# MaizeGDB STATUS REPORT

## A SUMMARY OF RECENT UPDATES AND ACTIVITIES AS WELL AS NEW INITIATIVES

USDA-ARS
Project No. 3625-21000-045 (Ames, IA)
and
Project No. 3622-21000-027 (Columbia, MO)
[formerly Project No. 3622-21000-026 (Columbia, MO)]

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**SEPTEMBER 2006**

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## Summary

Since the dissolution of the MaizeGDB Steering Committee just after their last meeting in August of 2004, the MaizeGDB team has sought to steadily improve the interfaces and data available at MaizeGDB and also improve our own internal procedures so that we are prepared for future growth. Outlined in the following submission to Nucleic Acids Research are improvements and changes in five broad areas:

- **Data Improvements** include a stable and organized pipeline for the incorporation of public sequence data into MaizeGDB and the regular acquisition of data from community sources, including the founding of an Editorial Board to collect relevant papers for community reading.
- **Public Interface Improvements** include new map displays, incremental improvements including faster and more accurate general searching and relevant search result pages, and the Morgan2McClintock tool which allows researchers to convert genetic maps into cytological maps and vice-versa.
- **Curation Tool Improvements** include the development and deployment of a module for the inclusion of QTL experiments, the development and deployment of “professional” curation tools at the University of Illinois by Marty Sachs’ team, and incremental improvements.
- **Maize Community Support** includes extensive support of the Maize Genetics Conference, including having two members of the MaizeGDB team serving as ex officio members of the conference planning committee, support of the Executive Committee including public surveys and elections, increased interactions with other groups – especially Gramene and the Maize Sequencing Project, and facilitation of community contacts.
- **Standard Operating Procedures** outlines our procedures for data storage, redundancy, and security.

OXFORD UNIVERSITY PRESS Nucleic Acids Research

# MaizeGDB's new data types, resources, and activities

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|---|---|
| Journal: | *Nucleic Acids Research* |
| Manuscript ID: | draft |
| Manuscript Type: | 6 Database Issue |
| Key Words: | maize, database, bioinformatics, website, zea |
| | |

# MaizeGDB's new data types, resources, and activities

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## ABSTRACT

MaizeGDB is the Maize Genetics and Genomics Database. Available at MaizeGDB are diverse data that support maize research including maps, gene product information, loci and their various alleles, phenotypes (both naturally occurring and as a result of directed mutagenesis), stocks, sequences, molecular markers, references, and contact information for maize researchers worldwide. Also available through MaizeGDB are various community support service bulletin boards including the Editorial Board's list of high-impact papers, information about the Annual Maize Genetics Conference, and the Jobs board where employment opportunities are posted. Reported here are data updates, improvements to interfaces, and changes to standard operating procedures that have been made during the past two years. MaizeGDB is freely available and can be accessed online at http://www.maizegdb.org.

# INTRODUCTION

Maize (*Zea mays* ssp. *mays*) has long been the number one production crop in the United States, and in 2001 it also became number one in the world. Because maize is economically important and also serves as a model organism for genetics research, it is one of the most highly researched organisms in existence. The maize genome has an especially high level of DNA sequence polymorphism and extended regions of non-homology between inbred lines (1,2), hence the diversity represented by the maize gene pool is unparalleled in both a phenotypic and molecular sense. This provides a unique vehicle to explore questions in evolution, domestication, development, trait expression, functional allelic diversity, and the interrelated processes that shape such events and their outcomes.

The application of new technologies and bioinformatic tools coupled with thorough phenotypic evaluation for useful traits and molecular characterization of diverse maize germplasm offers the potential for significant discovery via translational genomics. The goal of turning the identification and evaluation of functional and evolutionarily important allelic variation into a comprehensive genomics activity is dependent on being able to associate diverse information in a seamless manner. MaizeGDB is the community resource charged with developing informatic solutions for storing, displaying, and linking comprehensive maize data so that they are made easily accessible to researchers worldwide. Described here are updates and improvements to MaizeGDB that have been made over the course of the past two years.

## NEW DATA TYPES

Since the initial announcement in 2004 that MaizeGDB was up and running (3), the database has expanded to include new data types such as TILLING data (4; http://www.maizegdb.org/cgi-bin/displaylocusresults.cgi?term=mtp*), cytological maps with associated images (e.g., http://www.maizegdb.org/cgi-bin/displaymaprecord.cgi?id=892372), and the maize Recombination Nodule maps (5,6; http://www.maizegdb.org/RNmaps.php). All new data types are made available alongside related information and are accessible through mechanisms that seamlessly integrate with the site's existing functionalities. An example of how the new Recombination Nodule map data can be used to speed up experiments that utilize the maize translocation stocks follows.

A researcher wants to determine whether the gene product of her new mutant *gof1,* which maps to 3L within 1 cM of *tub6,* acts cell autonomously using a mosaic analysis. Since there are no suitable cell autonomous markers known to be proximal to *gof1*, she decides to use an A-A translocation to bring *gof1*+ distal to a cell autonomous marker on another chromosome. To do this, she needs to find a translocation stock with a breakpoint on 3L proximal to her gene of interest, and a breakpoint on another chromosome that is distal to a gene that can be used as a cell autonomous marker. To find a list of available translocations, she uses the link on the front page of MaizeGDB to get to the Stocks Data Center (Fig. 1a), scrolls down to Maize Genetics Cooperation Stock Center Resources (7), and clicks the link for the "Stock Center Catalog." She clicks the link for "Reciprocal Translocation (comprehensive list)" to arrive at http://www.maizegdb.org/cgi-bin/stockcatalog.cgi?id=3, and decides to try 1049B T1-3(5242) (3L.65; 1L.90). In order to determine the approximate positions of these breakpoints relative to genetically mapped loci, she goes to the Maps Data Center (Fig. 1b) and navigates to the Recombination

Nodule maps. From here, she clicks the link toward the bottom of the page to go to the Morgan2McClintock Translator (8; http://www.lawrencelab.org/Morgan2McClintock/). Here, she chooses chromosome 3, pastes the entire “Genetic 2005 3” map from MaizeGDB (accessible at http://www.maizegdb.org/cgi-bin/displaymaprecord.cgi?id=940882) into the text box and hits the button marked “Calculate!”. The output file shows that 3L.65 lies about 5 cM proximal to *tub6*. This means that the breakpoint is proximal to her gene of interest! Using the Translator again for chromosome 1, she finds the position of 1L.90 relative to the “Genetic 2005 1” map (accessible at http://www.maizegdb.org/cgi-bin/displaymaprecord.cgi?id=940880). The output table shows that *lw1*, a suitable cell autonomous marker (9), lies between *cent1* and the breakpoint. Using the stock for T1-3(5242), she can set up a stock heterozygous for *gof1*, *lw1*, and the translocation where *gof1*+ and *lw1*+ reside on the translocation, and the recessive mutant alleles reside on the normal (non-translocation) chromosomes. Without access to the maize Recombination Nodule map data and the Morgan2McClintock Translator, cytological and genetic maps cannot be integrated directly. Setting up such an experiment would have required many additional experiments using various translocation stocks.

## DATA UPDATES

All types of data (references, loci, maps, etc.) are updated regularly as time and human resources allow. Listed here are a few of the major recent updates to content.

MaizeGDB’s sequence set is made up of all public maize sequences including EST, cDNA, GSS, STS, HTC, and genomic DNA sequences from GenBank (10) as well as the Uniprot (11) protein sequence set. This dataset is updated monthly utilizing a custom pipeline set up by workers at PlantGDB (12). Whereas in the past only the *Zea* *mays* ssp. *mays* sequence set was included in the update, a recent change was made to the sequence set update pipeline to include sequences for all subspecies of *Zea mays*. Also stored at MaizeGDB is contig membership information for the PlantGDB GSS (genome survey sequence) and PUT (putative unique transcript) contigs as well as the TIGR TC (tentative consensus) EST contig set (12 October 2005 release; 13).

The IBM2 FPC0507 maps (http://www.maizegdb.org/cgi-bin/displaymapresults.cgi?term=fpc0507) represent the anchored BAC finger print contigs which are currently being used to guide the B73 Maize Genome Sequencing Project. These maps were derived using anchor information for 414 contigs as assigned in the July 2005 manually edited FPC product (14; http://www.genome.Arizona/fpc/maize). Represented on the map are loci where at least 2 BACs in the contig were empirically associated with a molecular marker. Positions for loci were derived using a hybrid coordinate comprised of an integer representing the nearest genetic anchor point followed by a decimal and the FPC consensus band (CB) coordinate. Loci are associated with the defining BACs, markers, and marker sequences, and are linked to the current contig representation at Arizona. This map adds over 25,000 new loci to MaizeGDB, most of which are associated with overgo probes designed to detect full-length cDNAs (15).

Initiated to assist in anchoring BAC contigs and continued to support maize genetics research, the IBM Neighbors product approximates the genetic map orders of all loci mapped to better than 5 cM and most recently includes the loci which have only been placed onto anchored FPC contigs. Like the anchored BAC FPC contigs, the IBM Neighbors representation utilizes the IBM2 map as the framework. Each version is maintained, and the primary map source for a locus coordinate is displayed. The most recent version (http://www.maizegdb.org/cgi-bin/displaymapresults.cgi?term=ibm2*2005*neighbors) includes well-ordered mutants based on the Genetic 2005 compilation (16), which incorporated the UMC 98 maps (17).

Over 5,300 newly mapped loci, based on sequenced probes where most were derived from a cDNA, were provided to MaizeGDB from mapping projects that are using high-resolution intermated recombinant inbred panels of stocks. These came from: the Schnable lab (3,391 insertion-deletion loci on 2 map versions, IBM IDP +MMP versions 4 and 5; http://maize-mapping.plantgenomics.iastate.edu), Matthieu Falque (1,680 RFLP loci on IBM GNP and GNP LHRF maps; 18), and the Community Mapping Service (289 loci; described below).

## NEW FUNCTIONALITIES

Along with additions of new data, MaizeGDB personnel remain committed to maintaining and improving upon the interface to the database. New map displays have “sequence view” (which shows the sequences associated with each locus on the map) and “primer view” (which shows the primers and probes for each locus on the map) options which are accessible toward the top of all default map views (e.g., http://www.maizegdb.org/cgi-bin/displaymaprecord.cgi?id=143431). Search algorithms have been refined to allow researchers to simply enter a term in the search field toward the top of any page at MaizeGDB (see Fig. 1c) and quickly find relevant results, and summary information is now available on search results pages so that the most relevant records can easily be identified. For example, if a researcher were to search all records with the string “r1”, over 170 loci would be found. To help with locating the locus for an exact match, i.e., the locus *r1 colored1*, the exact match is shown at the top of the list of results. In addition, though the appearance of many data displays has not changed, the underlying code has been rewritten to improve load times and to optimize computational efficiency.

In an effort to improve access to diverse maize data, the MaizeGDB interface has been modified to include an abundance of linkages to other databases including the Plant Ontology Consortium (19; http://www.plantontology.org), Gramene (20; http://www.gramene.org) and (soon) the Maize Sequencing Project's genome browser. Data displays provide abundant context-sensitive linkages to records in other databases, enabling users to visit, for example, a gene record at MaizeGDB and with just a click quickly find related sequences, annotated maps, and similar sequences at other Web sites.

Recently the Community Curation Tools (accessible through the "tools" link at the top of any page at MaizeGDB; Fig. 1d) were updated to enable the entry of QTL data. Insights gained from experience with QTL data entry into the legacy MaizeDB (21) were leveraged in planning the functionality of this module, and linking of trait and map location to germplasm containing the superior allele is enforced. New automatic nomenclature features ensure consistency and minimize data entry effort. General functionality of the QTL module is consistent with that of the other Community Curation Tools described previously (22).

## COMMUNITY SUPPORT ACTIVITIES

MaizeGDB hosts an Editorial Board (Fig. 1e) whose members communicate with MaizeGDB personnel monthly to report their selections of current and historic literature germane to maize research. The list of Editorial Board selections is appropriate to guide journal clubs or for use by individuals keen to remain abreast of the advances relevant to maize research. It can be accessed at http://www.maizegdb.org/editorial_board.php.

MaizeGDB personnel support the Maize Genetics Executive Committee (MGEC; Fig. 1f) by providing a venue for them to contact and interact with the community of maize researchers. MaizeGDB personnel create and administer customized community surveys and handle and monitor elections for the MGEC (which involves the creation of methods for anonymous balloting and key-based restrictions to preclude stuffing the ballot box). These services help the MGEC to understand the needs of and communicate clearly with the community of maize researchers. Note also that author M.L.S. is a member of the MGEC.

The Annual Maize Genetics Conference (see Fig. 1g) is growing by leaps and bounds, with a nearly 20% increase in attendance within the last three years and a near doubling in the number of abstracts submitted. Workers at MaizeGDB created a set of tools to accept abstract submissions and to manage review of the abstracts by Conference Steering Committee members. MaizeGDB personnel also maintain the mailing list for the Conference Steering Committee, and authors T.E.S. and M.L.S. serve on the conference steering committee in an *ex officio* capacity and also assemble and print the conference program.

MaizeGDB hosts the Maize Newsletter (MNL), and MaizeGDB Curator M.L.S. is a co-editor of that publication. The main MNL site is at MaizeGDB (http://www.maizegdb.org/mnl.php), and new volumes are staged at the University of Missouri-Columbia (http://www.agron.missouri.edu). Contributions from collaborators are posted as received, and, with minor editing, redacted for printing once a year. The MNL also includes annual reports from the Maize Genetics Cooperation – Stock Center, the MaizeGDB, and any new map syntheses developed by MaizeGDB and collaborators. Funding for the redaction, printing, and mailing are from an endowment established by contributions from collaborators.

CIMDE is the community mapping service originally provided by personnel working on the Maize Mapping Project (23; http://www.maizemap.org/bioinformatics.htm). Author M.L.S. currently manages

CIMDE. Map positions are determined using 580 framework loci and MapMaker software (24), and are returned within 2 weeks of submission of raw map scores. When those data become public, they are incorporated into the Community IBM Map (cIBM) along with related documentation such as the contributor, nucleotide sequence accessions, encoded proteins, and literature citations. The most recent update (cIBM2005; http://www.maizegdb.org/cgi-bin/displaymapresults.cgi?term=cIBM*2005) includes the published maps of the Genoplante Consortium (18) and data submitted for inclusion in the public IBM Neighbors map (described above). The data sources are attributed, and sequence accessions related to mapped loci as well as sequence details, such as primers required to reproduce the mappings, are actively solicited and annotated.

## DATABASE AND AVAILABILITY

Standard operating procedures, accessibility, and machine architecture are reviewed in detail elsewhere (22). The following is a brief description of how the project databases are administered and explains availability and methods of access. The MaizeGDB schema is accessible online at http://www.maizegdb.org/MaizeGDBSchema.pdf. Presently there are three copies of the database and interface, which exist on three identical servers. The interface on each server interacts with data on the local copy of the database, thereby allowing the maintenance of a production environment (i.e., the copy accessed through http://www.maizegdb.org), a curation or staging environment, and an isolated testing and development environment. The development environment functions as a playground where data manipulation and interface development are tested. The curation database stores the most current data. As data are entered into the curation database (by researchers using the Community Curation Tools and by professional curators), they are initially listed as non-public and can only be viewed by MaizeGDB staff members. Once the data are reviewed, a curation level tag is changed so that the new records will become publicly accessible. Updates to production are carried out by replacing the existing production copy of the database with a duplicate of the curation database and the latest sequence files from PlantGDB. This update generally occurs on the first Tuesday of each month (see Fig. 1h). The curation database is backed up on a daily basis and is available for download (http://goblin1.zool.iastate.edu/~oracle/) for those who have Oracle RDBMS installed locally. Requests to gain read-only SQL access to the database should be directed by email to mgdb@iastate.edu. Data housed at MaizeGDB are in the public domain, hence they are freely available for use without a license.

## FUTURE PLANS

The genome of maize inbred line B73 is being sequenced, and the creation and public availability of the official site (called the Maize Genome Browser; http://www.maizesequence.org) is in the offing. The Maize Genome Browser has embedded links to MaizeGDB throughout, and context-sensitive links from MaizeGDB into the Maize Genome Browser are planned. By creating links to the Maize Genome Browser, MaizeGDB can connect researchers with up-to-date views of the maize genome as it is sequenced without bearing the responsibility of supporting an independent genome browser for maize. To learn more about the Maize Genome Sequencing Consortium's plans and to find updates on their progress, visit http://www.maizegdb.org/sequencing_project.php (see also Fig. 1i).

In most cases, a model organism's official gene models are housed at the model organism database (MOD). Because the maize genome is being sequenced and it is anticipated that MaizeGDB (the MOD for maize) will be charged with storing and making available the official gene models, plans are in the works to put together an infrastructure for supporting the storage of this new data type and to create a version control system to allow for the storage of each major gene model release.

Not all datatypes are currently integrated with sequence data. Breeders find it difficult to locate all genomic and phenotypic data for plant germplasm collections because breeding and sequence data are housed in separate, disconnected databases. While MaizeGDB stores maize data related to genetics and genomics, most historical, geographic origin, characterization, and evaluation data associated with the National Plant Germplasm System's Plant Genetic Resources collections are housed in the Germplasm Resource Information Network (GRIN; http://www.ars-grin.gov/npgs/). Work to integrate MaizeGDB with GRIN is a high-priority item for development in the coming year so that breeders are enabled to more easily associate genetic and genomic data with traditional crop improvement information.

## ACKNOWLEDGMENTS

We thank the MaizeGDB Working Group (E. Buckler, K. Cone, M. Freeling, O. Hoekenga, L. Mueller, P. Schnable, T. Slezak, A. Sylvester, D. Ware, and especially M. Sachs and V. Brendel) for their help and guidance. The contributions of Editorial Board (2006 membership includes T. Brutnell, S. Chopra, K. McGinnis, W. Pawlowski, M. Timmermans, and J. Yu) are most appreciated. We also thank H. Sanchez-Villeda and M. McMullen for contributing a naming and tracking tool for loci defined by FPC*;* S. Schroeder, H. Sanchez-Villeda and others for maintaining the software and Web services associated with the CIMDE mapping services; S. Baran for coding the Community Curation Tools; and G. Davis, M. McMullen, and E. Coe for advice on mappings (though we take full credit for any errors). We thank V. Brendel's PlantGDB Group (M.

Wilkerson, Q.F. Dong, and A. Fu) for creating and maintaining the maize sequence pipeline.

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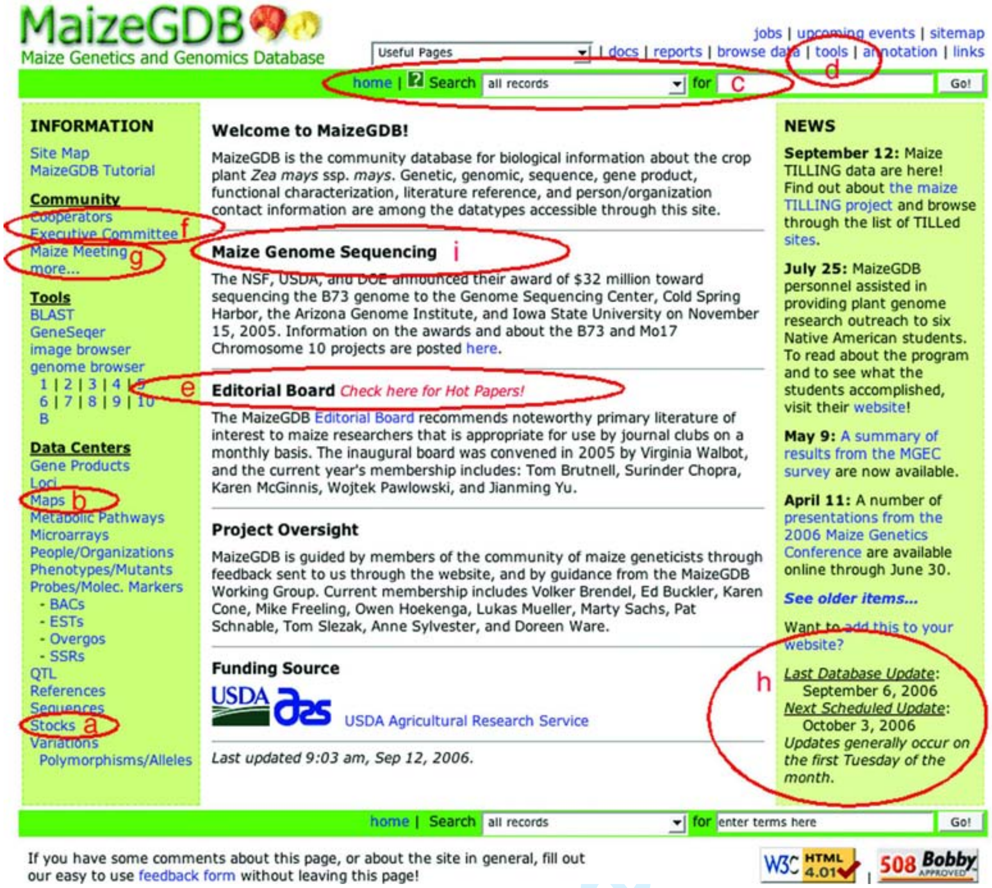
## LEGENDS TO FIGURES

**Figure 1. Important information, data centers, tools, and news items are accessible from the MaizeGDB home page.** Data and bulletin boards as well as links to noteworthy or high profile projects are accessible directly on the front page. The "Stocks" Data Center (a) enables queries by focus linkage group, genotypic variation, karyotypic variation, and other limitors. Likewise, the "Maps" Data Center (b) can limit results by contained loci, chromosome, source, or mapping panel and also allows direct access to unique map types including the Recombination Nodule maps through its "Map Reports and Tools" section. All MaizeGDB pages have the same header, which is loaded with functionality enabling, e.g., searches of all data from any page (c) and access to tools (d) including the Community Curation Tools. Bulletin boards that keep researchers connected with the community include the Editorial Board (e), the Maize Genetics Executive Committee pages (f), and the Annual Maize Genetics Conference (which is referred to simply as "The Maize Meeting") site (g). Dates of database updates are available directly on the front page (h), as are important major efforts of interest to all maize researchers like the Maize Genome Sequencing project (i).



**INFORMATION**

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- BACs
- ESTs
- Overgos
- SSRs
QTL
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Sequences
Stocks
Variations
Polymorphisms/Alleles

**Welcome to MaizeGDB!**

MaizeGDB is the community database for biological information about the crop plant *Zea mays* ssp. *mays*. Genetic, genomic, sequence, gene product, functional characterization, literature reference, and person/organization contact information are among the datatypes accessible through this site.

**Maize Genome Sequencing**

The NSF, USDA, and DOE announced their award of $32 million toward sequencing the B73 genome to the Genome Sequencing Center, Cold Spring Harbor, the Arizona Genome Institute, and Iowa State University on November 15, 2005. Information on the awards and about the B73 and Mo17 Chromosome 10 projects are posted here.

**Editorial Board** *Check here for Hot Papers!*

The MaizeGDB Editorial Board recommends noteworthy primary literature of interest to maize researchers that is appropriate for use by journal clubs on a monthly basis. The inaugural board was convened in 2005 by Virginia Walbot, and the current year's membership includes: Tom Brutnell, Surinder Chopra, Karen McGinnis, Wojtek Pawlowski, and Jianming Yu.

**Project Oversight**

MaizeGDB is guided by members of the community of maize geneticists through feedback sent to us through the website, and by guidance from the MaizeGDB Working Group. Current membership includes Volker Brendel, Ed Buckler, Karen Cone, Mike Freeling, Owen Hoekenga, Lukas Mueller, Marty Sachs, Pat Schnable, Tom Slezak, Anne Sylvester, and Doreen Ware.

**Funding Source**

USDA ars USDA Agricultural Research Service

*Last updated 9:03 am, Sep 12, 2006.*

**NEWS**

**September 12:** Maize TILLING data are here! Find out about the maize TILLING project and browse through the list of TILLed sites.

**July 25:** MaizeGDB personnel assisted in providing plant genome research outreach to six Native American students. To read about the program and to see what the students accomplished, visit their website!

**May 9:** A summary of results from the MGEC survey are now available.

**April 11:** A number of presentations from the 2006 Maize Genetics Conference are available online through June 30.

***See older items...***

Want to add this to your website?

*Last Database Update*:
September 6, 2006
*Next Scheduled Update*:
October 3, 2006
*Updates generally occur on the first Tuesday of the month.*

If you have some comments about this page, or about the site in general, fill out our easy to use feedback form without leaving this page!

# History-2

# History of the MaizeGDB Project

(Adapted from 1)

In the late 1920s it was recognized by the community of maize geneticists that the data they were recording needed organization, publication and curation. To this end, R. A. Emerson and others began publishing the Maize Genetics Cooperation Newsletter (MNL), which is compiled and published on a yearly basis. (The MNL is published in Columbia, MO, and is funded by an endowment administered by the University of Missouri.) To further the same goals, in 1991 the United States Department of Agriculture-Agricultural Research Service (USDA-ARS) charged Ed Coe, then editor of the MNL, to develop a maize genome database (2). MaizeDB (located in Columbia, MO) was one of the first biological databases to exist online, and became an indispensable research tool utilized by maize geneticists worldwide. Staff for the MaizeDB project included: Coe (USDA-ARS Category 1 Research Geneticist and Lead Scientist for the project), Mary Schaeffer (formerly Mary Polacco; USDA-ARS Category 4 Geneticist and Curator), and Denis Hancock (University of Missouri at Columbia Information Technology Specialist). The interfaces and database design were contracted for several years to Stan Letovsky in consultation with Mary Berlyn, Director of the *E. coli* Genetic Stock Center and Marty Sachs, currently USDA-ARS Director of the Maize Genetics Cooperation Stock Center. Postdoctoral associates, notably Georgia Davis and Partick Byrne, students, and others also contributed.

In 1998, the Maize Gene Discovery Project (MGDP), led by Stanford University professor Virginia Walbot and including 10 research groups, was funded by the National Science Foundation, [reviewed in (3)]. The MGDP discovered new maize genes and developed tools for characterizing maize mutants. The microarray slides, EST clones, library plates of indexed transposon insertions and seed generated by MGDP necessitated the implementation of a resource to make these materials publicly available and to organize the data generated by the project team. This need was met by ZmDB, a resource developed by Iowa State University professor Volker Brendel's group (4). In addition to making MGDP materials available, ZmDB also encompassed all public maize ESTs, GSSs and protein sequences.

In September of 2001 the USDA-ARS created a Specific Cooperative Agreement with Brendel to begin an initiative to combine MaizeDB and ZmDB, thus creating a single maize genetics and genomics database using state-of-the-art database architecture and Web design protocols. Brendel's staff working on the MaizeGDB project included: Qunfeng Dong (Assistant Scientist), Heike Kross (Postdoctoral Associate), Trent Seigfried and Darwin Campbell (Information Technology Specialists), and later Carolyn Lawrence (Postdoctoral Associate). In 2003, a set of Community Curation Tools was created by contract Web developer Sanford Baran in consultation with Mary Schaeffer. These tools were and reviewed by the Transition Steering Committee. On September 1 of 2003 MaizeGDB superseded MaizeDB and made available all data and resources that previously existed at MaizeDB and ZmDB.

On April 3 of 2004, USDA-ARS National Program Staff established a project (CRIS # 3625-21000-045) in the Corn Insects and Crop Genetics Research Unit in Ames Iowa. (This CRIS is the one that currently supports MaizeGDB and is the fund from which the SCA with Volker Brendel is now drawn.) Research Geneticist Paul Scott administered the project early on, and oversaw the hire of two Information Technology Specialists for the project: Seigfried and Campbell. Lawrence was hired to lead the project in June of 2005. At present, the staff of MaizeGDB is made up of four USDA-ARS employees working in two locations. In Ames, Iowa are Lawrence (Category 1 Research Geneticist and the project's Lead Scientist), Seigfried (IT Specialist and Bioinformatics Engineer specializing in interface design and development), and Campbell (IT Specialist and Database Administrator). In Columbia, Missouri is Mary Schaeffer (Category 4 Geneticist and the project's sole Curator).

1. Lawrence,CJ, Dong, Q, Polacco, ML, Seigfried, TE, and Brendel, V. MaizeGDB, the community database for maize genetics and genomics. Nucleic Acids Res., 31, 393-397.
2. Polacco,M. and Coe,E. (1999) MaizeDB: the maize genome database. In Letovsky,S.I. (ed.), Bioinformatics: Databases and Systems. Kluwer Academic Publishers, Norwell, MA, pp. 151-162.
3. Lunde,C.F., Morrow,D.J., Roy,L.M. and Walbot,V. (2003) Progress in maize gene discovery: a project update. Funct. Integr. Genomics, 3, 25-32.
4. Dong,Q., Roy,L., Freeling,M., Walbot,V. and Brendel,V. (2003) ZmDB, an integrated database for maize genome research. Nucleic Acids Res., 31, 244-247.

**Received by MaizeGDB Personnel on January 25, 2006**

## MaizeGDB Steering Committee Report September 3, 2004

On August 26, 2004 a Steering Committee (SC) meeting was held at Iowa State University (ISU) to review the progress and plans of the Maize Genetics Database (MaizeGDB). Several SC members attended a workshop on annotation tools developed by the MaizeGDB/PlantGDB team on the following day. The SC members are listed at the end of this report.

The SC was charged with reporting on the following topics:
- A clear understanding of the current status of MaizeGDB
- Opportunities for improving the project
- An examination of the project’s structure, staffing, timelines, and trajectory
- How MaizeGDB relates to other projects

### Managerial Summary

We find that the MaizeGDB team has done an excellent job of supporting the maize research community since MaizeGDB fully replaced MaizeDB in October, 2003. Large increases in site usage support the claims that users have transitioned effectively to the new system. A large set of user feedback messages also shows that the MaizeGDB team has been extremely responsive to user requests. The MaizeGDB team has instituted a robust infrastructure that provides both good responsiveness and data protection. Personnel changes since the last SC meeting have led to the establishment of an extremely competent and cooperative team; however, the project could use an additional biologist (curator) and a PhD-level bioinformatics specialist to fully exploit the available information. The SC continues to have some concerns about the evolving role(s) of MaizeGDB with respect to other community resources (e.g., NCBI, TIGR, Gramene, and other organism-specific databases), but this is an issue to be discussed and resolved at the funding agency level.

With the departure of Leland Ellis to DHS, MaizeGDB needs a replacement point of contact within USDA. We understand that a permanent individual will fulfill this role in the near future.

*Items indicated in Italics in the following section are to be addressed in a written response to the SC by the MaizeGDB team within a timeframe defined by the funding agency.*

### 1. Data curation and annotation

The MaizeGDB team has developed a set of Web-based tools for both expert data curation as well as community annotation. The SC has a number of comments on these tools:

- The large-scale data input/curation tools developed by Jason Carter for Marty Sachs’ stock center were impressive and highlighted significant design choice differences from the tools provided directly by MaizeGDB. Chief among these are the ability to think top down versus the bottom-up approach required by the MaizeGDB tools. (Top down means that the user can focus on the object of interest, (say, entering a new stock), with linked pop-ups appearing whenever it turns out that some lower-level item (say, a new person, etc.) must be added in order for the task to proceed. [NOTE: SC member Marty Sachs reports that discussions after the SC meeting concluded that Jason Carter should convert his tools to directly link to the MaizeGDB Oracle server (instead of a local MySQL copy), then share this code with the MaizeGDB team. This will provide MaizeGDB with a working code base and also allow the Stock Center to directly update MaizeGDB.]

  - *The MaizeGDB team should take a hard look at the top-down tools and either adopt these tools outright or provide equivalent user functionality in their current tools. An economic justification for the choice taken should be provided in writing to the SC and to the funding agency when the decision is made. (This can be separate from the overall response to this SC report, because adequate time is needed to make this choice.)*

- During discussions the MaizeGDB team noted that the error rate among legacy data is about 1%. The SC noted that a rather large effort was going into chasing down what would be considered an acceptable error rate in many databases. As MaizeGDB scales up, the return on investment for cleaning up old data has to be judged against the benefits that can be obtained by other uses of scarce skilled talent. The SC suggests that the community annotation mechanism be used to deal with errors in legacy data, leveraging the community to find, report, and “fix” problems in the data. *Please provide a plan for dealing with data curation/cleansing as the available information scales up rapidly.*
- The SC feels that too much emphasis is being put on the entry of references, especially given the comments of the 2004 editorial board about their experiences of using the new tools. MaizeGDB will not rival PubMed for most users. The key importance of references is their linkage to other data types (e.g., locus, variations, stocks, map data, etc). Resources should be put into encouraging authors to submit their own references to MaizeGDB as they are published. Automated downloading of references from PubMed into MaizeGDB is a reasonable goal, but this should not become a major resource sink. One idea was to send authors an email that their paper is now referenced in MaizeGDB, along with a 1-click URL to allow them to directly submit corrections to their record for review and incorporation. References could be tagged to show which ones had received author editing/approval. *Please provide an updated plan for dealing with references in MaizeGDB.*
- SC member Sarah Hake noted: I had a small comment about typing in references. I had time to cut and paste in two references from our lab. It is easy enough to paste in the abstract and the title, etc. However, typing in the important links, such as gene name and data type is way too slow with the pull down menus provided. I just typed in a couple sentences into the comments that a curator could then translate into the database. For example "In this paper in situ hybridization of tb1 was carried out in maize and teosinte. Double mutants were made between anther ear1 and tb1 as well as between ts2 and tb1." To type in that information with their tools would have been very slow. However, someone else might like to know that such double mutants were made and that information never appears in the abstract.

## 2. Data query and visualization

The current MaizeGDB interface is focused on a large set of views into the data (e.g., maps, probes, sequence, stocks, variations, etc.) These views are well-suited to a traditional tightly-focused use of information and the resulting displays are nicely designed and consistent across the views. The SC has a number of concerns related to the expansion of MaizeGDB as the community needs scale and evolve:

- The current user interfaces do not allow for complex queries that cut across the different provided views. For example, although the current phenotype browser allows for a few types of selections (images, traits, and body parts), but no ability to tie, for example, to genes that lie on sequenced BACs. The SC recommends that the MaizeGDB team design a separate "expert user" query interface. At a minimum, this should provide a query-by-example forms interface that allows complex combinations (AND, OR, and NOT) of specifications across the entire range of current data "view" categories. Output from this expert user query mechanism should be selectable in a variety of format (HTML, XML, text, CSV, etc.) and be accessible to users via programs as well as browsers. The team should resist the temptation to continually add new query capabilities, one user request at a time, to the existing interfaces. Such "creeping featurism" complexity will ultimately reduce the usability of the existing interfaces by average users, and can never be sufficient to support expert users. *Please comment on your vision and timetable for providing expert-level query interfacing.*
- The SC notes that the data on maize is nearing the point where "data mining" and other data discovery queries will begin to be feasible for some advanced users. The MaizeGDB team will need to consider how to best support such users, given that it is not feasible to expect MaizeGDB to support all possible queries and tools.
- Jo Messing noted that genetic line information should be presented wherever this makes sense in displays.
- As maize information rapidly moves towards being sequence-based, MaizeGDB needs to migrate towards better visualization tools to make it clear to users what data are known and how it all ties together. The chromosome-based views at TIGR are an example of one good approach. Volker Brendel noted that the next phase would be to move to use sequence data as the coordinate system to integrate data. *Please provide additional details on plans and timetable for this conversion.*

(The following comments came from SC member Mike Freeling, who was unable to attend in person. As they are all related to the user interface, they are included here intact.)

--**The Home page** should address the status of the maize genome sequencing effort, with links to the updated info, with date of update. This sequencing effort is the big thing! This might be a quarterly commentary. For example: "Genomic sequence of the maize B73 genome are in GenBank. The BAC/PAC sequence, usually annotated, are at XXXX and XXX and most easily fetched at XXX and the methy/cot filtered and RescueMu reads, and similar short sequences, are in GSS.... Smaller sequences have been assembled into larger sequences in at least two locations: TIGR (AZM) and Iowa State (MAGI). Assessment: Contigs of all available sequence are not yet able to reconstruct BAC sequence even when each BAC sequence is present in GSS. ... In summary, XX% of the genes have a model of sorts (PlantGDB) and XX% of gene space may be extracted, but with much manual effort at this time....... Tune in later for an update, blah, blah " Signed, Volker This commentary with links is sorely needed.

--I think there are several problems once a user clicks **"locus/loci"**

1) First, this link is about genes and alleles, not loci (loci are part of genetic maps, they do not encode unless they are specifically defined to do so). For Arabidopsis, for example, the AtXgXXXXX designations are loci because these numbers are assigned based on order in the chromosome. A term like "Adh1" is a gene. *Adh1-m335* is, for example, an allele. And "*Adh1%*" is all *Adh-like* genes. Marty Sachs would be an excellent person to advise on the details of nomenclature.

I suggest going to TAIR and typing in any gene name or its abbreviation. For example, *SHATTERPROOF* or *SHP*. Two gene models pop up reflecting two different genes in the genome: *SHP1* and *SHP2.* Each of these also has a locus designation (AtXGXXXXX) and, if the locus designation is modified to such as AtXGXXXXX**.1**, then that is the same as a gene designation and relates to a particular gene model. Although it take a lot of clicks to use TAIR to get to sequence, I like the way gene/locus nomenclatures are used.

2) Once a locus or loci have been entered into MaizeGDB, a list appears. It is unclear at the outset what is available for each allele/gene listed. Only after straining tendons for several minutes is the truth known. At least there should be links appearing if there **is** cDNA or an AZM/MAGI or a BAC sequence for this exact allele. If there are gene models, each should be linked right here! If the sequence is only to a wild-type allele at this gene, which is the usual case, that should be made clear. If it is too onerous to link to an in-progress sequence, then link to the search box of the appropriate database with the gene already filled in (E.G. TIGR maize AZM + singletons database). These links should be one click to model or sequence. As it is now, the GenBank link on the righthand scroll bar needs to be clicked, and this to get a long list of related sequences/links in GenBank, but not necessary sequence of the item clicked. The GenBank links must now be clicked to see what's what. That's a lot of clicking and mulling to find out there is, most often, no sequence available. I advise MaizeGDB that helping users find out what is available and what is NOT are equally important, and valuable.

If MaizeGDB did this, I would use it myself. As it stands, I simply go directly to what I think is the best site. **I would like MaizeGDB to know today's best site and link me up.** " Hook me up " would be a nice slogan to associate with MaizeGDB.

3. As time goes on, further links, to homeologs (no site at present) and orthologs (as PlantGDB and Gramene) in other plants, will need to be installed. All of these links are most useful if embedded right next to the gene designation the moment the gene designation

comes up. The structure of MaizeGDB should be able to accommodate an endless array of up-front links that might take the user directly to destination with the minimum of clicks.

- SC member Tom Slezak notes from his human genome project experience that "locus" rapidly gets overloaded to the point of becoming useless. The maize community appears to be at or near that point. When sufficient sequence is available, everything becomes "feature" coordinates on the sequence and "locus" becomes an anachronism. MaizeGDB should help prepare users for this transition.
- V. Walbot comments: The link to the site TUTORIAL should be made more prominent – it currently appears to be part of the education section.
- I second Mike Freeling's comments that when a "gene record" appears there should be an indication of whether or not it is mapped, whether a full-length cDNA exists, and whether there is a gene model. This sequence-based data should be no more than one click away. Currently the links are to places where you can type in a search.
- Imagine that PlantGDB no longer exists. How will MaizeDB obtain EST assemblies, gene models, etc. and the expertise to use them. Please give a plan of how data from other sources will be used. Who will keep in contact with non-ISU based bioinformatics groups?
- The front page should give a running total of the number of ESTs in the public domain, the date of the most current assembly (and a link to it), and the number and quantity of genomic sequences and a date of the most recent assembly (and a link to it). This information needs to be prominently featured on the front page.
- Apparently the majority of visitors to the site want map information. This is not surprising given the emphasis on mapping resources at MaizeGDB in its present form. Where do sequence-oriented people go for their information? Are their reciprocal links at every record at TIGR, for example, sending people to MaizeGDB to find out more about a gene? If not, how will this be accomplished?

- *Please comment on the above and provide the SC a prioritized plan and estimated timetable these issues.*

## 3. Relationship of MaizeGDB to other community resources

The SC finds it highly regrettable that Gramene chose to not send a representative to the SC meeting**.** Both TIGR and NCBI are at least equally important to consider as the large-scale and long-range future of agricultural genomics information are being planned. The SC has the following comments and concerns on this topic:

- The MaizeGDB team has done a nice job using available maize sequence data and synteny to begin to map Arabidopsis gene models to maize. The SC feels that this is an area of overlap with both Gramene and TIGR (not to mention PlantGDB, and eventually NCBI). MaizeGDB should take the moral high ground and provide explicit links to similar work by the other projects, in addition to making it clear what MaizeGDB is doing differently. *Please outline the long-term plans for mapping rice genes to maize, and define how you will determine the most constructive ways to collaborate with other community projects.*

- The SC felt that the distinctions between MaizeGDB and PlantGDB were at times both arbitrary and very confusing. For example, the maize gene models are not in MaizeGDB, but clearly should be seamlessly reached from there. Alternatively, the MaizeGDB home page should make it crystal clear that some maize resources are contained in PlantGDB (which currently isn't even mentioned on the MaizeGDB home page.) The two funding agencies involved are certainly amenable to tighter linkage between these databases. As mentioned above, the MaizeGDB plans should include a scenario for coping if PlantGDB ceases to exist. *Please outline a plan to reduce the confusion and better exploit the roles and strengths of each database.*
- The SC agrees with Volker Brendel that to better aid the maize research community, appropriate links should be liberally added to take users to other sites with relevant maize information and/or tools.
- The SC feels it would be appropriate for maizeGDB to maintain the maize pseudomolecules and make them available from a maizeGDB display and for download. The location of the sequences on the FPC map can be obtained from www.genome.arizona.edu/shotgun/maize/status, which is updated nightly with the latest sequence information.
- The project should work towards a time when the maize community can seek journal buy-in for deposit of data in MaizeGDB as a condition of publication.
- The funding agencies should explicitly require that relevant grantees submit their data to MaizeGDB in a timely fashion.
- A comment was made at the meeting about the desirability of a universal plant genome researcher login. Although this would take a considerable amount of cooperation across multiple projects, the SC finds it to be a laudable long-range goal that MaizeGDB should press forward. This would make a good topic for a PAG conference talk or workshop proposal, for example, especially if a few of the appropriate sites could be convinced to collaborate on the idea (and talk/workshop).
- SC member Ed Buckler, who was unable to attend, asks whether a meeting on diversity data (coordinated by MaizeGDB and Gramene) is still planned for this fall.
- *Please comment on the above and provide the SC a plan and estimated timetable for enhancing ties with other community resources.*

## 4. Future Objectives and Timelines

- Release schedules models need to be defined for:
    - Data
        - Release numbers, change logs, what's new, next scheduled release, etc.
    - Schema
    - Tools
    - Interfaces
- A reliable mirror site needs to be established.
- Growth and scaling issues can be expected now that the site has achieved a certain degree of user success and increased expectations. This will affect storage and both database and tools/services server capacity. A plan for this evolution should be provided.

  - *Please provide the SC your plans and timelines for each of the topics in this section.*

- **Next meeting(s)**

  The SC recommends that the funding agencies will convene a meeting of the relevant plant genome databases in the near future, in an attempt to coordinate a federation of all the available resources. Assuming this happens within the next year, the next SC meeting should be held in approximately a year and should focus on issues related to scaling and interaction. Representatives from Gramene, TIGR, and NCBI should be present, if possible. If components of these databases receive funding from the USDA, the agency should command their attendance.

- *Please provide the SC with your comments and suggestions for future meetings with the SC.*

**Steering Committee Maize Genetics Database August 26, 2004**

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# Future-3

**New hires for MaizeGDB:** Computational Biologist (Ames, IA) and Curator, (Albany, CA)

**Position Descriptions:**

*Computational Biologist (Ames, IA)*

A. Introduction

The position is in the Corn Insects and Crop Genetics Research Unit, Midwest Area, Ames, Iowa. The Unit conducts research on the biology of improving grain and forage crops. The incumbent is a Research Geneticist (Plants) in National Program (NP) 301, Plant, Microbial and Insect Genetic Resources, Genomics, and Genetic Improvement. The responsibilities include utilization of computational and experimental methods to better understand the evolution and structure of the maize genome and the genes contained within it, and to use this information in collaboration with other scientists in the unit to facilitate crop improvement. The incumbent will work in collaboration with laboratory scientists and other computational biologists to conduct research in bioinformatics, develop new computational and analytical methods, and serve as a technical resource and advisor to the MaizeGDB project in the area of computational biology.

B. Major Duties

Objectives are to conduct studies in basic and applied computational biology, including genome organization and function, control of gene expression, and other problems amenable to computational, mathematical, and statistical analyses of biological data and systems. Specifically, conducts studies using genomic approaches to identify genome structure and gene regulation. Work includes but is not limited to:

(a) Analysis and interpretation of maize sequence data.
(b) Use of data structures to efficiently represent and mine genetic and physical maps of maize.
(c) Development of representations of maize sequence data to be integrated into the MaizeGDB.

Provides guidance and advice on computational biology methods, techniques, and results to other ARS comoputational biologists and plant biologists in the Management Unit.

C. Evaluation Factors

FACTOR 1: KNOWLEDGE REQUIRED BY THE POSITION

- Background in computational science.
- Fundamental principles of biochemistry and molecular biology.
- Fundamental understanding of basic plant biology.

- Understanding of the practical and theoretical consequences of the nature and limitations of biological data and its application to agriculture.

- Knowledge of computational simulation techniques and appropriate statistical methods, and familiarity with methods for storage, retrieval, and manipulations of large data sets, especially sequences.

FACTOR 2: SUPERVISORY CONTROLS

- The incumbent receives administrative supervision from the Research Leader who provides broad guidance and advice regarding overall program objectives. The Lead Scientist for the MaizeGDB project provides technical guidance relative to collaborations with the MaizeGDB project. Within the objective of the research assignment the incumbent identifies, defines, and selects approaches and experimental procedures after consultation with supervisors.

- Minimal technical supervision is provided. The incumbent is responsible for choosing the research approach after consultation with the Research Leader and the MaizeGDB Lead Scientist. Incumbent has substantial freedom and responsibility in a broad problem area involving the responsibility for determining which studies will be conducted, approach and methods to be used, planning and organizing the work, and bringing it to conclusion. No technical guidance is received; however, incumbent discusses studies with Lead Scientist, RL, and National Program Staff to ensure they are in line with unit and Agency program goals. Incumbent is considered an expert in computational biology and has full responsibility for ensuring the scientific soundness and accuracy of reported research, subject to validation by the scientific community. Completed reports, manuscripts, and software packages are reviewed for compliance with Agency program and policy guidelines.

FACTOR 3: GUIDELINES

Literature relevant to this project is drawn from computer science, statistics, applied mathematics, bioinformatics, and biology. A variety of information is available via the Internet, but it is of uneven quality and requires careful evaluation. In many cases, insights and solutions will be derived from research areas outside biology in general, and bioinformatics in particular. Although the literature will be useful in suggesting general approaches, it will be less useful in providing immediate solutions to specific problems of biological and agricultural significance.

FACTOR 4: COMPLEXITY

Information from the literature rarely applies specifically to the problems of data storage and representation. The incumbent must use initiative, resourcefulness, and knowledge of the filed to adapt and modify procedures and data from the literature to fit a relational database representation. The incumbent has responsibility for creative functions necessary to synthesize a volume of data into a coherent tool for reference and research.

The work requires sophisticated computational approaches, the design of new algorithms as well as the application of existing algorithms, advanced methods for data modeling and representation, and other computational approaches to detect and analyze patterns inherent in biological data.

Substantial creativity is needed to integrate available knowledge from disparate sources to pursue interdisciplinary research objectives. In many cases, existing theoretical or computational methods will be applied to biological problems for the first time. In other cases, completely novel approaches, including new algorithms, will be required for the handling, analyses, integration, and presentation of very large amounts of genetic, phenotypic, genomic, and sequence data. The publication of insights and knowledge in combination with techniques and theory from fields including mathematics, statistics, molecular biology, biochemistry, and computer science will be critical.

## FACTOR 5: SCOPE AND EFFECT

- The work will result in documented increase in knowledge of the characteristics and utilization of the agriculturally important maize genome, and in logically constructive and computationally rigorous methods for extracting biological information from genome sequences.
- The results will facilitate new insights and experimental approaches by biological researchers studying gene structure and function, and theoretical and computational tools for analyzing the resulting data. The value of the results is their applicability for problems of biological and agricultural significance.

## FACTOR 6: PERSONAL CONTACTS

Personal contacts are with scientists at ARS, other Federal agencies, universities, and institutions, both domestic and abroad, as well as with administrative and other staff throughout the Midwest Area.

## FACTOR 7: PURPOSE OF CONTACTS

To discuss methodological problems and possible solutions with the technical support staff and other scientists, to discuss proposed plans and share practical experiences, discuss anticipated problems, and report progress and results obtained.

FACTOR 8: PHYSICAL DEMANDS

The work is sedentary and demands no physical exertion.

FACTOR 9: WORK ENVIRONMENT

The work is performed in a normal office and laboratory environment. Training sessions for scientists will be conducted at the target group's worksite and in conjunction with national and international meetings.

*Curator, (Albany, CA)*

A. Introduction

The position is in the Plant Gene Expression Center, Pacific West Area, Albany, California. The Center conducts fundamental research in plant molecular biology: essential genes are identified, isolated, and their function determined. The position is collaborative with the MaizeGDB, a project administered by the Corn Insects and Crop Genetics Research Unit in Ames, Iowa. The incumbent is a Geneticist in National Program (NP) 301, Plant, Microbial and Insect Genetic Resources, Genomics, and Genetic Improvement. The responsibilities include utilization of computational and data warehousing methods to improve the representation of maize genetics and genomics data in the MaizeGDB and the use of information, in collaboration with other scientists at the Center and beyond, to facilitate crop improvement. The incumbent will work in collaboration with laboratory scientists and computational biologists to: develop data resources for maize, help researchers to use the MaizeGDB, and serve as a technical resource to the project in the areas of genetics, cytogenetics, molecular biology, and development.

B. Major Duties

Objectives are to curate data for the MaizeGDB project. Specifically, conducts studies using genomic approaches to identify genome structure and gene regulation. Work includes but is not limited to:

(d) Integrate the RescueMu and EMS datasets at with the main MaizeGDB phenotype dataset.
(e) Manage the MaizeGDB Editorial Board and curate data from papers selected by Board members on a monthly basis.
(f) Increase documentation on maps (genetic, cytological, and otherwise).
(g) Train maize researchers to better utilize MaizeGDB.

Provides guidance and advice on computational biology methods, techniques, and results to other ARS scientists in the Management Unit.

C. Evaluation Factors

FACTOR 1: KNOWLEDGE REQUIRED BY THE POSITION

- Background in classical maize genetics and development to adapt RescueMu and EMS datasets to match the format of the existing MaizeGDB phenotype dataset.

- Fundamental principles of genetics, cytogenetics, transmission genetics, plant breeding, and molecular biology to create documentation for genetic, cytological, and fingerprint contig maps.

- Basic understanding of basic plant biology, genetics, cytogenetics, cell biology, transmission genetics, development, breeding, biochemistry, and physiology to curate data from the MaizeGDB Editorial Board's selections from the literature.

FACTOR 2: SUPERVISORY CONTROLS

- The incumbent receives administrative supervision from the Plant Gene Expression Center Director who provides broad guidance and advice regarding overall program objectives. The Lead Scientist for the MaizeGDB project provides technical guidance relative to collaborations with the MaizeGDB project. Within the objective of the research assignment the incumbent identifies, defines, and selects approaches and experimental procedures after consultation with supervisors.

- Minimal technical supervision is provided. The incumbent is responsible for choosing the research approach after consultation with the Center Director and the MaizeGDB Lead Scientist. In technical matters of maize genetics, cytogenetics, cell biology, physiology, and development the incumbent's recommendations are considered authoritative.

- For specified problems addressed, the incumbent formulates hypotheses, plans and carries out experiments, addresses experimental problems, and solicits input from maize geneticists and persons working at MaizeGDB and other plant genome databases. Completed reports, manuscripts, and software packages are reviewed for compliance with Agency program and policy guidelines.

FACTOR 3: GUIDELINES

The guidelines include a variety of information drawn from literature on plant biology, cytogenetics, cell biology, plant breeding, development, biochemistry, bioinformatics, and biology.

FACTOR 4: COMPLEXITY

Information from the literature rarely applies specifically to the problems of data storage and representation. The incumbent must use initiative, resourcefulness, and knowledge of the filed to adapt and modify procedures and data from the literature to fit a relational database representation. The incumbent has responsibility for creative functions necessary to synthesize a volume of data into a coherent tool for reference and research.

FACTOR 5: SCOPE AND EFFECT

- The work will result in documented increase in knowledge of the characteristics and utilization of the agriculturally important maize genome, and in logically constructive and computationally rigorous methods for extracting discrete biological information from MaizeGDB.

- The results will facilitate new insights and experimental approaches by biological researchers studying gene structure and function, and theoretical and computational tools for analyzing the resulting data.

- The value of the results is their applicability for problems of biological and agricultural significance.

FACTOR 6: PERSONAL CONTACTS

Personal contacts are with scientists at ARS, other Federal agencies, universities, and institutions, both domestic and abroad, as well as with administrative and other staff throughout the Pacific West Area.

FACTOR 7: PURPOSE OF CONTACTS

To discuss methodological problems and possible solutions with the technical support staff and other scientists, to discuss proposed plans and share practical experiences, discuss anticipated problems, and report progress and results obtained. Also to train scientists to better utilize MaizeGDB.

FACTOR 8: PHYSICAL DEMANDS

The work is sedentary and demands no physical exertion.

FACTOR 9: WORK ENVIRONMENT

The work is performed in a normal office and laboratory environment. Training sessions for scientists will be conducted at the target group’s worksite and in conjunction with national and international meetings.

***Draft: Sept. 18, 2006***

SUBJECT: Program Direction and Resource Allocation memo for ARS Corn Research Projects at Columbia, MO

TO: Stephen Shafer, Director
Midwest Area

THROUGH: Judith B. St. John, Deputy Administrator
Crop Production and Protection

FROM: Kay Simmons, National Program Leader
Plant Genetics and Grain Crops

Three ARS corn research projects at Columbia, MO, are to be consolidated into an existing project entitled: Genetic Mechanisms and Molecular Genetic Resources of Maize". This consolidation is directed to better coordinate ARS maize genetics and genomics research as part of the implementation of the next 5-year cycle of National Programs 301 (Plant Genetic Resources, Genomics, and Genetic Improvement) and 302 (Plant Biological and Molecular Processes).

<u>Before Consolidation:</u>

ARS project Genetic Mechanisms and Molecular Genetic Resources of Maize", Project Number: 3622-21000-027-00D, Michael McMullen, lead SY, National Program 302.

ARS Project: 3622-21000-024-00D, Breeding and Molecular Genetics of Corn, Oliver (vice-Darrah & Coe), National Program 301.

ARS Project 3622-21000-026-00D, Maize Genome Database, National Program 301

<u>After Consolidation:</u>

ARS project Genetic Mechanisms and Molecular Genetic Resources of Maize", Project Number: 3622-21000-027-00D, Michael McMullen, lead SY, National Program 302 (majority)/ National Program 301 (minority).

**Problem to be Addressed:**
A primary factor slowing crop improvement is limited knowledge of which genes control agronomic trait expression. Thus, the goal of this project is to develop and implement improved genetic/genomic approaches to systematically identify new gene targets, that are optimum candidates for improved trait expression

**Research Objectives:**

**Objective 1: Determine if altering expression of genes that exhibit evidence of past selection during maize domestication and improvement, modifies expression of currently relevant agronomic traits.**

**Objective 2: Conduct a comprehensive analysis of the role of the MYB class of transcription factors in controlling agronomic traits.**

**Objective 3: To develop strategies and mechanisms for improving drought-stress tolerance of maize.**

**Objective 4: Develop a next-generation maize genome database, which will be publicly accessible to users via the Web.**

**OSQR Review:**
Objectives 1 and 2 were reviewed successfully by the NP302 OSQR panel in 2005. Objective 3 is currently be reviewed by the 2006 Ad hoc OSQR review panel for NP301. Objective 4 is a shared objective with the ARS project, "Database of Maize Genome Information, Project Number: 3625-21000-045-00, Ames, Iowa. Carolyn Lawrence is the lead scientist. Objective 4 will be developed in collaboration with Dr. Lawrence, Ames, Iowa. That objective will be submitted for OSQR review in the Ames project plan as part of the upcoming planning and OSQR review of National Program 301.

**Cooperation/Collaboration with Other ARS Research Projects**
**Scientific Personnel:**
SYs (3.5)

**Cooperation/Collaboration with Other ARS Research Projects:**
Necessary (within ARS): Collaboration with Carolyn Lawrence, ARS, Ames, Iowa and cooperation with Doreen Ware, Gramene, Ithaca, New York. Collaboration will be with the other ARS laboratories involved in the Maize Diversity project, particularly Ed Buckler, USDA-ARS, Ithaca, New York; and Jim Holland, USDA-ARS, Raleigh, North Carolina. Collaboration with Bruce Hibbard, USDA-ARS, Columbia, Missouri, for field analysis of traits.

Necessary (external to ARS): Cooperation with the Maize Genetics and Genomics Database Working Group comprised of U.S. genomics/genetics scientists.

**Expected Outcomes with Relevance to Problem Areas and Components w/in the NP Action Plan:**
Potential Benefits: This project will link sequence variation to trait expression through the use of multiple quantitative trait loci (QTL), association analysis populations, gene insertion populations and near isogenic line populations derived from both diverse maize

inbred lines and teosinte accession. The long-term benefit will be that identification of the genes that control traits will lead to novel approaches for crop improvement.

Anticipated Products:

- Curation, and analysis of maize genetic and genomic data;
- Development of a new, powerful genetic strategy to identify candidates gene controlling agronomic traits.
- New knowledge of specific genes that affect a wide range of useful traits in maize.
- Sound testable hypothesis for genetic improvement of useful agronomic traits.
- Development of a new genetic selection strategy for more efficient maize genetic improvement

**Source of Funds and Funding Level:**
Net to Location:

# Current Project Title

ARS Project No. **362-521000-045-00D**

Principal Investigator: Carolyn J. Lawrence

**Expected Contribution to National Program 301 Action Plan:**
The work to be accomplished by the Maize Genetics and Genomics Database (MaizeGDB) Team will meet needs defined in component 2 (Crop Informatics, Genomics, and Genetic Analyses) of the Action Plan. Expected outputs primarily address the problem areas of: 2a) genome database stewardship and informatics tool development, but also will enable the 2b) structural comparison and analysis of crop genomes and 2c) genetic analyses and mapping of important traits. It should be noted that the majority of the work to meet maize researchers' needs is service oriented, but that research components are also an integral part of the work to be accomplished.

**Proposed Objectives**:

- Integrate novel data types and data connections into the MaizeGDB and develop the database into a resource for systems biology approaches to understanding complex genotype to phenotype relationships.
  - Create sequence-centric views of the data to enable full exploitation of the maize genome sequence from both B73 and chromosome 10 of Mo17.
  - Develop the cyberinfrastructure necessary to enable storage of the "official gene models" for maize as they are produced.
  - Integrate the divergent phenotypic datasets that are currently made available through MaizeGDB but that are stored in non-standardized ways.
  - Develop a portal to maize project websites to enable facile navigation to sites of interest and to help with keeping track of which data are available to be integrated into MaizeGDB.
- Deploy and customize available and develop novel software to analyze DNA sequences, genetic and cytological maps, and other data types so that the overall genome organization of maize and its structural relationship to the genomes of other organisms can be easily investigated and more clearly defined.
- Advance the field of plant breeding by enabling researchers to move from phenotype to sequence and from sequence to seed efficiently by interconnecting MaizeGDB and GRIN.

**Anticipated Products:**

- Software and data analysis tools that enable the analysis of genetic and genomic data sets.
- Long-term maintenance of reliable genetic, genomic, and phenotypic description data sets achieved via active data curation.
- Annotated gene sequences for candidate gene locations.
- Single points of access (portals) to multiple databases.
- Integrated genetic, physical, and cytogenetic maps.
- Interconnected and interoperable databases.

# *Genetic Mechanisms and Molecular Genetic Resources for Maize*

ARS Project No. **3622-21000-027-00D**

Principal Investigator: Michael D. McMullen

**Expected Contribution to National Program 301 Action Plan:**
Although the majority of this project is in National Program 302, the products of this research will contribute to NP 301 by providing maize breeders with novel candidate genes for maize improvement. One of the most important products of this research is the development of a new, powerful genetic strategy to identify candidate genes controlling agronomic traits. We have been contacted by a number of other scientists who will be attempting to test if our approaches for identifying genes with signatures of selection will work for their species. A second product of this research is the development of comprehensive transcription factor expression profiles both in stressed and non-stressed conditions that will be valuable to the maize community. We will test numerous candidate genes for their role in controlling various agronomic traits, including drought tolerance. The genes we show affecting traits become candidates for plant breeders for crop improvement either by introduction of alleles from exotic germplasm or by manipulation of expression in transgenic plants. Additionally, the MaizeGDB component of this project directly contributes to genome database stewardship and utility.

**Proposed Objectives:**

- Determine if altering expression of genes that exhibit evidence of past selection during maize domestication and improvement, modifies the expression of currently relevant agronomic traits. (M. McMullen & S. Flint-Garcia)
- Develop strategies and mechanisms for improving drought-stress tolerance of maize. (M. Oliver)
- Conduct an analysis of the role of transcription factors in controlling agronomic traits in maize. (M. Oliver & M. McMullen)
- Integrate new data, data types, data connections and documentation into the maize genome database (MaizeGDB) and develop high level syntheses, such as consensus maps, and ontologies to support user access and database interoperability. Develop the database into a resource for systems biology approaches to understanding complex genotype to phenotype relationships. (M. Schaeffer)

**Anticipated Products:**

- Identification of selected genes as novel candidates for maize improvement.
- New strategies for drought tolerance in maize.
- Candidate transcription factor targets for drought improvement.
- Improved content and functionality for MaizeGDB.

# Charge-4

Summary of Community Forum
48th Annual Maize Genetics Conference
Friday March 9, 2006

TALK BY JANE SILVERTHORNE, NSF

***After the genome….***

Learning from other genomic and post-genomic efforts

- Comments on the importance of workshops in developing tools
- Mt Fuji analogy – there's more than one mountain to climb and planning should be ongoing
- Need to re-evaluate at each milestone and even before the milestone

History of *Arabidopsis* sequencing effort

- 1990 - seminal plan that included international cooperation and coordination / plan for the db stock center – decision was made, for example, that full length cDNAs were important
- 1994 - NSF meeting
- 1996 - sequencing project
- 1998 - NPGI accelerated project
- 2000 - sequence completed ahead of schedule

History of *Arabidopsis* post-genomic effort and planning

- 1995 - planning for post-sequencing effort started
- 1998 - tools discussion
- 2000 - Salk meeting lead to 2010 program
- 2010 - program that included important midway checkpoints (see recent report http://www.nsf.gov/pubs/2006/bio0601/bio0601.pdf) and was driven by biology as well as tool development

History of rice sequencing effort was somewhat different because there was already an international and industry effort in place

- 1997 – sequencing project was already underway
- 1999 – planning session for functional genomics started early and lead to IRFGC (International Rice Functional Genomics Consortium)
- 2002 - first announcement from combined industry, US and international effort
- 2004 – "finished" genome announcement
- IRFGC – developed similar plan to *Arabidopsis* 2010 program but focused on agronomic traits, not just driven by biology

Lessons –

- Planning must be organized by scientists and the plans should be science-driven
- IP materials and data release policies must be spelled out
- IP clarity is especially for crop plant
- Plan needs to be flexible to accommodate new technology and new events
- Coordination of db activities is particularly important, especially possibility of incorporating tools from other countries
- Partnerships are most efficient and very important

Talk by V. Sundaresan

After the genome: Lessons from *Arabidopsis* and Rice

History of developing -*omics* since yeast was sequenced 10 years ago

Resources and tools that have been important for *Arabidopsis*

- Proper gene annotations
- Reverse genetics tools
- Expression arrays of all types (transcriptome and proteome)
- Full-length cDNAs
- Proteomic tools
- Stock centers with full availability and user friendly
- Unrestricted access -no MTA

Note that all *Arabidopsis* tools lead to the Salk lines, one of most important tools developed but others include: affy chips, 2hybrid screening tools, RNAi tools, VIGS, etc

For rice, same needs and same tools
- Stock centers have been less satisfactory for rice community because US (Arkansas) focuses on germplasm primarily
- Japan and Philippines also have centers but transport and access is restricted.

Road map of needs in post-genomics in rice
- Need to strengthen genetic resources
- Need to be able to translate research for breeders
- Need hi thru put phenotyping tools
- Need activation tagging lines
- Need fully efficient transformation of elite lines and decisions about which line to focus on.
- Need comprehensive stock center in US
- More international integration is still needed
- Accessibility still a major issue

For maize community – comparative genomics tools with rice very important.

Panel Discussion: see list of posed questions by panel members

Open Forum

COMMENTS AND DISCUSSION FROM MAIZE COMMUNITY

When projects end what happens to resources that have been developed?
- Community needs to be able to access and submit information
- Includes the need to simplify bioinformatics access
- The information is all out there but it is currently not centralized and have to go to individual and unique websites, learn all new tools each time – must be integrated
- There are many home pages but no guide to how to navigate, i.e. no single one stop shop that consolidates info

MaizeGDB as portal
- There needs to be more than links to other home pages, needs to be integration
- It is up to the researchers to establish and if there is a need, researchers should contact Carolyn Lawrence

Central field space
- Needed for smaller institutions and for those researchers who can't handle big growouts
- Need continued community phenotypic screens

NCGA comments
- Want to help maintain focus on agronomic significant tissues because NCGA needs the basic research to improve and increase production and ensure productivity
- What are the next genomes that need to be sequenced?
- How are the decisions made for what is most efficient? NCGA looks to the community for the next genome to be sequenced
- NCGA also needs to understand the connections between the basic science and the applications so they can bring specific examples back to Congress.
- How do we finally tie back to economic issues?

For comparative genomics, look to the human genome as a model
- Now there are 5-6 mammalian genomes available and effort now is to fill in diversity
- Now is the time to think abut having more cereal genomes since sorghum, brachypodium, rice, maize are all on the horizon
- But to accomplish this informatics resources need to be integrated so that cross genome comparisons can be made for agronomic traits, QTL etc
- Bioinformatics has been a major investment for human genomics, involved major integration issues

Stock center needs to be enlarged and supported
- More mutant lines are becoming available and the concern is that the stock center will be overwhelmed
- The stock center needs more resources to propagate, maintain and distribute

More on db issues
- Need to remember that TAIR is up to 23 people, so they can archive and also work on new bioinformatics tools
- db should include training for how to use the resources
- Need to deal with the fact that resources don't get integrated so the question is how to capture all the effort
- What should the relationship be between maizegdb and gramene?
- Should gramene develop further or should there be another centralized resource?
- Perhaps competition among two to three db is valuable to push the work forward (as was the case for human genome)
- Remember only 4 people associated with maize gdb and 12 associated with gramene

Need to develop full range of profiling arrays
- Need to augment standard transcription profiling with epigenetic profiling tools
- Other profiling arrays needed especially promoter, tiling arrays etc

# XI. COMMUNITY SURVEY RESULTS

## Maize Genetics Executive Committee (MGEC) Survey Results (172 responses)

Posted at MaizeGDB May 2006.
<http://www.maizegdb.org/mgec.php>

As follow-up to the open community forum held at the Maize Genetics Conference Asillomar 2005, a questionnaire was developed by the Maize Genetics Executive Committee (MGEC) and posted to cooperators from MaizeGDB. Results are summarized below.

A score of 1 was assigned for "highest priority".

### Question 1

### Prioritizing General Community Needs

1. High quality maize genome sequence annotation. (avg: 5.72)
2. Improved maize reverse genetics resources that allow investigator to move from sequence to seed. (avg: 6.72)
3. An improved maize database that allows investigator to move seamlessly between multiple genomic datasets and expression analysis. (avg: 7.12)
4. Improved maize transformation that is inexpensive, fast, and possible in multiple backgrounds. (avg: 7.16)
5. Resources for rapid mapping of all maize mutants. (avg: 8.66)
6. Functional studies that focus on individual genes, gene families or networks. (avg: 9.06)
7. High density markers (MaizeHapMap): SNPs for all genes and a catalog of genes not in B73. (avg: 9.35)
8. Enhanced capacity at the Maize Stock Center including increased seed storage space. (avg: 9.45)
9. Improved tools for quantitative genetics. (avg: 10.1)
10. Gene replacement tools. (avg: 10.2)
11. Support of training workshops in maize genetics, genomics, and bioinformatics. (avg: 10.8)
12. Further development of a maize global transcript profiling service. (avg: 11.0)
13. Proteomic tools and data for maize. (avg: 11.6)
14. Continued development of cytogenetic methods including chromosome painting techniques. (avg: 12.9)
15. Funded support for community field space. (avg: 14.0)
16. Other; see individual responses (avg: 14.8)

### Question 2

### Future Sequencing Strategies

Which survey sequences would be most valuable?

1. Full-length cDNAs (avg: 2.55)
2. ESTs (avg: 3.99)
3. Methylation filtered genomic sequences (avg: 4.20)
4. High-Cot genomic sequences (avg: 4.49)
5. Random shotgun genomic sequences (avg: 4.55)
6. Other; see individual responses (avg: 6.25)

Which lines would be most valuable to sequence after B73?

1. Mo17 (avg: 2.25)
2. W22 (avg: 3.72)
3. Other *Zea* species; see individual responses (avg: 4.52)
4. Other inbred line; see individual responses (avg: 4.91)
5. Other grass; see individual responses (avg: 5.15)

When comparing overall sequencing strategies, 52.3% of those surveyed stated that they preferred near-complete sequencing of one line over survey sequencing of multiple lines.

### Question 3

### Database and Annotation Issues

What features do you want to see in an improved community database?

1. Tools to navigate from maize sequence to map position and possible mutants or QTL (avg: 4.16)
2. Tools to navigate from gene to reverse genetics tools such as insertion sites (avg: 4.68)
3. Tools to navigate from maize sequence to homologous and syntenous sequence from other grasses (avg: 4.77)

4. Tools to navigate from maize sequence to a complete profile of expression studies (avg: 5.19)
5. Tools to navigate from maize sequence to homologous sequences in other species (avg: 5.62)
6. Increased interoperability between MaizeGDB and Gramene (avg: 6.14)
7. More tutorials on using existing database resources, both at MaizeGDB and at individual project sites (avg: 7.11)
8. Availability of a sequence browser such as Ensembl at/through MaizeGDB that supports and maintains user-contributed annotations in addition to automatic annotations (avg: 7.15)
9. Other; see individual responses (avg: 8.89)

### For a community annotation pipeline

47.0% of the respondents indicated that centralized annotation efforts by a single bioinformatics group was their preference
37.7% of the respondents indicated that decentralized annotation where individual groups contribute annotation to a curatorial site was their preference
15.1% of the respondents indicated an alternative solution was their preference (see individual responses)

### Optional Individual Responses to Question 1 - General Community Needs

(27 responses total)
Maize specific small molecule database (metabolomics)
Better support for computational biology
Improved software tools for maize curators
Studies of mechanisms of resistance of maize to pathogens
454 Sequence Multiple Diverse Maize Inbreds
Funding opportunity for pilot studies
Maize Activation Tagging resources for dominant phenotypes
Support for non-wet lab genetic analysis
Increased support for Gramene to provide end-user analytical tools for analysis of all cereal genomic sequences
Further development of off the shelf maize global transcript profiling platform
Improved affy chip, incorporation of quality checked data into MaizeGDB & PLEXdb
Agronomist trained in genomics to apply what we have learned to the field
Establishment of a metabolomics center and service (NMR and GC-MS and NIRS)
Better channels for communication & collaboration
Career development workshops for young scientists
Make important papers web-available when poorly accessible (e.g. Wilkes 1979)
More support for long-term public corn breeding programs
Affymetrix whole genome array
Richer BIOLOGICAL CONTENT in the maize database
Quantitative genetics
Complete maize genome sequence
Genetics of reproductive signs. Nuclear-cytoplasmic interaction.
History of Maize cooperators, contact with maize cooperators
Understanding cellular localization of maize gene products
MaizeGDB: capture the empirical data; a strong professional curation staff for maize and cereal genome peer-reviewed literature to capture the empirically confirmed information.
Maize genome evolution
Reverse genetics in rice

### Optional Individual Responses to Question 2(a) – which survey sequences would be most valuable?

(28 total responses)
Selected BAC clones of gene rich regions (6 responses)
MPSS developmental profiles (3)
454 sequencing (3)
Finish B73 to completion (2)
Selected gene amplicons for diversity resequencing & transposon flanking sequences (2)
Organelle genomes from many inbreds and relatives (shotgun) (2)
Ab10 in addition to chromosome 10 from B73 and Mo17
BAC/EST/GSS contigs from multiple inbreds anchored to a genetic map
ESTs from Normalized cDNA libraries
PCR amplicons corresponding to maize genes

Repetitive sequences
Affy-style arrays to discover SNPs across diverse germplasm or RIL pop. members
Gene enriched sequences (methyl & Cot are equivalent)
Set of BAC ends optimizing genome coverage

### Optional Individual Responses to Question 2(b) - Suggested Inbred Lines For Sequencing

(47 responses)
A188, tissue culture and transformation ability (7)
Gaspe flint - short flowering time inbreds will enable comparative adaptive studies (3)
The diverse germplasm lines being studied by Buckler/Doebley group. (2)
F7: european counterpart to B73 (2)
Oh43; another commonly used inbred line and a third heterotic group (2)
A619, mutants behave very differently in this inbred (2)
Mp313E (aflatoxin resistant inbred),
Iodent line (an expired PVP),
H99 (phenotypic penetrance has been altered)
NC89 and K55 (4x intermated population of 500 lines is being developed),
W23 (distinct from W22 and used by many on the west coast),
Michoacán 21 (best inbred for tropical lines),
CML247 (CIMMYT line with high market value but low (a)biotic stress tolerance -- commonly used in crop improvement programs for developing countries), Parthenogenetic maize lines-haploinductors,
M20W (good suppresser of many mutations),
Mo20W (drought and stress tolerance),
CML103 (a tropical source that is relatively early in the Midwest and results in reliable seed set),
PH207, recently public elite inbred line that is important progenitor to many current commercial hybrids
F2 (using INRA reference stock) as a representative of flint material, which represents an high divergence with dent material and has been used for genomic studies in France
27 linkage founders from NAM
The 16 progenitors of the Iowa Stiff Stalk Synthetic (BSSS). This would be a step toward understanding how genes respond to selection in populations. BSSS is the most economically important. pop
An inbred equidistant (by genetic distance) from B73 and Mo17
Other inbreds mentioned are P 165, KYS, KY21, popcorn, B37, W64A, Tzi8, CML69, P39, 4 Co63

### Optional Individual Responses to Question 2(b) - Suggested ***Zea*** Species For Sequencing

(68 total responses. most just suggested “teosinte”).
17 supported sequencing *Z. parviglumis*.
5 supported sequencing *Z. diploperennis*.
3 supported sequencing *Z. luxurians*.

### Optional Individual Responses to Question 2(b) - Suggested Grass Species For Sequencing

(43 responses)
12 suggested sequencing *Sorghum bicolor* (Important economically and phylogenetically, small genome, relative with desirable traits, closest relative that is a crop, sufficiently different from maize for numerous traits).
9 suggested sequencing *Tripsacum*. *T. andersonii* and *T. dactyloides* were suggested. (Closest genera to *Zea* to compare genome evolution with Zea)
4 suggested wheat (major polyploid grass species; Pooideae for comparative purposes)
2 suggested barley (major true diploid crop species, access to genes not tractable in maize)
2 suggested Brachypodium; it's a promising model
Switch grass- perennial, may have important agronomic properties
sugar cane( because of its economic importance).
foxtail millet, small genome, outgroup for maize and sorghum, rapid cycling, potential model
*Streptochaeta* from base of grasses for comparisons with rice and maize
*Eleusine indica*; fills gap grass taxonomy, is diploid, and has small genome
*Joinvillia* sp.-- outgroup to the pre-grass tetraploidy.
*Coix*; a close relative of *Zea*

### Optional Individual Responses to Question 3(a) What features do you want to see in an improved community database?

(23 responses)

Some 15% of respondents listed other, but lower ranked priorities. Notably, many focused on enhancing content of biological information, in particular phenotypic, both mutant and QTL. This aligns with the top navigation tool priority. Many indicated a need for a single unified genome browser, easier to use than gbrowse should be the navigation tool target. Others indicated a need for better access to machine-readable formats; deposit of all project data into the community database; more flexible BLAST; archival/historical information; interoperability with other databases (e.g. TIGR; GO; TAIR).

### Optional Individual Responses to Question 3(b) Community annotation pipeline

(26 responses)

Virtually all of the 15% 'write-in' respondents indicated a preference for an initial annotation by a single group, with support provided for updates by others in the community, with or without curation.

## *Prepared by Mary Schaeffer for the Maize Genetics Executive Committee*

***Major bioinformatics resources used by maize researchers.* Funding sources in parentheses.**

*GenBank* (NIH) – compiles all sequences from literature and from submissions; provides tailored BLAST searches and sequence views.
*GrainGenes* - Triticeae genome database
*Gramene* (NSF major source of funds, USDA-ARS minor) - Comparative sequence and map views of the cereal grains, based on rice; curated rice genome data.
*MAGI* (NSF) - assembled ~850,000 gene-enriched maize GSSs generated by the Consortium for Maize Genomics into MAGIs (Maize Assembled Genomic Islands).
*MaizeGDB* (USDA-ARS) – compiles and presents interlinked biological, trait, biochemical, genomic, and map data.
*PlantGDB* (NSF) - processes GenBank sequences for all plants, and has a pipeline to get raw and assembled sequences into MaizeGDB. Note that the pipeline to get sequences into MaizeGDB is supported by a Specific Cooperative Agreement with the USDA-ARS using MaizeGDB funds.
*TAIR* (NSF) - Arabidopsis genome database; protein functions; pathways; etc.
*TIGR* (NIH, NSF, other) - note the EST contigs are no longer updated at TIGR, last maize build was Oct 2005.
*UniProt* (European sources, NIH) - protein functions for sequences, both inferred and curated by SwissProt and PIR staff.

***Other project databases/views*. Funding sources in parentheses.**

*Maize sequencing* (NSF) – soon to be released
*FPC* (NSF, other)
*Panzea* (NSF)
*ChromDB* (NSF)

***Where does MaizeGDB need help?***

Staffing is not adequate to undertake many of the roles expected by the community of maize geneticists. Staffing also precludes many aspects of data representation that are expected from most Model Organism Databases (MODs). Note that TAIR, which serves only plant biologists and does serve a plant breeding community with data on field traits and technology, has a staff of some 19 (not including PI's), compared to 4 for MaizeGDB (see below), where one of the 4 is a research PI and has position responsibilities related to research beyond the scope of the database.

Below is a list of some data and services that are either poorly represented or non-existant at MaizeGDB at present. Note especially that MaizeGDB does not currently have the infrastructure to commit to maintaining the official maize gene models. This is a service proved by almost all MODs for their species, and will be a major concern once the B73 genome has been sequenced.

* Integration of project data from diverse studies, many of which are very large and complex, requires time; simple archiving means it is effectively lost. Two examples of many: microarray data from structured service projects and from individual studies; QTL studies, both raw data and analytical summaries.

* Much of the experimentally confirmed gene function data is not current, reported in the literature but not entered and integrated.

* Much of the experimental data on development and on plant structure and growth is not current, reported in the literature but not entered and integrated.

* Community curation is a desirable expectation but still takes time of a staff member, both to pro-actively solicit, and to monitor the entry for quality. Inevitably, community curation is uneven and requires professional closure of gaps.

* Gene Ontology or GO annotation is not performed at MaizeGDB, although it is an accepted standard for other genome databases. Plant Ontology or PO annotation is limited to genes in MaizeGDB that have mutant phenotypes. It could be enhanced to include gene expression experiments. These ontologies provide ways to link to gene function information in other genome databases.

* Metabolic pathway curation and representation. Note that the "Metabolic Pathways" datacenter at MaizeGDB is sorely outdated and does not provide the functionality presented by such projects as MetaCyc.

* Any new interfaces to accommodate retrieval of new data types, creative data mining requests from the community, or new annotation, such as GO or PO.

…* Interfaces that provide a conduit to project databases. *Note that PI C. Lawrence will prepare and submit a proposal to NSF-PGRP to create such a portal to project databases within the next few months.*

**Staffing of some MODs and CODs (Clade-Oriented Databases)**

Compiled primarily by Eva Huala (TAIR) Spring 2006 - PI 's for the databases (multiple, in most instances) are not included in the compilation.

| ***Common name, Genus, or [Family]*** | ***Database*** | ***Total FTE Equivalents*** | ***IT Total FTE Equivalents (if known)*** |
|---|---|---|---|
| mouse | MGI | 59 | 20 |
| rat | TGD | 2.6 | 1 |
| Zebra fish | ZFIN | 18 | 9 |
| *Drosophila* | Flybase | 29 | |
| *Drosophila* | CGD | 1.7 | 0.2 |
| *Caenorhabditis* | Wormbase | 27 | |
| *Dictyostelium* | Dictybase | 5 | 2 |
| yeast (*S. cerevisiae*) | SGD | 24 | 9 |
| yeast (*S. pombe*) | Pombe | 1 | 0.25 |
| *Arabidopsis* | TAIR | 18 | 6 |
| Maize | MaizeGDB | 3 | 2 |
| [Poaceae] | Gramene | 11* | |
| [Triticeae] | GrainGenes | 2 | .5 |

* This estimate was provided by E. Buckler to C. Lawrence as an unofficial "round number".

# Budget-5

## MaizeGDB Project in Ames, IA (3625-21000-045-00D)

**Total available:** **$566,671**
$466,671 permanent
$100,000 temporary transfer on yearly basis from Columbia, MO.

| **Item** | **Sub-items** | **$** | **%** |
|---|---|---:|---:|
| **Salaries and Benefits** | Lead Scientist | 89100 | 16 |
| **(current)** | IT Specialist | 88300 | 16 |
| | IT Specialist | 72300 | 13 |
| | 14% Administrative Assistant | 8078 | 1 |
| | 3% Research Leader | 4677 | 1 |
| **Salaries and Benefits** | Computational Biologist* | 84900 | 15 |
| **(new)** | Temp half time curator at PGEC† | 41000 | 7 |
| | 12% IT Specialist (unit systems administrator) | 10596 | 2 |
| | *Total Salaries* | *398951* | *71* |
| *__Recruitment and Moving Expenses__ | (Scientist) Computational Biologist | 15000 | 3 |
| †**PGEC Collaboration** | Travel (PAG, Maize Meeting, and three training visits to major sites) | 5000 | 1 |
| | Supplies | 3000 | 0 |
| | Infrastructure | 7000 | 1 |
| **Travel** | About 3 persons per meeting to: PAG (2K), Maize Meeting (1K), ISMB (3K), and incidental trips | 20000 | 4 |
| | Working Group | 12000 | 2 |
| **SCA Brendel** | Sequences, etc. | 30000 | 5 |
| **Contracts** | Oracle support | 8100 | 1 |
| **RSA** | On-campus supplies spending | 5000 | 1 |
| **All Other (Includes Supplies/Materials)** | Computer hardware, software, furniture, office supplies, publication costs, move to CGIL, etc. | 62620 | 11 |
| | *Total* | *566671* | *100* |

Note that without temporary transfer of funds, the PGEC collaboration (which amounts to the addition of a half time curator) is not allowed.

# POPcorn Proposal-6

# POPcorn Project Proposal

**NSF** RFP at http://www.nsf.gov/publications/pub_summ.jsp?ods_key=nsf06581, proposal due Oct 6

**DOE** RFP to be posted at http://www.science.doe.gov/production/bes/eb/Grants/grants.html, deadline to be announced early in calendar year 2007

In the physical binder, this section will have a draft of the POPcorn proposal for NSF. For the electronic copy, included here is a copy of the email that was sent out to request letters of collaboration. The list of persons contacted to send letters of collaboration as well as their responses (if any) are listed in the table at the end of this section.

**Email**
Date: Fri, 15 Sep 2006 15:24:28 -0500
To: EMAIL ADDRESSES IN TABLE BELOW
From: Carolyn Lawrence <noreplymaize@iastate.edu>
Reply-to: triffid@iastate.edu
Subject: Collaboration Request for a Maize Project of Interest

Dear Dr. XXXXXX,

You may recall from the recent discussion at the Maize Genetics Conference that a centralized resource for locating all maize research projects is lacking, and that many researchers voiced the desire for an online web portal to be created. I am putting together proposals to get funds to create just such a resource, which is described in some detail below. I plan to submit the proposal to two agencies, the NSF and the DOE. In case both are funded (which is, of course, a long-shot), the proposals will be slightly different to enable acceptance of one award and also some percentage of the other. I have attached to this email a template letter of collaboration that could be edited, put on your own letterhead, and returned if willing to work with us to SPECIFICS ABOUT THE RESEARCHERS' PROJECT WERE LISTED HERE.

For the DOE request for proposals, a section on maize as an energy crop will be included. For the NSF request for proposals, a BLAST service that searches all maize sequences then delivers to the user information on which sequences have associated data at a particular project database will be created. Because your letter of collaboration would be used for both proposals, please do not specifically mention either of these two services in the letter. Alternatively, two specific letters of collaboration could be drafted.

Thanks so much for considering helping us to get funding to create the POPcorn resource!

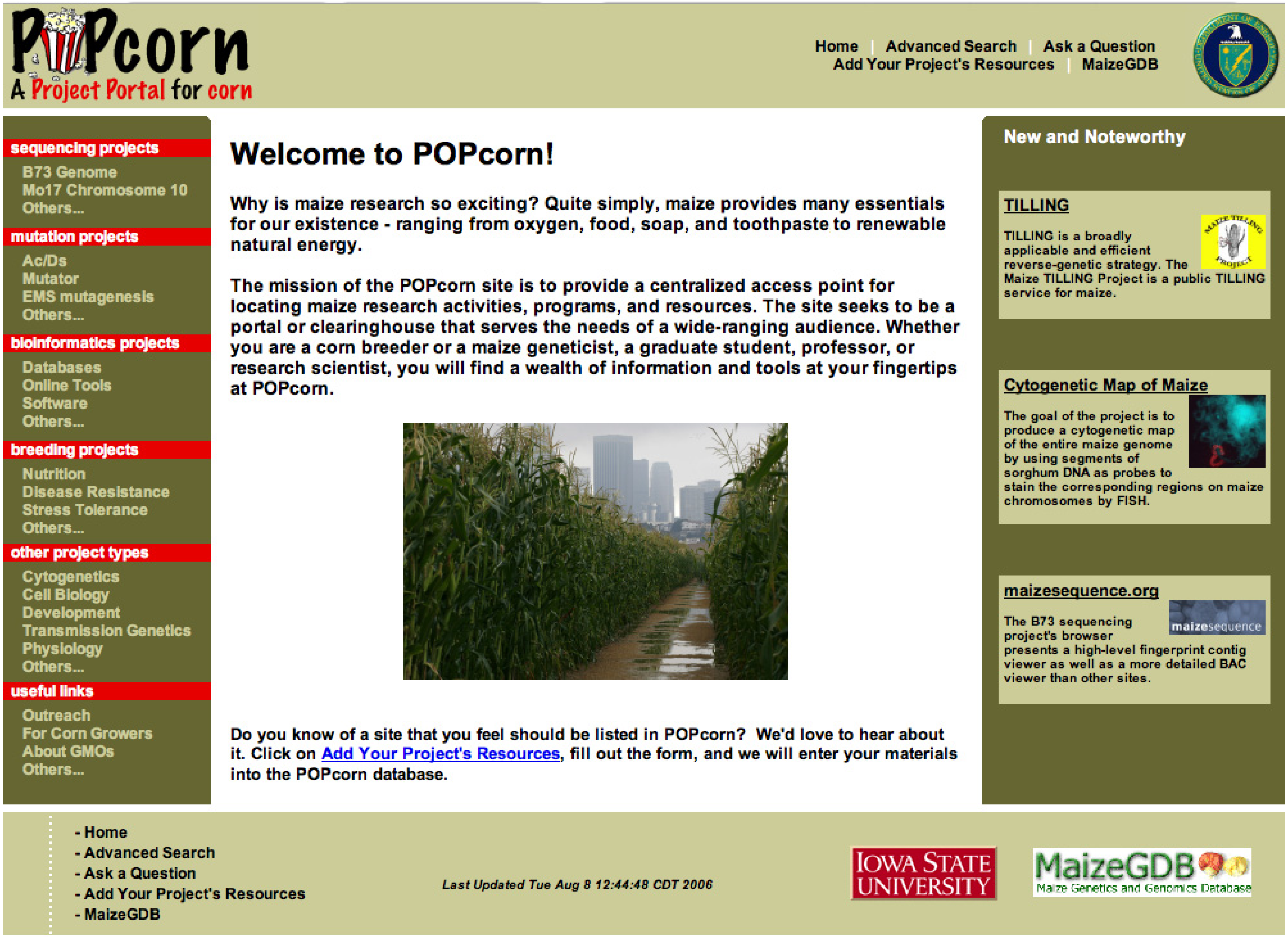
Sincerely,
Carolyn Lawrence

Project Description (see also attached mock-up screenshot tif for DOE):
It is almost impossible to locate all project sites that are available for maize research. A naive stab at collating a list of about fifty projects is available at MaizeGDB at http://www.maizegdb.org/maizeprojects.php, but that page becomes outdated regularly and stores little to no information about the work being reported by the listed project sites. While the MaizeGDB project page does serve as a list to inform researchers of others' work, it fails to get researchers to sites of interest, largely because the content at those sites is not something that can be searched simultaneously. We propose to create a portal (called POPcorn; see the tif image attached for a mockup of an entry page) which will will serve as a conduit to maize project data repositories. The POPcorn project code will be harvested out of an existing project site called PGROP (the Plant Genome Research Outreach Portal). That site is available at http://www.plantgdb.org/PGROP/pgrop.php.

Very little new code would have to be created for POPcorn, but existing code would need to be modified and participating groups would need to be contacted and also visited in person by POPcorn project personnel. The POPcorn project would require the hire of one Information Technology Specialist through Iowa State University on a 2-year appointment and of a data curator (also on a 2-year appointment). The IT Specialist would gain familiarity with the existing PGROP code while he/she is editing it for POPcorn, and once the POPcorn site is up and running (which will take about 6 months), the project will enter the maintenance stage of its lifecycle. During the subsequent 18 months, not only will an idea of what is required for its maintenance be gained, the software behind the site will be generalized so that anyone could download the software and create such a project portal by filling in some tables and choosing a color scheme, etc. During both years, the curator would be working with project databases to create mechanisms to connect the project websites and to create mechanisms and templates for data exchange. Once the two years of POPcorn funding are over, MaizeGDB personnel would inherit the maintenance of the POPcorn site, and it would be ancillary to MaizeGDB. In addition to serving as a portal to sites for researchers, the availability of the site will help MaizeGDB personnel to be aware of which data are available for incorporation into MaizeGDB as individual maize project sites get up and going.

Here's an example of how the BLAST mechanism (outlined for the NSF proposal only) would work for the user:
A researcher sends a BLAST query and POPcorn searches all maize sequences and returns hits with associated data from, e.g., Gramene, the Maize Genome Browser, MaizeGDB, PlantGDB, MAGI, TILLING, etc. That is, output at POPcorn would show for every sequence found which sites have data associated with that sequence. This means that researchers would be enabled to do a single BLAST and get results that have, for instance, contig membership information for the MAGI, PlantGDB, and the TIGR contigs. This means the researcher might get a result with sequences that have associated TILLING data, which would connote that there's seed for a line with a point mutation in the sequence returned. He/she might get a response from MaizeGDB that would let you know that the hits were present on a number of different maps.

## Email Attachment 1: Image of POPcorn



POPcorn
A Project Portal for corn

Home | Advanced Search | Ask a Question
Add Your Project's Resources | MaizeGDB

**sequencing projects**
- B73 Genome
- Mo17 Chromosome 10
- Others...

**mutation projects**
- Ac/Ds
- Mutator
- EMS mutagenesis
- Others...

**bioinformatics projects**
- Databases
- Online Tools
- Software
- Others...

**breeding projects**
- Nutrition
- Disease Resistance
- Stress Tolerance
- Others...

**other project types**
- Cytogenetics
- Cell Biology
- Development
- Transmission Genetics
- Physiology
- Others...

**useful links**
- Outreach
- For Corn Growers
- About GMOs
- Others...

# Welcome to POPcorn!

Why is maize research so exciting? Quite simply, maize provides many essentials for our existence - ranging from oxygen, food, soap, and toothpaste to renewable natural energy.

The mission of the POPcorn site is to provide a centralized access point for locating maize research activities, programs, and resources. The site seeks to be a portal or clearinghouse that serves the needs of a wide-ranging audience. Whether you are a corn breeder or a maize geneticist, a graduate student, professor, or research scientist, you will find a wealth of information and tools at your fingertips at POPcorn.

Do you know of a site that you feel should be listed in POPcorn? We'd love to hear about it. Click on Add Your Project's Resources, fill out the form, and we will enter your materials into the POPcorn database.

**New and Noteworthy**

**TILLING**

TILLING is a broadly applicable and efficient reverse-genetic strategy. The Maize TILLING Project is a public TILLING service for maize.

**Cytogenetic Map of Maize**

The goal of the project is to produce a cytogenetic map of the entire maize genome by using segments of sorghum DNA as probes to stain the corresponding regions on maize chromosomes by FISH.

**maizesequence.org**

The B73 sequencing project's browser presents a high-level fingerprint contig viewer as well as a more detailed BAC viewer than other sites.

- Home
- Advanced Search
- Ask a Question
- Add Your Project's Resources
- MaizeGDB

*Last Updated Tue Aug 8 12:44:48 CDT 2006*

## Email Attachment 2: Letter of collaboration template

September 15, 2006

SUBJECT: Letter of Collaboration for Proposal Entitled 'POPcorn: A consolidated online research project search mechanism for maize'

TO: Carolyn J. Lawrence, Ph.D.
1565 Agronomy Hall
Iowa State University
Ames, IA 50011

FROM: YOUR NAME AND ADDRESS HERE

Dear Carolyn,

I am writing this letter to convey my desire to collaborate with you and colleagues at the USDA-ARS and Iowa State University on the POPcorn project, which will enable online resources generated by maize research projects to be searched simultaneously. It is my understanding that you are proposing to collate information on all online research resources for maize (sequence-based and otherwise) and to make that information available through integrated browse and search mechanisms. This would enable researchers to have a list of current projects by type at their fingertips, and would help researchers to spend less time searching for data at the computer, and more time testing their hypotheses at the bench.

My group will be happy to provide a description of our project and relevant generated data to your group. I am sure that the availability of such a Web portal will increase the awareness of my own project, and I look forward to using the POPcorn site for my own research! At present it is nearly impossible to be sure that I am finding all of the right sites for data important to my research, and I believe POPcorn will help me (and other researchers) to locate maize project data.

I am happy that you have budgeted travel funds to enable POPcorn project group members to visit my location. Working with the staff to be sure that data exchange formats and protocols are well explained and that datasets to be exchanged are easy to generate is of the utmost importance for an endeavor such as this to succeed.

Finally, I am glad to hear that MaizeGDB has committed to inheriting the maintenance of the POPcorn project once the project deliverables have been generated and the funding for the project draws to a close. It is great to know that POPcorn itself will not disappear!

Sincerely,

YOUR SIGNATURE HERE
YOUR TYPED NAME HERE

**Table of researchers contacted and their responses.**

| Researcher | Email address | Response (if any) |
|---|---|---|
| Brad Barbazuk | bbarbazuk@danforthcenter.org | |
| Alice Barkan | abarkan@molbio.uoregon.edu | |
| Hank Bass | bass@bio.fsu.edu | |
| Jim Birchler | birchlerj@missouri.edu | yes |
| Volker Brendel | vbrendel@iastate.edu | yes |
| Tom Brutnell | tpb8@cornell.edu | yes |
| Karen Cone | conek@missouri.edu | yes |
| Carolyn Napoli | cnapoli@ag.arizona.edu | |
| Kelly Dawe | kelly@plantbio.uga.edu | |
| John Doebley | jdoebley@wisc.edu | |
| Hugo Dooner | dooner@waksman.rutgers.edu | |
| Damon Lisch | dlisch@berkeley.edu | yes |
| David Galbraith | galbraith@arizona.edu | |
| Michael Hahn | hahn@ccrc.uga.edu | Decided his project is not appropriate, so has chosen not to send a letter. |
| Sarah Hake | maizesh@nature.berkeley.edu | yes |
| David Jackson | jacksond@cshl.edu | yes |
| Leon Kochian | LVK1@cornell.edu | |
| Steve Moose | smoose@uiuc.edu | yes |
| Henry Nguyen | NguyenHenry@missouri.edu | |
| Mike Scanlon | mjs298@cornell.edu | yes |
| David Schwartz | dcschwartz@facstaff.wisc.edu | |
| Mark Settles | settles@ufl.edu | yes |
| Bill Sheridan | bill.sheridan@und.edu | yes |
| Lincoln Stein | lstein@cshl.edu | |
| Vicki Vance | vance@biol.sc.edu | |
| Klaas van Wijk | kv35@cornell.edu | |
| Doreen Ware | ware@cshl.edu | |
| Clliff Weil | cweil@purdue.edu | yes |
| Susan Wessler | sue@plantbio.uga.edu | yes |
| Roger Wise | rpwise@iastate.edu | |
| Yeisoo Yu | yeisooyu@ag.arizona.edu | yes |
| Jimmie Mowder | jmowder@ars-grin.gov | |
| Mike Blanco | mblanco@iastate.edu | |
| Pat Schnable | schnable@iastate.edu | |

# Publications-7

*Nucleic Acids Research, 2004, Vol. 32, Database issue* ***D393–D397***
*DOI: 10.1093/nar/gkh011*

# MaizeGDB, the community database for maize genetics and genomics

**Carolyn J. Lawrence[1], Qunfeng Dong[1], Mary L. Polacco[3], Trent E. Seigfried[1] and Volker Brendel[1,2,*]**

[1]Department of Genetics, Development and Cell Biology and [2]Department of Statistics, Iowa State University, Ames, IA 50011-3260, USA and [3]Department of Agronomy, University of Missouri and Agricultural Research Service, United States Department of Agriculture, Columbia, MO 65211, USA

Received August 15, 2003; Accepted August 27, 2003

## ABSTRACT

**The Maize Genetics and Genomics Database (MaizeGDB) is a central repository for maize sequence, stock, phenotype, genotypic and karyotypic variation, and chromosomal mapping data. In addition, MaizeGDB provides contact information for over 2400 maize cooperative researchers, facilitating interactions between members of the rapidly expanding maize community. MaizeGDB represents the synthesis of all data available previously from ZmDB and from MaizeDB—databases that have been superseded by MaizeGDB. MaizeGDB provides web-based tools for ordering maize stocks from several organizations including the Maize Genetics Cooperation Stock Center and the North Central Regional Plant Introduction Station (NCRPIS). Sequence searches yield records displayed with embedded links to facilitate ordering cloned sequences from various groups including the Maize Gene Discovery Project and the Clemson University Genomics Institute. An intuitive web interface is implemented to facilitate navigation between related data, and analytical tools are embedded within data displays. Web-based curation tools for both designated experts and general researchers are currently under development. MaizeGDB can be accessed at http://www.maizegdb.org/.**

## INTRODUCTION

Maize (commonly referred to as corn in the United States or by its botanical name *Zea mays* L. ssp. *mays*) is an important crop. Not only does maize feed both the world's people and its livestock, but its byproducts are also necessary for many industries where corn content is less apparent. Maize byproducts are used in the manufacture of diverse commodities including glue, soap, paint, insecticides, toothpaste, shaving cream, rubber tires, rayon, molded plastics and others [see (1) for review]. The Maize Genetics and Genomics Database (MaizeGDB; http://www.maizegdb.org) is a public database that serves the community of maize researchers by storing and curating data related to the genetics and genomics of maize. Such data include for example, locus information for genes, chromosomal variations (allelic diversity), map positions of genes, primers used for mapping analysis, probe sets used in mapping and phenotypic image data. These data types are intrinsically interrelated, and MaizeGDB's web interface recapitulates these relationships. Using MaizeGDB, a researcher can type a term (e.g., *adh1*) into the search field at the top of any page and should be able to navigate intuitively from the results page to pages containing the locus, related stocks, variations, primers, the position of the locus on a variety of maps and additional information. Also available on results pages are links to contact information for maize researchers who are experts on the query topic and who can provide valuable research materials (see Usage Example below).

## HISTORICAL BACKGROUND

Maize is an organism of historical importance to all biologists. A sample of seminal discoveries made by maize geneticists include: Emerson's contributions to the concepts of epistasis and quantitative genetics (2,3); Stadler's research showing that X-rays cause mutation (4,5); Beadle's doctoral dissertation describing how irregular behavior of meiotic chromosomes causes heritable pollen production defects (6); Creighton and McClintock's work showing that genetic crossing over is accompanied by physical crossovers between chromosomes (7); Rhoades' discovery of the cytoplasmic inheritance of male sterility (8); and McClintock's description and characterization of transposable elements, which ultimately won her the Nobel prize [reviewed in (9)].

In the late 1920s it was recognized by the community of maize geneticists that the data they were recording needed organization, publication and curation. To this end, R. A. Emerson and others began publishing the Maize Genetics Cooperation Newsletter (MNL), which is compiled and published on a yearly basis. To further the same goals, in 1991 the US Department of Agriculture-Agricultural Research Service (USDA-ARS) charged Ed Coe, then editor of the MNL, to develop a maize genome database (10). MaizeDB was one of the first biological databases to exist online, and it became an indispensable research tool utilized by maize geneticists worldwide.

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In 1998, the Maize Gene Discovery Project (MGDP) was funded by the National Science Foundation, led by Virginia Walbot and including 10 research groups [reviewed in (11)]. The MGDP discovers new maize genes and develops tools for characterizing maize mutants. The microarray slides, EST clones, library plates of indexed transposon insertions and seed generated by MGDP necessitated the implementation of a resource to make these materials publicly available and to organize the data generated by the project team. This need was met by ZmDB (12). In addition to making MGDP materials available, ZmDB also encompasses all public maize ESTs, GSSs and protein sequences. ZmDB's embedded similarity search tools and services (providing multiple sequence alignments, protein domain determination and spliced alignments) simplify sequence analysis, thus allowing researchers to spend more time making scientific discoveries at the bench. ZmDB was scheduled to shut down in September 2003 at the termination of the MGDP.

In September of 2001 the USDA-ARS began an initiative to combine MaizeDB and ZmDB, thus creating a single maize genetics and genomics database using state-of-the-art database architecture and web design protocols. As of September 1, 2003, this goal was realized. MaizeGDB supersedes MaizeDB, and makes available all data and resources that previously existed at either MaizeDB or ZmDB. Researchers working at MaizeGDB seek to serve the maize community's database resource needs by making maize data and materials available and by collaborating with researchers to store and display their important scientific findings.

## DATABASE COMPONENTS

The records contained within MaizeGDB can be grouped into four general classes of related information: genetic data, genomic and other DNA sequence files, gene product or functional characterization records, and literature reference and person or organization listings. Some of the connections within and among these four general classes are described below. (For a detailed depiction of how the data centers at MaizeGDB are interconnected see http://www.maizegdb.org/MaizeGDBSchema.pdf.)

### Genetic data centers

Maps, loci, quantitative trait loci, traits, variations and seed stocks constitute the genetic data centers. Since the first maize linkage maps were compiled and published in 1935, mapping data have been crucial to maize geneticists (13). At MaizeGDB, map queries can be restricted to a particular chromosome, map source, inbred line or background. Loci along the chromosome are linked to their respective locus records, and the coordinates of and bins containing each locus are listed. For maps that are also present at Gramene (a resource for comparative analysis of grass genomes) (14) and the National Center for Biotechnology Information (NCBI) (15), links are provided for navigation to those visualization resources. Individual loci or clusters of loci that are physically linked and that act together to modulate quantitative traits are called quantitative trait loci (QTL). QTL records can be searched by experiment, identified by the person who performed the experiment and year, or by trait. Selecting an individual QTL experiment creates a page showing the experimental overview, which includes the mapping panel, progeny for genotype evaluation, progeny for trait evaluation and marker summary. The page also will list trait evaluations, QTL detected by the experiment and links to any references describing the experiment. Alternative forms of QTL, loci, chromosomes and other genetic elements are called variations. Variation searches at MaizeGDB can be restricted to type, locus, viability, progenitor stock, dominance, mutagen, mutation, expressed phenotype and stock. Selecting a particular variant from the list of records matching the search criteria creates a page including the variant's name, allele descriptor, dominance, type (allele, QTL variant, transposition, etc.), phenotype(s) and a list of stocks known to carry the variation. To obtain seed for analysis of variations, links for ordering stocks are embedded within the variation and trait pages. Alternatively, specific seed stock searches can be performed and can be restricted by identifier, type (BA translocation, hybrid, inbred line, etc.), focus linkage group, genotypic variation, karyotypic variation, phenotype, availability and parentage. Results pages list the stock name, a descriptive name, type, focus linkage group and source. Stocks available from the Maize Genetics Cooperation Stock Center (http://www.uiuc.edu/ph/www/maize/) or NCRPIS (http://www.ars-grin.gov/ars/MidWest/Ames) can be ordered by following links that are embedded throughout MaizeGDB.

### Genomic/sequence data centers

Maize sequences, SSRs, probes, BACs and overgo probes are found within MaizeGDB's genomic and other DNA sequence data centers. Sequence searches query the database for ESTs (derived from http://www.ncbi.nlm.nih.gov/dbEST), GSSs (http://www.ncbi.nlm.nih.gov/dbGSS), HTGs (http://www.ncbi.nlm.nih.gov/HTGS), STSs (http://www.ncbi.nlm.nih.gov/dbSTS), complementary DNAs (cDNAs) and proteins using the sequence's accession number, GI number or a part of the sequence title. Sequences also can be searched using BLAST (16) and the GeneSeqer gene discovery tool (17). Links on sequence record pages make it possible to carry out BLAST searches at MaizeGDB, PlantGDB (18) or GenBank. Simple sequence repeats (SSRs) can be identified at MaizeGDB by repeat pattern [e.g., (AAAT)3 represents AAATAAATAAAT], and the SSR browser allows researchers to examine SSR records by name, bin location along a given chromosome and base sequence. Some sequence data are also included in MaizeGDB's probe data set, which is made up of a mix of both probe and sequence data types including amplified fragment length polymorphisms (AFLPs), restriction fragment length polymorphisms (RFLPs), non-EST cDNAs, DNA probes, genomic DNA, miniature inverted-repeat transposable elements (MITEs), random amplified polymorphic DNAs (RAPDs), yeast artificial chromosomes (YACs) and a small assortment of other probe types. Bacterial artificial chromosome (BAC) records can also be found within this data center. Contigs formed from multiple BACs can be visualized through links to WebFPC [http://www.genome.arizona.edu/fpc/maize and (19)]. Overlapping oligonucleotide pairs (overgos that were used to detect BACs) can be identified at MaizeGDB by name or using a short DNA sequence as the database query. Overgo results pages list primer pairs as a single sequence with the overlapping portions of the two sequences highlighted. Selecting a single overgo from the list creates a screen showing the two primers, their names, alignment and a list of the BACs detected by the overgo. Also listed are any ESTs that are known to contain either overgo sequence.

### Gene product/functional characterization data centers

MaizeGDB stores and curates detailed descriptions of gene products, metabolic pathways, and mutant or variation phenotypes. Gene product records display gene product type (storage protein, signal receptor, transcription factor, etc.), Enzyme Commission number(s) (as assigned by IUPAC-IUBMB; http://www.chem.qmw.ac.uk/iupac/jcbn), a list of motifs and features, a list of related gene products, and a link to references that describe the gene product. Searches can be limited by environmental or chemical induction conditions; subcellular localization; metabolic pathway; metabolic constituent; and sequence, structural, and gel migration rate information. Metabolic pathway records can be searched by pathway name, metabolic process (e.g., cell division) and key enzyme. Over 7000 phenotype records can be searched by name, trait, presence of related images and body part (plant organ) exhibiting the phenotype. Selecting a phenotype search result creates a page displaying links to related traits and associated stocks.

### Reference and person/organization data centers

Not all references important to maize researchers can be found using conventional journal search engines like the NCBI's 'Entrez Pubmed' (http://www.ncbi.nlm.nih.gov/PubMed). MaizeGDB contains both mainstream and cryptic references including MNL references (which cannot be cited without the author's permission but contain invaluable data, nonetheless) and references from other journals not supported by typical reference search engines. In addition, MaizeGDB maintains reference information and abstracts for works published in the annual Maize Genetics Conference Proceedings. To facilitate interactions among maize researchers, MaizeGDB also stores and curates data related to maize people and organizations. Because these records are tied to many other records in the site (such as references, probes and sequences) researchers can easily identify others with similar interests. The people or organizations search page allows for searches to be conducted by name, and the person or organization browser can be used to select information to be included in output tables.

### Major data centers are interconnected

To illustrate how the major groupings of data centers are interconnected, maize mutations containing a *RescueMu* transposable element and corresponding seed stocks and plant phenotypes can be used as a case in point. The MGDP (11) recovered small genomic libraries of DNA derived from a grid-based field of up to 2304 *RescueMu* plants. From these genomic sequences they made plasmid library plates (organized in rows and columns that mirrored the organization of the field) that can be screened for *RescueMu* insertions using PCR. By sequencing out from the transposon, sequences of genomic DNA flanking *RescueMu* were recovered from many grids. In addition, seed stocks were generated by self-pollination of each *RescueMu* grid plant and are maintained by the Maize Genetics Cooperation Stock Center. MaizeGDB facilitates searches for specific *RescueMu* sequences, plant phenotypes and seeds in the following way. BLAST (15) searches can be carried out from http://www.maizegdb.org/blast.php against the maize GSSs using a DNA or protein sequence as the query. Significantly similar sequences are identified, and links to retrieve particular sequence records from MaizeGDB are given. For GSSs that were produced by MGDP, links to view plant phenotypes associated with the *RescueMu* insertion are provided. Phenotype browser pages link to seed stock order forms from the Maize Genetics Cooperation Stock Center. Hence search tools and data centers warehousing sequence and phenotype data as well as forms for ordering seed stock online are logically interconnected, recapitulating the biological interrelationships conserved among these related data.

## USAGE EXAMPLE

A typical researcher seeking information related to his or her gene of interest (e.g., *alcohol dehydrogenase 1* or *adh1*) might go to MaizeGDB to gather information about the gene and to order seed for plants bearing mutations within the gene. (This conscientious researcher has already visited the first three pages shown in Table 1 and has learned how to use MaizeGDB.) The researcher proceeds to http://www.maizegdb.org to find out what information is available for *adh1* by searching all records using '*adh1*' as her query (see Fig. 1A; also note that maize researchers always italicize loci and gene names; however, searches at MaizeGDB do not require italics and will tolerate the use of all upper- or lower-case). She finds links to locus, phenotype, probe, reference, sequence, stock and variation records (Fig. 1B), and then selects the first stock. This stock happens to carry a genotypic variation called 'Adh1-3F1124r53' (Fig. 1C). Clicking the link to genotypic variations of 'Adh1-3F1124r53' would create a page (not shown) telling the researcher that the phenotypes associated with the 'Adh1-3F1124r53' allele are low and null activity of *adh1*, and that the allele is dominant. From the page shown in Figure 1C, the researcher orders the seed for 'Adh1-3F1124r53' from the Maize Genetics Cooperation Stock Center using the link labeled 'Order this stock' in the list of tools on the right of the record.

Going back to the list of original search results (Fig. 1B), the researcher decides to view the first locus record shown in the list (which represents the gene *adh1*). Browsing the locus page (Fig. 1D) she finds that the gene resides on the long arm of chromosome 1 and that images of *adh1* mutant phenotypes exist. By going to the phenotype images (not shown), the researcher finds that expected phenotypes for *adh1* mutant plants include failure to germinate in anaerobic conditions and pollen tube germination defects. This information tells the researcher what phenotypes to expect from the seed that will soon arrive in the mail from the Maize Genetics Cooperation Stock Center. Going back to the locus page (Fig. 1D) she scrolls down (not shown) to find the names of cooperators from whom RFLP probes for *adh1* can be obtained. Sequences for primers that the researcher can use to amplify the *adh1* gene are also displayed. Other data of interest she finds on this page include links to the genomic and EST sequences of *adh1*, recombination data and detailed comments about the gene product encoded by the *adh1* gene. For more information on how to navigate the MaizeGDB website, please visit each of the links listed in Table 1.

**Table 1.** Links for helpful and interesting sites at MaizeGDB

| | | |
|---|---|---|
| MaizeGDB tutorial | http://www.maizegdb.org/tutorial/index.php | A tutorial explaining how to use many of the features of MaizeGDB |
| Site tour | http://www.maizegdb.org/site_tour.php | A brief tour describing the highlights of MaizeGDB |
| Documentation | http://www.maizegdb.org/doc.php | A summary of documentation for the site including schema, credits, documentation of important maize projects, links and other resources |
| Credits | http://www.maizegdb.org/credit.php | A page providing credit to the software providers and other groups and individuals essential to MaizeGDB |
| Maize Genome Browser | http://www.maizegdb.org/cgi-bin/bin_viewer.cgi | A utility enabling researchers to browse through the maize chromosomes to find sequences, genes, BACs, SSRs and other genetic elements in various regions of the maize genome |
| Mapped BLAST | http://www.maizegdb.org/blast.php | A BLAST utility that also returns known map locations of sequence matches; linked throughout the site |
| GeneSeqer | http://www.maizegdb.org/geneseqer.php | A web interface to the GeneSeqer gene discovery tool that is also interlinked throughout the site for researchers to use dynamically |
| Image browser | http://www.maizegdb.org/cgi-bin/imagebrowser.cgi | A collection of image-browsing tools to help researchers locate images of maize appropriate for their educational needs |
| Educational resources | http://www.maizegdb.org/education.php | A selection of maize-related educational resources for both researchers and the general public |
| Job board | http://www.maizegdb.org/jobs.php | A page that allows members of the community to post or find jobs |
| Database statistics | http://www.maizegdb.org/cgi-bin/database_stats.cgi | A review of the counts of particular records of various types stored in MaizeGDB |
| Site statistics | http://www.maizegdb.org/cgi-bin/awstats.pl | Information on site usage |

**Site Search Results**

Matches were found in the following categories matching the term adh1. Click on the category to browse through those records.

4 locus record(s) was/were found.
4 phenotype record(s) was/were found.
3 probe record(s) was/were found.
122 reference record(s) was/were found.
170 sequence record(s) was/were found.
15 stock record(s) was/were found.
572 variation record(s) was/were found.

**118J (stock)**

This stock is also known by the following names:
**118J** (per Canonical Name)
**118J Adh1-3F1124r53**

**Available From:** Maize Genetics Cooperation - Stock Cente
**Co-op ID:** 118J
**Focus Linkage Group:** 1.
**Type:** CHROMOSOME MARKER

**Genotypic Variations:**
Adh1-3F1124r53

**Description:** 118J Adh1-3F1124r53

**GRIN Information:**
118J (known as *MGS 131379*)
See this germplasm at GRIN (Germplasm Resources Information Network)!
This is a genetic germplasm.

**Off-Site Resources:**
GRIN MGS 131379

You can try another stock search...
☐ Make this search case-sensitive

See record in a printer-friendly format

Return to the homepage

**118J Research Tools**

Here are some internet resources to aid your investigation into 118J.

**Order this stock**
**Stock Center Catalog**
Search Google for 118J
Search Usenet for 118J

**adh1 *alcohol dehydrogenase1* (locus)**

This locus is also known by the following names:
**Adh** (per Schwartz, D)
**Adh-1** (per Various)
**Adh2** (per Scandalios, J)
**bnl(adh1)**
**npi21(adh1)** (per Wright, S)
**npi21-adh1** (per Wright, S)
**rgpc496a(adh)**
**umc(adh1)** (per Burr, B)
**umc1726**

**Full Name:** alcohol dehydrogenase1
**Type:** GENE
**Species:** Zea mays ssp. mays
**Linkage Group:** 1.
**Arm:** L (long arm)
**Length:** 5.2 kbp
**Properties:** MNL GENE LIST
**Expression Induction:** Expression of this locus is induced by ANOXIA.
**See 3 images of adh1 expression.**

**Map Coordinates:** (* indicates the locus is on the backbone)

| Map | Coordinate | Bin |
|---|---|---|
| bins 1 | 1.1 | 1.10 |
| BNL 2002 1 | 233 | 1.10 |
| BNL 93 1 | 216 | 1.10 |
| BNL 95 1 | 217.9 | 1.10 |
| BNL 96 1 * | 217.9 | 1.10 |
| BNL 96 frame 1 * | 233 | 1.10 |
| CO159/T232 F2.B 1992 1 | 189.3 | 1.10 |
| CU 98 1 | 194.2 | 1.10 |
| CU 99 1 | 224.8 | 1.10 |
| Cytological 1 | .85 | 1.10 |
| Genetic 1 * | 200 | 1.10 |
| IBM neighbors v.2 1 | 807.5 | 1.10 |
| IBM2 neighbors 1 | 910.75 | 1.10 |
| IBM2 neighbors frame 1 | 910.75 | 1.10 |
| INRA composite 1996 1 | 250 | 1.10 |
| INRA Composite 1997 1 | 215.4 | 1.10 |
| Mycogen 1992 1 | 222.9 | 1.10 |
| NPI 1990 1 | 144 | 1.10 |
| SSR Consensus 1 * | 132.2 | 1.10 |
| SSR Tx303xCO159 1 * | 226.3 | 1.10 |
| UMC 93 1 | 248.3 | 1.10 |
| UMC 98 1 * | 205.2 | 1.10 |
| UMC Interval Map 93 1 | 219.7 | 1.10 |

**Brief Comments:**

electrophoretic mobility; null alleles are known; dimeric; intra/interlocus hybrid bands occur); SSR umc1726

**adh1 Research Tools**

Here are some internet resources to aid your investigation into adh1.

**Search Tools**
Search **PlantGDB** for adh1
Search **Gramene** for adh1
Search **AmiGO** (gene ontology) for adh1
Search **GenBank** for adh1
Search **TIGR ZmGI** for adh1

Search **Google** for alcohol dehydrogenase1
Search **Google Groups** for alcohol dehydrogenase1
Search **PubMed** for alcohol dehydrogenase1

MaizeGDB **Genome Browser**

**Locus Overview By Chrom.**
1 | 2 | 3 | 4 | 5
6 | 7 | 8 | 9 | 10

**Figure 1.** Example database search at MaizeGDB using the query 'adh1'. The group of screenshots shows an example of how researchers can search MaizeGDB for *alcohol dehydrogenase 1* (*adh1*). (**A**) All MaizeGDB pages have the same search bar at the top of the page. In this example all records are searched for the term '*adh1*'. (**B**) Records of various data types are retrieved. (**C**) Selecting one of the seed stock records creates a page showing information about the stock. In the list of tools to the right is a link for ordering it from the Maize Genetics Cooperation Stock Center. (**D**) Selecting the first of four locus records identified by the search creates a page (truncated here for space) showing data related to the locus *adh1*. Beyond 'Brief Comments' there are information and links to: related gene products (both internal and offsite), ESTs, probes, SSRs, primers, variations, phenotypes, nearby and related loci, sequences, map scores, recombination data, extensive comments, references and related offsite resources. A list of tools to the right links this page to search engines and other databases.

## FUTURE DIRECTIONS

The MaizeGDB team is dedicated to seeking out new data sources for evaluation as materials to be archived in support of research applications. Data types and efforts currently under evaluation include: (i) listing the availability of and contact information for tissue, organ and inbred line-specific cloned sequence libraries, (ii) creating a searchable maize transposon and repeat sequence database, (iii) utilizing an editorial board to provide in-depth annotation of selected publications and (iv) launching storage and display endeavors for chromosome fluorescence *in situ* hybridization (FISH) image data as it becomes available from the Cytogenetic Map of Maize project (ISGA-PGR; https://www.fastlane.nsf.gov/servlet/showaward?award=0321639). Researchers interested in helping to make these or other data types of interest available to the maize community through MaizeGDB are encouraged to contact the MaizeGDB team at mgdb@iastate.edu.

## AVAILABILITY

MaizeGDB is accessible at the URL http://www.maizegdb.org/. Inquiries concerning the database should be directed by email to mgdb@iastate.edu.

## ACKNOWLEDGEMENTS

We thank our national steering committee (Tom Slezak, Ed Buckler, Vicki Chandler, Mike Freeling, Sarah Hake, Marty Sachs, Cari Soderlund, Lincoln Stein and Virginia Walbot) and our local steering committee (Phil Becraft, Steve Howell, Robert Jernigan, Mike Lee, Alan Myers, Tom Peterson, Pat Schnable and Jonathan Wendel) for their collaboration, direction and helpful comments. We also thank Darwin Campbell (database developer), Sanford Baran (web developer) and Mike Brekke (systems support specialist) for their contributions to the success of the MaizeGDB project. This work is funded by USDA-ARS specific cooperative agreement no. 58-3625-1-192.

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# The Maize Genetics and Genomics Database. The Community Resource for Access to Diverse Maize Data[1]

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The Maize Genetics and Genomics Database (MaizeGDB) serves the maize (*Zea mays*) research community by making a wealth of genetics and genomics data available through an intuitive Web-based interface. The goals of the MaizeGDB project are 3-fold: to provide a central repository for public maize information; to present the data through the MaizeGDB Web site in a way that recapitulates biological relationships; and to provide an array of computational tools that address biological questions in an easy-to-use manner at the site. In addition to these primary tasks, MaizeGDB team members also serve the community of maize geneticists by lending technical support for community activities, including the annual Maize Genetics Conference and various workshops, teaching researchers to use both the MaizeGDB Web site and Community Curation Tools, and engaging in collaboration with individual research groups to make their unique data types available through MaizeGDB.

## MISSION AND SCOPE

The Maize Genetics and Genomics Database (MaizeGDB) is the community resource for maize (*Zea mays*) data and can be accessed online at http://www.maizegdb.org. Data types stored at MaizeGDB include (but are not limited to) sequence, locus, variation, probe, map, metabolic pathway, phenotype, quantitative trait locus (QTL) experiment, stock, and contact information for hundreds of maize researchers worldwide (for review, see Lawrence et al., 2004). Data visualization is facilitated by unique views such as the highly popular genome browser (http://www.maizegdb.org/cgi-bin/bin_viewer.cgi) that displays data within their chromosomal context. Furthermore, data analysis tools such as BLAST (Altschul et al., 1997) and GeneSeqer (Brendel et al., 2004) are available for researchers to carry out their own data analyses directly via MaizeGDB Web services.

The team of people who work at MaizeGDB seek to serve the community of maize geneticists not only by making data generated by maize researchers available through the MaizeGDB site, but also by engaging in various community service projects. The MaizeGDB team supports the annual Maize Genetics Conference by maintaining the conference Web site and facilitating the abstract collection process, provides technical assistance for training workshops (e.g. the Maize Genetics, Genomics and Bioinformatics Workshop, which took place in March 2004 at the International Maize and Wheat Improvement Center [CIMMYT] in Mexico City), and sends out announcements to the community of maize geneticists via e-mail as directed by the Maize Genetics Executive Committee (http://www.maizegdb.org/mgec.php). In addition, by providing data descriptions for the general public, which can be found on each data center page at MaizeGDB (e.g. a description for gene product can be viewed at http://www.maizegdb.org/gene_product.php#dld), the MaizeGDB team works to educate the general public about the importance of maize genetic research.

It is the aim of this article to illustrate the breadth of information made available through MaizeGDB, to convey the method by which the information is curated and made accessible, and to relate how the database infrastructure was built and is currently maintained. Detailed information regarding historical aspects of the MaizeGDB project and a review of various data types made available through the MaizeGDB site are described elsewhere (Lawrence et al., 2004).

## DISCUSSION AND FUTURE DIRECTIONS

In September 2004, under the guidance of the National Plant Genome Initiative (NPGI), the National Science Foundation (NSF), the U.S. Department of Energy (DOE), and the U.S. Department of Agriculture (USDA) announced that research funds would be made available to sequence the maize genome, and a solicitation for grant proposals was circulated (see http://www.nsf.gov/pubs/2004/nsf04614/nsf04614.txt). It was noted in this announcement that proposals should

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[1] This work was supported by a Specific Cooperative Agreement with the Agricultural Research Service, U.S. Department of Agriculture (no. 58–3625–1–192 to V.B.).

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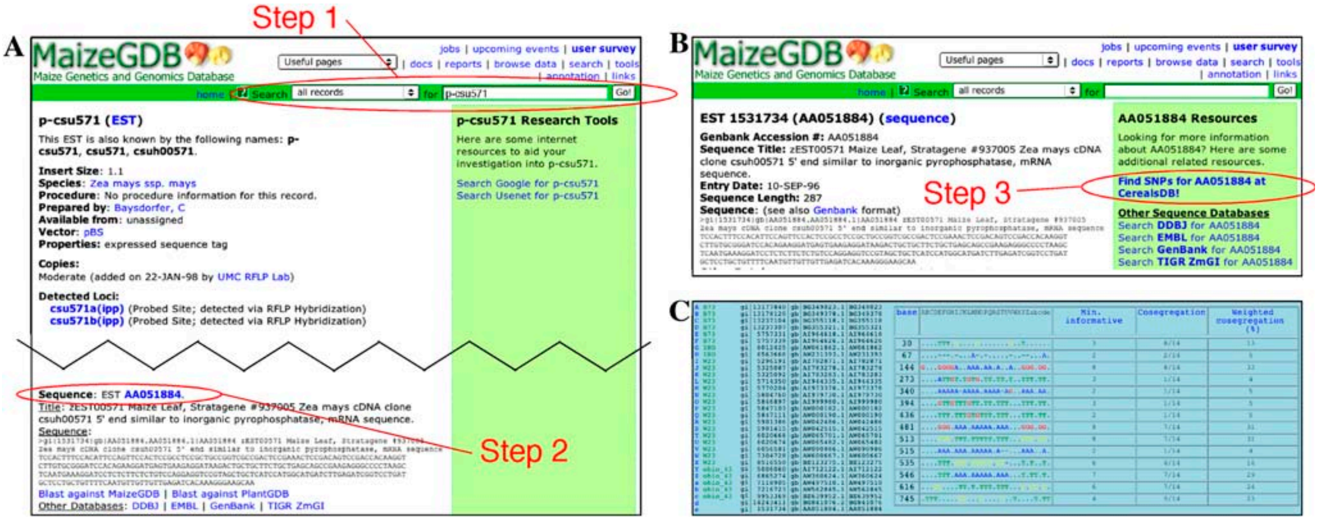
www.plantphysiol.org/cgi/doi/10.1104/pp.104.059196.



**p-csu571 (EST)**

This EST is also known by the following names: **p-csu571, csu571, csuh00571**.

**Insert Size**: 1.1
**Species**: Zea mays ssp. mays
**Procedure**: No procedure information for this record.
**Prepared by**: Baysdorfer, C
**Available from**: unassigned
**Vector**: pBS
**Properties:** expressed sequence tag

**Copies:**
Moderate (added on 22-JAN-98 by UMC RFLP Lab)

**Detected Loci:**
**csu571a(ipp)** (Probed Site; detected via RFLP Hybridization)
**csu571b(ipp)** (Probed Site; detected via RFLP Hybridization)

**Sequence**: EST **AA051884**.
Title: zEST00571 Maize Leaf, Stratagene #937005 Zea mays cDNA clone csuh00571 5' end similar to inorganic pyrophosphatase, mRNA sequence.
Sequence:

Blast against MaizeGDB | Blast against PlantGDB
Other Databases: DDBJ | EMBL | GenBank | TIGR ZmGI

**p-csu571 Research Tools**

Here are some internet resources to aid your investigation into p-csu571.

Search Google for p-csu571
Search Usenet for p-csu571

**EST 1531734 (AA051884) (sequence)**

**Genbank Accession #:** AA051884
**Sequence Title:** zEST00571 Maize Leaf, Stratagene #937005 Zea mays cDNA clone csuh00571 5' end similar to inorganic pyrophosphatase, mRNA sequence.
**Entry Date:** 10-SEP-96
**Sequence Length:** 287
**Sequence**: (see also Genbank format)

**AA051884 Resources**

Looking for more information about AA051884? Here are some additional related resources.

**Find SNPs for AA051884 at CerealsDB!**

**Other Sequence Databases**
Search **DDBJ** for AA051884
Search **EMBL** for AA051884
Search **GenBank** for AA051884
Search **TIGR ZmGI** for AA051884

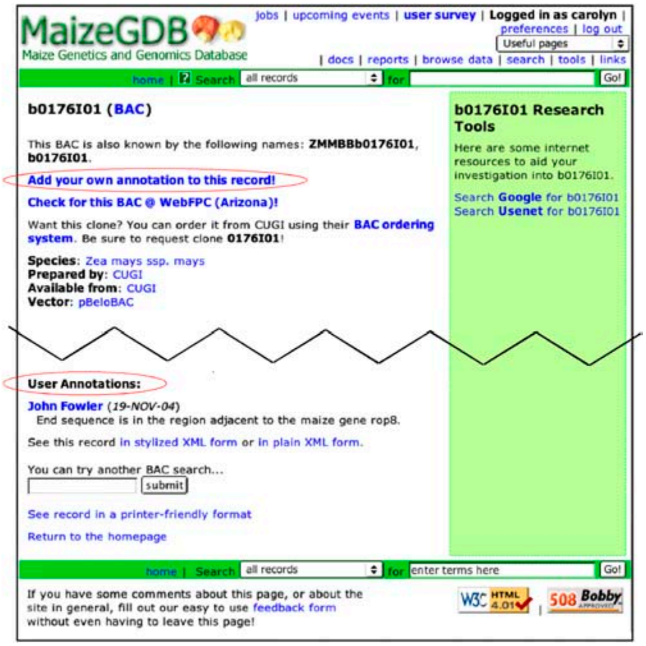
**Figure 1.** The name of a probe can be used at MaizeGDB to locate SNP data available at CerealsDB. The researcher first searches "all records" from the top of any MaizeGDB page (A; step 1, circled in red) using "p-csu571" as her query; she locates the probe record. From the probe page (A), the researcher follows a link (step 2, circled in red) to view the MaizeGDB sequence display page. From the sequence display page (B), she follows a link to CerealsDB (step 3, circled in red) to check for SNP contigs that include the sequence. Data describing a putative SNP contig (C) are presented directly via the CerealsDB site (http://www.cerealsdb.uk.net/maize_snips/snip_1563.htm). The sequence of interest (EST AA051884) is listed at the bottom of the group of sequences shown.

utilize existing, previously funded resources, one of the resources listed explicitly being the maize community genome database.

Currently, MaizeGDB provides a portal to maize genome sequencing information (which can be viewed at http://www.maizegdb.org/genome). Displayed on that page are documents outlining details concerning the maize genome sequencing endeavor, links to maize sequence repositories, information outlining the diversity of sequencing strategies currently employed, and a list of relevant publications germane to the maize genome sequencing project. As the maize genome gets sequenced, MaizeGDB will adapt to provide a sequence-centered portal to all maize data similar to the one provided by The Arabidopsis Information Resource (TAIR; http://www.arabidopsis.org; Rhee et al., 2003).

Presently, the number of people working at MaizeGDB is quite small when compared to the personnel associated with other database projects like TAIR (http://www.arabidopsis.org), Gramene (http://www.gramene.org), and the Solanaceae Genomics Network (SGN; http://www.sgn.cornell.edu). In order to serve as a central site for making large numbers of sequences, contigs, assemblies, and, eventually, a fully sequenced maize genome available at MaizeGDB, it is necessary that partnerships be forged between MaizeGDB and other databases, sequencing projects, and large-scale generators of maize data. In an initial effort to engage in such a collaboration, a pipeline for getting sequence data into MaizeGDB has been developed wherein all available maize sequences are downloaded from GenBank (http://www.ncbi.nih.gov/Genbank) by staff working at the Plant Genome Database (PlantGDB; http://www.plantgdb.org; Dong et al., 2004). Once the sequences have been cleaned, analyzed, and assembled into contigs at PlantGDB, they are delivered to MaizeGDB for long-term storage and display. By creating intuitive links to PlantGDB and facilitating database interoperability between MaizeGDB and PlantGDB, the weight of the burden to deliver high-quality sequence-based products to the community of maize geneticists is shared among mutually benefiting parties. Such collaborations are useful and are facilitated by initiatives like the Plant Ontology Consortium (http://www.plantontology.org; Bruskiewich et al., 2002), a group working to create controlled vocabularies for describing plant structures and growth and developmental stages to facilitate database interoperability among resources serving plant biologists working on a broad range of species. Forging new, useful partnerships with other databases and helping to develop methods to facilitate database interoperability are the highest priority tasks facing the MaizeGDB team in the coming year.

Over the course of the past year, cytological map images generated by the Cytogenetic Map of Maize project (http://www.cytomaize.org; Koumbaris and Bass, 2003) were added to the database, and displays for cytological map data were developed (e.g. http://www.maizegdb.org/cgi-bin/displayfishrecord.cgi?id=12098&map=892372). Community and Professional Curation Tools were developed for most data types, and the MaizeGDB Editorial Board began selecting noteworthy maize primary literature for rigorous professional data curation (see http://www.maizegdb.org/editorial_board.php). During the coming months, work will focus on associating Plant Ontology (http://www.plantontology.org) terms of type Plant Structure



**b0176I01 (BAC)**

This BAC is also known by the following names: **ZMMBBb0176I01**, **b0176I01**.

Add your own annotation to this record!

Check for this BAC @ WebFPC (Arizona)!

Want this clone? You can order it from CUGI using their BAC ordering system. Be sure to request clone **0176I01**!

**Species**: Zea mays ssp. mays
**Prepared by**: CUGI
**Available from**: CUGI
**Vector**: pBeloBAC

**User Annotations:**

John Fowler (*19-NOV-04*)
End sequence is in the region adjacent to the maize gene rop8.

See this record in stylized XML form or in plain XML form.

You can try another BAC search...

**b0176I01 Research Tools**

Here are some internet resources to aid your investigation into b0176I01.

Search **Google** for b0176I01
Search **Usenet** for b0176I01

If you have some comments about this page, or about the site in general, fill out our easy to use feedback form without even having to leave this page!

**Figure 2.** Researchers can add annotation to records at MaizeGDB. After having logged in to the site, the researcher's username appears in the upper right corner of the window, and links appear on pages allowing the researcher to add annotations (top red circle). Once an annotation has been added, it appears toward the bottom of the page (bottom red circle) along with the contributor's name and the date the annotation was submitted.

and Trait (an ontology currently under development) with records, and the raw data generated by QTL experiments will be made available. A Community Curation Tool module for QTL data is slated for development in the very near future.

## MATERIALS AND METHODS

### Web Interfaces Allow Access to Data within a Biological Context

The data stored at MaizeGDB are made available through a series of interconnected Web pages. Researchers can also contact the MaizeGDB team at mgdb@iastate.edu to request access to Web-based read-only SQL tools allowing direct queries on the curation copy of the database. These pages are coded in HTML, and most are automatically generated by PHP and Perl scripts. Through the Web interface (accessible at http://www.maizegdb.org), each data display page shows detailed information on a specific biological entity (e.g. a locus), as well as basic information about data associated with it (e.g. maps, variations, probes, and citations are among data types associated with loci), and links to related off-site resources (e.g. locus pages link directly to Gramene; Ware et al., 2002). Access to individual data displays is made possible through a number of different mechanisms, including a text search tool (available at the top right corner of each page) and a genome browser (located at the bottom left of the site's main page). These tools and interconnected pages allow researchers to easily navigate from point to point as they investigate research topics of interest. The interface design attempts to maximize the information available, requiring only a minimal amount of input from the researcher.

MaizeGDB's method of data delivery is aimed at making information available within the framework of its scientific meaning. Data displays place specific pieces of data within a biological context. For example, if you arrive at a map page by way of a locus page, the locus that was last visited is highlighted within the map display. Not only does using the biological relatedness of data types in conjunction with following a researcher's clickstream enable the interface to reflect real biological relationships, it also aids researchers by causing the site to seem to follow their actual train of thought. The following usage case demonstrates the interrelatedness of different types of biological information, reveals MaizeGDB's method of recapitulating those interrelationships, and highlights the placement of links to off-site resources that can help researchers gain access to related information that is not stored at MaizeGDB.

An intrepid researcher visits MaizeGDB in the hopes of finding information that would help her to design multiplex PCR primers to genotype $F_2$ plants. She is working to determine the transmission of different variants of chromosome 10, and wishes to develop a protocol for diagnosing which chromosome 10 variants are present in any given plant growing in a half-acre field. Because the researcher knows that the expressed sequence tag (EST) probe p-csu571 labels bands that migrate differentially on Southern blots between the two backgrounds of interest (Mroczek, 2003), she decides to start by investigating sequence data for that EST. In Step 1, by searching "all records" from the top of any MaizeGDB page (see Fig. 1A) using "p-csu571" as her query, she locates the probe record for p-csu571 (http://www.maizegdb.org/cgi-bin/displayestrecord.cgi?id=118621) and discovers that the sequence AA051884 is associated with p-csu571. In Step 2, she follows the sequence link to view the MaizeGDB copy of that sequence record. In Step 3, in the right bar on the sequence record page (http://www.maizegdb.org/cgi-bin/displayseqrecord.cgi?id=1531734; Fig. 1B), a link to "Find SNPs for AA051884 at CerealsDB" is displayed. By clicking that link to automatically search CerealsDB (http://www.cerealsdb.uk.net/discover.htm; Barker et al., 2003) for single-nucleotide polymorphisms (SNPs) that include AA051884 (gi 1531734), she identifies a putative SNP cluster (snip_1563; Fig. 1C) demonstrating that, among sequences similar to AA051884, multiple polymorphisms exist. This information will allow her to design a multiplex PCR experiment protocol that could enable her to genotype plants in the field without resorting to performing hundreds of time-consuming Southern blots.

Most of the continued development of the MaizeGDB interface is guided by members of the maize (*Zea mays*) genetics research community: Community members have sent hundreds of suggestions and requests concerning methods to find and display data. To aid in encouraging community feedback, a highly utilized context-sensitive feedback tool appears at the bottom of every page. The needs of researchers serve as the major impetus for interface development, and addressing those needs directly allows for tools to be developed that are both timely and germane to the needs of maize geneticists.

An example of a research need that guided interface development comes from Bill Sheridan, a maize geneticist working in the Department of Biology at the University of North Dakota. Dr. Sheridan contacted the MaizeGDB team seeking an easy method to summarize which simple sequence repeats (SSRs) detected bacterial artificial chromosomes that were also associated with genetically mapped markers. Dr. Sheridan worked with the MaizeGDB team to design a table-generating tool that provides approximate map locations for markers, the SSRs for those markers, and bacterial artificial chromosomes detected by the SSRs (see the links to each of the 10 maize chromosomes beneath the heading "Mapped & Anchored SSRs" at http://www.maizegdb.org/ssr.php). Dr. Sheridan was able to use this tool for his research and was pleased that his input guided the development of such a useful tool. This sort of interface development to address specific research needs typifies the method by which members of the MaizeGDB team work alongside researchers to help them gain access to complex relationships documented in the database. In summary, MaizeGDB's interface was initially designed to provide a context for interpreting maize data, and continued interface development is driven by specific input from and collaborative design with members of the maize research community at large.

### Data Curation: Driven by the Community of Maize Geneticists

At present, the MaizeGDB team does not have any individual member dedicated solely to data curation. Instead, all team members curate data as the need arises and in accordance with his or her particular knowledge base. Most data are added to the curation copy of the database (see below for a description of how each copy of the database is utilized) in bulk and are contributed by community members directly. Feedback from researchers often guides individual data additions and edits. By describing which data to associate with existing records or by explaining why mistakenly associated information should be updated, the community of maize geneticists contributes directly to curating the data stored at MaizeGDB. Moreover, community members can add annotations to records at MaizeGDB by logging in through the annotation link at the top of any MaizeGDB page. Once logged in, researchers can add notes like the one shown in Figure 2 (http://www.maizegdb.org/cgi-bin/displaybacrecord.cgi?id=424644) by clicking the link to "Add your own annotation to this record" shown at the top of virtually all data displays.

For researchers interested in contributing data directly to the database, a set of Java-based Community Curation Tools has been developed and is available for general use. Data types accessible through these tools include clone library, gel pattern, gene product, linkage group, locus, map, map scores, panel of stocks, person, phenotype, primer/enzyme, probe, recombination data, reference, species, stock, term, and variation. By creating data records, researchers become Community Curators who own the records they create and retain the ability to edit owned records directly.

To ensure that records entered by community members are complete, a curation level system has been implemented. Newly entered records are considered "submitted" and are checked by a professional curator. Once checked, the records are marked "approved" or "failed," and only "approved" records become publicly accessible through the Web interface. Each time a community member edits a record he or she owns, the record is reassigned the "submitted" curation level and must be reapproved to regain accessibility through the Web interface.

Workshops demonstrating the use of the Community Curation Tools were taught at Iowa State University (ISU) in August 2004 and at the Plant and Animal Genome Conference in San Diego, January 2005. To schedule an on-site training session for your research group, contact the MaizeGDB team at mgdb@iastate.edu.

Professional curators have access to a set of Java-based Professional Curation Tools that were originally created to interact with the Maize Genetics Cooperation Stock Center (MGCSC) MySQL copy of the database and that subsequently were adapted to interact with the ISU Oracle-based curation database. Whereas the Community Curation Tools were designed specifically to allow researchers from the community of maize geneticists to gain limited and controlled access to the database, the Professional Curation Tools allow less restricted access to data, enabling professional curators to create and edit records in an efficient and authoritative manner.

## Standard Operating Procedures, Accessibility, and Machine Architecture

Three copies of the MaizeGDB database exist at ISU: a production copy, a curation (staging) copy, and a test copy. Each copy is housed on a separate machine. The production copy of the database is accessible through http://www.maizegdb.org. This copy is not edited and is accessible by the public through the Web interface. The curation copy of the database is accessible by both community and professional curators via curation tools: It is the copy of the database to which new data are added and within which existing data are edited when the need to do so arises. The curation copy of the database is dumped in a compressed form to file each day. Compressed daily dumps of the curation database are formatted for Oracle and can be accessed at http://goblin1.zool.iastate.edu/~oracle. A typical dump file is currently approximately 750 MB in size (approximately 2 GB when uncompressed). Dumps from the curation database are housed on a different machine than the curation database itself. Individuals can request copies of the curation database (or individual tables contained therein; see http://www.maizegdb.org/MaizeGDBSchema.pdf for access to the current MaizeGDB schema) formatted for Oracle, MySQL, or Microsoft Access by e-mailing the MaizeGDB team at mgdb@iastate.edu. On the first Tuesday of each month, a duplicate of the curation copy of the database replaces the production copy. Scheduled replacements are announced at the bottom right of the main page (http://www.maizegdb.org). The test copy of the database serves as a testing ground for tool development and improvements to both Community and Professional Curation Tools and is also used as a training site for community curators to gain familiarity with the functionality of the Community Curation Tools before using them to access the curation copy of the database.

The servers that support MaizeGDB run Oracle 9i, which is licensed every 2 years. The machines that house the various copies of the database are Dell PowerEdge servers (Round Rock, TX) with 2 × 2.0 GHz Xeon processors, 4 GB of RAM, 5 × 73 GB Ultra 320 10K RPM drives with Red Hat Advanced Server 2.1 (Raleigh, NC) installed. All servers are nearly identically configured.

In addition to the copies of the database housed at ISU, a MySQL copy exists at the MGCSC in Urbana/Champaign, Illinois, enabling the staff of the MGCSC to keep track of data associated with maize stocks directly (a service described in detail in Scholl et al., 2003). The MGCSC copy of the database is accessible through the Professional Curation Tools and is synchronized with the ISU curation database at regular intervals.

## ACKNOWLEDGMENTS

We are indebted to Darwin A. Campbell for his work as the MaizeGDB database administrator; Qunfeng Dong for his work as the database manager at PlantGDB, the source for all sequence data made available through MaizeGDB; and Marty Sachs, Director of the MGCSC, for his work curating stock and associated data types. We also thank Michael Brekke, systems support specialist; Sanford B. Baran, contract Web developer and creator of the Community Curation Tools; and Jason Carter, information technology specialist for the MGCSC and creator of the Professional Curation Tools that enable the MGCSC and MaizeGDB to maintain data synchronization. MaizeGDB would not have been possible without the legacy work of Ed Coe and Mary Polacco on the original MaizeDB resource. We are grateful for their continued interest and contributions.

Received December 31, 2004; returned for revision January 28, 2005; accepted February 20, 2005.

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# Plant Biology Databases: A Needs Assessment
## November 16, 2005

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## ABSTRACT

We review the anticipated needs of the plant genome research community for long-lived data collections. We find that there is an increasing need for such repositories, and offer guidelines for balancing the funding of data production projects with those aimed to manage and integrate the data. In particular, we find that there is a pressing need to develop a trained cadre of skilled knowledge workers who are able to curate complex biological data, and to provide this cadre with a system of stable funding that enables data repositories to be established and maintained over extended periods of time. We note approvingly the current trend of species-specific databases to expand into comparative genomics-minded clade-oriented databases, but caution that new technologies are needed to facilitate the transparent integration of data among these databases.

**Conclusions and specific recommendations begin on page 34.**

## INTRODUCTION

A recent draft report from the National Science Board (NSB)—an oversight board of the National Science Foundation (NSF)—recommended that the NSF establish an "agency-wide umbrella strategy" for maintaining and enhancing long-lived data collections (Pennisi 2005; NSB 2005). "Data collections" is broadly inclusive of the digital data itself as well as the brick and mortar and personnel infrastructure needed to maintain the resource in a state that is useful to the scientific community. "Long-lived" refers to resources that have life spans that exceed technological generations, so they must adapt their technological implementations while maintaining or advancing their functionality.

The rationale for establishing such long-lived data collections is straightforward. The NSF and USDA together have invested hundreds of millions of dollars in research grants to generate large-scale data sets, most notably in the field of genomics. These data sets will have significance to the research community for an extended period of time, in some cases far longer than the duration of the research grant that originally funded their generation. In order to preserve this investment, the NSF and USDA need a strategy to identify and support groups to maintain these data sets. Another reason for investing in long-lived data collections arises from the value of data integration. It is often the case that two data sets, when integrated, are far more useful than the two data sets taken individually. An obvious example is the case of a genome sequence and a collection of clustered ESTs (expressed sequence tags). Taken individually, the genome sequence provides poor information about the location and nature of genes because of the inaccuracy of *ab initio* gene prediction, and the EST collection provides little information on gene structure and rarely provides the full-length coding sequence. Taken together, however, the genome sequence and EST collection provide a more accurate and comprehensive view of the content and structure of the genes in the genome. This latter point argues for the establishment of "living" data repositories in which the information is actively curated, as opposed to "dead" repositories of static FTP sites.

The establishment of long-lived data collections for plant biological data has been somewhat patchy to date. During the 1990's, the USDA-ARS established a series of species-specific databases for maize, rice, wheat, soy and other species of agronomic importance, but the results were not always satisfactory, possibly due to scarcity of resources. After a recent consolidation in the number of databases funded by the ARS, those databases that remained have shown robust growth, most notably MaizeGDB and the Legume Information System (LIS). The NSF DBI has been reluctant to commit long-term resources to database projects, but when it has committed substantial resources to data collections, it has had notable successes as evidenced by TAIR, Gramene and TIGR. However, it is unclear whether the current paradigm of establishing species-specific databases in response to investigator-initiated research proposals is the most efficient and forward-looking strategy.

This document looks at the nature of current and future biological data sets, and attempts to provide a framework on which administrators at NSF and USDA can manage the need for long-term data collections.

## Definitions

We lead this document with a number of definitions.

*Static Repository* – A static data repository is an unchanging archive of information. An example of a static repository is an FTP site containing data files from a SNP discovery project. Static repositories are typically read-only so that once published, they change rarely if at all. Compared to curated repositories, static repositories are relatively inexpensive to set up and maintain.

*Curated Repository* – A curated data repository is under active management. Data sets are reanalyzed on a regular basis in order to integrate them with each other and to find and correct inconsistencies within the data sets. The managers of this type of resource inject their own editorial judgment into the process in order to create an integrated data set that represents their best estimate of reality. Curated repositories are often built on top of database management systems and web-based interfaces that invite researchers to explore the connections among the component data sets.

*Stock Center* – A stock center is a repository of physical reagents, such as seed stocks, clones, vectors, and cell lines. It incorporates a database that describes its holdings and often offers an online catalog function that allows browsing and electronic ordering. The stock center database ideally should create a public interface for accessing its catalog, thereby allowing data repositories to create cross-references to stock center holdings.

*MOD* – Model organism database. This is a curated repository that focuses on a particular species. MODs are often been formed spontaneously by a research community in order to track reagents and other shared information resources needed by the community.

*COD* – Clade oriented database. These are a new breed of curated repositories that focus on multiple related species, for example vertebrates.

*Data Set Annotation* – Data set annotation is the process by which third parties add value to existing data sets using combinations of informatics tools and human judgment. Examples include predicting genes on genome sequences, identifying the genomic locations of genetic markers, establishing the correspondence between quantitative trait loci (QTLs) among two or more species based on common traits, or adding human-readable descriptions of gene function to gene records. Annotation is a service commonly made available at curated repositories.

*Automated Annotation* – Automated annotation is the result of running a computational pipeline on a data set. Examples of automated annotation include gene prediction, EST clustering, and ortholog set development. Automated annotation systems are expensive to set up because of the investment in software and algorithmic development required, but once established their maintenance costs are modest. A further characteristic of automated annotation is that these processes do not usually require personnel who have a detailed knowledge of the biology of the organism, because most automated annotation pipelines are species-independent. For example, an EST clustering system set up to work on poplar will also produce satisfactory results for tomato.

*Manual Annotation* – Manual annotation requires the judgment of a human being and is characterized by activities that require the integration of information from multiple data sets and from the scientific literature. Examples of manual annotation activities include gene ontology annotation, the interpretation of targeted gene knockout studies, and the classification of the traits measured in a QTL study. In contrast to automated annotation, manual annotation systems may have low startup costs (they can start with one postdoc's part-time activity and grow from there), but do not decrease in cost during the lifetime of the project.

*Data Providers* – These are the producers of data sets, typically teams of bench biologists, computational biologists, and bioinformaticians. The managers of data repositories, whether of the static or curated types, either create interfaces that allow data providers to submit their data without assistance, or actively seek out the data providers and assist them in making their data available through the repository.

*End-Users* – These are consumers of the data sets, typically bench biologists. Naïve end-users require easy-to-use and intuitive interfaces that nevertheless provide them with access to the full data set. These users are often satisfied with one-object-at-a-time interfaces, such as those provided by almost all biological databases. More sophisticated users require query interfaces that allow them to integrate multiple data sets within the current repository, functionality that a few of the larger databases provide. The most sophisticated users wish to integrate multiple data sets across multiple repositories, a type of functionality that is rare in all but a few restricted cases.

*Evidence and Attribution Tracking* – Evidence tracking links an assertion contained within a repository to the underlying evidence that supports that assertion. For example, an assertion about the genes a transcription factor regulates may be supported by a paper that describes a knockdown of the transcription factor. Curated repositories need to scrupulously document the chain of evidence in order to prevent unsubstantiated facts from "magically" appearing in the database. Attribution tracking links a data set and annotations on the data set to the individual or group that produced it. In actively curated data sets, there is always a risk of losing attribution information. Because the data has been heavily worked over, end users lose track of where the data originated. This is not ideal, as it discourages data providers from submitting their sets, while simultaneously encouraging end users to treat the information as if it had magically truthful properties. Managers of curated repositories try to avoid this trap by propagating correct attributions and evidence tracking throughout the data.

Attribution tracking links a data set and annotations on the data set to the individual or group that produced that data set. In actively curated data sets, there is always a risk of losing attribution data. Because the data has been heavily worked over, end users lose track of where the data originated. This is not ideal, as it discourages data providers from submitting their sets, while simultaneously encouraging end users to treat the

information as if it had magically truthful properties. Managers of curated repositories try to avoid this trap by propagating correct attributions throughout the data.

*Ontologies* – Ontologies are sets of vocabulary terms whose meanings and relations with other terms are explicitly stated in such a way as to be comprehensible to humans and computer programs. For example, the Gene Ontology describes the function of genes. Ontology-building has emerged as a major activity of curated repositories because by annotating data sets using a shared set of ontologies, repositories can establish connections both within the data sets they curate and across data sets contained within different repositories.

## The Bioinformatics Food Chain

Over time, a food chain of sorts has arisen within bioinformatics (Figure 1). An understanding of how this food chain works can assist in making decisions on how to balance competing demands on resources.

At the bottom of the food chain are LIMS (laboratory information management) systems. These are highly customized laboratory-specific systems responsible for managing the internal processes of a data provider. In the genome sequencing world, a typical LIMS system would manage the robots that set up automated sequencing runs.

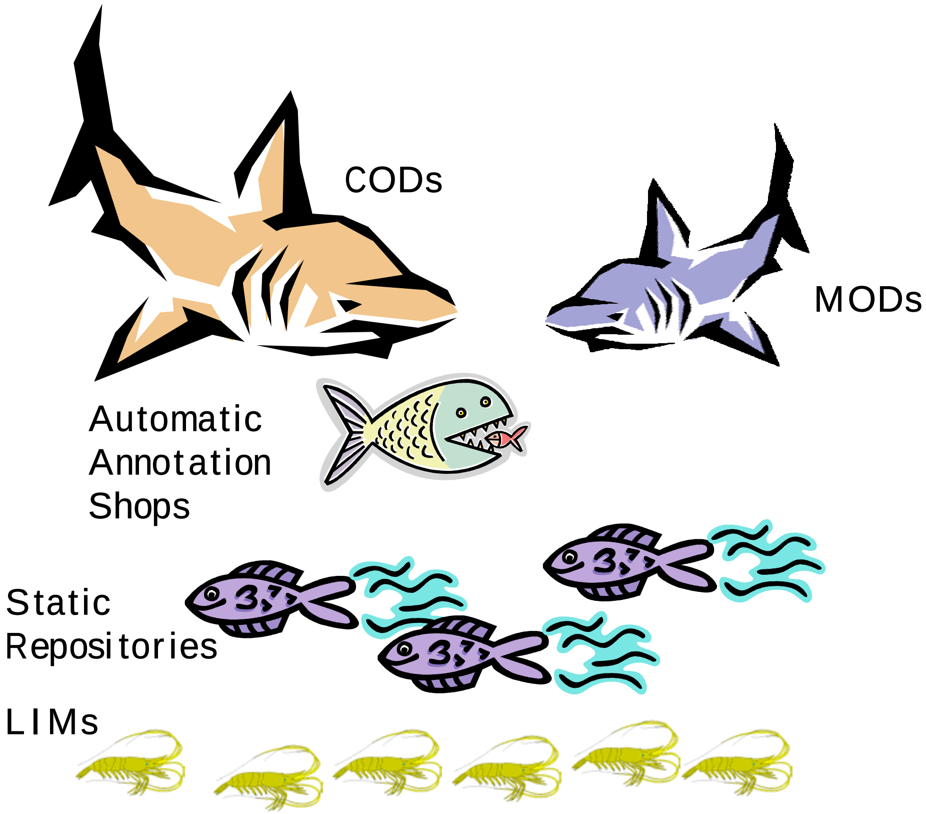

*Figure 1: The Bioinformatics Food Chain*

Next in the food chain are the static data repositories that are responsible for providing long-term storage for the information generated by the data providers. The primary duty of these repositories is to provide a stable, time-stamped and versioned record of the raw data. In genome sequencing, the classic example of this is GenBank (Benson *et al* 2004), which records sequence submissions. Other examples of static repositories include GEO (Barrett *et al* 2005), a repository of microarray expression data, and PDB (Westbrook *et al* 2003), a repository of x-ray crystallographic structures.

Above this level are the automatic annotation shops. These are enterprises that add value to the information contained in static repositories by performing automated annotation across the data set, producing a new set of annotations. Ensembl (Birney *et al.* 2004) is a good example of an automatic annotation shop. Its primary mission is to predict protein-coding genes on genomes using a highly automated and consistent pipeline. PlantGDB (Dong *et al.* 2005) performs consistent automatic EST assembly and annotation across multiple plant species.

The information produced by automatic annotation shops is in turn taken up by model organism databases (MODs). These are community databases focused on a single species or group of related species. MODs take the information provided by automatic annotation shops, enhance it with manual curation, integrate it with information from the literature, and relate it to other data sets and resources. In the plant genomics world, The Arabidopsis Information Resource, TAIR (Rhee *et al.* 2003), is the oldest and best established MOD.

At the top of the food chain is a new breed of databases that we call "clade-oriented databases" or CODs, for a want of a better term. The CODs are multi-species databases, which usually have a clade-specific emphasis. They integrate information from the static data repositories, annotation shops, and MODs into a single integrated database designed expressly for making comparisons among species. The best-known database of this type is the UCSC Genome Browser (Karolchik *et al.* 2003), which contains information on all vertebrate genomes and selected model organism animals such as yeast, fly and worm. The best extant examples in the plant genomics world are Gramene (Ware *et al.* 2002) and LIS (Gonzales *et al.* 2005), which are CODs for monocots and legumes respectively.

It is important to realize that these categories are not mutually exclusive. Many databases combine these categories. For example, NCBI manages GenBank, a static repository of nucleotide sequences, a curation shop, the NCBI human gene build, and EntrezGenes (REF), which is essentially a set of mini-MODs.

## PLANT BIOLOGY DATA SETS AND THEIR REQUIREMENTS

The next sections will describe the types of data sets relevant to plant biology and the long-term data gathering, integration, and analysis activities needed to maintain their value.

### *Genome Sequencing and Mapping*

The process of genome mapping and sequencing generates a large number of reagents and information resources, including:

1. Marker collections – PCR primer pairs, oligos, clone end sequences, and other collections of markers used for identifying genomic positions.

2. Clone libraries – cDNA libraries, BAC, fosmid and other libraries that act as a valuable laboratory reagent long after the mapping and sequencing is over.

3. Physical maps –All cytological and sequence-based maps are in fact physical maps, but most often the label "physical map" is used to describe the information that describes the order and orientation of the members of clone libraries on a given genome. (*Genetic Maps and Variation* discusses Genetic Maps).

4. Raw sequence reads – Sequencing trace files, nucleotide reads, and quality score

files that are the raw evidence for the genomic sequence.

5. Genome assemblies – Long-range genomic sequence assembled from raw reads using sequence assembly algorithms.

Both static and curated repositories are needed to support these activities (Table 1). Static repositories that allow occasional correction of the information are sufficient to manage the marker collections, raw sequence reads, and the information associated with clone libraries, because these data, once generated, do not change frequently. Stock centers can manage the probes needed to detect RFLP-based markers.

However, physical maps and sequence assemblies are dynamic, changing by way of each annotation and refinement update. Physical maps typically require active curation for a period of years after their initial generation, and genome assemblies, at least for eukaryotes, appear to require active curation indefinitely (even the oldest and simplest of the eukaryotic assemblies, that of *S. cerevisiae*, is still being updated). If the clone library is intended to be a long-lasting reagent, a stock center is needed to maintain and distribute it.

The assembly and curation of physical maps requires a group that is skilled in the operation of such software as FPC. Typically physical map assembly is an iterative process that involves experimental validation at the bench, making it useful for physical map assembly and maintenance to be co-located with the laboratory that develops the clone libraries and fingerprints. After a physical map has been published, the tasks of annotating and integrating it with other data can be taken up by the curated repositories, which will increase its usefulness and value to the community.

Genome assembly is a more complex situation. There are typically three phases of the process, a rough "draft" assembly followed by a finishing phase, followed in turn by a maintenance phase. The draft assembly is both computation-intensive and dependent on sophisticated (and somewhat finicky) software, but it requires no laboratory intervention once the first set of reads has been developed. One can envision draft assemblies being performed by a specialist third party group unaffiliated with the sequencing laboratories. The finishing phase, however, involves an iterative process of human and computational inspection of sequence, laboratory experimentation, and refinement of the assembly. Finishing always takes place in the sequencing laboratories.

After the genomic assembly is "finished," it enters an important maintenance phase that has not received much attention. As the assembly is annotated (see next section) and the scientific community uses the assembled sequence in their research, discrepancies and other problems are inevitably discovered. Ideally, these problems should be resolved -- or at least formally noted -- and used to incrementally improve the assembly. This task calls for a curated repository that can act as the focal point for genome annotation, community feedback, and the management of assembly updates and version-controlled releases.

Historically, sequencing centers have not been good fits for genome assembly maintenance and the responsibility for this activity has been taken on by MODs and more recently by CODs (crop monocots in Gramene and Medicago and Lotus in LIS). On occasion, the activity has been mired in disputes over the "ownership" of the sequence, leading to periods in which a genomic sequence has stagnated. The absence of a clearly-defined center that can receive and act on complaints about problems in the assembly leads to frustration among the end-users and loss of confidence in the assembly; this is an outcome to be avoided.

It is important to state clearly that physical mapping and genome sequencing and assembly are mutually dependent activities that are usually independent of the species or clade of the organism being sequenced. Therefore the static and curated repositories that support these activities can easily be managed by centers that operate on multiple species and do not need to bring any species-specific expertise to bear. There are also many existing facilities that can manage this type of data: for example, GenBank is the obvious choice for the static repositories for marker collections, sequence reads, traces and assembly versions.

| *Data Type* | *Static Repository* | *Curated Repository* | *Stock Center* | *Comments* |
|---|---|---|---|---|
| **Marker Collections** | X | X | X | Curation involves assignment of markers to genomes which is part of genome annotation; no species-specific knowledge needed. |
| **Clone Libraries** | X | | X | Use existing repositories for static data |
| **Physical Maps** | X | X | X | Does not require species-specific knowledge |
| **Draft Genome** | X | X | | Static repository needed for reads – use NCBI. Curated repository need for assembly, but no species-specific knowledge (usually) required |
| **Finished Genome** | | X | | Manage community input; species-specific knowledge helpful but not required |

*Table 1: Types of Data Repositories Needed for Genome Sequencing & Mapping*

**Summary recommendations** for genome sequencing and mapping projects:

- Molecular markers (genetic and physical) should be submitted to NCBI GenBank.

- Clone libraries should be submitted to stock centers.
- A standard file format should be developed for representing physical maps. Physical maps should be curated at the MOD or COD level.
- Genome assemblies must be curated and maintained after the original sequencing centers have moved on. Sequencing projects must develop a plan for the orderly handing over of the assembly to a repository that can manage updates of the assembly in response to community feedback and/or additional experimental data.

### *Genome Annotation*

After the production of a genome sequence, the next task is to add meaning to it via a process of annotation. Genome annotation spans the gamut from identifying the location of previously-identified cDNA sequences in the genome, to characterizing the interactions among different gene family members, and involves making inferences at the nucleotide, protein, and biological process levels (Stein 2001). The first steps of genome annotation are typically to identify repetitive elements, and to align ESTs, cDNAs, protein sequences and molecular markers (such as STSs) to the genome. The next step is to create a set of gene predictions, both for protein-coding and non-coding (e.g. miRNA) genes. This is followed by an involved process of annotating the genes and their products; typical steps involve identifying recognizable protein domains in the products of protein-coding genes, describing the function of gene products using the Gene Ontology and other controlled vocabularies, and integrating these annotations with information on gene product expression patterns and molecular interactions garnered from other high-throughput experimental data sets.

Much more so than mapping and sequencing, genome annotation is a dynamic ongoing process. This is so because the annotation of an organism's genome blends imperceptibly into the understanding of the organism's biology. An understanding of the genome's "parts list" leads to new discoveries at the bench. Techniques developed during the pursuit of hypothesis-driven research leads to new data sets that enhance the quality of genome annotation.

Genome annotation may be approached using fully automated methods, or a combination of automated annotation followed by manual curation. Automated genome annotation is essential both for the initial annotation of a newly sequenced genome and for keeping the annotation up to date. Following the automated steps, the annotation may be enhanced by manual curation in order to increase its reliability and coverage. Manual curation involves careful examination of the automated annotations by expert curators, who apply their biological knowledge to identifying flaws in gene predictions, Gene Ontology assignments, and other annotations. Manual curation is also necessary to link the annotated genome to the biological literature so as to provide the critical bridge between genomics and hypothesis-driven research.

Although requiring a higher initial investment, manual curation to a high standard will result in a dataset which can more easily be maintained by automated processes requiring only limited subsequent manual intervention. Automated pipelines can incorporate newly deposited sequence information much more easily when the initial gene models are confirmed as correct.

Because manual curation is labor intensive, it will not be economically practical to apply it to all genomes. In such a case it is important to choose a "reference genome" that will act as an exemplar for a clade under study. The reference genome should be heavily hand-curated so that its annotations can later be computationally propagated to genomes of related species. The fully-automatic annotation of a genome that has not had the benefit of a hand-annotated close relative is likely to be inferior to one that does.

Regardless of whether it was produced by a fully-automated effort or a combination of automatic and manual curation, the single most important output of an annotation effort is a canonical list of genes and their genomic structure and function. The gene list serves as a reference for the entire research community and is an absolute prerequisite for subsequent studies that attempt to leverage the genome sequence. To be most useful there must be a community consensus on the nature and ownership of the gene list, and there should be a process by which updates to the gene list are tracked so that researchers can recover the name and exact structure of a gene at the time a particular experiment was performed.

Significant long term efforts and costs are required to maintain an annotated genome sequence as a useful resource (Table 2). The maintenance tasks include 1) continuous refinement of gene structures and addition of splice variants using new data (for example new cDNAs or ESTs, genome sequences of related organisms) and improved gene prediction algorithms; 2) updates to gene function annotation (including gene product information and GO function, process and cellular component annotations using both computational and manual literature-based methods); 3) annotation of other objects that can be anchored on the genome, for example cDNA clones, transposons and repeats, mutations including insertional knockouts, and SNPs and other markers that serve as research tools for the utilization of the genome sequence.

| *Data Type* | *Static Repository* | *Curated Repository* | *Stock Center* | *Comments* |
|---|---|---|---|---|
| **Canonical Gene List** | | X | | Requires cooperation of both automatic and manual curation groups. Species-specific knowledge required for manual curation, but |

| *Data Type* | *Static Repository* | *Curated Repository* | *Stock Center* | *Comments* |
|---|---|---|---|---|
| | | | | not for automatic gene builds. |
| **Aligned reagents** | X | X | X | Requires extensive cooperation among static repositories, stock centers and curated repositories. |
| **Protein domains** | | X | | Does not require species-specific knowledge |
| **Gene function (e.g. GO)** | | X | | Automated assignment followed by manual curation. |

*Table 2: Types of Data Repositories Needed for Genome Annotation*

**Automatic annotation shops.** In plants, where comparative genomics seems likely to play an even more important role than in vertebrate genomics, uniform high-quality automatic annotation is vital both within and among plant genomes. A lack of uniformity has the potential to cripple efforts to achieve high quality genome annotation. However, automatic annotation of plant genomes has, to date, been *ad hoc.* The primary annotation of the Arabidopsis genome was performed by the sequencing group consortium, resulting in a genome in which different chromosomes were initially annotated to different standards (The Arabidopsis Genome Initiative 2000); this has since been remediated by manual curation. The *Oryza sativa* and *indica* genomes were also annotated in a piecemeal fashion, and the confusion is now being exacerbated by redundant, but perhaps unavoidable, genome annotation efforts that have given birth to multiple conflicting gene sets and assemblies. Although there are several sophisticated efforts in this direction, including the International Medicago Genome Annotation Group (IMGAG, www.medicago.org), PlantGDB, and the TIGR genome annotation group (www.tigr.org) it is fair to say that there has yet to emerge a specialist genome annotation shop on par with Ensembl that is widely trusted by the research community to produce a high quality, uniform automatic annotation. We feel there is a strong need for such a facility.

Another vital function of automatic annotation shops is the alignment of sequence-based reagents to the genome. These reagents include MPSS and SAGE tags, EST sequences, BAC end sequences, the oligonucleotides and cDNAs used in microarrays, the flanking sequences of SNPs, and genetic markers. Because of the dynamic nature of both the assembly and the gene annotations, these alignments must be performed on an ongoing basis, and changes in the alignments, such as the movement of an EST from one chromosome to another, must be versioned and tracked. The reason that active curation of alignments is so important is because biological inferences from sequence-based reagents are dependent on the correct relationship between reagent and the genome annotation. For example, if an Affymetrix array is built on top of one version of an annotated genome and then the genome assembly and its annotations are updated in light of new knowledge, the oligonucleotides chosen for the array may no longer correspond to the genes they were chosen to represent; it is critical for researchers to know how the oligonucleotides on the array relate to the current best gene annotations.

A large number of software tools for automated genome annotation have been developed (Table 3). In principle the automated tools allow any research group with access to a compute cluster to become an annotation shop. In practice, the tools need to be extensively tweaked to accommodate the idiosyncrasies of each genome, and this, in turn, requires a good understanding of the organism's biology. In addition, a considerable amount of computer science sophistication is required to construct and manage an automatic annotation pipeline. For this reason, there are currently only a handful of groups with the capability to perform consistent automated genome-wide annotation.

| *Annotation Type* | *Description* | *Representative Tools* |
|---|---|---|
| **Sequence cleansing** | The ability to remove superfluous sequences, i.e., vector removal, quality trimming, and poly A/T trimming | |
| **Repeat finding** | The ability to identify transposons, microsatellites, and other repetitive elements | RepeatMasker, TIGR's Plant Repeat Databases |
| **Sequence similarity searching** | The ability to compare sequences against known proteins and transcripts | BLAST, BLAT |
| **Protein domain identification** | The ability to identify protein families, domains and other functional sites | InterPro, BLOCKS, eMOTIFS |
| **Signal peptide cleavage sites** | The ability to identify signal peptide cleavage sites. | SignalP |
| **Transcription factor identification** | The ability to identify transcription factors and their binding sites | TRANSFAC |
| **Non-coding RNA gene identification** | The ability to identify non-coding RNA genes. | RFAM |
| **Gene prediction** | The ability to predict the presence and structure of a gene from the genomic nucleotide sequence. | GenScan Fgenesh |
| **GO mapping** | The ability to associate a sequence with Gene Ontology terms based on protein domain content and other characteristics. | Interpro2GO |
| **Miscellaneous sequence to genome mapping** | The ability to map other useful sequence-based features to the genome (e.g. cDNAs, ESTs, microarray elements, insertion flanks, SNPs, TILLing mutations) | |
| **Transcript mapping** | The ability to annotate new genes and update existing gene models based on transcript data | GeneWise, Exonerate, PASA |
| **Manual curation of gene structures** | The ability to manually adjust the structure of gene models (e.g. add new exons or splice variants) | Artemis, Apollo |

| *Annotation Type* | *Description* | *Representative Tools* |
|---|---|---|
| **Literature-based annotation of gene function** | The ability to assign functional annotations go genes from literature sources, using free text and/or ontologies. | PubSearch, Textpresso, Manatee |
| **Manage community curation** | The ability to accept corrections and new information from community submissions. | AtGDB, HAVANA |

*Table 3: Software tools for genome annotation*

Some effort has also gone into developing software frameworks for automated sequence annotation (Hoon *et al.* 2003; Potter *et al.* 2004). These frameworks use a machine-readable protocol to drive pipelines of the various sequence annotation tools. Although the frameworks show promise for facilitating the setting up of an annotation shop, they have a long way to go before they are ready to be used outside their group of origin.

**Manual curation.** As in the animal genomics world, responsibility for maintaining and enhancing plant genome annotations by manual curation has become the domain of several plant community MODs, including TAIR and TIGR (Lee *et al.* 2005). Because manual curation is strongly tied to the biological literature, to research community needs, and to the various experimental resources for the organism (knockout collections, genetic maps), it seems likely that additional community databases will be needed to come online as new genomes are completed.

As with automatic annotation, a variety of software systems have been developed to assist with manual curation (Table 3).

**Community Curation.** Community curation of the canonical gene set will be needed to maintain high quality genome annotation in the long term without excessive funding requirements, but community participation is currently quite low. There are technical and social reasons for this lack of participation. The primary technical reason for this is that tools to facilitate community participation are expensive to develop because they need to be robust, easy to use, and provide mechanisms for quality control. In addition they must be sufficiently adaptable to incorporate new kinds of data. The primary social reason for this is that there is little or no reward for curated contributions to community information resources. Furthermore, the tools to incorporate community annotation are currently much more restricted than other areas of genome annotation and with doubts regarding the level of enthusiasm on the part of the communtiy, creating further resources may prove difficult. Additionally while there is a high cost in developing such tools there is also a substantial cost in regard to the manual curation which will likely be required to verify community curation.

At the very least, however, all annotated genomes should have a community feedback mechanism so that those individuals who find errors and other problems in the canonical gene set can report them and be assured that their reports will be acted on.

**Static and curated repositories for genome annotation.** The primary repository for the static storage of genome annotation is the genome division of NCBI, also known as GenomeDB (www.ncbi.nlm.nih.gov/Genomes/). This division holds the original automatic annotations from sequencing groups. In some cases, plant MODs have reached agreement with NCBI to transmit the results of their manual curation to GenomeDB, enabling this repository to display up to date information as well. In other cases, the MODs remain the sole curated repository for genome annotation data.

GenomeDB, the MODs and CODs generally provide reliable access to the data and utilize best software engineering practices of versioning and keep information on history and evidence tracking. The main downside of having MODs be the sole repository of current genome annotation information is that this interferes with the ability of users to make comparisons among the genomes, due to historical differences in user interfaces and data representation. The Generic Model Organism Database (GMOD) project (Stein *et al. 2002*) is attempting to remediate this issue by establishing standards for representation of genomic annotation data (see for example, the Sequence Ontology (Eilbeck *et al.* 2005)), but the proposed standards have yet to be widely implemented and have yet to have a measurable impact on the research community.

**User interfaces.** GenomeDB provides a "one size fits all" user interface that provides basic genome visualization, browsing and querying.

The community databases provide user interfaces to genomic data based on community specifications. These include tools for graphical visualization of sequence data in relation to a genome map, query tools based on community needs, presentation of query results in the context of the biology for the species of interest, and customized bulk data access methods. As noted earlier, the use of highly customized user interfaces is a double-edged sword. While it enhances the user experience for members of a specific research community, it inhibits comparisons among species. For this reason the GMOD project has developed standardized user interface tools for viewing genome and for querying and downloading bulk data sets (Durinck *et al.* 2005). New community databases should be encouraged to adapt existing tools rather than inventing new ones.

**Funding**. Funding for the community databases is generally based on funding cycles of 3-5 years in length, while support for GenomeDB is tied to NCBI's more stable long-term funding. While plant biologists recognize the need for curation to keep information current, no stable long-term mechanisms for supporting such curation have been developed. In addition, effective management of the dependencies that exist between information resources is extremely difficult, given the lack of standards for versioning and update/release notification mechanisms. Finally, each data resource is typically provided with its own custom access and interface mechanisms, forcing users to learn a special form of interaction with each provider of data.

In summary, the most pressing needs for plant genome annotation are 1) one or more dedicated annotation shops that can create a set of automatic gene predictions from a virgin genome assembly using a well-understood, reproducible annotation pipeline; 2) a policy for assigning responsibility for the canonical gene list to a group charged with the long-term maintenance and curation of the list; 3) a mechanism for involving the research community in the upkeep of the genome annotation; and 4) a well-supported "portal" for access to aggregated plant genomic data.

**Summary recommendations** for genome annotation:

- Sequencing projects must develop a plan for developing a public, canonical set of gene predictions over a set period of time using generally accepted best practices for gene prediction. The plan should include a mechanism for accepting and responding to community feedback on incorrect or missing gene models.
- Use of standardized genome annotation pipelines should be encouraged. This will simplify the task of cross-species comparison, and reduce redundant effort.
- Encourage partnerships between manual curation groups and genome annotation shops.

### *Comparative Genomics*

Annotation and analysis of genomes are increasingly informed by comparisons among sequences from closely and distantly related organisms. The importance of these comparisons to plant biology will increase dramatically in the coming years as the number of available genomes grows. The identification and characterization of homologous sequences -- that is, sequences that are related by descent from a common ancestor -- is an essential step in the interpretation of genomes, since the evolutionary relatedness of these sequences across different genomes provides clues to conservation of gene and protein structure and function. Conversely, the sequence-level divergences that are overlaid upon this coarse conservation may be implicated in the diversification of gene function and the emergence of novel traits. Comparative analysis of the genomes provides the much-needed link between functional studies often pursued in model systems and the genetic mapping of traits (e.g. QTLs) that is widespread in crop species.

The dynamic nature of plant genomes makes this characterization particularly challenging, as modern genes or sequence elements may be related to each other through a series of local and/or genome-scale duplication events along one or both lineages. For example, it is not unusual for a single gene in the common angiosperm ancestor to have given rise to multiple surviving genes in modern plants through a series of shared and/or lineage-specific gene duplications. At the largest scales, networks of tens, hundreds, or even thousands of genes may be conserved across tens of megabases of genomic territory, resulting in long “syntenic” (literally, “same strand”) regions within and between genomes. At shorter scales, tandem duplication, divergence, transposition, and loss of individual genes and their associated regulatory sequences are important processes that need to be disentangled.

Ancient polyploidy and diploidization events are an essential part of plant history, including at least two in eurosid lineage leading to *Arabidopsis*, and one in the grass lineage leading to *Oryza*, with additional more recent polyploidizations known in maize, soybean, alfalfa, sugarcane, and other plant species. These superimposed duplications lead to complex hypotheses in which the function of the gene in the angiosperm ancestor may be partitioned, amplified, or otherwise distributed across multiple modern genes, in a potentially genome-specific manner. The analysis of ancient polyploidy is further complicated by the rampant loss of duplicated genes that follows these events, which makes them challenging to identify at the single gene level. Since polyploidy is not common in animals, computational advances in this area are likely to be driven by plant bioinformatics.

Commonly used "best hit" analyses are especially prone to error in the face of the dynamism of plant genomes. If used without the proper caution, such approaches to "functionally" annotate new gene sequences has the potential to contaminate plant sequence databases with faulty nomenclature that will become increasingly unreliable without a combination of new computational methods combined with machine-assisted manual curation of reference genomes distributed across plant phylogeny.

| *Data Type* | *Static Repository* | *Curated Repository* | *Stock Center* | *Comments* |
|---|---|---|---|---|
| **Genome to genome alignment** | | X | | Primarily automatic annotation. |
| **Gene families** | | X | | Automatic annotation supplemented by manual curation. Extensive knowledge of gene family properties required. Probably well-suited for community curation. |
| **Conserved functional elements** | | X | | Active research needed. Requires collaboration among computational groups, curatorial groups and experimental groups. |

*Table 4: Types of Data Repositories Needed for Comparative Genomics*

Active curation is needed to manage comparative genomics data (Table 4). Specific needs for comparative plant genomics are methods and tools for:

1. *Characterizing syntenic relationships among plant genomes.* This activity uses protein- and nucleotide-sequence similarity measures, supplemented by mapping data to relate the genomes of multiple species via their syntenic relationships. End-users should be able to navigate across the resulting web of synteny to understand the phylogenetic history of their segment of interest. This activity is a task for curated repositories and involves a combination of automated and manual annotation.

2. *Gene family characterization.* At the whole-gene level, characterize the pattern of duplication, divergence, and loss in each gene lineage in the context of these large-scale genomic events and local tandem events to lead to a complete understanding of the diversification of modern gene families is the long term goal. These phylogenetic efforts must be accompanied by visualization and query tools as well as easy-to-interpret confidence measures that make these, often arcane, studies accessible to the general user. This is largely an automated annotation task to be performed by curated repositories.

4. *Gene structure evolution.* At the sub-gene level, characterize the conservation of gene structure and probe the evolution of alternative splicing patterns, in order to understand possibilities for functional divergence. This annotation activity can probably be automated, but will require extensive research before it is a reality. As the experimental characterization of splice variants is unlikely to keep pace with the increase in raw genomic sequence, we will need computational methods to predict alternative splicing and to represent when and where these variants occur.

5. *Improved detection of non-coding sequences through comparative analysis of genomes.* This includes comparisons within and between genomes. We anticipate that these putative cis-regulatory sequences will be characterized systematically both empirically and computationally, through the integration of datasets from a wide array of experiments built upon genomic data, including expression microarrays, chromatin immunoprecipitation assays, proteomic studies, etc. This is also an automated annotation activity to be carried out by curated repositories, but like (4) it requires extensive research into new experimental methods. Also be aware that this is a type of genome annotation that dovetails with the requirements described in the corresponding section.

6. *User interface.* For this complex type of data to be manageable by end users, curated repositories must set up user interfaces that allow users to navigate the

> web of experimentally determined functional data across multiple plant species, with easy access to the source of evidence for functional annotations. In this manner, the true power of comparative genomics can be brought to bear by linking the relatively small number of functional studies to exponentially growing number of sequence resources. The GMOD project provides some portable tools for displaying synteny data (Pan *et al.* 2005; Ware *et al.* 2002) but more development work is needed to capture the full complexity of macro and micro-synteny across phylogenetic trees.

As noted earlier, comparative genomics standards and algorithms are still very much an active research topic. For this reason it is highly appropriate for research activities to be combined with active curation.

We see the plant community as requiring the following services: 1) one or more automatic annotation shops that provide the computes necessary to generate baseline genome to genome alignments and gene family identifications; 2) curated repositories that will take the resources produced by (1) and provide hand-curated management of synteny blocks, protein families, and conserved functional elements; 3) standardized user interfaces for displaying and manipulating this type of data.

**Summary recommendations** for comparative genomics projects:

- Encourage the use of standardized pipelines and/or annotation shops for performing genome to genome alignments.

- Encourage the development of standardized machine-readable representations of genome to genome alignments and synteny relationships.

*Genetic Mapping and Diversity*

Genetic maps of plants are of importance both as a key tool for unraveling the biology of the organism and as a resource for selective breeding and improvement of agronomically important species. Natural and induced genetic variability can be detected using both phenotypic (visible) traits and a wide range of molecular technologies. Detectable genetic polymorphisms include various forms of polyploidy, chromosomal rearrangements, gene rearrangements, insertions, deletions, microsatellite repeats, RFLPs, PCR-AFLPs, SNPs, MNPs and haplotype blocks. While genetic variants are often characterized in terms of the detection technology, the utility of information from genetic variants depends on context: genomic location, population attributes and phenotypic effects.

Because the reproductive biology of most plant species supports inbreeding, it is possible to maximize linkage disequilibrium across the genome for the inbred. Thus it is straightforward to generate large segregating families from a bi-parental cross of two inbred lines, thereby generating genetic linkage maps for most plant species of interest to plant biologists. These same genetic variants in segregating families are also the basis for identification of large genomic regions that are likely to be in linkage disequilibrium with genes that influence complex and quantitative traits.

The utility of genetic variants from a population genetics perspective, i.e., estimating allelic frequencies, finding regions under selection, constructing haplotypes and associating allelic effects with phenotypes, is determined in the context of the breeding population. In the extreme case of a population consisting of progeny from an inbred line all genetic markers are in complete linkage disequilibrium. This is the basis for associating specific lines or accessions with genomic haplotypes or fingerprints. Actual breeding populations consist of many individual accessions and determining how to sample the breadth of breeding populations and evaluate sub-structure within a species is an active area of research. Thus, estimating allelic frequencies, haplotype blocks and genetic effects of an allele all depend upon the definition of the breeding population.

| *Data Type* | *Static Repository* | *Curated Repository* | *Stock Center* | *Comments* |
|---|---|---|---|---|
| **Marker Collections** | X | X | X | Static repositories would be sufficient if standards for reporting polymorphic markers existed and were enforced. |
| **Linkage Maps** |  | X | X | Extensive manual curation currently required. Stock centers needed to capture germplasm of breeding populations and/or parental lines. |
| **Quantitative Trait Loci** |  | X | X | Extensive manual curation required. Controlled vocabularies to describe traits highly recommended. Stock centers needed to capture germplasm of breeding populations and/or parental lines. |
| **Diversity Data** |  | X | X | Extensive manual curation required. Stock centers needed to capture strains used in study. |

*Table 5: Types of Data Repositories Needed for Genetic Mapping & Diversity*

The long-term storage of genetic mapping and variation data is the domain of actively curated repositories such as MODs, CODs and stock centers (Table 5). This is largely due to the complexity of the data types that need to be described, such as breeding populations and phenotypes. However, another important impediment to automated storage is the absence of standards for describing genetic maps and their components.

Even the identifiers used for polymorphic molecular markers are not standardized, and researchers routinely change marker names when using markers described by other groups in their own studies. As a result, in order to make a genetic study comparable to other studies, curators must expend great effort in order to understand the idiosyncrasies of a genetic mapping study, to normalize marker names and pedigree information, and to describe the phenotype under study. Even with extensive curation, it is often impossible to associate a genetic mapping study with identifiable germplasm accessions, due to the lack of standards for identifying the breeding population upon which the study was based.

**The types of data** produced by genetic mapping and population genetics studies are as follows:

1. *Polymorphic markers.* These are naturally or induced polymorphisms that can be assayed by PCR or other detection techniques. Polymorphisms are the basic components of genetic linkage maps, phenotypic association studies and population-based surveys for natural selection. NCBI dbSNP (Wheeler *et al.* 2005) is a long term storage repository for polymorphic markers, but because it relies on voluntary submissions, and is not actively curated, its contents are heavily skewed towards large-scale dbSNP discovery efforts in human and model vertebrates. It has not been heavily utilized by the plant genetics community, and as a result it contains only a handful of Arabidopsis genetic variants and no genetic variants from other plant species. Instead, plant polymorphic marker information can be found in one or more of the MODs and CODs. In Arabidopsis, TAIR has curated a large number of SNPs as well as descriptions of most types of naturally occurring polymorphisms. Similarly, maize, soybean, rice, and wheat polymorphisms can be found in the curated databases MaizeGDB, Soybase (REF), LIS, Gramene and GrainGenes (REF).

2. *Linkage Maps.* These are ordered sets of polymorphic markers whose relative position and distance are determined by examining crossover frequencies during meitotic recombination in breeding populations. All of the active community databases provide access to this type of map through a process of active curation.

3. *Quantitative Trait Loci (QTLs).* These are maps of the association between a complex trait, such as plant height, against the alleles of a set of polymorphisms that have previously been assigned to a linkage map. QTL maps are the basis for scientific breeding programs as well as a key ingredient in positional gene cloning. Because of the difficulties inherent in describing phenotypes systematically, QTLs require heavy active curation and are handled by several of the extant plant MODs and CODs.

4. *Diversity data.* These are data sets gathered from plants "in the wild" and are key to reconstructing the historical processes of natural variation and selection on plant populations. For example, by comparing the frequencies of alleles in modern maize races to the frequencies in the wild ancestor of maize, teosinte, researchers have identified genetic variants that were selected for during domestication and improvement (Wright *et al.* 2005). Population diversity data is currently captured only by a very few extant plant databases, such as the Panzea database of maize diversity (www.panzea.org).

5. *Genetic mapping reagents.* In addition to generating information, genetic mapping and variation studies generate such physical reagents as PCR primers for detecting SNPs, genotyping arrays, hybridization probes for RFLPs and AFLPs, and recombinant inbred breeding populations. In order to be preserved for future use, these reagents need to be maintained and distributed by stock centers.

**Limitations of existing resources.** To date, genetic mapping and diversity data, as well as the physical reagents associated with them, have been gathered in a haphazard way. The maize and Arabidopsis genomics community databases do provide access to information on genetic mutants and stocks, but other plant genetics research communities have much more dispersed resources. The unpredictable nature of funding for curated plant databases has been to some extent responsible for this state of affairs.

As noted earlier, a critical issue is the lack of a reliable connection between molecular polymorphisms, genetic mapping studies, and germplasm resources. While all plant MODs and CODs provide information on molecular polymorphisms, they often lack links to the germplasm accessions on which the polymorphisms were characterized. Similarly, the germplasm collections at international stock centers typically provide little if any information on the molecular characterization of their stocks.

Another issue has been the lack of a standardized format for representing even simple genetic data types such as genetic linkage maps. The Polymorphism Markup Language (PML) has been proposed as a standard reporting format for this purpose (Sugawara, Mizushima et al. 2005).

In order to improve the capture and maintenance of this important type of data, we recommend 1) that researchers who develop molecular polymorphic markers be required to submit the information on these assays to dbSNP or another long term repository; 2) that the plant research community move quickly to adopt PML and other emerging standards for representing genetic mapping and variation data; and 3) that stock centers and MODs receive the support necessary to coordinate capture and curation of breeding population germplasm information.

**Summary recommendations for genetic mapping & diversity projects:**

- Genetic markers and maps should be submitted to long-term (static or curated) repositories using publicly-recognizable names. Genetic markers based on molecular sequences should use recognizable sequence IDs. Genetic maps are probably best handled by curated repositories (MODs or CODs).

- Encourage the development and use of standardized machine-readable representations for genetic maps, diversity data, association and QTL studies.

- When feasible, important germplasm (such as seed stock for parental lines used in mapping crosses) should be submitted to stock centers prior to publication.

### *Pathways*

Biological pathways connect the genes, proteins and chemical compounds of an organism into network of knowledge that represents a first step in understanding biology on a systems level. This knowledge can be used as a basis to model a system and to drive hypothesis driven research. Although almost any biological process can be thought of in the form of a pathway, biological pathways are usually considered to represent biochemical pathways or regulatory pathways. In the case of biochemical pathways, the proteins have enzymatic properties and usually operate on low molecular weight substrates and sometimes also bio-polymers derived from them. Regulatory pathways often involve protein-protein interactions, or covalent modifications of protein substrates, such as phosphorylation, methylation, acylation, etc., that change the activities of enzymes in regulatory or signal cascades. Obviously, biochemical and regulatory networks represent an important aspect of cell function, and their elucidation, description, and understanding provides insights into the nature of diseases and nutrition, and provides opportunities for the improvement of agriculture, biotechnology, and human well-being. In addition, the pathway data intersects naturally with large-scale genome analyses, such as genomics, proteomics, and metabolomics. Indeed, the community is turning increasingly towards network analysis tools to understand these heavily-funded data sets.

Pathway data are complex: pathways are networks of different data-types, can span different subcellular compartments which often involve transport reactions, enzymes consist of protein complexes, and reactions can require multiple co-factors, depend on substrate and enzyme concentrations, have complex enzymatic properties, and be affected by feedback and other types of inhibition. An adequate description of pathways is therefore a daunting task. Representing such knowledge is one of the primary functions of biological databases, and the curation of the metabolism of a species is best done at the MOD or COD level. However, because pathways are frequently conserved across wide evolutionary distances, several large projects take advantage of this conservation to create databases of biological pathways across multiple species. In Japan, the KEGG project at the University of Kyoto (Kaneshisa *et al.* 2000), provides a comprehensive website with overview diagrams of about 200 biochemical pathways, along with a number of analysis tools. In Russia, the EMP Project (www.empproject.com) has created a large curated database of pathways based on the comprising several thousand journal articles. In the US, reactome.org (www.reactome.org/), focuses on human and animal pathways and currently contains 659 pathways. Another large US effort, the Metacyc project (www.metacyc.org/), collects pathway information from the scientific literature. Currently, MetaCyc contains pathways from more than 240 species (including many bacterial species, but with a particular focus also on plants), comprising more than 500 pathways with 8000 metabolites. MetaCyc uses a model that should be particularly appealing to MODs: Species specific databases can be generated quickly using the MetaCyc collection of pathways and Pathologic, a program that pulls the appropriate pathways out of the MetaCyc databases. New pathways can then be added to the species specific database, which can be fed back to MetaCyc, where they are available for future predictions.

The discrepancy between the number of compounds and pathways found in nature and the number found in databases is considerable. This is particulary a concern for plants, for which hundreds of thousands of compounds have been described in the literature, mostly in secondary metabolism, yet the databases contain at most a few thousand. The need for manual curation of these data into databases cannot be overemphasized. An important consideration is that a large fraction of pathway annotation work has focused on prokaryotes and animal systems. However, many of the secondary metabolite pathways in plants do not occur in animals or bacteria. Therefore, curated plant repositories will need targeted funding to annotate the plant-specific pathways. Ideally, all the annotated pathways would flow into a central database that could be used to derive the pathway complement of a new genome to be annotated. The closest current example of such a database is the previously mentioned MetaCyc database.

In addition to these heavily manually curated, dynamic databases focusing on the pathway themselves, static repositories are needed for other data types, such as storing chemical, chromatographic, mass spec, and other information on small molecules (Table 6). This is particularly important to large-scale methodologies such as metabolomics which generate data for hundreds of compounds. ChEBI (www.ebi.ac.uk/chebi) is a good start at this, but currently has fewer than 6000 curated compounds. Other static collections for enzymatic reactions, such as the Enzyme Commission database, BRENDA and ENZYME, are also important resources.

In contrast to some of the other biological data types discussed in this document, standardized file formats for describing pathways exist and are now widely accepted. The two most important ones are the BioPAX format (www.biopax.org/ ) and the Systems Biology Markup Language format (www.sbml.org). The first is more suitable for describing regulatory networks, while the second is more suitable for describing biochemical reactions.

The availability of pathway data in an electronically accessible and computational format will greatly enhance the efficiency of biological and medical research and represent a first step towards a hypothesis-driven systems biology approach. Although some day it may be possible to predict pathways automatically from high-throughput data sets, pathway annotation is currently a painstaking process of human judgment and curation, and is a vital part of genome annotation.

| *Data Type* | *Static Repository* | *Curated Repository* | *Comments, Examples* |
|---|---|---|---|
| **Small molecules** | X | X | No comprehensive database available |
| **Enzyme nomenclature** |  | X | Enzyme Commission, BRENDA, MetaCyc |
| **Reference Pathway Set** |  | X | MetaCyc (automatic pathways based on curated data sets in reference species) |
| **Species-specific pathways** |  | X | AraCyc |

*Table 6: Types of Data Repositories Needed for Pathway Annotation*

**Summary recommendations** for pathway data:

- Plant pathway databases should be encouraged.
- Whenever feasible, such databases should make use of existing pathway resources, such as MetaCyc.

### *Ontologies & Controlled Vocabularies*

An ontology is a set of vocabulary terms whose meanings and relations with other terms are explicitly stated in such a way as to be comprehensible to humans and computer programs. Ontologies provide a way to unambiguously describe data and, in effect, are vehicles for standardizing data description.

A growing number of shared ontologies are being built and used in biology. Examples include ontologies for describing gene and protein function, cell types, anatomies and developmental stages of organisms, microarray experiments, and metabolic pathways. A list of open source ontologies used in biology can be found on the Open Biological Ontologies website (obo.sourceforge.net/). The Gene Ontology (www.geneontology.org) is a biological ontology that has garnered extensive community acceptance, and is a set of over 16,000 controlled vocabulary terms for the biological domains of ‘molecular function’, ‘subcellular compartment’, and ‘biological process’. Like other biological ontologies, GO is organized as a directed acyclic graph, a type of hierarchical tree that allows a term to exist as a specific concept belonging to more than one general term. Other examples of ontologies currently in development are the Sequence Ontology (SO) project, a collection of all the terms needed to describe genome sequence annotation, and the Plant Ontology (PO) project (www.plantontology.org), a set of terms describing structure and growth stages in flowering plants.

Ontologies are used mainly to annotate data such as sequences, gene expression clusters, experiments, and strains. Data sets that have been described in this systematic way can be efficiently compared, merged, and searched. Most importantly, ontology annotations can be used as the basis for interpreting noisy functional genomics experiments, thereby inferring knowledge. For example, when interpreting a gene expression array, one can ask whether any functions and processes, as represented by ontology terms, are statistically significantly over-represented at one measured time point versus another.

There are two linked tasks in the creation and use of biological ontologies (Table 7). The first task is to create the ontology framework. This is typically performed by a small team of domain experts who meet, develop the basic topology of the ontology (the root terms and the major branches), and then flesh out the term list and definitions with increasingly specific concepts. In latter phases of ontology development, community members are invited to contribute their expertise to specific portions of the ontology. This phase of ontology development may take months to years, after which the ontology enters a slower maintenance phase.

The second task is to put the ontology to work by associating its terms with biological data. This is an ongoing task that is usually performed by curators at MODs and CODs. The exact nature of the work depends on the ontology domain. For example, a phenotype ontology could be used to describe morphological traits of plant mutants and/or naturally occurring variants. The experience of the GO and Plant Ontology groups suggests that it is best to begin the association work while the ontology is still in development, so as to stress-test the ontology while it is still plastic.

A mature suite of software tools for using ontologies is available (www.geneontology.org/GO.tools.shtml), and these are sufficient for the basic tasks of creating ontologies, refining them, performing associations, and searching databases of ontologies and their associations. However, additional tools are needed to perform data integrity checks and to explore complex ontologies. For example, term definitions are currently given in natural language form, which is fine for human comprehension but does not easily allow computers and software to be developed that can help check for ontology integrity and provide more semantically powerful search functions. We also see an opportunity for the creation of an international repository of ontology standards that could oversee the development and maintenance of the ontologies.

| *Data Type* | *Static Repository* | *Curated Repository* | *Stock Center* | *Comments* |
|---|---|---|---|---|
| **Ontologies** |  | X |  | Curation involves development and updating ontologies |
| **Annotations** |  | X |  | Curation involves annotations of data objects using the ontologies |

*Table 7: Types of Data Repositories Needed for Ontology Development*

**Summary recommendations** for ontologies:

- Ontology development should be encouraged. Whenever possible, ontologies should leverage existing database schemas and software tools.

*Phenotypic (Functional) Data*

High-throughput methods for collecting, storing, and analyzing phenotypic data, also known as “functional genomics,” ties the structural information of the genome to the biology of the organism. It comprises a broad and expanding number of techniques that generate data collections that require all the types of data repositories that we have discussed previously:

1. Tissue- and stage-specific EST library analysis.
2. Oligo- and cDNA-based microarray expression studies.
3. SAGE (Series Analysis of Gene Expression) and MPSS (Massively Parallel Signature Sequencing) data.
4. Reporter-gene tissue-specific expression data. A typical example is a gene's promoter coupled to a GFP reporter.
5. High-throughput deletion analysis, including targeted and non-targeted gene knockouts and genome-wide RNAi.
6. Traditional mutation, recombinant inbred and QTL analysis based on morphological and/or quantitative traits.

7. Chromatin immunoprecipitation data, protein interactions information, and even crystallographic structures, which can be used to speculate about the function of a given gene product.

As described in the previous section, ontologies are vital for the interpretation of phenotypic data. For example, RNA-based techniques such as microarrays, SAGE and MPSS, require standard ontologies that describe the tissue, organ, and growth stage from which the RNA was extracted, as well as ontologies that describe the precise environmental and growth conditions of the source organism. For interventions that result in a measurable phenotype, ontologies are needed to describe the portion of the organism affected and the nature of the change. Without shared ontologies, it is impossible to compare the results of functional genomics experiments across multiple experiments or species.

Given the availability of suitable ontologies, much of the curation of EST, SAGE, and MPSS datasets can be generalized to the following tasks:

1. For EST-based data sets, cluster the ESTs. This is a computational task that, though not perfect, is well understood. It is a task that is independent of a given species and which can be performed by a number of extant groups including TIGR and PlantGDB.

2. Integrate the sequence information that underlies the data set (EST sequence, SAGE, or MPSS tag) with the genomic data, when available. This involves identifying the genomic location of the EST read, EST cluster, or sequence tag. This usually a highly-automatable task and can be done by groups that do not have any special species- or clade-specific expertise.

3. Associate the RNA source with the appropriate set of ontology terms. This is a task that requires detailed understanding of the developmental biology of the organism and is best suited to database groups that focus on species- or clade-specific biology. A logical alternative is to have the data providers document the association between an RNA source used in an experiment and a set of ontology terms, but there is so far no precedent for this type of activity.

Microarray data sets require a static repository for the raw microarray results as well as a curated repository for associating the target RNAs with ontology terms that describe the tissue, stage, and environment of the plant from which the RNA was derived. Whereas the static repository can be managed by a species-independent center, such as the NCBI GEO database, the association and annotation of the data set needs to be performed by a group that has extensive knowledge of the specific organism's biology.

Reporter gene data sets require a stock center to maintain and distribute the derived lines, and a curated repository to associate the stage- and tissue-specific expression patterns with ontology terms and to establish the connection between the reporter gene construct and the genome annotation. There may also be images associated with the data set which must be annotated. These tasks require a group with extensive knowledge of the specific organism's biology.

The requirements for the knockout and RNAi-based knockdown resources are similar to those for reporter gene sets. A stock center is needed to manage the knockout strain or the small hairpin library, and a curated repository is needed to associate the resulting phenotypes with the appropriate ontology terms as well as to establish connections to the genome annotation. Like reporter gene sets, this activity requires a group that has extensive knowledge of the specific organism's normal and abnormal biology.

Finally, the management of the traditional types of phenotypic analysis which studies spontaneously-arising variants, mutants derived from a mutagenesis screen, or agronomically important quantitative traits that differ among two strains usually requires the involvement of a stock center to curate the germplasm stocks that arise from the study and a curated repository to manage the information on the experimental design and the results. Good shared ontologies are key to managing this type of data so as to facilitate comparisons among multiple experimental studies. Manual annotation by biologists who have a detailed understanding of the organism's biology is required for anything but the most superficial curation of this type of data.

| *Data Type* | *Static Repository* | *Curated Repository* | *Stock Center* | *Comments* |
|---|---|---|---|---|
| **ESTs** | X | X | X | EST clustering can be performed in a species-independent way |
| **Microarray Expression Studies** | X | X | | Use existing repositories for static data |
| **SAGE, MPSS** | | X | | Genome mapping does not require species-specific knowledge, but ontology association does |
| **Knockouts, knockdowns** | | X | X | Species-specific knowledge required |
| **Reporter Constructs** | | X | X | Species-specific knowledge required |
| **Mutant & QTL Analysis** | | X | X | Species-specific knowledge required |

*Table 8: Types of Data Repositories Needed for Phenotypic Data:*

**Summary recommendations** for phenotypic data:

- Data sets that require species-independent computation or services, such as EST clustering and microarray storage and analysis, should leverage existing resources whenever feasible.

- Phenotypic data repositories should be encouraged to develop shared ontologies to describe assay and phenotype data.

### *Reagents and Stock Centers*

This section deals with the specific need for stock centers to manage and distribute the physical reagents that are created by genome-scale projects. The central task of a stock center is to (1) enable individual researchers who are not directly connected to the projects to locate the reagents generated by large-scale projects; and (2) to acquire those physical entities for use in their own experimental analyses. Although it is simple to state the need, further examination of the topic reveals several thorny issues.

Stock centers must deal with the logistics of receiving reagents, storing them, and distributing them in a timely and cost-effective manner. Given that reagents are often living organisms (seed stock or even growing plants that must be propagated vegetatively) the logistical issues are substantial. Stock centers have the additional challenge of maintaining the integrity of their stock. There needs to be a verifiable link between the reagent that was used in a published experiment and the reagent that the stock center ships out upon request. No system being perfect, there is always the chance of sample mixup or contamination (either within the stock center or before it even receives the reagent), and it is desirable that stock centers have mechanisms in place to identify each sample unambiguously, for example by using molecular polymorphism fingerprints.

Finally, stock centers must establish reciprocal connections with static and curated data repositories so that the experimental data described in the repository has an unambiguous connection to a physical reagent in the stock center. In practice, this means that stock centers must implement a system of stable public IDs that can be shared with the data repositories and updated at regular intervals. A good example of a working relationship between data generators, stock centers and data repositories are the SALK SIGnAL service, the ABRC (www.biosci.ohio-state.edu/ ~plantbio/Facilities/abrc/abrchome.htm), and TAIR, which together give researchers access to a valuable collection of Arabidopsis insertional mutant stocks. Some stock centers have been effective at providing integrated search and query facilities (for example the Nottingham Arabidopsis Stock Center, NASC), but many have not had the resources to develop more than a very simple online catalog of their stocks.

We now consider existing resources for several common types of plant biology reagents.

**Seed Stocks.** Many MODs and project databases offer resources for locating and ordering seed stocks for plants that are genetically modified and/or for natural germplasm accessions. An example can be found at TAIR (www.arabidopsis.org/), which collaborates with ABRC at Ohio State (www.biosci.ohio-state.edu/~plantbio/Facilities/abrc/abrchome.htm) to integrate genome annotation data with biological reagents. MODs often include varying levels of pedigree data, depending on the database and the thoroughness and availability of such information. Other resources providing data on seed stocks include MaizeGDB (www.maizegdb.org/), NASC (arabidopsis.info/), the CerealsDB SNP repository (www.cerealsdb.uk.net/discover.htm), Panzea (a project database for maize diversity data; www.panzea.org/), Gramene (www.gramene.org), IRRI (the International Rice Research Institute; www.irri.org), and GRIN (the Germplasm Resource Information Network; www.ars-grin.gov/npgs/).

GRIN is of particular interest because it houses information describing natural plant genetic resources for over 11,000 species of plants (nearly a half-million accessions) and allows available stocks to be ordered online. However, unlike the other repositories listed here, GRIN does not currently store molecular information with stock data, or provide connections to data repositories that do store such information. This makes it difficult for researchers to identify and acquire useful germplasm via sequence information, and makes it impossible to verify the correct identity of a seed stock.

**Transgenes.** A special case of a seed stock is a transgene, a piece of DNA (generally coding DNA) that has been introduced into cells or organisms to modify the genome. Transgenic plants are created using various methods including promoter-enhancer traps, T-DNA insertional mutagenesis, and EMS mutagenesis. In the case of a transgene, there is always some form of molecular characterization of the line, typically performed by the lab that generated it, and there is often some characterization of the phenotypic consequences of the transgenesis. The key to maintaining the usefulness of the transgene is for the data repository to index the transgene by its molecular signature (e.g. the insertion site of the engineered DNA), its phenotypic effect (typically using a searchable ontology), its stock center ID, and, when appropriate, a reference to the paper in which the transgene was published. The stock center, for its part, should be able to verify that the seed stock it receives carries the correct molecular change and should provide researchers to whom the stock is distributed the information needed to verify the identity of the stock.

**Vectors & Cloned Sequences.** Stock centers can be called upon to store vectors, clones, and whole clone libraries. For example, the Maize Gene Discovery Project (MGDP; PI Virginia Walbot) deposited its clones at stock centers located at Texas A&M and the Arizona Genomics Institute and transmitted the clones' molecular data to the maize data repository at MaizeGDB. Even though the MGDP project is now finished, researchers can still identify clones of interest to them and obtain the reagents. Without this foresightedness, the funding agencies' investment in the project might have been lost.

**Locating Resources.** A recurrent complaint from plant researchers is the difficulty of locating available data and reagents. In part this is because data providers have often established *ad hoc* solutions for archiving reagents and information about them, leading inevitably to a proliferation of distribution sites and online databases. One way to reduce the confusion would be to strongly encourage groups that are developing reagent resources to establish relationships with existing stock centers and data repositories. Some funding mechanism – perhaps subcontracts from the resource generator to the stock center and repository – would need to be found to allow this type of arrangement to scale.

Another way to make the existence of resources more transparent is the establishment of a plant molecular reagent data "portal" in which all resources are organized by species and resource type. This was the model preferred by an NSF discussion in 2000 (panel members included Howard Rines, Jennifer Normanly, David Frisch, Hongbin Zhang, Robin Buell, Jan Dvorak, and Virginia Walbot), in which it was concluded that stock centers and individual labs alone should suffice for making reagents available to researchers. We feel that the best location for such a portal is a MOD or COD, where data integration and organization happens routinely.

**Summary recommendations for stock centers:**

- Stock centers should be encouraged, and provided with sufficient resources, to collect, utilize and publish molecular characterization data on germplasm and other reagents.

### *Data Integration*

Currently, many information resources are encyclopedic. They excel at collecting, curating, indexing, and presenting a broad array of data types, both within and across species. With only a few mouse clicks, scientists can see visual layouts of gene sequences annotated with functional information, 3D protein structures, and a suite of alternative displays and analysis tools. As electronic encyclopedic reference portals, these data collections have helped set standards in electronic data organization and presentation.

Yet the very technologies that allow these collections to excel, such as their heavy reliance on keyword searches, pull-down menus, and the traditional web interface of HTML over HTTP, present substantial obstacles to empowering them as high-throughput research resources. Biology is increasingly becoming a high throughput, information science, and as such, this places demands on the necessity for machines to translate our simple requests into complex queries, execute those queries over distributed resources, filter and collate the returned information, and present the results in an organized manner. This demand is not well served by either the traditional point-and-click web browser interface or an *ad hoc* FTP download of bulk data. To see the severity of this problem, bring up a web browser and try to answer any of the following questions:

1. *Which drought tolerance genes in maize have homologs in Arabidopsis that are significantly up- or down-regulated when experimental plants are exposed to desiccating conditions?*

2. *TAIR returns 21 loci associated with the Gene Ontology term "meiosis." Arabidopsis is likely to have hundreds of genes involved in meiosis. Which ones share motifs suitable for determining ancient gene duplication events that could elucidate the process' evolution?*

3. *What information does PDB have on these genes that would support or refute common ancestry?*

The difference between asking these questions today versus ten years ago is that today much—if not all—of the information needed to make a reasonable advance is already available over the web; it is just not available in a readily-accessible, high throughput manner. In fact, the amount of point-and-click, cut-and-paste effort needed to answer them is so high that it can take a full-time postdoctoral fellow weeks to confidently discover and execute the manual workflow. The challenge for today's data collections is to allow scientists to access and extract the information the resources already have in a high throughput, efficient manner. This requirement is placed upon them because biology is increasingly becoming a high-throughput, information science.

Information must be integrated in order to answer the above questions, and a prerequisite for integration is interoperability. That is, we cannot expect machines to integrate before they can interoperate. Currently, there are neither broadly accepted nor implemented interoperability standards. Both interoperability and integration are hampered by the fact that HTML encoding tends to confound the raw data content with its structure and presentation. Disentangling the data from how it is organized and presented is an important benefit that is likely to arise from well-constructed interoperability standards, and one that will be key to achieving integration.

For us to move data collections from low-throughput, electronic encyclopedias, to high throughput, research resources, we will need to develop interoperability standards in a manner that allows machines to assess suitability-for-purpose on a request-by-request basis. This will require semantically tagging information and making it available for logical discrimination, either via document-based models, such as RDF (Resource Description Framework), OWL (Ontology Web Language), or SWRL (Semantic Web Rule Language); or via procedural access from traditional computer languages. We note approvingly that NSF has recently funded a research project to utilize these technologies in the creation of a Virtual Plant Information Network (BioMOBY 2005).

## CONCLUSIONS AND SPECIFIC RECOMMENDATIONS

Our plant biology database needs assessment has come back time and again to a single overriding conclusion: the research community's need for a system of curated data repositories where information is actively acquired, organized, maintained and distributed. This in turn requires a trained cadre of skilled knowledge workers who are able to curate complex biological data, as well as a system of stable funding that enables such repositories to be established and maintained for extended periods of time. We will discuss global recommendations first and then summarize recommendations reached earlier that are specific for particular types of biological data.

*1) Develop a funding mechanism that would give curated repositories a longer cycle time than currently feasible.*

Most curated databases are now funded as research projects under a process of competitive grant review for cycles of 3-5 years. This is insufficient to establish a stable resource and to create an environment that will be attractive to those biologists who wish to make a professional career of data curation. We recommend that funding agencies develop a mechanism to fund static and curated repositories for renewable periods of 7-10 years. During this time the repositories would be subject to annual review by an advisory board, and would be held to a defined set of milestones and objective measurements of performance. This would allow successful repositories to provide the community with long-term stable maintenance of data, while allowing funding agencies to weed out unsuccessful repositories.

*2) Foster curation as a career path.*

The funding agencies as well as educational institutions should put renewed emphasis on data curation as a respected career path. This will involve addressing issues of curriculum development, mentoring, specialty conferences, and the development of peer reviewed journals that specialize in curation research and methodology. One promising recent development is an embryonic movement to establish a Society of Biocurators (see biocurator.org), which we feel should be encouraged. A possible mechanism for supporting students who wish to explore curation as a career would be to establish a career development award for individuals seeking to enter the discipline.

*3) Balance data generation and information management.*

Because the storage of the data and/or reagents generated by high-throughput studies is so vital to the community, we feel that funding agencies should insist that potential data providers include in their proposals a plan for the long term storage and maintenance of the data set and any reagents, if any, associated with it. A minimum set of standards for the publication of data sets includes using publicly recognizable identifiers for biological data objects, using accepted nomenclature to describe the data set, using standard formats for data files, and linking the IDs of reagents submitted to stock centers to the IDs given in data files. Whenever possible, data providers should make arrangements with existing repositories and stock centers rather than planning to implement an entirely new information resource. If managing a data set will strain the existing resources of data repository and/or stock center, then the data provider should establish the appropriate subcontractual arrangements to close the gap.

*4) Separate the technical infrastructure from the human infrastructure.*

As noted earlier, there are many automated computational tasks that do not require specialized species- or clade-specific knowledge. These tasks include such things as gene prediction, EST assembly, genome alignment and protein family identification. In order to avoid redundant and inconsistent efforts, funding agencies should encourage partnerships between groups that can provide technical infrastructure for automated annotation tasks and groups that are skilled at manual curation. In the animal world, a successful example of this type of partnership is the relationship between Ensembl and MGD (www.informatics.jax.org); the former provides an automated gene prediction set on the mouse genome, while the latter integrates this information with allelic information, phenotypic data, genetic maps, and other heavily curated biological resources.

*5) Standardize data formats and user interfaces*

The lack of standard file formats for genetic maps and several other key biological data types provides friction that increases the cost and decreases the pace of active curation. The lack of standardization of data repository user interfaces leads to frustration on the part of researchers who cannot easily move from one repository to another.

Data providers should be encouraged to use standard file formats whenever available. Data repositories should provide standard user interfaces in addition to any custom ones they wish to develop. When suitable standards do not exist, there should be a push to develop them. We feel that it would be appropriate to establish a working group to develop a “Best Practices” document to describe recommended data formats and user interfaces for common biological data types. This could then be used as one guideline for evaluating data generation and management proposals.

*6) Encourage CODs*

Existing MODs should increasingly exchange data with and create reciprocal linkages to CODs currently in operation. In order to avoid an unsustainable proliferation of species-specific databases, and to encourage the emerging discipline of comparative genomics, we also recommend that existing MODs should be encouraged to take on new species and gradually evolve into CODs.

*7) Encourage the development and deployment of new technologies explicitly aimed at integrating across MODs and CODs.*

Just as MODs and CODs deliver value greater than the sum of their particulate data sets, the integration of data and services across MODs and CODs has enormous potential for achieving high value in comparative bioinformatics. Realizing this value will require work explicitly aimed at solving the distributed data integration equation. We recommend recognizing this is a distinct area of research and effort necessary to achieving a national network of integrated plant biology databases.

*8) Specific recommendations for genome sequencing and mapping projects*

- Molecular markers (genetic and physical) should be submitted to NCBI GenBank.
- Clone libraries should be submitted to stock centers.
- A standard file format should be developed for representing physical maps. Physical maps should be curated at the MOD or COD level.
- Genome assemblies must be curated and maintained after the original sequencing centers have moved on. Sequencing projects must develop a plan for the orderly handing over of the assembly to a repository that can manage updates of the assembly in response to community feedback and/or additional experimental data.

*9) Specific recommendations for genome annotation*

- Sequencing projects must develop a plan for developing a public, canonical set of gene predictions over a set period of time using generally accepted best practices for gene prediction. The plan should include a mechanism for accepting and responding to community feedback on incorrect or missing gene models.
- Use of standardized genome annotation pipelines should be encouraged. This will simplify the task of cross-species comparison, and reduce redundant effort.
- Encourage partnerships between manual curation groups and genome annotation shops.

*10) Specific recommendations for comparative genomics*

- Encourage the use of standardized pipelines and/or annotation shops for performing genome to genome alignments.
- Encourage the development of standardized machine-readable representations of genome to genome alignments and synteny relationships.

*11) Specific recommendations for genetic mapping*

- Genetic markers and maps should be submitted to long-term (static or curated) repositories using publicly-recognizable names. Genetic markers based on molecular sequences should use recognizable sequence IDs. Genetic maps are probably best handled by curated repositories (MODs or CODs).

- Encourage the development and use of standardized machine-readable representations for genetic maps, diversity data, association and QTL studies.

- When feasible, important germplasm (such as seed stock for parental lines used in mapping crosses) should be submitted to stock centers prior to publication.

*12) Specific recommendations for pathway data*

- Plant pathway databases should be encouraged.

- Whenever feasible, such databases should make use of existing pathway resources, such as MetaCyc.

*13) Specific recommendations for ontologies*

- Ontology development should be encouraged. Whenever possible, ontologies should leverage existing database schemas and software tools.

*14) Specific recommendations for phenotypic data*

- Data sets that require species-independent computation or services, such as EST clustering and microarray storage and analysis, should leverage existing resources whenever feasible.

- Phenotypic data repositories should be encouraged to develop shared ontologies to describe assay and phenotype data.

*15) Specific recommendations for stock centers*

- Stock centers should be encouraged, and provided with sufficient resources, to collect, utilize and publish molecular characterization data on germplasm and other reagents.

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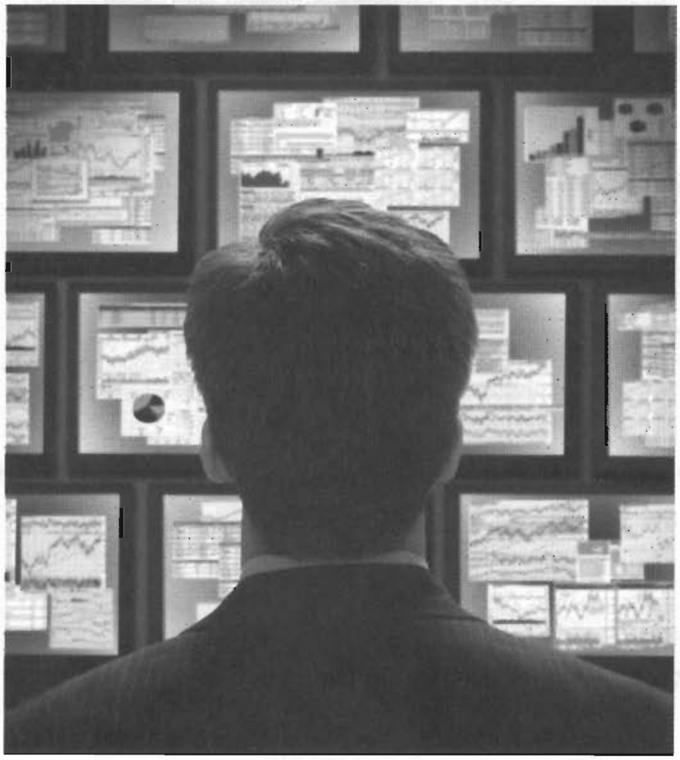
By The Plant Genome Database Working Group

WHITE PAPER

# Save our Data!

## Here's how to prevent critical biological data repositories from disappearing into the ether



The public research sector has invested hundreds of millions of dollars in grants to generate large-scale biological data sets, most notably in the field of genomics. These large data sets include genome sequences, gene expression array results, extensive surveys of sequence variation within populations, and findings from protein-protein interaction studies. Such data sets are housed in many online repositories, ranging in size and scope from small single-organism databases, to large multiorganism databases such as the comprehensive GenBank sequence database.

The problem is that the majority of these databases were established by the initiative of individual researchers, and their longevity is constrained by the continuing enthusiasm of their founders and their prospects for long-term funding. In other cases, online databases were established by individual researchers, who, in the absence of an obvious repository for the data they were generating, released their data through their own Web or FTP sites. When the database's founder moves on to other projects, loses interest, or loses funding, there is a clear and present risk that the database will slowly decay from lack of updating and may eventually break down completely and disappear from the Internet. When that happens, the data will become inaccessible.

In January 2005, representatives of the National Science Foundation's Plant Genome Program and the US Department of Agriculture's Agricultural Research Service asked us to form a working group to examine these issues. Although our primary focus was on the needs of plant biology, our discussion and conclusions apply to the maintenance of other genome-scale data sets, including those of animals, fungi, protists, and prokaryotes.

### Static Versus Curated Repositories

One of the core issues we wrestled with was the respective roles of static versus curated repositories. A static data repository – for example, the GenBank database, which contains chronologically ordered sequence submissions – is a relatively unchanging archive of information. The "business model" of a static repository is that of a self-service storage facility. The owner of the data checks his or her data set in, and only the owner has permission to modify it.

In contrast, a curated data repository can be likened to an art museum. Repository curators actively seek out new data sets to incorporate into the collection, and once a data set has been entered, they are free to reorganize and integrate it with other data sets, to find and annotate inconsistencies, and to add editorial comments. The National Center for Biotechnology Information has a well-known curated repository, EntrezGenes, which is a systematic collection of genes from multiple species that have been annotated by experts from each species' research community. Other curated repositories include model organism databases (MODs) focused on a single species, such as the WormBase database for *Caenorhabditis elegans* (www.wormbase.org), and TAIR, The *Arabidopsis* Information Resource (www.arabidopsis.org).

Researchers often prefer curated repositories, but supporting such a care-intensive facility comes at a cost: Such repositories are built and managed by biological curators, a specialized cadre of PhD-level biologists who combine their scientific expertise with information-management skills. A typical curated repository, with a staff of two curators and a half-time programmer, will cost in excess of $250,000 per year.

### MODs Versus CODs

MODs are typically formed by research communities and often start out as an online directory for shared resources. For example, MaizeGDB began life as an electronic catalog of maize mutants and their genetically mapped locations. As the cost of genome-scale technologies has decreased, research communities have moved from analyzing single species to analyzing entire phylogenetic clades of related organisms. Making comparisons among multiple species is a powerful way both to identify functional elements in the genome and to understand how genes evolved in response to selective constraints.

The need to perform such comparisons has led to the creation of CODs (clade-oriented databases) that contain information on multiple related species and provide researchers with analysis and visualization tools for making comparisons within and among species. The contents of CODs can be manually curated or built automatically with computational pipelines, and most CODs combine elements of both manual and automated annotation. Examples of CODs include the Gramene database of cereal genomes (www.gramene.org) and the Genome Browser of vertebrate genomes (http://genome.ucsc.edu) at the University of California, San Diego.

These fundamental issues and developments were the basis of the group's principal recommendations, highlights of which follow:

1. **Encourage CODs.** Because multispecies databases provide researchers with a level of information that is not available from traditional MODs, the working group recommended that the funding agencies promote the formation of repositories that look beyond a single model species and to encourage both the formation of repositories equipped to store and analyze data from multiple species simultaneously, and the use of technologies that allow the information held in multiple databases to be compared and integrated.

2. **Develop a funding mechanism** that would support biological databases for longer cycle times than under current mechanisms. Presently, most curated databases are funded as research projects for cycles of three to five years under a process of competitive grant review. This is insufficient to establish a stable resource and to create an environment attractive to those biologists who wish to make a professional career of data curation. We encourage the funding agencies to develop a mechanism to fund static and curated repositories for renewable periods of seven to 10 years, subject to annual review by an advisory board and assessed by a set of objective measurements of performance.

3. **Foster curation as a career path.** The specialized cadre of PhD-level biologists who acquire, develop, and maintain integrated data sets is insufficient to meet the current needs. We recommend that the funding agencies as well as educational institutions put renewed emphasis on data curation as a respected career path. This would involve addressing issues related to developing the proper curricula, mentoring scientists, supporting specialty conferences, and developing peer-reviewed journals specializing in curation research and methodology.

4. **Balance data generation and information management.** Because the storage of data and/or reagents generated by high-throughput studies is so vital to the research community, funding agencies should insist that potential data providers include in their proposals a plan for long-term storage and maintenance of the projects' generated data sets and reagents. A minimum set of standards for the publication of data sets includes using publicly recognizable identifiers for biological data objects, using accepted nomenclature to describe the data set, using standard formats for data files, and linking the identifiers of reagents submitted to stock centers to the identifiers used in data files. Whenever possible, data providers should make arrangements to collaborate with existing repositories and stock centers rather than implementing entirely new information resources.

5. **Advance comparative biology.** In order to avoid an unsustainable proliferation of species-specific databases, and to encourage the emerging discipline of comparative genomics, we recommend funding support for mergers and cooperative agreements among existing and proposed databases that allow for comparisons among species and for the integration of multiple types of data.

6. **Separate the technical infrastructure** from the human infrastructure. Many automated computational tasks do not require specialized species- or clade-specific knowledge. These tasks include, for example, gene prediction, EST assembly, genome alignment, and protein family identification. In order to avoid redundant and inconsistent efforts, funding agencies should encourage partnerships between groups that can provide technical infrastructure for automated annotation tasks and groups that are skilled at curation.

7. **Standardize data formats and user interfaces.** The lack of standardization among related data sets causes inability to integrate and analyze data using fixed procedures. Data providers should be encouraged to use standard file formats whenever available. Data repositories should provide standard user interfaces in addition to any custom ones they wish to develop. When suitable standards do not exist, support should be available to develop them.

With a coordinated funding and training plan for database maintenance and curation, the rapidly growing volume of high-throughput genomic and functional information will retain its value to the biological community for many years to come. ■

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For a longer version of the Working Group's recommendations, see www.gramene.org/resources/plant_databases.pdf.

DOI: 10.1534/genetics.105.054155

# Note

## Predicting Chromosomal Locations of Genetically Mapped Loci in Maize Using the Morgan2McClintock Translator

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Manuscript received December 1, 2005
Accepted for publication December 21, 2005

### ABSTRACT

The Morgan2McClintock Translator permits prediction of meiotic pachytene chromosome map positions from recombination-based linkage data using recombination nodule frequency distributions. Its outputs permit estimation of DNA content between mapped loci and help to create an integrated overview of the maize nuclear genome structure.

TWO fundamentally different but colinear types of gene maps can be produced, linkage maps and physical maps. Classical linkage (genetic) maps are based on allele-recombination frequencies, whereas physical maps are based on the linear DNA molecules that compose the chromosomes.

In maize, a model genetic and major agricultural species, >1200 high-resolution linkage maps composed of thousands of markers are available, whereas detailed physical maps of DNA sequence and chromosome structure are still in development. The three main types of maize physical maps differ in the level of molecular resolution. They are (1) genome sequence assembly maps at DNA base-pair resolution (see, *e.g.*, Dong *et al.* 2005; Fu *et al.* 2005); (2) fingerprint-contig maps, resolved at the level of overlapping restriction fragments from cloned segments of genomic DNA (see, *e.g.*, Pampanwar *et al.* 2005); and (3) cytological maps constructed by microscopic observation of pachytene chromosome structure (*e.g.*, the Cytogenetic FISH 9 map created by Koumbaris and Bass 2003 and Amarillo and Bass 2004).

Linkage and physical maps have different coordinate systems for positioning loci. The genetic map unit is called a "centiMorgan" (cM) in honor of Thomas Hunt Morgan. One centimorgan is equal to 1% crossing over between two linked loci. Fingerprint-contig and genomic-assembly maps are measured in base pairs, whereas physical maps based on pachytene chromosome structure (also called cytological or cytogenetic maps) position each locus as the fractional distance along the arm from the centromere to the telomere. Recently, maize researchers have begun to call the unit of this sort of map denomination a "centiMcClintock" (cMC) in honor of maize genetics pioneer Barbara McClintock. Here we formally define 1 cMC as 1% of the length of the chromosome arm upon which a given locus resides. For example, if the short arm of chromosome 9 is 8.70 µm in length and the *bronze1* (*bz1*) locus lies 5.66 µm from the centromere on that chromosome arm, *bz1* lies (5.66/8.70 × 100 =) 65% of the distance from the centromere to the chromosome tip or 65 cMC from the centromere. A locus at position 66 would lie exactly 1 cMC from the *bz1* locus. Because maize chromosome arm lengths vary and the centiMcClintock is a relative unit, 1 cMC on, *e.g.*, the short arm of chromosome 9 does not necessarily consist of the same number of micrometers as 1 cMC on any of the 19 other chromosome arms. The cytological conventions are further described and defined at http://www.maizegdb.org/coordinateDef.php.

Recombination rates vary tremendously along individual chromosomes such that the map distance between two loci on a linkage map may not accurately predict the physical distance between them (Anderson *et al.* 2004). This variation has made integrating the two types of maps difficult and also has important implications for genome-assembly efforts and positional-cloning strategies (Sadder and Weber 2002).

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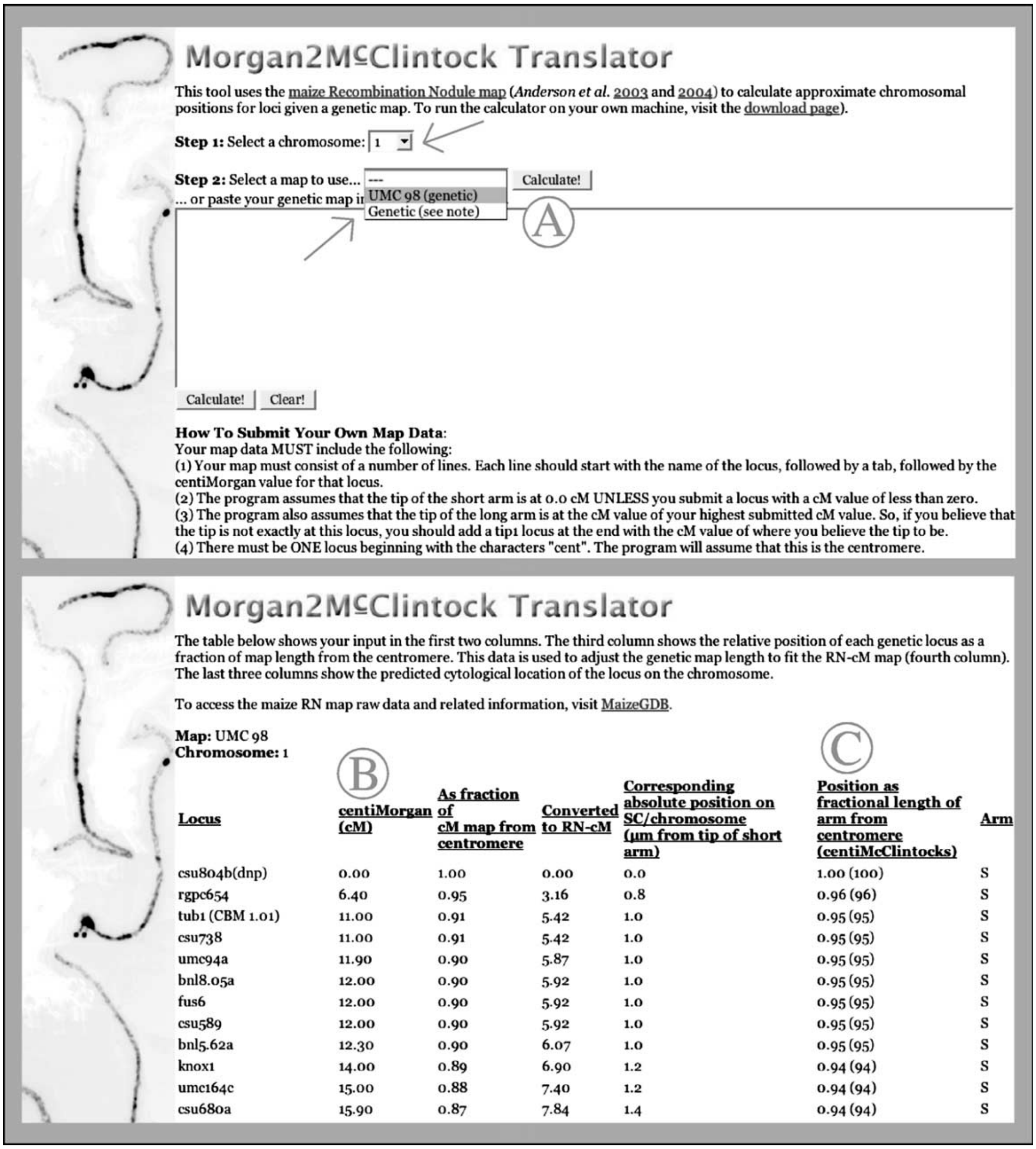

## Morgan2McClintock Translator

This tool uses the maize Recombination Nodule map (*Anderson et al.* 2003 and 2004) to calculate approximate chromosomal positions for loci given a genetic map. To run the calculator on your own machine, visit the download page).

**Step 1:** Select a chromosome: 1

**Step 2:** Select a map to use...
... or paste your genetic map i

**How To Submit Your Own Map Data**:
Your map data MUST include the following:
(1) Your map must consist of a number of lines. Each line should start with the name of the locus, followed by a tab, followed by the centiMorgan value for that locus.
(2) The program assumes that the tip of the short arm is at 0.0 cM UNLESS you submit a locus with a cM value of less than zero.
(3) The program also assumes that the tip of the long arm is at the cM value of your highest submitted cM value. So, if you believe that the tip is not exactly at this locus, you should add a tip1 locus at the end with the cM value of where you believe the tip to be.
(4) There must be ONE locus beginning with the characters "cent". The program will assume that this is the centromere.

## Morgan2McClintock Translator

The table below shows your input in the first two columns. The third column shows the relative position of each genetic locus as a fraction of map length from the centromere. This data is used to adjust the genetic map length to fit the RN-cM map (fourth column). The last three columns show the predicted cytological location of the locus on the chromosome.

To access the maize RN map raw data and related information, visit MaizeGDB.

**Map:** UMC 98
**Chromosome:** 1

| **Locus** | **centiMorgan (cM)** | **As fraction of cM map from centromere** | **Converted to RN-cM** | **Corresponding absolute position on SC/chromosome (μm from tip of short arm)** | **Position as fractional length of arm from centromere (centiMcClintocks)** | **Arm** |
|---|---|---|---|---|---|---|
| csu804b(dnp) | 0.00 | 1.00 | 0.00 | 0.0 | 1.00 (100) | S |
| rgpc654 | 6.40 | 0.95 | 3.16 | 0.8 | 0.96 (96) | S |
| tub1 (CBM 1.01) | 11.00 | 0.91 | 5.42 | 1.0 | 0.95 (95) | S |
| csu738 | 11.00 | 0.91 | 5.42 | 1.0 | 0.95 (95) | S |
| umc94a | 11.90 | 0.90 | 5.87 | 1.0 | 0.95 (95) | S |
| bnl8.05a | 12.00 | 0.90 | 5.92 | 1.0 | 0.95 (95) | S |
| fus6 | 12.00 | 0.90 | 5.92 | 1.0 | 0.95 (95) | S |
| csu589 | 12.00 | 0.90 | 5.92 | 1.0 | 0.95 (95) | S |
| bnl5.62a | 12.30 | 0.90 | 6.07 | 1.0 | 0.95 (95) | S |
| knox1 | 14.00 | 0.89 | 6.90 | 1.2 | 0.94 (94) | S |
| umc164c | 15.00 | 0.88 | 7.40 | 1.2 | 0.94 (94) | S |
| csu680a | 15.90 | 0.87 | 7.84 | 1.4 | 0.94 (94) | S |

FIGURE 1.—The Morgan2McClintock Translator. Screen capture images taken from http://www.lawrencelab.org/Morgan2McClintock show examples of data input (top) and output (bottom). (A) The user first chooses the maize linkage group as chromosome number (arrow at Step 1) and then the corresponding centimorgan linkage-map data set (arrow at Step 2). The linkage map data can be chosen from among stored data sets available for common maps or pasted directly into a text box for map data not currently stored. Clicking the "Calculate" button submits input data and calculates centiMcClintock values from the RN frequency distribution. The output web page contains a table that summarizes one locus per row and includes columns that describe the input data in centimorgans (B) and the output data in predicted locations along the pachytene chromosome, expressed in microns and in centiMcClintocks (C).

A method for linking genetic maps with chromosome structure has recently been developed. ANDERSON *et al.* (2003) determined the frequency distributions of recombination nodules (RN) along the 10 pachytene chromosomes of maize. Because each RN represents a crossover on the physical structure of the chromosome, these RN maps are unique in that they contain both linkage and cytological information that allows the prediction of the cytological position of any genetically mapped marker (ANDERSON *et al.* 2004). We have developed a tool, the Morgan2McClintock Translator (accessible at http://www.lawrencelab.org/Morgan2McClintock), which automates the cytological-position prediction process for any input linkage data.

Conversion of maize linkage map coordinates into cytological coordinates requires both linkage data and

RN frequencies as input. The Morgan2McClintock Translator includes as data files the maize RN map (Anderson *et al.* 2003) as well as two genetic maps, the University of Missouri at Columbia (UMC) 1998 map (Davis *et al.* 1999) and the 1997 genetic map (Neuffer *et al.* 1995). More than a thousand other genetic maps, which also can be used as input files, are available at MaizeGDB (Lawrence *et al.* 2005 and http://www.maizegdb.org/map.php). The translator itself was coded with PHP, and the equations that it uses to convert linkage maps into cytological maps are those described by Anderson *et al.* (2004). The application can be run online, or it can be downloaded for local use on any machine equipped to serve PHP. Aspects of the input and output displays for the translator for the UMC 98 genetic map are shown in Figure 1 (Davis *et al.* 1999).

The distribution of RNs provides an important connection between genetic maps and chromosomal structure, which has allowed the examination of gene distribution at the chromosomal level in maize (Anderson *et al.* 2006). This integration also permits estimation of DNA and chromosomal distances between genetic loci, a feature that will assist in the sequence assembly of the maize genome. Theoretically, this approach is applicable to other organisms with comparable cytological crossover-distribution data such as tomato (Sherman and Stack 1995) and mouse (Froenicke *et al.* 2002), and we plan to develop a set of similar tools for these organisms that should be useful in comparing genetic and chromosomal aspects of genomes in different species.

Use of the maize Morgan2McClintock Translator will allow researchers to integrate previously disparate views of maize genome structure. For example, the maize cytological maps (http://www.maizegdb.org/cgi-bin/displaycompletemaprecord.cgi?id=40028) are predominantly annotated with chromosomal translocation breakpoints (Coe 1994). For most breakpoints, corresponding germplasm is available from the Maize Genetics Cooperation Stock Center (Scholl *et al.* 2003). Integrating the cytological breakpoint positions with genetic linkage maps would enhance the application of available translocation stocks to genome research, breeding programs, and chromosome engineering efforts. This is one among many ways in which the Morgan2McClintock Translator could be used specifically to add value to maize genetics and structural genomics research and more generally to aid in meiotic chromosome research.

We thank Nigel Walker and Anne B. Thistle for critical reading of the manuscript. This work was supported by the U. S. Department of Agriculture–Agriculture Research Service and by the National Science Foundation (DBI-0321639 to H.W.B. and MCB-314644 to L.K.A.).

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Communicating editor: R. S. Hawley

**Maydica 51 (2006): 357-367**

# CONSENSUS QUANTITATIVE TRAIT MAPS IN MAIZE: A DATABASE STRATEGY

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Received October 14, 2005

**ABSTRACT** - Experimenters who seek to apply the many and diverse studies on quantitative trait loci (QTL) face complex problems in summarizing, interrelating, and integrating them. We report a strategy for consensus QTL maps that leverages the highly curated data in MaizeGDB, in particular, the numerous QTL studies and maps that are integrated with other genome data on a common coordinate system. In addition, we exploit a systematic QTL nomenclature and a hierarchical categorization of over 400 maize traits developed in the mid 90's; the main nodes of the hierarchy are aligned with the trait ontology at Gramene, a comparative mapping database for cereals. Consensus maps are presented for one trait category, insect response (80 QTL); and two traits, grain yield (71 QTL) and kernel weight (113 QTL), representing over 20 separate QTL map sets of 10 chromosomes each. The strategy is germplasm-independent and reflects any trait relationships that may be chosen. Whether the goal of the experimenter is to understand processes of growth, development, or stress response; to define and isolate genes specific to traits; or to mark QTL segments for selection in maize improvement, the elements of the strategy can be applied equally well.

KEY WORDS: QTL; Consensus; Maize; Trait ontology.

## INTRODUCTION

The earliest maize maps were compiled from many recombination studies involving only a few linked mutants each (Emerson *et al.*, 1935). These may be viewed in MaizeGDB under the name EBF 1935. The Genetic 2005 map is the most recent update of this map and now includes a framework of RFLP loci (Coe, 2005). The early 90's saw a rapid expansion of molecular marker maps, each with hundreds of newly mapped loci. The bins coordinates were developed to provide a consensus coordinate system for all mapped entities. Each bin is a chromosomal region spanning 10-20cM. The boundaries of each bin are defined by a public set of Core Markers (Gardiner *et al.,* 1993; Davis *et al.*, 1999). The bins maps represent over 15,000 loci and include genes, probed sites, cytological breakpoints and QTL. They integrate 130 independent map sets and include all mapped loci stored in MaizeGDB. A higher resolution integrated map, IBM neighbors, has recently been developed (MAIZEGDB www.maizegdb.org; Polacco *et al.*, 2003) to aid in BAC contig anchoring; this map purposely excludes loci where a chromosomal position cannot be ascertained to a higher resolution than a bin.

Recent tools for QTL consensus map building offer extensive analysis or 'meta analysis' of data prior to assigning a 'consensus' QTL location for a trait (CMTV, Sawkins *et al.,* 2004; BioMercator, Arcade *et al.,* 2004). We report a strategy that is quite straightforward, and does not invoke new algorithms. Instead, it uses a database, MaizeGDB, to capture community QTL data in a labor intensive, highly systematic manner so that there may be a facile output of the chromosome distribution for all QTL for a trait or a trait category.

## MATERIALS AND METHODS

### *Coordinates for map*

The level of resolution for most QTL is currently on the order of 10-20 cM, or about a bin (Fig. 1; Arcade *et al.,* 2004). The data curated in MaizeGDB are taken from several QTL mapping experiments referenced in Table 1. Both temperate and tropical germplasm are represented. Bin assignments of QTL were made computationally based on the bin coordinates of nearest flanking molecular markers. In certain cases, a QTL listed as spanning 2 or more bins may have higher resolution: (1) when the QTL is near

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TABLE 1 - *Data sources for QTL maps in MaizeGDB for the grain yield, kernel weight and the trait category, biotic response.*

| Map[a] | Number of QTL[b] Yield | Biotic | Weight | Reference |
|---|---|---|---|---|
| Mo17/H99 F3 1994 | 1 | | 6 | Veldboom and Lee (1994), Veldboom *et al.* (1994) |
| Mo17/H99 F3 1996 | 3 | | 16 | Veldboom and Lee (1996a,b) |
| Zagreb Composite 1996 | 3 | | | Kozumplik *et al.* (1996) |
| Mo17/H99 RI QTL 1998 | 5 | | 13 | Austin and lee (1998) |
| B73/A7 F3 1995 | 5 | | | Ajmone-Marsan *et al.* (1994, 1995) |
| SD334 x SD35 F2 1996 | 5 | | | Agrama and Moussa (1996) |
| Pioneer Composite 1998 | 6 | 3 | | Beavis *et al.* (1994) |
| Mo17/H99 RI QTL 1996 | 6 | | 12 | Austin and Lee (1996) |
| KW1265/D146 F2 1998 | 14 | | | Melchinger *et al.* (1998) |
| Ac7729/Ac7643 F2 Tropical 1996 | 23 | | | Ribaut *et al.* (1997) |
| B89/33-16 F2 1993 | | 10 | | Pe *et al.* (1993) |
| Va14/B73 F2 1996 | | 3 | | Saghai (1996) |
| Ki3/CML139 F2 1998 | | 7 | | Khairallah *et al.* (1998) |
| GE37/FF8 F3 1998 | | 7 | | Byrne *et al.* (1998) |
| B73/B52 F3 | | 7 | | Schon *et al.* (1993) |
| CML131 X CML67 F2 1996 | | 9 | 11 | Bohn *et al.* (1996) |
| CML131 x XML67 F2 1996 | | 16 | 10 | Bohn *et al.* (1997) |
| Bubeck Composite 1 (3 map sets) | | 28 | | Bubeck *et al.* (1993) |
| Pioneer Composite 1999 | | | 1 | Beavis *et al.* (1994) |
| KW1265/D146 F3 | | | 13 | Schon *et al.* (1994) |
| Pioneer Composite 1999 | | | 15 | Abler *et al.* (1991) |
| IHP/ILP F3 1994 | | | 15 | Goldman *et al.* (1993, 1994) |
| Total | 71 | 80 | 113 | |

[a] Name of the QTL map in MaizeGDB

[b] Number of QTL for a trait or trait category used in this report.

a bin edge, and flanking markers for a QTL fall into adjacent bins; and (2) when there is a low marker density for a region in a particular QTL map so that flanking markers span a region greater than 2 bins. Nonetheless, depending on the trait, 75%-80% of QTL represented here have been assigned to one or 2 bins. Exceptions include QTL for grain yield on chromosomes 5 and 6; and for biotic response on chromosomes 4 and 8 (Fig. 1).

### *Nomenclature*

Each QTL is provided a unique name that is based on a symbol assigned to a particular trait, e.g. *qplht* for plant height and *qgyld* for grain yield. A unique number is then added, e.g. for plant height, *qplht1, qplht2, qplht3;* and for grain yield, *qgyld1, qgyld2, qgyld3*. The purpose of the 'q' prefix is to distinguish this class of loci from other mapped loci. Numbers have no significance, other than to define QTL loci described in distinct experiments or germplasm. Many of these distinctly labeled QTL could represent allelic regions. This practice is comparable to the nomenclature standards for mutants with identical phenotypes, which map to the same chromosome and where allelism information is unknown (www.maizegdb.org/maize_nomenclature.php).

Trait names used in the literature have been modified so that identical traits, regardless of how measured, have the same descriptor. For example, "ear diameter" and "ear circumference" are assigned the name "ear diameter", the descriptor used by GRIN (www.ars-grin-gov/cgi-bin/npgs/html/desclist.pl?89); grain weight, 100-kernel weight, 300- kernel weight, and 1000-kernel weight are called "kernel weight". In the latter case the GRIN descriptor, "1000-kernel weight", was not chosen as it infers a method of measurement. Any term used in the public literature is maintained as a synonym for the selected trait descriptor. Detailed information about how a trait was measured, including measures of heritability, and overall contribution of a QTL to the trait, should also be available in MaizeGDB which retains, with modest modifications, the schema described by Byrne *et al.* (1995). QTL experiments in MaizeGDB are additionally documented by literature citation(s) and may include raw genotype and phenotype scoring data.

### *Trait categories*

The formal nomenclature for traits and QTL symbols is intimately tied to a hierarchical set of categories, also known as a trait ontology. A main goal of the trait ontology is to facilitate identifying intra and inter-species regions that may affect a group of traits, for example all traits involved in stress, or abiotic stress. The current maize trait ontology, initiated in the mid-90's at

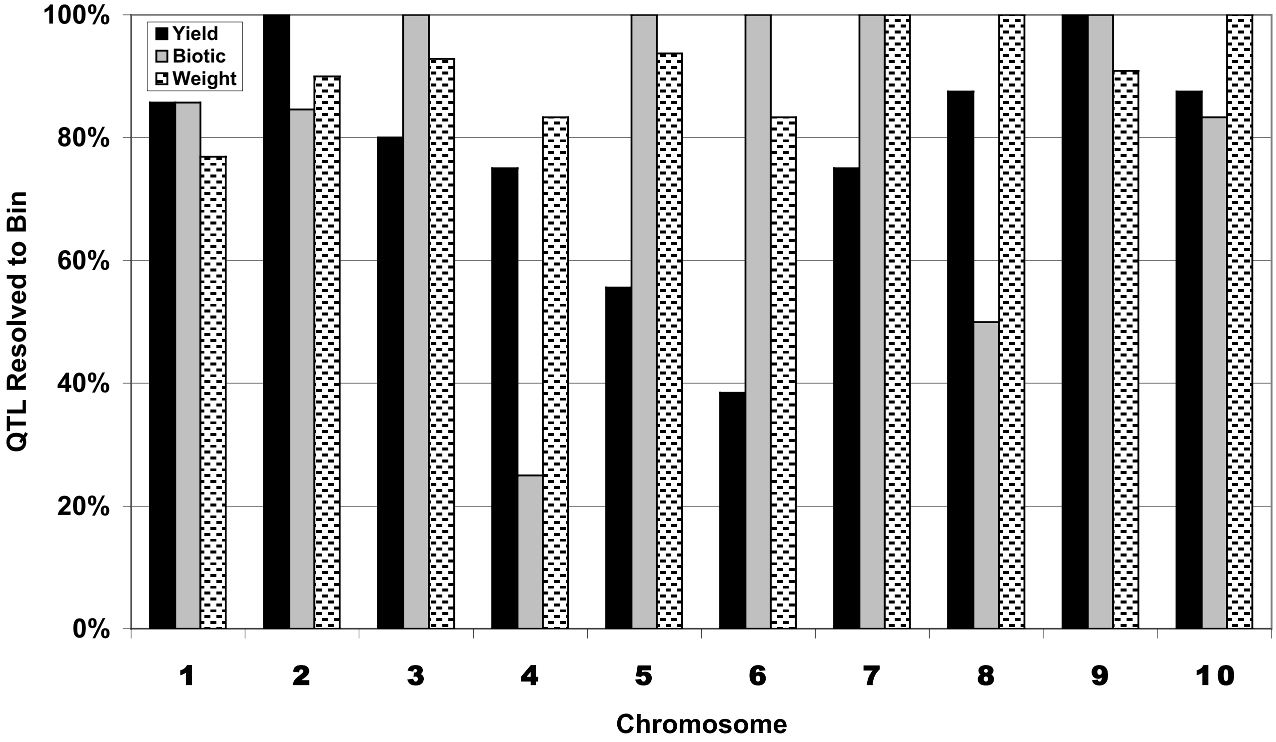

FIGURE 1 - Per cent QTL listed in Table 1 that are resolved to 2 of fewer bins for the traits grain yield (yield) and kernel weight (weight) and the trait category biotic response (Biotic).

MaizeDB, has undergone a modest refinement in MaizeGDB, so that the upper nodes of the hierarchy correspond with those in the trait ontology developed more recently by Gramene for rice (www.gramene.org/plant_ontology/index.html). At this time the maize and rice ontologies are closely aligned at the top node. Individual traits may be species specific, particularly with respect to disease responses. This is a work in progress and as more traits are described, the content of the ontologies is anticipated to change. The trait ontology currently follows the logic used for the Plant Ontology (PLANT ONTOLOGY™ CONSORTIUM, 2002) and the Gene Ontology (GENE ONTOLOGY CONSORTIUM, 2004). A small sample is shown in Table 2 and compares the current classification of insect response traits in MaizeGDB and Gramene.

### *Linked information*

To aid in interpretation of a QTL map position, a database user can follow links from a QTL name on a bins map to linked pages containing information on the mapping population, trait evaluation procedures, and statistical analysis methods. Each QTL is described by the significance level by which it was detected, the magnitude of its phenotypic effect, the percent phenotypic variation explained (%$R^2$), its type of gene action, and the parental source of the favorable allele. Comments on the presence or absence of epistasis and genotype-by-environment interaction can also be added. (Note that the amount of detail entered for a particular QTL depends on the content of the published information).

## RESULTS AND DISCUSSION

### *Consensus maps*

The consensus maps overview depicted in Fig. 2 shows the chromosomal bin distribution of QTL for 2 traits, grain yield and kernel weight, and a trait category, biotic response. Details about the various QTL are provided in Table 3. In addition to data represented in Fig. 2, we have added in Table 3 10 QTL for the trait, response to *Gibberella* stalk rot. All the data are stored in MaizeGDB, and use the nomenclature and coordinate assignments rules described above. Few of the studies report the same number of QTL for a given trait and most explore different sets of traits. For example, only one of the experiments selected includes QTL for both an insect response and grain yield; this is a Pioneer 1998 analysis of mapping populations involving inbred lines B73, Mo17 and V78 (Table 1, BEAVIS *et al.,* 1994).

The distribution of QTL for biotic responses indicates a number of regions where multiple QTL have been reported (Fig. 2; Table 3). On chromosome 3, bin 3.05, there are 4 biotic response QTL, *q1scb5,*

TABLE 2 - *Trait ontology. Comparison of the insect response node in MaizeGDB and Gramene.*

| MaizeGDB | Gramene |
|---|---|
| ● Stress response | ● Stress trait |
| ❍ Abiotic stress response | ❍ Abiotic stress trait |
| ❍ Biotic Stress Response | ❍ Biotic stress trait |
|  | >>Crop damage resistance trait<< [a] |
| ■ Disease response | ■ Microbial damage resistance |
| ■ Mimic response | ■ Mimic response |
| ■ Animal response | ■ Animal damage resistance |
| ● Insect response | ● Insect damage resistance |
| Response to [insect name][b] | [Insect name] resistance) |
| ❍ response to 1st generation sugarcane borer *q1scb* | ❍ army worm resistance |
| ❍ response to 1st generation southwestern corn borer *q1swc*b | ❍ rice skipper resistance |
| ❍ response to European corn borer (2nd brood) *q2ecb* | ❍ green leafhopper resistance |
| ❍ response to corn earworm *qcew* |  |
| ❍ response to southwestern corn borer *qswcb* |  |

[a] This Gramene category is not used by MaizeGDB

[b] The traits listed under Insect response have QTL used for this report

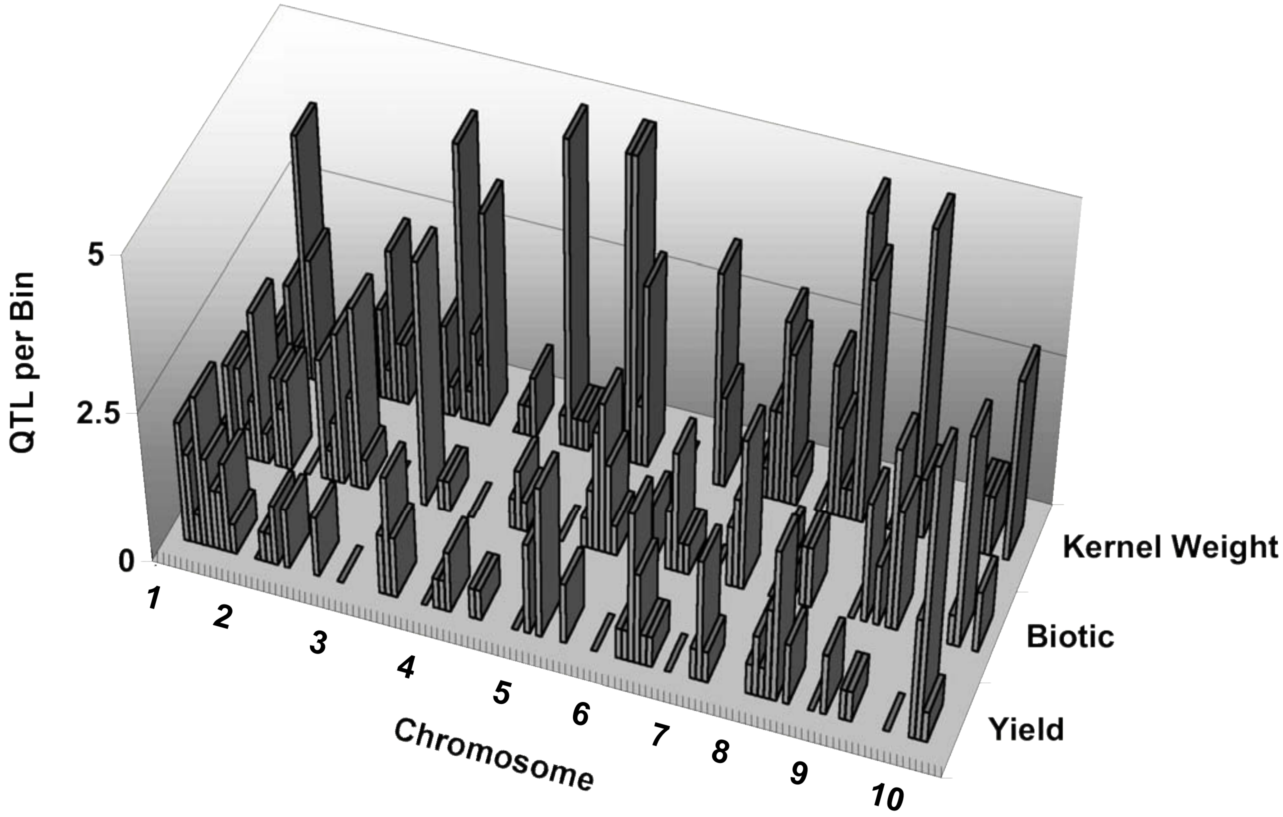

FIGURE 2 - Consensus QTL maps for grain yield (yield), biotic response (biotic) and kernel weight (weight). Values are the number of QTL/bin, for QTL resolved to one or two bins. For this Figure, when a QTL is assigned a 2 bin range, it was counted as 1/2 for each bin unit. More detail about the nature of the QTL in each bin is provided in Table 3.

TABLE 3 - *Bin locations of QTL for grain yield, kernel weight and biotic (pest) response traits.*

QTL that span one or two bins are represented by the symbol used by MaizeGDB. Data for the QTL mappings were taken directly from the published literature (Table 1). Bin coordinates were assigned as described in the Methods. MaizeGDB plans to display trait mappings in a manner similar to this table (T. Seigfreid, personal communication).

| **BIN** | **Biotic Response**[1] | **Grain Yield** | **Kernel Weight**[2] |
|---|---|---|---|
| 1.00 | | | |
| 1.00-1.01 | | | q300k7 |
| 1.01 | | | |
| 1.01-1.02 | q2ecb4 | | |
| 1.02 | qczm17 | | |
| 1.02-1.03 | | | |
| 1.03 | | qgyld21 | |
| 1.03-1.04 | | qgyld44, qgyld48 | |
| 1.04 | qcew5 | | q300k54 |
| 1.04-1.05 | qczm25 | qgyld14 | q300k22 |
| 1.05 | | | |
| 1.05-1.06 | | | |
| 1.06 | q1swcb1 | qgyld70 | |
| 1.06-1.07 | | qgyld35, qgyld39, qgyld49 | |
| 1.07 | qgsr1, qgsr6, q1scb1, q1swcb2 | | q300k23, q300k34 |
| 1.07-1.08 | q2ecb5 | | q300k1, q300k8, q300k47, q300k55 |
| 1.08 | | qgyld15 | |
| 1.08-1.09 | | | |
| 1.09 | | qgyld1 | |
| 1.09-1.10 | | | |
| 1.10 | q1swcb3 | qgyld40 | |
| 1.10-1.11 | qscb1 | qgyld56 | |
| 1.11 | | | |
| 1.11-1.12 | qczm6 | | q300k56 |
| 1.12 | q1scb2 | | |
| 2.00 | | | |
| 2.00-2.01 | | qgyld65 | |
| 2.01 | | | |
| 2.01-2.02 | | | qgrwt27 |
| 2.02 | qcew6, qscb2 | qgyld57 | |
| 2.02-2.03 | | | q300k57 |
| 2.03 | | | |
| 2.03-2.04 | q2ecb6 | | q1000k2 |
| 2.04 | qgsr7 | qgyld36 | qgrwt32 |
| 2.04-2.05 | qczm26 | | |
| 2.05 | qczm12, qczm18 | | |
| 2.05-2.06 | | | q300k9 |
| 2.06 | | | q300k24, q300k58 |
| 2.06-2.07 | | | |
| 2.07 | q1scb3 | | q300k48 |
| 2.07-2.08 | qscb3 | | |
| 2.08 | qcew7 | | q300k25 |
| 2.08-2.09 | q2ecb7 | | |
| 2.09 | | qgyld2 | |
| 2.09-2.10 | | | |
| 2.10 | | | |
| 3.00 | | | |
| 3.00-3.01 | | | |
| 3.01 | | | q300k42 |
| 3.01-3.02 | | | q300k59 |
| 3.02 | | | |
| 3.02-3.03 | | | |

TABLE 3 - *continued.*

| BIN | Biotic Response[1] | Grain Yield | Kernel Weight[2] |
|---|---|---|---|
| 3.03 | | | |
| 3.03-3.04 | | | |
| 3.04 | | | q300k26, q300k36, qgrwt1, qgrwt8 |
| 3.04-3.05 | qgsr2 | | q300k2 |
| 3.05 | q1scb5, q2ecb8, qczm19, qczm3 | | |
| 3.05-3.06 | | | |
| 3.06 | | qgyld66 | q300k27 |
| 3.06-3.07 | | | q1000k3 |
| 3.07 | | qgyld71 | |
| 3.07-3.08 | | qgyld30, qgyld32 | q300k11 |
| 3.08 | | | qgrwt11, qgrwt18, qgrwt23 |
| 3.08-3.09 | qswcb6 | | |
| 3.09 | | | |
| 3.09-3.10 | | | |
| 3.10 | | | |
| 4.00 | | | q300k60 |
| 4.00-4.01 | | | |
| 4.01 | | | |
| 4.01-4.02 | | qgyld41 | |
| 4.02 | | | q300k28 |
| 4.02-4.03 | | | |
| 4.03 | | qgyld3 | |
| 4.03-4.04 | | | |
| 4.04 | | | |
| 4.04-4.05 | | | |
| 4.05 | qgsr3, qgsr8 | | |
| 4.05-4.06 | | | |
| 4.06 | | | |
| 4.06-4.07 | qcew8 | | |
| 4.07 | | | |
| 4.07-4.08 | qczm9 | qgyld45 | q300k13 |
| 4.08 | | | q300k37, q30043, q300k50, qgrwt2, qgrwt5 |
| 4.08-4.09 | | | q300k3 |
| 4.09 | | | |
| 4.09-4.10 | | | |
| 4.10 | | | |
| 4.10-4.11 | | | q300k15 |
| 4.11 | | | |
| 5.00 | | | |
| 5.00-5.01 | | | |
| 5.00-5.02 | | qgyld27 | q300k16 |
| 5.01 | | qgyld16 | |
| 5.01-5.02 | | qgyld72 | |
| 5.02 | | | |
| 5.02-5.03 | | qgyld58 | |
| 5.03 | | qgyld4, qgyld22 | q300k29, q300k38, q300k4, q300k44, q300k51, q300k61 |
| 5.03-5.04 | qczm14 | qgyld59 | |
| 5.04 | qgsr4, qgsr9 | | qgrwt12, qgrwt15, qgrwt19, qgrwt21, qgrwt24 |
| 5.04-5.05 | qscb4 | | |
| 5.05 | qswcb3 | | |
| 5.05-5.06 | qswcb7 | | q1000k10, q1000k4 |
| 5.06 | q1scb6, qswcb8 | | qgrwt3, qgrwt9 |
| 5.06-5.07 | | | |
| 5.07 | q1swcb4 | qgyld60 | |

TABLE 3 - *continued.*

| **BIN** | **Biotic Response**[1] | **Grain Yield** | **Kernel Weight**[2] |
|---|---|---|---|
| 5.07-5.08 | qscb5 | | |
| 5.08 | | | |
| 5.08-5.09 | | | |
| 5.09 | | | |
| 6.00 | | | |
| 6.00-6.01 | | | |
| 6.01 | qcew9 | | |
| 6.00-6.02 | | qgyld33, qgyld31 | |
| 6.02 | | | |
| 6.02-6.03 | | | |
| 6.03 | | | |
| 6.03-6.04 | | qgyld67 | |
| 6.04 | | | |
| 6.04-6.05 | qswcb10, qswcb4 | | |
| 6.05 | qcew10 | qgyld17 | q1000k5, qgrwt33 |
| 6.05-6.06 | | qgyld8, qgyld24, qgyld73 | q300k17, q300k5, q300k52 |
| 6.06 | | | |
| 6.06-6.07 | | | |
| 6.07 | | | |
| 6.07-6.08 | qczm21 | qgyld68 | |
| 6.08 | | | |
| 7.00 | | | |
| 7.00-7.01 | | | q300k19 |
| 7.01 | | | |
| 7.00-7.02 | | | |
| 7.02 | q1swcb5 | | qgrwt6 |
| 7.02-7.03 | | | q300k20 |
| 7.03 | q2ecb2 | | q300k30 |
| 7.03-7.04 | qscb6 | qgyld69 | |
| 7.04 | q1scb7, q2ecb9 | qgyld18, qgyld42 | qgrwt4, qgrwt10 |
| 7.04-7.05 | | qgyld61 | q1000k11, q1000k6 |
| 7.05 | | | q300k62 |
| 7.05-7.06 | | | qgrwt28 |
| 7.06 | | | |
| 8.00 | | | |
| 8.00-8.01 | qczm15 | | |
| 8.01 | | | |
| 8.01-8.02 | | | |
| 8.02 | | | q300k31, q300k63 |
| 8.02-8.03 | | qgyld51 | q1000k12 |
| 8.03 | | | q1000k7 |
| 8.03-8.04 | | qgyld62 | |
| 8.04 | qscb7 | | |
| 8.04-8.05 | | | qgrwt29 |
| 8.05 | q1scb8 | qgyld7 | |
| 8.05-8.06 | | qgyld63 | |
| 8.06 | | qgyld37, qgyld74 | qgrwt13, qgrwt16, qgrwt20, qgrwt34, |
| 8.06-8.07 | | | q300k53, q300k6, qgrwt30, qgrwt35 |
| 8.07 | | | q300k40, q300k46 |
| 8.07-8.08 | | | |
| 8.08 | | qgyld19 | |
| 8.08-8.09 | | | |
| 8.09 | | | |

TABLE 3 - *continued.*

| BIN | Biotic Response[1] | Grain Yield | Kernel Weight[2] |
|---|---|---|---|
| 9.00 | | | |
| 9.00-9.01 | | | q300k21 |
| 9.01 | qczm16, qczm23 | qgyld5 | |
| 9.01-9.02 | | | q300k64 |
| 9.02 | | | |
| 9.02-9.03 | | | qgrwt7 |
| 9.03 | qscb8 | | q100k1, q300k32, q300k65, qgrwt17, qgrwt22, qgrwt31 |
| 9.03-9.04 | | | |
| 9.04 | | | qgrwt14 |
| 9.04-9.05 | | qgyld10 | |
| 9.05 | q1swcb6, qswcb12 | | |
| 9.05-9.06 | | | |
| 9.06 | qscb9, qswcb5 | | |
| 9.06-9.07 | | | |
| 9.07 | | | |
| 9.07-9.08 | | | |
| 9.08 | | | |
| 10.00 | | | |
| 10.00-10.01 | | | |
| 10.01 | | | qgrwt36 |
| 10.01-10.02 | | | |
| 10.02 | | | q300k66 |
| 10.02-10.03 | | | |
| 10.03 | | | qgrwt25 |
| 10.03-10.04 | q1scb10 | qgyld38, qgyld43, qgyld47, qgyld52 | |
| 10.04 | q2ecb10, qcew11, qscb10 | qgyld11, qgyld34 | |
| 10.04-10.05 | | qgyld64 | |
| 10.05 | | | |
| 10.05-10.06 | qgsr5, qgsr10 | | |
| 10.06 | | | q1000k14, q1000k8, q300k33 |
| 10.06-10.07 | | | |
| 10.07 | qczm24 | | |

[1] Symbols for biotic response traits: *q1scb*, response to 1st generation sugarcane borer; *q1swcb*, response to 1st generation southwestern corn borer; *q2ecb*, response to European corn borer (2nd brood); *qcew*, response to corn earworm; *qscb*, response to sugarcane borer; *qswcb*, response to southwestern corn borer; *qczm*, response to *Cercospora zeae-maydis; qgsr,* response to *Giberrella* stalk rot.

[2] All new QTL symbols for grain weight will be styled '*qgrwt*'; previously designated QTL in MaizeGDB will not be altered.

*q2ecb8* for the insect response traits: 1st generation sugarcane borer, 2nd brood European corn borer, and 2 QTL, *qczm19, qczm3* for response to the grey leaf spot fungus, *Cercospora zeae-maydis*. Both *qczm19* and *qczm3* are distinct, and mapped by the same experiment, with peaks separated by some 20 cM (BUBECK *et al.*, 1993). The others, *q1scb5* reported by BOHN *et al.* (1997) and *q2ecb8* by SCHON *et al.* (1993) were on distinct populations involving both tropical and temperate zones of origin. Using the Genome Browser tool at MaizeGDB (www.maizegdb.org/cgi-bin/chromosome_viewer.cgi?chrom=3), one can view in bin 3.05, a list of 41 SSR probes which could be useful for both finer mapping of QTL in this region, or for marker assisted selections. Since many of the SSR probes have been used successfully to anchor BAC contigs, or are associated with a cDNA mapped to a BAC, one immediately has a gateway to chromosome walking in maize as reported in a recent workshop at the Maize Genetics Meetings (HOLLICK, 2005). Interestingly, there are 2 genes, in bin 3.05, engaged in disease resistance: *mv1 resistance to maize mosaic virus1* and *wsm2 wheat streak mosaic virus resistance 2,* located within 4 cM of each other on the Genetic 2005 maps. While this report deals only with QTL, one may also extract from MaizeGDB, any genes with qualitative phenotypes that are assigned, as in this case, to the trait 'disease response'.

It is interesting to explore regions rich in variation for key traits such as grain yield and insect or disease response. One region on chromosome 3, bins 3.06 and 3.07, has several QTL for grain yield, apparently separated, although near the "hot spot", bin 3.05, described above for biotic response QTL. In contrast, on chromosome 10, bins 10.03-10.04 contain some 6 QTL, overlapping an insect response QTL-rich region, bin 10.04 (*q2ecb10, qcew11,qscb10, q1scb10*). Because several hundred genes may be present within a bin (103 bins for a genome with 40,000-60,000 genes), similarly located traits may likely be encoded by distinct genes, even for a particular category, such as the 2 virus resistance loci in bin 3.05. These correspondences serve to indicate regions that are highly variable for multiple important agronomic traits and therefore, where caution is needed in conventional breeding to avoid carrying over undesirable alleles. Given a choice between equivalent insect resistance alleles on the long arm of chromosome 9, or bin 10.04, for example, choosing the chromosome 9 allele would have less chance of an adverse effect on yield.

In the near future there will be available public QTL mapping data on high resolution populations such as the inter-mated B73 x Mo17 recombinant inbreds (LEE *et al.*, 2002; SHAROPOVA *et al.*, 2002). We expect that the data may show a higher resolution of map coordinates, as provided by the framework for IBM neighbors. When these data are integrated into MaizeGDB, the current IBM neighbors algorithm and software can be utilized without modification for a higher resolution QTL mapping. In addition, because both the bins map and IBM neighbors maps are imported by Gramene, the comparative strategies in place at Gramene will be supported by any transition to a higher resolution mapping.

Future upgrades of consensus QTL data in MaizeGDB will be facilitated by a new curation tool under development. It is similar to the tool suite described by LAWRENCE *et al.* (2005) for other datatypes in MaizeGDB and will be accessible to the community on request.

### *Relevance to plant breeding*

Although, strictly speaking, QTL results from a given study are applicable only to a specific mapping population, the compilation of results from multiple studies provides a broader picture of trait inheritance. Patterns of QTL number, location, effect size, type of gene action (additive or dominant), and environmental interactions add to an understanding of "trait architecture" that may help a breeder make decisions on breeding methodology, population size, or number of environments for trait evaluation. For example, a trait with evidence from multiple studies of large-effect QTLs that were consistently detected across a range of environments would be a promising trait to consider for marker-assisted selection. On the other hand, when numerous small-effect QTLs with variable expression are the norm, then marker-assisted selection would have a low probability of success.

The co-location of QTLs for different traits may provide insights into the genetic relationships among traits, or the physiological mechanisms or biochemical pathways involved in trait expression. The occurrence of QTLs for different traits in a single region may well be coincidental, but if QTLs for the traits overlap in more than one genomic location, especially in regions not known to be duplicated, then the evidence is much stronger for a true biological association (DE VIENNE *et al.*, 1999). Knowledge of trait associations, whether due to pleiotropy or linkage, is important information for a breeder, because these associations may either facilitate or hinder selection progress.

The compiled QTL data might also be useful in a breeding program by identifying genomic "hot spots" that affect expression of a trait or traits (e.g., bins 1.06-1.08 or 6.04-6.06 in Table 2). In a marker-assisted backcrossing program, for example, the breeding team would want to ensure that those regions were represented by linked markers to adequately capture the background genome of the recurrent parent.

## CONCLUSION

This report describes a very simple method for summarizing chromosomal distribution of QTL for a specific trait, or trait category. It relies on extensive curation of QTL data and is made useful by inclusion in MaizeGDB linked to extensive information about the QTL, and other linked information about markers and gene function. The output indicates the regions in the genome that (1) influence a selected trait or a category of traits; (2) have high variability for the trait or trait category. It is amenable to comparative map display of two or more trait distributions and can be applied equally well to experimental studies on plant processes and responses; on trait-specific genes; and on marking QTL segments for selection in maize improvement. Because the integration is a public database, it is freely accessible and can be used to support software tools for other analyses.

We anticipate that the extensive alignment of the trait categories for maize with those at Gramene for rice will facilitate database interoperability and discovery of candidate genes for QTL in both rice and maize.

ACKNOWLEDGEMENTS - Appreciation is expressed by M.S. to Don Duvick for his encouragement of myself when a new researcher to maize, his continued, lively interest in maize research, and, perhaps most important, his support of open scientific exchange between Pioneer and the public sector research communities.

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Plant Physiology Preview. Published on August 11, 2006, as DOI:10.1104/pp.106.085720

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Journal Research Area:
Bioinformatics, ontology, functional annotations, genome analysis

# Whole Plant Growth Stage Ontology for Angiosperms and its Application in Plant Biology

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Financial Source: NSF grant number 0321666

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## ABSTRACT

Plant growth stages are identified as distinct morphological landmarks in a continuous developmental process. The terms describing these developmental stages record the morphological appearance of the plant at a specific point in its lifecycle. The widely differing morphology of plant species consequently gave rise to heterogeneous vocabularies describing growth and development. Each species or family-specific community developed distinct terminologies for describing whole plant growth stages. This semantic heterogeneity made it impossible to use growth stage description contained within plant biology databases to make meaningful computational comparisons. The Plant Ontology Consortium (POC) (http://www.plantontology.org) was founded to develop standard ontologies describing plant anatomical as well as growth and developmental stages that can be used for annotation of gene expression patterns and phenotypes of all flowering plants. In this paper, we describe the development of a generic whole-plant growth stage ontology that describes the spatio-temporal stages of plant growth as a set of landmark events that progress from germination to senescence. This ontology represents a synthesis and integration of terms and concepts from a variety of species-specific vocabularies previously used for describing phenotypes and genomic information. It provides a common platform for annotating gene function and gene expression in relation to the developmental trajectory of a plant described at the organismal level. As proof of concept the POC used the PO growth stage ontology to annotate genes and phenotypes in plants with initial emphasis on those represented in The Arabidopsis Information Resource (TAIR), Gramene database and MaizeGDB.

## INTRODUCTION

Plant systems are complex, both structurally and operationally, and the information regarding plant development requires extensive synthesis to provide a coherent view of their growth and development. The difficulty of developing such a synthesis is exacerbated by the deluge of new technologies such as high throughput genotyping, microarrays, proteomics, transcriptomics etc that generate large amounts of data rapidly. The speed and magnitude of data deposition challenges our ability to represent and interpret this data within the context of any particular biological system (Gopalacharyulu et al., 2005). The ability to extract knowledge from historical sources and integrate it with new information derived from global datasets requires a sophisticated approach to data mining and integration.

Historically, the growth and development of cultivated plants have been monitored at the whole plant level with the help of scales of easily recognizable growth stages. Consequently, there exist large volumes of literature detailing growth stages for individual plant species or closely related groups of species. For example, Zadok's scale (Zadok et al., 1974) was developed for the Triticeae crops and is widely used to stage the growth and development of cereal crops in the United States. The flexibility of this scale has allowed it to be extended to other cultivated plants, and a uniform code called the BBCH (**B**iologische **B**undesanstalt, Bundessortenamt and **CH**emical industry) code was developed from it (Meier, 1997). The BBCH scale is quite generic and encompasses multiple crops, including monocot and eudicot species. It offers standardized descriptions of plant development in the order of phenological appearance, and has coded each stage for easy computer retrieval. It should be noted that Arabidopsis, as a representative of the Brassicaceae and by virtue of not being a cultivated species, did not have a specific growth stage vocabulary or scale until 2001 when (Boyes et al., 2001) developed an experimental platform describing the *Arabidopsis thaliana* growth stages using the BBCH scale. This work created a crucial semantic link between Arabidopsis and cultivated plants. In addition to facilitating the description and synthesis of large amounts of data within a crop species, vocabularies like the BBCH and Zadok’s scale also make possible transfer of information among researchers and provide a common language for comparative purposes (Counce et al., 2000) .

In the post genomic era, these scales have proved inadequate to handle the deluge of information that required large-scale computation for comparative analysis. This called for the conversion of existing scales into ontology that have an advantage over simple scales because their hierarchical organization facilitates computation across them. Terms in an ontology are organized in the form of a tree, the nodes of the tree represent entities at greater or lesser levels of detail (Smith, 2004). The branches connecting the nodes represent the relation between two entities such that the term ‘radicle emergence stage’ is a child of the parent term ‘germination stage’ (Fig-1). Individual stages of a scale are then parts that can be related to the whole by their order of appearance during plant growth. Each term carries a unique identifier and strictly-specified relationships between the terms allow systematic ordering of data within a database, this in turn improves input and retrieval of information (Bard and Rhee, 2004; Harris et al., 2004).

Consequently, several species-specific databases converted BBCH and other scales into formal ontologies (controlled vocabularies) to facilitate the annotation of genetic information. For example, the Gramene database (Jaiswal et al., 2006) designed its cereal growth stage ontology based on the stages described in the Standard Evaluation System (SES) for rice (INGER, 1996), and those described by Counce et al. (2000) for rice, by Zadok et al., (1974) for Triticeae (wheat, oat and barley) and by Doggett (1988) for sorghum. Except for the sorghum, which is a less studied crop, these species had fairly well-described growth staging vocabularies. MaizeGDB (Lawrence et al., 2005) developed a very extensive controlled vocabulary from a modified version of that described by Ritchie et al., (1993). TAIR (Rhee et al., 2003) developed the *Arabidopsis thaliana* growth stage ontology from the scale described by Boyes et al., (2001). However, ontologies created in these projects remained restricted to particular species or families, whereas comparative genomics requires that a common standard vocabulary be applied to a broad range of species. The uniform BBCH scale (Meier,

1997) appeared to be a suitable model to develop a unified ontology since this scale had already synthesized monocot and eudicot crop stages into a single vocabulary.

The Plant Ontology Consortium (POC) was inaugurated in 2003 for the purpose of developing common ontologies to describe the anatomy, morphology and growth stages of flowering plants (Jaiswal et al., 2005). Its primary task was to integrate and normalize existing species-specific ontologies or vocabularies that had been developed by several major databases for the purpose of annotating gene expression and mutant phenotype. The PO is divided into two aspects. The first is the Plant Structure Ontology (PSO) is a vocabulary of anatomical terms (Ilic *et al.* manuscript in preparation), which, since its release to the public domain in 2004, has become widely used by plant genome databases (Jaiswal et al., 2005). The second aspect is the Plant Growth and Developmental Stages Ontology. This component of PO is further divided into the Whole Plant Growth Stage Ontology and the Plant Part Developmental Stages. This paper focuses on the Whole Plant Growth Stage Ontology (GSO); we will discuss the history, design and applications of the GSO and show how it simplifies the description of a continuous and complex series of events in plant development. The Plant Part Developmental Stages will be reviewed elsewhere.

## RESULTS

The GSO was developed over a period of two years [2004-2006] by a team of plant biologists comprising systematists, molecular biologists, agronomists, plant breeders and bioinformaticians. We worked to develop a set of terms to describe plant development from germination to senescence that would be valid across a range of morphologically distinct and evolutionarily distant species. Although the rate of addition of new terms to the GSO has slowed since its initial stages of development, it is still under active development as we refine the ontology in response to user input and feedback from database curators.

Currently, the GSO has a total of 112 active terms; each organized hierarchically (Fig1, 2a) and associated with a human-readable definition. Although we started with existing systems such as the BBCH (Meier, 1997) as well as the controlled vocabularies developed for Arabidopsis by TAIR, for rice, Triticeae (wheat, oat and barley) and sorghum by Gramene database and for maize by MaizeGDB, the current version of GSO is quite distinct from its predecessors. We will first discuss the major design issues we dealt with during the development of the GSO, and then describe the structure of the GSO and its applications to real-world problems. The ontology terms, database and gene annotation statistics provided here are based on April 2006 release of the POC database.

## Architecture of the Ontology

We chose to make use of the data model originally developed for the Gene Ontology (GO) to describe the GSO. This data model uses a directed acyclic graph (DAG) to organize a hierarchy of terms such that the most general terms are located toward the top of the hierarchy while the most specific ones are located at the bottom of the hierarchy (Fig-1, 2a, 2b). Each “parent” term has one or more “children,” and the relationship between a parent and one of its children is named, either “IS_A” to indicate that the child term is a specific type of the parent term, or “PART_OF” to indicate that the child term is a component of the parent term (Smith, 2004). For example the “reproductive growth” and “flowering” terms are related by IS_A, because flowering is a type of reproductive growth. On the other hand “seedling growth” is related to its children terms “radicle emergence” and “shoot emergence” by PART_OF, because seedling growth is comprised of the two processes of radicle emergence and shoot emergence (Fig-1, 2a).

Each term is given a unique accession number named PO:XXXXXXX where the series of X’s is a seven-digit number (Fig-2a). Accession numbers are never reused, even when the term is retired or superseded. Obsolete terms are instead moved to a location in the hierarchy underneath a term named “obsolete_growth_and_developmental_stage (Fig-2a).” This ensures that there is never any confusion about which term an accession number refers to. Each term also has a human-readable name like “seedling growth”, a paragraph-length definition that describes the criteria for identifying the stage, and citations that attribute the term to a source database, journal article, or an existing staging system. Many terms also have a synonym list; these are described in more detail below.

Our choice of the GO data model was driven by numerous practical considerations, foremost of which was the fact that the data model is supported by a rich set of database schemas, editing tools, annotation systems and visualization tools.

### Naming of Plant Growth Stages

The next issue we dealt with was how to name plant growth stages. Although development in any organism is a continuous process, it is important to have landmarks that identify discrete milestones of the process in a way that is easily reproducible. Extant systems either name growth stages according to a landmark (e.g. 3-leaf stage) or by assigning a number or other arbitrary label to each stage. We chose to define growth stages using morphological landmarks that are visible to the naked eye (Counce et al., 2000), because such descriptive terms are more intuitive, self explanatory to the users and easy to record in an experiment. To minimize differences among species, we were able to describe many growth stages using measurements/landmarks that are in proportion to the fully mature state. For example, the inflorescence stages are described in progression starting from the “inflorescence just visible,” “1/4 inflorescence length reached”, “1/2 inflorescence length reached” to “full inflorescence length reached.” This provides an objective measurement of the degree of maturation of the inflorescence in a way that is not dependent on the absolute value of the inflorescence length.

### Synonyms

Because the GSO crosses species and community boundaries, we needed to acknowledge the fact that each community has its own distinct vocabulary for describing plant structures and growth stages. To accommodate this, we made liberal use of the GO data model's synonym lists, which allows any GSO term to have one or more synonyms from species specific vocabulary that are considered equivalent to the official term name. The GSO currently contains 997 synonyms taken from several plant species. On an average there are about 9 synonyms per GSO term (Table-I). Like terms, we attribute synonyms to the database, literature reference or textbook from which they were derived.

As an example of a synonym, consider 'dough stage in wheat' and 'kernel ripening in maize,' both of which essentially refer to the fruit ripening stage. These terms are included as synonyms to the generic (species-independent) GSO term “ripening” (PO:0007010) (http://www.plantontology.org/amigo/go.cgi?view=details&show_associations=terms&search_constraint=terms&depth=0&query=PO:0007010) . From the end-user's point of view, the synonyms can be used interchangeably with the generic terms when searching databases that use the PO. This means that data associated with the ripening stage of all plants is accessible even to a naïve user, irrespective of the variable terminology, diverse morphologies and differing developmental time-lines of plants such as wheat and maize.

By using synonyms, we were able to merge 98% of terms from the various species-specific source ontologies into unambiguous generic terms. In a few cases we encountered identical terms that are used by different communities to refer to biologically distinct stages. We resolved such cases by using the *sensu* qualifier to indicate that the term has a species-specific (not generic) meaning. One example of this, described in more detail later, is inflorescence visible (to the naked eye) vs. inflorescence visible (*sensu* Poaceae). In most plants the inflorescence becomes visible to the naked eye soon after it forms, whereas in Poaceae (grasses), the inflorescence only becomes visible much later in its development, after emergence from the flag leaf sheath.

## Spatio-temporal representation

Less satisfactory is the design compromise that we reached in order to represent the spatial and temporal ordering of terms. The existing plant growth scales are organized by the temporal progression of developmental events. However, the GO data model presents unique challenges in designing an ontology that represents the temporal ordering of terms across multiple species that display small but key variations in that ordering.

In particular, the GO data model does not have a standard mechanism for representing organisms' developmental timelines. This has forced each organism database that has sought to represent developmental events using the GO model to grapple with the issue of representing a dynamic process in a static representation. Some animal model organism databases, such as WormBase for *Caenorhabditis elegans*, Flybase for *Drosophila*, Zfin for Zebra fish, have developed developmental stage ontologies (OBO, 2005) in which temporal ordering is represented using either the DERIVED_FROM, DEVELOPS FROM or OCCURS_AT_OR_AFTER relationship to indicate that one structure is derived from another or that one stage follows another. However, we found these solutions to be unworkable for the GSO because of the requirement that the ontology must represent growth stages across multiple species. For example, consider the process of main shoot growth. In the wheat plant, main shoot growth may be completed at the 9 leaf stage, while in rice and maize, shoot growth may be completed at the 11 and 20 leaf stages respectively and this varies with different cultivars/germplasms (Fig-3). Transition to the subsequent stage of reproductive growth is thus staggered for each species, and cannot be accurately described by an ontology in which each stage rigidly follows another.

Our compromise is to visually order the display of terms in a temporal and spatial fashion, but not to build this ordering into the structure of the ontology itself. In practice, what we do is to add alphabetic and numeric prefixes to each term. When terms are displayed the user interface tools sort them alphabetically so that later stages follow earlier ones (Fig 2a). This compromise is similar to the one taken by the *Drosophila* developmental stages ontology (Flybase, http://flybase.org/) (OBO, 2005).

As an example of how this works, we describe the stages of leaf production using terms named “LP.01 one leaf visible”, “LP.02 two leaves visible,” “LP.03 three leaves visible” and so forth. When displayed using the ontology web browser, the terms appear in their natural order (Fig-2b). However, there is nothing hard-wired into the ontology that indicates that “LP.01 one leaf visible” precedes “LP.02 two leaves visible.”

A related issue is the observation that during plant maturation, multiple developmental programs can proceed in parallel. For instance, the processes of leaf production and stem elongation, although coupled, are temporally overlapping and can proceed at different relative rates among species and among cultivars within a species. We represent such processes as independent children of a more generic term. In the case of the previous example, both leaf production and stem elongation are represented as types of “main shoot growth” using the IS_A relationship (Fig-1, 2a).

## Description of the Ontology

The four main divisions of the GSO are “A_Vegetative growth”, “B_Reproductive growth,” “C_Senescence,” and “D_Dormancy” (Fig-2a). As described earlier, the alphabetic prefix is there to force these four divisions to be displayed in the order in which they occur during the plant’s lifecycle in general. The sub stages of Vegetative Growth are “0_Germination,” “1_Main Shoot Growth,” and “2_Formation of Axillary Shoot,” while the sub stages of Reproductive Growth are “3_Inflorescence Visible,” “4_Flowering,” “5_Fruit Formation,” and “6_Ripening.” Neither senescence nor dormancy currently has sub stages beneath them. Again, the numeric prefixes are there only to make the sub stages appear in a logical order. Each of the sub stages has multiple, more specific stages beneath it.

Although the BBCH scale (Meier, 1997) was the starting point for the GSO, we have diverged from it in many important aspects. A major difference is the number of top-level terms (Fig-1, 2a). The BBCH scale has 10 principle stages as its top level terms, but the GSO only has four. We collapsed four BBCH top-level stages (Germination, Leaf Development, Stem Elongation and Tillering) into our top level Vegetative Growth term, and collapsed another 6 BBCH top-level terms (Booting, Inflorescence Emergence, Flowering, Fruit Development and Ripening) into Reproductive Growth. We felt justified in introducing the binning terms vegetative growth and reproductive growth for several reasons; (1) to help annotate genes that act throughout these phases (2) persistent use in current scientific literature, especially when the specific stage of gene action or expression remains unclear; and (3) they were requested by our scientific reviewers to enhance the immediate utility of the ontology.

We now look in more detail at some of the more important parts of the ontology.

***Germination*** (PO:0007057). This node in the GSO has eight children that are broadly applicable to seed germination. The stages under “Seedling Growth” and “Shoot Emergence” are not given numerical prefixes, as it is not clear which event precedes the other among the various species. Only events of seed germination were considered in this ontology, whereas the BBCH scale equates seed germination with germination of vegetatively propagated annual plants and perennials such as bud sprouting. The two processes are in fact quite distinct in terms of organs developing at this stage, the physiology and various metabolic processes, and thus we felt that combining them was inappropriate.

***Main Shoot Growth*** (PO:0007112) refers to the stage of the plant when the shoot is undergoing rapid growth. It can be assessed in different ways depending on the species and the interests of the biologist. Plants may be equally well described in terms of leaves visible on the main shoot or in terms of the number of nodes detectable (Zadok et al., 1974), and biologists studying Arabidopsis commonly assess the size of the rosette. To accommodate existing data associated to these terms we created three instances of Main Shoot Growth, namely the “Leaf Production”, “Rosette Growth” and

“Stem Elongation”, with a strong recommendation to use “Leaf Production” wherever possible.

***Leaf Production*** (PO:0007133). Leaves are produced successively so that the progression through this stage can be measured by counting the number of visible leaves on the plant (Fig-2b, 3). In any species, leaves are always counted in the same way (Meier, 1997) (described in detail later). In plants other than monocotyledons, leaves are counted when they are visibly separated from the terminal bud. The recognition of the associated internode (below) follows the same rule (Fig-3). Leaves are counted singly unless they are in pairs or whorls visibly separated by an internode, in which case they are counted as pairs or whorls. In taxa with a hypogeal type of germination, the first leaf on the epicotyl is considered to be 'leaf one' and in grasses the coleoptile is 'leaf one'.

In the GSO the stages of leaf production continue up to twenty leaves/pairs/whorls of visible leaves (Fig-2a), but this can be emended to accommodate higher numbers, as new species are included. This is unlike the BBCH scale (Meier, 1997), where only nine leaves can be counted and all the rest would be annotated to ‘nine leaves or more’. This was done to accommodate the leaf development stages of maize, where depending on cultivars the number of leaves can be few as five or have 20 or more leaves. The maize community and the MaizeGDB database (Lawrence et al., 2005) use a modified version of Ritchie’s scale (Ritchie et al., 1993) in which the stages of the maize plant are measured solely by counting the leaves from the seedling through the vegetative stages, and the nodes are not counted.

Stem Elongation can be assessed by the number of visible nodes; this metric is commonly applied to the Triticeae, for which the Zadok’s (Zadok et al., 1974) or BBCH scales (Meier, 1997) were originally developed. Stem elongation begins when the first node becomes detectable. This is usually equivalent to node number seven (the number varies in different cultivars), since earlier nodes are not detectable before elongation commences in the grasses, (Boyes et al., 2001) considers Arabidopsis

“Rosette Growth” analogous to “Stem Elongation” in the grasses, and uses leaf expansion as the common factor linking the rosette growth and stem elongation stages. In our model, *Rosette Growth* (PO:0007113) and *Stem Elongation* (PO:0007089) are treated as separate instances of sibling stages (Fig-1, 2a), mainly to provide language continuity for users, rather than for biological reasons.

***Reproductive growth*** (PO:0007130) and its child terms are organized a little differently from vegetative growth. Reproductive growth has four instances: *Inflorescence Visible* (PO:0007047), *Flowering* (PO:0007026), *Fruit Formation* (PO:0007042) and *Ripening* (PO:0007010) (Fig-2a). The *Inflorescence Visible* (*sensu* Poaceae) (PO:0007012) specific to grass family is an instance of the generic term *Inflorescence Visible* (PO:0007047). This in turn has two instances: *Booting* (PO:0007014) and *Inflorescence Emergence from Flag Leaf Sheath* (PO:0007041). As described earlier, the generic *Inflorescence Visible* stage is considered separate from *Inflorescence Visible sensu Poaceae*, as the former includes all plants where inflorescence formation and visibility coincide, while in members of the Poaceae, many developmental events in the reproductive phase start during the vegetative phase but manifest themselves as visible morphological markers much later.

Other stages are similar in their organization to the existing scales, but as we continue including various species from families, Solanceae and Fabaceae we anticipate that changes in the organization may be required to accommodate them into the GSO.

## User Interface

The GSO terms are in a simple hierarchy that is intuitive to use. The GSO is a relatively small ontology and has a total of 112 terms, excluding the obsolete node. It has 4 top nodes, 15 interior nodes (terms associated with children terms) and 88 leaf nodes (terms without any children terms) (Fig-2a). New terms are added based on user requests after thorough discussions. A researcher can browse the GSO using the ontology browser available at (http://www.plantontology.org/amigo/go.cgi). This is a web-based tool for searching and browsing ontologies and their associations to data. It has been developed by the GO consortium (http://www.geneontology.org/GO.tools.shtml#in_house) and modified to suit our needs. To browse, clicking on the [+] sign in front of the term expands the tree to show children terms (Fig-2a). This view provides information on the PO ID of the GSO term, term name, followed by a number of associated data such as genes. For every green colored parent term a summary of the data associated to its children terms is presented as a pie chart. The user has an option to filter the number of associated data displayed based on species, data sources and evidence codes. The icons for [i] and [p] suggest the relationship types between the parent and child term as described in the legend. While browsing, a user can click on the term name to get the details at any time (figure-4b). The users will see the icon [d] for develops_from relationship type. This relationship type is used strictly in the PSO and not GSO. It suggests that a plant structure develops from another structure (Jaiswal et al., 2005).

In addition to the browse utility, users may search by entering the name of a term or a gene. For example, querying with “germination” results in three terms, of which two are from the GSO section of the ‘plant growth and development stage’ ontology and one from the PSO. To avoid getting a large list, users may choose the “exact match,” option before submitting the query. A search for “0 germination” choosing “exact match” gives one result (Fig-4a). A user may browse the parents and children of this term by clicking on the blue colored tree icon and following the [+] sign next to the term name, which suggests that there are additional terms under this term, or simply click on the term name “0 germination” for more details. The term detail page (Fig-4b) provides information on the ID, aspect ontology (plant structure or growth and development), species specific synonyms, if any, definition, external references and links, if any, and the associated data. The association section allows a user to select the source database, species name and the evidence code (Table-II) used to make the annotation to limit the data displayed. e.g. there are 138 gene associations to the term ‘0 germination (PO:0007057)’ (Fig-4b). The list of associated data (Fig-4c) gives information about the name, symbol, type (e.g. gene), the source and the species, in addition to the evidence used for inferring the association to the term. The gene symbol provides a hyperlink to the gene detail page (Fig-4d), and the data source links to the same entry on the provider's website. This allows a user to search for extended details that may not be provided in the POC database, such as information on genome location, biochemical characterization, associations to the Gene Ontologies (GO), etc. For help at any time, users can click on the 'help' menu at the bottom of the browser page or visit the link, http://www.plantontology.org/amigo/docs/user_guide/index.html.

## Annotations to GSO

Annotation is the process of tagging snippets of information to the genomic element by skilled biologists to extract its biological significance and deepen our understanding of the biological processes (Stein, 2001). The curator attributes the added information to its source by the use of evidence codes (http://www.plantontology.org/docs/otherdocs/evidence_codes.html) indicating the kind of experiment that was carried out to infer the association to a GSO term, such as 'inferred from expression pattern' (IEP) involving northern, western and/or microarray experiment or 'inferred from direct assay' (IDA) such as isolated enzyme and/or *in-situ* assays, etc. (Table-II). The user interface has query filter options to search for genes annotated with a given type of evidence code. Explicit spatio-temporal information related to the whole plant is extracted from literature by a curator and described using terms from the GSO. The current build of the GSO has over 600 genes associated to it from the TAIR and Gramene databases (Figure-5a). Analysis of the data at this point may not be entirely reflective of current research in Arabidopsis and rice, as manual curation is a dynamic and evolving process and will necessarily lag behind the actual state of research. In TAIR, about 130 genes associations to whole plant growth stages carry the evidence code IEP, while in the Gramene database, a majority of GSO annotations (about 480) carry the evidence code inferred from mutant phenotype (IMP) and a smaller number of IEP, and Inferred by Genetic Interaction (IGI) associations. A closer look at the number of genes associated to various terms and their immediate parents (Figure-5a, b) reveals that many of these genes with GSO annotations in TAIR are associated to germination stages which is a vegetative stage. Similarly the vegetative stages particularly 5 to 6 leaf stages (children of leaf production) and reproductive stages namely the Inflorescence Visible (*sensu* Poaceae) a child of Inflorescence visible, Fruit Formation and Fruit Ripening stages in the rice plant are of particular importance (Figure-5b). The Solanaceae Genome Network (SGN) has adapted the GSO and has created a mapping file for Solanaceae (Tomato) synonyms that is used to associate their data. Tomato mutants are initially being curated to these terms and, predictably, a large number of mutants will be associated to the ripening stages (data not shown). As we continue to solicit data from collaborating databases and annotate using the GSO, we obtain a global view of how data is associated with different stages of plant growth (Figure-5b).

## Application

This section provides examples of genetic analyses that typically uses whole-plant ontogeny as a feature of the experimental design and data analysis. It indicates some of the difficulties of extracting spatio-temporal information from the literature and shows the advantages of curating genomic information using the plant ontologies (GSO and PSO), which allow the users to query ‘when’ and ‘where’ a gene is assayed, expressed or its effects become visible during the lifecycle of a plant. In addition the PO database supports queries such as ‘what are the genes that are expressed during the germination stage in Arabidopsis and rice?’ or ‘show me all of the phenotypes in the reproductive stages of a rice plant when mutated’.

### Annotation examples of mutant phenotypes

The primary description of phenotypic data is usually at the whole-plant level and it is rarely a straight-forward exercise of term-to-term association for the curator. For example characterization of dwarf mutants is done in different ways, most often by the leaf or node number that is affected, counted either top-down or bottom-up; in this system the leaf and the internode below it can be used to define the same stage. This is distinct from node ‘visible’ stages that are less reliable, as the first node that is ‘visible’ is a variable number in grasses (Fig 3).

An example is provided by recording of internode elongation, the main morphological feature that is affected in dwarf plants, is attributed among others to the effect of gibberellin (GA) and brassinosteroids (BRs) (Chory, 1993; Ashikari et al., 1999). (Yamamuro et al., 2000) show that BR plays important roles in internode elongation in rice and have characterized dwarf mutants based on the specific internode that is affected. In the *dn*-type mutant all the nodes are uniformly affected (the total number of nodes in a given mature rice plant). However, in the *nl*-type mutant, only the fourth internode is affected, while in the case of the *sh*-type mutant, only the first internode is affected. However, in this case, the authors of the study number the internodes from top down - the uppermost internode below the panicle is the first internode. To be consistent with the GSO, these numbers have to be converted to the appropriate leaf/node counting from the base of the shoot (Fig-3). This has to be achieved by the curator’s personal knowledge of the plant, from legacy information available for the species and germplasm accession, or by contacting the authors.Unlike the above example, generally leaves are counted from below and the curator extracts information from statements such as ‘when the plant is at the 3 leaf stage.’ This permits an immediate visualization of the morphological appearance of the plant to the researcher and curator as well as the user (Fig 3). Currently by using the IMP filter, more than 500 genes annotated to different growth stages are available in the PO database.

## Cross-database comparison of gene annotations

Almost all organismal databases are mutually exclusive and provide little or no overlap in their schemas with other databases. Thus they cater to exclusive user communities. To illustrate how the use of ontologies can overcome database interoperability problems, we compare the related processes of flowering-time in *Arabidopsis thaliana* and heading date in rice (Fig 6). The gene network underlying the photoperiodic flowering response involves photoreceptors, circadian clock systems, and floral regulator genes (Yanovsky and Kay, 2002; Izawa et al., 2003; Putterill et al., 2004; Searle and Coupland, 2004). Interestingly, the molecular components that underlie the transition from vegetative to reproductive growth are conserved in Arabidopsis and rice (Hayama and Coupland, 2004; Putterill et al., 2004).

The three key regulatory genes in Arabidopsis are *GIGANTEA (GI) CONSTANS (CO)* and *FLOWERING TIME (FT)* and in rice they are *Oryza sativa Gigantea* (*OsGI)*, *Photosensitivity* (*Se*1) (synonymous with *Heading date 1, Hd1*) and *Hd3a* (Hayama et al., 2003) (Fig-6). *GI* is an activator of *CO* (Izawa et al., 2000) and literature provides evidence that the *Se1* (*Hd*1) gene from rice is an ortholog of a *CO* family member in Arabidopsis (Putterill et al., 1995; Yano et al., 2000). Furthermore, an allele at the *Hd3a* locus in rice promotes the transition to floral development (Kojima et al., 2002) and it appears to be an ortholog of *FT* (Kardailsky et al., 1999; Kobayashi et al., 1999). Thus, the relationship of *OsGI* to *Se1* (*Hd1*) and that of *Se1* (*Hd*1) to *Hd3a* in rice is similar to *GI, CO* and *FT* in Arabidopsis, despite the fact that Arabidopsis is a long day plant while rice is a short day plant (Kojima et al., 2002; Hayama et al., 2003) (Fig-6).

At present all the above genes are available in the PO database, annotated either or to both GSO and PSO terms (Table-III). The *Arabidopsis* databases, National Arabidopsis Stock Centre (NASC) and TAIR have used IMP, IEP, IDA and ‘Traceable author statement’ (TAS) evidence codes to annotate *GI, CO* and *FT* genes to the exact plant structure where they are expressed. Gramene database has used the IMP and IGI evidence codes to annotate *OsGi, Se1* (*Hd1)* and *Hd3a*. For rice the ‘Inferred from Genetic Interaction’ (IGI) code was used to describe the epistatic interaction between *Se1* (*Hd1)* and *Hd3a*. Table-III also includes the annotation of the same genes to the Gene Ontology (GO). Although this information is not provided by the POC database, it can be retrieved by visiting the respective source databases TAIR and Gramene from the gene detail pages. The information on GO annotations, further suggests the biochemical roles of these genes and their functional similarity or dissimilarity.

Cross-database querying is often difficult because of the way the stage of plant growth is described or the way a trait or phenotype is assayed and curated in species-specific databases. In Arabidopsis the time of flowering is indicated by the number of rosettes on a plant (Samach et al., 2000), while it is indicated by the number of days between planting (or transplanting) and heading of the primary panicle in rice (Yano et al., 2000). The phenology or growth stage studied in both plants is the same (appearance of reproductive structure), but the annotation typically used to identify that growth stage is very different. Once generic terminology describing plant phenology/growth stages is agreed upon and consistently utilized in database curation, these kinds of results will become more readily accessible with fewer queries.

## Standard growth stage vocabulary in experimental description and design.

Associated with the problem of database curation is the problem of data collection in laboratories and research groups, where data related to plant growth stages are typically collected based on chronological age alone such as 5-days after germination, 10-days after flowering, 1-month old plant, leaf tissue was harvested in the spring of 2005 etc. The widely differing developmental timelines do not allow meaningful comparisons, even among members of the same species, particularly when environmental conditions vary. However if critical studies can be performed on a few model genotypes from the same species across various environments they can serve as a reference. This kind of data has been described for 24 rice cultivars, including Nipponbare, Azucena, IR36, IR64, Koshihikari etc. (Yin and Kropff, 1996), for 19 genotypes of maize, including B73, Mo17, hybrid B73xMo17 and 16 additional hybrids (Padilla and Otegui, 2005) and a comparative study including wheat, barley and maize (McMaster et al., 2005). The overall outcome of all these studies suggested that although genotypes may differ in their growth profiles in terms of growth rate or flowering time as a result of environmental variables (i.e., light, temperature or water deficit conditions), the targeted vegetative growth stages recorded by counting the number of leaves almost always followed a predictable pattern for a given genotype. The responses to variables such as increase or decrease of growth rate or stem elongation, versus the leaf numbers, were not interdependent. This further proved that such experiments can be used by researchers to estimate the growth stage profile based on counting the number of leaves and that this estimate of growth stage was independent of the environment as long as the genotype is known. Thus, data collected with reference to a commonly defined series of whole plant growth stages such as the ones described in the GSO will provide greater coherence and facilitate comparisons between and within species (Boyes et al., 2001).

## DISCUSSION

The GSO is meant to link genetic and molecular information along the ontogenetic trajectory of plant growth, from germination to senescence in developmental time and space. Development is the execution of the genetic program for the construction of a given organism. The morphological structure is the product of many hundreds or thousands of genes that must be expressed in an orchestrated fashion in order to create any given tissue, body part or multicellular structure (Davidson, 2001). Development is thus the outcome of a vast network of genes whose expression is regulated both spatially and temporally. Suites of genes are expressed only during specific times during the life cycle of a plant, while other genes are turned on and off intermittently throughout the life cycle. Effective annotation of growth stage-specific gene markers in plant genome databases requires the development and use of ontologies, such as the GSO described here. Many genetic and developmental studies are initially conducted using a specific model system that is rich in genomic resources, but validation of hypotheses often depends on investigation of multiple plant systems (Cullis, 2004). Incorporation of information from multiple sources requires integration and synthesis of data across species and database boundaries. The use of common terminology to describe homologous features in diverse species is the first step. Inclusion of synonyms for growth stages of every plant species offers an effective solution for the immediate term, but may become unwieldy in the future. It is analogous to the approach taken by the WORDNET project that defines words using sets of synonyms and currently covers 150,000 English words (Fellbaum, 1998). We are working with our software developers to provide tools that will categorize synonyms eventually helping the user community to find the GSO terms that qualify as the growth stage terms for the plant species of their choice and automate the process of identifying derivative synonyms that can be queried in multiple ways. For example, a user may want to query on the term “sixth leaf/six leaves/6 leaves”, all of which are derivatives of each other. Improvements in developer’s tools will help prevent the ontology from becoming unwieldy and will greatly improve the efficiency of searches.

The GSO will also be valuable in describing high throughput experimental designs, where plant development is typically analyzed using global patterns of gene expression at defined developmental stages (Schnable et al., 2004). We further anticipate that the design of an experiment is likely to influence the potential to conduct comparative analyses. For example, a problem may arise when a normalized set of tissue samples, e.g. from leaf tissue harvested at the 3, 6 and 10 leaf stages, is used to isolate a protein sample for a proteomics experiment or mRNA for either the microarray experiment or for constructing an EST/cDNA library. Unless each sequence from the library is associated with a particular source tissue and growth stage, it is very difficult to ascertain the actual growth stage at which the mRNA was expressed. Further in the PSO and GSO annotations it is not necessary that one gene is associated with only one plant structure and growth stage description. There can be multiple annotations to accommodate the necessary information about an expression profile, e.g. an EST accession can be expressed in leaf tissue at both the 3 and 10 leaf stage but it may not be detected in 6 leaf stage. Hence, the use of well-defined growth stage ontology would be extremely useful to provide a framework for comparing gene expression patterns analyzed at different stages within and across species.

The generic design of the GSO aims to facilitate the process of integrating genomic information from diverse plant systems to deepen our understanding of plant form and function. Adoption of the ontology will contribute to its continued improvement and development and will promote an increasingly global view of plant biology. Members of the POC have used the emerging growth stage ontology to annotate genes and phenotypes in plants. As proof of concept, data associations from TAIR and Gramene are already available and users can now search over 600 annotated genes, updated on a monthly basis. The Gramene database (Jaiswal et al., 2006) will display the cereal growth stage ontology (GRO) together with the GSO and eventually retire the GRO, giving transition time for its users to familiarize themselves with the new terms. A similar approach will be taken by TAIR (Rhee et al., 2003) and MaizeGDB (Lawrence et al., 2005) is currently testing their annotations. Initially, emphasis was focused on the core databases but expanding use of the ontology by Soybase collaborators Rex Nelson and Randy Shoemaker and SGN collaborators Naama Menda and Lukas Mueller highlights its utility for comparative genomics. Soybase has adapted the GSO for description of soybean data. SGN adapted the GSO for taxonomic family-wide description of Solanaceous plants and is currently testing it for tomato mutant description. In subsequent releases associations to maize and tomato will become available in the PO database, followed by soybean.

As our understanding of the gene networks and underlying molecular details regarding the origin and diversification of complex pathways such as flowering time grows, a challenge is presented to test the ability to place this knowledge into a framework that can accommodate the information as it emerges and place it into an appropriate comparative context. Similarly our current understanding of genetics and evolution in plants raises many questions about orthology, paralogy and co-orthology in diverse species (Malcomber et al., 2006). The functional relationships among these genes and gene families will be reflected in databases that annotate such information using precise morphological terms from the GSO and the PSO. The effective use of controlled vocabularies also helps identify problems and gaps in knowledge related to the curation of genes in different species where the evolutionary relationships are not entirely clear. Drawing from the experience of its core databases, the POC in future will address the above issues by preparing and sharing annotation standards that can be used by other member databases to the benefit of the larger plant science community.

The current GSO design is based on annual plants, therefore discussions are underway with collaborators representing the poplar and citrus research communities to expand it to include perennials. We also hope that future software developments will allow us to hard wire temporal relationships into the ontology. We encourage databases and individual researchers to contact us if they are suggesting new terms, modification of existing definition(s), term to term relationships or even interested in joining the POC by contributing the associations to their genes and mutant phenotypes by writing an e-mail at po-dev@plantontology.org. More information about joining POC can be found online http://www.plantontology.org/docs/otherdocs/charter.html).

## MATERIALS AND METHODS

### Ontology development

Biologists from University of Missouri at St. Louis and Missouri Botanical Gardens, and curators from the TAIR, MaizeGDB and Gramene databases worked together to evaluate growth and development in Arabidopsis*,* maize and rice, examining the vocabularies and models used to describe the whole-plant growth stages in each species. Growth stages of Arabidopsis were described by (Boyes et al., 2001) based on the BBCH scale (Meier, 1997) that includes both monocot and non-monocot species The BBCH scale in turn is based on the Zadok scale, developed for Triticeae (Zadok et al., 1974), which forms one of the literature bases for the cereal growth stage ontology developed by Gramene database (Jaiswal et al., 2006). Rice terminology was derived from (INGER, 1996), for Triticeae, from (Zadok et al., 1974) and (Haun, 1973), and for sorghum from Doggett, (1988).  MaizeGDB (Lawrence et al., 2005) derives its growth stage vocabulary from a modified version of Ritchie's scale (Ritchie et al., 1996). The vocabulary developed by MaizeGDB was integrated into cereal growth stage ontology in the Gramene database as well.  With these preexisting interconnections in the core databases, we were able to begin synthesizing them into a generic ontology. Similar growth stage concepts for the above species were identified and mapped to the generic growth stages and stored in mapping files. The mapping files are available at (http://brebiou.cshl.edu/viewcvs/Poc/mapping2po/). More details about the project and ontology development is available on the documentation section of the plant ontology website (http://www.plantontology.org/docs/docs.html).

## Review of ontology

All aspects of the ontologies developed by the POC, including the GSO, are a collaborative effort and involve evaluation and assessment by numerous external experts. Before each ontology is released to the public, the POC's internal board of senior editors provides critical assessments and offers suggestions for substantive changes which are thoroughly discussed and incorporated into a revised version of the ontologies. The revised ontologies are then released to database curators and developers, who check for inconsistencies and provide critical feedback about problems and/or advantages associated with use of the new ontologies. In the final phase, the ontologies are subjected to review (http://www.plantontology.org/docs/growth/growth.html) by an external panel of experts. Over 15 outside scientists with expertise in the growth and development of diverse plant species have provided valuable input to the development of this ontology. (http://www.plantontology.org/docs/otherdocs/acknowledgment_list.html)

## Ontology editing tools and web-interface

The plant ontologies are built and maintained using the Directed Acyclic Graph editor (DAG-edit) developed by the GO software group. It is open source software implemented in Java and installed locally; flat files are used to store the ontologies. DAG-edit permits creating and deleting new terms, and adding synonyms in categories such as exact, broad, narrow or related synonyms. This software also supports a user-defined plug-in for reading, saving, importing and exporting (Harris et al., 2004). (http://sourceforge.net/project/showfiles.php?group_id=36855). The ontologies are shown using a tree structure. As the GSO is a relatively small ontology, the DAG-edit shows a good overview of the expanded tree in one window. The tool DAG-Edit was superseded by the OBO-Edit (Open Biomedical Ontology Editor) in its recent release by the GO software group. The same will be used in the future development and maintenance of the GSO.

The PO uses the Amigo ontology browser as the web interface for searching and displaying the ontologies (Fig 4). Querying can be done using term names, numerical identifier, synonyms or definitions. The associated annotations to terms from all the represented databases can be viewed on the term detail page (Jaiswal et al., 2005).

## Acknowledgements:

The POC is supported by National Science Foundation (NSF) grant 0321666. We thank Drs. Rex Nelson and Randy Shoemaker from Soybase and Naama Menda and Lukas Mueller of SGN for their participation in development and mapping of Soybean and Solanaceae terms to the GSO. We thank numerous researchers for reviewing the GSO and they are listed online (http://www.plantontology.org/docs/otherdocs/acknowledgment_list.html). We apologize to the countless scientists and farmers whose observations on growth stages and plant development were not incorporated into this manuscript for lack of space. We acknowledge the Gene Ontology Consortium for software support. We thank Drs. Dean Ravenscroft and Junjian Ni for reviewing the manuscript.

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## FIGURE LEGENDS

### FIGURE-1

The parent and child term organization in the whole plant growth stage ontology (GSO). The solid curved lines joining the terms represent IS_A relationship and the dotted curved lines suggest a PART_OF relationship between the child and the parent terms. A term may or may not have a child term. In this example, germination IS_A vegetative stage and flowering IS_A reproductive stage. Similarly vegetative stage, reproductive stage, senescence and dormancy are subtypes (IS_A) of whole plant growth stage. Root emergence and shoot emergence are PART_OF the seedling growth stage. The seedling growth stage and imbibition are PART_OF germination. In this figure not all the children terms are shown for every parent term in the GSO.

### FIGURE-2

The GSO as seen on the ontology browser available at http://www.plantontology.org/amigo/go.cgi. (a) For browsing, simply click on the [+] icon before the term name plant growth and developmental stages, and then on the [+] next to whole plant growth stages (GSO). This will expand the tree by opening the children terms. The PO ID is the term’s accession number, and the number followed by the term name is the total number of associations that have been curated to the genes for a given term. This number will change depending on the gene product filter a user may have chosen. Users can also get a pie chart showing the distribution of data associations to a term’s children term. In this figure, the general level (top level) terms in the GSO are “A Vegetative growth”, “B Reproductive growth”, “C Senescence”, and “D Dormancy”. The sub-stages of “A Vegetative Growth” are “0 Germination”, “1 Main Shoot Growth” and “2 Formation of Axillary Shoot”, while the sub-stages of “B Reproductive Growth” are “3 Inflorescence Visible” ,“4 Flowering” ,“5 Fruit Formation” and “6 Ripening”. Neither “C senescence” nor “D dormancy” currently has sub-stages beneath them. The alphanumeric prefixes serve to make the sub-stages appear in the order in which they occur during the plant’s lifecycle. If the temporal order is not defined consistently in all plants, the terms may not have these prefixes. The prefixes are usually abbreviations of the term name; for example, ‘LP’ is for leaf production, ‘SE’ is for stem elongation. The numerical portion uses double digits starting with 01, 02 and so on. Each of the sub-stages may have more specific stages beneath it. When a term is retired or superseded, it is considered ‘Obsolete’. Such terms are moved to a location in the hierarchy underneath a term named “obsolete_growth_and_developmental_stage”. (b) A detailed view of the sub-stage PO:0007133, ‘Leaf production’ and its children. Children terms up to 20 leaves visible were added to accommodate the growth stage requirements of the maize plant.

**FIGURE-3**

Corresponding growth stages in different plants and advantages of using broad and granular terms for annotations. In this example one can say flowering occurs in plant A at the 6-leaf visible stage, in plant B at the 9-leaf visible stage and in plant C at the11-leaf visible stage. Plants A-C represents either different germplasm accessions/cultivars of the same species or accessions/cultivars from different species. This nomenclature allows the researcher to record when a gene is expressed or a phenotype is observed by following the gradual progression of the plant’s lifecycle. For example, if a gene is expressed at the 6the leaf or the 5th internode stage, the meaning is now clear, while in the past, the information had to be recorded as the ‘5th leaf from the top of the plant’. Such annotation required that one wait until the plant completed its lifecycle to count the number of leaves from the top, or that one make an assumption how many leaves there would be in the plant/population used in the study. Note: the number of nodes and the number of leaves is always less than the number of internodes by one. The arrow pointing upwards suggests that the numbers are counted in that direction in ascending order starting with 1 and going up to ‘n’, where ‘n’ can be any number depending on the plant.

**FIGURE-4**

An example of a GSO search using the ontology browser and search web interface. (a) Ontology search results for ‘0 germination’ by using the ‘exact match’ and ‘terms’ filter. To start searching, visit the www.plantontology.org website and click on the ‘Search and

Browse Plant Ontology' link on the page menu. An ontology browser page opens that has a search option on the left hand side. Type the term name of interest, such as 'germination' for a generic search or '0 germination' for an exact match. Select the 'term' filter and 'submit query'. Click on the term name to visit the term detail page or browse the lineage of this term in the ontology by clicking the 'tree icon' next to the check box. (b) The term detail page provides information on the term name, accession/ID, synonyms, definition, comments and associations to genes. (c) The list of genes associated to the term are listed in the bottom half of the term detail page. A default list gives all the genes with every type of evidence code and source. The evidence type, species and source filters can be used to generate the list as desired. The list provides the gene symbol, name, source, evidence and a citation. The gene symbol links to the gene detail page and the source links to the original record in the contributor's database (e.g. TAIR/Gramene), the evidence code links to its details and the reference links to the original citation referred to by the contributor for inferring the ontology association to the gene. (d) The gene detail page provides information on the symbol, name, synonym, source, a list of all the terms in the GSO and PSO, evidence and the citations. This view suggests where and when a gene is expressed and/or an associated phenotype is observed.

**FIGURE-5**

Summary of the Arabidopsis and rice gene annotations to the GSO. (a) Growth stage-specific gene annotations from Arabidopsis and rice. The stages prefixed with A-D are the top most categories of the growth stages, namely vegetative, reproductive, senescence and dormancy. The stages prefixed with 0- 2 are vegetative sub-stages and those with 3-6 are reproductive sub-stages. 'All stages' means all the GSO terms. (b) A list of selected Arabidopsis and rice genes annotated to 5 specific growth stage terms, suggesting the current state of annotations and not the actual growth stage-specific profile. A similar list can be generated to get growth stage-specific gene expression profiles for a given species. In columns 2 and 3, the numbers [written in bold] appearing before the parentheses are the total number of gene annotations; species specific genes are written in italics.

**FIGURE-6**

Genes participating in the flowering time pathway. This figure illustrates the flowering time pathway genes from Arabidopsis, *GI*, *CO* and *FT*, and rice, *OsGI*, *Se1* (*Hd1*) and *Hd3a*. In the PO database, the annotation for these genes is provided by three databases, the National Arabidopsis Stock Centre (NASC), TAIR (for Arabidopsis) and Gramene (for rice). The curators have used terms (Table III) from the whole growth stage ontology (GSO) and plant structure ontology (PSO) to suggest when and where in a plant these genes were expressed or their phenotype was observed. Based on the experiment types (evidence codes) and citation evidences, the databases recorded information about the mutant/gene/gene product to the GSO and the PSO terms. Compared to the short day length promotion of flowering in rice, flowering is promoted by long day exposure in Arabidopsis. When rice is exposed to long days, it leads to a down regulation of the *Hd3a* gene by *Se1* (*Hd1*), leading to a delayed transition of the vegetative shoot apical meristem to the reproductive inflorescence meristem. In other words, the growth stage ‘inflorescence visible (*sensu* Poaceae)’, which is synonymous with ‘heading stage’, is delayed. The double headed arrows suggest that the Arabidopsis and rice genes are orthologous. The colored boxes around the genes represent the databases that provided the gene annotations. In the PO database, the putative orthology of these genes cannot currently be determined or displayed, but it can be inferred by visiting either the Gramene or the TAIR database.

**TABLE-I**

A summary of the number of synonyms integrated into the GSO from each species/family/source. The Integration of synonyms for Soybean and Solanaceae is in progress.

| **Species/source** | **Number of synonyms** |
|---|---|
| Arabidopsis | 93 |
| Rice | 23 |
| Maize | 162 |
| Wheat | 65 |
| Oat | 65 |
| Barley | 65 |
| Sorghum | 13 |
| BBCH and Zadok scales | 381 |
| Soybean | 79 |
| Solanaceae (mainly tomato) | 51 |
| All the species | 997 |
| Average number of synonyms per GSO term | About 9 |

**TABLE-II**

List of evidence codes for use in annotations to GSO. These are used in building the annotation inferences that indicate the type of experiment cited by the researcher whose data was used to determine the protein and/or transcript expression and phenotype of mutant(s) or quantitative trait loci (QTL).

| **Evidence code** | **Name** |
|---|---|
| IC | Inferred by curator |
| IDA | Inferred from direct assay |
| IEA | Inferred from electronic annotation |
| IEP | Inferred from expression pattern |
| IMP | Inferred from mutant phenotype |
| IGI | Inferred from genetic interaction |
| IPI | Inferred from physical interaction |
| ISS | Inferred from sequence or structural similarity |
| NAS | Non-traceable author statement |
| TAS | Traceable author statement |

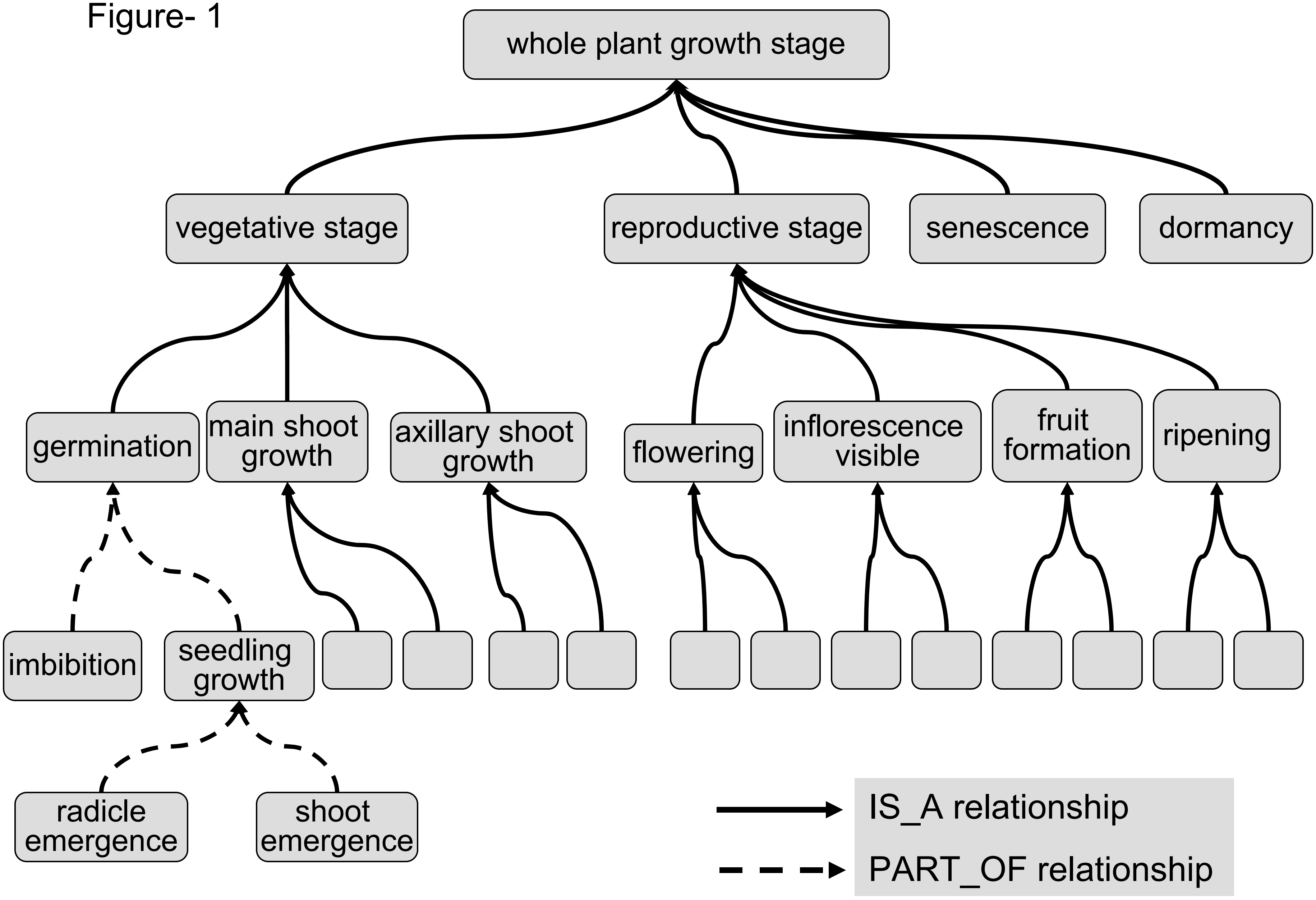
**TABLE-III**

Annotation of the three orthologous set of flowering time pathway genes from Arabidopsis and rice. The GSO and PSO annotations for Arabidopsis *GI, CO* and *FT* and rice *OsGI, Se1 (Hd1)* and *Hd3a* genes were imported from the PO database. The annotations to GO (column 4-6) were imported from TAIR and Gramene databases in order to give an overview on the functional characteristics of the orthologous genes. The curators assigned the ontology terms from the whole growth stage (GSO) and plant structure (PSO) aspect to suggest when and where in a plant these genes were expressed or phenotyped. Depending on the experiment type (evidence code) and citation evidence (references), the databases recorded information about the mutant/gene/gene product to GSO and PSO terms. The same procedure was used for GO annotations. Columns 2-6 provide information on the term names, ID, and the evidence code.

| Genes | Plant growth stage (GSO) | Plant structure (PSO) | GO: cellular component | GO: molecular function | GO: biological process |
|---|---|---|---|---|---|
| **Arabidopsis** | | | | | |
| *GI* | whole plant (PO:0000003) (TAS) | flower (PO:0009046) (IMP) | nucleoplasm (GO:0005654) (IDA)<br>nucleus (GO:0005634) (IDA) | Unknown | response to cold (GO:0009409) (IMP)<br>flower development (GO:0009908) (TAS)<br>regulation of circadian rhythm (GO:0042752) (IMP)<br>positive regulation of long-day photoperiodism, flowering (GO:0048578) (IMP) |

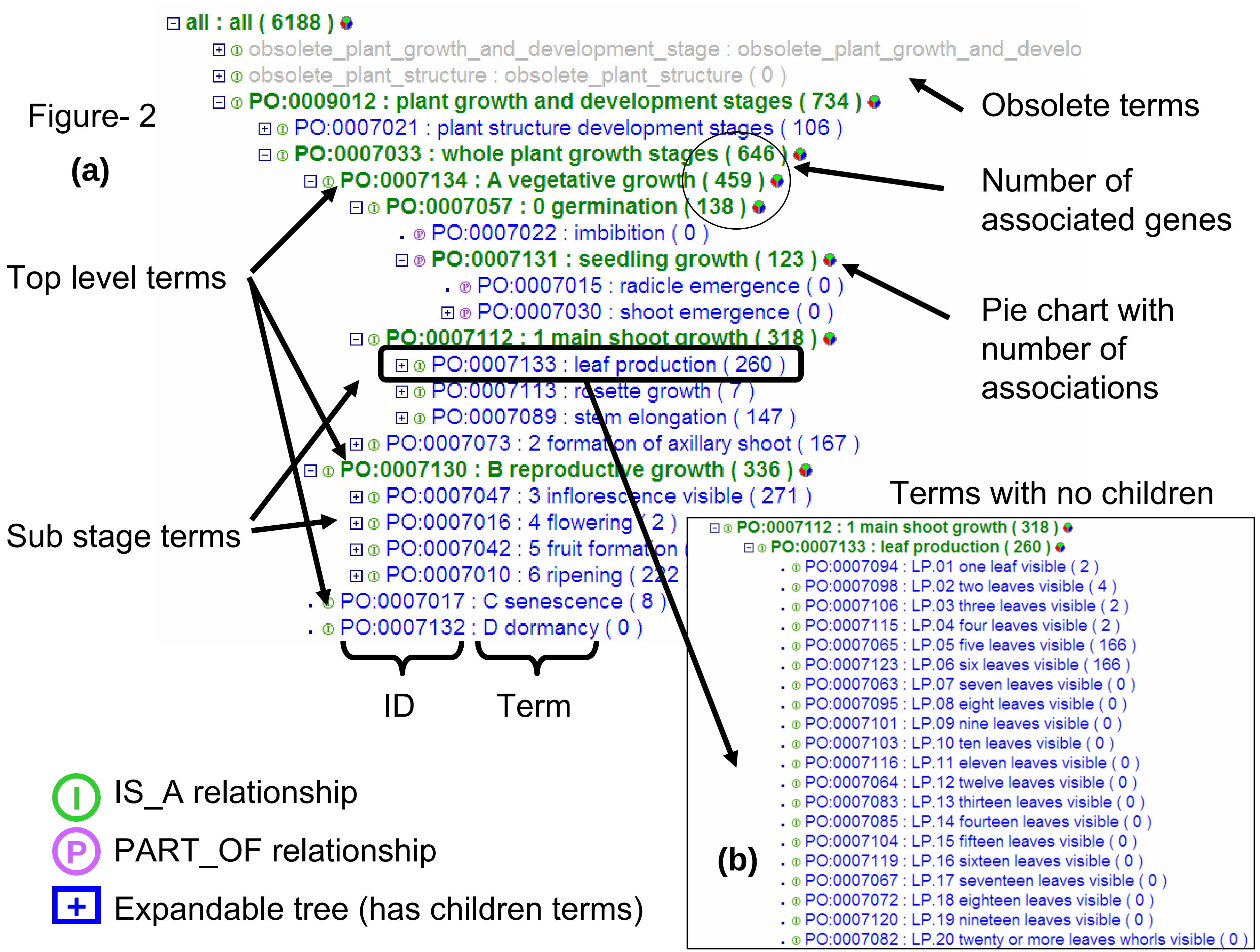
| | | | | | |
|---|---|---|---|---|---|
| *CO* | Not available | flower (PO:0009046) (IMP) | nucleus (GO:0005634) (NAS) | transcription factor activity (GO:0003700) (ISS) | regulation of flower development (GO:0009909) (IMP) |
| *FT* | Not available | leaf (PO:0009025) (TAS)<br>shoot apex (PO:0000037) (IDA) | unknown | phosphatidylethanolamine binding (GO:0008429) (ISS)<br>protein binding (GO:0005515) (IPI) | positive regulation of flower development (GO:0009911) (IMP) |
| **Rice** | | | | | |
| *OsGi* | inflorescence emergence from flag leaf sheath (PO:0000003) (IMP) | Inflorescence (PO:0009049) (IMP) | nucleus (GO:0005634) (IEP) | Unknown | inflorescence development (GO:0010229) (IMP) |
| *Se1 (Hd1, Fl1)* | inflorescence emergence from flag leaf sheath (PO:0007041) (IGI, IMP)<br>stem elongation (PO:0007089) (IMP)<br>FR.04 fruit ripening complete (PO:0007038) (IMP) | floret (sensu Poaceae) (PO:0006318) (IMP)<br>inflorescence (PO:0009049) (IGI, IMP)<br>inflorescence meristem (PO:0000230) (IMP)<br>seed (PO:0009010) (IMP) | nucleus (GO:0005634) (IEP) | DNA binding (GO:0003677) (ISS)<br>transcription factor activity (GO:0003700) (ISS)<br>zinc ion binding (GO:0008270) (ISS) | inflorescence development (GO:0010229) (IGI)<br>long-day photoperiodism (GO:0048571) (IEP, IGI)<br>short-day photoperiodism (GO:0048572) (IEP, IGI) |
| *Hd3a (Fl32a)* | inflorescence emergence from flag leaf sheath (PO:0007041) (IMP)<br>stem elongation (PO:0007089) (IMP)<br>FR.04 fruit ripening complete (PO:0007038) (IMP) | floret (sensu Poaceae) (PO:0006318) (IMP)<br>inflorescence (PO:0009049) (IMP)<br>inflorescence meristem (PO:0000230) (IMP)<br>seed (PO:0009010) (IMP)<br>sporophyte (PO:0009003) (IEP) | Unknown | phosphatidylethanolamine binding (GO:0008429) (ISS) | inflorescence development (GO:0010229) (IMP)<br>short-day photoperiodism (GO:0048572) (IMP)<br>regulation of timing of transition from vegetative to reproductive phase (GO:0048510) (IMP) |

Figure- 1



whole plant growth stage
vegetative stage
reproductive stage
senescence
dormancy
germination
main shoot growth
axillary shoot growth
flowering
inflorescence visible
fruit formation
ripening
imbibition
seedling growth
radicle emergence
shoot emergence
IS_A relationship
PART_OF relationship

Figure- 2



all : all ( 6188 )
obsolete_plant_growth_and_development_stage : obsolete_plant_growth_and_develo
obsolete_plant_structure : obsolete_plant_structure ( 0 )
PO:0009012 : plant growth and development stages ( 734 )
PO:0007021 : plant structure development stages ( 106 )
PO:0007033 : whole plant growth stages ( 646 )
PO:0007134 : A vegetative growth ( 459 )
PO:0007057 : 0 germination ( 138 )
PO:0007022 : imbibition ( 0 )
PO:0007131 : seedling growth ( 123 )
PO:0007015 : radicle emergence ( 0 )
PO:0007030 : shoot emergence ( 0 )
PO:0007112 : 1 main shoot growth ( 318 )
PO:0007133 : leaf production ( 260 )
PO:0007113 : rosette growth ( 7 )
PO:0007089 : stem elongation ( 147 )
PO:0007073 : 2 formation of axillary shoot ( 167 )
PO:0007130 : B reproductive growth ( 336 )
PO:0007047 : 3 inflorescence visible ( 271 )
PO:0007016 : 4 flowering ( 2 )
PO:0007042 : 5 fruit formation (
PO:0007010 : 6 ripening ( 222
PO:0007017 : C senescence ( 8 )
PO:0007132 : D dormancy ( 0 )

PO:0007112 : 1 main shoot growth ( 318 )
PO:0007133 : leaf production ( 260 )
PO:0007094 : LP.01 one leaf visible ( 2 )
PO:0007098 : LP.02 two leaves visible ( 4 )
PO:0007106 : LP.03 three leaves visible ( 2 )
PO:0007115 : LP.04 four leaves visible ( 2 )
PO:0007065 : LP.05 five leaves visible ( 166 )
PO:0007123 : LP.06 six leaves visible ( 166 )
PO:0007063 : LP.07 seven leaves visible ( 0 )
PO:0007095 : LP.08 eight leaves visible ( 0 )
PO:0007101 : LP.09 nine leaves visible ( 0 )
PO:0007103 : LP.10 ten leaves visible ( 0 )
PO:0007116 : LP.11 eleven leaves visible ( 0 )
PO:0007064 : LP.12 twelve leaves visible ( 0 )
PO:0007083 : LP.13 thirteen leaves visible ( 0 )
PO:0007085 : LP.14 fourteen leaves visible ( 0 )
PO:0007104 : LP.15 fifteen leaves visible ( 0 )
PO:0007119 : LP.16 sixteen leaves visible ( 0 )
PO:0007067 : LP.17 seventeen leaves visible ( 0 )
PO:0007072 : LP.18 eighteen leaves visible ( 0 )
PO:0007120 : LP.19 nineteen leaves visible ( 0 )
PO:0007082 : LP.20 twenty or more leaves whorls visible ( 0 )

Figure- 3

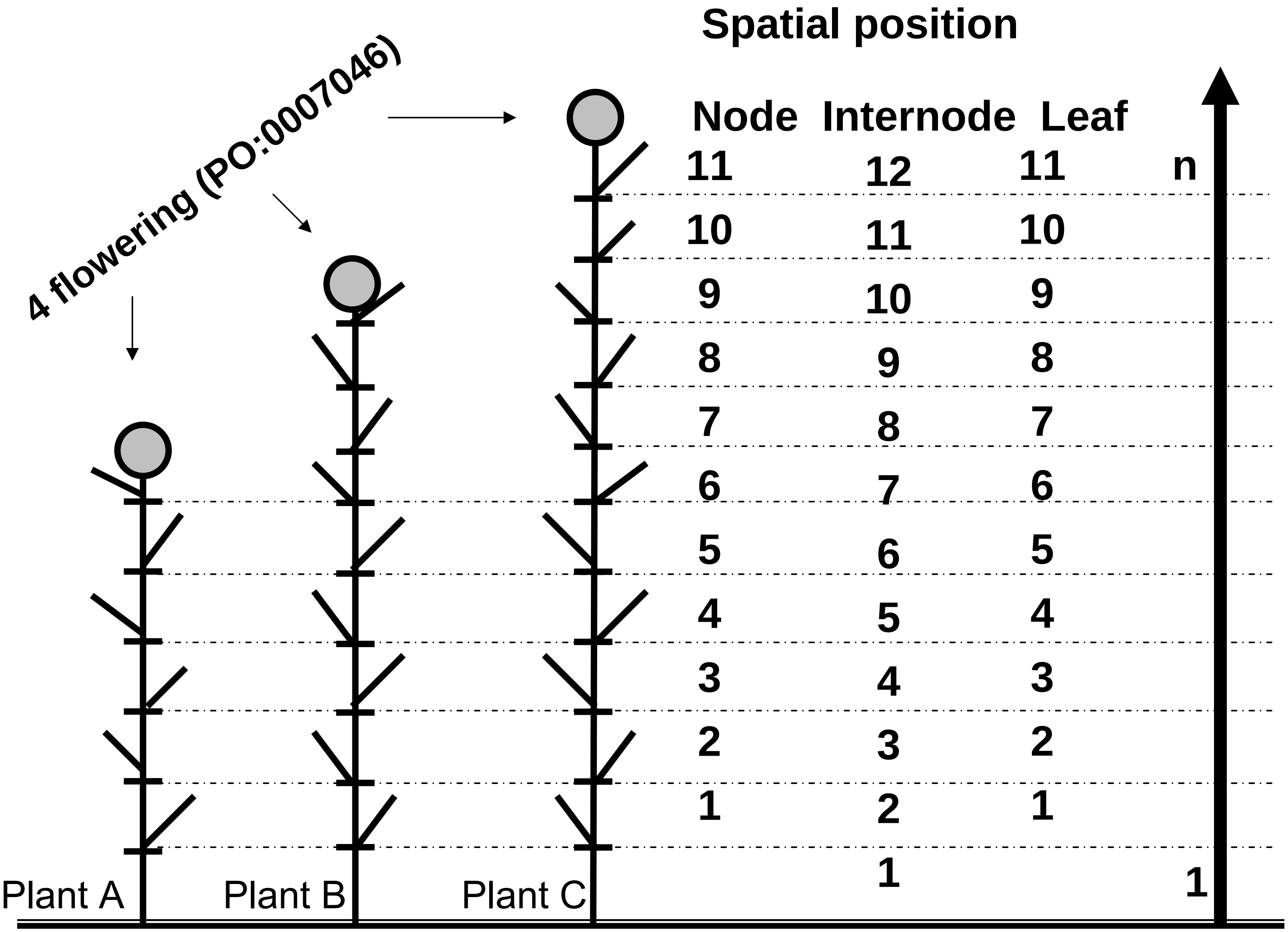
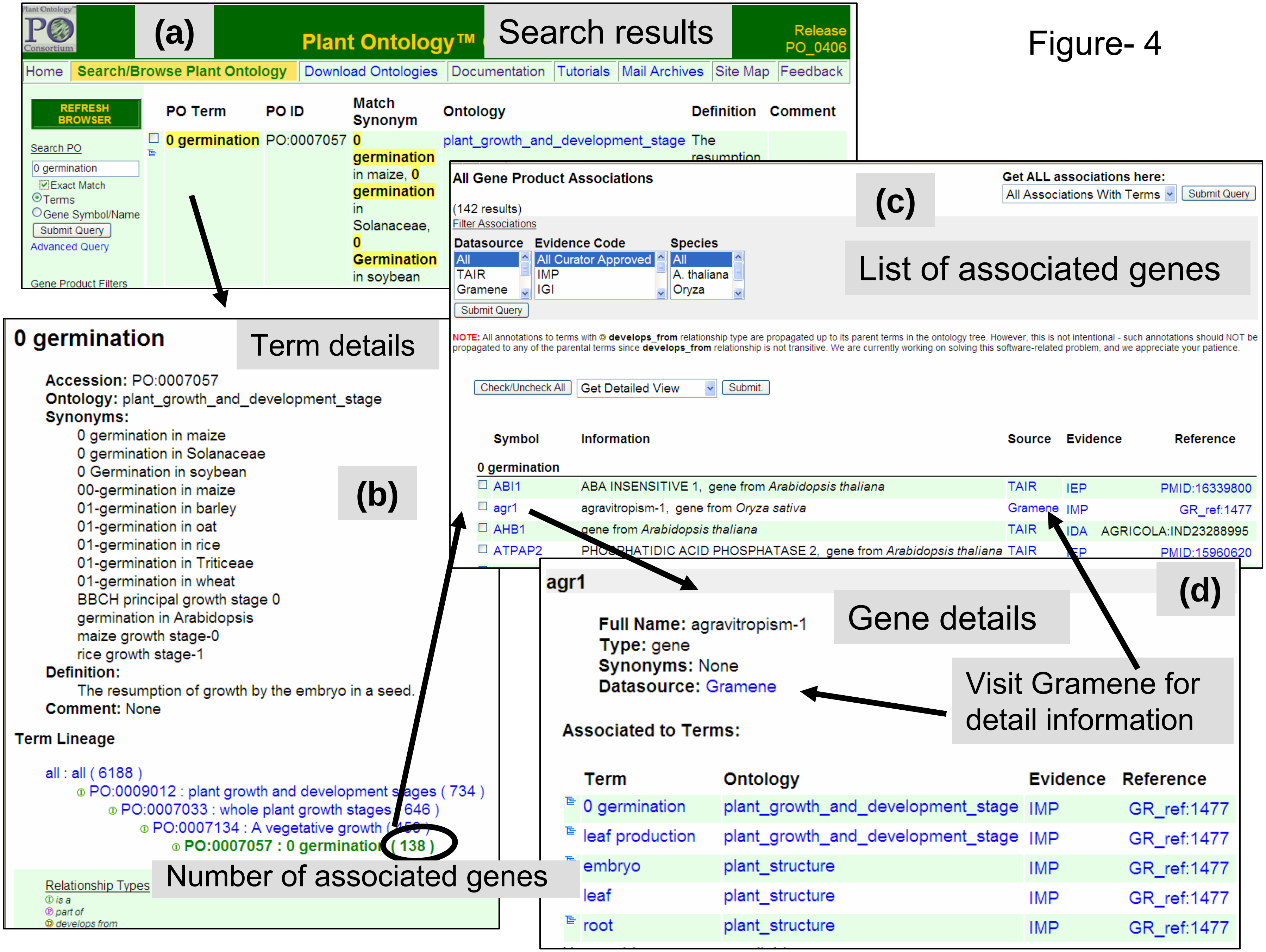

Spatial position
4 flowering (PO:0007046)
Node
Internode
Leaf
11 12 11 n
10 11 10
9 10 9
8 9 8
7 8 7
6 7 6
5 6 5
4 5 4
3 4 3
2 3 2
1 2 1
1
1
Plant A
Plant B
Plant C

Figure- 4



Search PO: 0 germination

☑ Exact Match

● Terms

○ Gene Symbol/Name

| | PO Term | PO ID | Match Synonym | Ontology | Definition | Comment |
|---|---|---|---|---|---|---|
| ☐ | 0 germination | PO:0007057 | 0 germination in maize, 0 germination in Solanaceae, 0 Germination in soybean | plant_growth_and_development_stage | The resumption | |

**0 germination**

**Accession:** PO:0007057

**Ontology:** plant_growth_and_development_stage

**Synonyms:**

- 0 germination in maize
- 0 germination in Solanaceae
- 0 Germination in soybean
- 00-germination in maize
- 01-germination in barley
- 01-germination in oat
- 01-germination in rice
- 01-germination in Triticeae
- 01-germination in wheat
- BBCH principal growth stage 0
- germination in Arabidopsis
- maize growth stage-0
- rice growth stage-1

**Definition:**

The resumption of growth by the embryo in a seed.

**Comment:** None

**Term Lineage**

all : all ( 6188 )
 Ⓘ PO:0009012 : plant growth and development stages ( 734 )
  Ⓘ PO:0007033 : whole plant growth stages ( 646 )
   Ⓘ PO:0007134 : A vegetative growth ( 458 )
    Ⓘ **PO:0007057 : 0 germination ( 138 )**

**All Gene Product Associations**

(142 results)

| Datasource | Evidence Code | Species |
|---|---|---|
| All | All Curator Approved | All |
| TAIR | IMP | A. thaliana |
| Gramene | IGI | Oryza |

**NOTE:** All annotations to terms with Ⓓ **develops_from** relationship type are propagated up to its parent terms in the ontology tree. However, this is not intentional - such annotations should NOT be propagated to any of the parental terms since **develops_from** relationship is not transitive. We are currently working on solving this software-related problem, and we appreciate your patience.

**0 germination**

| | Symbol | Information | Source | Evidence | Reference |
|---|---|---|---|---|---|
| ☐ | ABI1 | ABA INSENSITIVE 1, gene from *Arabidopsis thaliana* | TAIR | IEP | PMID:16339800 |
| ☐ | agr1 | agravitropism-1, gene from *Oryza sativa* | Gramene | IMP | GR_ref:1477 |
| ☐ | AHB1 | gene from *Arabidopsis thaliana* | TAIR | IDA | AGRICOLA:IND23288995 |
| ☐ | ATPAP2 | PHOSPHATIDIC ACID PHOSPHATASE 2, gene from *Arabidopsis thaliana* | TAIR | IEP | PMID:15960620 |

**agr1**

**Full Name:** agravitropism-1

**Type:** gene

**Synonyms:** None

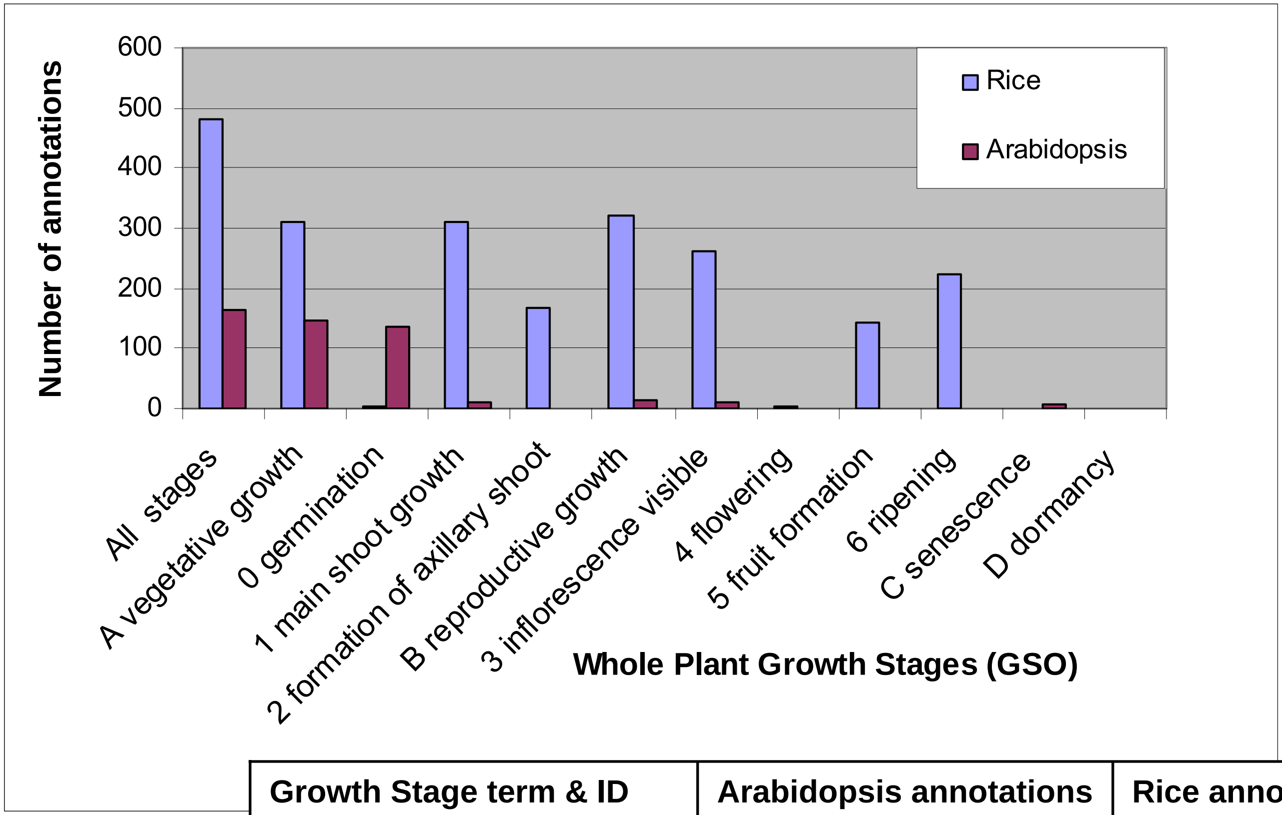
**Datasource:** Gramene

**Associated to Terms:**

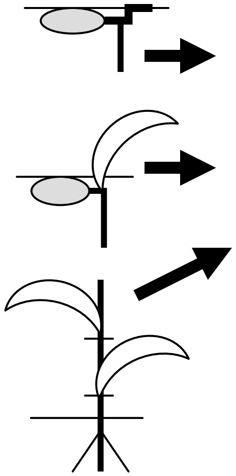
| Term | Ontology | Evidence | Reference |
|---|---|---|---|
| 0 germination | plant_growth_and_development_stage | IMP | GR_ref:1477 |
| leaf production | plant_growth_and_development_stage | IMP | GR_ref:1477 |
| embryo | plant_structure | IMP | GR_ref:1477 |
| leaf | plant_structure | IMP | GR_ref:1477 |
| root | plant_structure | IMP | GR_ref:1477 |

Figure-5

(a)



(b)



| Growth Stage term & ID | Arabidopsis annotations | Rice annotations |
|---|---|---|
| 0 Germination<br>PO:0007057 | **136** (*ABI1, COX6B, GA4, LEP, AAE7, TED3*) | **2** (*d10, agr1*) |
| LP.01 one leaf visible<br>PO:0007094 | none | **2** (*bierf1, gh2*) |
| LP.02 two leaves visible<br>PO:0007098 | **2** (*ATPRP2, PRP4*) | **2** (*bierf1, gh2*) |
| 3 Inflorescence visible<br>PO:0007047 | **11** (*AOX1B, ATRBP1, ATRAD51, PGA4*) | **260** (*Gi, gh1, gf1, sd1, prp1, Rcn1, Rcn2*) |
| C senescence<br>PO:0007017 | **8** (*SAG101, SRG1, CAT3, ASN1, SAG4*) | none |

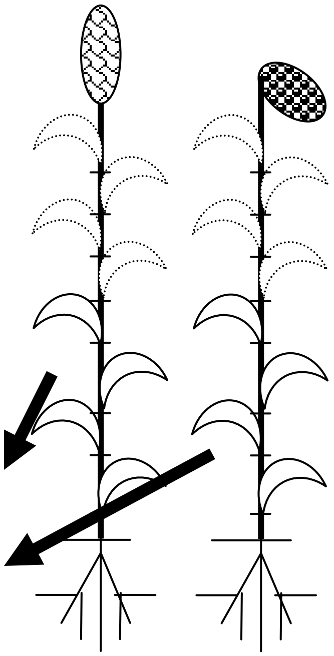
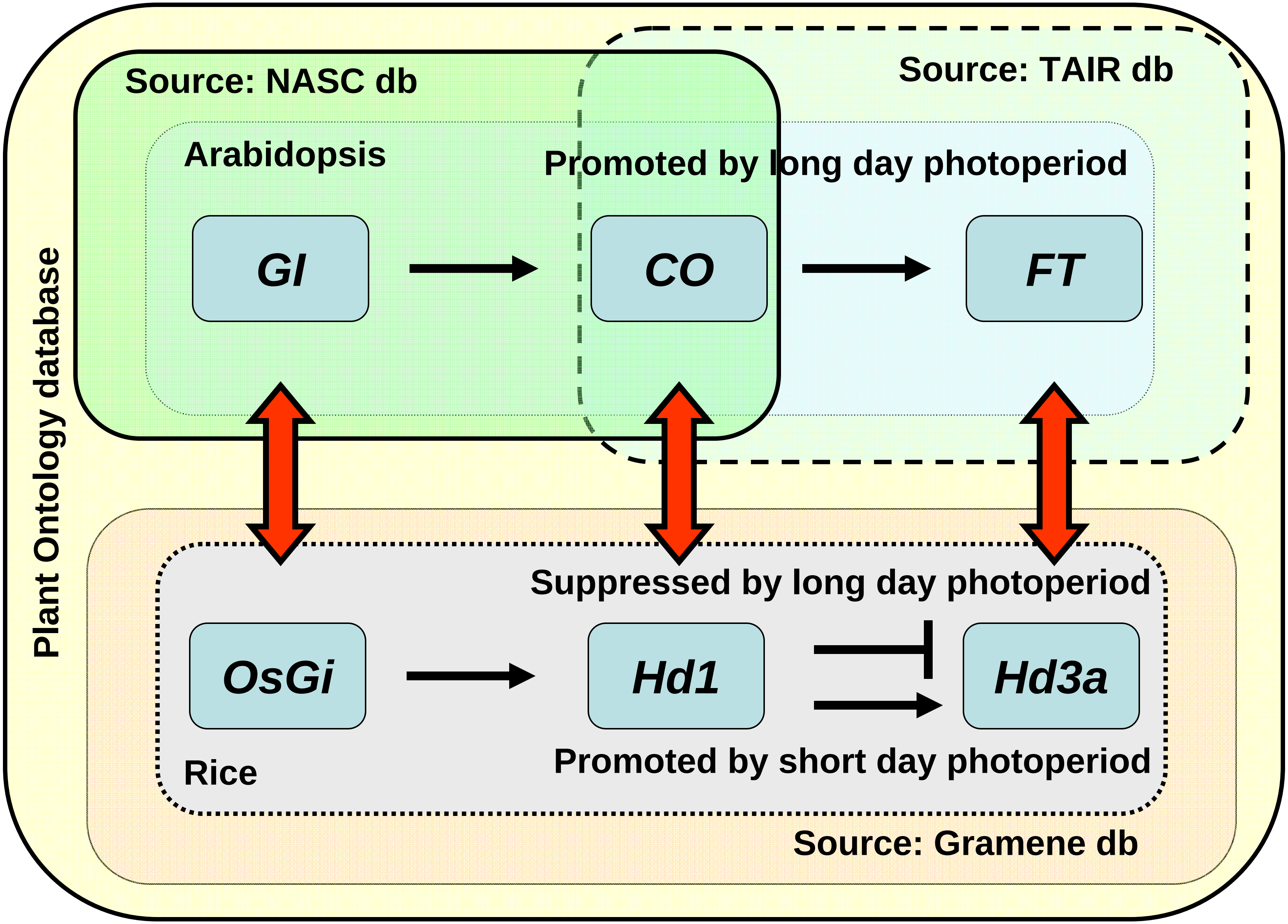


Figure- 6


Source: NASC db
Source: TAIR db
Arabidopsis
Promoted by long day photoperiod
GI
CO
FT
Plant Ontology database
Suppressed by long day photoperiod
OsGi
Hd1
Hd3a
Rice
Promoted by short day photoperiod
Source: Gramene db

To be published in *Plant Bioinformatics*, D. Edwards (Editor) for the series *Methods in Molecular Biology*. Humana Press, Totowa, New Jersey, USA.

## X

# MaizeGDB: The Maize Genetics and Genomics Database

**Carolyn J. Lawrence**

## Abstract

MaizeGDB is the community database for biological information about the crop plant *Zea mays*. Genetic, genomic, sequence, gene product, functional characterization, literature reference, and person/organization contact information are among the datatypes stored at MaizeGDB. At the project's website (http://www.maizegdb.org) are standardized custom interfaces enabling researchers to browse data and to seek out specific information matching explicit search criteria. In addition, pre-compiled reports are made available for particular types of data and bulletin boards are provided to facilitate communication and coordination among members of the community of maize geneticists.

**Key Words:** Maize; database; genetics; genomics; genome; model organism database.

## 1. Introduction

MaizeGDB is the repository for and interface to maize genetics and genomics data. Its content is comprised of records previously stored at the MaizeDB *(1)* and ZmDB *(2)* repositories (which are no longer in operation) as well as sequence data provided by workers at PlantGDB *(3)*, information gleaned from primary literature and entered into the database via manual curation, and data provided directly by the maize researchers who generated it. Because not all maize data are housed within MaizeGDB, contextual links are embedded throughout the data interface to enable navigation to other sites of interest (see **Table 1** for a list of linked sites).

In addition to storing and making available maize data, workers at MaizeGDB also provide services to the community of maize geneticists. Bulletin boards for news items, information of interest to cooperators, lists of websites for projects that focus on the scientific study of maize, an editorial board's recommended reading list, and educational outreach items are among the webpages made available through the MaizeGDB site (see **Table 2**). In addition, workers at MaizeGDB provide technical support for the Maize Genetics Executive Committee and the Annual Maize Genetics Conference.

Information about the history of MaizeGDB and the technical aspects of project's operation are described elsewhere ***(see 4 and 5, respectively)***. Reported here are the types of data that are made available at MaizeGDB, some generalized search strategies that can be applied across various datatypes, and a number of specialized example usage cases. Mechanisms for adding data to the database also are described in detail.

## 2. Materials

### *2.1. Genetic Data*

1. Loci including (but not limited to) genes, chromosomal segments, centromeres, introns, probed sites, and quantititative trait loci (QTL).

2. Variations including the set of alleles at a given locus, chromosomal structural variations, cytoplasmic variations, DNA polymorphisms, rearrangements, transpositions, etc.
3. QTL experiment environmental conditions, parental stocks, traits of interest, locus summaries, and raw data files.
4. Maps, over 1200 including high-resolution genetic maps and cytogenetic (cytological) maps along with associated data including mapping panel descriptors, population size, source information (usually a researcher's name), and related maps.
5. Seed stock descriptors consisting of a unique identifier (the stock name) and known synonyms, the stock source (e.g., an individual researcher's name or an organization name like the "Maize Genetics Cooperation – Stock Center"), and associated focus linkage group assignments, genotypic variations, karyotypic variations, phenotypes, and parental stock identifiers.

### 2.2. Genomic and Sequence Data

1. Sequences and sequence contig membership data.
2. Molecular probes including (but not limited to) BACs, YACs, cDNAs, and ESTs.
3. Molecular probe preparation methods for the amplification of, e.g., overgos, SSRs, RAPDs, RFLP, AFLPs, and other genomic DNAs.

**Table 1.** Contextually linked site list.

| ***Site Name*** | ***Web Address*** | ***Connection Context*** |
|---|---|---|
| NCBI Map Viewer | http://www.ncbi.nlm.nih.gov/mapview/ | Maps |
| Gramene | http://www.gramene.org/ | Loci, Maps |
| PlantGDB | http://www.plantgdb.org/ | Loci, Sequences, Sequence contigs |
| DDBJ<br>EMBL<br>TIGR<br>CerealsDB (SNPs) | http://www.ddbj.nig.ac.jp/<br>http://www.ebi.ac.uk/<br>http://maize.tigr.org/<br>http://www.cerealsdb.uk.net/cgi-bin/maize_snip.pl | Sequences |
| GenBank | http://www.ncbi.nih.gov/Genbank/ | Sequences, Probes |
| Maize Mapping Project (WebFPC) | http://www.genome.arizona.edu/fpc/WebAGCoL/maize/ | Probes |
| BioCyc<br>KEGG | http://www.biocyc.org<br>http://www.genome.ad.jp/kegg/ | Gene products |

| | | |
|---|---|---|
| SwissProt/TrEMBL | http://www.expasy.org/ | |
| AmiGO | http://www.godatabase.org<br>/cgi-bin/amigo/go.cgi | |
| PubMed | http://www.pubmed.gov/ | Person/Organization,<br>References |
| GRIN | http://www.ars-grin.gov/npgs/ | Stocks |

### *2.3. Gene Product and Functional Characterization Descriptions*

1. Gene products with associated Enzyme Commission (EC) numbers, expression induction conditions, subcellular localization data, metabolic pathway, known metabolic cofactors, mass (kDa), and links to loci that encode them.
2. Phenotypic descriptions that include trait descriptions and affected tissue types/organs (body parts) alongside mutant images.

### *2.4. Literature References and Person/Organization Records*

1. References from primary literature, the Maize Genetics Cooperation – Newsletter, and abstracts from the Annual Maize Genetics Conference; associated with virtually all other data types.

2. Contact information records for cooperators, authors, and organizations.

Table 2. Bulletin boards and static pages.

| ***Page Title and Web Address*** | ***Content Description*** |
|---|---|
| News Column<br>http://www.maizegdb.org/ | News bulletins are displayed in the right margin. Older items are accessible through a link near the bottom. |
| Tutorial<br>http://www.maizegdb.org/tutorial/ | Online step-by-step tutorial explains how to use the MaizeGDB website. |
| Data Contribution ‘How To’ Guide<br>http://www.maizegdb.org/data_contribution.php | Displays sources of currently stored data and how researchers can contribute their own data. |
| Editorial Board<br>http://www.maizegdb.org/editorial_board.php | A list of noteworthy references selected monthly by the MaizeGDB Editorial Board. |
| Cooperators’ Page<br>http://www.maizegdb.org/cooperators.php | Page of links to resources supporting the cooperative spirit shared among maize researchers. |
| Maize Genetics Cooperation – Newsletter | Makes accessible online copies of |

| | |
|---|---|
| http://www.maizegdb.org/mnl.php | the MNL and provides information on how to receive hard copies. |
| Maize Genetics Executive Committee<br>http://www.maizegdb.org/mgec.php | Explains the membership, goals, function, and history of the MGEC. |
| Maize Genetics Conference<br>http://www.maizegdb.org/maize_meeting/ | Online access to information about when and where the Maize Genetics Conference will take place, and access to online forms for submitting abstracts, etc. |
| Maize Research Projects List<br>http://www.maizegdb.org/maizeprojects.php | A list of maize projects and links to their respective project sites. |
| Educational Resources<br>http://www.maizegdb.org/education.php | Makes accessible materials for maize educational outreach. |

### *2.5. Terms, Controlled Vocabularies, and Ontologies*

1. Terms and term definitions that describe stored data of various types.
2. Controlled vocabularies, the set of terms that describe a given process or datatype. E.g., terms of type "Developmental Stage" make up one controlled vocabulary.
3. Ontologies, hierarchically related controlled vocabularies that serve to enable communication across different databases and data sets. Within

MaizeGDB are the Gene Ontologies ***(6)*** and the Plant Structure Ontology ***(7)***. Nascent ontologies like the Trait and Environment Ontologies, which are being developed by Gramene in collaboration with the Plant Ontology Consortium ***(***http://www.plantontology.org/ and ***8)***, are also incorporated and utilized as they emerge.

## 3. Methods

Navigating data to find specific, useful pieces of information is not always a simple task. Learning to use the tools that will enable facile data navigation is, therefore, a good use of time. By learning the general methods for browsing and searching MaizeGDB, the time required to locate information will be decreased, allowing for more to be spent testing hypotheses at the bench.

In each of the following sections, general techniques for efficiently and effectively navigating the MaizeGDB interface are described. Following each general description is an example usage case that explains how to access relevant and useful data to meet a specific research need.

### *3.1. Embedded Search and Feedback Mechanisms*

The fastest and easiest way to navigate to data of interest at MaizeGDB is by using the search bars. Search bars are available at the top and bottom of each page within a horizontal green band (*see* Fig. 1). Also present at the top of the page are the MaizeGDB icon (*see* **Note 1**) and links to bulletin boards including a job board, a list of upcoming events, and others. At the bottom of the page are the search bar and a link to send feedback to MaizeGDB personnel (*see* **Note 2**). The top and bottom search bars function identically. Virtually all datatypes can be queried simultaneously by selecting a type of record to search using the dropdown menu and entering a query word or phrase in the text box then pressing the button marked “Go!” (*see* **Note 3**). Described below is a protocol describing how to use the search bars to locate records of interest. Here, instructions are given to find information about available probes that mark the *bronze1* (*bz1*) locus as well as the information about how to obtain a cloned sequence of *bz1* for experimental use.

1. Go to http://www.maizegdb.org.
2. Locate the top search bar and click on the button marked with a question mark within the green band.
3. Read the note that appears in the popup window. (*See* **Note 4**).

4. Specify criteria to locate records about *bronze1* by selecting “locus / loci” from the dropdown menu and by typing `*bz1` into the field to the right. Click the button marked “Go!” (*See* **Note 5**).
5. The locus page for *bz1* gene is first in the results list (*see* **Note 6**). Click the link to the *bz1* gene.
6. On this page, scroll down to see the list of BACs, overgos, and other probes known to mark the *bz1* locus.
7. Click on the link to BAC a0020G06.
8. This BAC is listed as having been made available by Andrew Paterson. Click this link to access information about how to contact him to make arrangements to get the cloned a0020G06 BAC for experimental use.

### *3.2. Interrogation Tools*

Questions asked by biologists are complex, so tools that query the database must enable complex queries to be made. In the left margin of the main page (http://www.maizegdb.org) are links to various Data Centers (including Gene Products, Locus/Loci, Maps, Metabolic Pathways, etc.). Each Data Center name is linked to a page that makes available a Simple Search (similar in function to the search available through the search bar described in 3.1), an Advanced Search (which will be discussed more fully in this section), and a Discussion of the Data Type (written at a level comprehensible by the general public).

The use and functionality of the various Data Centers' Advanced Search tools are best explained by way of the following example. Two SSRs are known to flank a QTL of interest on maize chromosome 10 in bin 10.04. The two flanking SSRs' repeat patterns are (AG)28 and (TC)12. First, whether the repeat patterns are present and mapped (at the level of the chromosome bins) is determined. Next, BACs that contain the SSRs are identified and ones that contain both SSRs are selected. Finally, information on how to obtain the BACs for experimental use is accessed.

1. Go to http://www.maizegdb.org and look in the left bar for the Data Center called SSRs and click on it. (*See* **Note 7**).
2. In the Advanced Search Tool (the green box labeled "SSR Browser") use the checkbox and pulldown menus to limit the search to SSRs found in bin 10.04. Check the box to limit to a given repeat sequence and specify the repeat sequence as AG. Click the submit button toward the bottom of the green box.

3. In the results page, at least six results containing AG repeats are identified, but only one (p-umc2163) is anywhere near 28 units in length (the others are significantly shorter). Click the link labeled "p-umc2163."
4. Beneath the heading "Related Probes" 5 BACs are listed: b0045D05, b0161N11, b0256M13, b0187L03, and b0187C05. Make a note of these BAC identifiers (on paper or by other means).
5. Go back to the SSR Data Center (*see* **Note 8**),
6. Search for the SSR that is on the other side of your QTL by once again limiting your search within the green box to bin 10.04, and by specifying the repeat pattern (this time use TC). Click the submit button.
7. Of the results, the SSR p-MZETC34 has TC repeated 12 times. Click on "p-MZETC34" and scroll down to see the list of BACs that contain the repeat.
8. This probe detects four BACs: b0187L03, b0161N11, b0045D05, and b0256M13. Compare these BAC names to your notes (from step 4) to find that all four are also present in the first results set, so all could be used for sequencing to find out more about the QTL.

9. To find out how to order the BACs, click on the first BAC name, b0187L03. It is made available by CUGI (the Clemson University Genomics Institute).
10. Toward the top of this page, note the heading that reads, "**Want this clone? You can order it from CUGI using their BAC ordering system. Be sure to request clone b0187L03!**" Click the link within this heading to access the "BAC ordering system." A form for ordering the BAC directly from CUGI appears.

It should be noted that in instances where the SSRs of interest are known to be mapped, it is also possible to locate information using the "Mapped SSRs" browser toward the top of the SSR Data Center page. More specifically, if those SSRs are known to be mapped onto IBM2, it is possible to check for BACs anchoring those SSRs using the "Mapped & Anchored SSRs" browser, which also is accessible toward the top of the same page.

### *3.3. Analysis Tools*

In addition to methods enabling data access, tools for data analysis are also made available through MaizeGDB. Because the maize genome is currently being sequenced, sequence data are of particular interest at present. The sequence data analysis tools BLAST ***(9)*** and GeneSeqer ***(10)*** are accessible through links on the bottom left of the main page (http://www.maizegdb.org) and through links available on all sequence pages. BLAST enables the identification of sequences similar to a sequence of interest, while GeneSeqer creates spliced alignments of genomic DNA to cDNA/EST sequences to predict the exon-intron structure of genes.

Because the MaizeGDB sequence dataset is updated on a monthly basis, the BLAST service at MaizeGDB should not be considered to be the one-and-only place for searching for similar maize sequences! A sampling of other useful sites that host a BLAST service and that could be searched include NCBI (the site that hosts the most up-to-date sequence set), PlantGDB (which enables maize-specific BLAST searches and hosts a searchable assembly of the maize genome), Panzea (where sequence similarity searches can be carried out against sequence from a diverse set of maize lines), and the *Mu* Transposon Information Resource (where a sequence set tagged by the Robertson's *Mutator* elements is made available). All these BLAST services are accessible through their own sites, and links to them exist at the MaizeGDB BLAST page (http://www.maizegdb.org/blast.php).

Two distinct MaizeGDB BLAST services are available: one against the standard maize sequence set made available through NCBI (available at http://www.maizegdb.org/blast.php), and another against the “Cornsensus Sequence Set” ***(11)*** which is made accessible through a link toward the top of the standard MaizeGDB BLAST page. These two services are kept distinct in an effort to distinguish those sequences that exist in nature (the former) from the “Cornsensus Sequences” which represent alignments of similar sequences that are not guaranteed to have been derived from a single locus or even the same background of maize.

The MaizeGDB BLAST services are especially unique and useful in the following respect: results sets display the map locations of identified similar sequences and are linked to other records stored at MaizeGDB and offsite. The following example usage case shows these useful aspects of the MaizeGDB BLAST search utility using a sequence from B73 (the maize line that is currently being sequenced; see http://www.nsf.gov/awardsearch/showAward.do?AwardNumber=0527192) as the query. Here a sequence record of interest is located using its GenBank identifier, contextual links are followed to arrive at the MaizeGDB BLAST page, and a BLAST search against maize nucleotides is carried out. Within the results set, links to known map locations of matches are available. By following those links, maps are accessed and displayed with the locus of interest highlighted.

1. Using the search bar at the top of the page (as described in section 3.1), use the dropdown menu to select "sequences" and type **CG247295** into the field to the right. Click the submit button.
2. On the sequence page that appears, find the heading "Bioinformatics Tools" toward the bottom of the green bar on the right. Beneath the heading is a link to "BLAST against MaizeGDB." Click it.
3. On this page, scroll about half way down the page and fill in a sequence name, move right to choose the BLAST program (for this example, the default "blastn" is correct), continue right to choose "Maize Nucleotide" as the database to search, and to the right of that select an E-value (the default 0.0001 is appropriate for this example).
4. Note that the sequence query is already present (filled in from the sequence page from step 2), and click the button marked "Run BLAST" (*see* **Note 9**).

5. Scroll down the results set page (shown in Fig. 2) to view the results summary. Beneath the "Detailed Results Summary" for sequence AY772455.1 is a table consisting of three columns, the names of maps charting the position of this sequence's locus, the coordinate of the sequence on a given map, and the name of the marker or locus that was mapping (for AY772455.1, the locus listed is *umc95*). Click the link for the map named UMC 93 9, which is the second map from the top.
6. Note that on the UMC 93 9 map page that appears, the locus *umc95* is highlighted and that the page scrolls to show this locus. Note also that the epithet "CBM 9.05" is appended to the locus name. This connotes that the locus is the core marker for bin 9.05 (i.e., core bin marker 9.05).

### *3.4. Ways to Add Data to the Database*

MaizeGDB's sequence data comes from PlantGDB. That dataset is updated automatically on a monthly basis. Other datasets are classified as one of three types: large datasets, small datasets, and notes. Large datasets are generally added to the database in bulk by members of the MaizeGDB Team, and are contributed by researchers directly. To contribute a large dataset to the project (or to find out whether the dataset you have generated constitutes a “large” or “small” dataset), use the feedback button at the bottom of any MaizeGDB page to make an inquiry.

Researchers can add “notes” to records (like the one contributed by Hugo Dooner which is shown in Fig. 3). To add such a note, log in to the site using the “annotation” link displayed at the top right of any MaizeGDB page. Once logged in, click the link to "Add your own annotation to this record" shown at the top of virtually all data displays (*see* **Note 10**). Small datasets also can be added to the database by researchers directly by way of the MaizeGDB Community Curation Tools. The method for adding a small dataset is explained below, using a newly-published reference as the example usage case. The citation for our pretend reference is as follows:

Lawrence, CJ. (2005) How to use the reference curation module at MaizeGDB. *Plant Physiology* 9:3-4.

1. Click on the “annotation” link at the top of any MaizeGDB page. Click the link to “Create an Annotation Account” and fill out all information required. Be sure to check the box to become a MaizeGDB curator before clicking the submit button.

2. A confirmation email along with a Community Curation manual will be sent once the new account has been activated.
3. To begin adding data to the database, click on the link marked “tools” toward the top right of any MaizeGDB page.
4. Toward the bottom of this page click the link marked “Playground Community Curation Tools” (*see* **Note 11**).
5. Log in using the newly created username and password.
6. Click the link toward the center of the page to download the curation tools’ user manual for future reference.
7. In the left bar, click the link marked “Reference.”
8. Fill in the title and select “article” as the reference type. (Because you are working at the “Playground Community Curation Tools” feel free to make up pretend information for the purposes of this exercise.) When in doubt of what information to put into a given field, click on the buttons labeled with a question mark (see **Note 12**).
9. Fill in the year, volume, and pages information. For the “In Journal” field note the label “Lookup Field – Enter a Search String.” Fill in the journal title.
10. Click the link beneath the “Author” heading to “Add Authors.”

11. Half way down the page is a typing field where the name of an author can be typed to locate a person record to associate with the new reference. For this example, type **Lawrence**.
12. Lawrence is the first (and only) author on this imaginary publication, so leave the dropdown menu with "Author" selected, and type the number **1** into the box labeled "Order." Press the "Submit & Continue" button.
13. Note that "Lawrence, CJ" is available in the dropdown menu. Select this item from the dropdown menu that has replaced the typing field for Author, scroll to the bottom of the page, and click the button labeled "Add to List of Authors."
14. Note that "Lawrence, CJ" now appears in the list of authors at the top of the page. Click the button marked "Author List Complete."
15. Scroll to the bottom of the page and press the button marked "Submit & Continue." Returned in place of the "In Journal" search string are available instances of matching journal names. Select the records "Plant Physiol" (*see* **Note 13**).
16. Click the button at the bottom of the page marked "Insert into Database."

The newly created record enters a queue for approval by a worker at MaizeGDB. Once the record has been approved, it will become available through the MaizeGDB interface after the next database update. Other curation tool modules function similarly, and a detailed manual is available through the curation tools.

## 4. Notes

1. Clicking the icon within the top bar on any page results in a return to the main page, http://www.maizegdb.org.
2. When feedback is sent, the web address for the page from which the feedback was sent is included in the message automatically to enable workers to better understand how or why questions or concerns were submitted.
3. Instead of hitting "Go!" or "submit" buttons, it is also possible to simply press the "enter" or "return" key on the computer's keyboard to submit queries.
4. A wildcard is appended to the right ends of all queries automatically. This means that if **`bz1`** is typed into the search window, a search is carried out for all instances matching the pattern `bz1*`. Asterisks or percent signs can be appended manually to the left ends of search

strings to enable matching for instances where the string `bz1` is preceded by other characters.

5. In general, searches carried out via the search bars are simple searches that are limited to record names and synonyms. Names of probe records are those assigned by researchers, and are not subject to any standardized naming convention. For this reason, searching through probe records for `*bz1` is not guaranteed to yield a list of all probes that mark the *bz1* locus. Searching for the *bz1* locus record and subsequently browsing through associated probes is a better method to follow if the desire is to find all probe records associated with the *bz1* locus.
6. Had the asterisk not been appended to the left end of the query, the two "Probed Sites" and the one "YAC" shown in Fig. 2 would not have been found because the search phrase is preceded by other characters in those records' names. The gene *zp15* is found by the search because its synonym *bz15* contains the search string.
7. To return to the SSR Data Center, click on the upper left MaizeGDB icon then select the SSR Data Center from the left bar on the main page.
8. SSRs are a probe type. All probes can be searched by name through the "Probe" Data Center, but to search SSRs by sequence pattern, the SSR Data Center subset should be searched directly.

9. The search could be limited to find only those sequences with known map locations by selecting the check box just above the “Run BLAST” button.
10. This link is not displayed unless you are logged in to the site.
11. It is advisable to work first with the “Playground Community Curation Tools” before entering data into the real database. The “Playground Community Curation Tools” function just like the “Real Community Curation Tools,” but access a different copy of the database that intended for testing and training purposes. Using the “Playground Community Curation Tools” allows the entry of fictitious data while learning to use the tools without the possibility of compromising MaizeGDB’s content.
12. All fields required to create a complete reference record are marked with a red asterisk.
13. If the content of the dropdown menu returned in place of the field where a search string was entered does not contain the item desired, scroll to the bottom of the page and use the link to “Re-edit Search Fields.” If by making edits the item is still not found, use the link at the bottom of the left bar to “Email an Expert Curator.”

## Acknowledgments

The author would like to thank Trent Seigfried and Darwin Campbell for their work maintaining the MaizeGDB interface and database, respectively; Mary Schaeffer, Ed Coe, and Marty Sachs for their curatorial work;

PlantGDB partners Volker Brendel, Qunfeng Dong, and Matthew Wilkerson for building and maintaining the sequence update pipeline; Michael Brekke for technical support; and Sanford Baran and Jason Carter for developing the MaizeGDB curation toolsets. This work was supported by the USDA-ARS.

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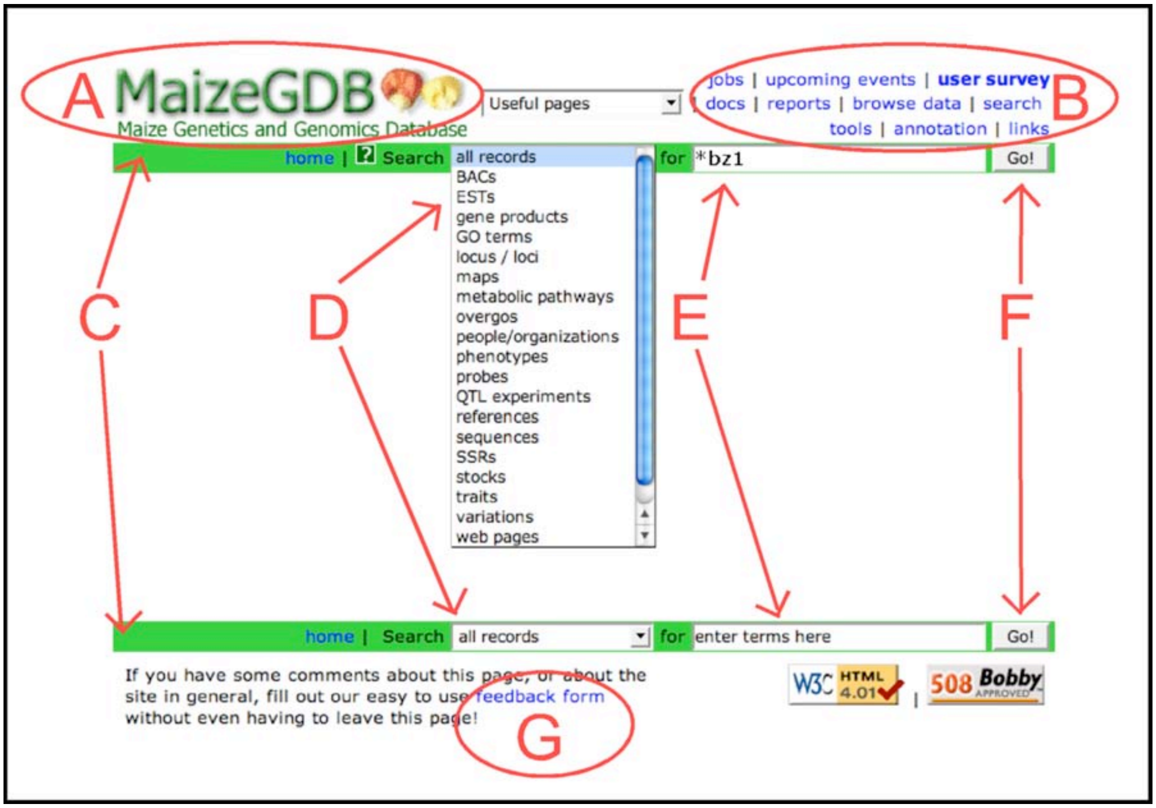
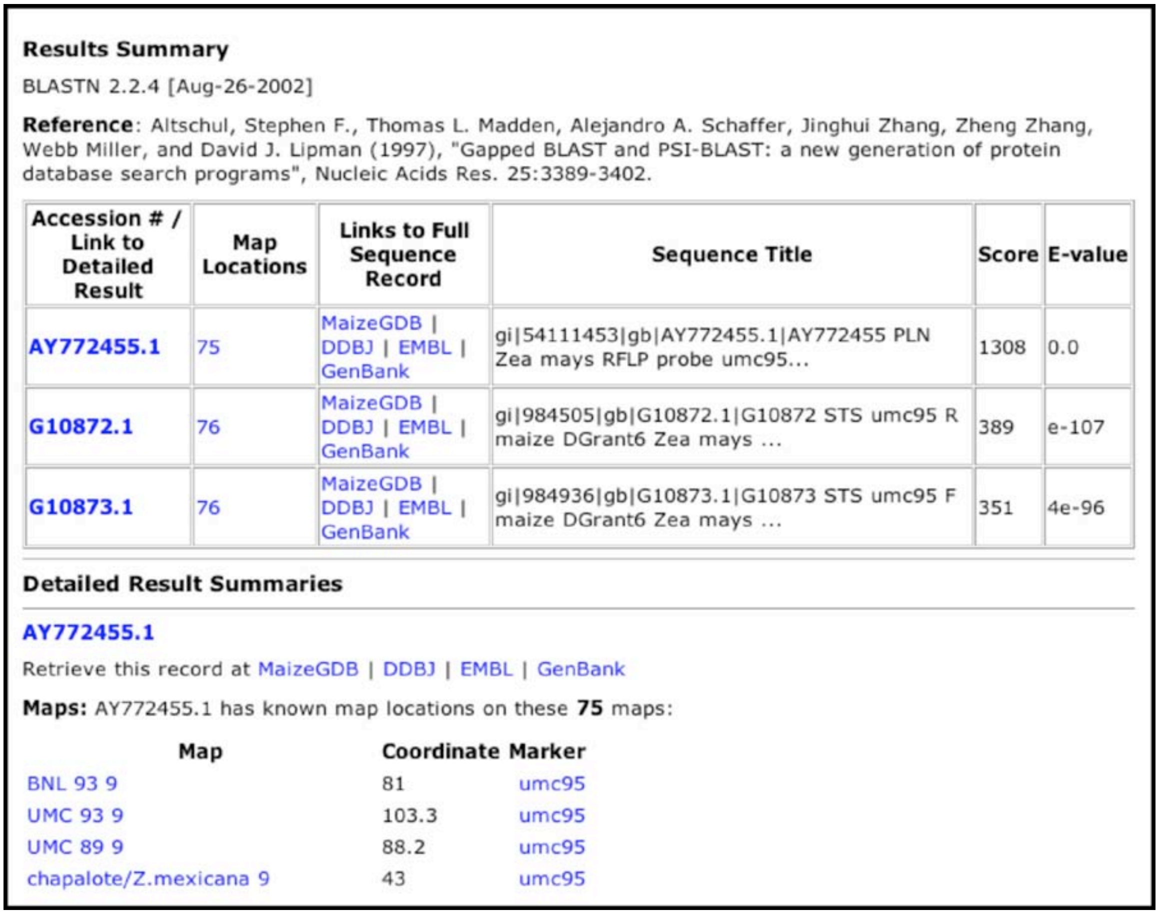


If you have some comments about this page, or about the site in general, fill out our easy to use feedback form without even having to leave this page!

Fig. 1. Search bars available at the top and bottom of all MaizeGDB pages. (A) The MaizeGDB icon is located at the top left of each page. Clicking the icon causes a return to the home page (http://www.maizegdb.org). (B) Links to bulletin boards and static pages are listed at the top right. (C) Within green bands located at the top and bottom of the page are the search bars. To carry out a search, choose a datatype (D) from the dropdown menu, type a search term (E) into the typing field, and press the button (E) marked “Go!”



**Results Summary**

BLASTN 2.2.4 [Aug-26-2002]

**Reference**: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

| Accession # / Link to Detailed Result | Map Locations | Links to Full Sequence Record | Sequence Title | Score | E-value |
|---|---|---|---|---|---|
| **AY772455.1** | 75 | MaizeGDB \| DDBJ \| EMBL \| GenBank | gi\|54111453\|gb\|AY772455.1\|AY772455 PLN Zea mays RFLP probe umc95... | 1308 | 0.0 |
| **G10872.1** | 76 | MaizeGDB \| DDBJ \| EMBL \| GenBank | gi\|984505\|gb\|G10872.1\|G10872 STS umc95 R maize DGrant6 Zea mays ... | 389 | e-107 |
| **G10873.1** | 76 | MaizeGDB \| DDBJ \| EMBL \| GenBank | gi\|984936\|gb\|G10873.1\|G10873 STS umc95 F maize DGrant6 Zea mays ... | 351 | 4e-96 |

**Detailed Result Summaries**

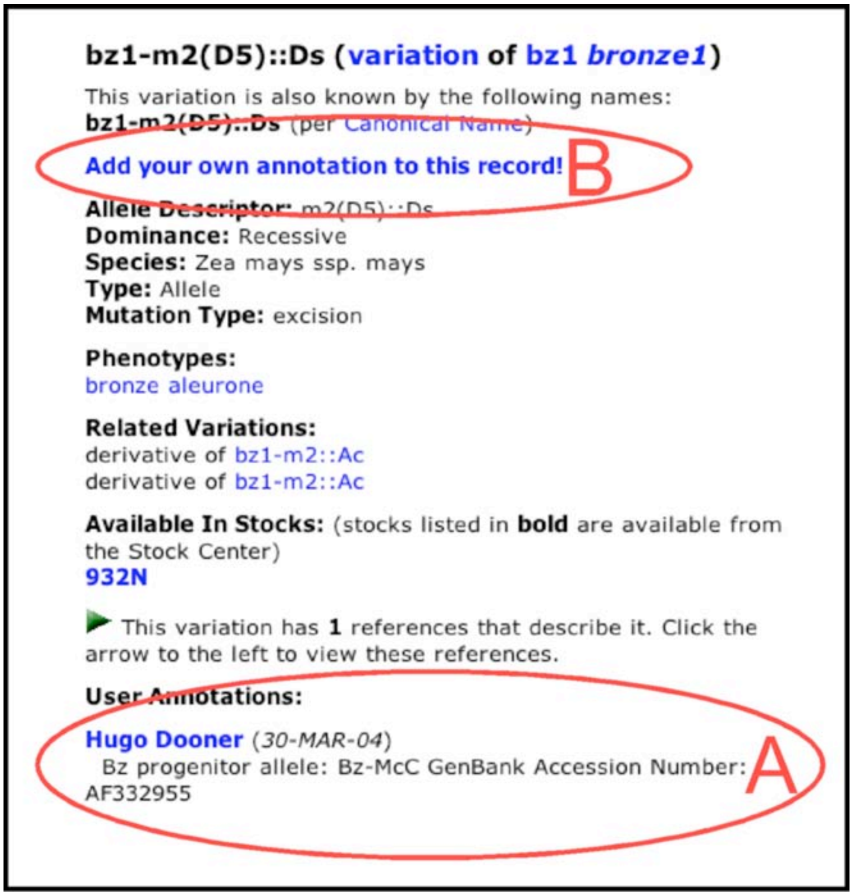
**AY772455.1**

Retrieve this record at MaizeGDB | DDBJ | EMBL | GenBank

**Maps:** AY772455.1 has known map locations on these **75** maps:

| Map | Coordinate | Marker |
|---|---|---|
| BNL 93 9 | 81 | umc95 |
| UMC 93 9 | 103.3 | umc95 |
| UMC 89 9 | 88.2 | umc95 |
| chapalote/Z.mexicana 9 | 43 | umc95 |

Fig. 2. BLAST results show map locations and are linked to other data. Within the "Results Summary" is a table showing the list of similar sequences matched by BLAST alongside those sequences' map locations, links to records at MaizeGDB and offsite, and the similarity scores and E-values. Below the table are "Detailed Results Summaries" which list the maps containing the sequences identified. Clicking on the map name results in access to a map display where the locus name for the sequence match identified highlighted.



**bz1-m2(D5)::Ds (variation of bz1 *bronze1*)**

This variation is also known by the following names:
**bz1-m2(D5)::Ds** (per Canonical Name)

**Add your own annotation to this record!**

**Allele Descriptor:** m2(D5)::Ds
**Dominance:** Recessive
**Species:** Zea mays ssp. mays
**Type:** Allele
**Mutation Type:** excision

**Phenotypes:**
bronze aleurone

**Related Variations:**
derivative of bz1-m2::Ac
derivative of bz1-m2::Ac

**Available In Stocks:** (stocks listed in **bold** are available from the Stock Center)
**932N**

This variation has **1** references that describe it. Click the arrow to the left to view these references.

**User Annotations:**

**Hugo Dooner** (*30-MAR-04*)
Bz progenitor allele: Bz-McC GenBank Accession Number: AF332955

Fig. 3. Researchers can add notes to records at MaizeGDB. (A) Hugo Dooner has annotated the *bz1-m2(D5)::Ds* allele as the *bz1* progenitor allele from the maize line McC. (B) Almost all datatypes stored can be annotated by following links to "**Add your own annotation to this record**" (*see* **Note 10**).

## V. MAIZE GENOME DATABASE

Transition to MaizeGDB: http://www.maizegdb.org
MaizeGDB is the next generation Maize Genome Database, with interfaces and all accesses to the data under the guidance of Volker Brendel, Ames, Iowa. It will completely replace the MaizeDB site, www.agron.missouri.edu, September 30, 2003. We welcome Volker's staff: Trent Seigfried, Darwin Campbell, Sanford Baran and Carolyn Lawrence to our community

Some history. In the fall of 2002, the first steering committee for a new Maize Genome Database, MaizeGDB, met to evaluate new interfaces to maize genome data. The Steering Committee for MaizeGDB is chaired by Tom Slezak, and currently includes: Ed Buckler, Vicki Chandler, Mike Freeling, Sarah Hake, Mary Polacco, Marty Sachs, Cari Soderlund, Lincoln Stein, and Virginia Walbot. At that time, a recommendation was made to target September 2003 as a final transition, with full migration of all data in MaizeDB to the new database, contingent on the development of a suite of curation tools. Missouri staff will continue to play a major role in curation of MaizeGDB; stocks will continure to be curated by Marty Sachs and his staff at Illinois. A major effort will be made to engage the community in curation (see below). The MaizeGDB was presented January 2003, at the Plant and Animal Genome Meetings, San Deigo, CA, and as a talk in the first general talks session of the 2003 Maize Meetings held in March at Lake Geneva, WI. It has been available for public review and inputs since Jan 2003 (see announcement on the Jan bionet bulletin board: http://bionet.hgmp.mrc.ac.uk/hypermail/maize/maize.200301/0005.html).

Community Curation of Literature – Coming soon
In May 2003, the MaizeGDB Steering Committee proposed an Editorial Board, whose membership would participate in curation of the literature. The inaugural board, convened by Ginny Walbot, will include: Hugo Dooner, Chief; Lisa Harper, Erich Grotewold, Bill Tracy, and Nathan Springer. This first group will be intimately involved in testing the data curation forms, their utility and friendliness. Once the forms have been vetted, there will be an open invitation to all cooperators to participate. Because the editorial board will curate a limited number of papers, it is highly important that we receive your support in this effort. Your paper could be high-lighted as a 'paper of the week' if comprehensively curated in MaizeGDB.

Community curation of larger research projects
This past year we have successfully developed protocols whereby 2 research projects handled much of the semantic and other checking of data at their site, so that it was consistent with MaizeDB, and supplied in a routine format to MaizeDB. In both cases, the project databases had SQL access to MaizeDB, permitting access to current tables of names and synonyms for loci, probes, and stocks. While the MaizeDB curator still needs to monitor for overall data quality prior to loading, most of the work has been performed by the experts for these data sets. We gratefully acknowledge the support of Marilyn Warburton, Ed Brandon, Carlos Lopez, Juan Alarcon, and Dave Hoisington (CIMMYT); and Mike McMullen, Ed Coe, Hector Sanchez-Villeda, Steve Schroeder and Georgia Davis (Missouri). The current curator of MaizeDB plans to similarly engage other projects in the near future.

Also of note:

- Consensus genetic maps with higher resolution than 'bins'. The current version is presented in this newsletter (pages 137-179). This map, IBM2 neighbors, forms the scaffold for the physical map; note that only loci listed as Backbone have statistically defendable order, being on-frame on the IBM map. We thank the Chromatin (www.chromdb.org) and Maize Mapping (www.maizemap.org) projects for providing new map data for this map. We plan to incorporate other community IBM map data in the near future. In all cases, sources of the data are acknowledged.

- Sorghum genetic maps were entered, courtesy of Andrew Paterson and John Bowers, with links to probes mapped on both the genetic and physical maps of maize. The Paterson BAC probes may be recognized as the 'SOG' markers on the Web FPC presentation at Arizona (http://genome.arizona.edu/fpc/maize).

- Links from maize to Gramene rice physical maps were kindly provided by Doreen Ware and Lenny Teytelman at Gramene. These links are based on sequence similarity of maize Cornsensus and ESTs to rice, and are posted at the Gramene site. These links are also regularly forwarded to Arizona for inclusion in the Web FPC presentation of the physical map of maize.

- A file of the mapped sequences of maize is one of our more requested items by larger projects and currently resides at: www.agron.missouri.edu/files_dl/SequenceMap directory. It lists sequence accessions, map coordinates on bins, IBM and IBM neighbors, and the locus name. A similar file will be maintained at the new site.

Mary Polacco
Curator, Maize Genome Database
July 23, 2003

# VI. A CONSENSUS GENETIC MAP

## Inter-mated B73 x Mo17 (IBM) Neighbors

## 5718 Loci July 2003

The IBM neighbors maps are a consensus map representation that is based on the high resolution IBM maps of the Maize Mapping Project (see Web site: www.maizemap.org). Both the IBM and the neighbors maps are used as scaffolding in assembly of the physical map (see also Web site: genome.Arizona.edu/fpc/maize). Note that the inter-mated B73xMo17 or IBM map, based on 4 rounds of random mating, is expanded 3-fold compared to F2 or IF2 (immortal F2) maps and has 15X greater resolving power compared to other public mapping populations (Sharopova et al., Plant Mol Biol 48:463-481, 2002; Lee et al., Plant Mol Biol 48: 453-461, 2002). Maps with loci in common with the IBM can be readily incorporated into IBM neighbors. The algorithm resolves any conflicts in order in favor of map orders with best statistical support. In the current representation, the below maps were included:

- IBM2 Dec 2002; IBM population, 302 individuals
- IBM1 Mar 2002; IBM population, 302 individuals; has a few loci not included on IBM2
- INDEL, April 2003; 302 individuals, subset of markers on IBM2 plus INDEL (insertion deletion polymorphism) and SNP (simple nucleotide polymorphism) markers
- ChromDB; Dec 2002; scored on mini-IBM with 94 individuals, but map computed using IBM 2002 map and all 302 scores. Map provided by Chromatin Mapping Project, see ChromDB Website, www.chromdb.org
- SSR popI, T218xGT119 population of Mike McMullen, 93 individuals
- SSR popII, Tx303xCO159, same population as UMC 98
- UMC 98,Tx303xCO159, immortal F2 population, 54 individuals; see Gardiner et al., Genetics 134:917-930, 1993; Davis et al., Genetics 152:1137-1172, 1999
- BNL 96, combined scores of 2 recombinant inbred mapping populations, T232xCM37 and Tx303xCO159, with 48, and 41 individuals, respectively; map provided by Ben Burr; see Website: acemaz.bnl.gov; see Burr et al., Genetics 118:519-526, 1988
- BNL 2002, population and map source same as BNL 96

**Fields in the table:**

**Locus:** Locus symbol.

**Contig:** C if the locus has a probe associated with a contig; AC if the contig has been anchored unambiguously to this genetic locus.

**Coordinate:** cM values; estimated for all maps save IBM2. Revisions can be expected as physical mapping progresses.

**Backbone:** Yes if on frame IBM2, as defined by MapMaker software, otherwise, ‘no’.

**Bin:** Bin location. Bins are stated numerically, as the linkage group or chromosome, followed by a decimal and then a value that defines the bin. Lower values are the distal region of the short arm. Revisions can be expected as physical mapping progresses.

**Source Map:** The map used to derive map order on IBM neighbors.

Mary Polacco, Hector Sanchez-Villeda, Ed Coe
Columbia, MO

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| bnl(tas1h) | | 1.00 | -55.80 | no | BNL 96 |
| csu804b(dnp) | | 1.00 | -30.50 | no | UMC 98 |
| umc1041 | C | 1.00 | -29.00 | no | SSR popII |
| bnl(tas1c) | | 1.00 | -11.70 | no | BNL 96 |
| rgpc654 | | 1.00 | -11.30 | no | UMC 98 |
| umc1619 | C | 1.00-1.01 | -8.00 | no | SSR popII |
| phi056(tub1) | C | 1.00-1.01 | -2.30 | no | IBM2 |
| umc1354 | AC | 1.00 | 0.00 | yes | IBM2 |
| tub1 | AC | 1.01 | 2.50 | yes | IBM2 |
| csu738 | | 1.00-1.01 | 2.50 | no | UMC 98 |
| umc1613 | C | 1.00-1.01 | 2.50 | no | SSR popII |
| dmt103b | C | 1.01 | 8.30 | no | ChromDB |
| bnlg149 | | 1.00 | 9.86 | no | BNL 2002 |
| umc1177 | AC | 1.01 | 10.50 | yes | IBM2 |
| umc1566 | AC | 1.01 | 16.50 | yes | IBM2 |
| bnl5.62a | | 1.01 | 22.80 | yes | IBM2 |
| fus6 | | 1.01 | 24.30 | no | IBM2 |
| mmp102 | | 1.01 | 26.10 | yes | IBM2 |
| AY110314 | C | 1.01 | 31.10 | yes | IBM2 |
| umc1292 | C | 1.01 | 32.08 | no | SSR popII |
| umc94a | | 1.01 | 40.30 | yes | IBM2 |
| csu589 | | 1.01 | 40.40 | no | UMC 98 |
| bnl8.05a | | 1.01 | 40.40 | no | UMC 98 |
| bnlg1124 | | 1.01 | 41.67 | no | BNL 2002 |
| knox1 | | 1.01 | 42.39 | no | UMC 98 |
| umc164c | | 1.01 | 43.39 | no | UMC 98 |
| lim179 | | 1.01 | 48.70 | yes | IBM2 |
| csu680a | C | 1.01 | 52.59 | no | UMC 98 |
| mmp49 | | 1.01 | 57.80 | yes | IBM2 |
| cdo1081a | | 1.01 | 59.50 | yes | IBM2 |
| bnlg1179 | | 1.01 | 64.14 | no | BNL 2002 |
| asg31 | C | 1.01 | 66.90 | yes | IBM2 |
| npi415 | | 1.01 | 67.70 | yes | IBM2 |
| AY110401 | C | 1.01 | 68.30 | no | IBM2 |
| cdo507a(ant) | | 1.01 | 68.52 | no | UMC 98 |
| umc1106 | | 1.00 | 68.71 | no | SSR popII |
| umc1305 | C | 1.00 | 69.70 | no | SSR popI |
| umc1281 | C | 1.05-1.06 | 69.70 | no | SSR popI |
| std20b(uce) | | 1.01 | 70.62 | no | UMC 98 |
| uaz104 | | 1.01 | 70.96 | no | BNL 96 |
| asg59a | | 1.01 | 71.10 | no | UMC 98 |
| php20537b | | 1.01 | 71.10 | yes | IBM2 |
| ufg31 | | 1.01 | 73.30 | yes | IBM2 |
| ufg33 | | 1.01 | 73.70 | yes | IBM2 |
| ufg32 | C | 1.01 | 74.50 | yes | IBM2 |
| ufg34 | | 1.01 | 76.10 | yes | IBM2 |
| PCO072650 | C | 1.01 | 79.25 | no | INDEL |
| umn857b | | 1.01 | 80.20 | no | UMC 98 |
| uaz260b(rpL5) | | 1.01 | 80.20 | no | UMC 98 |
| rgpc385a(rpL5) | | 1.01 | 80.20 | no | UMC 98 |
| bnlg1014 | C | 1.01 | 82.80 | yes | IBM2 |
| umc1363 | C | 1.01 | 83.70 | yes | IBM2 |
| umc1071 | C | 1.01 | 85.20 | yes | IBM2 |
| umc1269 | C | 1.01 | 86.30 | yes | IBM2 |
| umc2012 | C | 1.01 | 87.40 | no | IBM2 |
| tda47 | | 1.01 | 88.18 | no | UMC 98 |
| csu454(gst) | | 1.01 | 88.18 | no | UMC 98 |
| umc1977 | C | 1.01 | 89.20 | yes | IBM2 |
| PCO132874 | C | 1.01-1.02 | 90.85 | no | INDEL |
| umc1948 | AC | 1.01 | 91.50 | no | IBM2 |
| php20603 | | 1.01 | 91.70 | yes | IBM2 |
| npi97a | | 1.01 | 92.74 | no | UMC 98 |
| umc266b(ptk) | | 1.01 | 92.74 | no | UMC 98 |
| dpg12b | | 1.02 | 93.06 | no | BNL 2002 |
| umc2215 | | 1.01 | 93.88 | no | SSR popI |
| smt2 | | 1.01 | 94.18 | no | SSR popII |
| cdo20a | | 1.01-1.02 | 95.28 | no | BNL 2002 |
| prc3 | AC | 1.01 | 97.97 | no | SSR popII |
| rz444c | C | 1.01 | 98.29 | no | IBM1 |
| umc1484 | | 1.01 | 98.39 | no | SSR popII |
| php20689 | | 1.01 | 101.10 | yes | IBM2 |
| umc1685 | AC | 1.01 | 103.00 | yes | IBM2 |
| mmp93 | | 1.01 | 103.20 | yes | IBM2 |
| uaz182 | | 1.01 | 103.37 | no | BNL 2002 |
| bnlg1112 | | 1.01 | 104.48 | no | BNL 2002 |
| npi406 | | 1.02 | 105.64 | no | BNL 2002 |
| pbs11 | | 1.01 | 107.44 | no | BNL 2002 |
| cat2 | | 1.01 | 107.97 | no | BNL 2002 |
| umc1160 | AC | 1.01 | 108.30 | yes | IBM2 |
| umc2224 | AC | 1.01-1.02 | 110.90 | yes | IBM2 |
| npi579b | | 1.01 | 112.20 | yes | IBM2 |
| csic(rab30) | | 1.02 | 112.20 | no | BNL 2002 |
| bnlg1130 | | 1.01-1.02 | 114.33 | no | BNL 2002 |
| umc157(chn) | AC | 1.02 | 114.40 | yes | IBM2 |
| umc1222 | C | 1.01-1.02 | 114.40 | no | SSR popII |
| pmcb1 | | 1.02 | 115.20 | yes | IBM2 |
| uaz2a | | 1.02 | 123.57 | no | BNL 2002 |
| mmp68 | | 1.02 | 123.60 | yes | IBM2 |
| umc2225 | AC | 1.01-1.02 | 124.70 | yes | IBM2 |
| uaz146b(rps28) | | 1.01-1.02 | 125.60 | no | BNL 2002 |
| csu1171 | | 1.02 | 127.30 | yes | IBM2 |
| umc115 | | 1.02 | 127.30 | no | UMC 98 |
| umc194a(gpr) | | 1.02 | 127.30 | no | UMC 98 |
| csu1190 | | 1.02 | 127.39 | no | UMC 98 |
| tda50 | | 1.02 | 129.30 | no | UMC 98 |
| csu680c | C | 1.02 | 129.30 | no | UMC 98 |
| std2c(dba) | | 1.02 | 129.30 | no | UMC 98 |
| rgpc1122c(rpL15) | | 1.02 | 129.30 | no | UMC 98 |
| mmp171b | | 1.02 | 131.80 | no | IBM2 |
| umc1166 | AC | 1.02 | 133.60 | yes | IBM2 |
| PCO128140 | C | 1.02 | 139.41 | no | INDEL |
| umc1568 | AC | 1.02 | 141.80 | yes | IBM2 |
| bnlg1429 | AC | 1.02 | 143.50 | yes | IBM2 |
| umc1467 | AC | 1.02 | 143.50 | no | SSR popI |
| pds1 | C | 1.02 | 144.28 | no | BNL 96 |
| dnap9705(Ac) | | 1.02 | 144.28 | no | BNL 2002 |
| ensl001 | | 1.02 | 144.39 | no | BNL 2002 |
| ifbf33 | | 1.02 | 145.74 | no | BNL 2002 |
| php20640 | | 1.02 | 146.90 | yes | IBM2 |
| npi411b | | 1.02 | 149.13 | no | BNL 2002 |
| lim504 | | 1.02 | 151.60 | yes | IBM2 |
| npi423 | | 1.02 | 152.62 | no | BNL 2002 |
| csu691 | | 1.02 | 156.85 | no | UMC 98 |
| bnlg1614 | | 1.02 | 159.11 | no | BNL 2002 |
| npi209b | | 1.02 | 160.06 | no | BNL 2002 |
| bnlg1627 | | 1.02 | 160.06 | no | BNL 2002 |
| npi109a | | 1.02 | 160.06 | no | BNL 96 |
| umc1976 | AC | 1.02 | 160.60 | yes | IBM2 |
| bnlg176 | | 1.03 | 161.19 | no | BNL 2002 |
| csu860b | | 1.02 | 161.82 | no | UMC 98 |
| umc2226 | AC | 1.02 | 165.80 | no | IBM2 |
| mmp135 | | 1.02 | 166.00 | yes | IBM2 |
| bnlg1127 | | 1.02 | 167.50 | yes | IBM2 |
| bnlg1953 | AC | 1.02 | 170.00 | yes | IBM2 |
| bnlg1178 | | 1.02 | 171.40 | no | BNL 2002 |
| bnlg1007 | | 1.02 | 173.10 | no | BNL 2002 |
| umc2204 | C | 1.02 | 175.52 | no | SSR popI |
| umc1711 | | 1.02 | 176.69 | no | SSR popII |
| npi403b | | 1.02 | 183.80 | yes | IBM2 |
| csu320a | | 1.02 | 183.95 | no | UMC 98 |
| bnl9.13 | | 1.02 | 188.22 | no | BNL 2002 |
| bnlg109 | | 1.02 | 188.58 | no | BNL 2002 |
| umc2383 | C | 1.02-1.03 | 188.67 | no | SSR popII |
| uaz1 | | 1.02 | 193.14 | no | BNL 2002 |
| bnl5.21c | | 1.03 | 194.13 | no | BNL 2002 |
| bnlg1803 | | 1.02 | 198.32 | no | BNL 2002 |
| umc76 | C | 1.03 | 198.40 | yes | IBM2 |
| gln6 | AC | 1.02-1.03 | 198.40 | no | UMC 98 |
| umc243b | | 1.02-1.03 | 198.40 | no | UMC 98 |
| uaz120 | | 1.03 | 199.17 | no | BNL 2002 |
| isu2117c | | 1.03 | 199.17 | no | BNL 2002 |
| ufg78 | | 1.02-1.03 | 199.70 | no | IBM2 |
| uaz267 | | 1.03 | 200.03 | no | BNL 2002 |
| uox(bru1) | | 1.02-1.03 | 200.56 | no | BNL 2002 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| npi241b |  | 1.03 | 200.61 | no | BNL 2002 |
| bnl35d(blr) |  | 1.03 | 200.75 | no | BNL 2002 |
| mpik33h |  | 1.02-1.03 | 200.75 | no | BNL 2002 |
| bnlg1083 |  | 1.02 | 201.32 | no | BNL 2002 |
| cdo1387b(emp70) |  | 1.03 | 201.50 | yes | IBM2 |
| bnlg147 |  | 1.02 | 201.97 | no | BNL 2002 |
| lim122 |  | 1.03 | 205.00 | yes | IBM2 |
| umc1073 |  | 1.03 | 208.50 | yes | IBM2 |
| umc1403 | C | 1.03 | 210.60 | yes | IBM2 |
| npi439a |  | 1.03 | 216.80 | yes | IBM2 |
| umc230 |  | 1.03 | 218.40 | yes | IBM2 |
| umc11a |  | 1.03 | 218.80 | yes | IBM2 |
| npi425c |  | 1.03 | 218.80 | no | UMC 98 |
| npi234a |  | 1.03 | 219.00 | no | IBM2 |
| bnlg1484 | A C | 1.03 | 219.00 | no | IBM2 |
| bnl10.38a |  | 1.03 | 223.18 | no | BNL 2002 |
| mmp66 |  | 1.03 | 224.40 | yes | IBM2 |
| umc2397 |  | 1.03 | 224.76 | no | SSR popII |
| AY109929 | A C | 1.03 | 225.40 | no | IBM2 |
| csu315c |  | 1.03 | 225.80 | no | UMC 98 |
| umc1397 | A C | 1.03 | 226.40 | yes | IBM2 |
| AY110052 | C | 1.03 | 229.60 | yes | IBM2 |
| csu859(gol) |  | 1.03 | 242.15 | no | UMC 98 |
| AY110028 | C | 1.03 | 246.30 | yes | IBM2 |
| PCO074335 | C | 1.03 | 252.19 | no | INDEL |
| npi448 |  | 1.03 | 254.28 | no | BNL 96 |
| ifbf91 |  | 1.03 | 254.35 | no | BNL 2002 |
| ias8 |  | 1.03 | 254.77 | no | BNL 2002 |
| bnlg2204 |  | 1.03 | 254.86 | no | BNL 2002 |
| dgg9b |  | 1.03 | 255.13 | no | BNL 2002 |
| npi242b |  | 1.03 | 255.20 | yes | IBM2 |
| bnl1.326a |  | 1.06 | 255.31 | no | BNL 2002 |
| ts2 |  | 1.03 | 255.50 | no | BNL 2002 |
| ncr(sod4a) |  | 1.03 | 255.55 | no | BNL 2002 |
| mpik36 |  | 1.03 | 255.57 | no | BNL 2002 |
| csu181a |  | 1.03 | 256.62 | no | UMC 98 |
| csu254b |  | 1.03 | 256.62 | no | UMC 98 |
| csu214b(grp) |  | 1.03 | 256.62 | no | UMC 98 |
| csu179a(hsp70) |  | 1.03 | 256.62 | no | UMC 98 |
| umc1479 | A C | 1.03 | 257.40 | yes | IBM2 |
| umc8a |  | 1.03 | 257.47 | no | UMC 98 |
| csu238a(apx) |  | 1.03 | 257.47 | no | UMC 98 |
| csu710a(apx) |  | 1.03 | 257.55 | no | UMC 98 |
| asg26 | C | 1.03 | 257.90 | no | IBM2 |
| lim51 |  | 1.03 | 258.70 | no | IBM2 |
| bnlg439 | A C | 1.03 | 259.10 | no | IBM2 |
| bnlg1203 | A C | 1.03 | 259.30 | yes | IBM2 |
| fad8 | A C | 1.03 | 260.70 | yes | IBM2 |
| uaz139 |  | 1.03 | 261.74 | no | BNL 2002 |
| pbs16b |  | 1.03 | 262.46 | no | BNL 2002 |
| wusl1032 |  | 1.03 | 262.46 | no | BNL 2002 |
| AY110640 |  | 1.03 | 264.40 | yes | IBM2 |
| npi427b |  | 1.03 | 268.16 | no | BNL 96 |
| bnlg1458 | C | 1.03 | 268.90 | no | IBM2 |
| umc13 |  | 1.03 | 270.60 | yes | IBM2 |
| pdc3 |  | 1.03 | 270.60 | no | BNL 2002 |
| ibp2 |  | 1.03 | 271.37 | no | BNL 2002 |
| bnlg2180 |  | 1.03 | 272.53 | no | BNL 2002 |
| asg35b |  | 1.03 | 273.90 | yes | IBM2 |
| csu215b(grp) |  | 1.03 | 275.27 | no | UMC 98 |
| umc266a(ptk) |  | 1.03 | 275.39 | no | UMC 98 |
| dpg4 |  | 1.03 | 275.94 | no | BNL 2002 |
| dpg10 |  | 1.03 | 275.94 | no | BNL 2002 |
| uaz264b |  | 1.03 | 277.51 | no | BNL 2002 |
| dpg8 |  | 1.03 | 277.95 | no | BNL 2002 |
| AY110632 | A C | 1.03 | 278.10 | no | IBM2 |
| umc1701 |  | 1.03 | 279.13 | no | SSR popII |
| npi589 |  | 1.03-1.04 | 279.41 | no | BNL 2002 |
| p1 | C | 1.03 | 279.96 | no | SSR popI |
| csu814b |  | 1.03 | 279.96 | no | UMC 98 |
| ndp2 |  | 1.03 | 282.60 | yes | IBM2 |
| csu745d(rpPo) | C | 1.03 | 285.65 | no | UMC 98 |
| mmp23 |  | 1.03 | 286.20 | yes | IBM2 |
| AW400087 | C | 1.03 | 287.20 | no | IBM2 |
| npi286 |  | 1.03 | 288.50 | no | UMC 98 |
| ndp1 |  | 1.03 | 288.60 | yes | IBM2 |
| hcf3 |  | 1.03 | 290.10 | no | BNL 2002 |
| ynh21 |  | 1.03 | 290.10 | no | BNL 2002 |
| bnlg1866 | C | 1.03 | 290.10 | yes | IBM2 |
| bnlg182 |  | 1.03 | 290.10 | no | BNL 2002 |
| pge(phyB1) |  | 1.03 | 290.10 | no | BNL 2002 |
| umc1880 | C | 1.03 | 290.30 | no | IBM2 |
| phi109275 | C | 1.03 | 290.40 | no | IBM2 |
| umc1598 |  | 1.03 | 290.70 | yes | IBM2 |
| dpg11 |  | 1.03 | 290.73 | no | BNL 2002 |
| chs5054 |  | 1.03 | 290.82 | no | BNL 2002 |
| csu753 |  | 1.03 | 291.10 | no | UMC 98 |
| csu392b |  | 1.03 | 291.10 | no | UMC 98 |
| dpg9 |  | 1.03 | 291.25 | no | BNL 2002 |
| lim432 |  | 1.03 | 292.40 | yes | IBM2 |
| bnl12.06a |  | 1.03 | 293.00 | no | IBM2 |
| fmi1(pki) |  | 1.04 | 293.00 | no | UMC 98 |
| csu924(wsi) |  | 1.04 | 293.00 | no | UMC 98 |
| mmp151a |  | 1.03 | 297.20 | yes | IBM2 |
| umc1514 |  | 1.03 | 301.37 | no | SSR popII |
| AY110393 | C | 1.03 | 302.80 | no | IBM2 |
| mmp100 |  | 1.03 | 311.40 | yes | IBM2 |
| umc2145 |  | 1.03 | 319.00 | no | IBM2 |
| uaz146a(rps28) |  | 1.03-1.04 | 320.56 | no | BNL 2002 |
| mmp56 |  | 1.04 | 320.90 | yes | IBM2 |
| cdo938a |  | 1.04 | 323.10 | yes | IBM2 |
| asg69 | C | 1.04 | 323.61 | no | UMC 98 |
| csu633 |  | 1.04 | 323.61 | no | UMC 98 |
| csu941 |  | 1.04 | 323.61 | no | UMC 98 |
| umc227 |  | 1.04 | 323.61 | no | UMC 98 |
| csu632a |  | 1.04 | 323.61 | no | UMC 98 |
| asg45(ptk) | C | 1.04 | 323.61 | no | SSR popII |
| umc1452 |  | 1.03-1.04 | 323.80 | no | SSR popI |
| npi(sod4) |  | 1.03 | 325.24 | no | BNL 2002 |
| les22 |  | 1.04 | 325.30 | no | UMC 98 |
| bnlg2238 | A C | 1.04 | 326.70 | yes | IBM2 |
| bnlg1016 |  | 1.04 | 326.70 | no | BNL 2002 |
| umc2124 | A C | 1.04 | 328.50 | no | IBM2 |
| uaz266a(nad) |  | 1.03 | 328.69 | no | BNL 2002 |
| csu1082 |  | 1.04 | 329.37 | no | UMC 98 |
| cdo38a(ntp) | C | 1.03 | 330.43 | no | BNL 2002 |
| umc1849 |  | 1.04 | 335.00 | yes | IBM2 |
| asg75 |  | 1.04 | 336.50 | yes | IBM2 |
| umc1169 | C | 1.04 | 337.50 | yes | IBM2 |
| chr125b |  | 1.04 | 339.60 | no | ChromDB |
| asg30b |  | 1.04 | 340.70 | yes | IBM2 |
| rgpr44a |  | 1.04 | 340.70 | no | UMC 98 |
| csu737(npc) |  | 1.04 | 340.70 | no | UMC 98 |
| rgpc361(ppi) |  | 1.04 | 340.70 | no | UMC 98 |
| PCO099415 | C | 1.04 | 344.42 | no | INDEL |
| umc1472 | C | 1.04 | 345.85 | no | SSR popII |
| uaz3 |  | 1.03-1.04 | 348.99 | no | BNL 96 |
| csu389 |  | 1.04 | 349.88 | no | UMC 98 |
| rz672a(cgs) |  | 1.04 | 349.88 | no | UMC 98 |
| AY110330 | A C | 1.04 | 350.60 | yes | IBM2 |
| umc29a |  | 1.05 | 351.00 | no | BNL 2002 |
| sod4 |  | 1.04 | 351.10 | no | UMC 98 |
| rgpc198a(sik) |  | 1.04 | 351.10 | no | UMC 98 |
| bnl2.323 |  | 1.04 | 353.12 | no | BNL 2002 |
| csu207 |  | 1.04 | 356.00 | yes | IBM2 |
| csu452 |  | 1.04 | 356.00 | no | UMC 98 |
| rz251a |  | 1.04 | 356.00 | no | UMC 98 |
| csu649(scp) | A C | 1.04 | 356.00 | no | UMC 98 |
| umc2217 | C | 1.03-1.04 | 358.40 | no | SSR popI |
| uaz248a(his3) |  | 1.04 | 359.70 | no | IBM2 |
| umc2227 | A C | 1.04 | 360.90 | yes | IBM2 |
| bnlg652 |  | 1.05 | 365.51 | no | BNL 2002 |
| umc1144 | A C | 1.04 | 368.97 | no | SSR popII |
| ufg13b |  | 1.04 | 369.20 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| ufg77 | | 1.04 | 373.20 | yes | IBM2 |
| umc1917 | A C | 1.04 | 374.80 | no | IBM2 |
| umc2390 | | 1.04 | 376.98 | no | SSR popII |
| isu041b | | 1.04 | 377.20 | yes | IBM2 |
| csu323 | | 1.04 | 378.52 | no | UMC 98 |
| csu887 | | 1.04 | 378.52 | no | UMC 98 |
| isu61a | | 1.04 | 379.06 | no | IBM1 |
| ufg43 | | 1.04 | 383.60 | yes | IBM2 |
| npi262 | | 1.04 | 383.71 | no | UMC 98 |
| bcd450e | | 1.04 | 383.71 | no | UMC 98 |
| uaz198d(rpL10) | | 1.04 | 383.71 | no | UMC 98 |
| bnlg1811 | A C | 1.04 | 386.40 | yes | IBM2 |
| bnl7.21a | | 1.05-1.07 | 388.85 | no | BNL 2002 |
| umc275 | | 1.04 | 389.56 | no | BNL 2002 |
| bnl9.11b(lts) | C | 1.04 | 390.80 | yes | IBM2 |
| umc2228 | A C | 1.04 | 391.80 | no | IBM2 |
| umc1770 | A C | 1.04 | 392.10 | no | SSR popII |
| bnlg1886 | | 1.05 | 396.77 | no | BNL 2002 |
| umc2229 | A C | 1.04 | 397.30 | no | IBM2 |
| bnlg2295 | A C | 1.04 | 398.20 | yes | IBM2 |
| dpg12a | | 1.04 | 399.20 | no | BNL 2002 |
| bnlg2086 | A C | 1.04 | 401.20 | no | IBM2 |
| umc2112 | A C | 1.04 | 401.30 | no | IBM2 |
| asg3 | | 1.04 | 401.90 | yes | IBM2 |
| csu3 | C | 1.05 | 405.00 | yes | IBM2 |
| umc1243 | A C | 1.04-1.05 | 405.00 | no | SSR popI |
| csu694b(uce) | C | 1.05 | 408.21 | no | UMC 98 |
| CL34571_2 | C | 1.05 | 411.48 | no | INDEL |
| mmp61 | | 1.05 | 412.60 | yes | IBM2 |
| PCO099462 | C | 1.05 | 413.06 | no | INDEL |
| lim497 | | 1.05 | 413.70 | yes | IBM2 |
| rz500(stp) | A C | 1.05 | 415.58 | no | UMC 98 |
| umc2025 | C | 1.05 | 417.00 | yes | IBM2 |
| umc1558 | | 1.05 | 417.00 | no | SSR popI |
| bnlg1832 | | 1.05 | 422.81 | no | BNL 2002 |
| npi453 | | 1.04 | 422.81 | no | BNL 96 |
| umc1734 | A C | 1.05 | 423.00 | no | SSR popII |
| mmp39 | | 1.05 | 425.20 | yes | IBM2 |
| umc1244 | C | 1.05 | 427.60 | no | SSR popI |
| pop1 | | 1.05 | 429.38 | no | UMC 98 |
| csu822 | | 1.05 | 429.38 | no | UMC 98 |
| csu263b | | 1.05 | 429.38 | no | UMC 98 |
| csu781b | C | 1.05 | 429.38 | no | UMC 98 |
| rgpc316 | C | 1.05 | 429.38 | no | UMC 98 |
| csu653(fbn) | | 1.05 | 429.38 | no | UMC 98 |
| csu1041a(ptk) | | 1.05 | 429.38 | no | UMC 98 |
| umc1515 | A C | 1.05 | 430.60 | yes | IBM2 |
| AY109646 | A C | 1.05 | 431.20 | no | IBM2 |
| nfd104c | | 1.05 | 432.04 | no | ChromDB |
| umc2230 | A C | 1.05 | 432.40 | yes | IBM2 |
| AY111680 | A C | 1.05 | 433.60 | yes | IBM2 |
| umc1297 | C | 1.05 | 434.69 | no | SSR popII |
| umc1469 | A C | 1.05 | 435.09 | no | SSR popI |
| rz421 | | 1.05 | 435.47 | no | UMC 98 |
| uaz246c(mbf) | C | 1.05 | 436.40 | yes | IBM2 |
| csu793 | | 1.05 | 437.08 | no | UMC 98 |
| AY109678 | C | 1.05 | 437.30 | no | IBM2 |
| mmp143 | | 1.05 | 437.90 | yes | IBM2 |
| umc1461 | A C | 1.05 | 438.80 | no | IBM2 |
| csu1138 | | 1.05 | 439.00 | yes | IBM2 |
| umc260 | | 1.05 | 439.00 | no | UMC 98 |
| umc167a | | 1.05 | 439.00 | no | UMC 98 |
| csu781c | C | 1.05 | 439.00 | no | UMC 98 |
| uaz198c(rpL10) | | 1.05 | 439.00 | no | UMC 98 |
| rz323a | | 1.05 | 439.30 | no | IBM2 |
| umc1493 | | 1.05 | 439.30 | no | IBM2 |
| umc1076 | A C | 1.05 | 440.00 | yes | IBM2 |
| mmp101 | | 1.05 | 441.20 | yes | IBM2 |
| umc1689 | | 1.05 | 445.10 | no | SSR popII |
| AY110396 | A C | 1.05 | 445.50 | yes | IBM2 |
| umc1676 | A C | 1.05 | 450.80 | yes | IBM2 |
| umc2231 | A C | 1.05 | 453.50 | no | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| umc1703 | | 1.05 | 453.90 | yes | IBM2 |
| rs2 | | 1.05 | 457.00 | yes | IBM2 |
| umc1611 | A C | 1.05 | 458.40 | no | SSR popII |
| eno2 | | 1.05 | 460.60 | no | BNL 2002 |
| uaz9 | | 1.05 | 460.60 | no | BNL 2002 |
| pbs9b | | 1.05 | 460.60 | no | BNL 2002 |
| uaz7a | | 1.05 | 460.60 | no | BNL 2002 |
| npi214 | | 1.05 | 460.60 | no | BNL 2002 |
| cdo344c(rga) | | 1.05 | 460.60 | yes | IBM2 |
| mpik41d(mem1) | | 1.05 | 460.60 | no | UMC 98 |
| rz892a(alt) | | 1.05 | 461.50 | no | UMC 98 |
| umc1626 | | 1.05 | 464.08 | no | SSR popI |
| AI855190 | A C | 1.05 | 464.70 | no | IBM2 |
| CL14065_1 | C | 1.05 | 465.03 | no | INDEL |
| umc1906 | A C | 1.05 | 467.00 | yes | IBM2 |
| umc1903 | A C | 1.05 | 467.90 | no | IBM2 |
| mmp124 | | 1.05 | 469.40 | yes | IBM2 |
| umc2232 | | 1.05 | 470.90 | yes | IBM2 |
| umc1395 | A C | 1.05 | 471.70 | yes | IBM2 |
| umc1321 | A C | 1.05 | 473.20 | yes | IBM2 |
| umc1601 | | 1.05 | 473.80 | yes | IBM2 |
| umc2233 | A C | 1.05 | 474.50 | yes | IBM2 |
| csu710f(apx) | | 1.05 | 475.60 | no | UMC 98 |
| umc1603 | A C | 1.05 | 475.90 | yes | IBM2 |
| hac101b | | 1.05 | 481.90 | yes | IBM2 |
| npi304 | | 1.05 | 483.75 | no | BNL 2002 |
| rz296a | | 1.05 | 483.75 | no | BNL 2002 |
| npi598 | | 1.05 | 483.75 | no | BNL 96 |
| umc1323 | A C | 1.05 | 483.83 | no | SSR popI |
| uaz13 | | 1.05 | 484.68 | no | BNL 2002 |
| mmp95 | | 1.05 | 484.70 | no | IBM2 |
| uaz4 | | 1.05 | 484.75 | no | BNL 2002 |
| uaz5 | | 1.05 | 484.75 | no | BNL 2002 |
| uaz6 | | 1.05 | 484.75 | no | BNL 2002 |
| pbs6d | | 1.05 | 484.75 | no | BNL 2002 |
| npi401 | | 1.05 | 484.75 | no | BNL 2002 |
| bnl1.556 | | 1.05 | 484.75 | no | BNL 2002 |
| uaz276 | | 1.05 | 485.90 | yes | IBM2 |
| uaz203 | | 1.05 | 486.16 | no | BNL 2002 |
| npi279 | | 1.06 | 486.77 | no | BNL 2002 |
| uaz17a | | 1.06 | 486.93 | no | BNL 2002 |
| uaz273 | | 1.05-1.06 | 487.00 | no | IBM2 |
| uaz11 | | 1.04 | 488.19 | no | BNL 2002 |
| ucsd61g | | 1.00-1.05 | 489.17 | no | BNL 2002 |
| uaz253 | | 1.05 | 489.41 | no | BNL 2002 |
| npi272 | | 1.06 | 491.10 | no | BNL 2002 |
| umc67a | | 1.06 | 496.60 | yes | IBM2 |
| csu881(cys) | | 1.06 | 496.60 | no | UMC 98 |
| mbd106 | C | 1.06 | 496.60 | no | ChromDB |
| csu574b(eif2B) | C | 1.06 | 496.60 | no | UMC 98 |
| isu146 | | 1.06 | 501.20 | yes | IBM2 |
| umc1972 | | 1.06 | 503.30 | yes | IBM2 |
| umc1988 | | 1.06 | 504.93 | no | SSR popII |
| umc1754 | A C | 1.06 | 506.83 | no | SSR popII |
| umc1812 | A C | 1.06 | 508.20 | no | IBM2 |
| myb6 | | 1.06 | 514.70 | yes | IBM2 |
| asg11 | C | 1.06 | 516.33 | no | UMC 98 |
| umc196 | | 1.06 | 516.33 | no | UMC 98 |
| umc1590 | A C | 1.06 | 517.00 | yes | IBM2 |
| AY109499 | C | 1.06 | 517.70 | no | IBM2 |
| AY110566 | | 1.06 | 518.90 | no | IBM2 |
| bnl5.59 | | 1.06 | 520.40 | yes | IBM2 |
| csu92 | A C | 1.06 | 520.40 | no | UMC 98 |
| umc1508 | A C | 1.06 | 521.41 | no | SSR popII |
| php20654 | | 1.06 | 523.30 | yes | IBM2 |
| AY110296 | | 1.06 | 523.90 | yes | IBM2 |
| php20682 | | 1.06 | 524.50 | no | IBM2 |
| asg58 | | 1.06 | 525.70 | yes | IBM2 |
| umc1811 | A C | 1.06 | 526.40 | yes | IBM2 |
| csu675a(prh) | C | 1.06 | 527.06 | no | SSR popI |
| bnlg2057 | C | 1.06 | 527.60 | yes | IBM2 |
| csu194(mthr) | | 1.06 | 528.05 | no | UMC 98 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| csu503(met) | | 1.06 | 528.21 | no | UMC 98 |
| rgpc356 | | 1.06 | 528.71 | no | UMC 98 |
| umc177a | | 1.06 | 528.71 | no | UMC 98 |
| umc2234 | A C | 1.06 | 529.00 | no | IBM2 |
| csu256(hsp90) | | 1.06 | 532.18 | no | UMC 98 |
| bnlg1598 | A C | 1.06 | 532.80 | yes | IBM2 |
| umc1123 | A C | 1.06 | 535.10 | yes | IBM2 |
| npi429 | | 1.05-1.06 | 535.27 | no | BNL 96 |
| umc1398 | | 1.06 | 540.91 | no | SSR popII |
| AY104360 | C | 1.06 | 541.30 | yes | IBM2 |
| npi258 | | 1.06 | 542.31 | no | BNL 2002 |
| ptk3 | | 1.06 | 543.99 | no | UMC 98 |
| mmp156 | | 1.06 | 544.20 | yes | IBM2 |
| uaz15 | | 1.06 | 547.66 | no | BNL 2002 |
| bnl23b | | 1.06 | 547.66 | no | BNL 2002 |
| csu60b | | 1.06 | 547.66 | no | BNL 2002 |
| csu91b | | 1.06 | 547.66 | no | BNL 2002 |
| dup382 | | 1.06 | 547.66 | no | BNL 2002 |
| uaz14a | | 1.06 | 547.66 | no | BNL 2002 |
| bnl34 | | 1.06 | 547.66 | no | BNL 96 |
| bnlg1273 | | 1.06 | 547.70 | no | BNL 2002 |
| bnlg1908b | | 1.06 | 547.96 | no | BNL 2002 |
| cdo464a | | 1.06 | 547.97 | no | BNL 2002 |
| ucsd61a | | 1.06 | 548.17 | no | BNL 2002 |
| bnlg1057 | A C | 1.06 | 548.30 | no | IBM2 |
| isu2191i | | 1.06 | 548.30 | no | BNL 2002 |
| umc1396 | A C | 1.06 | 548.40 | yes | IBM2 |
| umc2235 | A C | 1.06 | 550.00 | yes | IBM2 |
| umc1748 | | 1.06 | 553.60 | yes | IBM2 |
| umc1919 | A C | 1.06 | 555.80 | yes | IBM2 |
| PCO116807 | C | 1.06 | 556.80 | no | INDEL |
| bnlg1615 | C | 1.06 | 557.60 | yes | IBM2 |
| csu805 | A C | 1.06 | 558.50 | no | IBM2 |
| csu899b(ant) | | 1.06 | 558.50 | no | UMC 98 |
| psr152a | | 1.06 | 559.80 | yes | IBM2 |
| uwo2 | | 1.06 | 560.05 | no | BNL 96 |
| AY111153 | C | 1.06 | 561.00 | no | IBM2 |
| umc2151 | | 1.06 | 563.90 | yes | IBM2 |
| cdo595 | | 1.06 | 565.55 | no | BNL 2002 |
| cdo475b | | 1.06 | 565.55 | no | BNL 2002 |
| umc1664 | | 1.06 | 566.63 | no | SSR popI |
| umc1668 | | 1.06 | 566.63 | no | SSR popI |
| uaz249a(ubf9) | | 1.06 | 567.08 | no | BNL 2002 |
| ntf1 | C | 1.06 | 570.80 | yes | IBM2 |
| csu590(rpL17) | | 1.06 | 570.80 | no | UMC 98 |
| csu505(rpL7) | | 1.06 | 573.18 | no | UMC 98 |
| umc58 | C | 1.06 | 575.90 | yes | IBM2 |
| umc119 | | 1.06 | 575.90 | no | UMC 98 |
| rz28a | | 1.06 | 576.75 | no | BNL 2002 |
| cdo116a | | 1.06 | 576.75 | no | BNL 2002 |
| zmm6 | | 1.06 | 577.19 | no | BNL 2002 |
| mpik34 | | 1.06 | 577.19 | no | BNL 2002 |
| ucsd72a | | 1.06 | 577.19 | no | BNL 2002 |
| asg16b | | 1.06 | 578.20 | yes | IBM2 |
| umc82b | | 1.06 | 581.27 | no | BNL 2002 |
| mmp123 | | 1.06 | 583.30 | yes | IBM2 |
| umc1035 | A C | 1.06 | 587.00 | no | IBM2 |
| umc1709 | A C | 1.06 | 588.20 | no | IBM2 |
| php20644 | | 1.06 | 589.60 | yes | IBM2 |
| bnlg421 | | 1.06 | 591.69 | no | BNL 2002 |
| umc1122 | C | 1.06 | 593.04 | no | SSR popII |
| umc1924 | A C | 1.06 | 593.80 | yes | IBM2 |
| umc2396 | | 1.06-1.07 | 594.96 | no | SSR popII |
| csu1150 | | 1.06 | 596.34 | no | UMC 98 |
| ufg50 | C | 1.06 | 597.50 | yes | IBM2 |
| umc1254 | A C | 1.06 | 598.60 | no | SSR popI |
| uaz147b | | 1.06 | 600.00 | yes | IBM2 |
| uaz18d | | 1.07 | 603.21 | no | BNL 2002 |
| csu1132 | | 1.06 | 603.80 | yes | IBM2 |
| umc2236 | A C | 1.06 | 604.80 | yes | IBM2 |
| hm1 | C | 1.06 | 605.95 | no | UMC 98 |
| umc1925 | A C | 1.06 | 606.50 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| dpg7b | | 1.06-1.07 | 607.27 | no | BNL 2002 |
| asg62 | A C | 1.07 | 607.30 | yes | IBM2 |
| umc1499 | C | 1.07 | 607.30 | no | SSR popII |
| npi224g | | 1.07 | 610.23 | no | BNL 2002 |
| wsu(nia4) | | 1.07 | 610.23 | no | BNL 96 |
| isu2117h | | 1.07 | 611.22 | no | BNL 2002 |
| ncr(nrA) | | 1.07 | 611.37 | no | BNL 2002 |
| isu2117a | | 1.07 | 615.35 | no | BNL 2002 |
| umc274 | | 1.06-1.07 | 615.89 | no | BNL 2002 |
| cuny21 | | 1.06-1.07 | 616.02 | no | BNL 2002 |
| uaz20a | | 1.07 | 617.33 | no | BNL 2002 |
| umc2237 | A C | 1.06 | 618.50 | yes | IBM2 |
| npi566 | | 1.07 | 619.06 | no | BNL 2002 |
| bnlg615 | | 1.07 | 626.63 | no | SSR popII |
| csh11 | | 1.07 | 626.86 | no | UMC 98 |
| umc1374 | A C | 1.06-1.07 | 627.10 | no | SSR popI |
| umc2239 | A C | 1.06 | 630.60 | yes | IBM2 |
| umc1486 | | 1.07 | 636.08 | no | SSR popII |
| umc2238 | A C | 1.06 | 638.30 | no | IBM2 |
| csu374b | | 1.07 | 642.30 | yes | IBM2 |
| php20855 | | 1.07 | 647.40 | yes | IBM2 |
| csh12 | | 1.07 | 647.73 | no | UMC 98 |
| bcd450d | | 1.07 | 649.50 | no | UMC 98 |
| bcd98a | A C | 1.07 | 649.50 | yes | IBM2 |
| csu614a | | 1.07 | 649.50 | no | UMC 98 |
| uaz19c | | 1.07 | 649.50 | no | BNL 2002 |
| umc1278 | C | 1.07 | 652.40 | no | SSR popII |
| umc1356 | | 1.07 | 652.65 | no | SSR popI |
| umc1661 | A C | 1.07 | 652.65 | no | SSR popI |
| umc1358 | A C | 1.07 | 653.40 | yes | IBM2 |
| npi605a | | 1.07 | 655.63 | no | BNL 96 |
| AY111834 | A C | 1.07 | 656.70 | yes | IBM2 |
| bnlg1556 | A C | 1.07 | 658.60 | yes | IBM2 |
| bnl7.08b | | 1.07 | 659.74 | no | BNL 2002 |
| umc1833 | | 1.07 | 662.18 | no | SSR popI |
| umc33a | | 1.07 | 664.17 | no | UMC 98 |
| agrp83b | | 1.07 | 664.17 | no | UMC 98 |
| std1b(his2B1) | | 1.07 | 664.17 | no | UMC 98 |
| dmt103c | C | 1.07 | 669.39 | no | ChromDB |
| umc23a | | 1.07 | 670.20 | yes | IBM2 |
| umc1706 | A C | 1.07 | 671.29 | no | SSR popII |
| uaz151(sar) | | 1.07 | 672.57 | no | BNL 2002 |
| uaz2b | | 1.07 | 674.08 | no | BNL 2002 |
| npi236 | | 1.07 | 677.45 | no | BNL 96 |
| uaz228d(his2b) | | 1.07 | 677.81 | no | BNL 2002 |
| umc2064 | | 1.07 | 678.49 | no | SSR popI |
| rz698a(ppy) | | 1.07 | 679.85 | no | UMC 98 |
| csu921b(ppp) | | 1.07 | 679.85 | no | UMC 98 |
| csu542 | | 1.07 | 682.27 | no | UMC 98 |
| hon105 | | 1.07 | 683.56 | no | ChromDB |
| lim442 | | 1.07 | 685.20 | yes | IBM2 |
| med63b | | 1.07 | 685.88 | no | UMC 98 |
| csu660a | C | 1.07 | 688.54 | no | UMC 98 |
| bcd98g | | 1.07 | 689.71 | no | BNL 96 |
| mmp189 | | 1.07 | 690.50 | yes | IBM2 |
| uaz205b(hsp70) | | 1.07 | 692.64 | no | UMC 98 |
| mmp173 | | 1.07 | 693.60 | yes | IBM2 |
| umc2387 | C | 1.07 | 697.22 | no | SSR popII |
| php20661 | | 1.07 | 699.90 | yes | IBM2 |
| php20713b | | 1.07 | 700.50 | no | IBM2 |
| bnlg1025 | C | 1.07 | 700.50 | yes | IBM2 |
| bnl17.15b(bt2) | C | 1.07 | 700.55 | no | BNL 2002 |
| dpg7c | | 1.07 | 700.58 | no | BNL 2002 |
| bcd207a | | 1.07 | 703.50 | yes | IBM2 |
| bcd98m | | 1.08 | 704.57 | no | BNL 2002 |
| AY110356 | C | 1.07 | 706.40 | yes | IBM2 |
| umc1128 | C | 1.07 | 711.50 | yes | IBM2 |
| bsd2 | | 1.05 | 712.12 | no | BNL 2002 |
| umc1147 | A C | 1.07 | 714.40 | yes | IBM2 |
| bcd386a | | 1.07 | 717.80 | yes | IBM2 |
| umc1848 | | 1.07 | 717.80 | no | SSR popI |
| bnlg1564 | | 1.07 | 718.50 | no | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| npi447a |  | 1.07 | 720.30 | yes | IBM2 |
| phi002 | C | 1.07-1.08 | 720.90 | yes | IBM2 |
| umc1245 | C | 1.07 | 721.90 | yes | IBM2 |
| AY110159 | C | 1.07-1.08 | 722.30 | no | IBM2 |
| umc128 | C | 1.08 | 722.40 | yes | IBM2 |
| mwg645f |  | 1.08 | 722.40 | no | BNL 2002 |
| rz583a(msb) |  | 1.08 | 722.40 | no | UMC 98 |
| umc37b |  | 1.02 | 723.74 | no | BNL 2002 |
| bnlg1629 |  | 1.08 | 723.82 | no | BNL 2002 |
| rny(pcr)a |  | 1.08 | 724.87 | no | BNL 2002 |
| umc37a |  | 1.08 | 726.10 | yes | IBM2 |
| npi224f |  | 1.05-1.12 | 727.83 | no | BNL 2002 |
| bnl17.06 |  | 1.08 | 728.23 | no | BNL 2002 |
| cdo94b |  | 1.07-1.08 | 730.48 | no | BNL 2002 |
| mdh4 |  | 1.08 | 734.42 | no | UMC 98 |
| AY110313 | C | 1.08 | 735.20 | yes | IBM2 |
| AY110191 | C | 1.08 | 740.40 | no | IBM2 |
| cdo98b | C | 1.08 | 744.70 | yes | IBM2 |
| umc1998 | C | 1.08 | 747.90 | no | IBM2 |
| npi614 |  | 1.08 | 748.92 | no | BNL 2002 |
| npi573 |  | 1.08 | 748.92 | no | BNL 96 |
| mmp99 |  | 1.08 | 750.00 | yes | IBM2 |
| csu12b(cin4) |  | 1.08 | 750.23 | no | UMC 98 |
| csu580a(mdh) |  | 1.08 | 750.23 | no | UMC 98 |
| bnlg2228 | A C | 1.08 | 755.20 | yes | IBM2 |
| csu1007(eif4F) |  | 1.08 | 756.19 | no | UMC 98 |
| umc83a | A C | 1.08 | 756.50 | yes | IBM2 |
| dup135a |  | 1.08 | 756.50 | no | BNL 2002 |
| umc1085 | A C | 1.08 | 757.22 | no | SSR popI |
| umc2029 |  | 1.08 | 760.13 | no | SSR popII |
| lim254 |  | 1.08 | 760.30 | yes | IBM2 |
| chr124 |  | 1.08 | 765.10 | no | ChromDB |
| npi120 |  | 1.08 | 765.90 | yes | IBM2 |
| umc2080 | C | 1.08 | 769.40 | no | IBM2 |
| umc1955 | C | 1.08 | 770.40 | yes | IBM2 |
| uce1 |  | 1.08 | 770.92 | no | UMC 98 |
| bnlg1044 |  | 1.08 | 772.50 | no | BNL 2002 |
| umc2181 | A C | 1.08 | 774.50 | yes | IBM2 |
| npi255 |  | 1.08 | 775.20 | yes | IBM2 |
| npi569a |  | 1.08 | 775.41 | no | BNL 2002 |
| id1 |  | 1.08 | 775.57 | no | BNL 2002 |
| rz561a |  | 1.08 | 776.90 | no | UMC 98 |
| umc1838 | C | 1.08 | 777.40 | yes | IBM2 |
| csh4(id1) |  | 1.08 | 779.20 | yes | IBM2 |
| umc1446 | C | 1.08 | 781.60 | yes | IBM2 |
| mpik37 |  | 1.08 | 781.90 | no | BNL 96 |
| umc1928 |  | 1.08 | 783.20 | yes | IBM2 |
| mmp22 |  | 1.08 | 784.70 | no | IBM2 |
| an1 | C | 1.08 | 785.30 | yes | IBM2 |
| mmc0041 | C | 1.08 | 787.49 | no | SSR popII |
| sdg123 | C | 1.08 | 789.30 | no | ChromDB |
| csu982(goa) |  | 1.08 | 790.84 | no | UMC 98 |
| bz2 | C | 1.08 | 792.42 | no | UMC 98 |
| AY110349 | C | 1.08 | 793.40 | yes | IBM2 |
| csu531 |  | 1.08 | 798.74 | no | UMC 98 |
| vp14 | A C | 1.08 | 798.74 | no | UMC 98 |
| csu780b |  | 1.08 | 798.74 | no | UMC 98 |
| rgps10558a |  | 1.08 | 798.74 | no | UMC 98 |
| csu66a(lhcb) |  | 1.08 | 798.74 | no | UMC 98 |
| csu889b(lhcb) |  | 1.08 | 798.74 | no | UMC 98 |
| umc1991 | C | 1.08 | 800.70 | yes | IBM2 |
| bnlg1643 |  | 1.08 | 802.89 | no | BNL 2002 |
| dup103 |  | 1.08 | 803.08 | no | BNL 2002 |
| umc2385 | C | 1.08-1.09 | 803.99 | no | SSR popII |
| umc1383 | A C | 1.08 | 805.30 | yes | IBM2 |
| umc1843 |  | 1.08 | 805.30 | no | SSR popII |
| bnl29d(pds) |  | 1.08 | 805.83 | no | BNL 2002 |
| bnlg100 |  | 1.09-1.10 | 805.95 | no | BNL 2002 |
| umc2240 | A C | 1.08-1.09 | 806.50 | no | IBM2 |
| ufg(vp2274a) |  | 1.08 | 807.63 | no | BNL 2002 |
| umc1914 | A C | 1.08-1.09 | 809.90 | no | IBM2 |
| lim247 |  | 1.08-1.09 | 811.00 | no | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| AY109506 | A C | 1.08-1.09 | 811.00 | no | IBM2 |
| cdj2 | A C | 1.09 | 812.30 | yes | IBM2 |
| csu1174 |  | 1.09 | 812.30 | no | UMC 98 |
| rgpr250 |  | 1.09 | 812.30 | no | UMC 98 |
| csu21a(ago) |  | 1.09 | 812.30 | no | UMC 98 |
| umc24b(lhcb) |  | 1.09 | 812.30 | no | UMC 98 |
| umc1512 | A C | 1.08-1.09 | 813.30 | no | IBM2 |
| csu745e(rpPo) | C | 1.09 | 813.60 | no | UMC 98 |
| rz474b(dnaj) |  | 1.08-1.09 | 813.60 | no | IBM2 |
| ufg53 |  | 1.09 | 815.20 | yes | IBM2 |
| bnl8.10a |  | 1.09 | 815.76 | no | BNL 96 |
| ufg10 | C | 1.08-1.09 | 817.30 | no | IBM2 |
| uaz268c |  | 1.09 | 817.60 | no | BNL 2002 |
| dup218b |  | 1.09 | 818.52 | no | BNL 2002 |
| nfc103a | C | 1.08 | 819.03 | no | ChromDB |
| csu696 |  | 1.09 | 821.50 | yes | IBM2 |
| rth1 |  | 1.09 | 824.40 | no | UMC 98 |
| cdo795a |  | 1.09 | 824.40 | no | UMC 98 |
| umc27b | C | 1.09 | 825.14 | no | BNL 2002 |
| rz403 |  | 1.09 | 825.80 | yes | IBM2 |
| umc1715 |  | 1.09 | 828.29 | no | SSR popII |
| npi615 |  | 1.09 | 828.36 | no | BNL 2002 |
| csu1097c |  | 1.09 | 828.75 | no | UMC 98 |
| chrom7 |  | 1.09 | 833.00 | yes | IBM2 |
| asg63b |  | 1.09 | 833.71 | no | UMC 98 |
| csu511a |  | 1.09 | 833.71 | no | UMC 98 |
| umc252b |  | 1.09 | 836.51 | no | UMC 98 |
| ias7 |  | 1.09 | 836.70 | no | BNL 96 |
| glb1 | A C | 1.09 | 839.30 | yes | IBM2 |
| umc2047 | A C | 1.09 | 842.30 | yes | IBM2 |
| umc140a |  | 1.09 | 846.10 | yes | IBM2 |
| umc129(geb) |  | 1.09 | 846.10 | no | UMC 98 |
| bnlg1331 | A C | 1.09 | 847.00 | yes | IBM2 |
| csu222a(wsi) |  | 1.09 | 847.30 | yes | IBM2 |
| umc1298 | A C | 1.09 | 850.27 | no | SSR popII |
| rgpc746(rnp) |  | 1.09 | 854.70 | no | UMC 98 |
| AY110452 |  | 1.09 | 855.40 | yes | IBM2 |
| tbp1 |  | 1.09 | 857.65 | no | BNL 96 |
| bnlg1041 |  | 1.06 | 858.18 | no | BNL 2002 |
| bnlg1720 |  | 1.09-1.10 | 858.39 | no | BNL 2002 |
| csu200b |  | 1.09 | 858.91 | no | UMC 98 |
| bnl17.04(tua) |  | 1.09-1.10 | 860.73 | no | BNL 2002 |
| msu2(iaglu) |  | 1.09 | 862.10 | yes | IBM2 |
| umc1411 | A C | 1.09 | 863.92 | no | SSR popII |
| rpa6b |  | 1.09 | 864.60 | no | UMC 98 |
| uat1(lox) |  | 1.09 | 864.60 | no | UMC 98 |
| umc197a(rip) |  | 1.09 | 864.60 | yes | IBM2 |
| bcd1072c(hsp70) |  | 1.09 | 864.60 | no | UMC 98 |
| ucsd61e |  | 1.08 | 869.20 | no | BNL 2002 |
| umc2411 |  | 1.09 | 869.42 | no | SSR popI |
| lpe1 |  | 1.03 | 871.90 | no | BNL 96 |
| ole4 | A C | 1.09 | 873.50 | no | SSR popI |
| csu110b |  | 1.09 | 874.30 | no | UMC 98 |
| csu554a(rnh) |  | 1.09 | 874.30 | yes | IBM2 |
| csu921a(ppp) |  | 1.09 | 874.30 | no | UMC 98 |
| ucsd113d |  | 1.09 | 875.17 | no | BNL 2002 |
| umc2028 |  | 1.09 | 875.58 | no | SSR popII |
| bnlg1502 |  | 1.09-1.10 | 875.60 | no | BNL 2002 |
| mmp195d |  | 1.09 | 879.70 | no | IBM2 |
| umc1306 |  | 1.09 | 881.24 | no | SSR popII |
| umc1082 | A C | 1.09 | 882.70 | yes | IBM2 |
| umc1431 | A C | 1.09 | 886.10 | yes | IBM2 |
| umc107a(croc) | A C | 1.10 | 886.90 | yes | IBM2 |
| gln2 | C | 1.10 | 887.30 | no | UMC 98 |
| cdo122a(nad) |  | 1.10 | 887.50 | yes | IBM2 |
| AI665421 | A C | 1.10 | 889.90 | yes | IBM2 |
| bnlg400 |  | 1.09 | 890.69 | no | BNL 2002 |
| bnlg1597a |  | 1.09-1.10 | 890.87 | no | BNL 2002 |
| AY110019 | C | 1.10 | 890.90 | no | IBM2 |
| rz912a(phy) |  | 1.10 | 891.48 | no | UMC 98 |
| bcd808a |  | 1.10 | 891.70 | yes | IBM2 |
| nfa103a |  | 1.10 | 892.10 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| umc2189 | A C | 1.10 | 892.20 | no | IBM2 |
| chb101b |  | 1.10 | 892.20 | no | ChromDB |
| chr106a |  | 1.10 | 892.20 | no | ChromDB |
| umc1290 | A C | 1.09 | 892.77 | no | SSR popII |
| PCO087393 | C | 1.10 | 892.91 | no | INDEL |
| mmp141 |  | 1.10 | 893.70 | yes | IBM2 |
| tua2 |  | 1.10 | 898.44 | no | UMC 98 |
| knox3 |  | 1.10 | 898.44 | no | UMC 98 |
| tua1 | C | 1.10 | 898.44 | no | UMC 98 |
| csu248 |  | 1.10 | 898.44 | no | UMC 98 |
| csu947 |  | 1.10 | 898.44 | no | UMC 98 |
| bnl15.18 |  | 1.10 | 898.44 | no | UMC 98 |
| csu272a(tua) |  | 1.10 | 898.44 | no | UMC 98 |
| umc2149 | A C | 1.10 | 898.70 | yes | IBM2 |
| mmp83 |  | 1.10 | 899.20 | yes | IBM2 |
| phyA1 |  | 1.10 | 900.00 | no | BNL 96 |
| bnl17.21(tua) |  | 1.10 | 900.00 | no | BNL 2002 |
| AY111936 | A C | 1.10 | 902.10 | yes | IBM2 |
| kn1 |  | 1.10 | 903.86 | no | BNL 2002 |
| BE639426 | A C | 1.10 | 907.10 | yes | IBM2 |
| umc2223 |  | 1.10 | 907.14 | no | SSR popI |
| uaz167a |  | 1.10 | 910.39 | no | BNL 2002 |
| adh1 |  | 1.10 | 910.77 | no | SSR popII |
| umc1885 |  | 1.10 | 910.77 | no | SSR popII |
| pge19 |  | 1.10 | 912.51 | no | BNL 2002 |
| umc72b |  | 1.10 | 912.51 | no | BNL 2002 |
| bnlg1268 |  | 1.09 | 912.51 | no | BNL 2002 |
| bnlg1671 | A C | 1.10 | 913.40 | yes | IBM2 |
| hxa102b |  | 1.10 | 913.40 | no | ChromDB |
| bnlg1116 |  | 1.09-1.10 | 913.57 | no | BNL 2002 |
| mmp172 |  | 1.10 | 915.20 | yes | IBM2 |
| npi407 |  | 1.10 | 916.70 | yes | IBM2 |
| umc1534 |  | 1.10 | 918.21 | no | SSR popII |
| npi98a |  | 1.10 | 920.10 | no | UMC 98 |
| rz632c |  | 1.10 | 920.10 | no | UMC 98 |
| umc106a |  | 1.10 | 920.10 | no | UMC 98 |
| rz630a(sat) |  | 1.10 | 920.10 | yes | IBM2 |
| umc1774 | C | 1.10 | 923.01 | no | SSR popI |
| vef101b | C | 1.10 | 923.99 | no | ChromDB |
| ucsd64c |  | 1.10 | 925.07 | no | BNL 2002 |
| ucsd104b(zag6) |  | 1.10 | 925.29 | no | BNL 2002 |
| lim99a |  | 1.10 | 926.30 | yes | IBM2 |
| bcd450b |  | 1.10 | 926.83 | no | UMC 98 |
| phi308707 | C | 1.10 | 927.40 | no | IBM2 |
| npi282b |  | 1.10 | 927.90 | yes | IBM2 |
| PCO095183 | C | 1.10 | 929.52 | no | INDEL |
| lim78 |  | 1.10 | 930.50 | yes | IBM2 |
| mta1 |  | 1.10 | 932.92 | no | UMC 98 |
| uat4a |  | 1.10 | 932.92 | no | UMC 98 |
| csu261 |  | 1.10 | 932.92 | no | UMC 98 |
| csu137b(ap) |  | 1.10 | 932.92 | no | UMC 98 |
| bnlg1347 |  | 1.10 | 933.09 | no | BNL 2002 |
| mpik22a(zmm4) |  | 1.10 | 934.49 | no | BNL 2002 |
| uaz130a(tlk) | C | 1.10 | 934.50 | yes | IBM2 |
| asg54a |  | 1.10 | 936.13 | no | UMC 98 |
| mmp165 |  | 1.10 | 939.70 | no | IBM2 |
| mmp87 |  | 1.10 | 942.40 | yes | IBM2 |
| knox8 |  | 1.10 | 944.47 | no | UMC 98 |
| npi581a |  | 1.10 | 948.17 | no | BNL 96 |
| ucsd106d |  | 1.10 | 949.67 | no | BNL 2002 |
| lim39 |  | 1.10 | 950.20 | yes | IBM2 |
| bnl7.25a |  | 1.10 | 951.20 | no | IBM2 |
| csu954 |  | 1.10 | 951.20 | no | UMC 98 |
| umc147b |  | 1.10 | 952.19 | no | BNL 2002 |
| bnl17.18b |  | 1.10 | 952.19 | no | BNL 96 |
| umc257 | C | 1.10 | 963.20 | no | IBM2 |
| phi1 |  | 1.11 | 963.60 | no | UMC 98 |
| rpa7a |  | 1.11 | 963.60 | no | UMC 98 |
| umc264 |  | 1.11 | 963.60 | no | UMC 98 |
| umc161a | C | 1.11 | 963.60 | yes | IBM2 |
| csu1169b |  | 1.11 | 963.60 | no | UMC 98 |
| uaz21a |  | 1.10 | 963.60 | no | BNL 2002 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| AY109834 | C | 1.11 | 970.00 | yes | IBM2 |
| phi265454 | A C | 1.11 | 973.00 | yes | IBM2 |
| npi75b |  | 1.10 | 973.80 | no | BNL 2002 |
| csu63a(cdj) |  | 1.11 | 973.97 | no | UMC 98 |
| csu570b(mtl) |  | 1.11 | 973.97 | no | UMC 98 |
| umc1500 | A C | 1.11 | 985.11 | no | SSR popII |
| ias13a |  | 1.11 | 985.24 | no | BNL 2002 |
| AY110426 | C | 1.11 | 987.30 | yes | IBM2 |
| uaz166a |  | 1.10 | 992.50 | no | BNL 2002 |
| ufg14 |  | 1.11 | 995.00 | no | IBM2 |
| mmp195g |  | 1.11 | 1000.90 | yes | IBM2 |
| bnl8.08a |  | 1.11 | 1001.46 | no | BNL 2002 |
| bnlg1023b |  | 1.06 | 1002.02 | no | BNL 2002 |
| npi238 |  | 1.11 | 1006.10 | yes | IBM2 |
| asg68b |  | 1.11 | 1006.10 | no | UMC 98 |
| jpsb239b |  | 1.11 | 1006.60 | no | IBM2 |
| usu1a(fnr) |  | 1.11 | 1006.90 | no | UMC 98 |
| cdo87b(ptk) | C | 1.11 | 1006.90 | yes | IBM2 |
| umc1553 | C | 1.11 | 1007.60 | yes | IBM2 |
| gdh1 |  | 1.11 | 1008.46 | no | BNL 2002 |
| umc1421 |  | 1.11 | 1010.20 | yes | IBM2 |
| umc1681 | A C | 1.11 | 1014.90 | yes | IBM2 |
| bnlg2331 |  | 1.11 | 1016.21 | no | BNL 2002 |
| uaz10 |  | 1.05 | 1018.62 | no | BNL 2002 |
| uaz12 |  | 1.04-1.05 | 1018.62 | no | BNL 2002 |
| csu868(trp) |  | 1.11 | 1019.06 | no | UMC 98 |
| umc1129 | A C | 1.11 | 1019.10 | yes | IBM2 |
| bnl8.29a |  | 1.11 | 1021.40 | yes | IBM2 |
| ohp1 | A C | 1.11 | 1021.40 | no | BNL 2002 |
| tum5 |  | 1.07-1.12 | 1021.40 | no | BNL 2002 |
| csu604a(trh) | A C | 1.11 | 1021.40 | no | UMC 98 |
| umc1111 | C | 1.11 | 1022.60 | yes | IBM2 |
| umc1862 |  | 1.11 | 1023.30 | no | SSR popII |
| npi241a |  | 1.11 | 1025.70 | yes | IBM2 |
| uaz240c |  | 1.11 | 1026.12 | no | BNL 2002 |
| hon110 |  | 1.11 | 1027.30 | no | ChromDB |
| umc1737 | A C | 1.11 | 1029.96 | no | SSR popI |
| csu33b | A C | 1.11 | 1030.14 | no | UMC 98 |
| umc2241 | A C | 1.11 | 1031.00 | yes | IBM2 |
| umc2242 | A C | 1.11 | 1031.80 | no | IBM2 |
| bnlg1055 |  | 1.11 | 1033.99 | no | BNL 2002 |
| umc1118 | A C | 1.11 | 1034.30 | yes | IBM2 |
| ccr1 |  | 1.11 | 1037.79 | no | UMC 98 |
| csu381 |  | 1.11 | 1037.79 | no | UMC 98 |
| csu755 |  | 1.11 | 1037.79 | no | UMC 98 |
| csu536(ccr) |  | 1.11 | 1037.79 | no | UMC 98 |
| csu663b(psaD) |  | 1.11 | 1037.79 | no | UMC 98 |
| bnlg667a | A C | 1.11 | 1039.42 | no | SSR popI |
| AY110479 | C | 1.11 | 1039.70 | yes | IBM2 |
| umc1538 |  | 1.11 | 1040.93 | no | SSR popII |
| umc1744 | C | 1.11 | 1051.10 | yes | IBM2 |
| umc84a | A C | 1.11 | 1054.20 | yes | IBM2 |
| umc86a |  | 1.11 | 1054.70 | yes | IBM2 |
| csu134a(thf) |  | 1.11 | 1054.73 | no | UMC 98 |
| umc1630 | C | 1.11 | 1055.90 | yes | IBM2 |
| ids1 |  | 1.11 | 1057.19 | no | SSR popII |
| php15058 |  | 1.11 | 1057.80 | no | IBM2 |
| PCO063726 | C | 1.11 | 1060.61 | no | INDEL |
| mpik9 |  | 1.12 | 1062.19 | no | BNL 2002 |
| AY110160 | C | 1.11 | 1063.80 | yes | IBM2 |
| bnlg504 |  | 1.11 | 1065.42 | no | BNL 2002 |
| bnlg131 | C | 1.11 | 1065.62 | no | SSR popI |
| csu175e(eif5A) |  | 1.11 | 1065.66 | no | UMC 98 |
| chi1 |  | 1.11 | 1070.58 | no | UMC 98 |
| bnlg2123 | C | 1.11 | 1073.46 | no | SSR popII |
| dpg1a |  | 1.11 | 1084.42 | no | BNL 2002 |
| bnlg257 |  | 1.07 | 1091.35 | no | BNL 2002 |
| cdo457b |  | 1.11 | 1091.89 | no | UMC 98 |
| lim228 |  | 1.11 | 1092.40 | yes | IBM2 |
| csu266 |  | 1.11 | 1095.02 | no | UMC 98 |
| umc1725 | A C | 1.12 | 1096.05 | no | SSR popII |
| CL62610_1 | C | 1.11 | 1096.12 | no | INDEL |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| umc1331 | AC | 1.11 | 1096.50 | yes | IBM2 |
| phi227562 | AC | 1.11 | 1097.40 | no | IBM2 |
| csu1089 |  | 1.11 | 1098.00 | yes | IBM2 |
| rz614(fdx) |  | 1.12 | 1098.00 | no | UMC 98 |
| fdx3 | AC | 1.11 | 1098.40 | no | IBM2 |
| umc2243 | AC | 1.11 | 1098.40 | no | IBM2 |
| umc2045 | C | 1.11 | 1099.30 | yes | IBM2 |
| phi064 | AC | 1.11 | 1103.00 | yes | IBM2 |
| uaz22 |  | 1.12 | 1103.73 | no | BNL 2002 |
| tum4 |  | 1.07-1.12 | 1110.28 | no | BNL 2002 |
| bnl6.32 |  | 1.12 | 1113.20 | yes | IBM2 |
| rgpr3239a |  | 1.11-1.12 | 1113.20 | no | UMC 98 |
| csu865(phb) |  | 1.11-1.12 | 1113.20 | no | UMC 98 |
| umc1605 | AC | 1.12 | 1117.10 | yes | IBM2 |
| umc1797 |  | 1.12 | 1119.09 | no | SSR popII |
| umc1819 | AC | 1.12 | 1119.20 | no | IBM2 |
| umc2244 | AC | 1.11 | 1120.30 | yes | IBM2 |
| AY110983 |  | 1.12 | 1121.19 | no | INDEL |
| mmp31 |  | 1.12 | 1121.90 | no | IBM1 |
| lim331 |  | 1.12 | 1121.90 | no | IBM1 |
| ufg35b |  | 1.12 | 1121.90 | no | IBM1 |
| ufg75a |  | 1.12 | 1121.90 | no | IBM1 |
| tufm1 | AC | 1.12 | 1121.90 | yes | IBM2 |
| csu1084 |  | 1.12 | 1122.42 | no | UMC 98 |
| csu1146 |  | 1.12 | 1122.42 | no | UMC 98 |
| csu1154 |  | 1.12 | 1122.42 | no | UMC 98 |
| npi294i |  | 1.12 | 1122.42 | no | UMC 98 |
| acp4 |  | 1.12 | 1122.42 | no | BNL 96 |
| csu1114 |  | 1.12 | 1128.24 | no | UMC 98 |
| csu1193 |  | 1.12 | 1132.60 | no | UMC 98 |
| AY109916 | AC | 1.12 | 1137.90 | yes | IBM2 |
| sdg119 |  | 1.12 | 1272.50 | no | ChromDB |
| PCO091677 | C | 2.00-2.01 | -47.10 | no | INDEL |
| AY110535 | AC | 2.00 | 0.00 | yes | IBM2 |
| crr1 |  | 2.00-2.01 | 2.60 | no | SSR popII |
| umc2246 | AC | 2.03 | 3.10 | no | IBM2 |
| isu53a |  | 2.00-2.01 | 3.80 | yes | IBM2 |
| bnl(tas1a) |  | 2.00 | 6.80 | no | BNL 96 |
| pgs1 |  | 2.00 | 13.10 | no | BNL 96 |
| umc1419 | AC | 2.00-2.01 | 15.20 | no | SSR popI |
| bnl8.45a | C | 2.01 | 18.80 | no | SSR popI |
| npi239 |  | 2.00-2.01 | 18.80 | no | UMC 98 |
| umc2Stelo-1 |  | 2.00-2.01 | 18.80 | no | UMC 98 |
| umc2Stelo-2 |  | 2.00-2.01 | 18.80 | no | UMC 98 |
| csu1192(apx) |  | 2.00-2.01 | 18.80 | no | UMC 98 |
| rny(pcr)c |  | 2.00 | 20.83 | no | BNL 96 |
| csu326 |  | 2.01 | 21.13 | no | UMC 98 |
| bnl10.38b |  | 2.01 | 21.39 | no | UMC 98 |
| npi417a |  | 2.00 | 22.51 | no | BNL 2002 |
| agrc805 |  | 2.01 | 23.72 | no | UMC 98 |
| uaz21b |  | 2.00 | 24.55 | no | BNL 2002 |
| AY109692 | C | 2.01 | 25.30 | no | IBM2 |
| isu144a |  | 2.01 | 27.40 | yes | IBM2 |
| phi96100 | AC | 2.01 | 28.10 | no | IBM2 |
| umc2245 | AC | 2.01 | 30.90 | yes | IBM2 |
| php20568b |  | 2.01 | 34.30 | yes | IBM2 |
| bnlg1092 |  | 2.01 | 36.78 | no | BNL 2002 |
| csu29a | AC | 2.01 | 37.96 | no | UMC 98 |
| umc2363 | C | 2.01 - 2.02 | 40.20 | no | SSR popII |
| jpsb485b |  | 2.01 | 43.30 | yes | IBM2 |
| umc1227 |  | 2.01 | 45.55 | no | SSR popII |
| umc1165 | AC | 2.01 | 47.40 | yes | IBM2 |
| csu300a |  | 2.01 | 48.31 | no | UMC 98 |
| umc53a |  | 2.02 | 50.90 | yes | IBM2 |
| csu1053 |  | 2.02 | 50.90 | no | UMC 98 |
| csu642 | AC | 2.02 | 52.02 | no | UMC 98 |
| mir3b(thp) |  | 2.02 | 53.23 | no | UMC 98 |
| fht1 |  | 2.01 - 2.02 | 53.39 | no | BNL 96 |
| rz590a |  | 2.02 | 54.54 | no | UMC 98 |
| bnlg1302 |  | 2.02 | 55.11 | no | BNL 2002 |
| cdo524 |  | 2.02 | 55.57 | no | UMC 98 |
| csu552 |  | 2.02 | 55.57 | no | UMC 98 |
| csu12d(cin4) |  | 2.02 | 55.57 | no | UMC 98 |
| npi254a |  | 2.02 | 55.60 | yes | IBM2 |
| csu1148 |  | 2.02 | 57.53 | no | UMC 98 |
| umc1542 | AC | 2.02 | 57.60 | yes | IBM2 |
| umc1552 |  | 2.01 - 2.02 | 59.51 | no | SSR popII |
| bnlg1297 |  | 2.02 | 59.90 | yes | IBM2 |
| cdo244b(crp) |  | 2.02 | 60.42 | no | UMC 98 |
| bnlg1017 |  | 2.02 | 65.70 | yes | IBM2 |
| npi577a |  | 2.02 | 73.44 | no | BNL 96 |
| umc1980 |  | 2.02 | 75.60 | yes | IBM2 |
| bcd98x |  | 2.02 | 76.96 | no | BNL 2002 |
| umc2403 |  | 2.02 | 77.44 | no | SSR popII |
| umc1265 |  | 2.02 | 77.70 | yes | IBM2 |
| uaz24b |  | 2.02 | 79.14 | no | BNL 2002 |
| AY109603 |  | 2.02 | 82.30 | yes | IBM2 |
| bnlg1338 |  | 2.01 | 85.65 | no | BNL 2002 |
| CL52019_1 | C | 2.01 - 2.02 | 87.02 | no | INDEL |
| BE640649 | C | 2.02 | 87.80 | yes | IBM2 |
| npi208c |  | 2.02 | 90.30 | yes | IBM2 |
| npi421a |  | 2.02 | 90.30 | yes | IBM2 |
| pbs5 |  | 2.02 | 90.30 | no | BNL 2002 |
| umc1961 | C | 2.02 | 92.00 | no | IBM2 |
| umc1824a | C | 2.02 | 92.60 | yes | IBM2 |
| umc1823 | C | 2.02 | 92.80 | no | IBM2 |
| sgb101 | C | 2.02 | 92.90 | no | ChromDB |
| mmc0111 | C | 2.02 | 93.30 | yes | IBM2 |
| AY109516 | AC | 2.02 | 94.40 | yes | IBM2 |
| uaz25b |  | 2.02 | 94.55 | no | BNL 2002 |
| uaz26a |  | 2.02 | 94.55 | no | BNL 2002 |
| uaz251b(rpS11) |  | 2.02 | 109.65 | no | BNL 2002 |
| dmt102b | C | 2.02 | 113.79 | no | ChromDB |
| cpx1 |  | 2.02 | 118.28 | no | BNL 2002 |
| npi290b |  | 2.02 | 118.28 | no | BNL 96 |
| eks1 | C | 2.02 | 122.40 | yes | IBM2 |
| agrc539a |  | 2.02 | 122.40 | no | UMC 98 |
| umc1756 | C | 2.02 | 141.60 | no | IBM2 |
| bnlg2277 | C | 2.02 | 143.10 | yes | IBM2 |
| csu1091 |  | 2.02 | 144.67 | no | UMC 98 |
| ucsd(lfyB) |  | 2.02 | 145.87 | no | BNL 96 |
| CL12768_1 | C | 2.02-2.03 | 146.85 | no | INDEL |
| ias6a |  | 2.02 | 148.10 | no | BNL 2002 |
| bnlg1327 | AC | 2.02 | 148.10 | yes | IBM2 |
| myb5 |  | 2.02 | 149.20 | yes | IBM2 |
| mpik4b |  | 2.03 | 150.00 | no | BNL 2002 |
| csu1113 |  | 2.02 | 150.40 | no | UMC 98 |
| umc2193 | C | 2.03 | 152.77 | no | SSR popI |
| umc1262 | C | 2.02 | 153.10 | yes | IBM2 |
| umc1261 | C | 2.02 | 154.60 | yes | IBM2 |
| umc1518 |  | 2.02 | 155.72 | no | SSR popII |
| csu425(gct) |  | 2.02 | 156.12 | no | UMC 98 |
| umc1422 | AC | 2.02 | 156.60 | yes | IBM2 |
| csu348a |  | 2.02 | 158.88 | no | UMC 98 |
| AY106040 | C | 2.03 | 163.50 | yes | IBM2 |
| bnlg125 | C | 2.03 | 164.33 | no | SSR popI |
| umc6 | C | 2.03 | 164.80 | yes | IBM2 |
| csu1058 |  | 2.03 | 165.03 | no | UMC 98 |
| umc6a | C | 2.03 | 165.03 | no | INDEL |
| si605074C02 | C | 2.03 | 168.64 | no | INDEL |
| lim328 |  | 2.03 | 171.50 | yes | IBM2 |
| mmc0231 |  | 2.03 | 179.40 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| umc44b | C | 2.03 | 182.30 | yes | IBM2 |
| nfd102 | C | 2.03 | 186.20 | no | ChromDB |
| bnlg1537 |  | 2.03 | 186.30 | no | BNL 2002 |
| inra1(tmp) |  | 2.03 | 189.79 | no | UMC 98 |
| bnlg1393 |  | 2.02 | 190.24 | no | BNL 2002 |
| npi287a |  | 2.03 | 191.50 | yes | IBM2 |
| umc61 |  | 2.03 | 193.30 | yes | IBM2 |
| bcd855a(ext) | C | 2.03 | 193.30 | no | UMC 98 |
| csh6 |  | 2.03 | 193.38 | no | UMC 98 |
| csh7 |  | 2.03 | 193.46 | no | UMC 98 |
| csu176 |  | 2.03 | 195.38 | no | UMC 98 |
| csu498 |  | 2.03 | 195.38 | no | UMC 98 |
| b1 | A C | 2.03 | 197.20 | yes | IBM2 |
| npi402 |  | 2.03 | 197.60 | no | BNL 96 |
| umc1845 |  | 2.03 | 197.89 | no | SSR popII |
| bnlg1621b |  | 2.03 | 200.33 | no | BNL 2002 |
| mmp33 |  | 2.03 | 203.10 | yes | IBM2 |
| bnlg2248 |  | 2.03 | 207.74 | no | BNL 2002 |
| agrr113a |  | 2.03 | 207.76 | no | UMC 98 |
| uaz27b |  | 2.03 | 207.76 | no | BNL 2002 |
| ufg3a(ivr) |  | 2.03 | 207.76 | no | UMC 98 |
| csu761 |  | 2.03 | 211.35 | no | UMC 98 |
| psr901 |  | 2.03 | 212.20 | yes | IBM2 |
| npi269a |  | 2.03 | 212.90 | no | BNL 96 |
| csu1167 |  | 2.03 | 212.95 | no | UMC 98 |
| ufg28b |  | 2.03 | 216.00 | no | IBM2 |
| bnl(plB) |  | 2.04 | 216.48 | no | BNL 2002 |
| ole1 | A C | 2.03 | 216.50 | yes | IBM2 |
| sdg104 | C | 2.03 | 216.50 | no | ChromDB |
| npi587 |  | 2.03 | 216.80 | no | IBM2 |
| mmp42 |  | 2.03 | 218.70 | yes | IBM2 |
| npi583 |  | 2.03 | 220.36 | no | BNL 96 |
| csu571a(ipp) |  | 2.03 | 221.34 | no | UMC 98 |
| AI920398 | A C | 2.03 | 221.40 | yes | IBM2 |
| agrr167a |  | 2.03 | 223.33 | no | UMC 98 |
| bnl10.42a |  | 2.03 | 223.33 | no | UMC 98 |
| umc1555 | A C | 2.03 | 225.38 | no | SSR popII |
| bnl12.36a |  | 2.03-2.04 | 225.70 | no | BNL 96 |
| bnlg1064 | A C | 2.03 | 227.10 | yes | IBM2 |
| bnl17.23b(pal) |  | 2.03 | 227.30 | no | BNL 2002 |
| sdg107 |  | 2.03 | 228.40 | no | ChromDB |
| AY104214 | A C | 2.03 | 236.40 | yes | IBM2 |
| csu861 |  | 2.03 | 236.51 | no | UMC 98 |
| csu821 |  | 2.03 | 238.51 | no | UMC 98 |
| si606023F08 | C | 2.03-2.04 | 242.86 | no | INDEL |
| umc34 | A C | 2.04 | 243.30 | yes | IBM2 |
| csu40(grx) |  | 2.03-2.04 | 243.30 | no | UMC 98 |
| phi109642 | A C | 2.03-2.04 | 244.00 | no | IBM2 |
| bnlg381 | A C | 2.04 | 244.70 | yes | IBM2 |
| npi607 |  | 2.04 | 247.20 | yes | IBM2 |
| bnl1.45b |  | 2.04 | 247.20 | no | BNL 2002 |
| npi248 |  | 2.04 | 248.54 | no | BNL 96 |
| umc1024 | A C | 2.04 | 250.10 | yes | IBM2 |
| umc1769 | C | 2.04 | 250.94 | no | SSR popI |
| umc2247 | A C | 2.04 | 251.10 | yes | IBM2 |
| bnl8.04 |  | 2.04 | 252.27 | no | UMC 98 |
| umc1026 |  | 2.04 | 256.05 | no | SSR popII |
| mpik35b |  | 2.04 | 258.34 | no | BNL 2002 |
| bnlg2287 |  | 2.04 | 258.96 | no | BNL 2002 |
| isu2117b |  | 2.04 | 262.54 | no | BNL 2002 |
| AY110266 | C | 2.04 | 262.60 | yes | IBM2 |
| PCO098412 | C | 2.04 | 263.84 | no | INDEL |
| csu348b |  | 2.04 | 266.76 | no | UMC 98 |
| csu350(gpdh) |  | 2.04 | 266.76 | no | UMC 98 |
| umc1326 | C | 2.04 | 266.80 | yes | IBM2 |
| cta1 | C | 2.04 | 267.21 | no | SSR popII |
| isu58a |  | 2.04 | 267.50 | no | IBM2 |
| umc2248 | A C | 2.04 | 267.80 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| umc259b | C | 2.04 | 268.40 | yes | IBM2 |
| csu735(geb) |  | 2.04 | 269.52 | no | UMC 98 |
| umc1448 | C | 2.04 | 269.60 | yes | IBM2 |
| PCO140184 | C | 2.04 | 269.87 | no | INDEL |
| umc234 |  | 2.04 | 271.59 | no | UMC 98 |
| hag103a | C | 2.04 | 273.60 | no | ChromDB |
| umc1465 | A C | 2.04 | 273.70 | yes | IBM2 |
| umc1541 | A C | 2.04 | 274.90 | yes | IBM2 |
| npi242c |  | 2.04 | 274.95 | no | BNL 96 |
| mmp122 |  | 2.04 | 275.60 | no | IBM2 |
| CL58207_1 | C | 2.04 | 276.17 | no | INDEL |
| umc135 |  | 2.04 | 277.80 | no | UMC 98 |
| npi220d | C | 2.04 | 277.80 | no | UMC 98 |
| mmp167 |  | 2.04 | 281.30 | yes | IBM2 |
| umc1579 |  | 2.04 | 284.40 | no | SSR popI |
| prp2 | A C | 2.04 | 284.70 | yes | IBM2 |
| CL10221_1 | C | 2.04 | 285.89 | no | INDEL |
| bnl12.09 |  | 2.04 | 287.11 | no | BNL 2002 |
| pbs12 |  | 2.04 | 288.13 | no | BNL 2002 |
| dpg6a |  | 2.04 | 288.53 | no | BNL 2002 |
| umc134b |  | 2.04 | 288.80 | yes | IBM2 |
| AY110485 | A C | 2.04 | 292.50 | yes | IBM2 |
| csu56c(ohp) | C | 2.04 | 292.87 | no | UMC 98 |
| lim86 |  | 2.04 | 293.80 | no | IBM2 |
| umc1580 | A C | 2.04 | 294.20 | yes | IBM2 |
| bnlg1018 | A C | 2.04 | 294.20 | yes | IBM2 |
| bnlg1175 | A C | 2.04 | 295.10 | yes | IBM2 |
| csu334 |  | 2.04 | 295.39 | no | UMC 98 |
| csu762 |  | 2.04 | 295.39 | no | UMC 98 |
| csu393(fbn) | C | 2.04 | 295.39 | no | UMC 98 |
| bnlg166 |  | 2.04 | 295.74 | no | BNL 2002 |
| umc2251 | A C | 2.04 | 295.80 | yes | IBM2 |
| umc2249 | A C | 2.04 | 296.30 | yes | IBM2 |
| bnlg1909 |  | 2.05 | 297.40 | no | BNL 2002 |
| bnl35e(blr) |  | 2.04 | 297.48 | no | BNL 2002 |
| mmp91 |  | 2.04 | 302.60 | yes | IBM2 |
| accA |  | 2.05 | 305.51 | no | BNL 96 |
| bnlg108 | C | 2.04 | 306.30 | yes | IBM2 |
| bnlg1861a |  | 2.04 | 307.02 | no | BNL 2002 |
| bnlg1818 |  | 2.04 | 307.69 | no | BNL 2002 |
| pic3 |  | 2.04 | 307.78 | no | BNL 2002 |
| bnlg1914 |  | 2.05 | 307.86 | no | BNL 2002 |
| csh(prl1) |  | 2.04 | 308.13 | no | BNL 2002 |
| uaz234 |  | 2.05 | 308.45 | no | BNL 2002 |
| uaz235(px) |  | 2.05 | 308.45 | no | BNL 2002 |
| npi271a |  | 2.05 | 308.66 | no | BNL 2002 |
| bnlg1085a |  | 2.04 | 308.98 | no | BNL 2002 |
| hcf106 |  | 2.05 | 309.37 | no | BNL 2002 |
| bnlg1063b | C | 2.05 | 309.37 | no | BNL 2002 |
| dupssr21 |  | 2.05 | 309.40 | no | BNL 2002 |
| bnlg1140 |  | 2.08 | 309.69 | no | BNL 2002 |
| msu1 |  | 2.04 | 309.84 | no | BNL 2002 |
| bnl29(pds3) |  | 2.05 | 309.84 | no | BNL 2002 |
| uaz25c |  | 2.05 | 309.96 | no | BNL 2002 |
| bnlg1613 |  | 2.04 | 309.96 | no | BNL 2002 |
| bnlg2328a |  | 2.05 | 309.96 | no | BNL 2002 |
| pbs15 |  | 2.05 | 309.96 | no | BNL 96 |
| umc1259 | C | 2.04 | 310.20 | yes | IBM2 |
| umc2030 | A C | 2.04 | 313.50 | yes | IBM2 |
| umc1861 | A C | 2.04 | 314.40 | yes | IBM2 |
| npi242a |  | 2.04 | 315.00 | yes | IBM2 |
| umc8b |  | 2.04 | 315.50 | no | IBM2 |
| sdg102a |  | 2.04 | 315.50 | no | ChromDB |
| umc2088 | A C | 2.04 | 316.70 | yes | IBM2 |
| csu1117b |  | 2.04 | 316.84 | no | UMC 98 |
| bnlg121 |  | 2.04 | 319.30 | yes | IBM2 |
| tug4 |  | 2.04 | 319.30 | no | BNL 2002 |
| umc2079 | A C | 2.04 | 320.70 | yes | IBM2 |
| php10012 |  | 2.04 | 321.00 | yes | IBM2 |
| hda102 | C | 2.04 | 322.20 | no | ChromDB |
| hrg1 | C | 2.04 | 323.30 | no | IBM2 |
| rgpg271 | C | 2.04 | 328.79 | no | UMC 98 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| umc2250 | C | 2.04 | 329.00 | yes | IBM2 |
| umc1485 | A C | 2.04 | 329.60 | no | SSR popI |
| mmp89 |  | 2.04 | 331.40 | yes | IBM2 |
| bcd450f |  | 2.04 | 331.93 | no | UMC 98 |
| umc184b(glb) |  | 2.04 | 331.93 | no | UMC 98 |
| umc2125 | A C | 2.04 | 332.20 | no | IBM2 |
| umc2007 |  | 2.04 | 334.20 | yes | IBM2 |
| csu255a |  | 2.04 | 335.34 | no | UMC 98 |
| uaz262 |  | 2.05 | 336.40 | no | IBM2 |
| umc1455 | A C | 2.04-2.05 | 338.13 | no | SSR popI |
| csu148b(clx) |  | 2.04 | 338.21 | no | UMC 98 |
| umc1454 | A C | 2.04 | 339.30 | yes | IBM2 |
| umc1235 | A C | 2.04 | 339.82 | no | SSR popII |
| umc1007 |  | 2.04-2.05 | 340.54 | no | SSR popII |
| umc131 |  | 2.05 | 342.40 | yes | IBM2 |
| umc1410 | A C | 2.04-2.05 | 342.40 | no | SSR popII |
| psr922b |  | 2.04-2.05 | 342.90 | no | IBM2 |
| isu89 |  | 2.05 | 343.00 | yes | IBM2 |
| psr666 |  | 2.05 | 344.20 | yes | IBM2 |
| umng2 |  | 2.05 | 344.26 | no | UMC 98 |
| umc1581 | C | 2.05 | 344.40 | no | IBM2 |
| csu1060 |  | 2.05 | 344.42 | no | UMC 98 |
| umng1 |  | 2.05 | 344.50 | no | UMC 98 |
| csu143 |  | 2.05 | 344.50 | no | UMC 98 |
| umc1635 | A C | 2.05 | 344.80 | no | IBM2 |
| csu4a |  | 2.05 | 344.90 | no | UMC 98 |
| csu833 |  | 2.05 | 344.90 | no | UMC 98 |
| csu842 |  | 2.05 | 344.90 | no | UMC 98 |
| csu1066 |  | 2.05 | 344.90 | no | UMC 98 |
| csu1163 |  | 2.05 | 344.90 | no | UMC 98 |
| umn1(acc) |  | 2.05 | 344.90 | no | UMC 98 |
| zpu1 | A C | 2.05 | 345.00 | yes | IBM2 |
| umc1922 |  | 2.05 | 345.20 | no | IBM2 |
| agrp173 |  | 2.05 | 345.71 | no | UMC 98 |
| csu671a |  | 2.05 | 345.71 | no | UMC 98 |
| PCO096835 | C | 2.05 | 346.24 | no | INDEL |
| mmp119 |  | 2.05 | 346.50 | yes | IBM2 |
| asg29b |  | 2.05 | 346.52 | no | UMC 98 |
| csu1059 |  | 2.05 | 346.84 | no | UMC 98 |
| bnlg1184 |  | 2.06 | 347.11 | no | BNL 2002 |
| bnlg1887 |  | 2.06 | 347.11 | no | BNL 2002 |
| uaz179 |  | 2.05 | 347.60 | no | BNL 2002 |
| uaz28b |  | 2.05 | 347.60 | no | BNL 2002 |
| umc1884 |  | 2.05 | 347.96 | no | SSR popI |
| ucsd1.8c |  | 2.05 | 348.28 | no | BNL 2002 |
| uaz135 |  | 2.05 | 348.74 | no | BNL 2002 |
| uaz181 |  | 2.05 | 348.74 | no | BNL 2002 |
| AY109687 | A C | 2.05 | 349.00 | yes | IBM2 |
| csu2a |  | 2.05 | 349.67 | no | UMC 98 |
| uaz236b(ser) |  | 2.05 | 349.69 | no | BNL 2002 |
| ssu2 |  | 2.05 | 350.00 | no | BNL 2002 |
| bnl20 |  | 2.05 | 350.00 | no | BNL 2002 |
| umc8c |  | 2.05 | 350.00 | no | BNL 2002 |
| psr109a |  | 2.05 | 350.00 | no | BNL 2002 |
| bnl17.25 |  | 2.05 | 350.00 | no | BNL 2002 |
| bnlg2039 |  | 2.05 | 350.00 | no | BNL 2002 |
| mwg645i |  | 2.05-2.06 | 350.00 | no | BNL 2002 |
| hsbp1 |  | 2.05 | 350.86 | no | SSR popII |
| csu850 |  | 2.05 | 351.13 | no | UMC 98 |
| csu851a |  | 2.05 | 351.13 | no | UMC 98 |
| umc8g |  | 2.05 | 352.18 | no | UMC 98 |
| AW681281 | C | 2.05 | 352.40 | no | IBM2 |
| csu1073a |  | 2.05 | 353.23 | no | UMC 98 |
| umc1459 | A C | 2.05 | 353.81 | no | SSR popII |
| csu1080b |  | 2.05 | 354.60 | yes | IBM2 |
| csu337 |  | 2.05 | 355.97 | no | UMC 98 |
| npi123c |  | 2.05 | 357.10 | no | UMC 98 |
| umc2110 | A C | 2.05 | 357.50 | no | IBM2 |
| umc255a | A C | 2.06 | 358.32 | no | SSR popII |
| mmc0401 | A C | 2.05 | 358.60 | yes | IBM2 |
| umc2252 | C | 2.05 | 359.10 | no | IBM2 |
| umc112a |  | 2.06 | 360.76 | no | UMC 98 |
| umc1028 | A C | 2.06 | 361.20 | yes | IBM2 |
| tda217b |  | 2.06 | 364.27 | no | UMC 98 |
| AY110336 | A C | 2.06 | 364.50 | no | IBM2 |
| npi297 |  | 2.06 | 367.20 | yes | IBM2 |
| rz509b(mip) |  | 2.06 | 367.33 | no | UMC 98 |
| umc176 | C | 2.06 | 368.00 | no | SSR popI |
| pbf1 | A C | 2.06 | 368.10 | no | IBM2 |
| umc1156 | A C | 2.06 | 368.57 | no | SSR popII |
| bnlg1831 | A C | 2.06 | 368.80 | no | IBM2 |
| bnlg180 |  | 2.05 | 369.18 | no | BNL 2002 |
| uaz18b |  | 2.05 | 369.24 | no | BNL 2002 |
| umc1079 | A C | 2.06 | 369.30 | yes | IBM2 |
| uaz265a(sbe1) |  | 2.05-2.06 | 369.51 | no | BNL 2002 |
| ici99 |  | 2.06 | 369.53 | no | BNL 2002 |
| umc2b | C | 2.06 | 369.53 | no | BNL 2002 |
| uaz194b(ugu) |  | 2.06 | 369.53 | no | BNL 2002 |
| uaz29 |  | 2.05 | 369.54 | no | BNL 2002 |
| bcd249a |  | 2.06 | 369.83 | no | BNL 2002 |
| bnlg371 |  | 2.05 | 369.90 | no | BNL 2002 |
| mpik33i |  | 2.05-2.06 | 369.91 | no | BNL 2002 |
| npi356a |  | 2.06 | 370.31 | no | BNL 96 |
| umc267(kapp) |  | 2.06 | 370.47 | no | UMC 98 |
| csu281b |  | 2.06 | 370.74 | no | UMC 98 |
| klp1d |  | 2.06 | 372.06 | no | UMC 98 |
| dia1 |  | 2.06 | 372.77 | no | BNL 96 |
| bnlg1036 | A C | 2.06 | 373.50 | yes | IBM2 |
| bnlg1225 |  | 2.06 | 373.68 | no | BNL 2002 |
| csu747a(arf) | C | 2.06 | 373.74 | no | UMC 98 |
| umc55a |  | 2.06 | 373.90 | no | UMC 98 |
| pbs13b |  | 2.06 | 373.90 | no | BNL 2002 |
| ucsd141b |  | 2.06 | 373.92 | no | BNL 2002 |
| bnl35c(blr) |  | 2.06 | 373.94 | no | BNL 2002 |
| bnlg1396 |  | 2.06 | 373.95 | no | BNL 2002 |
| bnlg2313b |  | 2.06 | 373.96 | no | BNL 2002 |
| uaz352b |  | 2.06 | 374.05 | no | UMC 98 |
| umc139a |  | 2.06-2.08 | 375.12 | no | UMC 98 |
| umc1658 | A C | 2.06 | 375.30 | yes | IBM2 |
| umc2253 | C | 2.05 | 376.10 | yes | IBM2 |
| ufg2(agp2) |  | 2.06 | 376.31 | no | BNL 96 |
| umc2178 | C | 2.06 | 377.40 | yes | IBM2 |
| umc2254 | A C | 2.05 | 378.70 | no | IBM2 |
| AY105915 | C | 2.06 | 378.90 | yes | IBM2 |
| tug3 |  | 2.06 | 379.20 | no | BNL 2002 |
| umc1875 | C | 2.06 | 379.20 | no | IBM2 |
| bnlg1138 | A C | 2.06 | 379.20 | yes | IBM2 |
| umc1763 |  | 2.06 | 379.20 | no | SSR popI |
| umc1923 | A C | 2.06 | 379.40 | no | IBM2 |
| bcd1087a |  | 2.06 | 379.85 | no | UMC 98 |
| umc2192 | C | 2.06 | 379.97 | no | SSR popI |
| umc1080 | A C | 2.06 | 380.00 | yes | IBM2 |
| jpsb365b |  | 2.06 | 380.50 | yes | IBM2 |
| umc2194 | C | 2.06 | 380.58 | no | SSR popI |
| umc1755 | A C | 2.06 | 380.60 | no | IBM2 |
| AY109981 | A C | 2.06 | 380.80 | no | IBM2 |
| ucsd1.8b |  | 2.06 | 380.99 | no | BNL 2002 |
| umc1004 | A C | 2.06 | 381.80 | yes | IBM2 |
| csu270 |  | 2.06 | 382.30 | no | UMC 98 |
| npi456 |  | 2.06 | 382.52 | no | BNL 96 |
| PCO063114 | C | 2.06-2.07 | 383.38 | no | INDEL |
| uky1(P450) |  | 2.06 | 383.98 | no | UMC 98 |
| npi565b |  | 2.05-2.06 | 384.60 | no | BNL 2002 |
| bnlg1047c |  | 2.05 | 384.76 | no | BNL 2002 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| bnl17.24 | | 2.06 | 385.07 | no | BNL 2002 |
| npi221b | | 2.06 | 386.59 | no | BNL 2002 |
| umc1806 | | 2.06 | 386.59 | no | SSR popII |
| npi277a | | 2.06-2.07 | 386.59 | no | BNL 96 |
| umc2372 | | 2.06 | 389.03 | no | SSR popII |
| uaz30c | | 2.06-2.07 | 389.79 | no | BNL 2002 |
| csu1051 | | 2.06 | 391.16 | no | UMC 98 |
| umc1749 | | 2.06 | 391.25 | no | SSR popII |
| umc2023 | | 2.06 | 391.41 | no | SSR popII |
| bnlg1329 | A C | 2.08 | 391.62 | no | BNL 2002 |
| bnlg1413 | | 2.07 | 393.38 | no | BNL 2002 |
| bnlg2103 | | 2.06 | 394.48 | no | BNL 2002 |
| npi47a | | 2.07 | 394.52 | no | UMC 98 |
| umc98a | | 2.07 | 394.52 | no | UMC 98 |
| bnl27 | | 2.07 | 394.52 | no | BNL 2002 |
| umc5a | C | 2.07 | 394.52 | no | SSR popI |
| umc29b | | 2.06-2.07 | 394.52 | no | UMC 98 |
| tjp1(thp) | | 2.06-2.07 | 394.52 | no | UMC 98 |
| umc1946 | | 2.06-2.07 | 394.52 | no | SSR popII |
| umc2019 | A C | 2.07 | 394.97 | no | SSR popII |
| bnlg1258 | | 2.08 | 395.59 | no | BNL 2002 |
| npi613 | | 2.07 | 396.04 | no | BNL 2002 |
| uaz228a(his2b) | | 2.06 | 396.32 | no | BNL 2002 |
| amy3 | A C | 2.07 | 399.43 | no | UMC 98 |
| umc1637 | | 2.07 | 399.72 | no | SSR popI |
| umc1108 | A C | 2.07 | 401.50 | yes | IBM2 |
| umc2402 | | 2.07-2.08 | 406.80 | no | SSR popII |
| bcd926b | C | 2.07 | 409.30 | yes | IBM2 |
| asg72a | | 2.07 | 411.40 | no | UMC 98 |
| php20005 | | 2.07 | 411.40 | yes | IBM2 |
| umc1497 | | 2.07 | 411.98 | no | SSR popI |
| umc2129 | A C | 2.07 | 414.10 | yes | IBM2 |
| ucsd64i | | 2.07 | 415.88 | no | BNL 96 |
| mmp177b | | 2.07 | 416.60 | no | IBM2 |
| umc2220 | | 2.07 | 416.73 | no | SSR popI |
| umc1554 | C | 2.07 | 417.98 | no | SSR popII |
| umc2205 | | 2.07 | 420.56 | no | SSR popI |
| umc1890 | A C | 2.07 | 422.70 | yes | IBM2 |
| umc2032 | A C | 2.04 | 424.49 | no | SSR popII |
| csu1103 | | 2.07 | 424.60 | no | UMC 98 |
| umc1285 | C | 2.04 | 425.23 | no | SSR popII |
| AY110410 | A C | 2.07 | 427.90 | yes | IBM2 |
| php20569b | | 2.07 | 428.45 | no | BNL 96 |
| uaz269b(kri) | | 2.07 | 433.88 | no | BNL 2002 |
| mmc0271 | | 2.07 | 438.30 | no | SSR popI |
| nfc104b | | 2.07 | 443.41 | no | ChromDB |
| rz474c(dnaj) | | 2.07 | 446.90 | yes | IBM2 |
| uaz194a(ugu) | | 2.07 | 450.40 | yes | IBM2 |
| ugp1 | | 2.07 | 450.99 | no | UMC 98 |
| asg84a | | 2.07 | 450.99 | no | UMC 98 |
| csu635 | | 2.07 | 450.99 | no | UMC 98 |
| umc22a | | 2.07 | 450.99 | no | UMC 98 |
| mpik27a(zmm7) | | 2.07 | 450.99 | no | UMC 98 |
| AY109917 | C | 2.07 | 452.20 | no | IBM2 |
| nfd101b | | 2.07 | 452.20 | no | ChromDB |
| sdg106 | | 2.07 | 452.40 | no | ChromDB |
| phi251315 | C | 2.07 | 453.80 | yes | IBM2 |
| umc2380 | C | 2.07-2.08 | 459.13 | no | SSR popII |
| AY109722 | | 2.07 | 461.70 | yes | IBM2 |
| umc1042 | | 2.07 | 466.65 | no | SSR popI |
| csu54a | | 2.07 | 467.16 | no | BNL 96 |
| bnlg1633 | | 2.07 | 468.70 | no | BNL 2002 |
| umc88(P450) | | 2.07 | 469.10 | no | BNL 2002 |
| bnlg1267 | A C | 2.08 | 470.73 | no | BNL 2002 |
| bnlg1045 | | 2.07 | 470.99 | no | BNL 2002 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| bnlg2144 | | 2.08 | 471.22 | no | BNL 2002 |
| sdg116b | | 2.07 | 471.40 | no | ChromDB |
| umc36b | | 2.07 | 472.90 | yes | IBM2 |
| php20017a | | 2.07 | 474.40 | yes | IBM2 |
| chr119 | | 2.07 | 474.40 | no | ChromDB |
| bnlg2077 | A C | 2.07-2.08 | 474.80 | no | IBM2 |
| umc1560 | A C | 2.07 | 475.10 | yes | IBM2 |
| psr135b | | 2.07-2.08 | 477.90 | no | IBM2 |
| asg20 | A C | 2.08 | 478.70 | yes | IBM2 |
| umc4a | C | 2.08 | 478.70 | no | UMC 98 |
| agrr85a | | 2.08 | 478.70 | no | UMC 98 |
| umc1536 | | 2.08 | 478.70 | no | SSR popII |
| csu658(mam) | | 2.08 | 478.70 | no | UMC 98 |
| csu657(atpd) | | 2.08 | 478.70 | no | UMC 98 |
| csu800(lhca) | | 2.08 | 478.70 | no | UMC 98 |
| csu847a(lhcb) | | 2.08 | 478.70 | no | UMC 98 |
| csu154a(eif5A) | C | 2.08 | 478.70 | no | UMC 98 |
| umc1049 | A C | 2.08 | 480.70 | yes | IBM2 |
| mmp116 | | 2.08 | 482.20 | yes | IBM2 |
| umc1745 | | 2.08 | 485.58 | no | SSR popI |
| mmc0191 | | 2.07-2.08 | 486.45 | no | SSR popII |
| tua5 | | 2.08 | 490.00 | no | UMC 98 |
| csu749b | | 2.08 | 490.00 | no | UMC 98 |
| umc125a | | 2.08 | 490.00 | no | UMC 98 |
| mmc0143 | | 2.07-2.08 | 491.43 | no | SSR popII |
| umc2374 | C | 2.07-2.08 | 492.54 | no | SSR popII |
| csu17b(rnp) | | 2.08 | 494.53 | no | UMC 98 |
| umc122a | | 2.08 | 496.03 | no | UMC 98 |
| csu203b(eif5A) | A C | 2.08 | 496.03 | no | UMC 98 |
| bcd808c | | 2.08 | 496.10 | no | IBM2 |
| rgpg99 | | 2.08 | 496.79 | no | UMC 98 |
| mmp84 | | 2.08 | 498.30 | yes | IBM2 |
| umc116b | | 2.08 | 501.31 | no | UMC 98 |
| umc1126 | C | 2.08 | 503.61 | no | SSR popII |
| AY109583 | A C | 2.08 | 507.40 | yes | IBM2 |
| bnlg1233 | A C | 2.08 | 509.20 | no | IBM2 |
| asg23 | | 2.08 | 509.60 | no | UMC 98 |
| umc137a | | 2.08 | 509.60 | yes | IBM2 |
| rgpc74c | | 2.08 | 509.60 | no | UMC 98 |
| bnl5.21b | | 2.08 | 509.60 | no | UMC 98 |
| csu175a(eif5A) | | 2.08 | 509.60 | no | UMC 98 |
| umc2005 | | 2.08 | 511.48 | no | SSR popI |
| AI668346 | A C | 2.08 | 515.80 | yes | IBM2 |
| umc1526 | | 2.08 | 516.90 | no | SSR popII |
| hda109 | C | 2.08 | 519.60 | no | ChromDB |
| chr122 | C | 2.08 | 520.00 | no | ChromDB |
| phi435417 | C | 2.08 | 520.50 | yes | IBM2 |
| bnl8.21b | | 2.07 | 521.71 | no | BNL 96 |
| umc1947 | C | 2.08 | 522.40 | yes | IBM2 |
| bnlg1335 | | 2.08 | 522.84 | no | BNL 2002 |
| umc1604 | C | 2.08 | 523.50 | yes | IBM2 |
| csu894a | | 2.08 | 524.73 | no | UMC 98 |
| csu920a | | 2.08 | 524.73 | no | UMC 98 |
| umc1618 | | 2.08 | 528.53 | no | SSR popII |
| bnlg1316 | C | 2.08 | 529.20 | no | IBM2 |
| bnlg198 | | 2.08 | 529.50 | no | BNL 2002 |
| ucsd106f | | 2.08 | 529.50 | no | BNL 2002 |
| bnl17.30b | | 2.08 | 529.50 | no | BNL 2002 |
| rgpc1122a(rpL15) | | 2.07 | 529.50 | no | UMC 98 |
| csh1b(chi) | | 2.07-2.08 | 529.50 | no | BNL 96 |
| bnlg1141 | | 2.08 | 529.52 | no | BNL 2002 |
| bnlg1908a | | 2.08 | 529.56 | no | BNL 2002 |
| bnlg1721 | | 2.08 | 529.57 | no | BNL 2002 |
| uaz31b | | 2.08 | 529.59 | no | BNL 2002 |
| bnlg1662 | | 2.08 | 529.59 | no | BNL 2002 |
| bnlg1767 | | 2.08 | 529.59 | no | BNL 2002 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| uaz32 |  | 2.08 | 529.61 | no | BNL 2002 |
| npi591 |  | 2.08 | 529.61 | no | BNL 2002 |
| uaz23b |  | 2.08 | 529.61 | no | BNL 2002 |
| bnl6.20 |  | 2.08 | 529.80 | yes | IBM2 |
| hag105 |  | 2.08 | 532.00 | no | ChromDB |
| csu909 |  | 2.08 | 535.99 | no | UMC 98 |
| npi210 |  | 2.08 | 536.50 | yes | IBM2 |
| dup1390 |  | 2.06 | 536.79 | no | BNL 2002 |
| bnlg1169 |  | 2.08 | 536.79 | no | BNL 2002 |
| dupssr24 |  | 2.08 | 536.79 | no | BNL 2002 |
| ast(amyBS2)b |  | 2.08 | 536.79 | no | BNL 96 |
| mmp137 |  | 2.08 | 537.10 | no | IBM2 |
| chc101b | C | 2.08 | 537.20 | no | ChromDB |
| umc1464 | C | 2.08 | 538.49 | no | SSR popII |
| AY109645 | C | 2.08 | 538.80 | yes | IBM2 |
| bnl5.61b |  | 2.08 | 539.05 | no | BNL 96 |
| uaz241b |  | 2.08 | 539.58 | no | BNL 2002 |
| asg28c |  | 2.08 | 539.95 | no | UMC 98 |
| csu1097b |  | 2.08 | 539.95 | no | UMC 98 |
| rgpc643c |  | 2.08 | 539.95 | no | UMC 98 |
| uaz140 |  | 2.07 | 540.36 | no | BNL 2002 |
| npi274 |  | 2.08 | 541.11 | no | BNL 2002 |
| bnlg1109 |  | 2.06 | 541.56 | no | BNL 2002 |
| ias4a |  | 2.08 | 543.32 | no | BNL 2002 |
| PCO102097 | C | 2.08 | 544.27 | no | INDEL |
| umc2085 | C | 2.08 | 544.40 | yes | IBM2 |
| npi413a |  | 2.08 | 546.59 | no | BNL 2002 |
| npi113b |  | 2.08 | 548.10 | no | IBM2 |
| npi298 | C | 2.08 | 548.30 | yes | IBM2 |
| npi452 |  | 2.08 | 548.30 | no | BNL 2002 |
| umc1633 | C | 2.08 | 548.50 | no | IBM2 |
| npi45a |  | 2.06-2.07 | 550.00 | no | BNL 2002 |
| bnl8.44b |  | 2.08 | 551.09 | no | UMC 98 |
| umc1798 |  | 2.08 | 551.13 | no | SSR popI |
| umc2202 | C | 2.08 | 551.13 | no | SSR popI |
| AY109575 | C | 2.08 | 552.70 | yes | IBM2 |
| umc1992 | C | 2.08 | 556.21 | no | SSR popII |
| mmp34 |  | 2.08 | 562.50 | yes | IBM2 |
| umc31b | C | 2.08 | 564.30 | no | BNL 96 |
| mmp138 |  | 2.08 | 565.90 | no | IBM2 |
| psr119b |  | 2.08 | 566.00 | no | IBM2 |
| npi610 |  | 2.08 | 567.40 | yes | IBM2 |
| bcd249h |  | 2.08 | 567.61 | no | BNL 2002 |
| pur1 |  | 2.08 | 570.10 | no | UMC 98 |
| uaz239b |  | 2.08 | 570.73 | no | BNL 2002 |
| mmc0381 | C | 2.08 | 572.40 | yes | IBM2 |
| dpg6d |  | 2.08 | 573.15 | no | BNL 2002 |
| mmp188 |  | 2.08 | 573.30 | yes | IBM2 |
| cdo38c(ntp) | C | 2.08 | 573.30 | no | IBM2 |
| bnlg1746 | C | 2.08 | 573.60 | yes | IBM2 |
| bnlg1606 |  | 2.08 | 573.95 | no | BNL 2002 |
| bcd98l |  | 2.09 | 575.19 | no | BNL 2002 |
| isu115 |  | 2.08 | 575.20 | no | IBM2 |
| isu91b |  | 2.08 | 575.40 | yes | IBM2 |
| bnlg1940 | A C | 2.08 | 577.60 | yes | IBM2 |
| psr144a |  | 2.08 | 579.50 | yes | IBM2 |
| psr144c |  | 2.08 | 581.10 | yes | IBM2 |
| rDNA5S |  | 2.08 | 582.60 | no | BNL 96 |
| umc1516 | A C | 2.08 | 584.30 | yes | IBM2 |
| mpik(chs1b) |  | 2.09 | 589.98 | no | BNL 2002 |
| umc171b(oec23) |  | 2.09 | 589.98 | no | UMC 98 |
| umc49a | A C | 2.09 | 591.50 | yes | IBM2 |
| umc1230 |  | 2.08-2.09 | 593.56 | no | SSR popII |
| umc1551 | C | 2.09 | 597.97 | no | SSR popII |
| umc1256 | C | 2.09 | 600.70 | yes | IBM2 |
| umc1252 | C | 2.09 | 600.90 | yes | IBM2 |
| AY109592 | C | 2.09 | 601.60 | no | IBM2 |
| csu304a |  | 2.09 | 601.78 | no | UMC 98 |
| csu728b | C | 2.09 | 601.78 | no | UMC 98 |
| npi47c |  | 2.09 | 603.73 | no | UMC 98 |
| whp1 |  | 2.09 | 603.73 | no | SSR popI |
| mpik26 |  | 2.09 | 605.83 | no | BNL 2002 |
| bnlg1520 |  | 2.09 | 605.83 | no | BNL 2002 |
| npi294d |  | 2.09 | 605.83 | no | BNL 96 |
| csu64a(grf) |  | 2.09 | 606.13 | no | UMC 98 |
| betl1 |  | 2.09 | 606.40 | no | UMC 98 |
| umc1525 |  | 2.09 | 612.29 | no | SSR popII |
| mpik38 |  | 2.09 | 618.93 | no | BNL 2002 |
| uaz33a |  | 2.09 | 622.05 | no | BNL 96 |
| csu622 |  | 2.09 | 622.94 | no | UMC 98 |
| agrc39b |  | 2.09 | 622.94 | no | UMC 98 |
| csu315d |  | 2.09 | 622.94 | no | UMC 98 |
| fco1b(pex) |  | 2.09 | 622.94 | no | UMC 98 |
| fco1a(pex) |  | 2.09 | 627.01 | no | UMC 98 |
| umc1736 |  | 2.09 | 627.98 | no | SSR popII |
| bnl(tas1g) |  | 2.10 | 631.06 | no | BNL 2002 |
| csu200a |  | 2.09 | 634.74 | no | UMC 98 |
| mmp195e |  | 2.09 | 636.80 | yes | IBM2 |
| srk1 |  | 2.09 | 642.88 | no | UMC 98 |
| bnlg469b | C | 2.09 | 650.10 | yes | IBM2 |
| bnlg2042 |  | 2.02 | 650.17 | no | BNL 2002 |
| bcd98k |  | 2.09 | 650.26 | no | BNL 2002 |
| bnlg1893 | C | 2.09 | 654.80 | yes | IBM2 |
| csu109a | C | 2.09 | 660.38 | no | SSR popI |
| umc36a |  | 2.10 | 661.10 | yes | IBM2 |
| npi294a |  | 2.09 | 661.10 | no | BNL 2002 |
| pbs10 |  | 2.09 | 665.81 | no | BNL 2002 |
| mha1 |  | 2.09 | 665.81 | no | BNL 96 |
| ucsd61c |  | 2.10 | 669.92 | no | BNL 2002 |
| csu611a(grp) |  | 2.09 | 669.98 | no | UMC 98 |
| csu665a(adt) |  | 2.09 | 674.42 | no | UMC 98 |
| AY110389 | C | 2.10 | 681.80 | yes | IBM2 |
| csu810a |  | 2.10 | 688.69 | no | UMC 98 |
| umc1704 |  | 2.08-2.10 | 689.93 | no | SSR popII |
| umc2184 | C | 2.10 | 692.40 | yes | IBM2 |
| mmp183 |  | 2.10 | 694.60 | yes | IBM2 |
| php20581b(tb) |  | 2.10 | 695.99 | no | SSR popI |
| bnl17.14 |  | 2.10 | 702.50 | yes | IBM2 |
| csu251b |  | 2.10 | 702.50 | no | UMC 98 |
| npi400b |  | 2.10 | 702.50 | no | BNL 2002 |
| lim104 |  | 2.10 | 706.50 | yes | IBM2 |
| nfa103b |  | 2.10 | 708.10 | yes | IBM2 |
| chr106b |  | 2.10 | 708.10 | no | ChromDB |
| umc2Ltelo |  | 2.10 | 708.33 | no | UMC 98 |
| ufg55 |  | 2.10 | 711.00 | yes | IBM2 |
| bnl17.19b |  | 2.10 | 711.07 | no | BNL 96 |
| phi101049 | A C | 2.10 | 712.10 | yes | IBM2 |
| AY109586 | A C | 2.10 | 713.10 | no | IBM2 |
| cdo938c |  | 2.10 | 716.30 | no | IBM1 |
| umc1696 |  | 2.10 | 716.30 | yes | IBM2 |
| knox4 |  | 2.10 | 716.30 | no | BNL 2002 |
| bcd98n |  | 2.10 | 718.24 | no | BNL 2002 |
| rgpc12b |  | 2.10 | 721.36 | no | UMC 98 |
| ucsd113b |  | 2.10 | 724.27 | no | BNL 2002 |
| bnl(tas1p) |  | 2.10 | 724.27 | no | BNL 2002 |
| ucsd106a |  | 2.10 | 724.27 | no | BNL 96 |
| AY111236 | A C | 2.10 | 725.30 | yes | IBM2 |
| umc2214 |  | 2.10 | 728.36 | no | SSR popI |
| ucsd113c |  | 2.10 | 768.59 | no | BNL 96 |
| uaz109 |  | 3.00 | -21.30 | no | BNL 96 |
| bnl(tas4l) |  | 3.00 | -1.20 | no | BNL 96 |
| umc32a | C | 3.01 | -1.10 | no | SSR popI |
| umc2118 | A C | 3.00 | 0.00 | yes | IBM2 |
| g2 | C | 3.00 | 2.00 | yes | IBM2 |
| umc1931 | A C | 3.00 | 5.60 | yes | IBM2 |
| umc1746 | C | 3.00 | 7.10 | no | IBM2 |
| phi453121 | A C | 3.00 | 7.50 | yes | IBM2 |
| umc2255 | C | 3.01 | 9.50 | yes | IBM2 |
| phi404206 | C | 3.01 | 11.00 | yes | IBM2 |
| umc1780 | C | 3.01 | 11.20 | yes | IBM2 |
| bnl8.15 | C | 3.01 | 11.40 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| umc3Stelo | | 3.00-3.01 | 14.68 | no | UMC 98 |
| umc1394 | C | 3.01 | 21.80 | yes | IBM2 |
| umc2256 | C | 3.01 | 23.40 | yes | IBM2 |
| umc1970 | C | 3.01 | 28.20 | yes | IBM2 |
| umc2071 | C | 3.01 | 29.20 | yes | IBM2 |
| asg64 | | 3.01 | 29.60 | yes | IBM2 |
| umc2257 | C | 3.01 - 3.02 | 30.50 | no | IBM2 |
| mmp158a | | 3.01 | 31.80 | yes | IBM2 |
| umc1892 | C | 3.01 | 35.50 | yes | IBM2 |
| php20905 | | 3.01 | 37.20 | yes | IBM2 |
| phi104127 | C | 3.01 | 38.00 | yes | IBM2 |
| umc2049 | C | 3.01 | 38.70 | yes | IBM2 |
| mmp38 | | 3.01 | 42.60 | yes | IBM2 |
| e8 | | 3.01 | 44.22 | no | UMC 98 |
| csu628 | | 3.01 | 44.22 | no | UMC 98 |
| umc249 | | 3.01 | 44.22 | no | UMC 98 |
| umc1793 | | 3.00 | 45.17 | no | SSR popII |
| umc2376 | C | 3.01 | 45.37 | no | SSR popII |
| umc2377 | C | 3.01 | 47.91 | no | SSR popII |
| umc121 | | 3.01 | 54.30 | no | IBM2 |
| asg30c | | 3.01 | 58.00 | yes | IBM2 |
| csu32a | C | 3.02 | 60.00 | yes | IBM2 |
| bnl44 | | 3.01 | 61.47 | no | BNL 2002 |
| csu1062 | | 3.02 | 64.85 | no | UMC 98 |
| umc1458 | A C | 3.02 | 67.20 | yes | IBM2 |
| mpik24b(zmm2) | | 3.02 | 74.10 | no | UMC 98 |
| zem1 | | 3.02 | 75.04 | no | BNL 2002 |
| zpia | | 3.02 | 75.04 | no | BNL 2002 |
| bnlg1144 | A C | 3.02 | 77.00 | yes | IBM2 |
| umc1886 | A C | 3.02 | 78.50 | yes | IBM2 |
| bnlg1523 | | 3.03 | 81.50 | no | BNL 2002 |
| uaz210(hsp18) | | 3.03 | 82.86 | no | BNL 2002 |
| csu230 | | 3.02 | 83.56 | no | UMC 98 |
| umc1814 | | 3.02 | 86.84 | no | SSR popII |
| hsp18f | | 3.03 | 91.22 | no | BNL 2002 |
| AY109549 | A C | 3.02 | 95.40 | yes | IBM2 |
| cko1 | A C | 3.02 | 97.60 | yes | IBM2 |
| csu75a | | 3.02 | 98.91 | no | UMC 98 |
| asg16a | C | 3.02 | 100.80 | no | UMC 98 |
| me3 | A C | 3.02 | 101.02 | no | UMC 98 |
| csu199b | | 3.02 | 101.30 | no | UMC 98 |
| php20042a | | 3.02 | 101.30 | yes | IBM2 |
| bnlg1647 | A C | 3.02 | 103.30 | yes | IBM2 |
| csu324b(cts) | | 3.02 | 107.90 | yes | IBM2 |
| csu728c | C | 3.03 | 109.00 | no | UMC 98 |
| asg24a(gts) | A C | 3.03 | 109.00 | yes | IBM2 |
| csu56b(ohp) | C | 3.03 | 109.00 | no | UMC 98 |
| zag4 | | 3.02 | 115.93 | no | BNL 96 |
| umc2369 | C | 3.03 | 117.03 | no | SSR popII |
| bnlg1325 | | 3.03 | 117.76 | no | BNL 2002 |
| lim66 | | 3.03 | 124.80 | yes | IBM2 |
| umc2258 | A C | 3.02-3.03 | 127.80 | yes | IBM2 |
| bnlg1447 | C | 3.03 | 129.40 | yes | IBM2 |
| mus2 | | 3.02-3.03 | 130.73 | no | BNL 2002 |
| umc2259 | A C | 3.02-3.03 | 131.70 | no | IBM2 |
| mmp79 | | 3.03 | 139.30 | yes | IBM2 |
| mmp186 | | 3.03 | 145.30 | yes | IBM2 |
| asg48 | A C | 3.04 | 152.70 | yes | IBM2 |
| umc2024 | | 3.03-3.04 | 152.70 | no | SSR popII |
| csu242 | | 3.04 | 153.40 | no | UMC 98 |
| bnl8.35a | | 3.04 | 153.40 | yes | IBM2 |
| bcd98j | | 3.04 | 153.64 | no | BNL 2002 |
| chs566 | | 3.04 | 153.70 | no | BNL 2002 |
| npi249a | | 3.04 | 153.86 | no | BNL 2002 |
| isu91a | | 3.04 | 153.97 | no | BNL 2002 |
| npi276a | | 3.04 | 154.00 | yes | IBM2 |
| uaz164d | | 3.03-3.04 | 154.06 | no | BNL 2002 |
| csh(prl2) | | 3.04 | 154.42 | no | BNL 2002 |
| uaz159b | | 3.04 | 157.30 | no | IBM2 |
| umc1030 | | 3.04 | 159.00 | yes | IBM2 |
| umc59e | A C | 3.04 | 159.00 | yes | IBM2 |
| me1 | | 3.02-3.03 | 160.45 | no | BNL 96 |
| std1d(his2B1) | | 3.04 | 162.05 | no | UMC 98 |
| phi234966 | | 3.04 | 163.50 | no | IBM1 |
| umc1772 | A C | 3.04 | 163.50 | no | IBM2 |
| npi446 | | 3.04 | 163.80 | yes | IBM2 |
| phi243966 | C | 3.02 | 163.80 | no | IBM2 |
| umc1425 | C | 3.04 | 165.00 | yes | IBM2 |
| umc2000 | A C | 3.04 | 166.90 | yes | IBM2 |
| umc1729 | | 3.04 | 167.36 | no | SSR popI |
| umc1608 | A C | 3.04 | 168.00 | yes | IBM2 |
| umc154 | | 3.04 | 172.87 | no | UMC 98 |
| csu949a | | 3.04 | 172.87 | no | UMC 98 |
| bnlg2136 | | 3.04 | 174.67 | no | BNL 2002 |
| umc2158 | A C | 3.04 | 176.60 | yes | IBM2 |
| umc1495 | A C | 3.04 | 177.40 | yes | IBM2 |
| nfc104c | | 3.04 | 179.44 | no | ChromDB |
| umc1392 | A C | 3.04 | 181.10 | yes | IBM2 |
| rgpc601b | | 3.04 | 181.52 | no | UMC 98 |
| umc2033 | A C | 3.04 | 181.70 | yes | IBM2 |
| haf101 | C | 3.04 | 183.65 | no | ChromDB |
| rgpc131a | A C | 3.04 | 184.77 | no | UMC 98 |
| psr754b | | 3.04 | 186.00 | yes | IBM2 |
| umc1742 | A C | 3.04 | 189.00 | yes | IBM2 |
| umc2117 | C | 3.04 | 190.20 | yes | IBM2 |
| bnlg1019a | A C | 3.04 | 190.60 | no | IBM2 |
| umc1717 | A C | 3.04 | 190.80 | no | IBM2 |
| bnlg1113 | A C | 3.04 | 190.80 | yes | IBM2 |
| bnlg1452 | A C | 3.04 | 190.80 | yes | IBM2 |
| umc1655 | A C | 3.04 | 191.10 | no | IBM2 |
| tpi4 | A C | 3.04 | 192.34 | no | UMC 98 |
| ucsd201 | | 3.04 | 192.35 | no | BNL 2002 |
| umc1025 | | 3.04 | 192.54 | no | SSR popII |
| bnlg1638 | | 3.04 | 193.10 | yes | IBM2 |
| pbs14e | | 3.04 | 193.10 | no | BNL 2002 |
| uaz34a | | 3.04 | 193.10 | no | BNL 2002 |
| umc42b | | 3.04 | 193.10 | no | BNL 2002 |
| dup183b | | 3.04 | 193.10 | no | BNL 2002 |
| bnlg1628 | | 3.04 | 193.10 | no | BNL 2002 |
| bnlg2047 | | 3.04 | 193.10 | no | BNL 2002 |
| isu1719h | | 3.04 | 193.10 | no | BNL 2002 |
| mpik32e(zag2) | | 3.04 | 193.10 | no | BNL 2002 |
| uaz249b(ubf9) | | 3.04 | 193.10 | no | BNL 2002 |
| npi(tpi) | | 3.04 | 193.33 | no | BNL 2002 |
| isu2117i | | 3.04 | 193.71 | no | BNL 2002 |
| rz543a | C | 3.04 | 193.96 | no | UMC 98 |
| pbs14a | | 3.04 | 194.27 | no | BNL 2002 |
| bnlg1085b | | 3.04 | 195.01 | no | BNL 2002 |
| bnlg1957 | | 3.05 | 195.13 | no | BNL 2002 |
| bet1 | | 3.04 | 195.22 | no | BNL 2002 |
| dup104 | | 3.04 | 195.22 | no | BNL 2002 |
| uaz34b | | 3.04 | 195.22 | no | BNL 2002 |
| dup287a | | 3.04 | 195.22 | no | BNL 2002 |
| dup53 | | 3.04 | 195.63 | no | BNL 2002 |
| isu2191c | | 3.04 | 195.63 | no | BNL 2002 |
| klp1a | | 3.04 | 196.12 | no | UMC 98 |
| umc92a | | 3.04 | 196.12 | no | UMC 98 |
| asg46a | C | 3.04 | 196.12 | no | UMC 98 |
| ttu1(hsp18) | | 3.04 | 196.12 | no | UMC 98 |
| mmp144 | | 3.04 | 196.90 | yes | IBM2 |
| npi398a | | 3.04 | 197.54 | no | BNL 2002 |
| isu1719b | | 3.04 | 197.68 | no | BNL 2002 |
| ucla(obf6) | | 3.04 | 197.87 | no | BNL 2002 |
| tis903.6a | | 3.04 | 198.08 | no | BNL 2002 |
| umc1351 | C | 3.04 | 199.97 | no | SSR popII |
| umc1965 | | 3.04 | 200.65 | no | SSR popII |
| e4 | | 3.04 | 200.71 | no | UMC 98 |
| umc1721 | | 3.04 | 202.67 | no | SSR popII |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| mmp36 | | 3.04 | 203.40 | yes | IBM2 |
| mmc0132 | A C | 3.04 | 208.60 | yes | IBM2 |
| cdo244d(crp) | | 3.04 | 208.60 | yes | IBM2 |
| umc2261 | A C | 3.04 | 210.40 | yes | IBM2 |
| mmc0312 | A C | 3.04 | 212.70 | yes | IBM2 |
| umc1908 | A C | 3.04 | 213.60 | yes | IBM2 |
| npi247 | | 3.04 | 213.80 | yes | IBM2 |
| npi114b | | 3.04 | 213.80 | no | BNL 2002 |
| dup162 | | 3.04 | 213.96 | no | BNL 2002 |
| isu76a | | 3.04 | 214.16 | no | BNL 2002 |
| php20509 | | 3.04 | 214.70 | no | IBM2 |
| php20576 | | 3.04 | 214.70 | no | IBM2 |
| umc2262 | A C | 3.04 | 214.70 | no | IBM2 |
| ens1004 | | 3.04 | 214.89 | no | BNL 2002 |
| umc161b | C | 3.04 | 214.89 | no | BNL 2002 |
| ufg44 | | 3.04 | 214.90 | no | IBM2 |
| bnl43 | | 3.04 | 215.26 | no | BNL 2002 |
| isu157 | | 3.03-3.04 | 215.26 | no | BNL 2002 |
| isu148 | | 3.04 | 215.44 | no | BNL 2002 |
| mmp69 | | 3.04 | 215.60 | yes | IBM2 |
| uaz255 | | 3.04 | 215.60 | no | BNL 2002 |
| ici273c | | 3.04 | 215.82 | no | BNL 2002 |
| AY109870 | C | 3.04 | 219.50 | yes | IBM2 |
| PCO107756 | C | 3.04 | 220.24 | no | INDEL |
| csu621 | | 3.04 | 223.64 | no | UMC 98 |
| rz382a | | 3.04 | 224.10 | yes | IBM2 |
| csu2b | | 3.04 | 224.46 | no | UMC 98 |
| bnlg1816 | | 3.04 | 226.90 | yes | IBM2 |
| umc2263 | A C | 3.04 | 227.80 | yes | IBM2 |
| umc1504 | A C | 3.04 | 228.20 | no | IBM2 |
| umc1347 | A C | 3.04 | 228.34 | no | SSR popII |
| mmp29 | | 3.04 | 228.50 | no | IBM2 |
| rz244b(dia) | | 3.04 | 230.10 | yes | IBM2 |
| chr110a | | 3.04 | 230.70 | no | ChromDB |
| php10016c | | 3.04 | 231.50 | yes | IBM2 |
| umc50a | | 3.04 | 232.16 | no | BNL 96 |
| umc1900 | | 3.04 | 232.40 | no | IBM2 |
| umc1223 | | 3.04 | 234.40 | yes | IBM2 |
| csu29b | C | 3.04 | 236.69 | no | UMC 98 |
| PCO068796 | C | 3.04 | 237.40 | no | INDEL |
| AY110403 | C | 3.04 | 238.10 | no | IBM2 |
| csu1070 | | 3.04 | 241.55 | no | UMC 98 |
| csh10b(cycII) | | 3.04 | 241.55 | no | UMC 98 |
| PCO141323 | C | 3.04 | 242.64 | no | INDEL |
| AY110297 | C | 3.04 | 244.70 | yes | IBM2 |
| tha1 | | 3.04 | 246.96 | no | UMC 98 |
| rps25 | | 3.04 | 246.96 | no | UMC 98 |
| umc97 | | 3.04 | 246.96 | no | UMC 98 |
| csu795 | | 3.04 | 246.96 | no | UMC 98 |
| umc175 | | 3.04 | 246.96 | no | UMC 98 |
| bnl5.33e | | 3.04 | 246.96 | no | UMC 98 |
| umc1968 | C | 3.04 | 250.40 | no | IBM2 |
| csu212b | | 3.04 | 254.53 | no | UMC 98 |
| AY110151 | A C | 3.04 | 254.60 | yes | IBM2 |
| umc1920 | | 3.04 | 258.40 | yes | IBM2 |
| umc10a | C | 3.04 | 259.40 | yes | IBM2 |
| chr126b | | 3.04 | 259.40 | no | ChromDB |
| php20558a | | 3.04 | 260.10 | yes | IBM2 |
| mbd105 | | 3.04 | 260.10 | no | ChromDB |
| php20511 | | 3.04 | 260.30 | no | IBM2 |
| umc2264 | A C | 3.04 | 261.10 | yes | IBM2 |
| rz995b(fbp) | | 3.04 | 261.22 | no | UMC 98 |
| npi220b | C | 3.04 | 261.22 | no | BNL 96 |
| mmp9 | | 3.04 | 262.90 | yes | IBM2 |
| csu851b | | 3.04 | 264.81 | no | UMC 98 |
| csu408(grp) | | 3.04 | 264.81 | no | UMC 98 |
| umc1683 | C | 3.04 | 266.00 | no | IBM2 |
| bnl13.05b | | 3.04 | 266.85 | no | BNL 96 |
| csu404b | | 3.04 | 266.97 | no | UMC 98 |
| umc1449 | A C | 3.04 | 269.40 | yes | IBM2 |
| umc1835 | | 3.04 | 270.88 | no | SSR popII |
| bnlg602 | C | 3.04 | 270.88 | no | SSR popII |
| csu290 | | 3.04 | 275.62 | no | UMC 98 |
| cdo1160b(kri) | C | 3.04 | 275.62 | no | UMC 98 |
| hac101a | | 3.04 | 276.60 | yes | IBM2 |
| lg3 | | 3.04 | 276.61 | no | BNL 2002 |
| uaz35 | | 3.04 | 276.77 | no | BNL 2002 |
| umc1527 | A C | 3.04 | 279.30 | yes | IBM2 |
| umc1773 | C | 3.04 | 280.40 | yes | IBM2 |
| psr628 | | 3.04 | 280.60 | yes | IBM2 |
| ici286b | | 3.04 | 283.72 | no | BNL 96 |
| jpsb527a | | 3.04 | 283.90 | yes | IBM2 |
| umc1386 | A C | 3.04 | 284.39 | no | SSR popII |
| umc2002 | A C | 3.04 | 290.60 | yes | IBM2 |
| bnlg1399 | | 3.05 | 291.50 | no | BNL 2002 |
| mpik35d | | 3.04 | 292.06 | no | BNL 2002 |
| cdo459 | | 3.04 | 294.50 | no | BNL 2002 |
| cdo344a(rga) | | 3.04 | 294.50 | yes | IBM2 |
| bnlg1022b | | 3.04 | 296.00 | no | BNL 2002 |
| umc102 | C | 3.05 | 296.10 | yes | IBM2 |
| mpik35e | | 3.04 | 296.63 | no | BNL 2002 |
| bnlg1246b | | 3.05 | 297.57 | no | BNL 2002 |
| bnlg1456 | | 3.05 | 298.57 | no | BNL 2002 |
| uaz19a | | 3.04 | 298.62 | no | BNL 2002 |
| bnl31b | | 3.05 | 298.64 | no | BNL 2002 |
| nabr1 | | 3.04 | 298.89 | no | BNL 2002 |
| umc1174 | A C | 3.05 | 299.20 | yes | IBM2 |
| umc1600 | A C | 3.05 | 301.00 | yes | IBM2 |
| umc1300 | | 3.05 | 301.44 | no | SSR popII |
| tda30 | | 3.05 | 301.78 | no | UMC 98 |
| rgpc529 | | 3.05 | 301.78 | no | UMC 98 |
| mmp80 | | 3.05 | 303.70 | yes | IBM2 |
| rgpc6(rpS9) | C | 3.05 | 304.80 | no | UMC 98 |
| uaz288a(ppi) | | 3.05 | 305.30 | yes | IBM2 |
| umc1693 | A C | 3.05 | 305.80 | no | IBM2 |
| umc1907 | | 3.05 | 306.10 | no | IBM2 |
| bnlg1601 | A C | 3.05 | 306.10 | no | IBM2 |
| umc1874 | | 3.05 | 306.10 | no | SSR popI |
| umc1616 | | 3.05 | 306.71 | no | SSR popI |
| phys2 | C | 3.05 | 307.00 | yes | IBM2 |
| rz261b(sad) | | 3.05 | 307.39 | no | UMC 98 |
| npi612 | | 3.05 | 307.69 | no | BNL 2002 |
| npi609 | | 3.05 | 307.69 | no | BNL 96 |
| cdo250 | | 3.05 | 308.00 | no | BNL 96 |
| rz296b | | 3.05 | 309.50 | yes | IBM2 |
| tda64 | | 3.05 | 310.84 | no | UMC 98 |
| umc1750 | | 3.05 | 310.97 | no | SSR popI |
| umc1102 | A C | 3.05 | 312.80 | yes | IBM2 |
| chr109b | C | 3.05 | 313.10 | no | ChromDB |
| bnlg1035 | A C | 3.05 | 313.40 | yes | IBM2 |
| AY110352 | A C | 3.05 | 315.40 | yes | IBM2 |
| csu229b(oec) | | 3.05 | 316.88 | no | UMC 98 |
| mmc0022 | A C | 3.05 | 318.20 | yes | IBM2 |
| umc2020 | A C | 3.05 | 318.20 | yes | IBM2 |
| php20508 | | 3.05 | 318.40 | no | IBM2 |
| cyp7 | | 3.05 | 319.04 | no | UMC 98 |
| umc1167 | A C | 3.05 | 319.20 | yes | IBM2 |
| atp1 | C | 3.05 | 319.47 | no | UMC 98 |
| bnl8.08g | | 3.05 | 319.56 | no | BNL 2002 |
| rz390c(cyb5) | | 3.05 | 319.80 | no | IBM2 |
| pgd2 | | 3.05 | 323.35 | no | UMC 98 |
| csu561a | | 3.05 | 323.35 | no | UMC 98 |
| npi611b | | 3.05 | 323.35 | no | UMC 98 |
| umc252a | | 3.05 | 323.35 | no | UMC 98 |
| bnl6.06a | | 3.05 | 323.35 | no | UMC 98 |
| csu234a(gbp) | | 3.05 | 323.35 | no | UMC 98 |
| umc1501 | | 3.05 | 325.40 | yes | IBM2 |
| AY112215 | A C | 3.05 | 326.20 | no | IBM2 |
| psr119a | | 3.05 | 327.90 | yes | IBM2 |
| cdo105 | | 3.05 | 330.60 | yes | IBM2 |
| AY111507 | A C | 3.05 | 331.30 | yes | IBM2 |
| bnl(tas1l) | | 3.05 | 332.94 | no | BNL 2002 |
| uaz37 | | 3.06 | 333.04 | no | BNL 2002 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| isu68 | | 3.04 | 333.30 | no | BNL 2002 |
| bnlg1904 | | 3.04 | 334.22 | no | BNL 2002 |
| AY111541 | A C | 3.05 | 334.60 | yes | IBM2 |
| isu52 | | 3.05 | 336.49 | no | BNL 2002 |
| isu118b | | 3.04 | 336.75 | no | BNL 2002 |
| umc1307 | | 3.05 | 339.61 | no | SSR popI |
| vp1 | | 3.05 | 340.35 | no | BNL 96 |
| asg52b | | 3.05 | 341.04 | no | UMC 98 |
| asg67b | | 3.05 | 341.04 | no | UMC 98 |
| umc1954 | A C | 3.05 | 341.05 | no | SSR popII |
| ldp1 | C | 3.05 | 344.20 | no | UMC 98 |
| umc26a | | 3.05 | 344.20 | yes | IBM2 |
| umc268 | | 3.05 | 344.20 | no | UMC 98 |
| uiu8(geb) | | 3.05 | 344.20 | no | UMC 98 |
| csu44(gst) | | 3.05 | 344.20 | no | UMC 98 |
| csu961(fnr) | | 3.05 | 344.20 | no | UMC 98 |
| umc18a(psaN) | | 3.05 | 344.20 | no | UMC 98 |
| csu237b(psaN) | | 3.05 | 344.20 | no | UMC 98 |
| csu439(trm) | A C | 3.05 | 344.20 | no | UMC 98 |
| rz141a(emp70) | | 3.05 | 344.20 | no | UMC 98 |
| bnlg420 | | 3.05 | 345.99 | no | BNL 2002 |
| klp3 | | 3.05 | 346.80 | no | UMC 98 |
| myb2 | C | 3.05 | 346.80 | no | ChromDB |
| umc1839 | | 3.05 | 346.92 | no | SSR popII |
| csu382c(cld) | C | 3.05 | 349.67 | no | UMC 98 |
| si618046E03 | C | 3.05 | 352.15 | no | INDEL |
| umc2265 | A C | 3.05-3.06 | 354.00 | no | IBM2 |
| asg1b | | 3.05 | 358.30 | no | UMC 98 |
| sps2 | A C | 3.05 | 358.30 | yes | IBM2 |
| umn41 | | 3.05 | 358.30 | no | UMC 98 |
| csu362 | | 3.05 | 358.30 | no | UMC 98 |
| mwg645c | | 3.05 | 358.30 | no | BNL 2002 |
| csu636 | | 3.05 | 361.10 | yes | IBM2 |
| rz14 | C | 3.05 | 362.51 | no | UMC 98 |
| uaz189(rpL5) | | 3.05 | 365.94 | no | BNL 2002 |
| csu268 | | 3.05 | 366.03 | no | UMC 98 |
| umc1973 | A C | 3.05 | 371.40 | yes | IBM2 |
| ici98 | | 3.06 | 374.87 | no | BNL 96 |
| umn857a | | 3.05 | 375.17 | no | UMC 98 |
| AY106230 | C | 3.05 | 377.90 | yes | IBM2 |
| AY111296 | A C | 3.05 | 384.90 | yes | IBM2 |
| rgpc385b(rpL5) | | 3.05 | 386.86 | no | UMC 98 |
| AI770873 | A C | 3.05 | 388.10 | yes | IBM2 |
| mmp184 | | 3.05 | 389.10 | no | IBM2 |
| npi296 | | 3.05 | 389.70 | yes | IBM2 |
| umc1539 | A C | 3.05-3.06 | 390.30 | yes | IBM2 |
| bnl5.37b | | 3.05-3.06 | 390.80 | yes | IBM2 |
| bnl5.37a | | 3.06 | 391.40 | no | IBM2 |
| npi108a | | 3.05-3.06 | 391.40 | no | UMC 98 |
| umc1400 | A C | 3.05-3.06 | 391.40 | no | SSR popII |
| uaz260a(rpL5) | | 3.05-3.06 | 391.40 | no | UMC 98 |
| umc1311 | C | 3.06 | 394.80 | yes | IBM2 |
| umc1593b | | 3.06 | 394.80 | no | SSR popII |
| umc1730 | A C | 3.06 | 398.40 | yes | IBM2 |
| ucsd72d | | 3.06 | 400.17 | no | BNL 2002 |
| uaz8b(spr1) | | 3.06 | 400.89 | no | BNL 2002 |
| umc1027 | A C | 3.06 | 401.20 | yes | IBM2 |
| asg61a | | 3.06 | 401.80 | no | UMC 98 |
| bnl5.14 | | 3.06 | 401.80 | no | UMC 98 |
| bnl10.24a | | 3.06 | 401.80 | yes | IBM2 |
| lim486 | | 3.06 | 405.30 | yes | IBM2 |
| rz538b | | 3.06 | 411.10 | yes | IBM2 |
| csu1029 | | 3.06 | 411.10 | no | UMC 98 |
| npi268b | C | 3.06 | 411.10 | no | UMC 98 |
| umc1266 | A C | 3.06 | 411.60 | no | IBM2 |
| umc1876 | | 3.06 | 414.69 | no | SSR popI |
| asg39 | | 3.06 | 416.10 | yes | IBM2 |
| asg15 | | 3.06 | 416.10 | no | UMC 98 |
| asg34b(msd) | C | 3.06 | 416.10 | no | UMC 98 |
| umc165a | | 3.06 | 423.29 | no | UMC 98 |
| bnl8.01 | | 3.06 | 423.29 | no | BNL 96 |
| rz630d(sat) | | 3.06 | 423.54 | no | BNL 2002 |
| BE639846 | | 3.06 | 423.60 | yes | IBM2 |
| bnl47g | | 3.04 | 425.35 | no | BNL 2002 |
| PCO089398 | C | 3.06 | 428.85 | no | INDEL |
| umc2266 | A C | 3.06 | 434.30 | yes | IBM2 |
| umc164b | | 3.06 | 435.65 | no | BNL 96 |
| isu166b | | 3.04 | 436.83 | no | BNL 2002 |
| bnlg1047a | | 3.06 | 438.02 | no | BNL 2002 |
| bnlg1063a | C | 3.06 | 441.26 | no | BNL 2002 |
| bnlg1350a | | 3.08 | 443.99 | no | BNL 2002 |
| phi102228 | A C | 3.06 | 445.00 | yes | IBM2 |
| ksu1a | | 3.06 | 447.70 | no | UMC 98 |
| csu776b | | 3.06 | 447.70 | no | UMC 98 |
| csu38a(taf) | | 3.06 | 447.70 | no | UMC 98 |
| lg2 | | 3.06 | 449.04 | no | BNL 2002 |
| AY110055 | | 3.06 | 450.30 | yes | IBM2 |
| bnlg1449 | | 3.06 | 450.38 | no | BNL 2002 |
| npi328b | | 3.06 | 450.59 | no | BNL 96 |
| mmp27 | | 3.06 | 451.40 | no | IBM2 |
| mmp88 | | 3.06 | 451.40 | no | IBM2 |
| jpsb79 | | 3.06 | 451.50 | yes | IBM2 |
| umc60 | A C | 3.06 | 452.70 | yes | IBM2 |
| zag2 | | 3.05 | 453.36 | no | BNL 2002 |
| mpik2 | | 3.05 | 453.36 | no | BNL 2002 |
| uaz36 | | 3.05 | 453.36 | no | BNL 2002 |
| abp1 | A C | 3.05 | 453.36 | no | BNL 2002 |
| bnlg1505 | | 3.05 | 453.36 | no | BNL 2002 |
| gst4 | | 3.05 | 453.41 | no | BNL 2002 |
| isu131 | | 3.04 | 454.16 | no | BNL 2002 |
| bnlg1117 | | 3.05 | 454.24 | no | BNL 2002 |
| mpik30a | | 3.05 | 454.31 | no | BNL 2002 |
| bnlg2241 | | 3.06 | 454.31 | no | BNL 2002 |
| umc1951 | A C | 3.06 | 456.70 | no | SSR popI |
| psr754a | | 3.06 | 459.90 | yes | IBM2 |
| umc2268 | A C | 3.06 | 461.10 | yes | IBM2 |
| umc2408 | | 3.06 | 467.36 | no | SSR popII |
| umc1644 | | 3.06 | 473.10 | yes | IBM2 |
| bnlg2243 | | 3.08 | 474.75 | no | BNL 2002 |
| mmp5 | | 3.06 | 477.50 | yes | IBM2 |
| umc1674 | | 3.06 | 479.31 | no | SSR popII |
| csu1183 | | 3.06 | 480.10 | yes | IBM2 |
| bnlg1951 | A C | 3.06 | 481.60 | yes | IBM2 |
| rz444b | C | 3.06 | 481.72 | no | UMC 98 |
| csu351 | A C | 3.06 | 481.72 | no | UMC 98 |
| cdo251a | | 3.06 | 481.92 | no | BNL 2002 |
| mpik39b(myb) | | 3.04 | 482.06 | no | BNL 2002 |
| umc82c | | 3.06 | 482.30 | yes | IBM2 |
| umc2269 | A C | 3.06 | 482.30 | no | IBM2 |
| pho2 | | 3.04 | 482.67 | no | BNL 2002 |
| bnlg1798 | | 3.06 | 482.73 | no | BNL 2002 |
| csu215a(grp) | | 3.06 | 482.73 | no | UMC 98 |
| ufg42 | C | 3.06 | 486.20 | yes | IBM2 |
| tub6 | | 3.06 | 488.00 | no | UMC 98 |
| csu264 | | 3.06 | 488.00 | no | UMC 98 |
| csu191 | A C | 3.06 | 488.00 | yes | IBM2 |
| umc252c | | 3.06 | 488.00 | no | UMC 98 |
| csu223b(psei) | | 3.06 | 488.00 | no | UMC 98 |
| sdg113 | | 3.06 | 489.85 | no | ChromDB |
| bnlg1160 | A C | 3.06 | 491.40 | yes | IBM2 |
| umc2271 | A C | 3.06 | 494.00 | yes | IBM2 |
| umc2270 | A C | 3.06-3.07 | 494.00 | yes | IBM2 |
| csu96a(psei) | | 3.06 | 495.36 | no | UMC 98 |
| umc1985 | | 3.06 | 495.69 | no | SSR popII |
| csu180 | | 3.06 | 496.18 | no | UMC 98 |
| CL13054_1 | C | 3.06 | 499.82 | no | INDEL |
| lim424 | | 3.06 | 503.00 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
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| lim269 | | 3.06 | 504.70 | no | IBM2 |
| umc2381 | C | 3.06-3.07 | 505.18 | no | SSR popII |
| php20026 | | 3.07 | 505.19 | no | BNL 96 |
| ucla(obf3A) | | 3.07 | 506.11 | no | BNL 2002 |
| bnlg1931 | | 3.07 | 506.96 | no | BNL 2002 |
| AY111125 | A C | 3.06 | 507.20 | yes | IBM2 |
| umc39a | | 3.06 | 510.07 | no | UMC 98 |
| php15033 | | 3.06 | 511.10 | yes | IBM2 |
| bnlg197 | A C | 3.06 | 511.50 | yes | IBM2 |
| chs13d | | 3.04 | 511.50 | no | BNL 2002 |
| bnlg1796 | | 3.06 | 511.51 | no | BNL 2002 |
| bnl3.18 | | 3.07 | 511.71 | no | UMC 98 |
| bnlg1779 | | 3.07 | 512.00 | no | BNL 2002 |
| csu690 | | 3.06 | 512.53 | no | UMC 98 |
| AI770795 | A C | 3.06 | 512.70 | yes | IBM2 |
| uaz38a | | 3.07 | 515.53 | no | BNL 2002 |
| asg7b | | 3.06 | 517.00 | yes | IBM2 |
| dupssr17 | A C | 3.06-3.07 | 517.95 | no | SSR popI |
| bnl6.16a | | 3.07 | 520.70 | yes | IBM2 |
| cdo241a | | 3.06-3.07 | 520.70 | no | UMC 98 |
| bcd738b(pgk) | C | 3.06-3.07 | 520.70 | no | UMC 98 |
| umc1949 | | 3.06-3.07 | 527.06 | no | SSR popI |
| umc3b | | 3.06-3.07 | 529.40 | no | IBM2 |
| si618016E09 | C | 3.07 | 529.90 | no | INDEL |
| bnl15.20 | | 3.06-3.07 | 535.82 | no | BNL 96 |
| umc2050 | A C | 3.07 | 538.20 | yes | IBM2 |
| ici273a | | 3.07 | 538.47 | no | BNL 2002 |
| si605077F08 | C | 3.07 | 539.74 | no | INDEL |
| umc1135 | A C | 3.07 | 540.20 | yes | IBM2 |
| umc1767 | | 3.07 | 542.00 | yes | IBM2 |
| umc2272 | C | 3.07 | 544.20 | yes | IBM2 |
| umc1528 | A C | 3.07 | 544.40 | yes | IBM2 |
| PCO142509 | C | 3.07 | 544.56 | no | INDEL |
| umc1399 | C | 3.07 | 544.60 | yes | IBM2 |
| bnlg1605 | A C | 3.07 | 544.60 | yes | IBM2 |
| umc1690 | A C | 3.07 | 544.60 | no | SSR popII |
| bnl54 | | 3.04 | 544.81 | no | BNL 2002 |
| ufg21 | | 3.07 | 544.97 | no | BNL 2002 |
| npi212b | | 3.07 | 545.00 | yes | IBM2 |
| bnl45c | | 3.04 | 545.09 | no | BNL 2002 |
| hox3 | | 3.07 | 547.05 | no | UMC 98 |
| umc1148 | | 3.07 | 552.14 | no | SSR popII |
| umc1659 | | 3.07 | 552.14 | no | SSR popII |
| csu567(ces) | | 3.07 | 552.67 | no | UMC 98 |
| cdo1395d | | 3.07 | 554.22 | no | UMC 98 |
| csu680b | C | 3.07 | 554.22 | no | UMC 98 |
| csu706 | A C | 3.07 | 554.22 | no | UMC 98 |
| asg4 | | 3.07 | 554.39 | no | UMC 98 |
| bcd805 | | 3.07 | 554.39 | no | UMC 98 |
| bnl1.297a | | 3.07 | 554.39 | no | UMC 98 |
| bnl1.326b | | 3.07 | 554.39 | no | UMC 98 |
| bnl5.33b | | 3.07 | 554.39 | no | BNL 96 |
| AY104511 | A C | 3.07 | 562.10 | yes | IBM2 |
| umc1286 | C | 3.07 | 566.23 | no | SSR popI |
| AY109828 | | 3.07 | 566.50 | yes | IBM2 |
| asg10 | | 3.07 | 567.40 | no | IBM2 |
| gps4 | | 3.04 | 567.56 | no | BNL 2002 |
| umc1489 | A C | 3.07 | 567.60 | yes | IBM2 |
| umc2273 | A C | 3.07 | 568.00 | no | IBM2 |
| umc1404 | C | 3.07 | 568.30 | yes | IBM2 |
| csu1130 | | 3.07 | 571.61 | no | UMC 98 |
| rgpc643b | | 3.07 | 571.61 | no | UMC 98 |
| php20521 | | 3.07 | 572.70 | yes | IBM2 |
| sdg117a | C | 3.07 | 573.96 | no | ChromDB |
| umc15b | | 3.08 | 574.65 | no | BNL 96 |
| hon108 | C | 3.07 | 576.47 | no | ChromDB |
| umc1825 | C | 3.07 | 579.50 | yes | IBM2 |
| dhn6 | | 3.08 | 585.50 | no | BNL 2002 |
| umc16a | | 3.08 | 585.50 | no | UMC 98 |
| umc17a | A C | 3.08 | 585.50 | yes | IBM2 |
| umc228b | | 3.08 | 585.50 | no | UMC 98 |
| umc103b | | 3.08 | 585.50 | no | BNL 2002 |
| csu189(thr) | | 3.08 | 585.50 | no | UMC 98 |
| rny(atpb) | | 3.08 | 585.50 | no | BNL 2002 |
| bcd828a(atpb) | | 3.08 | 585.50 | no | BNL 2002 |
| uaz243a(atpb) | | 3.08 | 585.50 | no | BNL 2002 |
| csu240 | | 3.08 | 589.16 | no | UMC 98 |
| umc231 | | 3.08 | 591.16 | no | UMC 98 |
| bcd1127a | | 3.08 | 594.72 | no | BNL 2002 |
| csu772a | | 3.08 | 596.49 | no | UMC 98 |
| npi432 | C | 3.08 | 596.49 | no | UMC 98 |
| umc226a | | 3.08 | 596.49 | no | UMC 98 |
| uaz176b | | 3.08 | 596.49 | no | BNL 2002 |
| cdo345b | C | 3.08 | 596.53 | no | BNL 2002 |
| bnl17.27 | | 3.08 | 597.38 | no | BNL 2002 |
| dgc13 | | 3.08 | 597.51 | no | BNL 2002 |
| AY105849 | C | 3.08 | 597.60 | yes | IBM2 |
| npi201a | | 3.08 | 597.64 | no | BNL 2002 |
| rz527a | | 3.08 | 598.16 | no | BNL 2002 |
| uaz251e(rpS11) | | 3.08 | 599.30 | no | BNL 96 |
| bnl24b | | 3.08 | 599.38 | no | BNL 2002 |
| csu1117a | | 3.08 | 599.82 | no | UMC 98 |
| bnlg1861b | | 3.08 | 604.12 | no | BNL 2002 |
| umc1844 | | 3.08 | 605.81 | no | SSR popII |
| umc2274 | | 3.07-3.08 | 608.60 | no | IBM2 |
| umc1140 | C | 3.08 | 609.20 | yes | IBM2 |
| umc2275 | C | 3.07-3.08 | 610.20 | yes | IBM2 |
| mmc0251 | | 3.08 | 611.40 | yes | IBM2 |
| cdo118 | | 3.08 | 611.80 | no | IBM2 |
| npi91a | | 3.08 | 612.04 | no | BNL 2002 |
| npi257a | | 3.08 | 612.04 | no | BNL 2002 |
| cdo1160c(kri) | C | 3.07 | 612.22 | no | BNL 2002 |
| uaz18c | | 3.08 | 612.27 | no | BNL 2002 |
| umc1915 | A C | 3.08 | 617.50 | yes | IBM2 |
| bnlg1108 | A C | 3.08 | 618.60 | yes | IBM2 |
| umc2081 | | 3.08 | 627.10 | yes | IBM2 |
| umc1521 | | 3.08 | 627.13 | no | SSR popII |
| csu744 | C | 3.08 | 629.36 | no | UMC 98 |
| csu456(uce) | | 3.08 | 629.36 | no | UMC 98 |
| sdg115 | C | 3.08 | 630.00 | no | ChromDB |
| mdh3 | | 3.08 | 632.40 | no | UMC 98 |
| php10080 | | 3.08 | 632.40 | yes | IBM2 |
| isu158 | | 3.08-3.08 | 632.40 | no | BNL 2002 |
| umc1320 | A C | 3.08 | 633.80 | yes | IBM2 |
| umc1273 | A C | 3.08 | 634.80 | yes | IBM2 |
| AY109934 | A C | 3.08 | 638.30 | yes | IBM2 |
| si946021A07 | C | 3.08-3.09 | 640.58 | no | INDEL |
| umc2276 | A C | 3.08-3.09 | 652.40 | yes | IBM2 |
| uaz164c | | 3.08 | 681.62 | no | BNL 2002 |
| umc2174 | | 3.08 | 683.60 | yes | IBM2 |
| csu703 | | 3.08 | 688.71 | no | UMC 98 |
| AY110540 | | 3.08 | 691.20 | yes | IBM2 |
| a1 | | 3.09 | 697.20 | no | UMC 98 |
| umc63a | C | 3.09 | 697.20 | yes | IBM2 |
| csu869(cah) | | 3.09 | 697.20 | no | UMC 98 |
| csu125a(cah) | | 3.09 | 697.20 | no | UMC 98 |
| csu397(cah) | C | 3.09 | 697.20 | no | UMC 98 |
| umc184d(glb) | | 3.09 | 697.20 | no | UMC 98 |
| bnl47f | | 3.08-3.09 | 697.20 | no | BNL 2002 |
| csu303 | | 3.09 | 699.20 | yes | IBM2 |
| med68 | | 3.09 | 699.87 | no | UMC 98 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| bnl1.67 | | 3.09 | 699.87 | no | UMC 98 |
| csu845 | | 3.09 | 702.20 | yes | IBM2 |
| sh2 | A C | 3.09 | 702.20 | no | UMC 98 |
| bnl1.123 | | 3.09 | 702.20 | no | BNL 2002 |
| bnl12.30b | | 3.09 | 702.20 | no | BNL 2002 |
| pge25c | | 3.09 | 703.99 | no | BNL 2002 |
| bcd134b | | 3.09 | 712.91 | no | UMC 98 |
| cdo920b(egl) | | 3.09 | 712.91 | no | UMC 98 |
| CL29988_-2 | C | 3.09 | 713.08 | no | INDEL |
| jpsb107c | | 3.09 | 728.10 | yes | IBM2 |
| cdo962b | | 3.09 | 728.49 | no | BNL 96 |
| csu305b | | 3.09 | 728.70 | no | UMC 98 |
| dupssr33 | | 3.09 | 731.26 | no | BNL 2002 |
| jpsb41 | | 3.09 | 732.50 | yes | IBM2 |
| jpsb443 | | 3.09 | 732.50 | yes | IBM2 |
| sho38 | | 3.09 | 732.60 | no | IBM2 |
| jpsb106 | | 3.09 | 732.60 | no | IBM2 |
| sho89 | | 3.09 | 732.70 | yes | IBM2 |
| umc2152 | A C | 3.09 | 738.70 | yes | IBM2 |
| lim182 | | 3.09 | 743.00 | yes | IBM2 |
| csu768 | | 3.09 | 745.05 | no | UMC 98 |
| etm3 | | 3.09 | 746.54 | no | BNL 2002 |
| umc2008 | A C | 3.09 | 747.00 | no | IBM2 |
| umc2277 | A C | 3.08-3.09 | 747.50 | no | IBM2 |
| umc1813 | A C | 3.09 | 748.50 | yes | IBM2 |
| csu780a | | 3.09 | 750.69 | no | UMC 98 |
| csu919a | | 3.09 | 750.69 | no | UMC 98 |
| cdo455b | C | 3.09 | 750.69 | no | UMC 98 |
| dup214 | | 3.09 | 750.69 | no | BNL 2002 |
| rgps10558b | | 3.09 | 750.69 | no | UMC 98 |
| ici94 | | 3.09 | 751.67 | no | BNL 2002 |
| bnlg1536 | | 3.09 | 752.10 | yes | IBM2 |
| bnlg1182 | | 3.09 | 752.10 | no | BNL 2002 |
| isu102c | | 3.09 | 753.02 | no | BNL 2002 |
| pic6a | | 3.09 | 754.15 | no | BNL 2002 |
| lhcb1 | | 3.09 | 755.76 | no | UMC 98 |
| csu1086 | | 3.09 | 755.76 | no | UMC 98 |
| csu1142 | | 3.09 | 755.76 | no | UMC 98 |
| bnlg1754 | | 3.09 | 757.00 | yes | IBM2 |
| ias21 | | 3.09 | 757.10 | no | BNL 2002 |
| bnlg1257 | | 3.09 | 757.18 | no | BNL 2002 |
| uiu1a(pog) | | 3.09 | 757.31 | no | BNL 2002 |
| uaz110 | | 3.09 | 757.34 | no | BNL 2002 |
| bnlg2118 | | 3.09 | 757.41 | no | BNL 2002 |
| uaz114 | | 3.10 | 757.48 | no | BNL 2002 |
| uaz133 | | 3.09 | 757.54 | no | BNL 2002 |
| dup216 | | 3.09 | 757.71 | no | BNL 2002 |
| uaz213b | | 3.09 | 757.98 | no | BNL 2002 |
| csu58a | C | 3.09 | 758.02 | no | UMC 98 |
| ias22a | | 3.09 | 758.02 | no | BNL 2002 |
| uaz117a | | 3.10 | 758.02 | no | BNL 2002 |
| csu21b(ago) | | 3.09 | 758.02 | no | UMC 98 |
| csu899a(ant) | | 3.09 | 758.02 | no | UMC 98 |
| npi457 | | 3.09 | 758.20 | yes | IBM2 |
| umc1578 | A C | 3.09 | 758.41 | no | SSR popII |
| npi425a | A C | 3.09 | 759.90 | yes | IBM2 |
| bnlg1496 | A C | 3.09 | 760.90 | no | IBM2 |
| umc96 | | 3.09 | 764.78 | no | UMC 98 |
| csu289 | | 3.09 | 764.78 | no | UMC 98 |
| umc187 | | 3.09 | 764.78 | no | UMC 98 |
| php20726 | | 3.09 | 764.78 | no | UMC 98 |
| isu57a | | 3.09 | 766.61 | no | BNL 2002 |
| AY110567 | A C | 3.09 | 769.00 | yes | IBM2 |
| mmc0001 | C | 3.09 | 772.43 | no | SSR popII |
| isu1410h | | 3.09 | 773.24 | no | BNL 2002 |
| mwg645j | | 3.09 | 774.37 | no | BNL 2002 |
| uaz39 | | 3.09 | 774.81 | no | BNL 2002 |
| bnl7.26 | | 3.09 | 780.57 | no | UMC 98 |
| umc1361 | C | 3.09 | 786.39 | no | SSR popII |
| pbs13f | | 3.10 | 790.20 | no | BNL 2002 |
| npi420 | | 3.09 | 791.60 | yes | IBM2 |
| csu36c(rpL19) | | 3.09 | 791.99 | no | BNL 2002 |
| bnlg1098 | | 3.10 | 792.16 | no | BNL 2002 |
| umc2a | C | 3.10 | 801.50 | no | BNL 96 |
| umc1052 | C | 3.09 | 806.39 | no | SSR popI |
| umc1641 | A C | 3.09 | 806.90 | yes | IBM2 |
| nph1 | A C | 3.09 | 807.64 | no | SSR popII |
| lim444 | | 3.09 | 817.00 | yes | IBM2 |
| lim96 | | 3.09 | 823.50 | yes | IBM2 |
| lim82 | | 3.09 | 824.70 | yes | IBM2 |
| umc1639 | | 3.09 | 825.24 | no | SSR popII |
| csu320b | | 3.09 | 827.33 | no | IBM1 |
| plt2 | A C | 3.09 | 827.40 | no | IBM2 |
| mmp191 | | 3.09 | 828.90 | no | IBM1 |
| mmp193 | | 3.09 | 828.90 | no | IBM1 |
| umc1594 | A C | 3.09 | 828.90 | yes | IBM2 |
| umc1136 | A C | 3.10 | 830.70 | no | SSR popII |
| cyp1 | A C | 3.10 | 831.31 | no | SSR popII |
| umc2048 | A C | 3.10 | 858.62 | no | SSR popI |
| tda117 | | 3.10 | 870.84 | no | UMC 98 |
| csu728a | A C | 3.10 | 870.84 | no | UMC 98 |
| csu1061a | | 3.10 | 870.84 | no | SSR popI |
| chr126a | | 3.09 | 913.40 | no | ChromDB |
| agrr43b | | 3.10 | 914.76 | no | UMC 98 |
| uaz198a(rpL10) | | 3.10 | 914.76 | no | UMC 98 |
| bnlg372 | | 4.00 | -149.20 | no | BNL 96 |
| umc1232 | | 4.00 | -116.50 | no | SSR popI |
| agrr115 | C | 4.01 | -105.40 | no | INDEL |
| bnlg1318 | | 4.01 | -50.03 | no | BNL 2002 |
| bnlg1370 | C | 4.00 | -43.98 | no | BNL 2002 |
| bnlg1241 | | 4.01 | -36.04 | no | BNL 2002 |
| npi294j | | 4.01 | -19.74 | no | UMC 98 |
| cyp1710 | | 4.01 | -11.63 | no | UMC 98 |
| cyp2707 | | 4.01 | -11.63 | no | UMC 98 |
| csu618(P450) | | 4.01 | -11.63 | no | UMC 98 |
| cyp3 | C | 4.01 | -6.83 | no | SSR popII |
| umc1276 | C | 4.01 | -6.83 | no | SSR popII |
| AY109715 | A C | 4.00 | -4.10 | no | IBM2 |
| umc2278 | A C | 4.00 | 0.00 | yes | IBM2 |
| ufg26 | | 4.01 | 1.80 | yes | IBM2 |
| mtl1 | A C | 4.00-4.01 | 2.90 | no | IBM2 |
| bnlg1434 | A C | 4.01 | 4.30 | yes | IBM2 |
| ufg52 | C | 4.01 | 7.00 | yes | IBM2 |
| rca1 | A C | 4.01 | 9.90 | yes | IBM2 |
| umc4Stelo | | 4.00-4.01 | 10.67 | no | UMC 98 |
| mmp192 | | 4.01 | 13.70 | no | IBM2 |
| msf1 | C | 4.01 | 15.80 | yes | IBM2 |
| uaz103a | | 4.01 | 17.03 | no | BNL 2002 |
| csu221 | | 4.01 | 18.70 | yes | IBM2 |
| umc2279 | C | 4.01 | 22.90 | no | IBM2 |
| umc1228 | C | 4.01 | 23.40 | yes | IBM2 |
| bx1 | | 4.01 | 23.48 | no | SSR popI |
| bx5 | | 4.01 | 23.55 | no | BNL 2002 |
| bnl(tas1e) | | 4.00 | 23.82 | no | BNL 2002 |
| uaz59 | | 4.00-4.05 | 24.14 | no | BNL 2002 |
| umc123 | C | 4.01 | 24.60 | yes | IBM2 |
| umc1561 | | 4.00-4.01 | 25.93 | no | SSR popII |
| uaz58a | | 4.01 | 29.77 | no | BNL 2002 |
| mmp174 | | 4.01 | 30.40 | yes | IBM2 |
| uaz53a | | 4.01 | 37.30 | no | BNL 2002 |
| bx4 | C | 4.01 | 37.50 | yes | IBM2 |
| bx3 | | 4.01 | 37.50 | no | BNL 2002 |
| bx2 | | 4.01 | 38.96 | no | BNL 2002 |
| uaz41d | | 4.01 | 42.31 | no | BNL 2002 |
| cyp5 | A C | 4.01 | 47.60 | yes | IBM2 |
| umc1669 | | 4.01 | 57.50 | yes | IBM2 |
| rz329b(bga) | | 4.01 | 64.12 | no | UMC 98 |
| umc2409 | | 4.01 | 70.05 | no | SSR popII |
| uaz43b | | 4.01 | 73.44 | no | BNL 2002 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| umc1855 | | 4.01 | 74.18 | no | SSR popII |
| uaz54 | | 4.01 | 75.74 | no | BNL 2002 |
| uaz47b | | 4.01 | 75.74 | no | BNL 2002 |
| uaz129 | | 4.02 | 77.62 | no | BNL 2002 |
| uaz51 | | 4.01 | 78.04 | no | BNL 2002 |
| zpl1d | | 4.02 | 78.04 | no | BNL 2002 |
| npi604a | | 4.01 | 79.74 | no | BNL 96 |
| umc1757 | AC | 4.01 | 81.00 | no | IBM2 |
| umc1759 | AC | 4.01 | 81.00 | yes | IBM2 |
| phi295450 | AC | 4.01 | 81.00 | yes | IBM2 |
| umc1758 | | 4.01 - 4.02 | 81.93 | no | SSR popI |
| uaz30a | | 4.02 | 83.05 | no | BNL 2002 |
| ias10 | | 4.01 - 4.02 | 83.05 | no | BNL 2002 |
| php20725a | | 4.02 | 83.05 | no | INDEL |
| uaz184(hfi) | | 4.02 | 86.90 | no | BNL 2002 |
| uaz61a | | 4.01 - 4.02 | 87.64 | no | BNL 2002 |
| uaz60 | | 4.01 - 4.02 | 87.97 | no | BNL 2002 |
| uaz185(zp22) | | 4.02 | 88.32 | no | BNL 2002 |
| uaz55 | | 4.01 | 89.53 | no | BNL 2002 |
| uaz43d | | 4.01 | 89.53 | no | BNL 2002 |
| uaz52a | | 4.01 | 89.53 | no | BNL 2002 |
| uaz50 | | 4.01 | 90.57 | no | BNL 2002 |
| uaz14b | | 4.01 | 90.57 | no | BNL 2002 |
| uaz26b | | 4.01 | 90.57 | no | BNL 2002 |
| uaz42b | | 4.01 | 90.57 | no | BNL 2002 |
| uaz45b | | 4.01 | 90.57 | no | BNL 2002 |
| uaz46a | | 4.01 | 90.57 | no | BNL 2002 |
| uaz48a | | 4.01 | 90.57 | no | BNL 2002 |
| uaz49b | | 4.01 | 90.57 | no | BNL 2002 |
| uaz44b(zp19) | | 4.01 | 90.57 | no | BNL 2002 |
| cdo520(ser) | C | 4.02 | 90.60 | no | UMC 98 |
| umc2410 | | 4.02 | 91.57 | no | SSR popII |
| uaz57a | | 4.01 | 91.72 | no | BNL 2002 |
| uaz38b | | 4.02 | 92.14 | no | BNL 2002 |
| uaz149(zp19) | | 4.02 | 92.14 | no | BNL 2002 |
| uaz70c | | 4.02 | 92.49 | no | BNL 2002 |
| zpl1b | | 4.02 | 92.87 | no | BNL 2002 |
| zpl1c | | 4.02 | 92.87 | no | BNL 2002 |
| zpl1a | | 4.01 - 4.02 | 92.87 | no | BNL 2002 |
| umc277 | | 4.02 | 94.20 | no | UMC 98 |
| uaz17b | | 4.02 | 97.22 | no | BNL 2002 |
| uaz64b | | 4.02 | 97.22 | no | BNL 2002 |
| zpl1f | | 4.02 | 97.54 | no | BNL 2002 |
| umc1509 | | 4.02 | 100.08 | no | SSR popII |
| umc1943 | AC | 4.02 | 101.10 | yes | IBM2 |
| uaz67 | | 4.02 | 101.81 | no | BNL 2002 |
| uaz65b | | 4.02 | 101.81 | no | BNL 2002 |
| uaz66a | | 4.02 | 101.81 | no | BNL 2002 |
| uaz69a | | 4.02 | 101.81 | no | BNL 2002 |
| uaz68b(zp19) | | 4.02 | 101.81 | no | BNL 2002 |
| bnl17.13b | | 4.02 | 101.81 | no | BNL 96 |
| uaz41c | | 4.02 | 105.09 | no | BNL 2002 |
| uaz103b | | 4.02 | 105.95 | no | BNL 2002 |
| inra2(prp) | | 4.02 | 106.42 | no | UMC 98 |
| umc1288 | C | 4.02 | 107.04 | no | SSR popI |
| umc1294 | C | 4.02 | 108.43 | no | SSR popII |
| PCO146629 | C | 4.02- 4.03 | 110.44 | no | INDEL |
| uaz40a | | 4.02- 4.03 | 113.26 | no | BNL 2002 |
| dnap3 | | 4.01 | 114.81 | no | BNL 2002 |
| chs556 | | 4.03 | 126.23 | no | BNL 2002 |
| umc55b | | 4.03 | 126.28 | no | BNL 2002 |
| uaz63a | | 4.02 | 129.64 | no | BNL 2002 |
| php20713a | | 4.01 | 129.64 | no | BNL 2002 |
| zpl1e | | 4.01 - 4.02 | 129.64 | no | BNL 2002 |
| uaz62a | | 4.01 - 4.02 | 129.64 | no | BNL 2002 |
| psr144b | | 4.02 | 130.10 | yes | IBM2 |
| umc171a(oec23) | | 4.02- 4.03 | 130.86 | no | UMC 98 |
| umc87a | C | 4.02 | 134.10 | yes | IBM2 |
| chr117c | | 4.02 | 134.10 | no | ChromDB |
| umc31a | AC | 4.03 | 135.10 | no | IBM2 |
| bnlg1126 | | 4.03 | 135.30 | no | IBM2 |
| AY110398 | AC | 4.03 | 135.70 | no | IBM2 |
| umc1926 | | 4.03 | 140.90 | yes | IBM2 |
| umc2082 | | 4.03 | 141.60 | no | IBM2 |
| csu235 | | 4.03 | 143.40 | yes | IBM2 |
| csu63b(cdj) | | 4.03 | 143.40 | no | UMC 98 |
| csu583 | | 4.03 | 143.82 | no | UMC 98 |
| csu585 | | 4.03 | 143.82 | no | UMC 98 |
| rgpc496b(adh) | | 4.03 | 143.82 | no | UMC 98 |
| adh2 | AC | 4.03 | 147.10 | no | IBM2 |
| rz53b | | 4.03 | 147.20 | no | IBM2 |
| AY110253 | C | 4.03 | 152.90 | yes | IBM2 |
| isu144b | | 4.03 | 157.60 | yes | IBM2 |
| umc2281 | AC | 4.03 | 158.60 | yes | IBM2 |
| umc2280 | AC | 4.03 | 158.80 | no | IBM2 |
| AY110573 | | 4.03 | 163.90 | yes | IBM2 |
| uaz180 | | 4.03 | 164.49 | no | BNL 2002 |
| bnlg1162 | | 4.03 | 168.17 | no | BNL 2002 |
| umc2176 | | 4.03 | 174.60 | yes | IBM2 |
| bnl5.46a | | 4.03 | 177.34 | no | UMC 98 |
| uaz298(PDsI) | | 4.03 | 177.34 | no | UMC 98 |
| uaz239a | | 4.03 | 181.34 | no | BNL 96 |
| umc1902 | AC | 4.03 | 181.40 | yes | IBM2 |
| dpg2 | | 4.03 | 186.63 | no | BNL 2002 |
| pdi1 | C | 4.03 | 187.61 | no | SSR popII |
| mmp111 | | 4.03 | 189.10 | yes | IBM2 |
| uaz46b | | 4.05 | 189.63 | no | BNL 2002 |
| uaz48b | | 4.05 | 189.63 | no | BNL 2002 |
| dpg14 | | 4.02- 4.03 | 192.15 | no | BNL 2002 |
| rz630b(sat) | | 4.03 | 192.49 | no | UMC 98 |
| agrr109 | | 4.03 | 195.71 | no | UMC 98 |
| umc2039 | AC | 4.03 | 196.40 | yes | IBM2 |
| pgd3 | C | 4.03 | 200.30 | yes | IBM2 |
| fl2 | | 4.00- 4.04 | 200.30 | no | UMC 98 |
| csu449 | | 4.03- 4.04 | 200.30 | no | UMC 98 |
| agrc39a | | 4.03- 4.04 | 200.30 | no | UMC 98 |
| csu1135 | | 4.03- 4.04 | 200.30 | no | UMC 98 |
| uaz57b | | 4.04 | 201.89 | no | BNL 2002 |
| uaz145(ahh) | | 4.04 | 201.89 | no | BNL 96 |
| umc2211 | | 4.03 | 203.68 | no | SSR popI |
| wip2 | | 4.03 | 205.00 | yes | IBM2 |
| uaz62b | | 4.04 | 211.40 | no | BNL 2002 |
| uaz63b | | 4.04 | 211.40 | no | BNL 2002 |
| csu855 | | 4.03- 4.04 | 211.40 | no | UMC 98 |
| med63c | | 4.03- 4.04 | 211.40 | no | UMC 98 |
| bnl8.45c | C | 4.03- 4.04 | 211.40 | no | IBM1 |
| csu1185 | | 4.03- 4.04 | 211.40 | no | UMC 98 |
| csu298a | | 4.03- 4.04 | 211.40 | no | UMC 98 |
| npi386(eks) | AC | 4.04 | 211.40 | yes | IBM2 |
| rz900a(ahh) | | 4.03- 4.04 | 211.40 | no | UMC 98 |
| uaz53b | | 4.04 | 213.86 | no | BNL 2002 |
| umc49e | C | 4.04 | 213.91 | no | IBM1 |
| umc1821 | C | 4.04 | 214.47 | no | SSR popII |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| uaz30b | | 4.03-4.04 | 216.89 | no | BNL 2002 |
| umc1117 | A C | 4.04 | 218.50 | yes | IBM2 |
| csu12c(cin4) | | 4.04-4.05 | 219.81 | no | BNL 2002 |
| lim415 | | 4.04 | 223.60 | yes | IBM2 |
| umc1963 | A C | 4.04 | 225.70 | yes | IBM2 |
| bnlg1741 | | 4.06 | 226.91 | no | BNL 2002 |
| umc1652 | A C | 4.04 | 228.40 | yes | IBM2 |
| jpsb527b | | 4.04 | 230.40 | yes | IBM2 |
| zp1 | A C | 4.04 | 232.20 | no | IBM2 |
| mmc0471 | A C | 4.04 | 232.20 | yes | IBM2 |
| sdg108a | C | 4.04 | 232.20 | no | ChromDB |
| umc2206 | C | 4.04 | 234.85 | no | SSR popI |
| bnlg490 | A C | 4.04 | 237.80 | yes | IBM2 |
| psb3 | C | 4.04 | 239.38 | no | UMC 98 |
| uaz69b | | 4.05 | 239.42 | no | BNL 2002 |
| rgps2470 | | 4.04 | 239.79 | no | UMC 98 |
| agrr37b | C | 4.05 | 244.53 | no | SSR popII |
| aco1 | | 4.04-4.05 | 245.47 | no | BNL 2002 |
| bnl17.13c | | 4.05 | 245.47 | no | BNL 2002 |
| npi574a | | 4.05 | 245.47 | no | BNL 96 |
| bm3 | C | 4.05 | 245.50 | no | UMC 98 |
| agrr301 | | 4.05 | 245.50 | yes | IBM2 |
| agrr321 | | 4.05 | 245.50 | no | UMC 98 |
| csu599a | | 4.05 | 245.50 | no | UMC 98 |
| bap2 | | 4.05 | 246.97 | no | UMC 98 |
| agrp67 | | 4.05 | 246.97 | no | UMC 98 |
| agrp54b | | 4.05 | 247.79 | no | UMC 98 |
| umc1969 | | 4.05 | 248.60 | yes | IBM2 |
| uaz42c | | 4.05 | 248.79 | no | BNL 2002 |
| uaz48c | | 4.05 | 248.79 | no | BNL 2002 |
| umc2061 | A C | 4.05 | 250.80 | yes | IBM2 |
| orp1 | | 4.05 | 253.02 | no | UMC 98 |
| gpc1 | A C | 4.05 | 254.00 | yes | IBM2 |
| csu294 | | 4.05 | 254.00 | no | UMC 98 |
| csu1098 | | 4.05 | 254.00 | no | UMC 98 |
| csu1125 | | 4.05 | 254.00 | no | UMC 98 |
| rz143b(gpc) | | 4.05 | 254.00 | no | IBM2 |
| csu565(rpPo) | | 4.05 | 254.00 | no | UMC 98 |
| csu474(rpS14) | A C | 4.05 | 254.00 | no | UMC 98 |
| bnlg1937 | | 4.05-4.06 | 254.11 | no | BNL 2002 |
| uaz49A | | 4.05 | 254.20 | no | BNL 2002 |
| umc2282 | A C | 4.05 | 254.90 | no | IBM2 |
| bnlg1217 | | 4.05 | 255.32 | no | BNL 2002 |
| uaz61b | | 4.05 | 256.24 | no | BNL 2002 |
| uaz212 | | 4.05 | 256.83 | no | BNL 2002 |
| bnl17.10 | | 4.05 | 256.83 | no | BNL 2002 |
| npi289 | | 4.05 | 257.70 | no | BNL 2002 |
| npi95a | | 4.05 | 257.70 | no | BNL 96 |
| umc191(gpc1) | C | 4.05 | 258.60 | yes | IBM2 |
| uaz216 | | 4.05 | 261.77 | no | BNL 2002 |
| uaz230a | | 4.05 | 261.77 | no | BNL 2002 |
| uaz157(rpL19) | | 4.05 | 261.77 | no | BNL 2002 |
| uaz265c(sbe) | | 4.05 | 261.77 | no | BNL 96 |
| agrc567 | | 4.05 | 263.58 | no | UMC 98 |
| bnlg1265 | A C | 4.05 | 268.40 | yes | IBM2 |
| uaz218a(gss) | | 4.05 | 268.81 | no | BNL 2002 |
| agrr89 | | 4.05 | 269.06 | no | UMC 98 |
| umc193d(orp) | | 4.05 | 269.06 | no | UMC 98 |
| umc1303 | A C | 4.05 | 270.30 | yes | IBM2 |
| umc1382 | C | 4.05 | 270.30 | no | SSR popII |
| uaz41b | | 4.05 | 270.36 | no | BNL 2002 |
| uaz42a | | 4.05 | 270.36 | no | BNL 2002 |
| uaz45a | | 4.05 | 270.36 | no | BNL 2002 |
| uaz46c | | 4.05 | 270.36 | no | BNL 2002 |
| zpl2a | | 4.04-4.05 | 270.36 | no | BNL 2002 |
| uaz44a(zp19) | | 4.05 | 270.36 | no | BNL 2002 |
| uaz43a | | 4.05 | 270.78 | no | BNL 2002 |
| umc1964 | A C | 4.05 | 271.40 | no | IBM2 |
| bnl17.23c(pal) | | 4.05 | 272.44 | no | BNL 2002 |
| AY110290 | C | 4.05 | 274.70 | yes | IBM2 |
| uaz56 | | 4.05 | 274.77 | no | BNL 2002 |
| uaz246a(mbf) | C | 4.05 | 274.77 | no | BNL 2002 |
| bnlg2209 | | 4.05 | 276.54 | no | BNL 2002 |
| dnap4 | | 4.05 | 276.59 | no | BNL 96 |
| umc1390 | | 4.05 | 277.57 | no | SSR popI |
| psr152b | | 4.05 | 277.80 | yes | IBM2 |
| csu509 | A C | 4.05 | 279.90 | yes | IBM2 |
| umc1662 | | 4.05 | 282.04 | no | SSR popII |
| mmp125 | | 4.05 | 283.30 | yes | IBM2 |
| umc1031 | A C | 4.05 | 286.00 | yes | IBM2 |
| chr112a | C | 4.05 | 287.20 | no | ChromDB |
| umc1175 | A C | 4.05 | 287.30 | no | IBM2 |
| hda108 | | 4.05 | 287.70 | no | ChromDB |
| umc1896 | | 4.05 | 288.09 | no | SSR popII |
| umc1362 | C | 4.05 | 288.09 | no | SSR popII |
| umc1451 | C | 4.05 | 288.09 | no | SSR popII |
| umc42a | | 4.05 | 288.40 | yes | IBM2 |
| bnlg252 | | 4.06 | 288.42 | no | BNL 2002 |
| pic1b | | 4.05 | 288.60 | no | BNL 2002 |
| zpl3a | | 4.04-4.05 | 288.62 | no | BNL 2002 |
| bnlg1729 | | 4.05 | 288.67 | no | BNL 2002 |
| uaz72 | | 4.05 | 288.71 | no | BNL 2002 |
| mpik11f | | 4.05 | 288.71 | no | BNL 2002 |
| mpik15b | | 4.05 | 288.71 | no | BNL 2002 |
| uaz261b | | 4.05 | 288.71 | no | BNL 2002 |
| ucsd72l | | 4.05 | 288.71 | no | BNL 2002 |
| umc(orp1) | | 4.05 | 288.71 | no | BNL 2002 |
| ucsd62j(zag4) | | 4.05 | 288.71 | no | BNL 2002 |
| bnl(tas3a) | | 4.05 | 289.92 | no | BNL 96 |
| isu61d | | 4.05 | 291.30 | yes | IBM2 |
| jpsb67 | | 4.05 | 292.40 | no | IBM2 |
| bt2 | C | 4.05 | 292.90 | no | UMC 98 |
| bet2 | | 4.05 | 292.90 | no | BNL 2002 |
| csu902 | | 4.05 | 292.90 | no | UMC 98 |
| med63a | | 4.05 | 292.90 | no | UMC 98 |
| agrr286 | | 4.05 | 292.90 | no | UMC 98 |
| agrr62b | | 4.05 | 292.90 | no | UMC 98 |
| bnl15.45 | | 4.05 | 292.90 | yes | IBM2 |
| csu1026 | | 4.05 | 292.90 | no | UMC 98 |
| dpg7a | | 4.05 | 292.90 | no | BNL 2002 |
| umc242 | C | 4.05 | 292.90 | no | UMC 98 |
| umc263 | C | 4.05 | 292.90 | no | UMC 98 |
| umc47a | C | 4.05 | 292.90 | no | UMC 98 |
| npi367b | | 4.05 | 292.90 | no | BNL 2002 |
| bnlg1168 | | 4.05 | 292.90 | no | BNL 2002 |
| bnlg1790 | | 4.05 | 292.90 | no | BNL 2002 |
| bnlg667b | | 4.05 | 292.90 | no | BNL 2002 |
| bnl12.06b | | 4.05 | 292.90 | no | BNL 2002 |
| bnl15.27a | | 4.05 | 292.90 | no | BNL 2002 |
| std1a(his2B1) | | 4.05 | 292.90 | no | UMC 98 |
| csu19(colp) | | 4.04-4.05 | 293.14 | no | BNL 2002 |
| umc1953 | A C | 4.05 | 294.30 | no | IBM2 |
| umc2283 | A C | 4.05 | 294.40 | no | IBM2 |
| bnlg1159a | A C | 4.05 | 294.86 | no | BNL 2002 |
| umc1511 | A C | 4.05 | 295.20 | yes | IBM2 |
| wsu(nia2) | | 4.05 | 296.55 | no | BNL 2002 |
| pbs13a | | 4.05 | 296.88 | no | BNL 2002 |
| bnl17.09 | | 4.05 | 296.88 | no | BNL 2002 |
| umc2054 | | 4.05 | 296.99 | no | SSR popII |
| csu74(fdx) | | 4.05 | 297.06 | no | UMC 98 |
| psr128 | | 4.05 | 297.40 | yes | IBM2 |
| uaz195(ms) | | 4.05 | 297.49 | no | BNL 2002 |
| umc33b | | 4.05 | 297.53 | no | UMC 98 |
| csu716 | C | 4.05 | 297.53 | no | UMC 98 |
| cdo395a(ypt) | | 4.05 | 297.53 | no | UMC 98 |
| umc1791 | A C | 4.05 | 298.10 | no | IBM2 |
| mmp190 | | 4.05 | 298.40 | no | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| mmp140 | | 4.05 | 298.90 | yes | IBM2 |
| umc1895 | | 4.05 | 298.93 | no | SSR popI |
| ncr(nrB) | | 4.05 | 299.39 | no | BNL 2002 |
| uaz71a | | 4.05 | 299.48 | no | BNL 2002 |
| bnlg1755 | A C | 4.05 | 299.90 | yes | IBM2 |
| mmp45 | | 4.05 | 300.20 | no | IBM2 |
| umc1851 | | 4.05 | 302.33 | no | SSR popII |
| umc1142 | A C | 4.05 | 302.50 | yes | IBM2 |
| uaz73 | | 4.05 | 302.94 | no | BNL 2002 |
| bnl35b(blr) | | 4.05 | 302.97 | no | BNL 2002 |
| csu81b(ank) | | 4.05 | 303.33 | no | BNL 2002 |
| dup(als1) | | 4.05 | 303.76 | no | BNL 2002 |
| agrp83a | | 4.05 | 304.00 | no | UMC 98 |
| csu93c | C | 4.05 | 304.00 | no | UMC 98 |
| bnl5.71b | | 4.05 | 304.00 | no | UMC 98 |
| umc1346 | C | 4.05 | 304.30 | yes | IBM2 |
| mpik19b | | 4.05 | 304.51 | no | BNL 2002 |
| ucsd72g | | 4.05 | 304.64 | no | BNL 2002 |
| mpik11d | | 4.05 | 304.90 | no | BNL 2002 |
| nfd104e | | 4.05 | 304.97 | no | ChromDB |
| umc1702 | A C | 4.05 | 305.20 | no | IBM2 |
| mmp155 | | 4.05 | 305.50 | no | IBM2 |
| mmp149 | | 4.05 | 306.40 | yes | IBM2 |
| npi284 | | 4.05 | 306.96 | no | BNL 96 |
| mmp86 | | 4.05 | 307.40 | no | IBM2 |
| cdo497 | | 4.05 | 308.63 | no | UMC 98 |
| tda62b | | 4.05 | 308.63 | no | UMC 98 |
| cdo116b | | 4.05 | 308.63 | no | UMC 98 |
| bnl5.33a | | 4.05 | 308.63 | no | UMC 98 |
| std16a(blr) | | 4.05 | 308.63 | no | UMC 98 |
| mmp78 | | 4.05 | 310.70 | yes | IBM2 |
| ias12 | | 4.05 | 311.36 | no | BNL 2002 |
| CL65845_1 | C | 4.05-4.06 | 312.07 | no | INDEL |
| umc1317 | C | 4.05 | 313.00 | no | SSR popI |
| ucsd64f | | 4.05 | 313.15 | no | BNL 2002 |
| csu84 | | 4.05 | 313.25 | no | UMC 98 |
| npi267 | | 4.05 | 313.25 | no | UMC 98 |
| bnl7.20 | | 4.05 | 313.25 | no | UMC 98 |
| npi594b | | 4.05 | 313.25 | no | UMC 98 |
| umc273b | | 4.05 | 313.25 | no | UMC 98 |
| npi259a | | 4.05 | 313.25 | no | BNL 2002 |
| csu100(ptk) | | 4.05 | 313.25 | no | UMC 98 |
| csu693(lrr) | | 4.05 | 313.25 | no | UMC 98 |
| csu742b(rpS7) | | 4.05 | 313.25 | no | UMC 98 |
| nfa104 | | 4.05 | 314.90 | no | IBM2 |
| csu1063 | | 4.05 | 317.42 | no | UMC 98 |
| csu358b(pal) | C | 4.05 | 317.42 | no | UMC 98 |
| umc1548 | | 4.05 | 318.73 | no | SSR popI |
| umc1891 | | 4.05 | 318.73 | no | SSR popI |
| AY110562 | A C | 4.05 | 320.40 | yes | IBM2 |
| bnlg1930 | | 4.05-4.06 | 324.68 | no | BNL 2002 |
| umc23b | | 4.05 | 324.80 | no | BNL 2002 |
| AY110355 | A C | 4.05 | 326.50 | yes | IBM2 |
| uaz170 | | 4.06 | 327.59 | no | BNL 2002 |
| umc156a | C | 4.06 | 327.59 | no | SSR popI |
| php20597a | | 4.06 | 329.60 | yes | IBM2 |
| npi340b | | 4.06 | 329.89 | no | BNL 96 |
| uaz47a | | 4.06 | 331.26 | no | BNL 2002 |
| mmc0371 | A C | 4.06 | 331.30 | yes | IBM2 |
| umc2284 | A C | 4.05 | 332.40 | no | IBM2 |
| csu638 | | 4.06 | 332.50 | no | UMC 98 |
| umc1945 | A C | 4.06 | 333.20 | yes | IBM2 |
| mmp74 | | 4.06 | 335.20 | no | IBM2 |
| ucsd61i(zag4) | | 4.05-4.06 | 336.12 | no | BNL 96 |
| npi396 | | 4.06 | 338.41 | no | BNL 2002 |
| umc2391 | | 4.06 | 345.35 | no | SSR popII |
| nfd105 | | 4.06 | 346.72 | no | ChromDB |
| csu661 | A C | 4.06 | 349.68 | no | UMC 98 |
| umc2027 | | 4.06 | 349.80 | yes | IBM2 |
| mmp97 | | 4.06 | 354.50 | yes | IBM2 |
| csu640 | | 4.06 | 355.20 | no | UMC 98 |
| mmp176 | | 4.06 | 355.40 | yes | IBM2 |
| AY110310 | A C | 4.06 | 362.40 | yes | IBM2 |
| rgpr663a | | 4.06 | 366.25 | no | UMC 98 |
| mpik3 | | 4.06 | 367.20 | yes | IBM2 |
| uaz144a | | 4.06 | 367.29 | no | BNL 96 |
| bnl8.08h | | 4.06 | 371.62 | no | BNL 2002 |
| dupssr16 | | 4.06 | 371.71 | no | BNL 2002 |
| csu816 | | 4.06 | 371.77 | no | UMC 98 |
| csu587a | | 4.06 | 371.77 | no | UMC 98 |
| umc1299 | A C | 4.06 | 372.84 | no | SSR popII |
| uaz228c(his2b) | | 4.06 | 372.84 | no | BNL 2002 |
| rz567b(klc) | A C | 4.06 | 373.30 | yes | IBM2 |
| npi584 | | 4.06 | 375.04 | no | BNL 2002 |
| uaz257 | | 4.06 | 375.04 | no | BNL 2002 |
| bnlg1023a | | 4.06 | 378.95 | no | BNL 2002 |
| rz273a(ant) | | 4.06 | 379.30 | yes | IBM2 |
| uaz130b(tlk) | C | 4.05 | 379.99 | no | BNL 2002 |
| umc1869 | | 4.06 | 380.19 | no | SSR popII |
| umc2070 | A C | 4.06 | 380.58 | no | SSR popII |
| ias11 | | 4.06 | 382.26 | no | BNL 2002 |
| dge18 | | 4.06 | 383.37 | no | BNL 2002 |
| csu643b | | 4.06 | 384.04 | no | UMC 98 |
| csu907a | | 4.06 | 384.04 | no | UMC 98 |
| umc1329 | C | 4.06 | 384.91 | no | SSR popI |
| mpik11e | | 4.05 | 385.55 | no | BNL 2002 |
| mpik15a | | 4.05 | 385.55 | no | BNL 2002 |
| mpik16e | | 4.05 | 385.55 | no | BNL 2002 |
| rgpc601a | | 4.06 | 388.03 | no | UMC 98 |
| trg1 | | 4.06 | 389.92 | no | BNL 96 |
| bnlg2291 | A C | 4.06 | 392.20 | no | IBM2 |
| bnlg1137 | A C | 4.06 | 392.40 | yes | IBM2 |
| gln5 | | 4.06 | 393.24 | no | UMC 98 |
| ucsd64g | | 4.06 | 393.64 | no | BNL 2002 |
| bnlg1784 | | 4.07 | 395.80 | no | BNL 2002 |
| dupssr34 | | 4.07 | 395.81 | no | BNL 2002 |
| uaz263 | | 4.07 | 396.73 | no | BNL 2002 |
| uaz74 | | 4.07 | 397.13 | no | BNL 2002 |
| umc66 | C | 4.07 | 397.40 | yes | IBM2 |
| pbs13c | | 4.07 | 397.73 | no | BNL 2002 |
| prh1 | | 4.07 | 399.69 | no | UMC 98 |
| csu525(rpL17) | | 4.07 | 399.69 | no | UMC 98 |
| umc66a(lcr) | C | 4.07 | 399.69 | no | INDEL |
| rz446a | | 4.07 | 402.95 | no | UMC 98 |
| klp1e | | 4.07 | 405.49 | no | UMC 98 |
| umc104a | | 4.07 | 408.70 | yes | IBM2 |
| bnlg1621a | | 4.06 | 409.59 | no | BNL 2002 |
| pbs16c | | 4.07 | 410.74 | no | BNL 2002 |
| mmp147 | | 4.07 | 410.80 | yes | IBM2 |
| umc2038 | A C | 4.07 | 411.30 | yes | IBM2 |
| umc1651 | | 4.07 | 412.12 | no | SSR popII |
| umc19 | C | 4.07 | 414.20 | yes | IBM2 |
| umc229a | | 4.07 | 414.20 | no | UMC 98 |
| uaz66b | | 4.07 | 414.20 | no | BNL 2002 |
| bnl8.08i | | 4.07 | 414.20 | no | BNL 2002 |
| umc1994 | A C | 4.07 | 414.40 | no | SSR popII |
| agrp168c | | 4.07 | 415.30 | no | UMC 98 |
| bnl5.67a | | 4.07 | 415.30 | no | UMC 98 |
| umc1847 | | 4.07 | 418.20 | no | SSR popII |
| umc244a | | 4.07 | 418.66 | no | UMC 98 |
| mmp115 | | 4.07 | 420.60 | yes | IBM2 |
| zag3 | | 4.05-4.06 | 421.23 | no | BNL 2002 |
| umc1620 | | 4.07 | 421.25 | no | SSR popII |
| umc126b | C | 4.06 | 425.54 | no | BNL 2002 |
| umc1194 | | 4.07 | 427.56 | no | SSR popI |
| bnlg1189 | A C | 4.07 | 428.00 | no | IBM2 |
| uaz222 | | 4.07 | 428.21 | no | BNL 2002 |
| bnl5.24b | | 4.07 | 430.20 | yes | IBM2 |
| wsu(nia3) | | 4.07 | 432.69 | no | BNL 96 |
| umc127c | | 4.08 | 436.72 | no | SSR popII |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| PCO119336 | C | 4.07-4.08 | 436.95 | no | INDEL |
| asg33 | C | 4.07 | 437.50 | yes | IBM2 |
| csu672b | C | 4.07 | 437.50 | no | UMC 98 |
| csu597d(dah) | C | 4.07 | 437.50 | no | UMC 98 |
| asg9a |  | 4.07 | 440.88 | no | UMC 98 |
| uaz171 |  | 4.08 | 441.91 | no | BNL 2002 |
| mmc0341 | A C | 4.07 | 443.19 | no | SSR popl |
| umc1775 | C | 4.08 | 443.20 | yes | IBM2 |
| asg74b |  | 4.08 | 443.92 | no | UMC 98 |
| umc2009 |  | 4.08 | 446.76 | no | SSR popl |
| npi292 |  | 4.07 | 448.98 | no | BNL 96 |
| umc1667 |  | 4.08 | 449.40 | yes | IBM2 |
| asg85a |  | 4.08 | 451.01 | no | UMC 98 |
| AY109534 | A C | 4.08 | 452.10 | no | IBM2 |
| umc1808 |  | 4.08 | 452.90 | yes | IBM2 |
| mmp3 |  | 4.08 | 455.90 | yes | IBM2 |
| asg27a |  | 4.08 | 458.10 | yes | IBM2 |
| npi253b |  | 4.08 | 458.92 | no | BNL 96 |
| umc1476 | C | 4.08 | 462.10 | no | IBM2 |
| bnlg1444 |  | 4.08 | 462.50 | yes | IBM2 |
| dupssr28 |  | 4.08 | 462.58 | no | BNL 2002 |
| bnlg1927 | A C | 4.07 | 462.58 | no | BNL 2002 |
| bnl22 |  | 4.08 | 462.61 | no | BNL 2002 |
| npi208a |  | 4.08 | 462.66 | no | BNL 2002 |
| fer1 |  | 4.08 | 463.30 | no | UMC 98 |
| gol1 | C | 4.08 | 463.30 | yes | IBM2 |
| csu91a |  | 4.08 | 463.30 | no | UMC 98 |
| umc1871 |  | 4.08 | 464.39 | no | SSR popII |
| bnl7.65 |  | 4.08 | 464.80 | no | IBM2 |
| rgpg24 |  | 4.08 | 464.80 | no | UMC 98 |
| umc133a |  | 4.08 | 464.80 | no | UMC 98 |
| rgpg124a | C | 4.08 | 464.80 | no | UMC 98 |
| bnl10.05 |  | 4.08 | 466.10 | yes | IBM2 |
| bnlg2244 | A C | 4.08 | 467.10 | yes | IBM2 |
| bnl8.45b | C | 4.08 | 468.75 | no | SSR popl |
| umc2384 |  | 4.08 | 468.77 | no | SSR popII |
| umc1899 | A C | 4.08 | 470.60 | yes | IBM2 |
| pdh1 | A C | 4.08 | 471.86 | no | SSR popII |
| umc2404 |  | 4.08 | 471.86 | no | SSR popII |
| umc158 |  | 4.08 | 473.90 | yes | IBM2 |
| umc14a |  | 4.05-4.06 | 473.90 | no | UMC 98 |
| csu720b |  | 4.05-4.06 | 473.90 | no | UMC 98 |
| uaz252a(ptk) |  | 4.08 | 473.90 | no | BNL 2002 |
| csu428(cyb561) |  | 4.05-4.06 | 473.90 | no | UMC 98 |
| umc1418 | A C | 4.08 | 475.60 | no | SSR popII |
| bnlg2162 | A C | 4.08 | 475.70 | no | IBM2 |
| mmp70 |  | 4.08 | 476.00 | no | IBM2 |
| umc2405 |  | 4.08 | 476.46 | no | SSR popII |
| umc2635 |  | 4.08 | 477.90 | no | SSR popII |
| PCO129009 | C | 4.08 | 478.89 | no | INDEL |
| npi570 |  | 4.08 | 480.70 | yes | IBM2 |
| umc2041 |  | 4.08 | 483.93 | no | SSR popl |
| AY112127 | A C | 4.08 | 487.70 | yes | IBM2 |
| ufg23 |  | 4.08 | 499.90 | yes | IBM2 |
| umc1086 | C | 4.08 | 500.59 | no | SSR popII |
| AY110631 |  | 4.08 | 510.00 | yes | IBM2 |
| umc2285 | A C | 4.08 | 514.90 | yes | IBM2 |
| npi270 |  | 4.08 | 516.60 | yes | IBM2 |
| npi300c |  | 4.08 | 516.69 | no | BNL 2002 |
| php20071 |  | 4.08 | 518.10 | yes | IBM2 |
| rgpl102 |  | 4.08 | 518.10 | no | UMC 98 |
| cdo127a(pyk) | C | 4.08 | 518.10 | no | UMC 98 |
| mmc0321 | A C | 4.08 | 518.34 | no | SSR popl |
| uaz122 |  | 4.08 | 519.55 | no | BNL 2002 |
| bnl17.05(ssu) |  | 4.08 | 520.12 | no | BNL 96 |
| ssu1 | A C | 4.08 | 522.10 | yes | IBM2 |
| CL12681_1 | C | 4.08 | 523.23 | no | INDEL |
| umc1612 | A C | 4.08 | 523.40 | no | SSR popII |
| npi444 |  | 4.08 | 524.10 | yes | IBM2 |
| umc15a |  | 4.08 | 525.80 | yes | IBM2 |
| umn433 |  | 4.08 | 525.80 | no | UMC 98 |
| csu166a |  | 4.08 | 525.80 | no | UMC 98 |
| rgpg111 |  | 4.08 | 525.80 | no | UMC 98 |
| csu1038b |  | 4.08 | 525.80 | no | UMC 98 |
| csu1073b |  | 4.08 | 525.80 | no | UMC 98 |
| cdo365(pet) | A C | 4.08 | 525.80 | no | UMC 98 |
| csu597a(dah) | C | 4.08 | 525.80 | no | UMC 98 |
| php20562 |  | 4.08 | 526.00 | no | UMC 98 |
| c2 | C | 4.08 | 526.57 | no | SSR popl |
| tda44 |  | 4.08 | 526.57 | no | UMC 98 |
| csu178a |  | 4.08 | 526.57 | no | UMC 98 |
| npi910 |  | 4.08 | 526.57 | no | BNL 2002 |
| umc1051 | A C | 4.08 | 526.57 | no | SSR popl |
| csu202(rpL7) |  | 4.08 | 526.57 | no | UMC 98 |
| PCO136722 | C | 4.08 | 530.42 | no | INDEL |
| umc2187 | C | 4.08 | 531.70 | yes | IBM2 |
| npi410 |  | 4.08 | 533.87 | no | BNL 2002 |
| psr109b |  | 4.08 | 533.87 | no | BNL 2002 |
| umc1842 |  | 4.08 | 534.80 | yes | IBM2 |
| umc1856 |  | 4.08 | 534.80 | no | SSR popII |
| umc1371 | C | 4.08 | 534.80 | no | SSR popII |
| AY109980 | C | 4.06 | 535.40 | no | IBM2 |
| umc1132 | A C | 4.08 | 535.50 | no | IBM2 |
| nfd106 | C | 4.08 | 535.55 | no | ChromDB |
| AY105971 | A C | 4.08 | 536.30 | yes | IBM2 |
| AY110989 | A C | 4.08 | 536.90 | yes | IBM2 |
| ensl002a |  | 4.08 | 537.11 | no | BNL 2002 |
| rz596b |  | 4.08 | 539.00 | yes | IBM2 |
| bnl23a |  | 4.08 | 542.87 | no | BNL 2002 |
| bnl29(pds2) |  | 4.08 | 542.87 | no | BNL 2002 |
| umc2200 | C | 4.08 | 543.44 | no | SSR popl |
| umc2135 |  | 4.08 | 544.10 | yes | IBM2 |
| uaz33b |  | 4.09 | 548.95 | no | BNL 2002 |
| mmp178 |  | 4.08 | 551.00 | yes | IBM2 |
| umc1834 |  | 4.08 | 551.21 | no | SSR popII |
| csu704 | C | 4.08 | 553.34 | no | UMC 98 |
| umc2286 | A C | 4.08 | 553.70 | no | IBM2 |
| mpik(chs1a) |  | 4.08 | 553.81 | no | BNL 2002 |
| umc2188 | A C | 4.08 | 554.10 | yes | IBM2 |
| umc2360 | C | 4.08-4.09 | 554.90 | no | SSR popII |
| uaz142 |  | 4.08 | 558.11 | no | BNL 2002 |
| umc52 | C | 4.09 | 559.00 | yes | IBM2 |
| csu39 | C | 4.08-4.09 | 559.00 | no | UMC 98 |
| csu50a | C | 4.08-4.09 | 559.00 | no | UMC 98 |
| umc1559 |  | 4.08-4.09 | 559.00 | no | SSR popII |
| AY110170 | C | 4.09 | 561.50 | no | IBM2 |
| umc1313 | C | 4.08-4.09 | 562.75 | no | SSR popl |
| lim446 |  | 4.09 | 565.40 | yes | IBM2 |
| csu201 |  | 4.09 | 567.32 | no | UMC 98 |
| mwg645e |  | 4.09 | 570.61 | no | BNL 96 |
| csu241b |  | 4.09 | 570.64 | no | UMC 98 |
| rgpc643a |  | 4.09 | 570.64 | no | UMC 98 |
| uaz115 |  | 4.09 | 570.99 | no | BNL 2002 |
| csu304b |  | 4.09 | 571.47 | no | UMC 98 |
| uaz41a |  | 4.09 | 571.95 | no | BNL 2002 |
| cuny9 |  | 4.09 | 572.37 | no | BNL 2002 |
| bnlg1019b | C | 4.09-4.10 | 573.11 | no | BNL 2002 |
| bnlg2148 |  | 4.09 | 573.69 | no | BNL 2002 |
| bnlg292b | C | 4.08-4.09 | 573.71 | no | SSR popl |
| umc2139 | A C | 4.09 | 574.80 | yes | IBM2 |
| csu674(gts) |  | 4.09 | 578.13 | no | UMC 98 |
| php10025 |  | 4.09 | 579.80 | yes | IBM2 |
| ensl002b |  | 4.09 | 580.08 | no | BNL 2002 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| PCO104784 | C | 4.09 | 580.31 | no | INDEL |
| umc1939 |  | 4.09 | 580.69 | no | SSR popII |
| umc1940 | A C | 4.09 | 581.80 | no | IBM2 |
| umc1999 | A C | 4.09 | 581.80 | yes | IBM2 |
| ris2 |  | 4.09 | 583.12 | no | BNL 96 |
| uaz137 |  | 4.08 | 584.64 | no | BNL 2002 |
| mgs2 | C | 4.09 | 589.37 | no | BNL 2002 |
| umc1854 |  | 4.09 | 595.70 | yes | IBM2 |
| rgpr3235b | C | 4.09 | 597.00 | no | UMC 98 |
| csu862b(rpL11) |  | 4.09 | 597.00 | no | UMC 98 |
| mmp24 |  | 4.09 | 598.60 | no | IBM2 |
| umc1989 |  | 4.09 | 599.40 | no | SSR popII |
| mmp134 |  | 4.09 | 599.50 | yes | IBM2 |
| rz476a |  | 4.09 | 601.40 | no | IBM2 |
| rz599b | C | 4.09 | 601.40 | no | IBM2 |
| npi449b |  | 4.09 | 601.60 | yes | IBM2 |
| umc1650 |  | 4.09 | 602.10 | no | IBM2 |
| umc1803 |  | 4.09 | 602.20 | no | IBM2 |
| asg22 |  | 4.09 | 603.30 | yes | IBM2 |
| csu745b(rpPo) | C | 4.09 | 603.30 | no | UMC 98 |
| mmp94 |  | 4.09 | 605.50 | yes | IBM2 |
| umc1740 | A C | 4.09 | 611.90 | no | SSR popI |
| AY109933 | A C | 4.09 | 613.00 | yes | IBM2 |
| CL2227_3 | C | 4.09 | 613.42 | no | INDEL |
| AY110064 | C | 4.09 | 616.70 | no | IBM2 |
| umc1328 | A C | 4.09 | 618.10 | yes | IBM2 |
| umc1631 |  | 4.09 | 618.10 | no | SSR popII |
| umc2287 | A C | 4.09 | 619.40 | yes | IBM2 |
| rpd3 | A C | 4.09 | 621.42 | no | SSR popII |
| umc1643 |  | 4.09 | 621.61 | no | SSR popI |
| umc1820 |  | 4.09 | 622.93 | no | SSR popII |
| cdo534a(cts) |  | 4.09 | 623.20 | yes | IBM2 |
| csu324a(cts) |  | 4.09 | 623.20 | no | UMC 98 |
| csu34b(rpS8) | C | 4.09 | 623.20 | no | UMC 98 |
| cdo534c(cts) |  | 4.09 | 623.40 | no | IBM2 |
| umc2382 | C | 4.09 | 624.36 | no | SSR popII |
| npi333 |  | 4.09-4.10 | 625.99 | no | BNL 96 |
| AY110231 | A C | 4.09 | 635.20 | yes | IBM2 |
| cdo1395c |  | 4.09 | 635.91 | no | UMC 98 |
| csu1107 |  | 4.09 | 637.21 | no | UMC 98 |
| csu719(lox) |  | 4.09 | 637.21 | no | UMC 98 |
| umc1284 |  | 4.09 | 641.02 | no | SSR popI |
| csu631 |  | 4.09 | 643.08 | no | UMC 98 |
| sbp2 | A C | 4.09 | 644.30 | yes | IBM2 |
| bnlg1565 |  | 4.09 | 645.70 | no | IBM2 |
| bnlg572b |  | 4.09 | 647.82 | no | BNL 2002 |
| uaz65a |  | 4.09 | 648.81 | no | BNL 2002 |
| bnlg2299 |  | 4.09 | 650.44 | no | BNL 2002 |
| knox7 |  | 4.09-4.10 | 650.48 | no | BNL 2002 |
| npi116a |  | 4.09 | 651.61 | no | BNL 2002 |
| npi593a |  | 4.09 | 651.70 | yes | IBM2 |
| npi294g |  | 4.09 | 652.20 | no | UMC 98 |
| uaz123b |  | 4.09-4.10 | 652.92 | no | BNL 2002 |
| PCO088312 | C | 4.09-4.10 | 654.70 | no | INDEL |
| umc1101 | C | 4.09 | 655.00 | yes | IBM2 |
| umc2046 | A C | 4.09 | 657.00 | yes | IBM2 |
| bnlg2186 |  | 4.11 | 657.66 | no | BNL 2002 |
| uaz279(cbp) |  | 4.09 | 658.07 | no | UMC 98 |
| csu848a(vpp) |  | 4.09 | 658.07 | no | UMC 98 |
| ici281 |  | 4.10 | 659.03 | no | BNL 2002 |
| uwo3 |  | 4.10 | 666.64 | no | BNL 96 |
| csu283a |  | 4.10 | 669.80 | no | UMC 98 |
| csu758 | A C | 4.10 | 669.80 | no | UMC 98 |
| csu330(ubi) |  | 4.10 | 669.80 | no | UMC 98 |
| csu377a(ubi) |  | 4.10 | 669.80 | no | UMC 98 |
| php20608a | A C | 4.09-4.10 | 669.80 | yes | IBM2 |
| uwo8 |  | 4.11 | 670.20 | no | BNL 2002 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| bnlg589 | A C | 4.10 | 670.20 | yes | IBM2 |
| isu2191a |  | 4.10 | 670.20 | no | BNL 2002 |
| umc1503 | A C | 4.09-4.10 | 671.48 | no | SSR popI |
| umc1532 |  | 4.10 | 671.90 | yes | IBM2 |
| umc124b(chk) |  | 4.10 | 672.40 | yes | IBM2 |
| pge17 |  | 4.11 | 678.18 | no | BNL 2002 |
| uaz247(ubi) |  | 4.10 | 679.17 | no | BNL 2002 |
| dpg15a |  | 4.10 | 680.28 | no | BNL 2002 |
| agrr169 |  | 4.10 | 682.59 | no | INDEL |
| bnl32 |  | 4.11 | 685.82 | no | BNL 2002 |
| umc1109 | A C | 4.10 | 687.80 | yes | IBM2 |
| umc1720 |  | 4.10 | 688.03 | no | SSR popII |
| lim471 |  | 4.10 | 688.70 | yes | IBM2 |
| npi451 |  | 4.11 | 688.91 | no | BNL 2002 |
| bnl(tas1o) |  | 4.11 | 689.21 | no | BNL 2002 |
| umc2011 |  | 4.10 | 689.25 | no | SSR popI |
| dba1 |  | 4.10 | 691.20 | no | UMC 98 |
| bnl15.07a |  | 4.10 | 691.20 | yes | IBM2 |
| umc2288 | A C | 4.10 | 692.10 | yes | IBM2 |
| umc1699 |  | 4.10 | 692.94 | no | SSR popI |
| asg41 |  | 4.10 | 695.50 | yes | IBM2 |
| umc2044 |  | 4.10 | 696.05 | no | SSR popII |
| umc1180 | A C | 4.10 | 698.90 | yes | IBM2 |
| csu36a(rpL19) |  | 4.10 | 699.17 | no | UMC 98 |
| PCO109372 | C | 4.10 | 699.66 | no | INDEL |
| cas1 |  | 4.10 | 701.86 | no | UMC 98 |
| AY109668 | C | 4.10 | 702.20 | yes | IBM2 |
| bnlg1917 |  | 4.10 | 703.52 | no | BNL 2002 |
| csh2a(cdc2) |  | 4.10 | 704.21 | no | BNL 96 |
| bnlg1337 |  | 4.11 | 707.24 | no | BNL 2002 |
| umc2289 | A C | 4.10 | 707.80 | yes | IBM2 |
| AY109859 | A C | 4.11 | 708.50 | yes | IBM2 |
| AY109611 | A C | 4.11 | 715.50 | yes | IBM2 |
| umc1738 | A C | 4.10 | 720.48 | no | SSR popII |
| bnl8.23a |  | 4.10-4.11 | 726.30 | no | UMC 98 |
| ncr(cat3) |  | 4.10 | 727.63 | no | BNL 96 |
| csu380 |  | 4.11 | 728.50 | no | UMC 98 |
| umc169 | A C | 4.11 | 728.50 | yes | IBM2 |
| umc111a(psy) |  | 4.11 | 728.50 | no | UMC 98 |
| cpn10 |  | 4.10-4.11 | 728.50 | no | SSR popII |
| umc1719 | A C | 4.10-4.11 | 730.75 | no | SSR popI |
| umc1716 | A C | 4.11 | 732.99 | no | SSR popI |
| umc112c |  | 4.11 | 733.63 | no | UMC 98 |
| umc2290 | A C | 4.11 | 736.70 | no | IBM2 |
| bip2 | A C | 4.11 | 737.80 | yes | IBM2 |
| umc1649 | A C | 4.11 | 739.30 | no | IBM2 |
| mmp182 |  | 4.11 | 740.70 | yes | IBM2 |
| csu710b(apx) |  | 4.11 | 742.68 | no | UMC 98 |
| csu315b |  | 4.11 | 743.41 | no | UMC 98 |
| cat3 | A C | 4.11 | 744.10 | yes | IBM2 |
| umc1707 | C | 4.11 | 748.30 | yes | IBM2 |
| bnlg1890 |  | 4.11 | 750.20 | yes | IBM2 |
| ncr(b70b) |  | 4.10 | 752.97 | no | BNL 2002 |
| isu61b |  | 4.11 | 753.50 | no | IBM1 |
| ufg(ivr2a) |  | 4.10 | 804.83 | no | BNL 96 |
| umc1491 | A C | 5.00 | -32.40 | no | SSR popI |
| bnl(tas1n) |  | 5.00 | -13.30 | no | BNL 96 |
| bnl(tas2g) |  | 5.00 | -9.34 | no | BNL 2002 |
| bnl(tas2b) |  | 5.00 | -3.07 | no | BNL 2002 |
| AI676903 | A C | 5.00 | 0.00 | yes | IBM2 |
| umc1308 | A C | 5.00 | 6.30 | no | SSR popI |
| AY110625 | A C | 5.00 | 10.70 | yes | IBM2 |
| CL21419_1 | C | 5.00 | 13.70 | no | INDEL |
| tum3 |  | 5.00-5.03 | 14.66 | no | BNL 2002 |
| umc1240 | C | 5.00 | 16.30 | no | SSR popII |
| AY109758 | C | 5.00 | 17.10 | yes | IBM2 |
| uaz75 |  | 5.00 | 17.21 | no | BNL 2002 |
| ufg36 | C | 5.00 | 20.80 | yes | IBM2 |
| mmc0151 | A C | 5.00 | 22.60 | no | SSR popII |
| umc1253 | A C | 5.00 | 22.70 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| umc2292 | A C | 5.00 | 22.70 | yes | IBM2 |
| umc2291 | A C | 5.00 | 23.30 | yes | IBM2 |
| csu1087 |  | 5.00 | 24.50 | yes | IBM2 |
| uaz214 |  | 5.00 | 29.69 | no | BNL 2002 |
| umc1423 | A C | 5.00 | 30.00 | yes | IBM2 |
| csu277 |  | 5.00 | 31.50 | no | UMC 98 |
| csu527(crm) | C | 5.00 | 31.50 | no | UMC 98 |
| uaz259 |  | 5.00 | 31.52 | no | BNL 2002 |
| PCO062666 | C | 5.00 | 34.14 | no | INDEL |
| umc1445 | A C | 5.00 | 37.60 | yes | IBM2 |
| umc1496 | A C | 5.00 | 38.52 | no | SSR popl |
| csh1c(chi) |  | 5.00 | 39.20 | no | BNL 96 |
| umc2022 | A C | 5.00 | 39.40 | no | IBM2 |
| umc1097 | A C | 5.00 | 40.80 | yes | IBM2 |
| npi890 |  | 5.00 | 42.25 | no | BNL 2002 |
| mmp6 |  | 5.00 | 42.40 | yes | IBM2 |
| bnl8.33 | C | 5.00 | 46.80 | yes | IBM2 |
| cdo457a |  | 5.00 | 46.80 | no | UMC 98 |
| bnlg1006 | A C | 5.00 | 47.50 | no | IBM2 |
| umc1901 | A C | 5.00 | 50.10 | yes | IBM2 |
| umc86b |  | 5.00 | 52.80 | yes | IBM2 |
| uaz76a |  | 5.00 | 54.13 | no | BNL 2002 |
| umc1325 | A C | 5.00 | 54.60 | yes | IBM2 |
| asg60 |  | 5.00 | 57.48 | no | UMC 98 |
| rgpg164 | A C | 5.00 | 61.16 | no | UMC 98 |
| umc1260 | A C | 5.00 | 68.10 | yes | IBM2 |
| sca1 | C | 5.00 | 68.50 | yes | IBM2 |
| npi409 | A C | 5.01 | 69.50 | yes | IBM2 |
| bnl6.25a |  | 5.01 | 69.50 | no | UMC 98 |
| csu33a | A C | 5.01 | 69.50 | no | UMC 98 |
| csu663a(psaD) |  | 5.01 | 69.50 | no | UMC 98 |
| umc1679 | A C | 5.01 | 71.50 | no | IBM2 |
| umc1523 | A C | 5.01 | 71.90 | yes | IBM2 |
| csu604b(trh) | C | 5.01 | 73.04 | no | UMC 98 |
| mmp43 |  | 5.01 | 73.30 | no | IBM2 |
| bnl7.21c |  | 5.01 | 74.40 | yes | IBM2 |
| ohp2 | A C | 5.01 | 75.66 | no | BNL 2002 |
| umc1478 |  | 5.01 | 79.17 | no | SSR popII |
| cdo87a(ptk) | C | 5.01 | 83.67 | no | UMC 98 |
| jpsb239a |  | 5.01 | 83.70 | yes | IBM2 |
| bnl8.29b |  | 5.01 | 83.92 | no | BNL 96 |
| lim407 |  | 5.01 | 85.10 | yes | IBM2 |
| tua3 |  | 5.01 | 90.17 | no | UMC 98 |
| rpa7b |  | 5.01 | 90.17 | no | UMC 98 |
| umc144a |  | 5.01 | 90.17 | no | UMC 98 |
| csu1169a |  | 5.01 | 90.17 | no | UMC 98 |
| csu570a(mtl) |  | 5.01 | 90.17 | no | UMC 98 |
| AY109733 | C | 5.01 | 90.20 | yes | IBM2 |
| umc1365 | A C | 5.01 | 97.95 | no | SSR popII |
| umc147a |  | 5.01 | 99.03 | no | UMC 98 |
| umc240 | C | 5.01 | 99.03 | no | UMC 98 |
| bnl17.18a |  | 5.01 | 99.03 | no | UMC 98 |
| npi75a |  | 5.01 | 99.05 | no | BNL 2002 |
| npi579a |  | 5.01 | 99.05 | no | BNL 96 |
| uaz134 |  | 5.02 | 103.23 | no | BNL 2002 |
| bnl7.24b |  | 5.01 | 103.69 | no | BNL 2002 |
| uaz201(tua) |  | 5.01 | 104.40 | no | BNL 2002 |
| csu707 |  | 5.01 | 104.93 | no | UMC 98 |
| bnlg1836 |  | 5.01 | 106.08 | no | BNL 2002 |
| asg54b |  | 5.01 | 107.88 | no | UMC 98 |
| umc1766 |  | 5.01 | 111.76 | no | SSR popl |
| bnlg143 |  | 5.01 | 114.17 | no | BNL 96 |
| uat4b |  | 5.01 | 116.45 | no | UMC 98 |
| uaz163 |  | 5.01 | 122.34 | no | BNL 2002 |
| bcd450a |  | 5.01 | 123.24 | no | UMC 98 |
| csu137a(ap) |  | 5.01 | 123.24 | no | UMC 98 |
| umc2036 | A C | 5.01 | 124.70 | yes | IBM2 |
| umc1781 | A C | 5.01 | 124.70 | no | SSR popl |
| npi282a |  | 5.01 | 129.30 | yes | IBM2 |
| cuny7 |  | 5.01 | 129.30 | no | BNL 2002 |
| npi581b |  | 5.01 | 129.30 | no | BNL 2002 |
| ucsd104a(zag6) |  | 5.01 | 129.30 | no | BNL 2002 |
| hxa102a |  | 5.01 | 130.00 | no | ChromDB |
| ucsd64a |  | 5.01 | 133.17 | no | BNL 96 |
| mpik22b(zmm4) |  | 5.01 | 133.17 | no | BNL 2002 |
| rgpc975(rpS27) |  | 5.01 | 134.46 | no | UMC 98 |
| npi305a |  | 5.01 | 137.04 | no | BNL 2002 |
| ucsd72j |  | 5.01 | 137.04 | no | BNL 96 |
| uaz166b |  | 5.01 | 137.50 | no | BNL 2002 |
| rz630f(sat) |  | 5.01 | 138.00 | yes | IBM2 |
| hcf108 |  | 5.01 | 141.18 | no | BNL 2002 |
| csu318 |  | 5.01 | 141.25 | no | UMC 98 |
| umc72a |  | 5.01 - 5.02 | 141.25 | no | UMC 98 |
| umc90 | A C | 5.02 | 142.43 | no | SSR popl |
| ucsd106c |  | 5.01 | 144.67 | no | BNL 2002 |
| tua4 | C | 5.02 | 147.50 | yes | IBM2 |
| bnlg1382 |  | 5.01 | 148.43 | no | BNL 2002 |
| asg73 |  | 5.02 | 149.70 | yes | IBM2 |
| umc144b |  | 5.01 - 5.02 | 149.70 | no | UMC 98 |
| bnlg565 | A C | 5.02 | 150.90 | yes | IBM2 |
| ole3 | A C | 5.03- 5.04 | 151.75 | no | BNL 2002 |
| bcd808d |  | 5.02 | 152.00 | no | IBM2 |
| psr922a |  | 5.02 | 153.80 | yes | IBM2 |
| chb101a |  | 5.02 | 153.80 | no | ChromDB |
| umc1587 | A C | 5.02 | 156.90 | yes | IBM2 |
| rz632a |  | 5.02 | 158.15 | no | UMC 98 |
| umc107b(croc) | A C | 5.02 | 160.20 | yes | IBM2 |
| csu554b(rnh) |  | 5.02 | 161.60 | no | IBM2 |
| umc1894 |  | 5.01 - 5.02 | 164.59 | no | SSR popl |
| cdo122b(nad) |  | 5.02 | 164.60 | yes | IBM2 |
| uaz167b |  | 5.02 | 165.17 | no | BNL 2002 |
| pgm2 |  | 5.02 | 165.17 | no | BNL 96 |
| umc106b |  | 5.02 | 173.44 | no | BNL 2002 |
| phyA2 |  | 5.02 | 177.16 | no | BNL 2002 |
| ufg27 | C | 5.02 | 179.30 | no | IBM2 |
| mmp130 |  | 5.02 | 179.60 | yes | IBM2 |
| csu10a |  | 5.02 | 181.70 | no | UMC 98 |
| bcd1072a(hsp70) |  | 5.02 | 181.70 | yes | IBM2 |
| uaz211 |  | 5.02 | 182.23 | no | BNL 2002 |
| uaz219(hsp) |  | 5.02 | 182.91 | no | BNL 2002 |
| uaz215b(odo) |  | 5.02 | 183.23 | no | BNL 2002 |
| uaz205a(hsp70) |  | 5.03 | 184.27 | no | BNL 2002 |
| uwm2(rnp) |  | 5.02 | 185.09 | no | UMC 98 |
| bnlg105 | A C | 5.02 | 185.09 | no | SSR popl |
| csu108(gbp) | C | 5.02 | 185.09 | no | UMC 98 |
| bnlg1879 | A C | 5.03 | 189.80 | yes | IBM2 |
| ufg25 | C | 5.03 | 190.90 | no | IBM2 |
| umc2293 | C | 5.03 | 196.90 | yes | IBM2 |
| tub4 | C | 5.03 | 200.46 | no | SSR popII |
| mbd109 |  | 5.03 | 203.20 | no | ChromDB |
| csu164b | C | 5.03 | 203.30 | yes | IBM2 |
| csu511b |  | 5.03 | 204.10 | no | UMC 98 |
| rz474a(dnaj) |  | 5.03 | 204.10 | yes | IBM2 |
| csu222b(wsi) |  | 5.03 | 204.10 | no | UMC 98 |
| csu574a(eif2B) | C | 5.03 | 204.10 | no | UMC 98 |
| umc2388 | C | 5.02- 5.03 | 206.86 | no | SSR popII |
| bnlg1660 |  | 5.03 | 207.75 | no | BNL 2002 |
| knox10 |  | 5.02- 5.03 | 207.75 | no | BNL 2002 |
| csic(mah9) |  | 5.03 | 207.75 | no | BNL 96 |
| csu150b |  | 5.03 | 208.66 | no | BNL 2002 |
| nfc103b | C | 5.03 | 208.78 | no | ChromDB |
| csy1 |  | 5.03 | 209.19 | no | BNL 2002 |
| uaz25d |  | 5.03 | 209.38 | no | BNL 2002 |
| umc1686 |  | 5.03 | 210.30 | yes | IBM2 |
| tbp2 | A C | 5.03 | 211.74 | no | UMC 98 |
| rpa6a |  | 5.02 | 211.90 | no | UMC 98 |
| niu2::Bs1 |  | 5.03 | 212.30 | no | BNL 2002 |
| mmp112 |  | 5.03 | 212.70 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| bnlg557 | | 5.03 | 213.46 | no | BNL 2002 |
| mpik33e | | 5.03 | 213.46 | no | BNL 2002 |
| umc1852 | | 5.03 | 213.91 | no | SSR popI |
| cdo795b | | 5.03 | 214.50 | yes | IBM2 |
| bnlg1046 | A C | 5.03 | 216.30 | yes | IBM2 |
| dnap2 | | 5.03 | 216.41 | no | BNL 2002 |
| npi434 | | 5.03 | 216.41 | no | BNL 2002 |
| umc1597 | A C | 5.03 | 217.80 | yes | IBM2 |
| umc27a | C | 5.03 | 217.85 | no | BNL 96 |
| ici97 | | 5.03 | 218.35 | no | BNL 2002 |
| bnl7.56 | | 5.03 | 219.20 | yes | IBM2 |
| umc2060 | | 5.03 | 220.70 | no | SSR popI |
| rps15 | A C | 5.03 | 220.95 | no | SSR popII |
| csu340 | | 5.03 | 222.50 | yes | IBM2 |
| rgpc643d | | 5.03 | 222.50 | no | UMC 98 |
| rgpr440a(gap) | | 5.03 | 222.50 | no | UMC 98 |
| csu175c(eif5A) | | 5.03 | 222.50 | no | UMC 98 |
| uaz159a | | 5.03 | 223.44 | no | BNL 2002 |
| psr544 | | 5.03 | 227.20 | yes | IBM2 |
| umc1468 | | 5.03 | 227.35 | no | SSR popII |
| bcd207b | | 5.03 | 229.00 | yes | IBM2 |
| mmp180 | | 5.03 | 229.90 | no | IBM2 |
| mmc0351 | A C | 5.03 | 230.40 | yes | IBM2 |
| umc2035 | A C | 5.03 | 231.00 | yes | IBM2 |
| PCO135705 | C | 5.03 | 232.17 | no | INDEL |
| rny(pcr)b | | 5.03 | 235.25 | no | BNL 96 |
| AY111142 | C | 5.03 | 235.60 | yes | IBM2 |
| cdo98a | C | 5.03 | 239.60 | yes | IBM2 |
| umc1705 | | 5.03 | 240.80 | no | IBM2 |
| mdh5 | | 5.03 | 241.20 | no | UMC 98 |
| bnl5.02a | | 5.03 | 241.20 | yes | IBM2 |
| umc166a | | 5.03 | 241.20 | no | UMC 98 |
| umc83b | C | 5.03 | 241.20 | no | UMC 98 |
| csu580b(mdh) | | 5.03 | 241.20 | no | UMC 98 |
| bnlg2309 | | 5.03 | 241.25 | no | BNL 2002 |
| umc1048 | A C | 5.03 | 242.60 | yes | IBM2 |
| umc1557 | C | 5.03 | 245.10 | no | IBM2 |
| umc2294 | A C | 5.03 | 245.50 | no | IBM2 |
| umc1447 | A C | 5.03 | 247.60 | yes | IBM2 |
| AY109995 | | 5.03 | 250.30 | no | IBM2 |
| AY109606 | C | 5.03 | 250.30 | no | IBM2 |
| cpn1 | C | 5.03 | 251.24 | no | UMC 98 |
| rz561b | | 5.03 | 251.24 | no | UMC 98 |
| cdo475d | | 5.03 | 251.24 | no | UMC 98 |
| uky2(P450) | | 5.03 | 251.24 | no | UMC 98 |
| px13 | A C | 5.03 | 251.59 | no | SSR popI |
| lim175 | | 5.03 | 254.00 | yes | IBM2 |
| bnlg1700 | | 5.03 | 255.13 | no | BNL 2002 |
| hag101 | | 5.03 | 256.10 | no | ChromDB |
| std2b(dba) | | 5.03 | 256.76 | no | UMC 98 |
| rz892b(alt) | | 5.03 | 256.76 | no | UMC 98 |
| umc2295 | C | 5.03 | 257.80 | yes | IBM2 |
| umc1315 | A C | 5.03 | 260.20 | yes | IBM2 |
| umc1274 | C | 5.03 | 263.13 | no | SSR popII |
| umc1151 | A C | 5.03 | 263.82 | no | SSR popI |
| ufg49 | | 5.03 | 265.10 | yes | IBM2 |
| bnl5.27 | | 5.03 | 265.80 | no | BNL 2002 |
| umc43 | | 5.03 | 266.30 | yes | IBM2 |
| umc1830 | | 5.03 | 266.30 | no | IBM2 |
| bnl6.10 | | 5.03 | 266.30 | yes | IBM2 |
| rgpc1122e(rpL15) | | 5.03 | 266.30 | no | UMC 98 |
| umc2296 | A C | 5.03 | 267.50 | no | IBM2 |
| umc1935 | A C | 5.03 | 267.70 | yes | IBM2 |
| mmp8 | | 5.03 | 269.10 | no | IBM2 |
| umc1850 | | 5.03 | 270.10 | no | SSR popII |
| npi256 | | 5.03 | 270.23 | no | BNL 96 |
| rz242b | | 5.03 | 270.50 | yes | IBM2 |
| umc1692 | A C | 5.03 | 271.50 | no | IBM2 |
| umc1475 | A C | 5.03 | 271.50 | no | SSR popII |
| csu419 | | 5.03 | 273.55 | no | UMC 98 |
| ucr1b(eif) | | 5.03 | 273.55 | no | UMC 98 |
| xet1 | | 5.03 | 273.70 | no | BNL 2002 |
| umc1609 | A C | 5.03 | 275.90 | yes | IBM2 |
| uaz77 | | 5.03 | 277.27 | no | BNL 2002 |
| umc1373 | | 5.03 | 277.34 | no | SSR popI |
| isu2192a | | 5.03 | 277.90 | no | BNL 2002 |
| umc2297 | A C | 5.03 | 279.10 | yes | IBM2 |
| umc1 | | 5.03 | 280.80 | yes | IBM2 |
| cat1 | C | 5.03 | 280.80 | no | UMC 98 |
| csu338 | | 5.03 | 280.80 | no | UMC 98 |
| npi275 | | 5.03 | 280.80 | no | BNL 2002 |
| umc1784 | | 5.03 | 281.00 | no | SSR popII |
| umc1355 | C | 5.03 | 281.20 | yes | IBM2 |
| csu168a | | 5.03 | 281.54 | no | BNL 2002 |
| php20557b | | 5.03 | 281.90 | no | IBM2 |
| isu45b | | 5.03 | 282.00 | no | IBM2 |
| bnl1.380 | | 5.03 | 283.22 | no | BNL 2002 |
| bnl7.43 | | 5.03 | 283.44 | no | BNL 2002 |
| bnl6.22a | | 5.03 | 283.51 | no | BNL 2002 |
| mmp108a | | 5.03 | 284.30 | yes | IBM2 |
| umc1870 | A C | 5.03 | 285.50 | no | IBM2 |
| umc1731 | A C | 5.03 | 285.50 | no | SSR popII |
| phi109188 | A C | 5.03 | 285.70 | no | IBM2 |
| bnl10.06 | | 5.03 | 285.93 | no | BNL 2002 |
| ici287 | | 5.03 | 285.93 | no | BNL 96 |
| ncr200b(rip) | | 5.03 | 286.28 | no | UMC 98 |
| umc1389 | A C | 5.03 | 286.50 | yes | IBM2 |
| umc1429 | A C | 5.03 | 286.60 | no | IBM2 |
| psr167 | | 5.03 | 286.70 | yes | IBM2 |
| uaz186 | | 5.04 | 287.94 | no | BNL 2002 |
| ncr(b70a) | | 5.03 | 288.49 | no | BNL 2002 |
| isu61e | | 5.03 | 288.70 | no | IBM2 |
| isu61c | | 5.03 | 288.90 | no | IBM2 |
| php15018 | | 5.03 | 288.90 | no | IBM2 |
| php15024 | | 5.03 | 289.30 | yes | IBM2 |
| ivr2 | | 5.03 | 289.76 | no | BNL 2002 |
| npi213 | | 5.03-5.04 | 290.08 | no | BNL 2002 |
| mmp154 | | 5.03 | 290.20 | no | IBM2 |
| ufg60 | | 5.03 | 291.20 | yes | IBM2 |
| uaz226(cat1) | | 5.04 | 291.83 | no | BNL 2002 |
| umc2063 | | 5.03 | 292.60 | no | SSR popII |
| AY104079 | C | 5.03 | 292.90 | no | IBM2 |
| umc1226 | A C | 5.03 | 292.96 | no | SSR popI |
| gtc101 | | 5.03 | 293.80 | no | ChromDB |
| gtc102 | C | 5.03 | 293.80 | no | ChromDB |
| uaz213a | | 5.04 | 294.85 | no | BNL 2002 |
| mmp58 | C | 5.03 | 295.00 | yes | IBM2 |
| bnlg150 | | 5.04 | 297.40 | no | BNL 2002 |
| bnlg1902 | A C | 5.03 | 297.50 | yes | IBM2 |
| csu252a(cdc2) | | 5.03 | 297.73 | no | UMC 98 |
| knox6 | | 5.04 | 298.03 | no | BNL 2002 |
| umc1110 | A C | 5.03 | 298.10 | no | SSR popII |
| uwo4 | | 5.04 | 299.25 | no | BNL 2002 |
| ncr(cat1) | | 5.03 | 299.25 | no | BNL 96 |
| csu720c | | 5.03 | 299.67 | no | UMC 98 |
| csu652(rpL27) | C | 5.03 | 299.67 | no | UMC 98 |
| uaz275 | | 5.04 | 301.60 | no | UMC 98 |
| umn388 | | 5.04 | 301.60 | no | UMC 98 |
| bnl4.36 | C | 5.04 | 301.60 | yes | IBM2 |
| csu283b | | 5.04 | 301.60 | no | UMC 98 |
| csu305a | | 5.04 | 301.60 | no | UMC 98 |
| csu315a | | 5.04 | 301.60 | no | UMC 98 |
| csu670 | C | 5.04 | 301.60 | no | UMC 98 |
| csu660b | C | 5.04 | 301.60 | no | UMC 98 |
| csu377b(ubi) | | 5.04 | 301.60 | no | UMC 98 |
| uaz132a(dts) | | 5.04 | 301.60 | no | UMC 98 |
| csu36b(rpL19) | | 5.04 | 301.60 | no | UMC 98 |
| csu774(lhcb) | A C | 5.04 | 301.60 | no | UMC 98 |
| sbp1 | | 5.04 | 306.62 | no | SSR popII |
| umc2066 | | 5.04 | 306.62 | no | SSR popII |
| umc2373 | | 5.04 | 306.62 | no | SSR popII |
| umc2400 | | 5.04 | 306.62 | no | SSR popII |
| umc1815 | C | 5.04 | 306.62 | no | SSR popII |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| umc2298 | A C | 5.04 | 307.00 | yes | IBM2 |
| umc40 | | 5.04 | 308.20 | yes | IBM2 |
| umc250 | | 5.04 | 309.60 | no | UMC 98 |
| csu562b(ubi) | | 5.04 | 309.60 | no | UMC 98 |
| umc2299 | A C | 5.04 | 310.00 | no | IBM2 |
| mmp60 | | 5.04 | 310.20 | yes | IBM2 |
| umc1563 | C | 5.04 | 311.30 | no | SSR popII |
| umc2406 | C | 5.04 | 311.30 | no | SSR popII |
| asg51a | | 5.04 | 312.80 | no | UMC 98 |
| bnlg1829c | | 5.04 | 312.80 | no | IBM1 |
| rz87(clp) | | 5.04 | 312.80 | yes | IBM2 |
| umc1283 | A C | 5.04 | 313.28 | no | SSR popI |
| bnlg1892c | C | 5.04 | 313.30 | no | IBM2 |
| umc1629 | | 5.04 | 313.98 | no | SSR popII |
| umc1860 | | 5.04 | 313.98 | no | SSR popII |
| umc1591 | A C | 5.04 | 314.10 | yes | IBM2 |
| umc1224 | | 5.04 | 314.64 | no | SSR popII |
| umc2300 | A C | 5.04 | 315.20 | no | IBM2 |
| umc2301 | A C | 5.04 | 315.30 | no | IBM2 |
| umc2302 | A C | 5.04 | 316.80 | yes | IBM2 |
| umc1060 | A C | 5.04 | 317.60 | yes | IBM2 |
| umc1162 | A C | 5.04 | 317.66 | no | SSR popI |
| umc2407 | | 5.04 | 317.99 | no | SSR popII |
| umc1990 | | 5.04 | 318.90 | yes | IBM2 |
| BE639933 | C | 5.04 | 320.10 | no | IBM2 |
| umc1747 | C | 5.04 | 321.00 | yes | IBM2 |
| bnlg603 | A C | 5.04 | 321.00 | no | SSR popI |
| uwo7 | | 5.04 | 321.39 | no | BNL 2002 |
| uwo6 | | 5.04 | 321.39 | no | BNL 96 |
| a2 | C | 5.04 | 321.61 | no | BNL 2002 |
| isu2191j | | 5.04 | 321.62 | no | BNL 2002 |
| dupssr1 | | 5.02 | 321.63 | no | BNL 2002 |
| bnl17.30a | | 5.04 | 321.90 | no | BNL 2002 |
| bnlg1287 | | 5.04 | 321.94 | no | BNL 2002 |
| rny2(rita) | | 5.03-5.04 | 322.10 | no | BNL 2002 |
| bnlg1208 | A C | 5.04 | 323.10 | yes | IBM2 |
| php20589 | | 5.04 | 323.70 | no | IBM2 |
| lim4 | | 5.04 | 324.30 | yes | IBM2 |
| mip1 | | 5.04 | 324.62 | no | UMC 98 |
| asg43 | C | 5.04 | 324.62 | no | UMC 98 |
| bnl7.71 | | 5.04 | 324.62 | no | UMC 98 |
| csu241a | | 5.04 | 324.62 | no | UMC 98 |
| dupssr10 | A C | 5.04 | 324.62 | no | UMC 98 |
| csu862a(rpL11) | | 5.04 | 324.62 | no | UMC 98 |
| bnlg2323 | | 5.04 | 328.50 | yes | IBM2 |
| bt1 | | 5.04 | 328.99 | no | BNL 2002 |
| npi408 | | 5.04 | 328.99 | no | BNL 2002 |
| npi424 | | 5.04 | 328.99 | no | BNL 2002 |
| npi571 | | 5.04 | 328.99 | no | BNL 2002 |
| npi449a | | 5.04 | 331.40 | yes | IBM2 |
| rz476b | | 5.04 | 331.80 | no | IBM2 |
| mmp19 | | 5.04 | 332.70 | no | IBM2 |
| AY110906 | C | 5.04 | 336.50 | yes | IBM2 |
| ris1 | | 5.04 | 336.77 | no | BNL 96 |
| npi(pmr15) | | 5.04 | 336.77 | no | BNL 2002 |
| AY105029 | A C | 5.04 | 338.00 | no | IBM2 |
| csu302 | | 5.04 | 339.40 | yes | IBM2 |
| dpg15b | | 5.03-5.04 | 339.62 | no | BNL 2002 |
| chs572 | | 5.04 | 339.68 | no | BNL 2002 |
| npi53b | | 5.04 | 339.68 | no | BNL 2002 |
| bnlg653 | | 5.04 | 340.99 | no | BNL 2002 |
| npi104a | | 5.04 | 342.24 | no | BNL 2002 |
| uaz70a | | 5.04 | 342.67 | no | BNL 2002 |
| umc1092 | C | 5.04 | 342.70 | no | SSR popII |
| umc1192 | A C | 5.04 | 342.70 | no | SSR popII |
| bnl31a | | 5.04 | 342.90 | no | BNL 2002 |
| PCO103687 | C | 5.04 | 344.20 | no | INDEL |
| umc1349 | C | 5.04 | 346.50 | yes | IBM2 |
| bnlg1063c | C | 5.03 | 346.92 | no | BNL 2002 |
| AY109532 | A C | 5.04 | 351.20 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| mpik33a | | 5.04 | 352.45 | no | BNL 2002 |
| amp3 | | 5.04 | 354.81 | no | BNL 96 |
| koln2a(hox) | | 5.04 | 357.72 | no | BNL 2002 |
| myb3 | | 5.04 | 358.90 | yes | IBM2 |
| ici273b | | 5.04 | 358.99 | no | BNL 2002 |
| uaz131 | | 5.04 | 363.14 | no | BNL 2002 |
| koln10a(hox2) | | 5.04 | 365.17 | no | BNL 2002 |
| umc1332 | | 5.04 | 366.60 | no | SSR popI |
| umc1221 | A C | 5.04 | 368.40 | yes | IBM2 |
| umc1975 | | 5.04 | 370.79 | no | SSR popII |
| csu308 | | 5.04 | 371.20 | yes | IBM2 |
| csu765 | | 5.04 | 371.20 | no | UMC 98 |
| dup(als2) | | 5.04 | 374.29 | no | BNL 2002 |
| uaz238(ppi) | | 5.04 | 374.29 | no | BNL 96 |
| uaz248b(his3) | | 5.05 | 375.52 | no | BNL 2002 |
| incw1 | A C | 5.04 | 376.40 | yes | IBM2 |
| csu600 | A C | 5.04 | 377.00 | no | IBM2 |
| umc1966 | A C | 5.04 | 377.90 | no | IBM2 |
| ucsd64h | | 5.04-5.05 | 379.13 | no | BNL 2002 |
| umc1482 | | 5.05 | 383.80 | yes | IBM2 |
| npi295a | | 5.04 | 383.88 | no | BNL 2002 |
| bnl5.71a | | 5.05 | 387.00 | yes | IBM2 |
| mmc0081 | A C | 5.05 | 389.90 | yes | IBM2 |
| mpik14(Cin4) | | 5.05 | 390.91 | no | BNL 2002 |
| AY109682 | A C | 5.05 | 392.70 | no | IBM2 |
| phi333597 | A C | 5.05 | 394.40 | yes | IBM2 |
| bnl35a(blr) | | 5.04 | 394.61 | no | BNL 2002 |
| umc1348 | | 5.04-5.05 | 396.10 | no | SSR popI |
| umc1937 | | 5.04-5.05 | 396.10 | no | SSR popI |
| umc1822 | | 5.05 | 396.60 | yes | IBM2 |
| umc2026 | A C | 5.05 | 397.00 | yes | IBM2 |
| PCO060271 | C | 5.05 | 400.89 | no | INDEL |
| mmp47 | A C | 5.05 | 402.20 | yes | IBM2 |
| ufg18 | C | 5.05 | 404.00 | no | IBM2 |
| bnl10.12 | | 5.05 | 404.34 | no | BNL 96 |
| umc1264 | A C | 5.05 | 404.90 | yes | IBM2 |
| csu1080a | | 5.05 | 406.20 | no | UMC 98 |
| csu93b | C | 5.05 | 406.20 | no | SSR popII |
| PCO078116 | C | 5.05 | 408.36 | no | INDEL |
| rz166(nac) | | 5.05 | 408.44 | no | UMC 98 |
| umc2303 | A C | 5.05 | 408.80 | yes | IBM2 |
| tda62a | | 5.05 | 410.01 | no | UMC 98 |
| std16b(blr) | | 5.05 | 410.01 | no | UMC 98 |
| umc1155 | A C | 5.05 | 410.80 | yes | IBM2 |
| csu713 | | 5.05 | 412.18 | no | UMC 98 |
| csu95b | C | 5.05 | 412.18 | no | UMC 98 |
| CL11475_1 | C | 5.05 | 413.29 | no | INDEL |
| csu173 | C | 5.05 | 413.60 | no | IBM2 |
| gl8 | A C | 5.05 | 413.80 | no | UMC 98 |
| nbp35 | C | 5.05 | 413.80 | yes | IBM2 |
| rgpc174a | | 5.05 | 413.80 | no | UMC 98 |
| gte102 | | 5.05 | 414.07 | no | ChromDB |
| uaz79 | | 5.05 | 414.13 | no | BNL 2002 |
| mmp90 | | 5.05 | 414.70 | yes | IBM2 |
| PCO099796 | C | 5.05-5.06 | 415.78 | no | INDEL |
| umc1800 | | 5.05 | 415.95 | no | SSR popII |
| CL16923_1 | C | 5.05-5.06 | 419.02 | no | INDEL |
| mmc0282 | A C | 5.05 | 419.09 | no | SSR popII |
| npi237 | | 5.05 | 419.26 | no | BNL 2002 |
| umc2386 | C | 5.05 | 423.27 | no | SSR popII |
| uaz261a | | 5.05 | 425.07 | no | BNL 2002 |
| uaz190(gpc) | | 5.05 | 425.07 | no | BNL 96 |
| bnlg1847 | | 5.06 | 425.21 | no | BNL 2002 |
| serk2 | C | 5.05 | 428.30 | yes | IBM2 |
| umc1687 | A C | 5.05 | 429.19 | no | SSR popII |
| pal1 | | 5.05 | 436.68 | no | UMC 98 |
| asg71 | | 5.05 | 436.68 | no | UMC 98 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| csu1105 | | 5.05 | 436.68 | no | UMC 98 |
| umc1502 | | 5.05 | 439.29 | no | SSR popII |
| bnlg278 | | 5.05 | 441.69 | no | SSR popI |
| umc1853 | | 5.05 | 449.40 | no | SSR popII |
| uaz164a | | 5.05-5.06 | 450.22 | no | BNL 96 |
| csu550 | | 5.05 | 453.42 | no | UMC 98 |
| bnlg1237 | | 5.05-5.06 | 454.01 | no | BNL 2002 |
| umc1722 | A C | 5.05 | 456.01 | no | SSR popII |
| mmp104 | | 5.05 | 457.40 | yes | IBM2 |
| bnl5.40 | | 5.06 | 458.44 | no | UMC 98 |
| rpl19 | | 5.05 | 461.79 | no | UMC 98 |
| AY110063 | C | 5.05 | 467.20 | yes | IBM2 |
| umc126a | C | 5.06 | 469.60 | yes | IBM2 |
| AY109938 | C | 5.06 | 470.10 | yes | IBM2 |
| mmc0481 | A C | 5.06 | 476.60 | yes | IBM2 |
| umc2305 | A C | 5.06 | 479.70 | no | IBM2 |
| umc54 | C | 5.06 | 481.20 | yes | IBM2 |
| csu777 | | 5.06 | 481.20 | no | UMC 98 |
| umc14c | | 5.06 | 481.20 | no | UMC 98 |
| umc156b | C | 5.06 | 481.20 | no | BNL 2002 |
| cdo395b(ypt) | | 5.06 | 481.20 | no | UMC 98 |
| nfd104a | | 5.06 | 483.73 | no | ChromDB |
| umc1752 | A C | 5.06 | 488.40 | yes | IBM2 |
| uaz78 | | 5.05 | 489.59 | no | BNL 2002 |
| npi562 | | 5.06 | 491.49 | no | BNL 2002 |
| umc1941 | A C | 5.06 | 492.60 | no | IBM2 |
| umc141 | | 5.06 | 493.26 | no | UMC 98 |
| umc1524 | A C | 5.06 | 493.50 | yes | IBM2 |
| umc1680 | A C | 5.06 | 493.50 | yes | IBM2 |
| umc51a | A C | 5.06 | 493.70 | no | IBM2 |
| csu434 | | 5.06 | 493.96 | no | UMC 98 |
| csu440 | C | 5.06 | 493.96 | no | UMC 98 |
| php20531 | | 5.06 | 494.20 | yes | IBM2 |
| bnlg1246a | | 5.05 | 495.77 | no | BNL 2002 |
| csh10a(cycII) | | 5.06 | 496.87 | no | UMC 98 |
| uaz138c | | 5.06 | 497.13 | no | BNL 2002 |
| csu26c(ant) | | 5.05 | 498.71 | no | BNL 2002 |
| npi458a | | 5.06 | 499.70 | yes | IBM2 |
| zag5 | | 5.06 | 499.95 | no | BNL 2002 |
| umc2306 | A C | 5.06 | 500.10 | yes | IBM2 |
| rgpg57 | | 5.06 | 500.57 | no | UMC 98 |
| umc262 | | 5.06 | 500.57 | no | UMC 98 |
| umc253a | | 5.06 | 500.57 | no | UMC 98 |
| bnlg609 | A C | 5.06 | 500.70 | yes | IBM2 |
| uaz215a(odo) | | 5.06 | 500.70 | no | BNL 2002 |
| asg81a | | 5.06 | 504.54 | no | UMC 98 |
| csu587b | | 5.06 | 504.54 | no | UMC 98 |
| csu615a | A C | 5.06 | 504.54 | no | UMC 98 |
| uaz204 | | 5.06 | 510.88 | no | BNL 2002 |
| PCO111982 | C | 5.06-5.07 | 511.07 | no | INDEL |
| rz567a(klc) | C | 5.06 | 511.30 | yes | IBM2 |
| ici229 | | 5.06 | 511.87 | no | BNL 96 |
| php20566 | | 5.06 | 512.00 | yes | IBM2 |
| sdg117b | C | 5.06 | 512.00 | no | ChromDB |
| uaz254a | | 5.06 | 515.75 | no | BNL 2002 |
| mmp169 | | 5.06 | 516.30 | yes | IBM2 |
| umc2216 | | 5.06 | 518.37 | no | SSR popI |
| csu1164 | | 5.06 | 520.10 | no | UMC 98 |
| csu643a | | 5.06 | 520.10 | no | UMC 98 |
| csu907b | | 5.06 | 520.10 | no | UMC 98 |
| rz273b(ant) | | 5.06 | 520.10 | yes | IBM2 |
| cdo507b(ant) | | 5.06 | 520.10 | yes | IBM2 |
| csu26a(ant) | | 5.06 | 520.10 | no | UMC 98 |
| uaz144b | | 5.06 | 524.40 | no | BNL 2002 |
| gln4 | A C | 5.06 | 528.70 | yes | IBM2 |
| npi442 | | 5.06 | 530.00 | yes | IBM2 |
| umc108 | A C | 5.07 | 536.60 | yes | IBM2 |
| bnl9.07b | | 5.07 | 536.60 | no | BNL 2002 |
| psr3b | | 5.07 | 537.57 | no | BNL 2002 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| umc2201 | C | 5.07 | 542.05 | no | SSR popI |
| bnlg1346 | | 5.07 | 544.64 | no | BNL 2002 |
| npi253c | | 5.07 | 550.21 | no | BNL 2002 |
| umc1537 | A C | 5.07 | 553.61 | no | SSR popII |
| umc2198 | C | 5.07 | 554.92 | no | SSR popI |
| klp5 | | 5.07 | 555.46 | no | UMC 98 |
| asg84b | | 5.07 | 555.46 | no | UMC 98 |
| mpik10 | | 5.07 | 557.09 | no | BNL 2002 |
| bnlg1306 | | 5.07 | 557.09 | no | BNL 2002 |
| bnlg2305 | | 5.07 | 557.09 | no | BNL 2002 |
| umc68a | | 5.07 | 557.09 | no | BNL 96 |
| umc241 | | 5.07 | 559.61 | no | UMC 98 |
| umc1646 | | 5.07 | 566.30 | no | SSR popI |
| umc1375 | | 5.07 | 571.66 | no | SSR popI |
| umc2013 | | 5.07 | 571.66 | no | SSR popI |
| csu288 | | 5.07 | 574.70 | no | UMC 98 |
| asg9b | | 5.07 | 578.47 | no | UMC 98 |
| lhcb4 | | 5.07 | 578.47 | no | UMC 98 |
| ppp1 | C | 5.07 | 578.47 | no | UMC 98 |
| asg74a | | 5.07 | 578.47 | no | UMC 98 |
| cdo516a | | 5.07 | 578.47 | no | UMC 98 |
| csu1074 | | 5.07 | 578.47 | no | UMC 98 |
| ucsd106e | | 5.05 | 583.55 | no | BNL 2002 |
| agrc563a | | 5.07 | 586.39 | no | UMC 98 |
| csu672a | C | 5.07 | 586.39 | no | UMC 98 |
| wsu(nia5) | | 5.07 | 588.07 | no | BNL 96 |
| bnlg1118 | A C | 5.07 | 590.40 | yes | IBM2 |
| pbs6a | | 5.07 | 590.95 | no | BNL 2002 |
| bnlg1416 | | 5.07 | 592.07 | no | BNL 2002 |
| nnr2 | | 5.07 | 599.50 | yes | IBM2 |
| umc1072 | A C | 5.07 | 600.00 | yes | IBM2 |
| AY110369 | A C | 5.07 | 600.40 | no | IBM2 |
| mmp118 | | 5.07 | 601.30 | yes | IBM2 |
| bnl5.24a | | 5.08 | 609.40 | yes | IBM2 |
| bnlg118 | A C | 5.08 | 609.40 | yes | IBM2 |
| bnlg1597c | | 5.08 | 613.80 | yes | IBM2 |
| ias13b | | 5.09 | 615.76 | no | BNL 2002 |
| mmp170 | | 5.08 | 619.70 | yes | IBM2 |
| umc1792 | A C | 5.08 | 625.80 | yes | IBM2 |
| uaz71b | | 5.08 | 628.30 | no | BNL 2002 |
| AY110413 | | 5.08 | 630.80 | yes | IBM2 |
| npi288a | | 5.08 | 632.60 | yes | IBM2 |
| umc57d | | 5.08 | 638.50 | no | IBM2 |
| php20523b | | 5.08 | 638.80 | yes | IBM2 |
| umc1225 | A C | 5.08 | 641.40 | yes | IBM2 |
| uaz240a | | 5.08 | 641.75 | no | BNL 2002 |
| AY110182 | A C | 5.08 | 643.60 | no | IBM2 |
| mmp175 | | 5.08 | 645.40 | yes | IBM2 |
| got2 | | 5.08 | 648.23 | no | BNL 96 |
| csu834(mss) | | 5.08 | 649.24 | no | UMC 98 |
| csu799(rpCL9) | | 5.08 | 656.15 | no | UMC 98 |
| AY105910 | A C | 5.08 | 656.70 | yes | IBM2 |
| bnlg1695 | | 5.07 | 657.08 | no | BNL 2002 |
| bnlg1885 | | 5.07 | 657.08 | no | BNL 2002 |
| csu695(rpL9) | | 5.08 | 657.14 | no | UMC 98 |
| umc104b | | 5.08 | 660.10 | yes | IBM2 |
| bnlg389 | | 5.09 | 661.56 | no | BNL 2002 |
| rz446b | | 5.08 | 661.80 | yes | IBM2 |
| bnlg386 | | 5.09 | 661.94 | no | BNL 2002 |
| AW065811 | | 5.08 | 664.30 | yes | IBM2 |
| bnlg1711 | | 5.07 | 666.54 | no | BNL 2002 |
| php10017 | A C | 5.09 | 669.40 | yes | IBM2 |
| umc1829 | | 5.09 | 671.53 | no | SSR popII |
| umc2307 | | 5.09 | 672.60 | yes | IBM2 |
| umc2308 | C | 5.09 | 672.60 | no | IBM2 |
| mmp109 | | 5.09 | 676.70 | no | IBM1 |
| umc1153 | A C | 5.09 | 676.70 | yes | IBM2 |
| umc2209 | C | 5.09 | 678.29 | no | SSR popI |
| umc49f | C | 6.00 | 0.00 | yes | IBM2 |
| csu150a | | 6.00 | 4.57 | no | BNL 96 |
| fdx2 | | 6.00 | 9.10 | no | SSR popI |
| isu139 | | 6.00 | 17.30 | no | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| umc2208 |  | 6.00 | 17.39 | no | SSR popI |
| umc1143 | A C | 6.00 | 17.50 | yes | IBM2 |
| bnlg238 |  | 6.00 | 23.20 | yes | IBM2 |
| bnlg161b |  | 6.00 | 23.20 | yes | IBM2 |
| csu926(frk) |  | 6.00 | 25.75 | no | UMC 98 |
| umc2310 | A C | 6.00 | 27.60 | yes | IBM2 |
| umc2309 | A C | 6.00 | 27.80 | no | IBM2 |
| PCO069699 | C | 6.00-6.01 | 39.27 | no | INDEL |
| umc2068 |  | 6.00 | 47.80 | no | SSR popII |
| agrp144 |  | 6.00 | 49.00 | no | IBM2 |
| uaz18a |  | 6.00 | 51.97 | no | BNL 2002 |
| npi340a |  | 6.00 | 51.97 | no | BNL 96 |
| rz143a(gpc) |  | 6.00 | 56.70 | yes | IBM2 |
| rgpc174b |  | 6.00 | 60.32 | no | UMC 98 |
| bnlg1433 |  | 6.01 | 60.64 | no | BNL 2002 |
| bnlg1246d |  | 6.01 | 61.69 | no | BNL 2002 |
| bnlg1139 |  | 6.01 | 61.72 | no | BNL 2002 |
| csu178b |  | 6.00 | 63.34 | no | UMC 98 |
| csu710d(apx) |  | 6.00 | 63.34 | no | UMC 98 |
| AY110100 | A C | 6.00 | 63.60 | yes | IBM2 |
| umc1883 |  | 6.00 | 63.70 | no | SSR popII |
| umc1996 | C | 6.00 | 63.70 | no | SSR popII |
| mpik11b |  | 6.01 | 64.87 | no | BNL 2002 |
| nor |  | 6.01 | 64.87 | no | BNL 96 |
| mpik(DH7) |  | 6.01 | 64.87 | no | BNL 2002 |
| uiu1b(pog) |  | 6.01 | 64.87 | no | BNL 2002 |
| isu2232h |  | 6.01 | 64.90 | no | BNL 2002 |
| bnlg2097 |  | 6.01 | 64.95 | no | BNL 2002 |
| csu70 |  | 6.01 | 66.40 | no | UMC 98 |
| umc159a |  | 6.00 | 66.40 | no | UMC 98 |
| umc85a | A C | 6.01 | 66.40 | yes | IBM2 |
| gpc2 | A C | 6.00-6.01 | 66.40 | no | SSR popII |
| isu85a |  | 6.01 | 67.70 | yes | IBM2 |
| pic7b |  | 6.05 | 68.50 | no | BNL 2002 |
| uaz102 |  | 6.01 | 68.83 | no | BNL 2002 |
| bnl17.28 |  | 6.01 | 68.83 | no | BNL 2002 |
| umc1606 | A C | 6.01 | 69.20 | yes | IBM2 |
| sdg102b |  | 6.01 | 69.20 | no | ChromDB |
| hon104b | C | 6.01 | 69.20 | no | ChromDB |
| uaz269c(kri) |  | 6.01 | 69.61 | no | BNL 2002 |
| umc1753 | C | 6.00-6.01 | 70.37 | no | SSR popI |
| cdo1173c |  | 6.01 | 71.10 | yes | IBM2 |
| uaz258a |  | 6.01 | 71.20 | no | BNL 2002 |
| umc2311 | A C | 6.01 | 71.50 | no | IBM2 |
| mmp163 |  | 6.01 | 71.80 | no | IBM2 |
| bnlg1600 |  | 6.00 | 71.89 | no | BNL 2002 |
| bnlg1371 | A C | 6.01 | 72.70 | yes | IBM2 |
| bnl6.29a |  | 6.01 | 73.30 | yes | IBM2 |
| bnlg1165 |  | 6.01 | 73.87 | no | BNL 2002 |
| npi235a |  | 6.01 | 73.87 | no | BNL 96 |
| bnlg1043 |  | 6.00 | 73.94 | no | BNL 2002 |
| uaz150 |  | 6.01 | 74.80 | no | BNL 2002 |
| uaz197b(cdpk) |  | 6.01 | 74.80 | no | BNL 2002 |
| isu1410b |  | 6.01 | 75.39 | no | BNL 2002 |
| umc2312 | A C | 6.01 | 75.80 | yes | IBM2 |
| bnlg1867 | A C | 6.01 | 78.30 | yes | IBM2 |
| mmp13 |  | 6.01 | 79.60 | no | IBM2 |
| pge23 |  | 6.01 | 80.17 | no | UMC 98 |
| csu699 |  | 6.01 | 80.17 | no | UMC 98 |
| csu700 |  | 6.01 | 80.17 | no | UMC 98 |
| bnl7.28 |  | 6.01 | 80.17 | no | UMC 98 |
| bnlg426 | A C | 6.01 | 80.17 | no | UMC 98 |
| cdo580b(ivd) |  | 6.01 | 80.17 | no | UMC 98 |
| umc1229 | A C | 6.01 | 80.70 | yes | IBM2 |
| umc1625 |  | 6.01 | 81.72 | no | SSR popI |
| csu680e | C | 6.01 | 83.27 | no | UMC 98 |
| uaz80(iron) |  | 6.01 | 84.32 | no | BNL 2002 |
| bnlg1432 |  | 6.01 | 84.61 | no | BNL 2002 |
| tug2 |  | 6.01 | 84.61 | no | BNL 96 |
| php20528 |  | 6.01 | 85.50 | yes | IBM2 |
| rz390d(cyb5) |  | 6.01 | 86.30 | no | IBM2 |
| isu1410j |  | 6.01 | 86.50 | no | BNL 2002 |
| pic7a |  | 6.01 | 86.54 | no | BNL 2002 |
| umc2196 | C | 6.01 | 86.83 | no | SSR popI |
| cdo545 |  | 6.01 | 86.90 | yes | IBM2 |
| csu243 |  | 6.01 | 87.05 | no | UMC 98 |
| csu809 |  | 6.01 | 87.05 | no | UMC 98 |
| agrr221 |  | 6.01 | 87.05 | no | UMC 98 |
| csu1120 |  | 6.01 | 87.05 | no | UMC 98 |
| psr160a |  | 6.01 | 87.70 | no | IBM2 |
| php20854 |  | 6.01 | 87.70 | yes | IBM2 |
| uaz197a(cdpk) |  | 6.01 | 87.74 | no | BNL 2002 |
| npi594a |  | 6.01 | 88.11 | no | BNL 2002 |
| umc2313 | A C | 6.01 | 91.90 | yes | IBM2 |
| pgd1 |  | 6.01 | 96.00 | no | UMC 98 |
| uck1 | C | 6.01 | 96.00 | yes | IBM2 |
| csu1187 |  | 6.01 | 96.00 | no | UMC 98 |
| csu1196 |  | 6.01 | 96.00 | no | UMC 98 |
| csu94a |  | 6.01 | 97.38 | no | UMC 98 |
| umc36c |  | 6.01 | 97.38 | no | UMC 98 |
| umc1832 |  | 6.01 | 97.80 | no | IBM2 |
| umc2074 | A C | 6.01 | 98.00 | no | IBM2 |
| umc1444 | C | 6.01 | 98.40 | no | IBM2 |
| AY110213 | A C | 6.01 | 98.40 | no | IBM2 |
| bnlg1641 | A C | 6.01 | 98.40 | no | IBM2 |
| umc1133 | A C | 6.01 | 98.60 | yes | IBM2 |
| umc2315 |  | 6.01 | 98.80 | no | IBM2 |
| umc2056 | A C | 6.01 | 99.00 | no | IBM2 |
| umc2314 | A C | 6.01 | 99.30 | yes | IBM2 |
| nfa101 |  | 6.01 | 99.30 | no | ChromDB |
| uaz232b(sci) |  | 6.01 | 100.30 | yes | IBM2 |
| zp15 |  | 6.01 | 100.91 | no | BNL 2002 |
| uaz23a |  | 6.01 | 100.91 | no | BNL 2002 |
| bnlg249 |  | 6.01 | 100.91 | no | BNL 2002 |
| isu1774a |  | 6.01 | 100.91 | no | BNL 2002 |
| npi606 |  | 6.01 | 100.91 | no | BNL 96 |
| mmp160 |  | 6.01 | 101.90 | yes | IBM2 |
| mmp76 |  | 6.01 | 103.80 | yes | IBM2 |
| umc1498 | A C | 6.01 | 104.45 | no | SSR popI |
| ufg69 | C | 6.01 | 104.80 | yes | IBM2 |
| mmp20 |  | 6.01 | 105.90 | yes | IBM2 |
| bnl6.22b |  | 6.02 | 107.37 | no | UMC 98 |
| csu56a(ohp) | C | 6.02 | 107.37 | no | UMC 98 |
| csu146a(cdc48) |  | 6.02 | 107.37 | no | UMC 98 |
| mmp10 |  | 6.01 | 110.40 | yes | IBM2 |
| cyc3 | A C | 6.01 | 114.25 | no | SSR popII |
| mmp4 |  | 6.01 | 116.20 | yes | IBM2 |
| mmp108b |  | 6.01 | 118.30 | yes | IBM2 |
| umc1517 |  | 6.01 | 119.19 | no | SSR popII |
| umc1195 |  | 6.01 | 120.41 | no | SSR popII |
| y1 | A C | 6.01 | 120.50 | yes | IBM2 |
| mpik33d |  | 6.01 | 120.50 | no | BNL 2002 |
| si1 |  | 6.02 | 120.57 | no | BNL 2002 |
| bnlg1188 |  | 6.01 | 120.66 | no | BNL 2002 |
| rz444e | C | 6.02 | 123.70 | yes | IBM2 |
| umc59a | A C | 6.02 | 124.12 | no | SSR popII |
| umc1376 |  | 6.01 - 6.02 | 124.12 | no | SSR popII |
| enp1 |  | 6.02 | 124.50 | no | UMC 98 |
| agrr189 |  | 6.02 | 124.50 | no | IBM2 |
| csu548 |  | 6.02 | 124.50 | no | UMC 98 |
| oec33 |  | 6.02 | 124.60 | no | UMC 98 |
| csu395a | C | 6.02 | 124.60 | no | UMC 98 |
| umc51b |  | 6.02 | 124.64 | no | UMC 98 |
| umn361 |  | 6.02 | 124.64 | no | UMC 98 |
| bnlg1047b |  | 6.01 | 124.77 | no | BNL 2002 |
| bnlg1422 |  | 6.01 | 124.81 | no | BNL 2002 |
| mpik1 |  | 6.02 | 124.87 | no | BNL 2002 |
| bnlg107 |  | 6.01 | 124.87 | no | BNL 2002 |
| bnl28(sbe1) |  | 6.02 | 124.87 | no | BNL 2002 |
| umc1006 | A C | 6.02 | 125.00 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| csu183a(cdc48) | | 6.02 | 125.58 | no | SSR popI |
| mir2 | A C | 6.02 | 126.46 | no | SSR popII |
| bnlg1538 | | 6.01 | 127.02 | no | BNL 2002 |
| npi373 | | 6.02 | 127.02 | no | BNL 96 |
| mir1 | | 6.02 | 127.10 | yes | IBM2 |
| mir4(thp) | | 6.02 | 127.10 | no | UMC 98 |
| uiu5(chn) | | 6.02 | 127.10 | no | UMC 98 |
| uiu6(chn) | | 6.02 | 127.10 | no | UMC 98 |
| ucr1a(eif) | | 6.02 | 127.10 | no | UMC 98 |
| rz242a | | 6.02 | 127.80 | yes | IBM2 |
| agrr87a | | 6.02 | 127.80 | no | UMC 98 |
| umc1083 | A C | 6.02 | 127.80 | no | IBM2 |
| psu1a(spe) | | 6.02 | 128.18 | no | UMC 98 |
| csu309(atpc) | | 6.02 | 128.57 | no | UMC 98 |
| pbs8 | | 6.01 | 128.97 | no | BNL 2002 |
| phi077 | | 6.01 | 129.05 | no | BNL 2002 |
| saur1 | | 6.02 | 129.06 | no | SSR popII |
| npi377 | | 6.02 | 129.57 | no | BNL 2002 |
| bnlg2151 | | 6.02 | 129.71 | no | BNL 2002 |
| mpik18 | | 6.02 | 129.77 | no | BNL 2002 |
| uaz162 | | 6.02 | 129.96 | no | BNL 2002 |
| umc1656 | A C | 6.02 | 133.40 | yes | IBM2 |
| mmp117 | | 6.02 | 139.50 | yes | IBM2 |
| php20045a | | 6.02 | 142.12 | no | BNL 96 |
| mmp51 | | 6.02 | 143.20 | yes | IBM2 |
| sdg102c | | 6.02 | 145.10 | no | ChromDB |
| umc1257 | C | 6.02 | 145.70 | yes | IBM2 |
| umc1628 | | 6.02 | 147.60 | no | SSR popI |
| psr129b | | 6.02 | 147.90 | yes | IBM2 |
| bnlg2191 | A C | 6.02 | 148.70 | no | IBM2 |
| bnlg1753 | | 6.01 | 148.86 | no | BNL 2002 |
| bnlg391 | | 6.01 | 148.93 | no | BNL 2002 |
| uaz237b(prc) | | 6.01 | 148.95 | no | BNL 2002 |
| mwg645b | | 6.01 | 148.96 | no | BNL 2002 |
| uaz169 | | 6.01 | 149.29 | no | BNL 2002 |
| bcd98f | | 6.01 | 149.32 | no | BNL 2002 |
| uaz233b(act) | | 6.01 | 149.32 | no | BNL 2002 |
| uaz233d(act) | | 6.01 | 149.32 | no | BNL 2002 |
| jpsb108 | | 6.02 | 151.10 | yes | IBM2 |
| csu605 | | 6.02 | 151.27 | no | UMC 98 |
| php06007 | | 6.02 | 151.27 | no | UMC 98 |
| csu747b(arf) | C | 6.02 | 151.27 | no | UMC 98 |
| mmp65 | | 6.02 | 152.60 | no | IBM2 |
| sbp3 | C | 6.02 | 153.70 | yes | IBM2 |
| uaz227(end) | | 6.01 | 153.78 | no | BNL 2002 |
| npi100 | | 6.00-6.01 | 154.86 | no | BNL 2002 |
| csu923(sec61) | | 6.02 | 158.70 | yes | IBM2 |
| npi393 | | 6.03 | 161.87 | no | SSR popI |
| umc2316 | A C | 6.02-6.03 | 166.60 | no | IBM2 |
| umc1887 | A C | 6.03-6.04 | 166.80 | no | IBM2 |
| AY104775 | A C | 6.04 | 167.60 | yes | IBM2 |
| uaz106a | | 6.03 | 169.35 | no | BNL 96 |
| csu226b(elf1A) | | 6.03 | 170.96 | no | UMC 98 |
| AY111964 | A C | 6.04 | 171.20 | yes | IBM2 |
| csu199a | | 6.03 | 172.41 | no | UMC 98 |
| bnl(tas1i) | | 6.04 | 173.71 | no | BNL 2002 |
| npi98b | | 6.03 | 175.68 | no | BNL 96 |
| umc65a | A C | 6.04 | 181.90 | yes | IBM2 |
| std6b(dba) | | 6.03-6.04 | 181.90 | no | UMC 98 |
| umc1796 | | 6.04 | 189.50 | yes | IBM2 |
| umc1918 | A C | 6.04 | 189.90 | no | IBM2 |
| rz476d | | 6.04 | 191.30 | yes | IBM2 |
| bnlg480 | | 6.04 | 196.12 | no | BNL 2002 |
| npi223a | | 6.04 | 196.30 | yes | IBM2 |
| uaz160 | | 6.04 | 196.66 | no | BNL 2002 |
| umc1105 | A C | 6.04 | 199.00 | yes | IBM2 |
| umc1979 | A C | 6.04 | 200.30 | yes | IBM2 |
| uaz161a(elf) | | 6.04 | 202.74 | no | BNL 2002 |
| umc1857 | A C | 6.04 | 203.20 | yes | IBM2 |
| PCO075489 | C | 6.04 | 204.62 | no | INDEL |
| rgpc74b | | 6.04 | 207.68 | no | UMC 98 |
| si606044D05 | C | 6.04 | 208.86 | no | INDEL |
| umc113b | | 6.04 | 209.63 | no | BNL 2002 |
| pl1 | C | 6.04 | 211.50 | yes | IBM2 |
| gta105 | | 6.04 | 212.56 | no | ChromDB |
| mmc0523 | | 6.04 | 219.51 | no | SSR popII |
| tug8 | | 6.04 | 223.54 | no | BNL 96 |
| umc2006 | A C | 6.04 | 228.90 | yes | IBM2 |
| pic2a | | 6.04 | 229.71 | no | BNL 2002 |
| umc248b | | 6.04 | 230.01 | no | UMC 98 |
| agrr118a | | 6.04 | 232.64 | no | UMC 98 |
| npi253d | | 6.04 | 235.26 | no | UMC 98 |
| rz144b | A C | 6.04 | 235.26 | no | UMC 98 |
| umc2317 | C | 6.04 | 235.80 | yes | IBM2 |
| dzs23 | | 6.04 | 235.98 | no | BNL 96 |
| dup1375 | | 6.04 | 236.12 | no | BNL 2002 |
| umc1614 | | 6.04 | 236.94 | no | SSR popII |
| tda51 | | 6.04 | 238.18 | no | UMC 98 |
| rgpc643e | | 6.04 | 238.18 | no | UMC 98 |
| uat2(noi) | | 6.04 | 238.18 | no | UMC 98 |
| isu61f | | 6.04 | 238.70 | yes | IBM2 |
| hex2 | | 6.04 | 239.60 | no | BNL 96 |
| umc21 | | 6.05 | 240.80 | yes | IBM2 |
| tug6 | | 6.04 | 240.80 | no | BNL 2002 |
| npi617 | | 6.04 | 240.80 | no | BNL 2002 |
| bnlg1617 | | 6.05 | 240.80 | no | BNL 2002 |
| bnlg1922 | | 6.05 | 240.80 | no | BNL 2002 |
| PCO152525 | C | 6.04-6.05 | 241.23 | no | INDEL |
| isu111a | | 6.05 | 243.30 | no | IBM2 |
| csu578a | | 6.05 | 243.79 | no | UMC 98 |
| csu1083a | | 6.05 | 243.79 | no | UMC 98 |
| umc2318 | C | 6.05 | 244.70 | no | IBM2 |
| umc2319 | A C | 6.05 | 244.90 | yes | IBM2 |
| umc1795 | C | 6.05 | 245.29 | no | SSR popII |
| chr117d | | 6.05 | 246.60 | no | ChromDB |
| ufg11 | C | 6.05 | 248.10 | yes | IBM2 |
| umc2055 | | 6.04-6.05 | 248.62 | no | SSR popI |
| uaz280c(ppp) | | 6.05 | 251.70 | yes | IBM2 |
| asg52c | | 6.05 | 252.44 | no | UMC 98 |
| csu835 | | 6.05 | 252.44 | no | UMC 98 |
| csu382a(cld) | A C | 6.05 | 252.44 | no | UMC 98 |
| bnlg1154 | A C | 6.05 | 253.00 | no | IBM2 |
| npi265 | | 6.05 | 253.00 | no | BNL 2002 |
| umc1250 | A C | 6.05 | 254.50 | yes | IBM2 |
| umc1751 | | 6.05 | 254.50 | no | SSR popII |
| ucsd78a(zag1) | | 6.05 | 255.65 | no | BNL 2002 |
| psr108 | | 6.04 | 255.89 | no | BNL 2002 |
| tug7 | | 6.04 | 256.39 | no | BNL 2002 |
| uaz244a(prh) | | 6.04 | 258.61 | no | BNL 2002 |
| ici96 | | 6.04 | 258.87 | no | BNL 2002 |
| csu481 | | 6.05 | 261.10 | yes | IBM2 |
| csu310(ptk) | | 6.05 | 262.11 | no | UMC 98 |
| PCO146525 | C | 6.05 | 262.46 | no | INDEL |
| csu225 | | 6.05 | 262.79 | no | UMC 98 |
| umc265(ptk) | | 6.05 | 263.97 | no | UMC 98 |
| bnl3.03 | | 6.05 | 263.97 | no | BNL 96 |
| umc1826 | C | 6.05 | 267.70 | yes | IBM2 |
| zag1 | A C | 6.05 | 269.80 | yes | IBM2 |
| csu259 | | 6.05 | 269.80 | no | UMC 98 |
| umc1352 | C | 6.05 | 271.50 | yes | IBM2 |
| npi224i | | 6.04 | 272.10 | no | BNL 2002 |
| AI665560 | A C | 6.05 | 273.20 | no | IBM2 |
| umc1413 | A C | 6.05 | 277.10 | yes | IBM2 |
| uaz220(elf) | | 6.05 | 277.33 | no | BNL 2002 |
| bnlg2249 | A C | 6.05 | 278.00 | no | IBM2 |
| bnl15.37a | | 6.05 | 279.83 | no | BNL 2002 |
| csu360(elf1A) | C | 6.05 | 281.45 | no | UMC 98 |
| umc1114 | | 6.05 | 281.70 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| pge20 | | 6.05 | 282.07 | no | BNL 2002 |
| umc137b | | 6.05 | 283.65 | no | BNL 2002 |
| umc1314 | A C | 6.05 | 284.30 | no | IBM2 |
| csu1065 | | 6.05 | 286.14 | no | UMC 98 |
| csu782 | C | 6.05 | 286.14 | no | UMC 98 |
| rgpc74a | | 6.05 | 286.14 | no | UMC 98 |
| csu1189 | | 6.05 | 286.67 | no | UMC 98 |
| AY110542 | A C | 6.05 | 290.60 | yes | IBM2 |
| PCO134814 | C | 6.05 | 291.08 | no | INDEL |
| dhn1 | C | 6.05 | 291.88 | no | UMC 98 |
| uky3b(P450) | | 6.05 | 291.88 | no | UMC 98 |
| csu116a(elf1) | | 6.05 | 291.88 | no | UMC 98 |
| ynh(me2) | | 6.05 | 293.69 | no | BNL 96 |
| umc2141 | A C | 6.05 | 295.40 | yes | IBM2 |
| AY110435 | A C | 6.05 | 296.30 | no | IBM2 |
| umc1379 | C | 6.05 | 297.10 | yes | IBM2 |
| npi560 | | 6.05 | 299.20 | yes | IBM2 |
| ncr(sod3a) | | 6.05 | 299.24 | no | BNL 2002 |
| umc2040 | C | 6.05 | 299.26 | no | SSR popII |
| csu71a | | 6.01 | 299.34 | no | BNL 2002 |
| csu236 | | 6.05 | 301.80 | no | UMC 98 |
| csu60a | | 6.05 | 301.80 | no | UMC 98 |
| csu807b | | 6.05 | 301.80 | no | UMC 98 |
| npi294c | | 6.05 | 301.80 | no | UMC 98 |
| umc1388 | C | 6.05 | 302.00 | yes | IBM2 |
| mmp62 | | 6.05 | 304.10 | yes | IBM2 |
| mmc0241 | C | 6.05 | 306.59 | no | SSR popII |
| npi616a | | 6.05 | 308.30 | yes | IBM2 |
| AY110260 | A C | 6.05 | 310.70 | yes | IBM2 |
| npi252 | A C | 6.05 | 312.00 | yes | IBM2 |
| csu760a | | 6.05 | 312.07 | no | UMC 98 |
| umc46 | | 6.05 | 312.07 | no | BNL 96 |
| bcd855b(ext) | C | 6.05 | 312.07 | no | UMC 98 |
| csu666(his2A1) | | 6.05 | 312.07 | no | UMC 98 |
| dup400(pac) | | 6.05 | 313.32 | no | BNL 96 |
| jpsb107b | | 6.05 | 314.00 | yes | IBM2 |
| AY109873 | C | 6.05 | 314.80 | no | IBM2 |
| ufg16 | | 6.05 | 315.40 | no | IBM1 |
| bnlg1174 | A C | 6.05 | 315.40 | yes | IBM2 |
| chs562 | | 6.05 | 317.40 | no | BNL 96 |
| bnl17.26 | | 6.05 | 317.44 | no | BNL 2002 |
| AY110050 | A C | 6.05 | 318.60 | no | IBM2 |
| umc2321 | A C | 6.05 | 319.00 | no | IBM2 |
| chr116a | | 6.05 | 319.50 | no | ChromDB |
| bnlg1702 | | 6.05 | 320.70 | yes | IBM2 |
| AY110873 | A C | 6.05 | 321.90 | no | IBM2 |
| csu812 | | 6.05 | 322.67 | no | UMC 98 |
| umc2320 | A C | 6.05 | 322.90 | yes | IBM2 |
| csu1095 | | 6.05 | 323.36 | no | UMC 98 |
| csu1101a | | 6.05 | 323.36 | no | UMC 98 |
| mbd101b | C | 6.05 | 323.36 | no | ChromDB |
| pdk1 | A C | 6.05 | 323.50 | yes | IBM2 |
| umc1462 | | 6.06 | 325.10 | no | SSR popI |
| pmg1 | A C | 6.05 | 325.90 | yes | IBM2 |
| rgpc43b | | 6.05 | 330.59 | no | UMC 98 |
| csu581b(tua) | | 6.05 | 330.59 | no | UMC 98 |
| umc2065 | A C | 6.05 | 335.71 | no | SSR popII |
| npi608 | | 6.05 | 342.70 | yes | IBM2 |
| npi63b | | 6.05 | 342.70 | no | BNL 2002 |
| bnl5.47a | | 6.05 | 344.42 | no | BNL 96 |
| umc1805 | | 6.05 | 346.22 | no | SSR popII |
| umc1474 | A C | 6.06 | 356.72 | no | SSR popII |
| bnl8.06b | | 6.05 | 359.57 | no | BNL 96 |
| uaz400 | | 6.05 | 362.00 | no | IBM2 |
| uaz121a | | 6.05 | 362.40 | yes | IBM2 |
| mmp145 | | 6.05 | 367.40 | yes | IBM2 |
| bnl17.22 | | 6.05 | 371.76 | no | BNL 96 |
| bnlg1732 | C | 6.05 | 373.80 | yes | IBM2 |
| rz444d | C | 6.05 | 375.80 | yes | IBM2 |
| isu1410i | | 6.05 | 376.98 | no | BNL 2002 |
| mmp150 | | 6.05 | 378.40 | yes | IBM2 |
| si606039C09 | C | 6.05-6.06 | 378.99 | no | INDEL |
| uaz209 | | 6.05 | 379.02 | no | BNL 2002 |
| umc152c | | 6.05 | 380.12 | no | UMC 98 |
| bnlg345 | | 6.06 | 381.41 | no | BNL 2002 |
| umc38a | C | 6.06 | 385.80 | yes | IBM2 |
| bnlg1443 | | 6.05 | 385.80 | no | BNL 2002 |
| cdo89(aat) | | 6.05-6.06 | 385.80 | no | UMC 98 |
| bnl8.08c | | 6.06 | 387.24 | no | BNL 2002 |
| umc1912 | A C | 6.06 | 388.70 | yes | IBM2 |
| umc1859 | A C | 6.06 | 391.40 | yes | IBM2 |
| roa2 | C | 6.05-6.06 | 393.76 | no | SSR popI |
| umc1463 | C | 6.06 | 393.90 | yes | IBM2 |
| uaz256 | | 6.06 | 393.96 | no | BNL 96 |
| umc160a | | 6.06 | 393.96 | no | BNL 96 |
| umc1762 | C | 6.06 | 394.10 | yes | IBM2 |
| umc1424 | | 6.06 | 396.06 | no | SSR popI |
| CL10251_1 | C | 6.06 | 396.78 | no | INDEL |
| dup1373 | | 6.06 | 398.17 | no | BNL 2002 |
| umc2162 | C | 6.06 | 398.50 | yes | IBM2 |
| gtb101 | | 6.06 | 399.20 | no | ChromDB |
| sdg111a | | 6.06 | 399.20 | no | ChromDB |
| asg50a | | 6.06 | 400.30 | no | UMC 98 |
| umc138a | | 6.06 | 400.30 | no | UMC 98 |
| ufr1(cal) | | 6.06 | 400.30 | no | UMC 98 |
| bcd738a(pgk) | C | 6.06 | 400.30 | yes | IBM2 |
| mmp1 | | 6.06 | 401.70 | no | IBM2 |
| umc2389 | C | 6.06 | 404.12 | no | SSR popII |
| umc2322 | C | 6.06 | 404.40 | yes | IBM2 |
| AY104923 | C | 6.06 | 410.30 | yes | IBM2 |
| bnl8.08j | | 6.06 | 413.43 | no | BNL 2002 |
| npi280 | | 6.06 | 413.43 | no | BNL 96 |
| umc1520 | | 6.06 | 414.48 | no | SSR popII |
| uaz19d | | 6.06 | 419.46 | no | BNL 2002 |
| csu727(trh) | | 6.06 | 419.46 | no | UMC 98 |
| lim379 | | 6.06 | 420.40 | yes | IBM2 |
| php20904 | | 6.06 | 421.90 | no | UMC 98 |
| lim151 | | 6.06 | 423.00 | yes | IBM2 |
| gte101 | C | 6.06 | 423.70 | no | ChromDB |
| uaz243b(atpb) | | 6.06 | 424.37 | no | BNL 2002 |
| uaz43e | | 6.06 | 426.38 | no | BNL 2002 |
| AY105728 | A C | 6.06 | 426.40 | yes | IBM2 |
| AY105785 | C | 6.06 | 427.20 | yes | IBM2 |
| psr162 | | 6.06 | 428.40 | yes | IBM2 |
| umc2375 | C | 6.06-6.07 | 431.04 | no | SSR popII |
| csu841a | | 6.06 | 433.05 | no | UMC 98 |
| umc2170 | A C | 6.06 | 435.10 | yes | IBM2 |
| bnl17.12 | | 6.06 | 437.14 | no | BNL 96 |
| asg6a | | 6.06 | 441.80 | yes | IBM2 |
| hox2 | | 6.06-6.07 | 444.20 | no | UMC 98 |
| umc237 | | 6.06-6.07 | 444.20 | no | UMC 98 |
| umc132a(chk) | A C | 6.07 | 444.20 | yes | IBM2 |
| umc1296 | | 6.06-6.07 | 444.20 | no | SSR popII |
| csu238b(apx) | | 6.06-6.07 | 444.20 | no | UMC 98 |
| hdt103 | C | 6.07 | 444.70 | no | ChromDB |
| nfa102 | | 6.07 | 447.90 | yes | IBM2 |
| mmp50 | | 6.07 | 448.50 | no | IBM2 |
| umc266c(ptk) | | 6.07 | 450.13 | no | UMC 98 |
| phi299852 | A C | 6.07 | 450.70 | yes | IBM2 |
| mlg3 | A C | 6.07 | 452.70 | yes | IBM2 |
| bcd828b(atpb) | | 6.07 | 456.07 | no | UMC 98 |
| asg18 | | 6.07 | 462.00 | no | UMC 98 |
| umc1490 | A C | 6.07 | 466.50 | yes | IBM2 |
| asg47 | | 6.07 | 469.33 | no | UMC 98 |
| umc1897 | | 6.07 | 471.61 | no | SSR popII |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| AY110400 | C | 6.07 | 472.30 | yes | IBM2 |
| npi419a | | 6.07 | 481.00 | yes | IBM2 |
| csu928 | | 6.07 | 482.25 | no | UMC 98 |
| umc2323 | C | 6.07 | 483.50 | no | IBM2 |
| umc1779 | C | 6.07 | 484.29 | no | SSR popII |
| umc246 | | 6.07 | 490.63 | no | UMC 98 |
| umc238a | | 6.07 | 490.63 | no | UMC 98 |
| umc1248 | | 6.07 | 491.24 | no | SSR popII |
| mmp113 | | 6.07 | 491.80 | yes | IBM2 |
| AY109797 | AC | 6.07 | 498.70 | yes | IBM2 |
| AY104289 | AC | 6.07 | 501.20 | yes | IBM2 |
| umc2165 | AC | 6.07 | 502.90 | yes | IBM2 |
| bnlg1759a | AC | 6.07 | 503.40 | yes | IBM2 |
| uaz81 | | 6.06 | 503.87 | no | BNL 2002 |
| uaz269d(kri) | | 6.07 | 504.46 | no | BNL 2002 |
| idh2 | | 6.07 | 504.59 | no | UMC 98 |
| npi597a | | 6.07 | 504.59 | no | BNL 2002 |
| umc1350 | C | 6.07 | 504.80 | yes | IBM2 |
| bnlg1740 | C | 6.07 | 510.60 | yes | IBM2 |
| csu291 | | 6.07 | 511.22 | no | UMC 98 |
| csu293 | | 6.07 | 511.22 | no | UMC 98 |
| umc62 | C | 6.07 | 513.80 | yes | IBM2 |
| ufg(vp2274b) | | 6.06 | 513.80 | no | BNL 2002 |
| AY109996 | | 6.07 | 521.90 | yes | IBM2 |
| mdh2 | | 6.07 | 524.83 | no | UMC 98 |
| umc1621 | C | 6.07 | 526.01 | no | SSR popII |
| npi561 | | 6.07 | 526.80 | yes | IBM2 |
| bnlg1136 | C | 6.07 | 531.80 | yes | IBM2 |
| php20599 | | 6.07 | 532.80 | yes | IBM2 |
| umc133b | | 6.08 | 532.80 | no | BNL 2002 |
| mmp105 | | 6.07 | 534.60 | yes | IBM2 |
| umc1653 | C | 6.07 | 534.60 | no | IBM2 |
| agp2 | C | 6.07 | 536.40 | yes | IBM2 |
| bnlg1521 | | 6.07-6.08 | 537.12 | no | BNL 2002 |
| umc28 | | 6.08 | 538.45 | no | UMC 98 |
| asg7a | | 6.08 | 538.45 | no | SSR popII |
| uaz229 | | 6.08 | 538.45 | no | BNL 2002 |
| ufg(agp1) | | 6.08 | 538.45 | no | BNL 2002 |
| uaz123c | | 6.07-6.08 | 538.45 | no | BNL 2002 |
| PCO068526 | C | 6.08 | 540.18 | no | INDEL |
| umc1127 | | 6.07-6.08 | 540.47 | no | SSR popII |
| chr121 | | 6.07 | 541.00 | no | ChromDB |
| umc2059 | AC | 6.08 | 542.70 | yes | IBM2 |
| umc2324 | AC | 6.08 | 544.50 | yes | IBM2 |
| cdo345c | C | 6.08 | 545.80 | yes | IBM2 |
| csu68a(mcf) | | 6.08 | 548.57 | no | UMC 98 |
| cdo202a(mcf) | C | 6.08 | 548.70 | yes | IBM2 |
| umc134a | | 6.08 | 549.33 | no | UMC 98 |
| uaz240b | | 6.08 | 559.39 | no | BNL 96 |
| uor1a(rpS12) | | 6.08 | 579.29 | no | UMC 98 |
| bnlg1642 | | 7.00-7.01 | -27.20 | no | BNL 2002 |
| umc7Stelo | | 7.00 | -7.10 | no | UMC 98 |
| ucsd106b | | 7.00 | -3.80 | no | BNL 96 |
| bnlg1686 | | 7.00 | -1.40 | no | BNL 2002 |
| bnlg1367 | AC | 7.00 | -0.05 | no | BNL 2002 |
| umc2177 | | 7.00 | 0.00 | yes | IBM2 |
| csu582 | | 7.00 | 2.70 | yes | IBM2 |
| hsp3 | AC | 7.00 | 5.10 | no | IBM2 |
| bnl25 | | 7.00 | 6.76 | no | BNL 2002 |
| npi576a | | 7.00 | 10.45 | no | BNL 2002 |
| umc1241 | AC | 7.00 | 13.80 | yes | IBM2 |
| npi567 | | 7.00 | 14.80 | no | BNL 96 |
| umc1788 | AC | 7.00 | 19.90 | no | SSR popII |
| umc1642 | AC | 7.00 | 27.20 | no | IBM2 |
| umc1378 | AC | 7.00 | 27.40 | yes | IBM2 |
| rs1 | | 7.00 | 30.40 | no | BNL 96 |
| umc1672 | AC | 7.00 | 43.80 | yes | IBM2 |
| umc1694 | C | 7.00 | 45.00 | yes | IBM2 |
| umc1695 | AC | 7.00 | 45.60 | no | IBM2 |
| umc1426 | AC | 7.00 | 47.80 | yes | IBM2 |
| bnlg2132 | AC | 7.00 | 53.30 | yes | IBM2 |
| knox8b | | 7.00 | 55.07 | no | UMC 98 |
| rgpg124b | C | 7.00 | 56.77 | no | UMC 98 |
| asg8(myb) | | 7.01 | 61.30 | yes | IBM2 |
| csu251a | | 7.00-7.01 | 61.30 | no | UMC 98 |
| mmc0171 | | 7.00-7.01 | 66.28 | no | SSR popII |
| usu1b(fnr) | | 7.01 | 67.63 | no | UMC 98 |
| si945036H05 | C | 7.01 | 68.06 | no | INDEL |
| AY104465 | AC | 7.01 | 69.10 | yes | IBM2 |
| umc1840 | | 7.00-7.01 | 70.67 | no | SSR popI |
| php20581a(tb) | | 7.01 | 74.20 | yes | IBM2 |
| PCO143084 | C | 7.01 | 75.45 | no | INDEL |
| bnlg1292 | | 7.01 | 79.52 | no | BNL 2002 |
| cuny12 | | 7.01 | 79.70 | no | BNL 2002 |
| AW308691 | AC | 7.01 | 86.30 | yes | IBM2 |
| hda110 | C | 7.01 | 89.96 | no | ChromDB |
| umc1159 | AC | 7.01 | 92.00 | yes | IBM2 |
| isu84c | | 7.01 | 93.30 | no | IBM2 |
| uaz20b | | 7.01 | 96.92 | no | BNL 96 |
| csu486b | | 7.01 | 103.86 | no | UMC 98 |
| uaz83 | | 7.01 | 106.73 | no | BNL 2002 |
| umc2364 | C | 7.01 | 107.65 | no | SSR popII |
| mdh6 | | 7.01 | 109.56 | no | UMC 98 |
| csu810b | | 7.01 | 109.56 | no | UMC 98 |
| npi400a | | 7.01 | 109.56 | no | UMC 98 |
| csu129 | AC | 7.01 | 109.56 | no | UMC 98 |
| rgpc1122b(rpL15) | | 7.01 | 109.56 | no | UMC 98 |
| umc1409 | C | 7.01 | 110.59 | no | SSR popII |
| mmp18 | | 7.01 | 113.40 | yes | IBM2 |
| umc2392 | | 7.01 | 114.68 | no | SSR popII |
| mmp81 | AC | 7.01 | 115.80 | yes | IBM2 |
| umc235 | | 7.01 | 118.69 | no | UMC 98 |
| o2 | AC | 7.01 | 122.40 | yes | IBM2 |
| umc1270 | C | 7.01 | 123.50 | yes | IBM2 |
| his1a | C | 7.01 | 125.20 | yes | IBM2 |
| umc1632 | C | 7.01 | 126.30 | no | IBM2 |
| csu611b(grp) | | 7.01 | 127.46 | no | UMC 98 |
| umc2325 | AC | 7.01 | 127.60 | yes | IBM2 |
| csu794 | | 7.01 | 129.60 | no | UMC 98 |
| zds1 | | 7.02 | 130.98 | no | BNL 2002 |
| hon102 | C | 7.01 | 131.10 | no | ChromDB |
| asg34a(msd) | C | 7.02 | 132.00 | yes | IBM2 |
| umc1428 | AC | 7.01 - 7.02 | 132.00 | no | SSR popII |
| bnlg2160 | | 7.01 | 132.76 | no | BNL 2002 |
| npi294b | | 7.02 | 140.01 | no | BNL 2002 |
| isu1410c | | 7.02 | 140.01 | no | BNL 2002 |
| ast(dcm1) | | 7.02 | 140.01 | no | BNL 96 |
| gta101a | | 7.02 | 148.50 | yes | IBM2 |
| AY109536 | AC | 7.02 | 151.50 | yes | IBM2 |
| ufg1 | | 7.02 | 152.72 | no | BNL 2002 |
| uaz85 | | 7.02 | 152.72 | no | BNL 2002 |
| uaz86 | | 7.02 | 152.72 | no | BNL 2002 |
| uaz87 | | 7.02 | 152.72 | no | BNL 2002 |
| uaz88 | | 7.02 | 152.72 | no | BNL 2002 |
| in1 | | 7.02 | 152.72 | no | BNL 96 |
| bnlg1003 | | 7.02 | 152.72 | no | BNL 2002 |
| ucsd141a | | 7.02 | 152.72 | no | BNL 2002 |
| rny(pcr)d | | 7.02 | 152.72 | no | BNL 2002 |
| bnl17.13a | | 7.01 - 7.02 | 152.72 | no | BNL 2002 |
| csu93d | | 7.01 | 152.93 | no | BNL 2002 |
| umc1401 | AC | 7.02 | 153.00 | yes | IBM2 |
| umc1986 | AC | 7.02 | 153.30 | no | IBM2 |
| umc1036 | AC | 7.02 | 153.95 | no | SSR popI |
| umc2326 | AC | 7.02 | 154.80 | yes | IBM2 |
| mmp75 | | 7.02 | 155.20 | no | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| sdg101 | C | 7.02 | 155.20 | no | ChromDB |
| mmc0162 |  | 7.02 | 155.50 | no | IBM2 |
| kpp1 | C | 7.02 | 155.80 | yes | IBM2 |
| umc1978 | AC | 7.02 | 156.90 | yes | IBM2 |
| bnlg398 |  | 7.02 | 157.38 | no | BNL 2002 |
| umc2327 | AC | 7.02 | 158.00 | yes | IBM2 |
| AY105589 | AC | 7.02 | 162.40 | yes | IBM2 |
| psu2(bZip) |  | 7.02 | 164.66 | no | UMC 98 |
| csu4b |  | 7.02 | 165.01 | no | BNL 96 |
| tug9 |  | 7.02 | 165.39 | no | BNL 2002 |
| npi600 |  | 7.02 | 167.40 | yes | IBM2 |
| zpl2b |  | 7.02 | 167.40 | no | BNL 2002 |
| uaz64a |  | 7.02 | 167.40 | no | BNL 2002 |
| uaz68a(zp19) |  | 7.02 | 167.40 | no | BNL 2002 |
| umc1927 |  | 7.02 | 168.50 | no | IBM2 |
| umc1549 |  | 7.02 | 169.48 | no | SSR popI |
| crt2 | C | 7.02 | 170.80 | yes | IBM2 |
| uaz7b |  | 7.01 | 171.40 | no | BNL 2002 |
| tug5 |  | 7.02 | 171.70 | no | BNL 2002 |
| bcd98i |  | 7.02 | 171.70 | no | BNL 2002 |
| uaz173 |  | 7.02 | 174.11 | no | BNL 2002 |
| npi568 |  | 7.02 | 175.17 | no | BNL 96 |
| uaz89 |  | 7.02 | 176.23 | no | BNL 2002 |
| AY110576 | AC | 7.02 | 176.80 | yes | IBM2 |
| npi367a |  | 7.02 | 177.72 | no | BNL 2002 |
| uaz268b |  | 7.02 | 177.72 | no | BNL 2002 |
| umc(nabp1) |  | 7.02 | 177.72 | no | BNL 2002 |
| php20690b |  | 7.01 - 7.02 | 177.72 | no | BNL 96 |
| AY110473 | AC | 7.02 | 178.00 | no | IBM2 |
| cyp6 |  | 7.02 | 179.90 | yes | IBM2 |
| tda45 |  | 7.02 | 179.90 | no | UMC 98 |
| npi294e |  | 7.02 | 179.90 | no | UMC 98 |
| uaz352a |  | 7.02 | 179.90 | no | UMC 98 |
| bcd1087b |  | 7.02 | 179.90 | no | UMC 98 |
| bnl5.33g |  | 7.02 | 179.90 | no | UMC 98 |
| csu848b(vpp) |  | 7.02 | 179.90 | no | UMC 98 |
| bnlg1759b | AC | 7.02 | 179.93 | no | BNL 2002 |
| ucsd81c(zag2) |  | 7.02 | 180.26 | no | BNL 2002 |
| bnlg1094 | AC | 7.02 | 180.50 | yes | IBM2 |
| mmp187 |  | 7.02 | 181.30 | no | IBM2 |
| umc1433 | AC | 7.02 | 181.79 | no | SSR popI |
| rz509a(mip) |  | 7.02 | 181.96 | no | UMC 98 |
| psr371b |  | 7.02 | 182.60 | yes | IBM2 |
| ufg121 |  | 7.02 | 183.10 | no | IBM2 |
| umc1879 | AC | 7.02 | 183.40 | no | IBM2 |
| umc1666 |  | 7.02 | 183.40 | no | SSR popII |
| uaz187 |  | 7.02 | 183.70 | yes | IBM2 |
| mmp26 |  | 7.02 | 184.40 | no | IBM2 |
| umc270 |  | 7.02 | 184.70 | no | UMC 98 |
| rz698e(ppy) |  | 7.02 | 185.00 | no | IBM2 |
| umc112b |  | 7.02 | 185.16 | no | UMC 98 |
| uor1c(rpS12) |  | 7.02 | 185.39 | no | UMC 98 |
| rz698d(ppy) |  | 7.02 | 185.60 | yes | IBM2 |
| umc193c(orp) |  | 7.02 | 185.62 | no | UMC 98 |
| bnlg1247 | AC | 7.02 | 186.30 | yes | IBM2 |
| epl101 |  | 7.02 | 186.30 | no | ChromDB |
| vef101a | C | 7.02 | 186.30 | no | ChromDB |
| bnlg2233 |  | 7.02 | 186.50 | yes | IBM2 |
| bnlg1380 | C | 7.02 | 188.10 | yes | IBM2 |
| csu7a |  | 7.02 | 188.73 | no | BNL 96 |
| zpc2 |  | 7.02 | 189.97 | no | BNL 2002 |
| ciw(S10) |  | 7.02 | 190.16 | no | BNL 2002 |
| zp50 |  | 7.00-7.01 | 190.19 | no | BNL 2002 |
| bnlg1792 | AC | 7.02 | 190.40 | no | IBM2 |
| bnlg2203 | AC | 7.02 | 190.60 | yes | IBM2 |
| hag102 | C | 7.02 | 190.60 | no | ChromDB |
| sdg110 |  | 7.02 | 190.70 | no | ChromDB |
| mpik4a |  | 7.02 | 190.78 | no | BNL 2002 |
| uaz19b |  | 7.02 | 190.78 | no | BNL 2002 |
| npi596 |  | 7.02 | 190.90 | no | BNL 2002 |
| bnlg1200 |  | 7.01 | 190.98 | no | BNL 2002 |
| AY109809 | C | 7.02 | 192.50 | yes | IBM2 |
| lim333 |  | 7.02 | 195.60 | yes | IBM2 |
| npi224a |  | 7.02 | 197.63 | no | BNL 96 |
| uaz143 |  | 7.02 | 199.79 | no | BNL 2002 |
| umc1932 | AC | 7.02 | 204.80 | yes | IBM2 |
| CL4745_2 | C | 7.02 | 207.60 | no | INDEL |
| ucsd107b |  | 7.02 | 212.37 | no | BNL 2002 |
| chs606 |  | 7.02 | 212.84 | no | BNL 2002 |
| psr3a |  | 7.02 | 212.88 | no | BNL 2002 |
| npi111 |  | 7.02 | 212.88 | no | BNL 2002 |
| npi221a |  | 7.02 | 212.88 | no | BNL 2002 |
| bnl15.40 |  | 7.02 | 212.88 | no | BNL 96 |
| umc1339 |  | 7.02 | 214.12 | no | SSR popII |
| uaz351a(rpS12) |  | 7.02 | 215.06 | no | UMC 98 |
| bcd450c |  | 7.02 | 215.54 | no | UMC 98 |
| gl1 |  | 7.02 | 217.75 | no | BNL 2002 |
| csu11 |  | 7.02 | 217.96 | no | UMC 98 |
| csu233 |  | 7.02 | 217.96 | no | UMC 98 |
| csu936 |  | 7.02 | 217.96 | no | UMC 98 |
| csu241c |  | 7.02 | 217.96 | no | UMC 98 |
| csu281a |  | 7.02 | 217.96 | no | UMC 98 |
| csu919b |  | 7.02 | 217.96 | no | UMC 98 |
| uaz84 |  | 7.02 | 217.96 | no | BNL 2002 |
| csu81a(ank) |  | 7.02 | 217.96 | no | UMC 98 |
| bnlg1579 |  | 7.03 | 220.72 | no | BNL 2002 |
| zpb36 |  | 7.02 | 227.28 | no | BNL 96 |
| AY109968 | AC | 7.02 | 228.70 | yes | IBM2 |
| umc1983 | AC | 7.02 | 244.30 | yes | IBM2 |
| umc2142 | AC | 7.02 | 246.30 | yes | IBM2 |
| umc1138 | C | 7.02 | 247.70 | yes | IBM2 |
| umc1929 | AC | 7.02 | 249.10 | yes | IBM2 |
| umc2057 |  | 7.02 | 249.87 | no | SSR popI |
| npi112a |  | 7.02 | 251.86 | no | BNL 96 |
| umc1787 | AC | 7.02 | 252.40 | yes | IBM2 |
| umc2092 | AC | 7.02 | 252.90 | yes | IBM2 |
| PCO115023 | C | 7.02 | 254.02 | no | INDEL |
| umc1393 | AC | 7.02 | 258.40 | yes | IBM2 |
| umc258 | C | 7.02 | 259.00 | no | IBM2 |
| umc98b |  | 7.02 | 259.00 | no | UMC 98 |
| bnlg1164 |  | 7.02 | 260.11 | no | BNL 2002 |
| umc1585 | AC | 7.02 | 261.03 | no | SSR popII |
| npi47b |  | 7.02 | 261.39 | no | BNL 2002 |
| umc5b | C | 7.02 | 261.50 | yes | IBM2 |
| isu86 |  | 7.02 | 262.50 | yes | IBM2 |
| mmp21 |  | 7.02 | 265.30 | no | IBM2 |
| bnlg657 |  | 7.02 | 276.79 | no | BNL 2002 |
| bnlg1022a |  | 7.02 | 277.98 | no | SSR popII |
| umc1881 |  | 7.02 | 280.19 | no | SSR popII |
| ufg54 |  | 7.02 | 280.50 | yes | IBM2 |
| ufg65 | C | 7.02 | 280.70 | no | IBM2 |
| cdo412b |  | 7.02 | 285.40 | yes | IBM2 |
| bnlg1808 |  | 7.02 | 286.30 | yes | IBM2 |
| asg49 | AC | 7.03 | 286.57 | no | SSR popII |
| uaz205c(hsp70) |  | 7.02-7.03 | 286.57 | no | UMC 98 |
| dupssr11 |  | 7.02-7.03 | 287.70 | no | BNL 2002 |
| dupssr9 |  | 7.02-7.03 | 288.18 | no | BNL 2002 |
| umc116a |  | 7.03 | 288.90 | yes | IBM2 |
| mmp127 |  | 7.03 | 290.20 | yes | IBM2 |
| mmc0411 |  | 7.03 | 292.70 | yes | IBM2 |
| umc1713 | AC | 7.03 | 298.40 | yes | IBM2 |
| php20569a | AC | 7.03 | 300.00 | yes | IBM2 |
| umc1567 |  | 7.03 | 300.00 | no | SSR popII |
| bcd926a | C | 7.03 | 307.40 | yes | IBM2 |
| bnl15.21 |  | 7.03 | 309.90 | yes | IBM2 |
| bnl15.37b |  | 7.03 | 310.09 | no | UMC 98 |
| bnl5.46c |  | 7.03 | 310.60 | no | IBM2 |
| csu274(hsp90) |  | 7.03 | 311.43 | no | UMC 98 |
| mmp177c |  | 7.03 | 314.70 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| tda37b | | 7.03 | 314.87 | no | UMC 98 |
| csu395c | C | 7.03 | 314.87 | no | UMC 98 |
| umc1450 | C | 7.03 | 315.90 | yes | IBM2 |
| umc1987 | A C | 7.03 | 318.00 | yes | IBM2 |
| mmp46 | | 7.03 | 319.60 | yes | IBM2 |
| bnlg1070 | A C | 7.03 | 322.70 | yes | IBM2 |
| bnlg1305 | | 7.03 | 322.77 | no | BNL 2002 |
| npi122 | | 7.03 | 322.83 | no | BNL 2002 |
| bnlg434 | A C | 7.03 | 323.30 | yes | IBM2 |
| ij1 | A C | 7.03 | 324.42 | no | UMC 98 |
| umc222(fgh) | | 7.03 | 324.42 | no | UMC 98 |
| umc1333 | | 7.03 | 325.00 | no | SSR popII |
| csu296 | | 7.03 | 327.48 | no | UMC 98 |
| umc1456 | | 7.03 | 329.65 | no | SSR popII |
| npi394 | A C | 7.03 | 330.60 | yes | IBM2 |
| mpik27b(zmm7) | | 7.03 | 333.28 | no | UMC 98 |
| uaz123d | | 7.03 | 334.64 | no | BNL 2002 |
| uaz118b | | 7.03 | 335.59 | no | BNL 2002 |
| csu253 | | 7.03 | 336.64 | no | UMC 98 |
| bnlg339 | A C | 7.03 | 336.64 | no | SSR popI |
| umc1718 | C | 7.03 | 338.66 | no | SSR popII |
| PCO071075 | C | 7.03 | 342.21 | no | INDEL |
| umc1275 | C | 7.03 | 344.76 | no | SSR popII |
| brd103 | | 7.03 | 344.80 | no | ChromDB |
| mmp152 | | 7.03 | 345.40 | yes | IBM2 |
| AY110374 | A C | 7.03 | 347.20 | yes | IBM2 |
| umc1660 | C | 7.03 | 351.40 | yes | IBM2 |
| sdg116a | | 7.03 | 353.60 | no | ChromDB |
| rz596c | | 7.03 | 354.02 | no | IBM1 |
| npi389 | | 7.03 | 354.90 | yes | IBM2 |
| npi455a | | 7.03 | 354.90 | no | BNL 2002 |
| umc1481 | | 7.03 | 356.97 | no | SSR popII |
| ucsd106g | | 7.03 | 358.39 | no | BNL 2002 |
| umc56 | C | 7.03 | 361.90 | yes | IBM2 |
| umc110a | | 7.03 | 364.80 | yes | IBM2 |
| umc1408 | C | 7.03 | 365.40 | no | IBM2 |
| umc1837 | A C | 7.03 | 368.90 | yes | IBM2 |
| csu820 | | 7.03 | 369.88 | no | UMC 98 |
| csu1124 | | 7.03 | 371.46 | no | UMC 98 |
| umc149a | | 7.03 | 372.10 | no | UMC 98 |
| rz404(ccp) | C | 7.03 | 374.00 | yes | IBM2 |
| si614054G01 | C | 7.03 | 375.11 | no | INDEL |
| bnl6.27 | | 7.03 | 375.61 | no | BNL 96 |
| bnlg155 | | 7.03 | 376.90 | yes | IBM2 |
| PCO101826 | C | 7.03 | 377.90 | no | INDEL |
| umc111b(psy) | | 7.03 | 379.00 | yes | IBM2 |
| umc1865 | A C | 7.03 | 380.60 | no | IBM2 |
| umc1841 | | 7.03 | 380.60 | no | SSR popI |
| umc1134 | A C | 7.03 | 381.20 | yes | IBM2 |
| isu84a | | 7.03 | 381.50 | no | IBM2 |
| mmp194 | | 7.03 | 381.50 | no | IBM2 |
| umc2328 | A C | 7.03 | 381.50 | no | IBM2 |
| AY109644 | A C | 7.03 | 381.50 | no | IBM2 |
| nfd101a | | 7.03 | 381.60 | no | ChromDB |
| psr371a | | 7.03 | 381.80 | yes | IBM2 |
| ndk1 | | 7.03 | 382.60 | yes | IBM2 |
| bnlg2271 | C | 7.03 | 383.80 | yes | IBM2 |
| npi283a | | 7.04 | 383.84 | no | BNL 2002 |
| umc2329 | A C | 7.03 | 384.40 | no | IBM2 |
| umc1112 | A C | 7.03 | 385.10 | yes | IBM2 |
| uaz91(ndk) | | 7.04 | 385.50 | no | BNL 2002 |
| uaz31c | | 7.04 | 385.74 | no | BNL 2002 |
| tum2 | | 7.02-7.06 | 385.97 | no | BNL 2002 |
| csh2b(cdc2) | | 7.03 | 385.97 | no | BNL 2002 |
| bnl13.24 | | 7.04 | 386.44 | no | BNL 2002 |
| umc1324 | A C | 7.03 | 387.50 | yes | IBM2 |
| umc1888 | A C | 7.03 | 390.50 | yes | IBM2 |
| oec6 | A C | 7.03 | 391.00 | no | SSR popI |
| bnlg1805 | A C | 7.03 | 392.10 | yes | IBM2 |
| bnlg572 | | 7.03 | 392.19 | no | BNL 2002 |
| uaz28a | | 7.04 | 392.46 | no | BNL 2002 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| npi435 | | 7.04 | 392.71 | no | BNL 96 |
| isu150 | | 7.03 | 393.10 | yes | IBM2 |
| uaz221(his2a) | | 7.03 | 393.61 | no | BNL 2002 |
| bcd249i | | 7.04 | 394.42 | no | BNL 2002 |
| uaz224(eif2) | | 7.02 | 394.42 | no | BNL 2002 |
| rz596a | | 7.03 | 395.26 | no | IBM1 |
| ias5 | | 7.04 | 395.32 | no | BNL 2002 |
| tif1 | | 7.03 | 399.30 | yes | IBM2 |
| ast(amyBS2)a | | 7.04 | 401.26 | no | BNL 96 |
| psr135a | | 7.03 | 403.40 | yes | IBM2 |
| umc1301 | A C | 7.03 | 405.50 | yes | IBM2 |
| umc1936 | A C | 7.03 | 405.50 | yes | IBM2 |
| umc1001 | | 7.03 | 407.23 | no | SSR popII |
| PCO102751 | C | 7.03-7.04 | 407.78 | no | INDEL |
| umc254 | | 7.04 | 408.10 | yes | IBM2 |
| asg5 | | 7.03-7.04 | 408.10 | no | UMC 98 |
| bas1 | | 7.03-7.04 | 408.10 | no | UMC 98 |
| csh14 | | 7.03-7.04 | 408.10 | no | UMC 98 |
| rgpg20 | | 7.03-7.04 | 408.10 | no | UMC 98 |
| bnl4.24 | | 7.03-7.04 | 408.10 | no | UMC 98 |
| uor2(crp) | | 7.03-7.04 | 408.10 | no | UMC 98 |
| rz753(cdpk) | | 7.03-7.04 | 408.10 | no | UMC 98 |
| csu229a(oec) | | 7.03-7.04 | 408.10 | no | UMC 98 |
| cdo59a(gos2) | C | 7.03-7.04 | 408.10 | no | UMC 98 |
| umc2330 | C | 7.04 | 408.40 | no | IBM2 |
| umc2331 | C | 7.04 | 408.40 | no | IBM2 |
| uaz90 | | 7.04 | 409.99 | no | BNL 2002 |
| umc1710 | C | 7.04 | 410.50 | yes | IBM2 |
| umc1251 | C | 7.04 | 412.10 | yes | IBM2 |
| umc1684 | | 7.03 | 414.15 | no | SSR popI |
| asg32 | C | 7.04 | 416.50 | yes | IBM2 |
| csu847b(lhcb) | | 7.04 | 416.50 | no | UMC 98 |
| bnl5.21a | | 7.04 | 423.77 | no | UMC 98 |
| bnl5.61a | | 7.04 | 423.77 | no | UMC 98 |
| csu21d(ago) | | 7.04 | 423.77 | no | UMC 98 |
| umc2062 | | 7.04 | 426.40 | no | SSR popII |
| ufg17 | C | 7.04 | 427.50 | yes | IBM2 |
| AY110023 | C | 7.04 | 429.20 | no | IBM2 |
| bnlg1666 | C | 7.04 | 430.50 | yes | IBM2 |
| uaz117c | | 7.04 | 430.55 | no | BNL 2002 |
| uaz200 | | 7.03 | 430.56 | no | BNL 2002 |
| uaz225(lox) | | 7.04 | 430.57 | no | BNL 2002 |
| npi413b | | 7.04 | 430.66 | no | BNL 2002 |
| bnlg1161 | | 7.04 | 430.67 | no | BNL 2002 |
| uaz199 | | 7.04 | 430.82 | no | UMC 98 |
| uaz207 | | 7.04 | 430.82 | no | UMC 98 |
| csu213a | | 7.04 | 430.82 | no | UMC 98 |
| npi240a | | 7.04 | 432.30 | yes | IBM2 |
| npi263 | | 7.04 | 433.20 | yes | IBM2 |
| tda66c | | 7.04 | 438.65 | no | UMC 98 |
| npi352 | | 7.04 | 439.90 | yes | IBM2 |
| csu1055 | | 7.04 | 440.22 | no | UMC 98 |
| csu818b(lhca) | | 7.04 | 440.22 | no | UMC 98 |
| chr111 | C | 7.04 | 441.90 | no | ChromDB |
| bnl8.29c | | 7.04 | 442.30 | yes | IBM2 |
| umc1029 | C | 7.04 | 444.70 | yes | IBM2 |
| umc1342 | C | 7.04 | 444.70 | no | SSR popII |
| tua6 | | 7.04 | 447.27 | no | UMC 98 |
| bnl8.32 | | 7.04 | 447.27 | no | UMC 98 |
| csu749a | | 7.04 | 447.27 | no | UMC 98 |
| umc125b | | 7.04 | 447.27 | no | UMC 98 |
| npi217 | | 7.04 | 447.27 | no | BNL 2002 |
| uaz92 | | 7.03 | 447.28 | no | BNL 2002 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| uaz922 | | 7.03 | 447.28 | no | BNL 2002 |
| uaz233c(act) | | 7.03 | 447.28 | no | BNL 2002 |
| uaz82 | | 7.03 | 447.43 | no | BNL 2002 |
| php20563a | | 7.04 | 449.33 | no | BNL 2002 |
| umc1593a | | 7.03 | 450.17 | no | SSR popI |
| uaz123a | | 7.02 | 451.00 | no | BNL 2002 |
| bnlg1892a | C | 7.04 | 452.76 | no | BNL 2002 |
| bcd249b | | 7.04 | 453.19 | no | BNL 2002 |
| ukd(hotr) | | 7.04 | 453.19 | no | BNL 2002 |
| rip2 | | 7.04 | 453.91 | no | SSR popII |
| e1 | | 7.04 | 455.10 | no | UMC 98 |
| csu996 | | 7.04 | 455.10 | no | UMC 98 |
| bnl7.61 | | 7.04 | 455.10 | no | UMC 98 |
| bnl8.21a | | 7.04 | 455.10 | no | UMC 98 |
| bnl8.37a | | 7.04 | 455.10 | no | UMC 98 |
| bnl14.07 | C | 7.04 | 455.10 | no | UMC 98 |
| umc1543 | | 7.04 | 457.44 | no | SSR popI |
| mus1 | | 7.04 | 459.33 | no | BNL 2002 |
| pge3 | | 7.04 | 459.33 | no | BNL 2002 |
| ncr(b32c3b) | | 7.04 | 459.33 | no | BNL 2002 |
| isc(b32b) | | 7.04 | 459.33 | no | BNL 96 |
| uaz292(gdh) | | 7.04 | 464.18 | no | BNL 2002 |
| bcd349 | | 7.04 | 464.50 | yes | IBM2 |
| npi398b | | 7.04 | 465.04 | no | BNL 2002 |
| umc1944 | | 7.04 | 466.00 | no | SSR popI |
| csu5 | C | 7.04 | 468.72 | no | UMC 98 |
| umc1708 | C | 7.04 | 471.40 | yes | IBM2 |
| rgpc12a | | 7.04 | 472.17 | no | UMC 98 |
| umc137d | | 7.04 | 472.17 | no | UMC 98 |
| csu175d(eif5A) | | 7.04 | 472.17 | no | UMC 98 |
| umc2332 | C | 7.04 | 472.60 | yes | IBM2 |
| phi328175 | C | 7.04 | 472.90 | no | IBM2 |
| AY110439 | C | 7.04 | 473.00 | yes | IBM2 |
| ufg79 | | 7.04 | 473.40 | no | IBM2 |
| rgpr440b(gap) | | 7.04 | 475.40 | no | UMC 98 |
| bnl8.39 | | 7.04 | 475.51 | no | BNL 96 |
| dupssr13 | | 7.04 | 475.77 | no | BNL 2002 |
| csu8 | | 7.04 | 476.00 | yes | IBM2 |
| rz395 | | 7.04 | 476.00 | no | UMC 98 |
| umc1768 | C | 7.04 | 481.10 | yes | IBM2 |
| asg14a | | 7.04 | 487.51 | no | UMC 98 |
| asg36a | | 7.04 | 487.51 | no | UMC 98 |
| bnlg2259 | C | 7.04 | 489.20 | yes | IBM2 |
| umc1103 | C | 7.04 | 493.39 | no | SSR popII |
| umc1295 | C | 7.04 | 494.80 | yes | IBM2 |
| csu906 | | 7.04 | 497.10 | no | UMC 98 |
| ufg57 | C | 7.04 | 497.60 | yes | IBM2 |
| uaz119b(rpS6) | | 7.04 | 505.23 | no | BNL 96 |
| csu904 | | 7.04 | 511.67 | no | UMC 98 |
| rgpr663b | | 7.04 | 511.67 | no | UMC 98 |
| csu597c(dah) | C | 7.04 | 511.67 | no | UMC 98 |
| bnlg2328b | | 7.05 | 517.41 | no | BNL 2002 |
| AW267377 | C | 7.04 | 517.50 | no | IBM2 |
| umc1412 | C | 7.04 | 518.90 | yes | IBM2 |
| uaz241a | | 7.04 | 520.70 | no | BNL 2002 |
| uaz245(gbp) | | 7.04 | 520.70 | no | BNL 2002 |
| umc1125 | C | 7.04 | 522.79 | no | SSR popII |
| umc80a | | 7.04 | 524.71 | no | UMC 98 |
| PCO136133 | C | 7.04-7.05 | 525.04 | no | INDEL |
| PCO061754 | C | 7.04-7.05 | 529.89 | no | INDEL |
| umc245 | | 7.05 | 532.00 | yes | IBM2 |
| umc151 | | 7.04-7.05 | 532.00 | no | UMC 98 |
| umc251 | | 7.04-7.05 | 532.00 | no | UMC 98 |
| npi380 | | 7.05 | 533.70 | yes | IBM2 |
| rgpr44c | | 7.05 | 535.19 | no | UMC 98 |
| php20523a | | 7.05 | 535.71 | no | BNL 96 |
| npi433 | | 7.05 | 536.70 | yes | IBM2 |
| ias4b | | 7.04 | 536.70 | no | BNL 2002 |
| npi385 | | 7.04 | 536.96 | no | BNL 2002 |
| csu894b | | 7.05 | 537.27 | no | UMC 98 |
| npi113a | | 7.05 | 537.27 | no | BNL 96 |
| php20593 | | 7.05 | 537.77 | no | UMC 98 |
| php20909b | | 7.05 | 538.70 | yes | IBM2 |
| npi300b | | 7.04 | 539.25 | no | BNL 2002 |
| asg28b | | 7.05 | 540.74 | no | UMC 98 |
| csu920b | | 7.05 | 540.74 | no | UMC 98 |
| bnl16.06 | | 7.05 | 540.74 | no | UMC 98 |
| mmp67 | | 7.05 | 540.80 | no | IBM2 |
| php20690a | | 7.05 | 542.71 | no | UMC 98 |
| csu1106 | | 7.05 | 542.93 | no | UMC 98 |
| csu1097a | | 7.05 | 542.93 | no | UMC 98 |
| mmp25 | | 7.05 | 543.40 | no | IBM2 |
| ncr(sod2) | | 7.05 | 543.51 | no | BNL 2002 |
| umc2368 | | 7.05 | 544.55 | no | SSR popII |
| phi069 | | 7.05 | 545.20 | yes | IBM2 |
| umc1671 | A C | 7.05 | 547.28 | no | SSR popII |
| umc45 | | 7.05 | 547.30 | no | UMC 98 |
| umc91a | | 7.05 | 547.30 | no | UMC 98 |
| csu27 | A C | 7.05 | 547.30 | no | UMC 98 |
| csu578b | | 7.05 | 547.30 | no | UMC 98 |
| mmp17 | | 7.05 | 547.70 | no | IBM2 |
| umc2379 | C | 7.05-7.06 | 555.46 | no | SSR popII |
| bnl8.44a | | 7.05 | 558.45 | no | UMC 98 |
| csu163a | A C | 7.05 | 558.45 | no | UMC 98 |
| std16c(blr) | | 7.05 | 558.45 | no | UMC 98 |
| umc1154 | A C | 7.05 | 558.55 | no | SSR popII |
| csu632b | | 7.05 | 564.79 | no | UMC 98 |
| cdo38b(ntp) | A C | 7.05 | 564.79 | no | UMC 98 |
| csu814a | | 7.05 | 568.07 | no | UMC 98 |
| bnlg469c | C | 7.05 | 572.56 | no | BNL 2002 |
| pbs7 | | 7.06 | 584.14 | no | BNL 2002 |
| cdo938d | | 7.05 | 586.60 | yes | IBM2 |
| umc2197 | C | 7.05 | 587.92 | no | SSR popI |
| umc2333 | A C | 7.05 | 593.40 | yes | IBM2 |
| umc2222 | | 7.05 | 598.35 | no | SSR popI |
| umc1406 | A C | 7.05 | 598.90 | yes | IBM2 |
| umc35a | C | 7.05 | 600.20 | no | IBM1 |
| umc1407 | A C | 7.05 | 600.20 | yes | IBM2 |
| umc2334 | A C | 7.05-7.06 | 600.40 | no | IBM2 |
| umc1799 | | 7.04-7.06 | 600.79 | no | SSR popI |
| ufg39 | C | 7.05 | 602.90 | yes | IBM2 |
| umc1760 | A C | 7.05 | 607.60 | no | IBM2 |
| umc168 | A C | 7.06 | 608.20 | yes | IBM2 |
| npi45b | | 7.06 | 608.20 | no | BNL 2002 |
| kin1 | | 7.06 | 609.01 | no | BNL 2002 |
| phi116 | A C | 7.06 | 611.50 | yes | IBM2 |
| php20020 | | 7.06 | 611.90 | yes | IBM2 |
| csu705 | | 7.05-7.06 | 611.90 | no | UMC 98 |
| npi611a | | 7.06 | 614.80 | yes | IBM2 |
| php20728 | | 7.06 | 615.42 | no | BNL 96 |
| abg373 | | 7.06 | 616.31 | no | BNL 2002 |
| AY109703 | A C | 7.06 | 618.40 | yes | IBM2 |
| bnl(tas1j) | | 7.06 | 640.08 | no | BNL 96 |
| pbs13d | | 8.00-8.02 | -43.20 | no | BNL 96 |
| cuny19 | | 8.00 | -35.19 | no | BNL 2002 |
| pbs6c | | 8.00 | -34.86 | no | BNL 2002 |
| npi220a | C | 8.01 | 0.00 | yes | IBM2 |
| csu891(rpL30) | | 8.00-8.01 | 0.00 | no | UMC 98 |
| csu597b(dah) | C | 8.00-8.01 | 1.36 | no | UMC 98 |
| csu319 | | 8.01 | 5.90 | yes | IBM2 |
| rz382b | | 8.01 | 6.70 | yes | IBM2 |
| npi114a | | 8.01 | 10.10 | yes | IBM2 |
| umc1786 | C | 8.01 | 10.58 | no | SSR popII |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| rz995a(fbp) | | 8.00-8.01 | 10.68 | no | UMC 98 |
| csu312 | | 8.00-8.01 | 11.56 | no | UMC 98 |
| npi222b | | 8.01 | 14.22 | no | BNL 2002 |
| csu1076 | | 8.00-8.01 | 17.96 | no | UMC 98 |
| csu368(phr) | | 8.00-8.01 | 17.96 | no | UMC 98 |
| umc1139 | A C | 8.01 | 26.80 | yes | IBM2 |
| umc2042 | | 8.01 | 30.30 | yes | IBM2 |
| mmp148 | | 8.01 | 31.80 | yes | IBM2 |
| umc1592 | | 8.01 | 33.80 | yes | IBM2 |
| bnl13.05c | | 8.01 | 36.48 | no | SSR popI |
| rnp2 | | 8.01 | 40.68 | no | UMC 98 |
| csu29c | C | 8.01 | 40.68 | no | UMC 98 |
| bnlg1252 | | 8.00-8.01 | 42.39 | no | BNL 2002 |
| bnl8.08k | | 8.01 | 42.69 | no | BNL 2002 |
| bnl13.05a | | 8.01 | 44.40 | yes | IBM2 |
| umc1414 | | 8.01 | 48.00 | yes | IBM2 |
| CL16874_1 | C | 8.01 | 49.05 | no | INDEL |
| AY109699 | A C | 8.01 | 49.40 | yes | IBM2 |
| umc1327 | A C | 8.01 | 55.00 | yes | IBM2 |
| umc1075 | | 8.01 | 59.88 | no | SSR popII |
| ufg38 | | 8.01 | 64.52 | no | IBM1 |
| ncr(sod3b) | | 8.01 | 70.23 | no | BNL 96 |
| ufg61 | | 8.01 | 74.41 | no | IBM1 |
| csu332 | | 8.01 | 74.41 | no | UMC 98 |
| mpik41b(mem1) | | 8.01 | 74.41 | no | UMC 98 |
| umc1483 | A C | 8.01 | 83.10 | yes | IBM2 |
| isu1410a | | 8.02 | 84.14 | no | BNL 96 |
| csu675b(prh) | C | 8.01 | 98.40 | no | UMC 98 |
| mmp85 | | 8.01 | 99.60 | yes | IBM2 |
| bnlg1194 | A C | 8.02 | 105.40 | yes | IBM2 |
| bnl9.11a(lts) | A C | 8.02 | 106.40 | no | SSR popII |
| umc2352 | A C | 8.02 | 107.30 | yes | IBM2 |
| hon107b | C | 8.02 | 110.33 | no | ChromDB |
| npi110a | | 8.02 | 112.00 | yes | IBM2 |
| npi218a | | 8.02 | 112.00 | no | BNL 2002 |
| bnlg2037 | | 8.01 | 114.45 | no | BNL 2002 |
| cdo460 | | 8.02 | 115.10 | yes | IBM2 |
| umc1817 | A C | 8.02 | 115.30 | no | IBM2 |
| rz543b | C | 8.02 | 115.32 | no | UMC 98 |
| mmp57 | | 8.02 | 116.40 | yes | IBM2 |
| bnlg1073 | | 8.01 | 116.62 | no | BNL 2002 |
| mpik17d | | 8.02 | 126.57 | no | BNL 2002 |
| pic8b | | 8.02 | 127.80 | no | BNL 2002 |
| umc1304 | A C | 8.02 | 128.60 | yes | IBM2 |
| umc2004 | | 8.02 | 131.95 | no | SSR popII |
| bnlg2235 | A C | 8.02 | 132.40 | yes | IBM2 |
| bnlg1352 | | 8.02 | 132.40 | no | BNL 2002 |
| rgpc131b | A C | 8.02 | 133.53 | no | UMC 98 |
| chr117a | | 8.02 | 135.00 | no | ChromDB |
| bcd1823b | | 8.02 | 135.60 | no | IBM1 |
| bcd1823a | | 8.02 | 135.60 | yes | IBM2 |
| AY106269 | A C | 8.02 | 136.80 | yes | IBM2 |
| mmp166 | | 8.02 | 139.70 | yes | IBM2 |
| umc1790 | | 8.02 | 142.80 | no | SSR popII |
| umc103a | | 8.02 | 145.42 | no | UMC 98 |
| npi585a | | 8.02 | 149.00 | yes | IBM2 |
| npi276b | | 8.02 | 149.00 | no | BNL 2002 |
| csu949b | | 8.02 | 152.49 | no | UMC 98 |
| umc1974 | A C | 8.02 | 153.30 | yes | IBM2 |
| umc1872 | | 8.02 | 153.30 | no | SSR popII |
| hsp18c | | 8.02 | 155.66 | no | BNL 2002 |
| tpi3 | | 8.02 | 156.27 | no | BNL 2002 |
| wusl1042 | | 8.02 | 156.27 | no | BNL 2002 |
| psr598 | | 8.02 | 156.60 | yes | IBM2 |
| cdo328 | A C | 8.02 | 159.20 | yes | IBM2 |
| umc1913 | A C | 8.02 | 160.80 | yes | IBM2 |
| bnl21 | | 8.02 | 163.70 | no | BNL 2002 |
| uaz252b(ptk) | | 8.03 | 164.29 | no | BNL 2002 |
| uaz243c(atpb) | | 8.03 | 164.29 | no | BNL 2002 |
| uaz251a(rpS11) | | 8.03 | 164.29 | no | BNL 2002 |
| bcd98b | | 8.02 | 169.48 | no | BNL 2002 |
| bnlg669 | | 8.03 | 174.17 | no | BNL 2002 |
| bnlg1067 | | 8.03 | 174.17 | no | BNL 2002 |
| umc1868 | | 8.02 | 175.50 | no | SSR popII |
| csu329 | | 8.02 | 175.90 | yes | IBM2 |
| klp1b | | 8.02-8.03 | 176.60 | no | UMC 98 |
| umc124a(chk) | | 8.03 | 176.60 | yes | IBM2 |
| umc1530 | C | 8.03 | 179.50 | yes | IBM2 |
| umc1778 | C | 8.03 | 180.53 | no | SSR popII |
| mmp120 | | 8.03 | 191.00 | yes | IBM2 |
| tda52 | | 8.03 | 193.25 | no | UMC 98 |
| umc1034 | A C | 8.02-8.03 | 193.83 | no | SSR popI |
| CL51477_1 | C | 8.03 | 193.96 | no | INDEL |
| mmp72 | | 8.03 | 194.10 | yes | IBM2 |
| csu849(atpb) | | 8.03 | 195.50 | no | UMC 98 |
| umc2147 | A C | 8.03 | 197.10 | no | IBM2 |
| mmp158b | | 8.03 | 197.90 | yes | IBM2 |
| umc2146 | A C | 8.03 | 198.40 | no | IBM2 |
| umc32b | C | 8.03 | 199.10 | yes | IBM2 |
| bnlg2082 | C | 8.03 | 200.30 | yes | IBM2 |
| AW244963 | | 8.03 | 202.00 | yes | IBM2 |
| umc2353 | C | 8.03 | 203.00 | no | IBM2 |
| AY110450 | A C | 8.03 | 203.00 | no | IBM2 |
| umc120a | | 8.03 | 203.60 | no | IBM2 |
| ksu1c | | 8.03 | 203.90 | no | UMC 98 |
| csu279 | | 8.03 | 203.90 | no | UMC 98 |
| csu910 | | 8.03 | 203.90 | no | UMC 98 |
| csu1175 | | 8.03 | 203.90 | no | UMC 98 |
| umc236 | C | 8.03 | 203.90 | no | UMC 98 |
| umc238b | | 8.03 | 203.90 | no | UMC 98 |
| rz244a(dia) | | 8.03 | 203.90 | yes | IBM2 |
| umc206(hsp70) | | 8.03 | 203.90 | no | UMC 98 |
| bnlg1834 | A C | 8.03 | 204.80 | yes | IBM2 |
| chr110b | | 8.03 | 204.80 | no | ChromDB |
| umc1807 | | 8.03 | 205.80 | yes | IBM2 |
| umc1157 | A C | 8.03 | 206.00 | yes | IBM2 |
| umc1904 | A C | 8.03 | 206.60 | yes | IBM2 |
| npi260b | | 8.03 | 211.00 | yes | IBM2 |
| rpa5c | | 8.03 | 215.06 | no | UMC 98 |
| gpa1 | | 8.03 | 215.11 | no | UMC 98 |
| lhcb3 | | 8.03 | 215.11 | no | UMC 98 |
| tda164 | | 8.03 | 215.11 | no | UMC 98 |
| rgpc161 | | 8.03 | 215.11 | no | UMC 98 |
| cdo1160a(kri) | C | 8.03 | 215.60 | yes | IBM2 |
| umc2354 | C | 8.03 | 216.20 | no | IBM2 |
| umc1910 | | 8.03 | 216.90 | yes | IBM2 |
| asg24b(gts) | C | 8.03 | 217.14 | no | SSR popI |
| stp1 | | 8.03 | 217.46 | no | UMC 98 |
| mmp195f | | 8.03 | 220.60 | yes | IBM2 |
| mpik35f | | 8.02 | 221.77 | no | BNL 2002 |
| cdo202e(mcf) | C | 8.03 | 224.80 | yes | IBM2 |
| php3818 | | 8.03 | 226.10 | yes | IBM2 |
| zmm2 | | 8.02 | 226.26 | no | BNL 2002 |
| mpik12b | | 8.02 | 226.26 | no | BNL 2002 |
| mpik15d | | 8.02 | 226.26 | no | BNL 2002 |
| mpik15e | | 8.02 | 226.26 | no | BNL 2002 |
| mpik17c | | 8.02 | 226.26 | no | BNL 2002 |
| ucsd64b | | 8.02 | 226.26 | no | BNL 2002 |
| umc1415 | C | 8.03 | 228.60 | yes | IBM2 |
| umc1470 | A C | 8.03 | 231.20 | yes | IBM2 |
| umc2355 | A C | 8.03 | 232.90 | no | IBM2 |
| umc1984 | | 8.03 | 234.80 | yes | IBM2 |
| umc1236 | A C | 8.03 | 239.99 | no | SSR popII |
| AY103821 | C | 8.03 | 240.70 | yes | IBM2 |
| isu2191h | | 8.03 | 242.08 | no | BNL 2002 |
| bnl17.20 | | 8.03 | 242.08 | no | BNL 96 |
| bnlg1229 | | 8.03 | 242.12 | no | BNL 2002 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| pge2 | | 8.03 | 242.85 | no | BNL 2002 |
| mdh1 | | 8.03 | 243.50 | no | BNL 2002 |
| npi618 | | 8.03 | 243.90 | no | BNL 2002 |
| pbs4 | | 8.03 | 244.02 | no | BNL 2002 |
| ici277 | | 8.03 | 244.02 | no | BNL 2002 |
| umc2075 | C | 8.03 | 244.90 | no | IBM2 |
| isu1719c | | 8.03 | 245.23 | no | BNL 2002 |
| isu2191b | | 8.03 | 245.23 | no | BNL 2002 |
| bnlg1863 | A C | 8.03 | 245.70 | no | IBM2 |
| tug1 | | 8.03 | 245.73 | no | BNL 2002 |
| AY105457 | A C | 8.03 | 245.90 | no | IBM2 |
| bnlg1460 | | 8.03-8.04 | 247.08 | no | BNL 2002 |
| uaz249c(ubf9) | | 8.03 | 248.61 | no | BNL 2002 |
| bnl9.44 | | 8.03 | 251.01 | no | UMC 98 |
| ici286a | | 8.03 | 251.01 | no | BNL 2002 |
| ucsd61f | | 8.03 | 251.01 | no | BNL 2002 |
| niu1::Bs1 | | 8.03 | 251.01 | no | BNL 2002 |
| uaz269a(kri) | | 8.03 | 251.01 | no | BNL 2002 |
| uaz290(SDAg) | | 8.03 | 251.01 | no | BNL 2002 |
| AY110032 | A C | 8.03 | 254.80 | yes | IBM2 |
| umc2366 | C | 8.03 | 257.31 | no | SSR popII |
| rps28 | | 8.03 | 257.67 | no | SSR popI |
| umc1802 | | 8.03 | 257.67 | no | SSR popI |
| uaz244b(prh) | | 8.03 | 259.05 | no | BNL 2002 |
| uky3a(P450) | | 8.03 | 262.16 | no | UMC 98 |
| umc1617 | C | 8.03 | 262.74 | no | SSR popI |
| csu760b | | 8.03 | 263.40 | no | UMC 98 |
| csu244(imp) | | 8.03 | 263.40 | no | UMC 98 |
| umc1377 | | 8.03 | 263.76 | no | SSR popI |
| umc1289 | C | 8.03 | 264.40 | no | SSR popII |
| umc1385 | | 8.03 | 265.51 | no | SSR popI |
| umc1615 | | 8.03 | 265.51 | no | SSR popI |
| csu275a(mtl) | | 8.03 | 268.36 | no | UMC 98 |
| AY109740 | A C | 8.03 | 268.60 | yes | IBM2 |
| bnl1.45a | | 8.03 | 274.56 | no | UMC 98 |
| phi100175 | A C | 8.03 | 274.90 | yes | IBM2 |
| umc1735 | A C | 8.03 | 279.90 | yes | IBM2 |
| AY109626 | A C | 8.03 | 282.70 | no | IBM2 |
| umc1457 | A C | 8.03 | 284.60 | yes | IBM2 |
| umc1471 | | 8.03 | 285.04 | no | SSR popI |
| oec23 | | 8.03 | 286.23 | no | SSR popII |
| umc1302 | | 8.03 | 287.42 | no | SSR popII |
| uor1b(rpS12) | | 8.03 | 289.43 | no | UMC 98 |
| phi121 | C | 8.03 | 289.80 | yes | IBM2 |
| php20714 | | 8.03 | 291.30 | yes | IBM2 |
| tub2 | C | 8.03 | 291.91 | no | UMC 98 |
| tda217e | | 8.03 | 293.15 | no | UMC 98 |
| mbd101a | C | 8.03 | 294.20 | no | ChromDB |
| bnl8.06a | | 8.03 | 294.24 | no | BNL 96 |
| umc2154 | A C | 8.03 | 295.30 | yes | IBM2 |
| dupssr3 | | 8.03 | 296.42 | no | BNL 2002 |
| bnlg2289 | | 8.02 | 297.68 | no | BNL 2002 |
| ncr(sod3c) | | 8.03 | 298.21 | no | BNL 2002 |
| uaz121b | | 8.03 | 299.32 | no | BNL 2002 |
| csu620 | | 8.03 | 300.59 | no | UMC 98 |
| bnlg119 | | 8.04 | 302.36 | no | BNL 2002 |
| uaz25a | | 8.03 | 302.65 | no | BNL 2002 |
| bnl9.08 | | 8.03-8.04 | 303.04 | no | BNL 2002 |
| umc1460 | A C | 8.04 | 304.20 | yes | IBM2 |
| PCO147505 | C | 8.03-8.04 | 304.73 | no | INDEL |
| umc1427 | C | 8.03 | 307.33 | no | SSR popI |
| umc1487 | | 8.03 | 307.33 | no | SSR popII |
| bnl7.08a | | 8.04 | 309.27 | no | SSR popII |
| umc1765 | | 8.03 | 310.37 | no | SSR popI |
| AY110056 | A C | 8.04 | 310.40 | yes | IBM2 |
| act1 | C | 8.03 | 311.97 | no | BNL 2002 |
| agrc1 | | 8.04 | 312.38 | no | UMC 98 |
| umc1858 | A C | 8.04 | 312.40 | yes | IBM2 |
| ucsd106h | | 8.04 | 312.45 | no | BNL 2002 |
| uaz202 | | 8.04 | 312.90 | no | BNL 2002 |
| umc209(prk) | | 8.04 | 313.60 | no | UMC 98 |
| umc1343 | | 8.04 | 314.51 | no | SSR popII |
| bnlg2046 | C | 8.04 | 315.20 | yes | IBM2 |
| pdc1 | C | 8.04 | 315.20 | no | SSR popII |
| ufg58 | C | 8.04 | 315.70 | no | IBM2 |
| bnl17.16(bt2) | C | 8.03 | 315.87 | no | BNL 2002 |
| bnl10.39 | | 8.03 | 316.22 | no | BNL 2002 |
| csu1101b | | 8.04 | 316.72 | no | UMC 98 |
| npi224c | | 8.04 | 316.94 | no | BNL 2002 |
| bnlg1446 | | 8.05 | 316.94 | no | BNL 2002 |
| npi(pdk2) | | 8.04 | 316.94 | no | BNL 2002 |
| csu226a(elf1A) | | 8.04 | 319.39 | no | UMC 98 |
| AY104017 | C | 8.04 | 320.60 | no | IBM2 |
| wusl(pdc1) | | 8.04 | 320.63 | no | BNL 2002 |
| csu720a | | 8.04 | 322.95 | no | UMC 98 |
| gta101d | | 8.04 | 323.80 | yes | IBM2 |
| csu807a | | 8.04 | 323.95 | no | UMC 98 |
| uwm1a(uce) | | 8.04 | 324.06 | no | UMC 98 |
| csu179d(hsp70) | | 8.04 | 324.06 | no | UMC 98 |
| csu204(uce) | | 8.04 | 324.17 | no | UMC 98 |
| caat1 | | 8.04 | 324.73 | no | UMC 98 |
| cdo1395e | | 8.04 | 324.73 | no | UMC 98 |
| csu254d | | 8.04 | 326.29 | no | UMC 98 |
| pge21 | | 8.03 | 327.31 | no | BNL 2002 |
| sdg105a | | 8.04-8.05 | 327.47 | no | ChromDB |
| sb32 | | 8.04 | 328.29 | no | UMC 98 |
| csh9(cyc1) | | 8.04 | 328.40 | no | UMC 98 |
| bnl2.369 | A C | 8.05 | 329.40 | yes | IBM2 |
| rgpg81 | | 8.04-8.05 | 329.40 | no | UMC 98 |
| umc1130 | | 8.05 | 330.10 | yes | IBM2 |
| bnlg1176 | C | 8.05 | 330.40 | no | IBM2 |
| bnl24a | | 8.04 | 331.06 | no | BNL 2002 |
| ucsd113a | | 8.03-8.04 | 331.06 | no | BNL 96 |
| bnlg2313a | | 8.03 | 331.37 | no | BNL 2002 |
| hox1 | A C | 8.05 | 337.20 | yes | IBM2 |
| koln2c | | 8.04-8.05 | 340.35 | no | BNL 96 |
| AY104566 | A C | 8.05 | 342.00 | yes | IBM2 |
| rop7 | | 8.05 | 342.86 | no | SSR popII |
| pdk2 | C | 8.04 | 343.02 | no | UMC 98 |
| npi294f | | 8.04 | 343.02 | no | UMC 98 |
| rip1 | C | 8.04 | 343.02 | no | BNL 96 |
| uaz147a | | 8.04 | 343.58 | no | BNL 2002 |
| npi224h | | 8.04 | 344.26 | no | BNL 2002 |
| umc2367 | | 8.05 | 344.50 | no | SSR popII |
| csu66b(lhcb) | | 8.04 | 346.14 | no | BNL 2002 |
| bnlg1246c | | 8.05 | 346.35 | no | BNL 2002 |
| uaz165 | | 8.04 | 346.73 | no | BNL 2002 |
| mmp15 | | 8.05 | 348.20 | yes | IBM2 |
| umc1959 | A C | 8.05 | 352.20 | yes | IBM2 |
| csu841b | | 8.05 | 352.80 | no | UMC 98 |
| umc1562 | A C | 8.05 | 353.30 | yes | IBM2 |
| umc1263 | A C | 8.05 | 353.90 | yes | IBM2 |
| chr117b | | 8.05 | 353.90 | no | ChromDB |
| jpsb107a | | 8.05 | 356.60 | yes | IBM2 |
| umc1846 | C | 8.05 | 357.90 | no | IBM2 |
| csu292 | | 8.05 | 358.40 | no | IBM2 |
| ufg80 | C | 8.05 | 359.50 | yes | IBM2 |
| ici222 | | 8.05 | 360.75 | no | BNL 2002 |
| mmp195b | | 8.05 | 361.20 | no | IBM2 |
| bnlg1812 | | 8.05 | 362.52 | no | BNL 2002 |
| bnlg1599 | C | 8.05 | 362.71 | no | BNL 2002 |
| ucb(anp1) | | 8.05 | 362.71 | no | BNL 2002 |
| ufg74 | C | 8.05 | 363.40 | yes | IBM2 |
| bnl8.26 | | 8.05 | 364.43 | no | BNL 2002 |
| umc160b | | 8.04 | 366.75 | no | BNL 2002 |
| bnlg2181 | A C | 8.05 | 366.80 | no | IBM2 |
| bnlg162 | A C | 8.05 | 367.00 | no | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| bnlg666 | A C | 8.05 | 367.00 | yes | IBM2 |
| umc89a | C | 8.05 | 369.60 | yes | IBM2 |
| umc12a | C | 8.05 | 372.60 | yes | IBM2 |
| dgg9h |  | 8.05 | 372.60 | no | BNL 2002 |
| knox5 |  | 8.05 | 372.60 | no | BNL 2002 |
| npi595 |  | 8.05 | 372.60 | no | BNL 2002 |
| mwg645k |  | 8.04 | 372.60 | no | BNL 2002 |
| npi101b |  | 8.05 | 372.60 | no | BNL 2002 |
| csu829 |  | 8.05 | 372.66 | no | UMC 98 |
| knox11 |  | 8.05 | 372.66 | no | UMC 98 |
| umc2c | C | 8.05 | 372.66 | no | UMC 98 |
| csu1023 |  | 8.05 | 372.66 | no | UMC 98 |
| scri1(msf) |  | 8.05 | 372.66 | no | UMC 98 |
| rgpc597(prs) |  | 8.05 | 372.66 | no | UMC 98 |
| uaz233a(act) |  | 8.05 | 372.66 | no | BNL 2002 |
| rz390b(cyb5) |  | 8.05 | 372.67 | no | UMC 98 |
| dgg9a |  | 8.05 | 372.70 | no | BNL 2002 |
| mwg645a |  | 8.05 | 372.70 | no | BNL 2002 |
| cdo580a(ivd) |  | 8.05 | 372.70 | no | BNL 2002 |
| uiu1c(pog) |  | 8.05 | 372.75 | no | BNL 2002 |
| cdo708 |  | 8.05 | 372.84 | no | BNL 2002 |
| rz390a(cyb5) |  | 8.05 | 373.50 | no | IBM2 |
| bnlg1651 | A C | 8.05 | 374.50 | yes | IBM2 |
| umc1889 | A C | 8.05 | 374.90 | yes | IBM2 |
| umc1712 | C | 8.05 | 374.90 | no | SSR popI |
| umc2401 | C | 8.05 | 374.90 | no | SSR popII |
| hdt102 | C | 8.05 | 374.90 | no | ChromDB |
| umc1864 |  | 8.05 | 375.05 | no | SSR popI |
| bcd134a |  | 8.05 | 376.90 | no | UMC 98 |
| umc1340 | A C | 8.05 | 377.70 | yes | IBM2 |
| bnl12.36b |  | 8.05 | 377.79 | no | SSR popI |
| umc2378 | C | 8.05 | 377.94 | no | SSR popII |
| umc1882 |  | 8.05 | 378.34 | no | SSR popII |
| hda103 |  | 8.05 | 379.20 | yes | IBM2 |
| csu1041b(ptk) |  | 8.05 | 381.20 | no | UMC 98 |
| umc1316 | A C | 8.05 | 381.70 | yes | IBM2 |
| isu114 |  | 8.05 | 382.70 | yes | IBM2 |
| chr112b | C | 8.05 | 382.80 | no | ChromDB |
| umc1777 | A C | 8.05 | 382.90 | no | IBM2 |
| uaz164b |  | 8.05-8.06 | 383.08 | no | BNL 2002 |
| bnl12.30a |  | 8.05 | 385.50 | yes | IBM2 |
| cdo455a | C | 8.05 | 385.50 | no | UMC 98 |
| csu742a(rpS7) |  | 8.05 | 385.50 | no | UMC 98 |
| umc2199 | C | 8.05 | 387.37 | no | SSR popI |
| hon107a | C | 8.05 | 389.60 | no | ChromDB |
| umc1665 |  | 8.05 | 390.26 | no | SSR popI |
| umc2210 |  | 8.05 | 390.26 | no | SSR popI |
| uaz138b |  | 8.06 | 391.16 | no | BNL 2002 |
| pic6b |  | 8.05 | 394.24 | no | BNL 2002 |
| bnl17.01 |  | 8.06 | 394.69 | no | BNL 96 |
| umc1121 | A C | 8.05 | 395.86 | no | SSR popII |
| umc1824b | C | 8.05 | 397.86 | no | SSR popI |
| umc1287 | C | 8.05 | 399.47 | no | SSR popI |
| umc184c(glb) |  | 8.05 | 400.68 | no | UMC 98 |
| umc93a |  | 8.05 | 400.99 | no | UMC 98 |
| umc189(a1) |  | 8.05 | 400.99 | no | UMC 98 |
| dba2 |  | 8.05 | 401.47 | no | UMC 98 |
| umn430 |  | 8.05 | 401.47 | no | UMC 98 |
| csu125b(cah) |  | 8.05 | 401.47 | no | UMC 98 |
| csu31a | C | 8.06 | 404.15 | no | SSR popII |
| idh1 |  | 8.06 | 406.30 | no | UMC 98 |
| ici95 |  | 8.06 | 406.94 | no | BNL 2002 |
| pbs6b |  | 8.06 | 406.94 | no | BNL 2002 |
| umc53b |  | 8.06 | 406.94 | no | BNL 2002 |
| uaz176a |  | 8.06 | 406.94 | no | BNL 2002 |
| isu1774b |  | 8.06 | 406.94 | no | BNL 2002 |
| csu384 |  | 8.06 | 407.97 | no | UMC 98 |
| umc1670 |  | 8.06 | 408.29 | no | SSR popII |
| umc1141 | A C | 8.05 | 408.69 | no | SSR popI |
| umc2212 |  | 8.05 | 412.34 | no | SSR popI |
| umc2356 | C | 8.05 | 412.90 | no | IBM2 |
| umc1960 | C | 8.05 | 413.20 | no | IBM2 |
| umc1828 |  | 8.06 | 413.75 | no | SSR popII |
| umc1149 | C | 8.06 | 413.90 | yes | IBM2 |
| sdg118 | C | 8.05 | 413.90 | no | ChromDB |
| bnlg1152 | C | 8.06 | 414.10 | no | IBM2 |
| bnlg240 | C | 8.06 | 414.10 | no | SSR popI |
| umc48a |  | 8.06 | 415.59 | no | UMC 98 |
| csu110a |  | 8.06 | 415.59 | no | UMC 98 |
| csu772b |  | 8.06 | 415.59 | no | UMC 98 |
| PCO079694 | C | 8.06 | 415.69 | no | INDEL |
| AY109883 |  | 8.06 | 415.70 | no | IBM2 |
| mmp32 |  | 8.06 | 416.00 | no | IBM2 |
| csu2c |  | 8.06 | 420.83 | no | UMC 98 |
| ksu1d |  | 8.06 | 420.83 | no | UMC 98 |
| umc30a |  | 8.06 | 420.83 | no | UMC 98 |
| npi299 |  | 8.06 | 420.83 | no | BNL 2002 |
| uaz119a(rpS6) |  | 8.06 | 421.48 | no | BNL 2002 |
| npi201b |  | 8.06 | 421.73 | no | BNL 2002 |
| bnlg1782 |  | 8.05-8.06 | 422.30 | no | BNL 2002 |
| tum1 |  | 8.06 | 422.38 | no | BNL 2002 |
| bnl5.33d |  | 8.06 | 423.69 | no | UMC 98 |
| aba2 |  | 8.06 | 425.84 | no | UMC 98 |
| rgpc112 |  | 8.06 | 426.32 | no | UMC 98 |
| uaz94 |  | 8.06 | 428.18 | no | BNL 2002 |
| pbs9a |  | 8.06 | 429.37 | no | BNL 2002 |
| bcd134c |  | 8.06 | 429.65 | no | UMC 98 |
| bnl17.17 |  | 8.06 | 430.33 | no | BNL 96 |
| umc117 |  | 8.06 | 431.08 | no | UMC 98 |
| umc71a |  | 8.06 | 431.08 | no | UMC 98 |
| umc1728 | A C | 8.06 | 432.40 | yes | IBM2 |
| umc2031 | C | 8.06 | 432.63 | no | SSR popII |
| hdt105 |  | 8.06 | 434.41 | no | ChromDB |
| umc1161 |  | 8.06 | 434.55 | no | SSR popII |
| ald1 |  | 8.06 | 436.56 | no | UMC 98 |
| asg17 |  | 8.06 | 436.56 | no | UMC 98 |
| umc84c | C | 8.06 | 436.56 | no | UMC 98 |
| csu597e(dah) | C | 8.06 | 436.56 | no | UMC 98 |
| asg1a |  | 8.06 | 438.71 | no | UMC 98 |
| asg53 |  | 8.06 | 438.94 | no | UMC 98 |
| asg52a |  | 8.06 | 438.94 | no | UMC 98 |
| umc1905 | A C | 8.06 | 439.60 | yes | IBM2 |
| sbe3 |  | 8.06 | 440.07 | no | SSR popII |
| ksu1b |  | 8.06 | 441.09 | no | UMC 98 |
| csu382b(cld) | C | 8.06 | 441.09 | no | UMC 98 |
| rgpc198b(sik) |  | 8.06 | 441.09 | no | UMC 98 |
| uaz95 |  | 8.06 | 443.40 | no | BNL 2002 |
| sps1 | C | 8.06 | 443.40 | no | BNL 96 |
| umc2037 | A C | 8.06 | 444.96 | no | SSR popII |
| bnlg1607 |  | 8.06 | 445.76 | no | BNL 2002 |
| csu685 |  | 8.06 | 448.00 | no | UMC 98 |
| umc271 |  | 8.06 | 448.00 | no | UMC 98 |
| rgpc949 |  | 8.06 | 448.00 | no | UMC 98 |
| chr116b |  | 8.06 | 448.94 | no | ChromDB |
| umc2361 | C | 8.06 | 451.29 | no | SSR popII |
| npi108b |  | 8.06 | 451.50 | no | BNL 96 |
| mmc0181 | A C | 8.06 | 453.25 | no | SSR popII |
| umc2395 |  | 8.06 | 453.45 | no | SSR popII |
| uaz174 |  | 8.07 | 453.92 | no | BNL 2002 |
| bnlg1031 | C | 8.06 | 455.10 | yes | IBM2 |
| bnl10.24b |  | 8.06 | 455.50 | no | IBM2 |
| cuny20(psy) |  | 8.06-8.07 | 456.56 | no | BNL 2002 |
| umc1724 | C | 8.06 | 457.29 | no | SSR popII |
| CL9311_1 | C | 8.06-8.07 | 457.57 | no | INDEL |
| asg61b |  | 8.06 | 458.21 | no | UMC 98 |
| bnl10.11 |  | 8.07 | 459.01 | no | BNL 96 |
| npi268a | C | 8.07 | 459.20 | yes | IBM2 |
| bnl10.38c |  | 8.06-8.07 | 459.20 | no | UMC 98 |
| bnlg1065 | C | 8.07 | 460.80 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| umc164a | | 8.07 | 460.87 | no | BNL 2002 |
| umc2014 | | 8.07 | 463.03 | no | SSR popII |
| rz538a | | 8.07 | 464.00 | yes | IBM2 |
| umc165b | | 8.07 | 464.03 | no | UMC 98 |
| rgpc86(ptk) | C | 8.07 | 464.03 | no | UMC 98 |
| npi224b | | 8.08 | 464.38 | no | BNL 96 |
| csu254c | | 8.07 | 466.01 | no | UMC 98 |
| umc1607 | C | 8.07 | 466.50 | yes | IBM2 |
| bnlg1350b | | 8.07 | 466.93 | no | BNL 2002 |
| ucla(obf3B) | | 8.08 | 472.87 | no | BNL 2002 |
| csu96b(psei) | | 8.08 | 472.87 | no | BNL 96 |
| bnlg1056 | | 8.08 | 473.10 | no | BNL 2002 |
| umc7 | | 8.08 | 473.49 | no | UMC 98 |
| npi438b | | 8.08 | 473.49 | no | UMC 98 |
| csu223a(psei) | | 8.08 | 473.79 | no | UMC 98 |
| uwo1 | | 8.08 | 476.38 | no | BNL 96 |
| umc39b | | 8.09 | 477.61 | no | BNL 2002 |
| umc3a | | 8.09 | 482.43 | no | BNL 96 |
| cdo241b | | 8.08 | 482.84 | no | UMC 98 |
| bnlg1823 | C | 8.07 | 483.40 | yes | IBM2 |
| AY110569 | C | 8.07 | 486.90 | no | IBM2 |
| csu1155b | | 8.09 | 489.22 | no | UMC 98 |
| psy2 | C | 8.07 | 489.70 | yes | IBM2 |
| csu163b | | 8.07-8.08 | 490.27 | no | BNL 2002 |
| csu110c | | 8.07 | 490.63 | no | UMC 98 |
| umc266d(ptk) | | 8.07 | 490.63 | no | UMC 98 |
| AY110539 | | 8.07 | 494.20 | no | IBM2 |
| umc1268 | C | 8.07 | 494.70 | yes | IBM2 |
| csu776a | | 8.07 | 494.71 | no | UMC 98 |
| csu38b(taf) | | 8.07 | 494.71 | no | UMC 98 |
| uwm1c(uce) | | 8.07 | 495.97 | no | UMC 98 |
| umc1055 | | 8.07 | 496.12 | no | SSR popI |
| csu179c(hsp70) | | 8.07 | 498.49 | no | UMC 98 |
| dupssr14 | | 8.09 | 500.12 | no | UMC 98 |
| lim301 | | 8.07 | 504.30 | yes | IBM2 |
| bnlg1828 | | 8.07 | 506.80 | yes | IBM2 |
| umc1384 | | 8.07 | 507.36 | no | SSR popI |
| npi414a | A C | 8.08 | 509.80 | yes | IBM2 |
| tpi5 | | 8.07-8.08 | 509.80 | no | BNL 2002 |
| csu1155a | | 8.08 | 511.87 | no | UMC 98 |
| umc2357 | | 8.08 | 514.20 | no | IBM2 |
| mmp64 | | 8.08 | 515.00 | yes | IBM2 |
| umc82d | | 8.08 | 522.00 | no | UMC 98 |
| php20793 | | 8.08 | 522.40 | yes | IBM2 |
| AY109593 | C | 8.08 | 524.60 | yes | IBM2 |
| umc1005 | | 8.08 | 526.60 | yes | IBM2 |
| csu786(uce) | | 8.08 | 526.60 | no | UMC 98 |
| sb21 | | 8.08 | 529.82 | no | UMC 98 |
| csu591(uce) | | 8.08 | 529.82 | no | UMC 98 |
| umc2218 | | 8.08 | 533.24 | no | SSR popI |
| csu165a | | 8.08 | 534.65 | no | UMC 98 |
| csu922(arf) | | 8.08 | 534.65 | no | UMC 98 |
| csh8a(cyc4) | | 8.08 | 536.96 | no | UMC 98 |
| umc1032 | | 8.08 | 538.76 | no | SSR popII |
| umc1933 | A C | 8.08 | 540.30 | yes | IBM2 |
| mmp146 | | 8.08 | 544.70 | yes | IBM2 |
| umc2052 | | 8.08 | 545.52 | no | SSR popI |
| umc1673 | | 8.08 | 546.90 | yes | IBM2 |
| AY110053 | C | 8.08 | 550.40 | yes | IBM2 |
| npi107 | | 8.08 | 562.50 | yes | IBM2 |
| asg50b | | 8.08-8.09 | 562.50 | no | UMC 98 |
| npi112b | | 8.08 | 564.30 | yes | IBM2 |
| AY103806 | C | 8.08 | 569.00 | yes | IBM2 |
| gst1 | A C | 8.08 | 571.50 | yes | IBM2 |
| bcd98e | | 8.09 | 572.17 | no | BNL 2002 |
| uaz128 | | 8.08 | 573.45 | no | BNL 2002 |
| umc4b | C | 8.09 | 574.98 | no | BNL 2002 |
| csu146b(cdc48) | | 8.08 | 575.40 | yes | IBM2 |
| agrr21 | A C | 8.09 | 580.10 | yes | IBM2 |
| AY110127 | A C | 8.09 | 596.40 | yes | IBM2 |
| umc1663 | A C | 8.09 | 608.10 | no | IBM2 |
| phi233376 | A C | 8.09 | 609.10 | yes | IBM2 |
| umc1638 | A C | 8.09 | 621.60 | yes | IBM2 |
| umc1916 | | 8.09 | 626.70 | yes | IBM2 |
| bnlg1131 | | 8.09 | 628.20 | yes | IBM2 |
| AY109853 | A C | 8.09 | 632.00 | yes | IBM2 |
| agrr118b | | 9.00 | -41.50 | no | UMC 98 |
| bnl9.07a | | 9.00 | -11.20 | no | UMC 98 |
| umc1279 | C | 9.00 | -7.60 | no | SSR popII |
| umc1957 | A C | 9.00 | 0.00 | yes | IBM2 |
| umc109 | A C | 9.01 | 5.00 | yes | IBM2 |
| umc148 | | 9.01 | 7.30 | no | UMC 98 |
| rz144a | A C | 9.01 | 9.86 | no | UMC 98 |
| bnlg1724 | A C | 9.01 | 11.80 | yes | IBM2 |
| npi253a | | 9.01 | 14.00 | yes | IBM2 |
| umc2393 | | 9.00-9.01 | 16.20 | no | SSR popII |
| umc1370 | C | 9.01 | 17.70 | yes | IBM2 |
| rz144c | A C | 9.01 | 20.10 | no | UMC 98 |
| umc1040 | A C | 9.01 | 21.20 | no | IBM2 |
| bnlg2122 | A C | 9.01 | 21.30 | yes | IBM2 |
| umc1867 | A C | 9.01 | 24.30 | yes | IBM2 |
| php10005 | | 9.01 | 28.80 | yes | IBM2 |
| ucsd72f | | 9.01 | 32.83 | no | BNL 2002 |
| csu95a | C | 9.01 | 41.68 | no | UMC 98 |
| umc248a | | 9.01 | 41.68 | no | UMC 98 |
| bnlg1288 | | 9.01 | 43.23 | no | BNL 2002 |
| lim343 | | 9.01 | 46.20 | yes | IBM2 |
| ufg41 | | 9.01 | 50.40 | yes | IBM2 |
| gta106b | | 9.01 | 55.51 | no | ChromDB |
| koln10b(hox2) | | 9.01 | 56.00 | no | BNL 2002 |
| bnlg1583 | A C | 9.01 | 62.30 | yes | IBM2 |
| bnlg1810 | A C | 9.01 | 62.30 | yes | IBM2 |
| mir3a(thp) | | 9.01 | 63.43 | no | UMC 98 |
| c1 | C | 9.01 | 64.70 | yes | IBM2 |
| koln2b(hox) | | 9.01 | 65.19 | no | BNL 96 |
| umc1809 | C | 9.01 | 65.20 | yes | IBM2 |
| isu1146 | | 9.01 | 73.23 | no | BNL 96 |
| bnl17.11 | | 9.01 | 73.23 | no | BNL 96 |
| umc2335 | A C | 9.01 - 9.02 | 74.80 | yes | IBM2 |
| bnlg1272 | | 9.00 | 74.94 | no | BNL 2002 |
| umc113a | | 9.01 | 75.86 | no | UMC 98 |
| sh1 | A C | 9.01 | 80.30 | yes | IBM2 |
| umc1588 | A C | 9.01 | 82.30 | yes | IBM2 |
| umc1967 | A C | 9.01 | 84.30 | yes | IBM2 |
| umc2362 | | 9.01 - 9.02 | 86.67 | no | SSR popII |
| csu250b(aba) | | 9.01 | 86.72 | no | UMC 98 |
| umc1596 | A C | 9.01 | 86.80 | yes | IBM2 |
| bz1 | A C | 9.02 | 90.10 | yes | IBM2 |
| umc1958 | | 9.01 - 9.02 | 90.10 | no | SSR popII |
| umc1764 | A C | 9.02 | 94.28 | no | SSR popII |
| umc1131 | C | 9.02 | 94.70 | no | SSR popII |
| AY104252 | A C | 9.02 | 95.80 | yes | IBM2 |
| umc82a | | 9.02 | 96.33 | no | BNL 2002 |
| csu665b(adt) | | 9.02 | 99.07 | no | UMC 98 |
| dupssr6 | | 9.02 | 101.00 | no | SSR popI |
| umc1170 | A C | 9.02 | 101.10 | yes | IBM2 |
| chr113 | | 9.02 | 103.86 | no | ChromDB |
| csu471 | | 9.02 | 105.80 | yes | IBM2 |
| csu466(lhcb) | | 9.02 | 105.80 | no | UMC 98 |
| asg82 | | 9.02 | 106.01 | no | UMC 98 |
| asg19a | | 9.02 | 106.01 | no | UMC 98 |
| umc256a | | 9.02 | 106.01 | no | UMC 98 |
| bnl5.67b | | 9.02 | 106.01 | no | UMC 98 |
| csu733(rpL39) | | 9.02 | 106.01 | no | UMC 98 |
| csu651(rpL39) | C | 9.02 | 106.01 | no | UMC 98 |
| umc1647 | | 9.00 | 109.37 | no | SSR popI |
| umc1430 | | 9.02 | 115.36 | no | SSR popI |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| csu486a | | 9.02 | 115.39 | no | UMC 98 |
| isu111b | | 9.02 | 116.60 | yes | IBM2 |
| agrc255b | | 9.02 | 124.37 | no | UMC 98 |
| csu1083b | | 9.02 | 124.37 | no | UMC 98 |
| umc2336 | A C | 9.02-9.03 | 125.70 | yes | IBM2 |
| umc2219 | C | 9.02 | 127.70 | no | SSR popl |
| csu1077 | | 9.02 | 130.49 | no | UMC 98 |
| umc1636 | A C | 9.02 | 131.10 | yes | IBM2 |
| npi266 | | 9.02 | 134.12 | no | BNL 96 |
| prc1 | | 9.02 | 134.57 | no | UMC 98 |
| rz2a | | 9.02 | 134.57 | no | UMC 98 |
| klp1c | | 9.02 | 134.57 | no | UMC 98 |
| mpik11c | | 9.02 | 136.88 | no | BNL 2002 |
| mmp162 | | 9.02 | 139.00 | yes | IBM2 |
| dup1379 | | 9.02 | 139.47 | no | BNL 2002 |
| mpik19a | | 9.01 | 139.64 | no | BNL 2002 |
| ucsd62k(zag4) | | 9.02 | 142.12 | no | BNL 2002 |
| bnlg244 | A C | 9.02 | 142.60 | yes | IBM2 |
| bnlg1401 | A C | 9.02 | 147.50 | yes | IBM2 |
| mpik25(zmm3) | | 9.02 | 148.44 | no | UMC 98 |
| umc105a | | 9.02 | 152.93 | no | UMC 98 |
| mmp77 | | 9.02 | 153.00 | yes | IBM2 |
| bnlg1372 | | 9.02 | 155.16 | no | BNL 2002 |
| umc1037 | A C | 9.02 | 160.03 | no | SSR popl |
| umc1893 | | 9.02 | 161.33 | no | SSR poplI |
| mmp30 | | 9.02 | 162.50 | yes | IBM2 |
| isu2191d | | 9.03 | 163.63 | no | BNL 96 |
| bnlg2107 | | 9.02 | 167.99 | no | BNL 2002 |
| uaz237a(prc) | | 9.02 | 168.67 | no | BNL 2002 |
| umc1698 | | 9.02 | 170.40 | yes | IBM2 |
| dup1384 | | 9.02 | 172.42 | no | BNL 2002 |
| csu94b | | 9.02 | 173.33 | no | UMC 98 |
| cdo475a | | 9.02 | 173.33 | no | UMC 98 |
| csu228(pfk) | | 9.02 | 173.33 | no | UMC 98 |
| umc2213 | | 9.02-9.03 | 176.14 | no | SSR popl |
| dupssr19 | | 9.02 | 176.32 | no | BNL 2002 |
| dpg1b | | 9.02-9.03 | 177.50 | no | BNL 2002 |
| npi300a | | 9.02 | 178.05 | no | BNL 2002 |
| bnlg1082 | | 9.02 | 178.39 | no | BNL 2002 |
| bnlg1913 | | 9.02 | 178.39 | no | BNL 2002 |
| d3 | C | 9.03 | 178.69 | no | BNL 2002 |
| bnl3.06 | | 9.02-9.03 | 183.67 | no | BNL 2002 |
| mgs3 | A C | 9.02-9.03 | 184.17 | no | BNL 2002 |
| AY109531 | C | 9.02 | 185.20 | yes | IBM2 |
| csu616 | | 9.02-9.03 | 189.65 | no | UMC 98 |
| tda66d | | 9.02-9.03 | 189.65 | no | UMC 98 |
| umc247 | | 9.02-9.03 | 189.65 | no | UMC 98 |
| npi215a | | 9.02-9.03 | 189.65 | no | UMC 98 |
| umc253b | | 9.02-9.03 | 189.65 | no | UMC 98 |
| cdo590(ppr) | | 9.02-9.03 | 189.65 | no | UMC 98 |
| rgpr1908a(acb) | | 9.02-9.03 | 189.65 | no | UMC 98 |
| lim286 | | 9.02 | 190.10 | yes | IBM2 |
| dhn2 | | 9.03 | 190.16 | no | BNL 2002 |
| wx1 | C | 9.03 | 191.70 | yes | IBM2 |
| umc1634 | A C | 9.03 | 193.20 | yes | IBM2 |
| bnl5.21d | | 9.03 | 195.27 | no | BNL 2002 |
| umc273a | | 9.03 | 195.36 | no | UMC 98 |
| umc1258 | A C | 9.03 | 195.70 | yes | IBM2 |
| AY109570 | A C | 9.03 | 196.40 | no | IBM2 |
| hon104a | C | 9.03 | 196.88 | no | ChromDB |
| umc1586 | A C | 9.03 | 199.70 | yes | IBM2 |
| AY109816 | C | 9.03 | 200.40 | no | IBM2 |
| bnlg469a | C | 9.03 | 200.41 | no | BNL 2002 |
| lim101 | | 9.03 | 202.30 | yes | IBM2 |
| ufg71 | C | 9.03 | 204.40 | yes | IBM2 |
| mmp170b | | 9.03 | 208.50 | yes | IBM2 |
| PCO061815 | C | 9.03 | 209.97 | no | INDEL |
| rf2 | | 9.03 | 212.52 | no | UMC 98 |
| cdo17 | | 9.03 | 212.52 | no | UMC 98 |
| csu680d | C | 9.03 | 212.52 | no | UMC 98 |
| uwm1b(uce) | | 9.03 | 212.52 | no | UMC 98 |
| ucsd1.8a | | 9.03 | 214.22 | no | BNL 96 |
| psr160d | | 9.03 | 216.20 | yes | IBM2 |
| umc2338 | A C | 9.05 | 219.40 | yes | IBM2 |
| umc2337 | A C | 9.03 | 220.10 | yes | IBM2 |
| psr160c | | 9.03 | 220.70 | yes | IBM2 |
| chr120 | | 9.03 | 221.80 | no | ChromDB |
| bnl5.33c | | 9.03 | 222.36 | no | UMC 98 |
| bnl7.24a | | 9.03 | 222.36 | no | UMC 98 |
| umc2370 | C | 9.03 | 222.51 | no | SSR poplI |
| rz273c(ant) | | 9.03 | 223.90 | yes | IBM2 |
| rz953 | | 9.03 | 226.30 | yes | IBM2 |
| umc81 | C | 9.03 | 226.30 | yes | IBM2 |
| csu321 | | 9.03 | 226.30 | no | UMC 98 |
| pbs14b | | 9.03 | 226.30 | no | BNL 2002 |
| rgpr3235a | C | 9.03 | 226.30 | no | UMC 98 |
| php20075b(ext) | C | 9.03 | 226.30 | no | BNL 2002 |
| bnlg1626 | | 9.03-9.04 | 226.88 | no | BNL 2002 |
| bcd1421 | | 9.03 | 227.40 | yes | IBM2 |
| php20052 | | 9.03 | 228.30 | yes | IBM2 |
| asg37 | | 9.03 | 229.10 | no | UMC 98 |
| asg65a | | 9.03 | 229.10 | no | UMC 98 |
| asg66a | | 9.03 | 229.10 | no | UMC 98 |
| asg67a | | 9.03 | 229.10 | no | UMC 98 |
| bnl5.10 | | 9.03 | 229.10 | yes | IBM2 |
| csu193 | | 9.03 | 229.10 | no | UMC 98 |
| umc153 | | 9.03 | 229.10 | no | UMC 98 |
| bnl26 | | 9.03 | 229.10 | no | BNL 2002 |
| bnlg1730 | | 9.03 | 229.10 | no | BNL 2002 |
| std6a(dba) | | 9.03 | 229.10 | no | UMC 98 |
| bnl5.46b | | 9.03 | 230.00 | no | IBM2 |
| umc1599 | A C | 9.03 | 230.10 | no | IBM2 |
| csu623 | A C | 9.03 | 230.60 | yes | IBM2 |
| umc1191 | C | 9.03 | 232.80 | yes | IBM2 |
| mmp2 | | 9.03 | 235.50 | yes | IBM2 |
| umc1420 | | 9.03 | 236.88 | no | SSR popl |
| asg63a | | 9.03 | 238.00 | yes | IBM2 |
| umc2340 | A C | 9.03 | 238.40 | no | IBM2 |
| umc2339 | A C | 9.03 | 238.90 | yes | IBM2 |
| gtd101 | C | 9.03 | 238.90 | no | ChromDB |
| umc1271 | A C | 9.03 | 240.50 | yes | IBM2 |
| si605086B11 | C | 9.03 | 242.58 | no | INDEL |
| umc1691 | A C | 9.03 | 244.10 | yes | IBM2 |
| umc2412 | | 9.03-9.04 | 247.06 | no | SSR poplI |
| umc1688 | A C | 9.03 | 247.60 | yes | IBM2 |
| acp1 | | 9.03 | 249.20 | no | UMC 98 |
| umc20 | C | 9.03 | 249.20 | yes | IBM2 |
| asg68a | | 9.03 | 249.20 | no | UMC 98 |
| csu857 | | 9.03 | 249.20 | no | UMC 98 |
| gl15 | A C | 9.03 | 249.20 | no | UMC 98 |
| pbs14d | | 9.03 | 249.20 | no | BNL 2002 |
| npi222a | | 9.03 | 249.27 | no | BNL 2002 |
| umc1921 | | 9.03 | 249.60 | yes | IBM2 |
| uaz223(vpp) | | 9.03 | 250.40 | no | BNL 2002 |
| mwg645g | | 9.04 | 250.89 | no | BNL 2002 |
| uaz161b(elf) | | 9.03 | 251.65 | no | BNL 2002 |
| umc1700 | A C | 9.03 | 251.80 | yes | IBM2 |
| umc2087 | A C | 9.03 | 252.30 | no | IBM2 |
| npi454 | | 9.03-9.04 | 253.02 | no | BNL 2002 |
| AW257883 | A C | 9.03 | 253.70 | no | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| bnlg127 |  | 9.03 | 253.77 | no | BNL 2002 |
| umc1743 | A C | 9.03 | 254.00 | yes | IBM2 |
| umc114 | C | 9.03 | 254.30 | yes | IBM2 |
| AY103770 | A C | 9.03 | 254.60 | no | IBM2 |
| mmc0051 |  | 9.03-9.04 | 254.74 | no | SSR popII |
| bnl5.04 |  | 9.03 | 256.10 | yes | IBM2 |
| csu181b |  | 9.03-9.04 | 256.10 | no | UMC 98 |
| csu252b(cdc2) |  | 9.03-9.04 | 256.10 | no | UMC 98 |
| csu179b(hsp70) |  | 9.03-9.04 | 256.10 | no | UMC 98 |
| umc1267 | A C | 9.03 | 257.60 | no | IBM2 |
| rz682 | C | 9.03 | 258.20 | yes | IBM2 |
| csu147 | A C | 9.04 | 258.51 | no | SSR popII |
| knox2 |  | 9.03 | 258.91 | no | BNL 2002 |
| bnlg430 |  | 9.03 | 258.91 | no | BNL 2002 |
| bnlg1687 |  | 9.03 | 258.91 | no | BNL 2002 |
| bnlg1688 |  | 9.03-9.04 | 259.76 | no | BNL 2002 |
| lim99b |  | 9.04 | 259.80 | yes | IBM2 |
| fd1 |  | 9.03 | 261.09 | no | BNL 2002 |
| pic1a |  | 9.04 | 263.11 | no | BNL 96 |
| umc2394 |  | 9.03-9.04 | 263.79 | no | SSR popII |
| bnl7.13 | C | 9.04 | 264.90 | yes | IBM2 |
| hm2 | C | 9.03-9.04 | 264.90 | no | UMC 98 |
| csu254a |  | 9.03-9.04 | 264.90 | no | UMC 98 |
| csu214a(grp) |  | 9.03-9.04 | 264.90 | no | UMC 98 |
| csu778(lhcb) |  | 9.03-9.04 | 264.90 | no | UMC 98 |
| sbp4 | C | 9.04 | 266.00 | yes | IBM2 |
| bnlg1714 |  | 9.04 | 266.40 | no | IBM2 |
| isu2191k |  | 9.03 | 266.46 | no | BNL 2002 |
| ici266 |  | 9.04 | 267.04 | no | BNL 2002 |
| lim166 |  | 9.04 | 268.40 | yes | IBM2 |
| csu263a |  | 9.04 | 272.79 | no | UMC 98 |
| csu56d(ohp) | C | 9.04 | 272.79 | no | UMC 98 |
| csu183b(cdc48) |  | 9.04 | 272.79 | no | SSR popI |
| bnlg1209 | A C | 9.04 | 273.20 | yes | IBM2 |
| umc1522 |  | 9.04 | 275.14 | no | SSR popII |
| psr547 |  | 9.04 | 278.90 | yes | IBM2 |
| psr129a |  | 9.04 | 283.10 | yes | IBM2 |
| uaz112 |  | 9.04 | 283.36 | no | BNL 2002 |
| umc2398 |  | 9.04 | 283.58 | no | SSR popII |
| umc1107 | C | 9.04 | 285.80 | yes | IBM2 |
| bnlg1159b | C | 9.04 | 287.00 | yes | IBM2 |
| pbs14c |  | 9.04 | 287.79 | no | BNL 2002 |
| gta101c |  | 9.04 | 290.10 | yes | IBM2 |
| bnlg1012 | A C | 9.04 | 298.00 | yes | IBM2 |
| umc1878 |  | 9.04 | 298.43 | no | SSR popII |
| ufg66 |  | 9.04 | 300.00 | no | IBM2 |
| ufg73 |  | 9.04 | 300.00 | no | IBM2 |
| ufg70 | C | 9.04 | 300.20 | yes | IBM2 |
| ufg35a |  | 9.04 | 300.60 | no | IBM2 |
| npi580a |  | 9.04 | 302.30 | yes | IBM2 |
| csu43 | C | 9.04 | 302.89 | no | UMC 98 |
| csu557 |  | 9.04 | 302.89 | no | UMC 98 |
| rz251b |  | 9.04 | 302.89 | no | UMC 98 |
| csu212a |  | 9.04 | 302.89 | no | UMC 98 |
| csu404a |  | 9.04 | 302.89 | no | UMC 98 |
| rgpc524 |  | 9.04 | 302.89 | no | UMC 98 |
| wsu1(ptk) |  | 9.04 | 302.89 | no | UMC 98 |
| isu41a |  | 9.04 | 304.90 | yes | IBM2 |
| ufg68 |  | 9.04 | 306.20 | yes | IBM2 |
| umc1492 | A C | 9.04 | 308.00 | yes | IBM2 |
| umc1120 | A C | 9.04 | 309.90 | yes | IBM2 |
| sus1 | A C | 9.04 | 311.50 | yes | IBM2 |
| npi293a |  | 9.05 | 311.50 | no | BNL 2002 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| rgpr3239b |  | 9.04 | 311.50 | no | UMC 98 |
| AY109764 | A C | 9.04 | 311.90 | no | IBM2 |
| uaz236a(ser) |  | 9.04 | 312.12 | no | BNL 2002 |
| bnlg1270 |  | 9.05-9.06 | 312.20 | no | BNL 2002 |
| mmp96 |  | 9.04 | 312.50 | yes | IBM2 |
| mmp37 |  | 9.04 | 314.30 | yes | IBM2 |
| csu694a(uce) | C | 9.04 | 315.56 | no | UMC 98 |
| umc2121 | A C | 9.04 | 315.70 | yes | IBM2 |
| umc38c | C | 9.04 | 317.00 | yes | IBM2 |
| bnl7.50 |  | 9.04-9.05 | 317.01 | no | UMC 98 |
| umc1771 | A C | 9.04 | 317.27 | no | SSR popII |
| bnl8.17 | C | 9.04 | 320.20 | no | IBM2 |
| umc95 |  | 9.05 | 320.60 | yes | IBM2 |
| umc1519 |  | 9.04 | 320.60 | no | SSR popII |
| rgpr44b |  | 9.04-9.05 | 320.60 | no | UMC 98 |
| uaz119c(rpS6) |  | 9.04 | 321.79 | no | BNL 2002 |
| umc140b |  | 9.05 | 321.90 | yes | IBM2 |
| umc1078 | A C | 9.05 | 322.60 | yes | IBM2 |
| lim458 |  | 9.05 | 324.20 | yes | IBM2 |
| ufg13a |  | 9.05 | 326.00 | yes | IBM2 |
| ufg64 |  | 9.05 | 329.30 | yes | IBM2 |
| ufg63 | C | 9.05 | 331.20 | yes | IBM2 |
| umc1654 |  | 9.05 | 332.24 | no | SSR popII |
| umc1387 | A C | 9.04-9.05 | 334.54 | no | SSR popI |
| ufg48 |  | 9.05 | 335.80 | no | IBM2 |
| mmp153 |  | 9.05 | 336.10 | no | IBM2 |
| php20554 |  | 9.05 | 338.10 | yes | IBM2 |
| umc1357 | A C | 9.05 | 340.38 | no | SSR popI |
| umc1231 | A C | 9.05 | 342.00 | yes | IBM2 |
| chr125a |  | 9.05 | 343.10 | no | ChromDB |
| mmp41 |  | 9.05 | 343.70 | yes | IBM2 |
| hsp18a |  | 9.05 | 344.57 | no | BNL 2002 |
| umc1657 | A C | 9.05 | 344.80 | no | IBM2 |
| csu395b | C | 9.05 | 348.57 | no | UMC 98 |
| mmp151d |  | 9.05 | 348.80 | yes | IBM2 |
| dpg6c |  | 9.05 | 350.07 | no | BNL 2002 |
| pge(phyB2) |  | 9.05 | 350.07 | no | BNL 96 |
| bnlg1091 |  | 9.05-9.06 | 351.23 | no | BNL 2002 |
| mmp179 |  | 9.05 | 354.40 | no | IBM2 |
| uaz266b |  | 9.04 | 356.53 | no | BNL 2002 |
| ncr(sod4b) |  | 9.05 | 356.53 | no | BNL 2002 |
| rpa8 |  | 9.05 | 358.24 | no | UMC 98 |
| csu392a |  | 9.05 | 358.24 | no | UMC 98 |
| csu355(ext) |  | 9.05 | 358.24 | no | UMC 98 |
| ufg67 |  | 9.05 | 361.40 | yes | IBM2 |
| ufg47 |  | 9.05 | 362.20 | yes | IBM2 |
| uaz125 |  | 9.05 | 362.23 | no | BNL 2002 |
| AY109792 | A C | 9.05 | 369.30 | yes | IBM2 |
| csu710e(apx) |  | 9.05 | 372.40 | no | UMC 98 |
| uaz264a |  | 9.05 | 372.64 | no | BNL 2002 |
| AY110217 | A C | 9.05 | 373.20 | no | IBM2 |
| umc1494 | A C | 9.05 | 373.66 | no | SSR popI |
| csu219(tgd) |  | 9.05 | 376.55 | no | UMC 98 |
| csu58b |  | 9.05 | 378.34 | no | BNL 2002 |
| umc2095 | A C | 9.05 | 378.90 | yes | IBM2 |
| umc2341 | A C | 9.05-9.06 | 381.10 | yes | IBM2 |
| ibp1 |  | 9.05 | 382.70 | no | UMC 98 |
| csu634 | A C | 9.05 | 382.70 | yes | IBM2 |
| bnl8.08d |  | 9.05 | 383.14 | no | BNL 2002 |
| rz574b(cwp) |  | 9.05 | 383.80 | yes | IBM2 |
| umc2344 | A C | 9.05-9.06 | 384.80 | no | IBM2 |
| umc2342 | A C | 9.05-9.06 | 384.90 | no | IBM2 |
| si687046G05 | C | 9.05 | 385.03 | no | INDEL |
| umc2343 | A C | 9.05-9.06 | 385.30 | no | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| npi427a | | 9.05 | 386.80 | yes | IBM2 |
| ufg24 | C | 9.05 | 392.50 | yes | IBM2 |
| umc2134 | | 9.05 | 404.30 | yes | IBM2 |
| umc1732 | | 9.05 | 405.02 | no | SSR popI |
| npi443 | | 9.05 | 409.90 | yes | IBM2 |
| umc1417 | C | 9.05 | 411.95 | no | SSR popII |
| umc2371 | C | 9.05-9.06 | 418.60 | no | SSR popII |
| umc1794 | C | 9.05 | 420.18 | no | SSR popII |
| mmp142 | | 9.06 | 421.60 | yes | IBM2 |
| csu59a | AC | 9.05 | 425.25 | no | UMC 98 |
| csu61a | AC | 9.06 | 425.25 | no | SSR popII |
| csu145a(pck) | | 9.05 | 427.70 | no | UMC 98 |
| AY109550 | | 9.06 | 429.70 | no | IBM2 |
| uaz96a | | 9.06 | 430.51 | no | BNL 2002 |
| npi439b | | 9.06 | 431.70 | yes | IBM2 |
| npi425d | | 9.05 | 433.35 | no | UMC 98 |
| mmp132 | | 9.06 | 433.50 | yes | IBM2 |
| dba4 | | 9.06 | 438.50 | no | UMC 98 |
| csu28a(rpS22) | | 9.06 | 438.50 | no | UMC 98 |
| asg44 | | 9.06 | 441.20 | yes | IBM2 |
| mmp131 | | 9.06 | 458.50 | yes | IBM2 |
| umc2346 | C | 9.06 | 461.60 | yes | IBM2 |
| bnlg292a | C | 9.06 | 462.87 | no | BNL 2002 |
| csu93a | C | 9.06 | 463.90 | yes | IBM2 |
| cdo1387a(emp70) | | 9.06 | 465.16 | no | UMC 98 |
| bnlg1191 | | 9.07 | 467.46 | no | BNL 2002 |
| ufg75c | | 9.06 | 477.20 | yes | IBM2 |
| bnl7.57 | | 9.06 | 480.19 | no | BNL 96 |
| mmp168 | | 9.06 | 486.50 | yes | IBM2 |
| nfd104d | | 9.06 | 489.40 | no | ChromDB |
| chs5046 | | 9.05-9.06 | 489.80 | no | BNL 2002 |
| umc1366 | | 9.06 | 489.90 | yes | IBM2 |
| umc2345 | C | 9.06 | 492.30 | yes | IBM2 |
| hb1 | C | 9.06 | 494.50 | no | IBM2 |
| bnl5.09a | | 9.06 | 500.10 | yes | IBM2 |
| uom1(hb) | | 9.06 | 500.17 | no | UMC 98 |
| uaz148 | | 9.06 | 501.12 | no | BNL 2002 |
| bnlg1588 | | 9.07 | 501.46 | no | BNL 2002 |
| mmp110 | | 9.06 | 504.60 | yes | IBM2 |
| mpik28(zmm8) | | 9.06 | 508.79 | no | UMC 98 |
| AY110141 | C | 9.06 | 517.50 | yes | IBM2 |
| umc1310 | AC | 9.06 | 517.73 | no | SSR popII |
| cdo1395a | | 9.06 | 519.32 | no | UMC 98 |
| umc2207 | | 9.06 | 520.76 | no | SSR popI |
| csu1004 | | 9.06 | 525.07 | no | UMC 98 |
| AY109819 | AC | 9.06 | 526.00 | yes | IBM2 |
| csu877 | | 9.06 | 528.90 | no | UMC 98 |
| bnl14.28a | | 9.06 | 528.90 | yes | IBM2 |
| npi403a | | 9.06 | 528.90 | no | BNL 2002 |
| isu49 | | 9.06 | 530.80 | yes | IBM2 |
| umc2358 | | 9.06-9.07 | 531.03 | no | SSR popII |
| umc1789 | AC | 9.06 | 534.20 | yes | IBM2 |
| asg12 | AC | 9.07 | 536.10 | yes | IBM2 |
| npi209a | | 9.06-9.07 | 536.10 | no | UMC 98 |
| bnlg1525 | | 9.07 | 536.65 | no | BNL 2002 |
| phi448880 | AC | 9.06-9.07 | 536.80 | no | IBM2 |
| AY109543 | AC | 9.07 | 538.50 | yes | IBM2 |
| umc1675 | | 9.07 | 541.40 | yes | IBM2 |
| csu1005 | | 9.07 | 541.42 | no | UMC 98 |
| csu860a | | 9.07 | 541.42 | no | UMC 98 |
| umc1804 | | 9.07 | 542.26 | no | SSR popII |
| npi291 | | 9.07 | 542.48 | no | BNL 96 |
| std2a(dba) | | 9.07 | 544.97 | no | UMC 98 |
| bnlg1506 | | 9.07-9.08 | 547.75 | no | BNL 2002 |
| dupssr29 | | 9.07 | 550.43 | no | BNL 2002 |
| umc2359 | | 9.07 | 550.46 | no | SSR popII |
| bnlg1375 | | 9.07 | 551.02 | no | BNL 2002 |
| AY110382 | AC | 9.07 | 551.30 | no | IBM2 |
| bnlg619 | AC | 9.07 | 554.40 | yes | IBM2 |
| csu870 | | 9.07 | 554.44 | no | UMC 98 |
| csu1118 | | 9.07 | 554.44 | no | UMC 98 |
| ucsd61b | | 9.07 | 554.57 | no | BNL 2002 |
| mmp136 | | 9.07 | 556.40 | yes | IBM2 |
| umc2089 | AC | 9.07 | 562.70 | yes | IBM2 |
| umc2131 | AC | 9.07 | 566.80 | yes | IBM2 |
| umc1714 | AC | 9.07 | 567.30 | no | IBM2 |
| jpsb596 | | 9.07 | 567.70 | yes | IBM2 |
| npi97b | | 9.07 | 571.04 | no | BNL 96 |
| mmp171a | | 9.07 | 577.20 | yes | IBM2 |
| umc2347 | AC | 9.07-9.08 | 578.60 | no | IBM2 |
| bnlg128 | AC | 9.07 | 585.93 | no | SSR popI |
| AY106323 | AC | 9.08 | 587.90 | yes | IBM2 |
| csu50b | | 9.08 | 596.44 | no | BNL 2002 |
| dpg12c | | 9.08 | 601.89 | no | BNL 2002 |
| umc1137 | C | 9.08 | 603.50 | yes | IBM2 |
| csh2c(cdc2) | | 9.08 | 604.50 | no | BNL 2002 |
| asg59b | | 9.07 | 604.73 | no | UMC 98 |
| ucsd107a | | 9.08 | 606.53 | no | BNL 2002 |
| uaz31a | | 9.08 | 607.91 | no | BNL 2002 |
| umc94b | | 9.08 | 607.91 | no | BNL 96 |
| PCO127444 | C | 9.08 | 622.15 | no | INDEL |
| rz632b | | 9.07 | 626.03 | no | UMC 98 |
| csu883(rpL21) | | 9.07 | 628.99 | no | UMC 98 |
| dmt103a | C | 9.08 | 631.09 | no | ChromDB |
| umc1982 | C | 9.08 | 633.20 | no | IBM2 |
| bnlg1129 | C | 9.08 | 633.60 | no | IBM2 |
| bnl1.297b | | 9.08 | 635.20 | no | IBM1 |
| umc1505 | C | 9.08 | 635.20 | yes | IBM2 |
| mmp53 | | 9.08 | 636.20 | no | IBM2 |
| rz561c | | 9.07 | 636.68 | no | UMC 98 |
| umc272(vfa) | | 9.07 | 636.68 | no | UMC 98 |
| AI901738 | C | 9.08 | 637.10 | yes | IBM2 |
| AW216329 | C | 9.08 | 638.70 | yes | IBM2 |
| umc1104 | AC | 9.07 | 660.54 | no | SSR popII |
| umc1942 | | 9.07 | 678.34 | no | SSR popII |
| std20a(uce) | | 9.07 | 686.38 | no | UMC 98 |
| csu285(his2B) | | 9.07 | 691.11 | no | UMC 98 |
| klp6 | | 9.07 | 701.76 | no | UMC 98 |
| csu54b | C | 9.08 | 708.86 | no | SSR popI |
| umc1277 | C | 9.07-9.08 | 708.86 | no | SSR popII |
| csu804a(dnp) | | 9.07-9.08 | 708.86 | no | UMC 98 |
| ucsd72b | | 10.00 | -24.00 | no | BNL 96 |
| mmp48a | | 10.00 | 0.00 | yes | IBM2 |
| mmp48b | | 10.00 | 11.00 | yes | IBM2 |
| bnl10.17a | | 10.00 | 13.20 | no | UMC 98 |
| csu306(fer) | | 10.00 | 13.20 | no | UMC 98 |
| mpik13a | | 10.00 | 13.98 | no | BNL 2002 |
| umc1380 | C | 10.00 | 16.60 | yes | IBM2 |
| php20626 | | 10.00 | 19.10 | yes | IBM2 |
| AY110060 | | 10.00 | 22.30 | yes | IBM2 |
| psr119c | | 10.00 | 28.30 | yes | IBM2 |
| bnl3.04 | | 10.00 | 29.60 | yes | IBM2 |
| php20725b | | 10.00 | 29.90 | no | IBM2 |
| php20753a | | 10.00 | 30.00 | yes | IBM2 |
| phi041 | C | 10.00 | 30.90 | yes | IBM2 |
| ksu1e | | 10.00-10.01 | 34.80 | no | UMC 98 |
| php20075a(gast) | C | 10.01 | 34.80 | yes | IBM2 |
| umc1293 | C | 10.00 | 44.33 | no | SSR popI |
| ksu1f | | 10.01 | 44.70 | no | UMC 98 |
| mpik33::cin4 | | 10.01 | 48.08 | no | BNL 2002 |
| AW330564 | AC | 10.01 | 53.00 | yes | IBM2 |
| csu1061b | | 10.01 | 55.80 | yes | IBM2 |
| agrc561 | | 10.01 | 57.15 | no | UMC 98 |
| umc1291 | AC | 10.01 | 58.76 | no | SSR popII |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| csu136(plt) |  | 10.01 | 61.94 | no | UMC 98 |
| umc1318 | A C | 10.01 | 62.41 | no | SSR popI |
| AW225120 | A C | 10.01 | 64.10 | yes | IBM2 |
| csu1042 |  | 10.01 | 64.82 | no | UMC 98 |
| ksu2 |  | 10.01 | 71.20 | no | UMC 98 |
| ksu3 |  | 10.01 | 71.20 | no | UMC 98 |
| bnlg1451 |  | 10.02 | 74.44 | no | BNL 2002 |
| umc2053 | A C | 10.01 | 76.20 | yes | IBM2 |
| umc2018 | A C | 10.01 - 10.02 | 81.10 | yes | IBM2 |
| phi063 |  | 10.02 | 82.25 | no | BNL 2002 |
| umc1319 |  | 10.01 | 82.42 | no | SSR popII |
| csu577 |  | 10.01 | 85.25 | no | UMC 98 |
| csu359(alp) |  | 10.01 | 86.21 | no | UMC 98 |
| cdo127b(pyk) | C | 10.01 | 86.21 | no | UMC 98 |
| npi285a(cac) | A C | 10.02 | 91.00 | no | IBM2 |
| umc1152 | A C | 10.02 | 91.40 | yes | IBM2 |
| gdcp1 | A C | 10.02 | 97.90 | yes | IBM2 |
| umc1432 | A C | 10.02 | 99.63 | no | SSR popII |
| uaz21c |  | 10.01 | 100.78 | no | BNL 2002 |
| cr4 | C | 10.02 | 102.46 | no | UMC 98 |
| AY110360 | C | 10.02 | 104.00 | yes | IBM2 |
| ksu5 |  | 10.02 | 105.12 | no | UMC 98 |
| mmc0501 | A C | 10.02 | 106.70 | no | SSR popII |
| umc2034 | A C | 10.02 | 120.10 | yes | IBM2 |
| agrc714 |  | 10.02 | 121.64 | no | UMC 98 |
| csu250a(aba) |  | 10.02 | 121.64 | no | UMC 98 |
| csu103a(aba) | C | 10.02-10.03 | 123.02 | no | BNL 96 |
| rz400(gbp) |  | 10.02 | 126.17 | no | UMC 98 |
| AI795367 | A C | 10.02 | 134.80 | yes | IBM2 |
| umc1582 |  | 10.02 | 138.79 | no | SSR popI |
| tda217a |  | 10.02 | 140.82 | no | UMC 98 |
| AY109994 | C | 10.02 | 142.00 | yes | IBM2 |
| umc1337 | A C | 10.02 | 143.30 | no | IBM2 |
| phi059 | A C | 10.02 | 143.50 | yes | IBM2 |
| uaz153 |  | 10.03 | 144.73 | no | BNL 2002 |
| isu85b |  | 10.02 | 144.80 | yes | IBM2 |
| dpg3 |  | 10.03 | 144.92 | no | BNL 2002 |
| upen1 |  | 10.02 | 145.79 | no | BNL 2002 |
| rz900c(ahh) |  | 10.02 | 146.80 | no | IBM2 |
| rz900b |  | 10.02 | 146.80 | no | ChromDB |
| ucsd72k |  | 10.03 | 148.07 | no | BNL 2002 |
| ucsd72m |  | 10.03 | 148.07 | no | BNL 2002 |
| umc152a |  | 10.02 | 148.59 | no | BNL 96 |
| umc2114 | A C | 10.02 | 148.90 | no | IBM2 |
| csu561b |  | 10.02 | 150.41 | no | UMC 98 |
| csu1054 |  | 10.02 | 155.74 | no | UMC 98 |
| umc2069 |  | 10.02 | 155.90 | yes | IBM2 |
| PCO062847 | C | 10.02-10.03 | 156.93 | no | INDEL |
| umc130 | A C | 10.03 | 160.00 | yes | IBM2 |
| npi250a |  | 10.03 | 160.00 | no | BNL 2002 |
| csu625 |  | 10.03 | 160.40 | yes | IBM2 |
| ov23 |  | 10.03 | 160.88 | no | BNL 2002 |
| bnlg1547 |  | 10.03 | 161.85 | no | BNL 2002 |
| uaz24a |  | 10.03 | 161.97 | no | BNL 2002 |
| bnlg1085c |  | 10.03 | 162.40 | no | BNL 2002 |
| uaz178 |  | 10.03 | 162.98 | no | BNL 2002 |
| ias13c |  | 10.03 | 163.12 | no | BNL 2002 |
| npi105a |  | 10.03 | 163.20 | yes | IBM2 |
| uaz97 |  | 10.03 | 163.20 | no | BNL 2002 |
| uaz98 |  | 10.03 | 163.20 | no | BNL 2002 |
| npi417b |  | 10.03 | 163.20 | no | BNL 2002 |
| mpik41c(mem1) |  | 10.03 | 163.20 | no | UMC 98 |
| uaz242(clp) |  | 10.03 | 163.43 | no | BNL 2002 |
| umc18b(psaN) |  | 10.03 | 164.10 | yes | IBM2 |
| umc1863 |  | 10.03 | 165.52 | no | SSR popI |
| gcsh1 | C | 10.03 | 168.20 | yes | IBM2 |
| csu234b(gbp) |  | 10.03 | 168.20 | no | UMC 98 |
| csu237a(psaN) |  | 10.03 | 168.20 | no | UMC 98 |
| lim2 |  | 10.03 | 173.50 | yes | IBM2 |
| dpg5 |  | 10.03 | 176.43 | no | BNL 2002 |
| bcd1072b(hsp70) |  | 10.03 | 177.50 | yes | IBM2 |
| glu1 | C | 10.03 | 178.60 | no | UMC 98 |
| csu1050 |  | 10.03 | 178.60 | no | UMC 98 |
| php06005 |  | 10.03 | 178.60 | yes | IBM2 |
| csu745c(rpPo) | C | 10.03 | 178.60 | no | UMC 98 |
| php1 |  | 10.03 | 179.04 | no | BNL 2002 |
| npi98c |  | 10.03 | 179.04 | no | BNL 2002 |
| npi327b |  | 10.03 | 179.04 | no | BNL 2002 |
| npi597b |  | 10.03 | 179.04 | no | BNL 2002 |
| bnlg1762 |  | 10.03 | 179.04 | no | BNL 2002 |
| umc(orp2) |  | 10.03 | 179.04 | no | BNL 2002 |
| rz261a(sad) |  | 10.03 | 179.90 | no | UMC 98 |
| rgpc1122d(rpL15) |  | 10.03 | 179.90 | no | UMC 98 |
| rgpr440c(gap) |  | 10.03 | 180.23 | no | UMC 98 |
| umc1785 |  | 10.03 | 180.24 | no | SSR popI |
| umc1312 | A C | 10.03 | 180.24 | no | SSR popI |
| umc1962 | A C | 10.03 | 180.70 | yes | IBM2 |
| umc1866 |  | 10.03 | 180.70 | no | SSR popII |
| asg76a |  | 10.03 | 182.18 | no | UMC 98 |
| zmm1 |  | 10.03 | 182.96 | no | BNL 2002 |
| eoh1 |  | 10.03 | 183.15 | no | UMC 98 |
| rgpc496c(adh) |  | 10.03 | 183.15 | no | UMC 98 |
| bnlg210 | A C | 10.03 | 183.40 | yes | IBM2 |
| bnlg1037 |  | 10.03 | 183.41 | no | BNL 2002 |
| bnlg1716 |  | 10.03 | 183.41 | no | BNL 2002 |
| chs5008 |  | 10.03 | 183.44 | no | BNL 2002 |
| bcd98c |  | 10.03 | 183.62 | no | BNL 2002 |
| bnlg2216 |  | 10.03 | 183.62 | no | BNL 2002 |
| umc1367 | C | 10.03 | 183.80 | yes | IBM2 |
| chr109a | C | 10.03 | 183.80 | no | ChromDB |
| csu213b |  | 10.03 | 184.45 | no | UMC 98 |
| uaz116 |  | 10.03 | 184.70 | yes | IBM2 |
| sdg108b | C | 10.03 | 184.90 | no | ChromDB |
| php20646 |  | 10.03 | 185.10 | yes | IBM2 |
| umc1381 | A C | 10.03 | 187.00 | yes | IBM2 |
| ufg30a |  | 10.03 | 188.80 | no | IBM2 |
| AY110411 | C | 10.03 | 191.20 | yes | IBM2 |
| AY105746 | C | 10.03 | 193.60 | no | IBM2 |
| umc2067 | A C | 10.03 | 194.50 | no | IBM2 |
| umc2016 | A C | 10.03 | 195.40 | yes | IBM2 |
| bcd147(gbp) | C | 10.03 | 196.40 | yes | IBM2 |
| jpsb527c |  | 10.03 | 197.90 | yes | IBM2 |
| umc1345 | C | 10.03 | 199.50 | yes | IBM2 |
| AY110248 | C | 10.03 | 200.50 | yes | IBM2 |
| ufg59 | C | 10.03 | 203.00 | yes | IBM2 |
| mmp63 |  | 10.03 | 204.80 | no | IBM2 |
| rps3 |  | 10.03 | 208.50 | yes | IBM2 |
| bnlg1079 | A C | 10.03 | 213.10 | no | IBM2 |
| umc1239 | A C | 10.03 | 213.30 | yes | IBM2 |
| psr690 |  | 10.03 | 215.80 | yes | IBM2 |
| npi445a |  | 10.03 | 217.20 | yes | IBM2 |
| bnlg1712 | A C | 10.03 | 217.80 | yes | IBM2 |
| ensl003 |  | 10.03 | 217.80 | no | BNL 2002 |
| csh::stAc |  | 10.04 | 219.25 | no | BNL 2002 |
| AY112073 | A C | 10.03 | 220.10 | yes | IBM2 |
| npi602 |  | 10.03 | 222.50 | no | SSR popII |
| umc1938 |  | 10.03 | 222.50 | no | SSR popII |
| mpik20b |  | 10.03 | 225.11 | no | BNL 2002 |
| umc155 | A C | 10.03 | 225.70 | yes | IBM2 |
| AY111178 | C | 10.03 | 227.40 | yes | IBM2 |
| umc2349 | A C | 10.03-10.04 | 227.90 | no | IBM2 |
| umc1739 | A C | 10.03 | 228.00 | no | IBM2 |
| bnlg1655 | A C | 10.03 | 228.00 | no | IBM2 |
| umc1336 | A C | 10.03 | 228.30 | yes | IBM2 |
| umc2180 | A C | 10.03-10.04 | 228.30 | no | IBM2 |
| ncsu2 |  | 10.04 | 230.74 | no | BNL 96 |
| fgp1 | C | 10.03 | 234.30 | yes | IBM2 |
| umc64a |  | 10.04 | 242.30 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| orp2 | | 10.03-10.04 | 242.30 | no | UMC 98 |
| agrr62a | | 10.03-10.04 | 242.30 | no | UMC 98 |
| csu599b | | 10.03-10.04 | 242.30 | no | UMC 98 |
| umc243a | | 10.03-10.04 | 242.30 | no | UMC 98 |
| npi327a | | 10.04 | 242.39 | no | BNL 2002 |
| bnlg640 | A C | 10.03-10.04 | 242.39 | no | SSR popII |
| uaz100(prl) | | 10.03 | 242.84 | no | BNL 2002 |
| bnlg2336 | | 10.04 | 242.87 | no | BNL 2002 |
| bnlg1526 | | 10.04 | 243.01 | no | BNL 2002 |
| acc1 | | 10.04 | 243.12 | no | BNL 2002 |
| uaz99 | | 10.04 | 243.18 | no | BNL 2002 |
| sad1 | | 10.02 | 243.24 | no | BNL 2002 |
| uaz175a | | 10.04 | 243.29 | no | BNL 2002 |
| umc1873 | | 10.04 | 243.57 | no | SSR popII |
| uaz117b | | 10.04 | 243.61 | no | BNL 96 |
| csu815 | | 10.04 | 244.19 | no | UMC 98 |
| csu913 | | 10.04 | 244.19 | no | UMC 98 |
| csu929(his3) | | 10.04 | 244.19 | no | UMC 98 |
| uaz76b | | 10.04 | 244.26 | no | BNL 2002 |
| csu797(uce) | | 10.04 | 244.40 | no | UMC 98 |
| csu951(eno) | | 10.04 | 244.40 | no | UMC 98 |
| uaz228b(his2b) | | 10.05 | 244.48 | no | BNL 2002 |
| dupssr31 | | 10.04 | 244.55 | no | BNL 2002 |
| umc2348 | A C | 10.03-10.04 | 244.60 | no | IBM2 |
| hcf106c | | 10.04 | 245.64 | no | BNL 2002 |
| umc1995 | A C | 10.04 | 245.90 | yes | IBM2 |
| csu898 | | 10.04 | 246.51 | no | UMC 98 |
| nac1 | A C | 10.04 | 246.51 | no | UMC 98 |
| cdo1395b | | 10.04 | 246.51 | no | UMC 98 |
| umc1589 | C | 10.04 | 247.73 | no | SSR popII |
| umc1824c | C | 10.04 | 247.73 | no | SSR popII |
| isu1719a | | 10.04 | 247.96 | no | BNL 2002 |
| umc1246 | C | 10.04 | 248.20 | yes | IBM2 |
| csu276 | | 10.04 | 249.03 | no | UMC 98 |
| csu613(acb) | | 10.04 | 251.13 | no | UMC 98 |
| rgpr1908b(acb) | | 10.04 | 251.13 | no | UMC 98 |
| mmp16 | | 10.04 | 251.60 | yes | IBM2 |
| csu46a | | 10.04 | 253.24 | no | UMC 98 |
| umc1077 | A C | 10.04 | 253.30 | yes | IBM2 |
| rz69 | A C | 10.04 | 253.40 | no | IBM2 |
| AY110514 | A C | 10.04 | 254.50 | no | IBM2 |
| amo1 | C | 10.04 | 256.18 | no | UMC 98 |
| csu298b | | 10.04 | 256.18 | no | UMC 98 |
| AY109920 | C | 10.04 | 256.80 | yes | IBM2 |
| AY109876 | C | 10.04 | 259.40 | yes | IBM2 |
| csu864 | | 10.04 | 259.97 | no | UMC 98 |
| csu671b | | 10.04 | 259.97 | no | UMC 98 |
| mgs1 | A C | 10.04 | 260.50 | yes | IBM2 |
| csu333 | | 10.04 | 260.60 | no | UMC 98 |
| tda205 | | 10.04 | 260.60 | no | UMC 98 |
| psu1b(spe) | | 10.04 | 260.60 | no | UMC 98 |
| csu893(isp) | | 10.04 | 260.60 | no | UMC 98 |
| umc1836 | | 10.04 | 261.80 | no | IBM2 |
| AY109584 | | 10.04 | 261.90 | no | IBM2 |
| jpsb527d | | 10.04 | 264.20 | yes | IBM2 |
| npi305b | | 10.04 | 265.15 | no | BNL 96 |
| umc1827 | | 10.04 | 267.28 | no | SSR popI |
| mzetc34 | A C | 10.04 | 268.10 | no | IBM2 |
| PCO086427 | C | 10.04 | 268.32 | no | INDEL |
| mmp121 | A C | 10.04 | 269.60 | yes | IBM2 |
| AY110365 | A C | 10.04 | 271.30 | yes | IBM2 |
| incw3 | A C | 10.04 | 272.20 | yes | IBM2 |
| umc1911 | A C | 10.04 | 273.60 | yes | IBM2 |
| bnlg2127 | | 10.04 | 274.03 | no | BNL 2002 |
| npi264 | | 10.04 | 274.10 | no | IBM2 |
| npi303 | | 10.04 | 274.10 | no | BNL 2002 |
| umc1453 | A C | 10.04 | 274.40 | no | IBM2 |
| asg2 | C | 10.04 | 277.20 | yes | IBM2 |
| csu948 | | 10.04 | 277.23 | no | UMC 98 |
| umc261 | | 10.04 | 277.34 | no | UMC 98 |
| npi294h | | 10.04 | 277.63 | no | UMC 98 |
| AY109698 | A C | 10.04 | 280.70 | yes | IBM2 |
| umc2350 | A C | 10.04 | 283.50 | yes | IBM2 |
| bnlg137 | | 10.05 | 285.73 | no | BNL 2002 |
| umc1330 | C | 10.04 | 287.90 | yes | IBM2 |
| gpa2 | | 10.04 | 288.38 | no | UMC 98 |
| csu86 | C | 10.04 | 288.38 | no | UMC 98 |
| umc146 | | 10.04 | 288.38 | no | UMC 98 |
| csu981(eif5A) | | 10.04 | 288.38 | no | UMC 98 |
| dpg6b | | 10.05 | 288.57 | no | BNL 96 |
| ufg1433 | | 10.04-10.05 | 288.57 | no | BNL 2002 |
| umc1697 | C | 10.04 | 290.90 | no | IBM2 |
| php15013 | | 10.04 | 291.60 | yes | IBM2 |
| ufg8(grf) | | 10.04 | 291.97 | no | UMC 98 |
| umc1280 | C | 10.04 | 292.26 | no | SSR popI |
| grf2 | | 10.04 | 292.87 | no | UMC 98 |
| PCO126344 | C | 10.04-10.05 | 294.80 | no | INDEL |
| umc1115 | C | 10.04 | 295.90 | yes | IBM2 |
| umc159b | | 10.04 | 296.90 | no | UMC 98 |
| hag103b | C | 10.04 | 298.04 | no | ChromDB |
| umc1272 | C | 10.04 | 299.40 | yes | IBM2 |
| umc1648 | C | 10.04 | 299.80 | no | IBM2 |
| umc2003 | A C | 10.04 | 301.60 | no | IBM2 |
| std4(dba) | | 10.04 | 304.07 | no | UMC 98 |
| rz740(sam) | | 10.04 | 304.07 | no | UMC 98 |
| umc1930 | | 10.04 | 306.90 | yes | IBM2 |
| php20719a | | 10.04 | 308.40 | yes | IBM2 |
| npi563 | | 10.04 | 308.70 | no | IBM2 |
| umc1678 | | 10.04 | 308.70 | no | IBM2 |
| umc259a | C | 10.05 | 309.00 | yes | IBM2 |
| sam1 | | 10.04-10.05 | 309.00 | no | UMC 98 |
| umc162a | | 10.04-10.05 | 309.00 | no | UMC 98 |
| umc163a | | 10.04-10.05 | 309.00 | no | UMC 98 |
| umc1507 | A C | 10.04-10.05 | 309.00 | no | SSR popII |
| ufg7B | | 10.05 | 309.04 | no | BNL 2002 |
| npi582 | | 10.04-10.05 | 309.07 | no | BNL 2002 |
| npi578 | | 10.05 | 309.20 | yes | IBM2 |
| umc1898 | | 10.05 | 309.91 | no | SSR popI |
| umc1677 | C | 10.05 | 311.40 | yes | IBM2 |
| isu58b | | 10.05 | 315.20 | yes | IBM2 |
| npi269b | | 10.05-10.06 | 318.69 | no | BNL 2002 |
| AY110634 | A C | 10.05 | 319.50 | no | IBM2 |
| npi232a | | 10.05 | 323.05 | no | UMC 98 |
| PCO129934 | C | 10.05 | 324.99 | no | INDEL |
| mmp12 | | 10.05 | 327.30 | yes | IBM2 |
| PCO087182 | C | 10.05 | 328.44 | no | INDEL |
| umc1402 | | 10.05 | 330.98 | no | SSR popI |
| umc2221 | | 10.05-10.06 | 331.38 | no | SSR popI |
| bnlg1074 | A C | 10.05 | 332.10 | yes | IBM2 |
| bnlg1250 | A C | 10.05 | 335.50 | yes | IBM2 |
| ufg81 | C | 10.05 | 341.10 | yes | IBM2 |
| AY110167 | | 10.05 | 342.70 | no | IBM2 |
| csu745a(rpPo) | C | 10.05 | 343.40 | yes | IBM2 |
| umc1506 | | 10.05 | 344.80 | yes | IBM2 |
| ufg3b(ivr) | | 10.05 | 348.73 | no | UMC 98 |
| ufg37 | | 10.05 | 352.40 | yes | IBM2 |
| ufg28a | | 10.05 | 352.40 | yes | IBM2 |
| ufg72 | | 10.05 | 352.60 | no | IBM2 |
| umc1477 | A C | 10.05-10.06 | 366.30 | yes | IBM2 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| umc44a | C | 10.06 | 367.85 | no | SSR popII |
| bnl17.08 |  | 10.06 | 372.35 | no | BNL 2002 |
| r1 | C | 10.06 | 373.11 | no | SSR popI |
| umc1045 | C | 10.05-10.06 | 375.80 | no | IBM2 |
| umc57a | C | 10.06 | 375.98 | no | BNL 96 |
| npi287b |  | 10.06 | 376.04 | no | BNL 2002 |
| bnl10.13a | C | 10.06 | 376.30 | yes | IBM2 |
| mmp71 |  | 10.06 | 376.90 | no | IBM2 |
| bnlg1028 | C | 10.06 | 380.50 | yes | IBM2 |
| por2 | C | 10.06 | 381.04 | no | SSR popII |
| jpsb365a |  | 10.06 | 383.40 | yes | IBM2 |
| bnlg594 |  | 10.06 | 386.06 | no | SSR popII |
| csu615b | C | 10.06 | 387.50 | no | UMC 98 |
| cdo1417b(ptk) |  | 10.06 | 387.50 | no | UMC 98 |
| bnl17.02 |  | 10.06 | 387.90 | yes | IBM2 |
| bnl17.07 |  | 10.06 | 389.94 | no | BNL 2002 |
| uaz251c(rpS11) |  | 10.06 | 390.27 | no | BNL 2002 |
| bnlg153 |  | 10.06-10.07 | 390.28 | no | SSR popII |
| tip5 | C | 10.06 | 392.50 | yes | IBM2 |
| cpx2 |  | 10.06 | 393.75 | no | BNL 2002 |
| bnlg236 |  | 10.06 | 394.81 | no | BNL 2002 |
| ucsd(lfyA) |  | 10.06 | 394.81 | no | BNL 96 |
| umc1993 | A C | 10.06 | 410.60 | yes | IBM2 |
| bnlg2190 | A C | 10.06 | 412.30 | yes | IBM2 |
| ufg56 | C | 10.06 | 414.10 | no | IBM2 |
| dmt102a | C | 10.06 | 414.11 | no | ChromDB |
| ias6b |  | 10.06 | 416.42 | no | BNL 2002 |
| npi306 |  | 10.06 | 416.42 | no | BNL 96 |
| ufg62 |  | 10.06 | 416.60 | yes | IBM2 |
| klp1f |  | 10.06 | 418.25 | no | UMC 98 |
| npi290a |  | 10.06 | 418.25 | no | UMC 98 |
| ufg15 |  | 10.06 | 422.70 | no | IBM2 |
| isu2192b |  | 10.06-10.07 | 430.75 | no | BNL 96 |
| bnl7.49a(hmd) | A C | 10.07 | 437.60 | yes | IBM2 |
| cdo244a(crp) |  | 10.06-10.07 | 437.60 | no | UMC 98 |
| npi321a |  | 10.07 | 439.27 | no | BNL 2002 |
| agrr37c | A C | 10.07 | 442.20 | yes | IBM2 |
| rgpc285 |  | 10.07 | 442.78 | no | UMC 98 |
| umc1196 | A C | 10.07 | 444.80 | yes | IBM2 |
| umc1084 | A C | 10.07 | 445.70 | yes | IBM2 |
| npi421b |  | 10.07 | 445.75 | no | BNL 96 |
| csu1039 |  | 10.07 | 447.96 | no | UMC 98 |
| bnlg1677 | A C | 10.07 | 449.30 | yes | IBM2 |
| csu1028(lhcb) |  | 10.07 | 449.37 | no | UMC 98 |

| Locus | Contig | Bin | Coordinate, cM | Backbone | Source Map |
|---|---|---|---|---|---|
| AY110016 | A C | 10.07 | 450.80 | yes | IBM2 |
| rz590b |  | 10.07 | 453.14 | no | UMC 98 |
| npi208b |  | 10.07 | 454.60 | yes | IBM2 |
| mpik17f |  | 10.00 | 454.69 | no | BNL 2002 |
| mpik12a |  | 10.00 | 454.85 | no | BNL 2002 |
| mpik15f |  | 10.00 | 454.99 | no | BNL 2002 |
| ucsd64d |  | 10.00 | 454.99 | no | BNL 2002 |
| umc1249 | C | 10.06-10.07 | 456.65 | no | SSR popI |
| mmp181 |  | 10.07 | 464.60 | yes | IBM2 |
| ufg75b |  | 10.07 | 465.50 | no | IBM2 |
| asg50d |  | 10.07 | 466.33 | no | UMC 98 |
| mir3c(thp) |  | 10.07 | 466.33 | no | UMC 98 |
| bnlg1839 | A C | 10.07 | 466.40 | yes | IBM2 |
| bnlg279b |  | 10.06 | 467.15 | no | BNL 2002 |
| umc1176 |  | 10.07 | 468.40 | yes | IBM2 |
| umc2351 |  | 10.07 | 469.40 | no | IBM2 |
| bnlg1360 |  | 10.07 | 469.70 | yes | IBM2 |
| bnlg2025 |  | 10.07 | 470.89 | no | BNL 2002 |
| npi254b |  | 10.07 | 470.90 | yes | IBM2 |
| npi577b |  | 10.07 | 470.90 | no | BNL 2002 |
| npi604b |  | 10.07 | 475.10 | no | BNL 2002 |
| gln1 | C | 10.07 | 475.27 | no | UMC 98 |
| umc232 |  | 10.07 | 475.27 | no | UMC 98 |
| mwg645l |  | 10.07 | 478.97 | no | BNL 2002 |
| csu300b |  | 10.07 | 479.98 | no | UMC 98 |
| umc2203 |  | 10.07 | 481.42 | no | SSR popI |
| umc1640 | C | 10.07 | 483.61 | no | SSR popII |
| bnlg1450 | C | 10.07 | 483.70 | yes | IBM2 |
| umc1877 |  | 10.07 | 488.63 | no | SSR popII |
| bnlg1518 |  | 10.04 | 490.55 | no | BNL 2002 |
| csu844 |  | 10.07 | 495.05 | no | UMC 98 |
| php20568a |  | 10.07 | 496.60 | yes | IBM2 |
| crr2 |  | 10.07 | 505.50 | no | SSR popII |
| umc2021 | C | 10.07 | 505.50 | yes | IBM2 |
| bnlg1185 | C | 10.07 | 505.93 | no | BNL 2002 |
| AY109829 | A C | 10.07 | 509.90 | no | IBM2 |
| umc2126 | C | 10.07 | 513.20 | yes | IBM2 |
| isu53b |  | 10.07 | 522.60 | yes | IBM2 |
| asg19b |  | 10.07 | 524.10 | yes | IBM2 |
| umc1038 | A C | 10.07 | 525.11 | no | SSR popII |
| umc1556 | A C | 10.07 | 527.39 | no | SSR popII |
| umc269(ptk) |  | 10.07 | 527.55 | no | UMC 98 |
| csu781a | C | 10.07 | 528.02 | no | UMC 98 |
| csu571b(ipp) |  | 10.07 | 528.02 | no | UMC 98 |
| dba3 |  | 10.07 | 533.20 | no | UMC 98 |
| csu199d |  | 10.07 | 533.20 | no | IBM1 |
| csu48 | C | 10.07 | 533.20 | yes | IBM2 |
| umc1645 |  | 10.07 | 578.09 | no | SSR popI |

## V. COMMUNITY IBM (cIBM2004) MAPS

Map score data for the community IBM maps were supplied by various cooperators (Table 1) and are based on the IBM-94 panel of 94 stocks. These lines are a subset of the high resolution IBM-302 mapping population used to anchor the physical map (Cone et al., Plant Physiol 130:1686-1696, 2002). The IBM recombinant inbreds were developed from the Syn 5 generation, following 4 intermatings of B73xMo17 (Lee, M et al., Plant Mol Biol 48:453-461, 2002). Seed for the IBM-94 (Table 2) is distributed by the Maize Genetics Cooperation Stock Center <http://maizegdb.org/cgi-bin/stockcatalog.cgi?id=1>. DNA samples of the IBM-94 and the parent lines, along with protocols, are distributed at the University of Missouri-Columbia (<http://www.maizemap.org/dna_kits.htm>. Map score data submitted over the web <http://www.maizemap.org/CIMDE/cimde.html > will return map results within a week after submission; loci are placed based on a framework of 250 loci, also previously placed on the high resolution IBM maps. Each new marker is assigned to chromosome and mapped on the individual chromosomes using the build and place commands of Mapmaker.

With permission of individual cooperators, the community map will be published annually to MaizeGDB. Loci submitted to MaizeGDB are vetted, in consultation with the contributors, for nomenclature, and probe details, including relationships of probes to physical map probes. The first community map was provided to MaizeGDB Dec 2003 and is called cIBM2003. Information about associations to the physical map are additionally provided to Cari Soderland via the IBM neighbors (Polacco, M et al., Plant and Animal Genomes XII Conference, 2004, Maize Workshop < http://63.141.253.172/12/abstracts/W34_PAG12_159.html> for inclusion in the maize FPC product <http://www.genome.arizona.edu/fpc/maize/> and to the Maize Mapping Project iMap representation <http://www.maizemap.org/imap.htm>.

**Table 1. Cooperators providing raw map data include:**

**Ivan Acosta**, Yale University, New Haven, CT: *hlm2, tip1*

**Hank Bass**, University of Georgia, Athens, GA: *fsu1b(smh2), smh1.*

**Tom Brutnell**, Cornell University, Ithaca, NY <http://bti.cornell.edu/Brutnell_lab2/Projects/Tagging/BMGG_pro_tagging.html>: *bti00191a::Ac, bti00191b::Ac, bti03525::Ac, bti03526::Ac, bti03545::Ac, bti03557::Ac, bti03616::Ac, bti03702::Ac, bti03811::Ac, bti31132a::Ac, bti31132b::Ac, bti31192::Ac, bti99224::Ac, btilc175::Ac, mon00004::Ac, mon00030::Ac, mon00038::Ac, mon00044::Ac, mon00060::Ac, mon00072::Ac, mon00084::Ac, mon00088::Ac, mon00092::Ac, mon00106::Ac, mon00108::Ac, mon00122::Ac, mon00128::Ac, mon00150::Ac, mon00152::Ac, mon00178::Ac, mon00186::Ac, mon00192::Ac, mon00200::Ac, mon00218::Ac, mon00236::Ac, mon03068::Ac, mon03077::Ac, mon03078::Ac, mon03080::Ac.*

**ChromDB** <http://www.chromdb.org>, University of Arizona, Tucson, AZ. Chromatin RFLP: *ago108, bnlg182, brd101, brd102, brd103, chb101a, chb101b, chb102, chc101a, chc101b, chr106a, chr106b, chr109a, chr109b, chr110a, chr110b, chr111, chr112a, chr112b, chr113, chr116a, chr116b, chr117a, chr117b, chr117c, chr117d, chr118, chr118, chr119, chr120, chr122, chr124, chr125a, chr125b, chr126a, chr126b, crd101, dmt101, dmt102a, dmt102b, dmt103a, dmt103b, dmt103c, epl101, fie2, gta105, gta106b, gta107a, gta107b, gtb101, gtc101, gtc102, gtd101, gte101, gte102, hac101a, hac101b, haf101, hag101, hag102, hag103a, hag103b, hag105, hda102, hda108, hda109, hda110, hdt102, hdt103, hdt105, hmga101, hon104a, hon104b, hon105, hon106a, hon106b, hon107a, hon107b, hon110, hxa102a, hxa102b, mbd101a, mbd101b, mbd105, mbd106, mbd108, mbd109, mbd116, mbd119, mbd121, mez1, nfa101, nfa102a, nfa102b, nfa104, nfc101, nfc103a, nfc103b, nfc104a, nfc104b, nfc104c, nfc105, nfd101a, nfd101b, nfd102, nfd104a, nfd104c, nfd104d, nfd104e, nfd105, nfd106, nfd107, nfd108, nfd109, nfd110, nfd114, nfe101, sdg101, sdg102a, sdg102b, sdg102c, sdg104, sdg105a, sdg106, sdg107, sdg108a, sdg108b, sdg110, sdg111a, sdg113, sdg115, sdg116a, sdg116b, sdg117a, sdg117b, sdg118, sdg119, sdg123, sdg129, sgb101, sgb103, sgf101, smh4, vef101a, vef101b.*

**Genoplante**, France <http://genoplante-info.infobiogen.fr>. RFLP related to Overgos on the physical map: *gpm1, gpm10, gpm11, gpm12, gpm13, gpm14, gpm15, gpm16, gpm2, gpm3, gpm4, gpm5, gpm6, gpm7, gpm8, gpm9*

**Peter Rogowsky**, EDP ENS-Lyon, Lyon France: *ensl015, ensl016.*

**Mike McMullen**, USDA-ARS Columbia, MO. SNPs related to Overgos on the Physical map: *AI714808, AI737325, AI861369, AW036917, AW172071, AW231791, AW258116, AY103622, AY103942, AY103944, AY104188, AY104234, AY104686, AY105043, AY105132, AY105205, AY105451, AY105479, AY105872, AY106026, AY106137, AY106170, AY106313, AY106318, AY106439, AY106518, AY106592, AY106674, AY106825, AY107012, AY107018, AY107034, AY107053, AY107079, AY107121, AY107128, AY107193, AY107200, AY107292, AY107329, AY107414, AY107489, AY107496, AY107517, AY107629, AY107682, AY107743, AY107844, AY107881, AY107910, AY107911, AY108545, AY108825, AY108844, AY109061, AY109096, AY109128, AY109538, AY109804, AY110113, AY110240, AY110782, AY110827, AY110835, AY110853, AY111089, AY111254, AY111333, AY111822, AY111877, AY111962, AY112119, AY112175, AY112199, AY112283, AY112355, BE518809, BG266188*

**Sahtoh Namiko,** Cold Spring Harbor Laboratory, Cold Spring Harbor, NY: *shpl1.*

**Wolfgang Werr, Roman Zimmerman,** Institut für Entwicklungsbiologie,Universtaat Köln, Köln, Germany: *nact11, nact12, nact15, nact16a, ns1*

**Table 2. The IBM-94 panel includes the below lines**:

MO001 MO005 MO007 MO008 MO010 MO012 MO014 MO015 MO016 MO017 MO021 MO022 MO023 MO024 MO025 MO027 MO028
MO029 MO030 MO031 MO032 MO033 MO034 MO035 MO039 MO040 MO043 MO044 MO045 MO046 MO048 MO051 MO052 MO054
MO055 MO057 MO058 MO060 MO061 MO062 MO063 NO066 MO067 MO074 MO075 MO076 MO077 MO079 MO262 MO264 MO265
MO266 MO267 MO269 MO272 MO275 MO276 MO281 MO284 MO287 MO288 MO296 MO297 MO298 MO309 MO310 MO311 MO315

MO317 MO321 MO322 MO323 MO325 MO326 MO328 MO337 MO341 MO344 MO345 MO346 MO352 MO354 MO355 MO357 MO360 MO364 MO365 MO368 MO369 MO378 MO379 MO382 MO383 MO384
These line numbers are identical to the corresponding line in the larger panel of stocks, IBM 302, where seed is also maintained at the Stock Center.

*Acknowledgements.* This report would not have been possible without the considerable contributions of Karen Cone, Mike McMullen, Georgia Davis, Seth Haverman and Hector Sanchez-Villeda towards the design and implementation of the CIMDE (Community IBM map data entry) software package (Sanchez-Villeda et al., Bioinformatics 19:2022-2030, 2003) and the encouragement of Ed Coe, PI of the Maize Mapping Project, NSF DBI 9872655, which funded the software resources used for these maps.

Maps Legend.
Bin edges are indicated to the left of each chromosome; asterisks indicate a core marker. Positions of off-frame loci are indicated as an interval value, in parentheses, and refer to the interval 'down' from the framework locus to their immediate left. Note, due to the intermatings in this population, these map coordinates are not centiMorgan (cM) units as defined in the classical sense.

Submitted by
Mary Polacco
USDA-ARS
University of Missouri

# cIBM2004 CHROMOSOME 1

| BIN | Position | Locus | Locus Off Frame |
|---|---|---|---|
| 1.00 | 0 | ***umc1354*** | |
| 1.01 | 2.3 | ***tub1*** | |
| | 6.9 | ***dmt103b*** | |
| | 10.5 | ***umc1566*** | *(17.4)mon03077::Ac* |
| | 44.2 | ***lim179*** | *(7.7)AY107629* |
| | 68.1 | ***umc1977*** | |
| | 80.4 | ***AY110853*** | |
| 1.02 | 90.5 | ***umc157a*** | |
| | 107.3 | ***csu1171*** | |
| | 134.6 | ***bnlg1953*** | *(2.3)mon03080::Ac* |
| | 180.6 | ***mon00192::Ac, mon00106::Ac*** | |
| 1.03 | 180.7 | ***umc76a*** | |
| | 185.9 | ***umc1403*** | |
| | 234.1 | ***AY106592*** | |
| | 243.0 | ***asg35b*** | |
| | 254.0 | ***AY110240*** | |
| | 257.1 | ***AY107489*** | *(4.8)bnlg182* |
| | 262.5 | ***umc1598*** | |
| | 274.5 | ***mmp100*** | |
| 1.04* | 295.7 | ***umc1169*** | *(0.6)chr125b* |
| | 310.2 | ***bnl9.11b*** | *(3.1)AY103942* |
| 1.05 | 324.6 | ***csu3*** | *(5.5)btilc175::Ac* |
| | 339.0 | ***umc1515*** | |
| | 342.1 | ***nfd104c*** | |
| | 346.1 | ***AY106439*** | |
| | 347.2 | ***AY107682*** | |
| | 358.7 | ***hac101b*** | |
| 1.06* | 367.4 | ***mbd106*** | |
| | 369.8 | ***umc1972*** | *(1.1)gpm4* |
| | 385.5 | ***mbd119*** | |
| | 392.3 | ***asg58*** | |
| | 404.1 | ***nact15*** | |
| | 427.2 | ***ntf1*** | |
| | 448.5 | ***umc192*** | *(56.1)mon00186::Ac* |
| 1.07 | 449.1 | ***asg62*** | |
| | 510.4 | ***bnlg1556*** | |
| | 520.3 | ***dmt103c*** | |
| | 537.9 | ***hon105*** | *(8.7)bti03557::Ac* |
| | 547.4 | ***bnlg1025*** | |
| 1.08 | 561.1 | ***umc128*** | *(0.6)AY105132* |
| | 568.2 | ***bnlg2228*** | |
| | 570.7 | ***chr124*** | |
| | 574.3 | bti03545::Ac | |
| | 577.4 | ***sdg123*** | |
| | 586.5 | ***umc1991*** | |
| | 606.2 | ***nfc103a*** | |
| 1.09 | 611.1 | ***cdj2*** | *(3.7)AY106137* |

|  |  |  |  |
|---|---|---|---|
|  | 625.8 | ***umc2047*** |  |
|  | 639.7 | ***AY112283*** |  |
| 1.10 | 644.4 | ***umc107a*** |  |
|  | 650.8 | ***chb101b, chr106a*** |  |
|  | 650.9 | ***nfa103a*** |  |
|  | 656.2 | ***AY104234*** |  |
|  | 660.6 | ***hxa102b*** |  |
|  | 662.5 | ***vef101b*** |  |
| 1.11* | 671.6 | ***lim39*** | *(21.7)mon00200::Ac* |
|  | 696.7 | ***umc1421*** | *(2.7)hon110* |
|  | 714.2 | ***AY109096*** |  |
|  | 727.0 | ***AY106825, umc1630*** |  |
|  | 730.6 | ***AY112175*** |  |
|  | 741.5 | ***AY109128*** |  |
|  | 772.3 | ***phi064*** |  |
| 1.12 | 790.7 | ***bnl6.32*** |  |
|  | 792.6 | ***umc1605*** |  |
|  | 801.7 | ***AY104686*** |  |

## cIBM2004 CHROMOSOME 2

| BIN | Position | Locus | Locus Off Frame |
|---|---|---|---|
| 2.00 | 0 | ***isu53a*** | |
| 2.01* | 22 | ***umc1165, bti00191a::Ac*** | *(42.1)sgb101* |
| 2.02* | 64.7 | ***umc1824a*** | |
| | 78.4 | ***dmt102b*** | |
| | 84.2 | ***eks1*** | *(22.0)gpm7* |
| 2.03 | 110.1 | ***umc6a*** | |
| | 128.3 | ***nfd102*** | |
| | 139.4 | ***mmp33*** | |
| | 152.2 | ***sdg104*** | |
| | 157.1 | ***AY107034*** | |
| | 159.8 | ***sdg107*** | |
| 2.04* | 161.3 | ***phi109642*** | |
| | 169.2 | ***AY103944*** | |
| | 172 | ***umc1326*** | |
| | 174.3 | ***hag103a*** | |
| | 192.1 | ***AI714808*** | *(4.9)bti03811* |
| | 197.4 | ***umc2030*** | *(1.0)sdg102a* |
| | 200 | ***hda102*** | *(0.9)AY112119* |
| 2.05 | 206.1 | ***umc131*** | |
| | 207.4 | ***zpu1*** | *(0.4)AY107012* |
| | 212.6 | ***ns1*** | |
| | 214.6 | ***AY111877*** | |
| 2.06* | 217.3 | ***pbf1*** | |
| | 226.9 | ***umc1080*** | *(0.5)sdg119* |
| 2.07* | 238.9 | ***umc2129*** | *(3.1)AI861369* |
| | 244 | ***umc1890*** | |
| | 255.7 | ***nfc104b*** | |
| | 259.4 | ***sdg106, nfd101b*** | *(11.7)chr119,(9.7)sdg116b* |
| | 271.8 | ***umc1560*** | |
| 2.08 | 274.7 | ***asg20*** | |
| | 286.8 | ***mon00084::Ac*** | |
| | 296.4 | ***hda109, chr122*** | |
| | 303.1 | ***umc1604*** | |
| | 308 | ***hag105*** | |
| | 312.4 | ***chc101b*** | |
| | 326 | ***mmc0381*** | |
| | 336.2 | ***gpm16*** | |
| 2.09 | 346 | ***umc49a*** | |
| | 355.3 | ***umc1252*** | |
| | 380.9 | ***BG266188*** | |
| | 401.4 | ***bnlg469b*** | |
| 2.10* | 437.1 | ***AY106674*** | |
| | 446.7 | ***lim104*** | *(0.9)chr106b* |
| | 452.4 | ***umc1696*** | |

# cIBM2004 CHROMOSOME 3

| BIN | Position | Locus | Locus Off Frame |
|---|---|---|---|
| 3.01* | 0 | ***umc1931*** | |
| | 4.4 | ***bnl8.15*** | *()AY106313* |
| | 17.9 | ***AY112199*** | |
| | 20.5 | ***umc2049*** | |
| 3.02 | 40.1 | ***csu32a*** | |
| | 58.7 | ***umc1886*** | |
| 3.03 | 86.1 | ***asg24a*** | |
| | 104.7 | ***lim66*** | |
| 3.04 | 124.5 | ***asg48*** | |
| | 137.4 | ***umc1608*** | |
| | 147.7 | ***nfc104c*** | *(2.3)haf101,(12.6)AY107193* |
| | 160.9 | ***mmc0132*** | *(3.8)chr126b, (3.4)bti03702::Ac* |
| | 169.7 | ***umc1449*** | *(4.8)mbd105,(4.6)chr110a,(4.5)AY111333* |
| | 176.3 | ***hac101a*** | |
| | 179.9 | ***AY110827, gpm14*** | |
| 3.05 | 184.4 | ***umc102*** | *(7.6)bti03526::Ac* |
| | 190.7 | ***chr109b, umc1102*** | *(35.1)mon00178::Ac,(0.5)nact16a* |
| | 227.9 | ***csu636*** | |
| 3.06* | 236.5 | ***umc1539*** | |
| | 249.9 | ***asg39*** | |
| | 251.9 | ***AY106026*** | |
| | 309.4 | ***csu1183*** | |
| | 314.4 | ***sdg113*** | |
| | 320.4 | bti31083::Ac | |
| | 330.9 | ***asg7b*** | |
| 3.07 | 333.2 | ***bnl6.16a*** | |
| | 348.2 | ***AY107018*** | |
| | 369.4 | ***umc1404*** | |
| | 377 | ***sdg117a*** | |
| | 378.8 | ***nfc101, nfc105*** | |
| | 380.6 | ***hon108*** | |
| | 382.3 | ***AY106518*** | |
| 3.08 | 387.2 | ***umc17a*** | |
| | 389 | ***AW258116*** | |
| | 403.5 | ***gpm3*** | |
| | 408.7 | ***mmc0251*** | *(12.7)sdg115* |
| | 424 | ***umc1273*** | |
| 3.09 | 428.6 | ***umc63a*** | |
| | 436.7 | ***csu845*** | *(13.5)AY111254* |
| | 476.5 | ***lim182*** | |
| | 491.1 | ***bnlg1754, fsu1b*** | |
| | 527.2 | ***umc1641*** | |
| | 532.4 | bti03616::Ac | |
| | 538.3 | ***umc1594*** | |

## cIBM2004 CHROMOSOME 4

| BIN | Position | Locus | Locus Off Frame |
|---|---|---|---|
| 4.01* | 0 | ***msf1*** | |
| | 20.8 | ***bx4*** | |
| | 43.1 | ***umc1759*** | |
| 4.02 | 45.6 | ***php20725a*** | |
| | 67.4 | ***umc1943*** | |
| 4.03 | 104.8 | ***umc31a*** | *(1.5)chr117c* |
| | 116.6 | ***umc1926*** | |
| | 147.6 | ***umc2039*** | |
| | 212.5 | ***bnl8.45c*** | |
| 4.04* | 280 | ***bnlg490*** | |
| 4.05* | 286.1 | ***sdg108a*** | |
| | 292.1 | ***AY107128*** | |
| | 301.5 | ***csu509*** | |
| | 307.9 | ***chr112a, hda108*** | |
| | 310.8 | ***umc1511*** | |
| | 313.1 | ***nfa104*** | |
| | 314.8 | ***nfd104e*** | *(0.5)AY105043* |
| 4.06* | 321 | ***umc1945*** | |
| | 335.7 | ***nfd105*** | |
| | 344 | ***mpik3*** | |
| 4.07 | 371.4 | ***bti31094::Ac, umc66a*** | |
| | 377.2 | ***umc2038*** | |
| | 380.4 | ***mon00128::Ac*** | |
| | 382.9 | ***mon03078::Ac*** | |
| | 387.1 | ***bnl5.24b*** | |
| | 397.4 | bti00207::Ac | |
| 4.08* | 398.7 | ***umc1775*** | |
| | 409.4 | ***umc1808*** | |
| | 448.9 | ***ufg23*** | *(13.7)nfd106, (12.8)bti00245::Ac* |
| | 463.1 | ***umc1842*** | *(1.0)mbd121, (1.9)mon00150::Ac* |
| 4.09 | 468.2 | ***umc52*** | *(6.5)AY111962* |
| | 475.9 | ***umc1999*** | *(2.1)nfd107* |
| | 492.4 | ***AY107200*** | *(7.4)chb102* |
| | 501.4 | ***mbd116*** | *(14.5)bti31192::Ac* |
| | 517.6 | ***sbp2*** | *(4.4)AY107910* |
| 4.10 | 530.4 | ***php20608a*** | |
| | 547.8 | ***umc1109*** | *(15.2)AY111822* |
| | 563.6 | ***hon106b*** | |
| | 574.2 | ***bip2*** | |
| | 577.9 | ***umc1707*** | |

## cIBM2004 CHROMOSOME 5

| BIN | Position | Locus | Locus Off Frame |
|---|---|---|---|
| 5.00 | 0 | ***umc1253*** | |
| | 21.4 | ***tip1, umc1260*** | |
| 5.01 | 23.2 | ***npi409*** | |
| | 31.5 | ***lim407*** | |
| | 61.2 | ***umc2036*** | *(4.0)hxa102a* |
| 5.02* | 85.9 | ***asg73*** | |
| | 90.5 | ***chb101a*** | |
| | 94 | ***umc1587*** | *(23.4)ago108,(23.3)AY110835* |
| 5.03* | 119 | ***bnlg1879*** | |
| | 133 | ***rz474a*** | *(1.2)mbd109* |
| | 138.3 | ***nfc103b*** | |
| | 150 | ***umc2035*** | |
| | 158.8 | ***hag101*** | |
| | 165.7 | ***crd101*** | |
| | 168.8 | ***gpm5*** | |
| | 173 | ***umc1609*** | |
| | 178.3 | ***AY107414*** | |
| | 182.2 | ***shpl1*** | |
| | 187.1 | ***sdg129, AY107844*** | |
| | 187.2 | ***gtc101, gtc102*** | |
| | 188.3 | ***hon106a*** | |
| | 190.7 | ***bnlg1902*** | |
| 5.04* | 199.3 | ***mon00030::Ac*** | *(2.8)nfd108* |
| | 203.7 | ***umc1990*** | |
| | 218.4 | ***AY105205*** | |
| | 225.7 | ***umc1349*** | |
| | 233.3 | ***mon00152::Ac*** | |
| 5.05* | 242.3 | ***umc1482*** | |
| | 252.7 | ***nfe101*** | *(15.0)AY107329,(13.5)AY111089* |
| | 269.7 | ***nbp35*** | *(0.6)gte102* |
| | 281.8 | ***mon00044::Ac*** | |
| 5.06 | 290 | ***umc126a*** | |
| | 299.7 | ***nfd104a*** | |
| | 316 | ***bnlg609*** | |
| | 326.7 | ***sdg117b*** | |
| 5.07 | 347.1 | ***umc108*** | |
| | 397.9 | ***bnlg1118*** | |
| | 412.3 | ***bnlg118*** | |
| 5.08* | 443.5 | ***umc1225*** | |
| | 445.2 | ***mmp175*** | |
| | 454.4 | ***nfd109*** | |
| 5.09 | 463.3 | ***php10017*** | |

## cIBM2004 CHROMOSOME 6

| BIN | Position | Locus | Locus Off Frame |
|---|---|---|---|
| 6.00 | 0 | ***umc1143*** | |
| 6.01 | 19.9 | ***hon104b, umc85a*** | *sdg102b* |
| | 27.1 | ***bnlg1867*** | *(1.5)gpm8* |
| | 31.1 | ***nfa101*** | *(0.6)mez1,(0.5)mon00038::Ac* |
| | 32.3 | ***AY107121*** | |
| 6.02* | 36.1 | ***umc1006*** | |
| | 40.7 | ***sdg102c*** | |
| | 49.5 | ***csu923*** | |
| 6.04 | 61 | ***umc65a*** | |
| | 75.6 | ***umc1857*** | *(1.5)nact11,(1.2)AY108825,(1.8)AY109804* |
| | 78.5 | ***sgf101*** | |
| | 85.6 | ***gta107b, gta105*** | |
| | 90.5 | ***bti31132a::Ac, bti31132b::Ac*** | |
| | 103.3 | ***umc2006*** | *(7.8)AY107053* |
| 6.05* | 111.7 | ***isu111a*** | |
| | 114.8 | ***AY105479*** | *(0.7)AY107517* |
| | 116.9 | ***chr117d*** | |
| | 121.4 | ***uaz280c*** | |
| | 130.6 | ***umc1388*** | |
| | 143.6 | ***pmg1*** | *(1.5)mbd101b* |
| | 152.4 | ***chr116a, AY107881*** | |
| | 169.6 | ***AW036917*** | |
| | 192.5 | ***uaz121a*** | |
| | 199.4 | ***gpm9*** | |
| 6.06 | 213.3 | ***umc38a*** | |
| | 216.3 | ***umc1762*** | |
| | 218 | ***sdg111a, gtb101*** | |
| | 231.3 | ***lim379*** | |
| | 236.6 | ***lim151*** | *(0.9)gte101* |
| 6.07 | 257 | ***umc132a*** | *(0.7)hdt103* |
| | 260.2 | ***nfa102a*** | |
| | 265.5 | ***mlg3*** | |
| | 309.1 | ***umc1350*** | *(35.3)chr118,(35.3)chr121* |
| 6.08* | 346.2 | ***umc2059*** | |

## cIBM2004 CHROMOSOME 7

| BIN | Position | Locus | Locus Off Frame |
|---|---|---|---|
| 7.00 | 0 | ***csu582*** | |
| | 42.8 | ***umc1378*** | *(1.2)gpm12* |
| | 63.9 | ***umc1672*** | |
| 7.01 | 80.8 | ***asg8*** | |
| | 91.8 | ***php20581a*** | |
| | 102.8 | ***hda110*** | |
| | 122 | ***dmt101*** | |
| | 123.7 | ***o2, hon102*** | |
| 7.02 | 124.3 | ***asg34a*** | |
| | 142.5 | ***sdg101*** | |
| | 150.4 | ***cyp6*** | *(0.6)AY109061* |
| | 150.9 | ***AY106170*** | |
| | 152 | ***epl101, vef101a*** | |
| | 153.1 | ***hag102, sdg110*** | |
| | 169.2 | ***umc1983*** | |
| | 185.5 | ***mon03068::Ac*** | |
| | 194.6 | ***bnlg1808*** | |
| 7.03* | 196.9 | ***mmp127*** | |
| | 233 | ***bnlg1070*** | |
| | 241.8 | ***mbd108*** | |
| | 243 | ***brd103*** | *(1.6)bti31211::Ac* |
| | 245.4 | ***sdg116a*** | |
| | 247.7 | ***mon00072::Ac*** | |
| | 254.9 | ***umc56*** | |
| | 261.3 | ***brd101, nfd101a*** | *(3.2)AY107911* |
| | 279.8 | ***tif1*** | |
| 7.04* | 290.2 | ***umc1710*** | |
| | 313.2 | ***bnlg1666*** | |
| | 320.8 | ***chr111*** | |
| | 342.9 | ***mon00088::Ac*** | |
| | 345.7 | ***umc1708*** | |
| | 355.6 | ***AY108844*** | |
| | 368.5 | ***mon00060::Ac*** | |
| | 381 | ***umc1412*** | |
| | 389 | ***gpm2*** | |
| 7.05 | 395.9 | ***umc245*** | *(7.0)chc101a* |
| | 405.4 | ***phi069*** | *(6.0)AY106318* |
| | 449.3 | ***umc1406*** | |
| 7.06 | 455.3 | ***umc168*** | |
| | 459.7 | ***nfc104a*** | |

## cIBM2004 CHROMOSOME 8

| BIN | Position | Locus | Locus Off Frame |
|---|---|---|---|
| 8.01 | 0 | ***npi220a*** | |
| | 9.3 | ***csu319*** | |
| | 35 | ***umc1592*** | |
| | 57.9 | ***umc1327*** | |
| | 76.4 | ***mmp85*** | |
| 8.02* | 82 | ***hon107b*** | |
| | 83.9 | ***gpm11*** | |
| | 86.6 | ***cdo460*** | |
| | 107.3 | ***mmp166*** | |
| | 111.1 | ***chr117a*** | |
| | 126.8 | ***AI737325*** | |
| | 143.8 | ***nfd110, nfd114*** | |
| | 143.9 | ***umc124a*** | |
| | 145.6 | ***umc1530*** | |
| | 166.5 | ***gpm10, AY110113*** | |
| 8.03 | 166.6 | ***chr110b, chr126a*** | |
| | 169.4 | bti03525::Ac | |
| | 174.5 | ***umc1910*** | |
| | 180.4 | ***AW172071*** | |
| | 197.9 | ***umc1457*** | |
| | 201.7 | ***AY108545, mbd101a*** | |
| 8.04* | 204.1 | ***AW231791, AY107079*** | |
| | 213.8 | ***sdg105a*** | |
| 8.05* | 216.1 | ***umc1130*** | |
| | 229.6 | ***chr117b*** | *(6.1)nfa102b* |
| | 237.5 | ***umc1889*** | *(0.6)hdt102* |
| | 242.2 | ***chr112b*** | |
| | 242.8 | ***hon107a*** | |
| | 243.4 | ***fsu1a*** | |
| 8.06* | 264.4 | ***sdg118, umc1149*** | |
| | 287.2 | ***hdt105*** | |
| | 294.4 | ***chr116b*** | |
| | 300.1 | ***bnlg1031*** | *(18.8)mon00108::Ac* |
| 8.07* | 328.3 | ***umc1268*** | |
| 8.08 | 335.2 | ***npi414a*** | |
| | 364.8 | ***umc1933*** | *(20.2)mon00122::Ac* |
| 8.09 | 395.1 | ***agrr21*** | |
| | 469.4 | ***bnlg1131*** | |

## cIBM2004 CHROMOSOME 9

| BIN | Position | Locus | Locus Off Frame |
|---|---|---|---|
| 9.01 | 0 | ***umc109*** | *(9.6)AY112355* |
| | 47.4 | ***lim343*** | |
| | 50.6 | ***ufg41*** | |
| | 54.8 | ***gta106b, gta107a*** | |
| | 69.5 | ***umc1967*** | |
| | 71.2 | ***AY107496*** | |
| 9.02 | 73.5 | ***bz1*** | |
| | 90.6 | ***chr113*** | |
| | 93.5 | ***csu471*** | |
| | 99 | ***AY103622*** | |
| | 118.4 | ***bnlg1401*** | |
| | 149.5 | ***AY105451*** | |
| 9.03 | 159 | ***wx1*** | |
| | 160.9 | ***mon00236*** | |
| | 162.8 | ***umc1258*** | *(1.1)hon104a* |
| | 167.9 | ***gpm6*** | |
| | 174 | ***chr120*** | |
| | 175.3 | ***nact12*** | *(5.7)gtd101,(5.7)ensl015,(5.7)ensl016,(5.8) AY107743,(5.7)BE518809* |
| | 181.9 | ***umc1271*** | |
| | 189.9 | ***rz682*** | |
| 9.04* | 196.6 | ***bnlg1209*** | |
| | 208.2 | ***AY110782*** | |
| | 209.4 | ***umc1120*** | |
| 9.05 | 215.7 | ***umc95*** | |
| | 218.6 | ***chr125a*** | |
| | 225.7 | ***mmp151d*** | |
| | 248.2 | ***csu634*** | |
| | 253.7 | ***ufg24*** | |
| 9.06* | 269 | ***gpm1, mmp142*** | |
| | 293.5 | ***AY107292*** | |
| | 305.8 | ***mmp131*** | *(4.9)AY104188* |
| | 313.7 | ***mmp168*** | *(3.4)nfd104d,(19.2)mon00004* |
| 9.07 | 333.5 | ***asg12*** | |
| | 346.3 | ***bnlg619*** | |
| | 359 | ***brd102, mon00092*** | |
| | 378.5 | ***umc1137*** | *(25.8)dmt103a* |
| | 408.6 | ***umc1505*** | |

## cIBM2004 CHROMOSOME 10

| BIN | Position | Locus | Locus Off Frame |
|---|---|---|---|
| 10.00 | 0 | ***mmp48a*** | |
| | 10 | ***php20753a*** | |
| 10.01 | 14 | ***php20075a*** | |
| | 39.5 | ***umc2018*** | *(2.1)bti99224::Ac* |
| 10.02 | 48.5 | ***npi285a*** | |
| | 76.1 | ***umc2069*** | |
| 10.03 | 80.8 | ***umc130*** | *(8.9)chr109a,(4.5)AY105872* |
| | 90.2 | ***sdg108b*** | |
| | 92.9 | ***umc1345*** | |
| | 97.7 | ***hlm2*** | |
| | 100.8 | ***gpm13, fie2*** | |
| 10.04 | 102.5 | ***umc64a*** | |
| | 108.1 | ***umc1995*** | |
| | 116.1 | ***AY109538*** | |
| | 125.6 | ***umc1330*** | |
| | 131.6 | ***hag103b*** | |
| 10.05 | 136.3 | ***umc259a*** | |
| | 148 | ***umc1506*** | *(28.1)gpm15* |
| 10.06* | 177.3 | ***bnl10.13a*** | |
| | 187.9 | ***bnl17.02*** | |
| | 219.4 | ***umc1993*** | *(5.6)dmt102a* |
| 10.07 | 245.2 | ***bnl7.49a*** | |
| | 255 | ***bnlg1677*** | *(0.4)sgb103* |
| | 311.2 | ***bnlg1450*** | *(33.7)mon00218::Ac* |
| | 315.8 | ***bti00191b::Ac*** | *(0.4)sgb103* |
| | 341.1 | ***asg19b*** | *(33.7)mon00218::Ac* |

## VI. MAIZE GENOME DATABASE (MaizeGDB)

### Maps, Map Integration, and Community Curation

*www.maizegdb.org*

### Maps

Notable new maps provided this year to MaizeGDB include two major maps prepared using the public, 94 individual intermated B73XMo17 (IBM) population available from the Stock Center. This population is a subset of the larger population used to create the IBM2 map that anchors the physical, BAC contig map maintained at Arizona <www.genome.arizona.edu/fpc/maize>.

> IBM IDP + MMP bd (ver 4) maps from Pat Schnable.
> 1407 newly mapped insertion-deletions polymorphisms (IDP) <maize-mapping.plantgenomics.iastate.edu>. Some 655 IDP loci map to a statistically well-defended order. Probe details, including primer sequences and GenBank accessions have been made available to MaizeGDB.
>
> IBM GNP 2004, from Falque, M. et al., Genetics 170:1957-1966, 2005.
> 954 newly mapped maize ESTs. Details about probes, both RFLP and PCR based, have been provided to MaizeGDB and are also included as supplemental material in the publication. Probes monomorphic on the IBM are mapped on a second population, and those maps are called LHRFGnp2004.

Also newly added are the maize recombination nodule (RN) maps <http://www.maizegdb.org/RNmaps.php> reported by Anderson, L.K. et al., Genetics 165:849-865, 2003. Since the publication of the RN distribution for all ten chromosomes in maize, Anderson and others (Genetics 166:1923-1933, 2004) demonstrated that the distribution of RNs along the maize pachytene chromosome structure could be used to accurately predict physical, cytological map locations for loci mapped genetically (Anderson, L.K. et al.). In an effort to automate that process, a new tool called the 'Morgan2McClintock Translator' has been created by Lawrence, C.J., Seigfried, T.E., Bass, H.W., and Anderson, L.K. (manuscript in preparation). The alpha version of this new tool is currently accessible through the RN map data page (see above).

### Map Integration:

The Genetic 2005 maps, provided by Ed Coe (see this Newsletter, pages 116-126). This re-working includes a total of 2465 loci: a frame of 400 well-ordered loci largely from the Genetic 1997 maps, and also 754 from the UMC 98 RFLP maps. Establishing a well-ordered framework integrated with one of the maps that can be projected onto the IBM2 map means that many loci, in particular, those with empirically determined and confirmed functions, can be incorporated into the IBM neighbors consensus maps. Genes and breakpoints added to the IBM2 neighbors by this resource include:

> <u>Chromosome 1.</u> *T1-2a(1), T1-2b(1), T1-2c(1), T1-3a(1), T1-3k(1), T1-4b(1), T1-5(6899)(1), T1-6b(1), T1-6c(1), T1-7a(1), T1-7c(1), T1-9(8389)(1), T1-9b(1), T1-9c(1), TB-1La(1), TB-1Sb(1), ad1, amp1, bm2, br1, br2, cp3, d8, dek1, dia2, f1, gs1, gsr1, hsp26, ij2, l16, les2, lw1, mmm1, mpl1, ms17, ms9, msv1, nec2, obf1, pgm1, ptd1, rd1, sr1, tb1, ts6, vg1, vp5, vp8, zb4, zb7.*
> <u>Chromosome 2.</u> *T2-10a(2), T2-3(5304)(2), T2-3(6270)(2), T2-3a(2), T2-3c(2), T2-5a(2), T2-5g(2), T2-9b(2), agp1, akh2, al1, ba2, ch1, d5, emp2, fl1, gl11, gl14, gl2, gn1, ht1, les1, les10, les15, lg1, nec4, px1, rDNA5S, rf3, sk1, sks1, ts1, v24, v4, wlv1, ws3, wt1.*
> <u>Chromosome 3.</u> *K3L, T1-3(5597)(3), T1-3(8995)(3), T3-9(8447)(3), TB-3La(3), TB-3Lc(3), TB-3Sb(3), a3, ba1, brn1, cg1, cl1, cr1, d1, et1, ga7, gl6, hex1, ig1, lxm1, mv1, na1, pm1, ra2, rf1, rp3, rt1, sdw2, spc1, te1, ts4, w19, wlu1, wrk1, wsm2, y10, ys3.*
> <u>Chromosome 4.</u> *Dt6, T1-4b(4), T4-7(4698)(4), T4-9g(4), TB-4Sa(4), TB-4Sg(4), akh1, als1, cp2, dsc1, dzr1, gl3, gl4, gl5, gl7, la1, lw4, mdr1, ms41, ms44, ns2, o1, ra3, sos1, su1, tga1, tu1, v17, v8, zrp4.*
> <u>Chromosome 5.</u> *T1-5(8041)(5), T1-5b(5), T5-6b(5), T5-9(4817)(5), TB-5La(5), TB-5Lb(5), TB-5Ld(5), TB-5Sc(5),ae1, als2, am1, anl1, bm1, bv1, d9, dap1, dek33, ga2, gl17, got3, gpc4, hsf1, lu1, lw2, lw3, na2, nec3, nec6, nl2, pr1, ps1, ren1, sh4, td1, v12, v3, vp2.*
> <u>Chromosome 6.</u> *Dt2, NOR, T4-6(6623)(6), T4-6(8428)(6), T6-9(043-1)(6), T6-9(6019)(6), T6-9e(6), TB-6Lc(6), TB-6Ld(6), TB-6Sa(6), adk1, l10, l11, l12, l15, ln1, mdm1, mn3, ms1, pg11, po1, rgd1, rhm1, sm1, su2, tan1, w1, w14, w15, wi1, wsm1.*
> <u>Chromosome 7.</u> *TB-7Lb(7), TB-7Sc(7), les9, lhcb2, mn2, nbp1, o15, o5, pep4, px3, ra1, ren2, rs4, sl1, sod2, tp1, v5, va1, vp9, w16, w17, y8.*
> <u>Chromosome 8.</u> *TB-8Lc(8), clt1, emp3, fl3, ht2, htn1, j1, lg4, ms8, pdc2, pro1, rf4, rgh1.*
> <u>Chromosome 9.</u> *Dt1, T8-9a(9), T9-10b(9), TB-9La(9), TB-9Lc(9), TB-9Sb(9), TB-9Sd(9), ar1, baf1, bf1, bk2, bm4, eno1, g6, l7, les8, lo2, ms2, obf2, pg12, pyd1, rld1, trn1, v1, v30, v31, w11, wc1, wd1, yg2, zb8.*
> <u>Chromosome 10.</u> *TB-10L14(10), TB-10L15(10), TB-10L16(10), TB-10L18(10), TB-10L19(10), TB-10L2(10), TB-10L20(10), TB-10L21(10), TB-10L22(10), TB-10L23(10), TB-10L26(10), TB-10L32(10), TB-10L36(10), TB-10L6(10), TB-10L7(10), TB-10La(10), TB-10Lb(10), TB-10Sc(10), bf2, cx1, du1, g1, isr1, l1, l13, lc1, li1, mac1, ms10, ms11, mst1, nl1, o7, og1, oy1, rp1, rp5, rp6, rps11, sn1, sr2, tp2, w2, wsm3, y9, zn1.*

IBM2 2005 Neighbors, provided by MaizeGDB. These maps are computed by a reiterative projection algorithm (Polacco M. et al., MNL 77:137-179, 2003). IBM2 neighbors relies on the IBM2 framework of 1552 statistically well-defended ordered and maps curated in MaizeGDB which share some commonality with IBM2. The 2005 version adds new genetically mapped loci described above; and over 20,000 loci identified by SSR and Overgo probing of BACs and whose genetic map order is defined by their positions on anchored BAC contigs (www.genome.arizona.edu/fpc/maize).

### New 'Community Curation Tools'

Small datasets can be added directly to the database using a new set of Web-accessible Java-based Community Curation Tools that are currently available for general use. Datatypes accessible through these tools include: Clone Library, Gel Pattern, Gene Product, Linkage Group, Locus, Map, Map Scores, Panel Of Stocks, Person, Phenotype, Primer/Enzyme, Probe, Recombination Data, Reference, Species, Stock, Term, and Variation. A QTL data entry tool is under development and is expected to be available for use in the near future. As always, large datasets can be made available through MaizeGDB by special arrangement. Use the feedback form at the bottom of any page at MaizeGDB to request information on Community Curation or to enquire about how to get a large dataset into the database directly.

Other information about MaizeGDB may be found in 2 recent publications, accessible as full text through MaizeGDB:

Lawrence, CJ, Seigfried, TE, and Brendel, V., 2005. The Maize Genetics and Genomics Database. The community resource for access to diverse maize data. Plant Physiology 138:55-58.

Lawrence, CJ, Dong, Q, Polacco, ML, Seigfried, TE, and Brendel, V., 2004. MaizeGDB, the community database for maize genetics and genomics. Nucleic Acids Research 32:D393-D397.

Submitted by Mary Schaeffer and Carolyn Lawrence

## V. MAIZE GENOME DATABASE

*www.maizegdb.org*

Reverse Genetics: TILLING, *Ac* and *Ds* Toolkits, RNAi

Integration of the Maize TILLING Project's mutant information into MaizeGDB has been modeled, and will soon be available. Please visit http://genome.purdue.edu/maizetilling for projected release dates.

Information about stocks available from the Stock Center representing *Ds* or *Ac* tags from Hugo Dooner's and Tom Brutnell's projects is regularly updated. RNAi transgenic stocks available at the Stock Center are incorporated, using information provided by the Maize Chromatin Project and linked to targeted genes and constructs within MaizeGDB; links are also provided to the Chromatin Consortium database (http://www.chromdb.org). Query on the Stock page http://www.maizegdb.org/stock.php for stocks of type="Toolkit" and the focus linkage group of interest to retrieve the *Ac* and *Ds* insertion set; query for stocks of type="ChromDB" will retrieve RNAi stocks.

Sequences

Updated raw and assembled sequence sets are loaded into MaizeGDB on the first Tuesday of each month from a dataset prepared by Volker Brendel's PlantGDB project group (Dong et al., Plant Physiol. 139:610-618, 2005). The sequence set includes all maize sequences available at GenBank as well as PlantGDB's transcript contigs which are called PUTs (for "PlantGDB-assembled Unique Transcript Fragment") and GSS contigs (called GSStucs for "Genome Survey Sequence tentatively unique contigs"). For access to the most up-to-date sequence sets, visit PlantGDB (http://www.plantgdb.org) where the sequence set is updated daily. To gain access to sequences and their related data (e.g., map positions, probe information, etc.) visit MaizeGDB. Note that reciprocal linkages between both sites are present at both sites, enabling ease of navigation no matter where you start your sequence search.

Genetic Maps

The updated community IBM map (cIBM 2005) based on the IBM-94 mapping population includes some 1930 loci, where 580 now serve as the framework in the MapMaker computation, compared to 250 framework loci in previous versions of the cIBM maps. This framework was developed in collaboration with Ed Coe and is based on the framework used by Georgia Davis for quantitative trait mappings. Most of the new loci were incorporated from the Genoplante EST-based RFLP mapping (see also maps IBM GNP2004; Falque et al., Genetics 170:1957-1966, 2005). Other loci were mapped from data released by the Maize Chromatin Project (Karen Cone); the Maize Mapping Project (Mike McMullen); and the *Ac* Mutagensis Project (Tom Brutnell). The cIBM maps may be viewed, along with supporting data including map scores, probe details, etc., at MaizeGDB.

The new neighbors map (IBM2 neighbors 2005) now includes some 35,000 probed sites, most of which are related to public ESTs. In addition to the previously included genetic maps, this consensus map computation incorporates order information from several new maps,including Pat Schnable's IDP maps; RFLP maps from Genoplante (Falque et al., 2005); the Cornell University (CU) maps; the MITEs maps; and frame work loci on the Genetic 2005 maps, which encompass the UMC 98 RFLP maps in order to permit incorporation into neighbors. In addition, this build includes any locus ordered onto anchored BAC contigs in the maize FPC product (http://www.arizona.genome.edu). Only loci identified by at least 2 hits by a probe are included (see maps IBM2 FPC0507); probes represented include overgos, RFLPs, and SSRs. The IBM2 FPC0507 maps were built in collaboration with Mike McMullen as a part of the Maize Diversity Project.

Plant Ontology Curation

The Plant Ontology Consortium (http://www.plantontology.org) has developed over the past few years a logical structure for describing plant anatomy, development and growth. While the initial emphasis has been on 3 plants: *Arabidopsis*, rice, and maize, support for several other angiosperm crop plants is now included. At MaizeGDB, anatomical aspects of phenotypes have been associated with Plant Ontology accessions and the phenotype-inferred associations to loci, stocks and alleles have been supplied to the Plant Ontology database (http://www.plantontology.org. Curation tools for annotation of other types of gene expression are under development to add to associations inferred by mutant or trait phenotype.

Community Curation at MaizeGDB

A quantitative trait experiment module has added to the curation tool suite at MaizeGDB (Schaeffer et al., in preparation). This module builds on the earlier tools used at MaizeDB (Byrne et al., J. Agric. Genomics 1:1-11, 1995) and adds many automated and quality control features. For example, much of the nomenclature of objects (maps, QTL, alleles, and panels of stocks) are now auto-computed from symbols assigned to the trait and parental germplasm. Similar to the case for previous community curation tools, the record may be updated by the contributor up until the time it is considered ready for the monthly release. Changes made to data that have been released should be made by communicating with a staff curator. We encourage persons with publications in press to submit their data to MaizeGDB, beginning with the contact form provided on each page at MaizeGDB. Refer to http://www.maizegdb.org/data_contribution.php for more information about data submission to MaizeGDB.

### How You Can Help MaizeGDB to Succeed

As you know, MaizeGDB is a 'model organism database' and is the community of maize researchers' repository for genomic and genetic data pertaining to our favorite plant, *Zea mays* ssp. *mays*. At the Community Forum session during the Maize Genetics Conference this past year, the statement that MaizeGDB needs to evolve into a more TAIR-like resource (see http://www.arabidopsis.org) was made, and a desire for the community database to improve was communicated by many attendees, both during and after that session (minutes from the Community Forum can be accessed at http://www.maizegdb.org/maize_meeting/2006/ and in this MNL, pp. 111-113). Subsequently, the Maize Genetics Executive Committee surveyed the community to find out what issues were of the most importance to the community of maize geneticists. The survey's full report can be accessed at http://www.maizegdb.org/SurveyResults06.doc and in this MNL, pp. 114-117. The top three "General Community Needs" identified were:

1. High quality maize genome sequence annotation.
2. Improved maize reverse genetics resources that allow investigators to move from sequence to seed.
3. An improved maize database that allows investigators to move seamlessly between multiple genomic datasets and expression analysis.

Improving the MaizeGDB addresses needs one and two, and the desire for an improved database is stated per se as need three. Help us to meet your needs by voicing this concern! To find out how to help, read "Plant Biology Database s: A Needs Assessment", an advisory whitepaper to the NSF and USDA, which can be accessed at http://www.maizegdb.org/PDBNeeds.pdf, and contact us directly at mgdb@iastate.edu. For an abbreviated version of the Advisory Whitepaper's recommendations, see Stein et al. (The Scientist 20(4):24-25, 2006).

### Acknowledgements

We thank MaizeGDB's interface developer and bioinformatics engineer Trent Seigfried and database administrator Darwin Campbell for supporting the curation efforts described here. We are grateful for assistance from the MaizeGDB Working Group: Volker Brendel, Ed Buckler, Karen Cone, Mike Freeling, Owen Hoekenga, Lukas Mueller, Marty Sachs, Pat Schnable, Tom Slezak, Anne Sylvester, and Doreen Ware. We thank the MaizeGDB Editorial Board for recommending, on a monthly basis, noteworthy primary literature. This Board currently includes: Tom Brutnell, Surinder Chopra, Karen McGinnis, Wojtek Pawlowski and Jianming Yu.

Submitted by:
Mary Schaeffer (Polacco)
Carolyn J. Lawrence

## MGSC: Gramene and MaizeGDB cooperate to provide access to sequences and related data

--Lawrence, CJ; Ware, D

The NSF, USDA, and DOE announced on November 15, 2005 that together they had funded the sequencing of the genome of inbred line B73 as well as chromosome ten of Mo17 (a project that aims simultaneously to evaluate shotgun sequencing strategies for large genomes and to investigate maize diversity). In addition, the USDA-ARS contributed the MaizeGDB project resources. Because Gramene will be the primary portal to the maize B73 sequences (which are to be annotated by the Ware group), a description of past and present interactions between MaizeGDB and Gramene is presented here. This contribution describes our groups' interactions and also explains current and planned access points and portals to the maize sequence data. For a description of the maize sequencing project's deliverables and timelines, see pp. 71-72 in this volume of the Maize Newsletter.

MaizeGDB and Gramene personnel began collaborating early on, and have been involved in developing shared resources like the Plant Ontologies, (http://www.plantontology.org) a set of terms that describe plant anatomy and developmental stages, for the last three years. This hierarchical vocabulary enables data to be integrated by the use of common terms across different databases to describe divergent datasets, such as EST collections, mutant strains, and stocks, so that they can be simultaneously searched and analyzed. This set of terms currently is in place at both MaizeGDB and Gramene, enabling the annotation of various data types at both repositories, and is a resource upon which many connections can be built (between MaizeGDB and Gramene, and also with other resources like TAIR, the Solanacea Genomics Network, the Virtual Plant Information Network, and other plant databases).

In addition to working together, members of the MaizeGDB and Gramene teams have been apprised of and involved in the development of both resources. For instance, Gramene PI L. Stein contributed to guiding MaizeGDB's development by serving on the MaizeDB to MaizeGDB Transition Steering Committee, and Gramene co-PI D.W. currently serves as a member of the MaizeGDB Working Group. Similarly, MaizeGDB director C.J.L. has participated in Gramene Scientific Advisory Board meetings during the past two years. Curators from Gramene attended the MaizeGDB curation tools workshop in Ames, Iowa in the fall of 2004, and a working meeting to integrate maps and molecular markers was co-organized by MaizeGDB and Gramene personnel and was conducted one evening at the 2005 Maize Genetics Conference. Ideas and data are exchanged between the two groups on a regular basis.

The first of a number of sequence data meetings between the Ware maize sequence analysis group and the MaizeGDB team is slated to take place in June of 2006 at the Cold Spring Harbor Laboratory. During this meeting, we will work to identify means to synchronize data release and make accessing maize sequence data easier for researchers, irrespective of data storage location. We also will explore methods for addressing feedback from maize geneticists that is relevant to both projects. We expect that a joint feedback mechanism may be in order, but the logistics and implementation of such a mechanism will require serious consideration and discussion. It is expected that outcomes from the June meeting will serve to guide both groups' development strategies to maximize accessibility to sequence data while minimizing duplication of effort.

At present, the Gramene and MaizeGDB websites are linked throughout by way of shared data, common nomenclature, and a standard set of linking rules. New linkages and entry points to data will be made available at both sites as they are identified. For a list of some existing linkages, see Tables 1 and 2. Datasets shared by both groups include sequences, BACs, loci, markers, maps, and ontology terms. These datasets will serve as the basis for creating new linkages to increase the interconnectedness of the two resources. We solicit ideas you might have for how to improve both MaizeGDB and Gramene. Please send all comments and suggestions to both MaizeGDB and Gramene by way of our groups' shared email address: feedback@maizesequence.org. Your help, guidance, and continued support are greatly appreciated!

Table 1. Links from MaizeGDB to Gramene that are already in place.

| MaizeGDB Data Type | <Example Entry URL> and Link Placement to Gramene | Purpose |
|---|---|---|
| Sequences | <http://www.maizegdb.org/cgi-bin/displayseqrecord.cgi?id=AC149813><br>Right green bar, under "Search Tools". | Jump from MaizeGDB BAC data to the Gramene Finger Print Contig viewer |
| BACs | <http://www.maizegdb.org/cgi-bin/displaybacrecord.cgi?id=507533><br>Top of the page, in bold font. | Jump from MaizeGDB BAC data to the Gramene Finger Print Contig viewer |
| Loci | <http://www.maizegdb.org/cgi-bin/displaylocusrecord.cgi?id=12098><br>Right green bar, under "Search Tools". | View the locus within the context of its map location using CMap |
| Maps | <http://www.maizegdb.org/cgi-bin/displaymaprecord.cgi?id=143439><br>Right green bar, under "Other Map Views". | View the map visually using CMap |

Table 2. Links from Gramene to MaizeGDB that are already in place.

| Gramene Data Type | <Example Entry URL> and Link Placement to MaizeGDB | Purpose |
|---|---|---|
| BACs | < http://www.gramene.org/Zea_mays/cytoview?mapfrag=AC149813><br>Context menu for BAC on "Acc Clones" track. | Show associated marker data on MaizeGDB |
| Maps | <http://www.gramene.org/Zea_mays/cytoview?mapfrag=c0148C07><br>Context menu for clone on "FPC Map" track. | Show associated marker data on MaizeGDB |
| Markers | <http://www.gramene.org/Zea_mays/cytoview?contig=ctg129><br>Context menu for individual markers on "Markers" track. | Jump to marker info on MaizeGDB |
| Diversity | <http://www.gramene.org/db/cmap/feature?feature_acc=cmf1104a-ctg251-10><br>Cross-reference to MaizeGDB. | Jump to locus info on MaizeGDB |

# VII. BAC CONTIGS AND THEIR GENETIC ANCHORS

BAC contigs and CB positions of anchoring loci are from the maize FPC at Arizona (http://www.genome.arizona.edu/fpc/maize/). Genetic positions are based on the IBM2 high resolution map (http://www.maizegdb.org), computed from a 302 member panel of Stocks for intermated B73 x Mo17 recombinant inbreds. This mapping panel is available from the Maize Genetics Cooperation Stock Center and described by Lee et al. (Plant Mol. Biol. 48:453-461, 2003).

Columns:
***Bins*** are provided for the locus that approximates, on this list, the boundary of a bin; when it corresponds to a Core Marker, which define the bin boundaries, the corresponding locus and coordinate information is in bold face.

***Contig***: the number of the contig, as defined in the current (July 2005) FPC build.

***CB***: the position in a contig for a marker based on the consensus band (restriction fragment) for clones. In maize the CB is 4900 bp (http://www.genome.arizona.edu/fpc/maize/).

***IBM***: the IBM2 cM position, for loci flagged by an asterisk (*). Other loci have the approximate value from the IBM2 2005 neighbors computation. Contigs anchored by unpublished loci are provided the genetic position listed in FPC for a contig; in many instances these anchorings are based on rice-maize synteny of markers. Most of the FPC markers, both SSRs and overgos, were developed from maize cDNAs (ESTs; Unigenes). (Gardiner et al., Plant Physiol. 134:1317:1326, 2004).

***Locus***: Loci flagged by an asterisk are taken from the IBM2 map, which uses the high resolution 302 member inter-mated IBM mapping population of Mike Lee. Other loci are from the IBM2 2006 Neighbors map, a serial projection of genetic maps stored in MaizeGDB onto the IBM2 frame.

Shaded areas on each chromosome are approximate centromere locations, based on the Genetiic 2005 map compilations of Ed Coe (MNL 79; MaizeGDB).

Submitted by
Mary Schaeffer (Polacco)

Chromosome 1

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| 1.00 | 1 | 22 | -0.12 | *bnlg149* |
| | | 382 | -0.01 | *umc1613* |
| | | 413 | 0 | *umc1353* |
| | | 416 | 0 | *umc1354** |
| | | 440 | 0 | *bnlg1124* |
| 1.01 | | 454 | 2.5 | ***tub1**** |
| | 2 | 115 | 10.5 | *dmt103b* |
| | | 139 | 10.5 | *umc1177** |
| | | 159 | 16.5 | *umc1566** |
| | | 165 | 16.5 | *umc2183* |
| | 3 | 40 | 26.1 | *mmp102** |
| | | 40 | 31.1 | *AY110314** |
| | | 110 | 31.11 | *umc1619* |
| | | 129 | 31.11 | *csu589* |
| | | 229 | 48.7 | *lim179** |
| | | 330 | 48.71 | *AY107629* |
| | | 343 | 52.59 | *csu680a* |
| | | 343 | 48.71 | *umc1292* |
| | | 344 | 48.71 | *bnlg1179* |
| | 4 | 45 | 68.3 | *mlo1** |
| | | 50 | 68.3 | *umc1041* |
| | | 84 | 68.3 | *gpb1* |
| | | 114 | 68.31 | *umc1106* |
| | | 156 | 68.31 | *PCO072650* |
| | | 222 | 82.8 | *bnlg1014** |
| | | 291 | 87.4 | *umc2012** |
| | | 372 | 88 | *umc1071** |
| | | 410 | 86.3 | *umc1269** |
| | | 412 | 88.3 | *umc1305* |
| | | 422 | 88.3 | *smt2* |
| | | 437 | 88.3 | *gst31* |
| | | 483 | 89.2 | *umc1977** |
| | | 543 | 89.2 | *prc3* |
| | | 551 | 91.5 | *umc1948** |
| | 5 | 20 | 102.99 | *AY110853* |
| | | 68 | 103 | *umc2215* |
| | | 82 | 103 | *umc1685** |
| | | 382 | 108.3 | *umc1160** |
| | | 470 | 110.9 | *umc2224** |
| 1.02 | | 534 | 113.87 | ***umc157a(chn)**** |
| | 6 | 171 | 124.69 | *bnlg1178* |
| | | 172 | 124.69 | *esr2* |
| | | 300 | 124.7 | *umc2225** |
| | | 325 | 133.6 | *umc1166** |
| | | 410 | 133.61 | *PCO128140* |
| | | 488 | 141.8 | *umc1568** |
| | 7 | 18 | 143.5 | *bnlg1429** |
| | 8 | 48 | 160.53 | *pds1* |
| | | 314 | 160.55 | *bnlg1627* |
| | | 332 | 160.55 | *umc2191* |
| | | 562 | 160.58 | *umc1467* |
| | | 794 | 160.6 | *umc1976** |
| | | 819 | 165.8 | *umc2226** |
| | | 1033 | 166 | *mmp135** |
| | 9 | 20 | 170 | *bnlg1953** |
| | | 371 | 170.04 | *umc1711* |
| | | 621 | 170.06 | *bnlg1007* |
| | | 846 | 114.7 | *gln6* |
| | | 949 | 170.09 | *bnlg1803* |
| 1.03 | | 1097 | 198.06 | ***umc76a**** |
| | 10 | 98 | 204.95 | *umc2383* |

Chromosome 1

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | | 584 | 205 | *lim122** |
| | 11 | 40 | 210.6 | *umc1403** |
| | | 392 | 210.64 | *umc2397* |
| | | 405 | 219 | *bnlg1484** |
| | | 1167 | 225.4 | *AY109929** |
| | | 1230 | 225.41 | *umc2185* |
| | | 1274 | 226.4 | *umc1397** |
| | | 1316 | 229.6 | *AY110052** |
| | | 1565 | 229.63 | *ibp2* |
| | | 1739 | 229.64 | *PCO063726* |
| | | 2076 | 257.4 | *umc1479** |
| | | 2156 | 257.41 | *csu145c(pck)* |
| | | 2174 | 257.41 | *PCO074335* |
| | | 2176 | 259.1 | *bnlg439** |
| | | 2177 | 259.3 | *bnlg1203** |
| | | 2425 | 260.7 | *fad8** |
| | | 2512 | 260.71 | *umc1701* |
| | | 2587 | 260.72 | *pdc3* |
| | | 2723 | 270.6 | *umc13** |
| | | 2758 | 278.1 | *AY110632** |
| | | 3042 | 278.13 | *rth3* |
| | | 3153 | 278.14 | *p1* |
| | 12 | 12 | 287.14 | *p2* |
| | | 97 | 287.14 | *AY110240* |
| | | 396 | 287.18 | *AY107489* |
| | | 576 | 287.19 | *umc1514* |
| | | 632 | 302.8 | *AY110393** |
| | | 638 | 287.2 | *AW400087** |
| | | 680 | 287.2 | *bnlg182* |
| | | 680 | 290.3 | *umc1880** |
| | | 680 | 290.1 | *bnlg1866** |
| | | 699 | 290.32 | *umc2171* |
| | | 772 | 290.4 | *phi109275** |
| | | 825 | 290.41 | *asg45(ptk)* |
| | 13 | 120 | 292.4 | *lim432** |
| 1.04 | 14 | 26 | 328.57 | *umc1452* |
| | | 198 | 328.59 | *cdo38a(ntp)* |
| | | 308 | 328.6 | *umc49c* |
| | | 404 | 326.7 | *bnlg2238** |
| | | 494 | 326.71 | *bnlg1016* |
| | | 494 | 320.9 | *mmp56** |
| | | 667 | 328.5 | *umc2124** |
| | | 685 | 328.71 | *umc1254* |
| | | 723 | 328.71 | *les22* |
| | | 1441 | 337.69 | *sod4** |
| | | 1446 | 340.7 | *csu737(npc)* |
| | | 1636 | 337.71 | *umc2217* |
| | | 1858 | 350.6 | *AY110330** |
| | | 2013 | 374.8 | *umc1917** |
| | | 2272 | 350.64 | *umc1144* |
| | 15 | | 345 | unpublished |
| | 16 | 42 | 360.9 | *umc2227** |
| | | 324 | 360.93 | *umc2390* |
| | 17 | 237 | 386.4 | *bnlg1811** |
| | 18 | 389 | 390.8 | *bnl9.11b(lts)** |
| | | 472 | 391.8 | *umc2228** |
| | 19 | 552 | 392.73 | *aoc1* |
| | | 844 | 392.75 | *umc1770* |
| | 20 | 125 | 398.2 | *bnlg2295** |
| | | 156 | 397.3 | *umc2229** |
| 1.05 | 21 | 191 | 405 | ***csu3**** |

Chromosome 1

| BIN | BAC FPC: | | Genetic | Locus |
|---|---|---|---|---|
| | Contig | CB | IBM | |
| | | 309 | 408.21 | *csu694b(uce)* |
| | | 367 | 405.02 | *umc1243* |
| | | 367 | 401.3 | *umc2112** |
| | | 392 | 401.2 | *bnlg2086** |
| | | 673 | 413.06 | *mtl2* |
| | 22 | | 406 | unpublished |
| | 23 | 634 | 410.06 | *bnlg1884b* |
| | 24 | | 415 | unpublished |
| | 25 | 15 | 422.68 | *umc1734* |
| | 26 | 177 | 434.61 | *umc1297* |
| | | 498 | 430.6 | *umc1515** |
| | | 599 | 430.62 | *myc7** |
| | 27 | 352 | 432.4 | *umc2230** |
| | | 588 | 433.6 | *AY111680** |
| | 28 | 494 | 437.3 | *AY109678** |
| | 29 | 611 | 438.8 | *umc1461** |
| | | 1029 | 439 | *csu1138** |
| | | 1187 | 439.01 | *umc1689* |
| | 30 | 1899 | 440 | *umc1076** |
| | | 2729 | 473.5 | *obf1* |
| | | 2852 | 441.2 | *mmp101** |
| | | 2883 | 445.5 | *AY110396** |
| | 31 | 71 | 450.8 | *umc1676** |
| | | 828 | 450.87 | *umc1611* |
| | | 1403 | 450.92 | *AY106439* |
| | 32 | 234 | 453.5 | *umc2231** |
| | | 447 | 453.52 | *umc1626* |
| | | 700 | 453.54 | *bsd2* |
| | 33 | 22 | 463.9 | *CL14065_1* |
| | | 210 | 467 | *umc1906** |
| | | 321 | 467.9 | *umc1903** |
| | 34 | 23 | 464.7 | *AI855190** |
| | | 97 | 471.7 | *umc1395** |
| | | 217 | 473.2 | *umc1321** |
| | | 276 | 475.9 | *umc1603** |
| | | 276 | 474.5 | *umc2233** |
| | 35 | | 476 | unpublished |
| | 36 | 116 | 485.84 | *umc1323* |
| | | 745 | 485.9 | *uaz276** |
| | | 1138 | 485.94 | *mbd106* |
| 1.06 | | 1536 | 499.22 | *gpm4* |
| | 37 | 339 | 508.18 | *umc2083* |
| | | 435 | 508.19 | *uce1* |
| | | 556 | 508.2 | *umc1812** |
| | | 557 | 508.2 | *umc1754* |
| | | 837 | 508.23 | *csu61b* |
| | | 992 | 508.24 | *csu92a* |
| | | 1001 | 508.24 | *umc1508* |
| | | 1013 | 517 | *umc1590** |
| | 38 | 68 | 527.6 | *bnlg2057** |
| | | 590 | 529 | *umc2234** |
| | | 726 | 535.1 | *umc1123** |
| | | 726 | 532.8 | *bnlg1598** |
| | | 991 | 541.3 | *AY104360** |
| | | 1038 | 541.3 | *umc1281* |
| | | 1038 | 541.3 | *umc1398* |
| | | 1047 | 544.2 | *mmp156** |
| | | 1277 | 548.3 | *bnlg1057** |
| | 39 | 70 | 548.4 | *umc1396** |
| | | 133 | 550 | *umc2235** |
| | | 204 | 555.71 | *umc1919** |

Chromosome 1

| BIN | BAC FPC: | | Genetic | Locus |
|---|---|---|---|---|
| | Contig | CB | IBM | |
| | 40 | 82 | 557.6 | *bnlg1615** |
| | | 157 | 558.5 | *csu805** |
| | 41 | 19 | 570.8 | *ntf1** |
| | | 41 | 570.8 | *umc1668* |
| | | 146 | 587 | *umc1035** |
| | | 148 | 583.3 | *mmp123** |
| | | 174 | 587 | *PCO116807* |
| | | 201 | 588.2 | *umc1709** |
| | | 490 | 593.8 | *umc1924** |
| | | 522 | 593.8 | *umc1335* |
| | | 731 | 604.8 | *umc2236** |
| | | 855 | 606.5 | *umc1925** |
| 1.07 | | 859 | 607.3 | ***asg62**** |
| | | 1039 | 607.32 | *hm1* |
| | | 1236 | 618.5 | *umc2237** |
| | | 1414 | 618.52 | *umc1122* |
| | | 1527 | 630.6 | *umc2239** |
| | | 1535 | 642.27 | *umc2396* |
| | 42 | 27 | 648.5 | *umc1661* |
| | 43 | 218 | 649.5 | *bcd98a** |
| | | 373 | 652.08 | *umc1356* |
| | | 373 | 652.08 | *umc1374* |
| | | 452 | 653.4 | *umc1358** |
| | | 586 | 656.7 | *AY111834** |
| | 44 | 76 | 658.6 | *bnlg1556** |
| | | 555 | 658.65 | *umc1833* |
| | | 588 | 658.65 | *umc1486* |
| | | 727 | 658.67 | *umc1706* |
| | | 1505 | 658.74 | *umc1278* |
| | | 2620 | 658.85 | *umc2064* |
| | | 2841 | 658.88 | *bnl17.15b(bt2)* |
| | | 2846 | 658.88 | *btl2* |
| | 45 | 175 | 693.6 | *mmp173** |
| | | 218 | 693.6 | *umc2387* |
| | 46 | 21 | 700.5 | *bnlg1025** |
| | | 103 | 706.4 | *AY110356** |
| | | 131 | 711.5 | *umc1128** |
| | | 310 | 714.4 | *umc1147** |
| | | 593 | 735.2 | *AY110313** |
| | | 658 | 737.24 | *umc1848* |
| | | 758 | 740.4 | *AY110191** |
| 1.08 | | 938 | 722.4 | ***umc128**** |
| | | 1009 | 722.3 | *AY110159** |
| | | 1266 | 721.9 | *umc1245** |
| | | 1274 | 741.51 | *umc59c* |
| | | 1619 | 744.7 | *cdo98b** |
| | | 1737 | 747.9 | *umc1998** |
| | | 1766 | 747.9 | *bnlg1629* |
| | 47 | 151 | 755.2 | *bnlg2228** |
| | | 152 | 756.5 | *umc83a** |
| | | 244 | 756.51 | *umc2029* |
| | 48 | 49 | 760.3 | *lim254** |
| | | 244 | 770.4 | *umc1955** |
| | | 285 | 770.4 | *umc1085* |
| | | 586 | 774.5 | *umc2181** |
| | 49 | 389 | 776.51 | *mmc0041* |
| | | 452 | 776.51 | *umc1838** |
| | | 621 | 781.6 | *umc1446** |
| | | 717 | 785.3 | *an1** |
| | | 728 | 784.7 | *mmp22** |
| | | 759 | 785.3 | *bz2* |

Chromosome 1

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | | 943 | 793.05 | *AY110349** |
| | 50 | 98 | 800.7 | *umc1991** |
| | | 265 | 800.72 | *bnlg1643* |
| | | 619 | 805.3 | *umc1383** |
| | | 693 | 806.5 | *umc2240** |
| | | 719 | 806.5 | *umc2385* |
| | | 720 | 806.5 | *umc1843* |
| | 51 | 145 | 807.57 | *AY106137* |
| | 52 | 262 | 809.86 | *nfc103a* |
| | | 453 | 809.88 | *umc2116* |
| | | 495 | 809.89 | *vp14* |
| | | 623 | 809.9 | *umc1914** |
| | | 631 | 811 | *AY109506** |
| 1.09 | | 659 | 812.3 | ***cdj2**** |
| | 53 | 63 | 839.29 | *glb1** |
| | 54 | 356 | 847 | *umc1298* |
| | | 357 | 847 | *bnlg1331** |
| | 55 | 56 | 842.3 | *umc2047** |
| | | 410 | 825.14 | *umc27b* |
| | 56 | 418 | 849.01 | *lpe1* |
| | 57 | 11 | 883.03 | *AY112283* |
| | | 46 | 883.03 | *ole4* |
| | | 125 | 883.04 | *umc2028* |
| | | 295 | 883.06 | *umc1306* |
| | | 402 | 883.07 | *bnlg1720* |
| | | 410 | 883.07 | *tb1** |
| | | 693 | 886.1 | *umc1431** |
| 1.10 | | 833 | 886.9 | ***umc107a(croc)**** |
| | | 834 | 886.9 | *gln2* |
| | | 1035 | 889.9 | *AI665421** |
| | | 1296 | 889.93 | *PCO087393* |
| | | 1403 | 889.94 | *umc1290* |
| | | 1436 | 890.9 | *AY110019** |
| | | 1520 | 890.91 | *kn1* |
| | | 1579 | 890.91 | *knox3* |
| | | 1880 | 898.7 | *umc2149** |
| | | 1887 | 898.7 | *bnlg1268* |
| | | 1939 | 927.67 | *AY104234* |
| | | 2048 | 901.85 | *adh1** |
| | | 2289 | 907.1 | *BE639426** |
| | | 2322 | 907.11 | *umc1885* |
| | | 2355 | 907.12 | *umc1534* |
| | | 2355 | 913.4 | *bnlg1671** |
| | | 2614 | 934.5 | *uaz130a(tlk)** |
| | | 2838 | 926.3 | *PCO095183* |
| | 58 | 30 | 927.4 | *mta1* |
| | | 128 | 927.4 | *umc1774* |
| | | 209 | 927.4 | *phi308707** |
| | | 271 | 927.4 | *umc2223* |
| | 59 | | 930 | unpublished |
| | 60 | | 951.2 | unpublished |
| 1.11 | 61 | 291 | 963.6 | ***umc161a**** |
| | 62 | 410 | 972.99 | *umc1500* |
| | | 484 | 973.97 | *csu63a(cdj)* |
| | | 488 | 973 | *phi265454** |
| | | 675 | 1,007.60 | *umc1553** |
| | | 707 | 987.3 | *AY110426** |
| | 63 | 50 | 1,014.90 | *umc1681** |
| | | 60 | 1,014.90 | *ohp1* |
| | | 108 | 1,019.10 | *umc1129** |
| | 64 | 36 | 1,030.98 | *csu604a(trh)* |

Chromosome 1

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | | 152 | 1,030.99 | *umc1862* |
| | | 184 | 1,030.99 | *bnlg2331* |
| | | 255 | 1,031.80 | *umc2242** |
| | | 265 | 1,031.00 | *umc2241** |
| | | 272 | 1,031.80 | *csu33b* |
| | | 280 | 1,031.80 | *ccr1* |
| | | 282 | 1,031.80 | *umc1737* |
| | | 290 | 1,031.80 | *bnlg1055* |
| | | 318 | 1,034.30 | *umc1118** |
| | | 338 | 1,034.30 | *cesa5* |
| | | 492 | 1,034.32 | *bnlg667a* |
| | | 625 | 1,041.78 | *csu134a(thf)* |
| | | 642 | 1,034.33 | *AY109096* |
| | | 773 | 1,051.10 | *umc1744** |
| | | 815 | 1,051.10 | *ids1* |
| | | 832 | 1,051.11 | *chi1* |
| | | 860 | 1,051.11 | *umc1220* |
| | | 861 | 1,054.20 | *umc84a** |
| | | 965 | 1,054.21 | *AY106825* |
| | | 971 | 1,054.21 | *bnlg2123* |
| | | 972 | 1,054.21 | *bnlg131* |
| | | 972 | 1,055.90 | *umc1630** |
| | | 986 | 1,055.90 | *AY109128* |
| | 65 | 32 | 1,096.47 | *bnlg504* |
| | | 55 | 1,096.47 | *AY112175* |
| | | 249 | 1,096.49 | *CL62610_1* |
| | | 262 | 1,099.30 | *umc2045** |
| | | 307 | 1,098.40 | *fdx3** |
| | | 311 | 1,098.40 | *umc2243** |
| | | 333 | 1,096.50 | *umc1725* |
| | | 335 | 1,096.50 | *umc1331** |
| | | 339 | 1,097.40 | *phi227562** |
| | | 423 | 1,103.00 | *phi064** |
| 1.12 | 66 | 58 | 1,121.90 | *tufm1** |
| | | 98 | 1,119.20 | *umc1819** |
| | | 120 | 1,117.10 | *umc1605** |
| | | 120 | 1,120.30 | *umc2244** |
| | | 185 | 1,122.90 | *AY109916** |
| | 67 | 30 | 1136.0 | *umc1499* |
| | | 36 | 1,136.00 | *csu1114* |
| | | 229 | 1,136.02 | *umc1797* |
| | | 290 | 1,136.03 | *AY104686* |

Chromosome 2

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| 2.01 | 69 | 60 | 47.4 | umc1165* |
| | | 81 | 47.4 | umc2363 |
| | | 109 | 47.4 | csu642 |
| | | 133 | 47.41 | bnlg1338 |
| 2.02 | | 180 | 57.6 | umc1542* |
| | | 196 | 57.6 | umc1227 |
| | | 374 | 77.7 | umc1265* |
| | | 591 | 87.8 | BE640649* |
| | | 694 | 87.81 | umc2403 |
| | | 698 | 87.81 | sgb101 |
| | 70 | 78 | 92.6 | umc1824a* |
| | | 199 | 92.8 | umc1823* |
| | | 199 | 92 | umc1961* |
| | | 250 | 93.3 | mmc0111* |
| | | 260 | 93.3 | bnl7.49c(hmd) |
| | | 359 | 94.4 | AY109516* |
| | | 397 | 94.4 | CL52019_1 |
| | | 629 | 94.43 | bnlg1302 |
| | | 676 | 94.43 | dmt102b |
| | | 720 | 94.44 | umc1934 |
| | | 728 | 122.4 | eks1* |
| | 71 | 305 | 148.1 | bnlg1327* |
| | | 461 | 154.6 | umc1261* |
| | | 461 | 152.83 | umc1262* |
| | | 468 | 154.71 | bnlg125 |
| | | 468 | 154.71 | csu1091 |
| | | 468 | 154.71 | csu1113 |
| | | 522 | 156.6 | umc1422* |
| | | 533 | 156.6 | gpm7 |
| | 72 | 103 | 156.56 | umc2193 |
| | | 127 | 163.5 | AY106040* |
| 2.03 | | 161 | 164.55 | **umc6a*** |
| | 73 | 82 | 164.54 | si605074C02 |
| | 74 | 19 | 182.3 | umc44b* |
| | | 124 | 182.31 | nfd102 |
| | | 245 | 182.32 | bcd855a(ext) |
| | | 351 | 197.15 | b1* |
| | | 502 | 197.17 | umc1845 |
| | | 545 | 203.1 | mmp33* |
| | | 835 | 217.32 | ole1* |
| | | 938 | 217.33 | sdg104 |
| | | 1081 | 217.34 | AY107034 |
| | | 1111 | 221.4 | AI920398* |
| | | 1259 | 221.41 | bnlg2248 |
| | | 1362 | 221.42 | umc1769 |
| | | 1619 | 221.45 | umc1555 |
| | | 2020 | 227.1 | bnlg1064* |
| 2.04 | | 2255 | 243.3 | **umc34*** |
| | | 2255 | 244 | phi109642* |
| | | 2305 | 236.4 | AY104214* |
| | | 2337 | 244.7 | bnlg381* |
| | | 2337 | 244.01 | si606023F08 |
| | 75 | 15 | 250.1 | umc1026 |
| | | 15 | 250.1 | umc1024* |
| | 76 | 9 | 251.1 | umc2247* |
| | | 304 | 251.13 | AY103944 |
| | | 499 | 267.8 | umc2248* |
| | | 589 | 262.6 | AY110266* |
| | | 600 | 266.8 | umc1326* |
| | | 611 | 268.4 | umc259b* |
| | | 770 | 269.6 | umc1448* |

Chromosome 2

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | | 805 | 269.6 | cta1 |
| | 77 | 27 | 273.61 | PCO140184 |
| | | 604 | 273.67 | hag103a |
| | | 851 | 273.69 | CL58207_1 |
| | | 918 | 273.7 | umc1465* |
| | | 1019 | 274.9 | umc1541* |
| | | 1402 | 284.7 | prp2* |
| | | 1408 | 284.7 | CL10221_1 |
| | | 1450 | 284.7 | umc2032 |
| | 78 | 76 | 293.31 | grf1* |
| | | 118 | 293.32 | umc1579 |
| | | 118 | 294.2 | umc1580* |
| | | 171 | 293.8 | lim86* |
| | | 171 | 294.2 | bnlg1018* |
| | | 227 | 294.21 | cdo1328b |
| | | 278 | 295.1 | bnlg1175* |
| | | 444 | 295.8 | umc2251* |
| | | 528 | 296.3 | umc2249* |
| | | 797 | 292.87 | csu56c(ohp) |
| | | 1219 | 296.37 | AI714808 |
| | | 1294 | 306.3 | bnlg108* |
| | | 1327 | 306.3 | bnlg1909 |
| | | 1507 | 310.2 | umc1259* |
| | 79 | 189 | 313.5 | umc2030* |
| | | 315 | 314.4 | umc1861* |
| | | 497 | 314.41 | umc1285 |
| | | 1038 | 316.7 | umc2088* |
| | | 1191 | 316.72 | umc1485 |
| | | 1194 | 323.3 | hrg1* |
| | | 1590 | 320.7 | umc2079* |
| | 80 | 120 | 328.93 | hda102 |
| | | 398 | 328.96 | AY112119 |
| | | 825 | 329 | umc2250* |
| | 81 | 53 | 332.17 | bnlg1613 |
| | | 339 | 332.2 | umc2125* |
| | 82 | 400 | 339.3 | umc1454* |
| | | 402 | 339.3 | umc1455 |
| | | 615 | 339.32 | umc1410 |
| | 83 | 172 | 341.32 | umc1007 |
| 2.05 | 84 | 565 | 342.38 | npi220d |
| | 85 | 135 | 344.8 | umc1635* |
| | 86 | 408 | 344.4 | umc1581* |
| | | 2332 | 345.72 | zpu1* |
| | | 2775 | 345.74 | cdo456b |
| | | 2830 | 345.74 | umc1884 |
| | | 2830 | 349 | AY109687* |
| | 87 | 381 | 346.47 | AY107012 |
| | | 1118 | 346.5 | mmp119* |
| | 88 | 59 | 346.46 | bnlg1887 |
| | 89 | 1973 | 352.21 | hsbp1 |
| | | 3713 | 352.4 | AW681281* |
| | 90 | 366 | 357.45 | umc1459 |
| | | 394 | 358.6 | mmc0401* |
| | | 726 | 359.1 | umc2252* |
| | | 893 | 359.12 | AY111877 |
| | | 986 | 357.5 | umc2110* |
| | | 1192 | 361.2 | umc1028* |
| | 91 | 112 | 369.3 | umc1079* |
| | | 273 | 368.8 | bnlg1831* |
| | | 368 | 364.5 | AY110336* |
| 2.06 | | 371 | 369.32 | **umc255a** |

Chromosome 2

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | | 565 | 369.34 | *pbf1** |
| | | 619 | 369.34 | *bnlg371* |
| | | 1141 | 369.38 | *umc1235* |
| | | 1210 | 373.5 | *bnlg1036** |
| | | 1653 | 373.57 | *umc1156* |
| | | 1966 | 373.62 | *csu747a(arf)* |
| | | 2653 | 375.3 | *umc1658** |
| | | 3554 | 376.1 | *umc2253** |
| | | 3899 | 376.14 | *bnlg1396* |
| | | 3992 | 377.4 | *umc2178** |
| | | 4070 | 377.41 | *umc2194* |
| | | 4200 | 377.42 | *umc2192* |
| | 92 | 52 | 378.7 | *umc2254** |
| | | 156 | 379.2 | *bnlg1138** |
| | | 287 | 379.28 | *akh2* |
| | | 498 | 379.4 | *umc1923** |
| | | 608 | 380 | *umc1080** |
| | | 626 | 380.6 | *umc1755** |
| | 93 | | 380.2 | unpublished |
| | 94 | 81 | 380.8 | *AY109981** |
| | 95 | 135 | 381.8 | *umc1004** |
| | 96 | 56 | 382.8 | *PCO063114* |
| | | 781 | 382.87 | *umc1749* |
| | | 846 | 382.88 | *umc2023* |
| | 97 | 17 | 394.89 | *umc2019* |
| | | 48 | 394.89 | *umc1946* |
| | 98 | 45 | 401.94 | *umc2402* |
| | | 166 | 401.95 | *umc1637* |
| | | 190 | 401.95 | *bnlg1329* |
| | | 382 | 401.97 | *amy3* |
| | | 463 | 401.98 | *AI861369* |
| | | 742 | 414.1 | *umc2129** |
| | | 789 | 414.1 | *umc1497* |
| | | 1122 | 414.14 | *umc2380* |
| | 99 | | 416 | unpublished |
| | 100 | 10 | 422.68 | *mmc0271* |
| | | 10 | 178.78 | *mmc0231** |
| | | 163 | 427.9 | *AY110410** |
| | | 187 | 422.7 | *umc1890** |
| | 101 | 354 | 433.4 | *umc2205* |
| | 102 | | 450 | *unpublshed* |
| | 103 | 62 | 452.19 | *bnlg1633* |
| | | 100 | 453.8 | *phi251315** |
| | | 155 | 452.2 | *AY109917** |
| | | 245 | 453.81 | *bnlg1267* |
| | | 555 | 453.85 | *bnlg198* |
| | | 555 | 453.85 | *bnlg1335* |
| | | 868 | 475.1 | *umc1560** |
| | | 877 | 474.8 | *bnlg2077** |
| | | 925 | 475.11 | *umc1554* |
| | | 980 | 475.11 | *umc4a* |
| | | 1136 | 475.12 | *umc1536* |
| 2.08 | | 1234 | 478.7 | ***asg20**** |
| | | 1283 | 480.7 | *umc1049** |
| | | 1296 | 482.2 | *mmp116** |
| | 104 | 79 | 509.12 | *bnlg1662* |
| | | 143 | 509.13 | *umc1126* |
| | | 154 | 509.13 | *bnlg1721* |
| | | 192 | 509.13 | *bnlg1767* |
| | | 501 | 509.16 | *bnlg1169* |
| | | 687 | 509.18 | *umc1526* |
| | | 837 | 509.2 | *umc2005* |
| | | 869 | 509.2 | *bnlg1233** |
| | | 895 | 515.85 | *hda109* |
| | | 927 | 515.8 | *AI668346** |
| | | 1053 | 520.5 | *phi435417** |
| | | 1167 | 522.4 | *umc1947** |
| | | 1252 | 136.1 | *umc1604** |
| | | 1437 | 529.2 | *bnlg1316** |
| | | 1739 | 529.23 | *chc101b* |
| | | 1739 | 538.8 | *AY109645** |
| | | 1893 | 538.82 | *PCO102097* |
| | | 1898 | 538.82 | *umc1992* |
| | | 1898 | 544.4 | *umc2085** |
| | | 1954 | 547.68 | *npi298a** |
| | | 1959 | 548.5 | *umc1633** |
| | | 2075 | 562.5 | *mmp34** |
| | 105 | 92 | 572.4 | *bnlg1606* |
| | | 92 | 573.3 | *cdo38c(ntp)** |
| | | 98 | 572.4 | *mmc0381** |
| | | 99 | 573.3 | *bnlg1141* |
| | | 153 | 573.6 | *bnlg1746** |
| | | 183 | 573.6 | *umc1798* |
| | | 496 | 577.6 | *bnlg1940** |
| | 106 | 161 | 579.81 | *umc2202* |
| | 107 | 9 | 584.3 | *umc1516** |
| | | 19 | 584.3 | *gpm16* |
| | 108 | 15 | 591.47 | *umc2374* |
| | | 225 | 591.49 | *umc1230* |
| 2.09 | | 383 | 591.5 | ***umc49a**** |
| | | 474 | 591.51 | *umc1551* |
| | | 598 | 591.52 | *bnlg1520* |
| | | 778 | 343.7 | *umc1252** |
| | | 778 | 600.7 | *umc1256** |
| | | 891 | 601.6 | *AY109592** |
| | | 1172 | 601.63 | *umc1525* |
| | | 2027 | 601.71 | *umc1736* |
| | 109 | 279 | 650.1 | *bnlg469b** |
| | | 317 | 654.8 | *bnlg1893** |
| | | 334 | 654.8 | *csu109a* |
| | | 637 | 692.4 | *umc2184** |
| | | 670 | 692.4 | *umc2077* |
| | | 672 | 681.8 | *AY110389** |
| | | 707 | 694.6 | *mmp183** |
| | 110 | 46 | 713.1 | *AY109586** |
| | | 120 | 712.1 | *phi101049** |
| | | 186 | 713.11 | *umc2214* |
| | | 331 | 725.3 | *AY111236** |
| | | 398 | 725.31 | *AY106674* |

Chromosome 3

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| 3.00 | 111 | 265 | 0 | *umc2118** |
| | | 296 | 5.59 | *g2** |
| 3.01 | | 334 | 5.6 | *umc1931** |
| | | 334 | 9.5 | *umc2255** |
| | | 338 | 7.5 | *phi453121** |
| | | 340 | 7.1 | *umc1746** |
| | | 352 | 9.5 | *umc32a* |
| | | 420 | 9.5 | *AY106313* |
| | | 427 | 9.5 | *umc1793* |
| | | 427 | 11.2 | *umc1780** |
| | | 427 | 11 | *phi404206** |
| | | 491 | 21.8 | *umc1394** |
| | | 520 | 23.4 | *umc2256** |
| | | 539 | 28.2 | *umc1970** |
| | | 543 | 29.2 | *umc2071** |
| | | 630 | 30.5 | *umc2257** |
| | | 673 | 30.5 | *AY112199* |
| | | 679 | 35.5 | *umc1892** |
| | | 687 | 38 | *phi104127** |
| | | 699 | 38.7 | *umc2049** |
| | | 704 | 38.7 | *umc2377* |
| | | 709 | 37.35 | *umc2376* |
| | | 712 | 38.7 | *cdo345b* |
| 3.02 | | 766 | 60 | ***csu32a**** |
| | | 916 | 67.2 | *umc1458** |
| | | 1029 | 77 | *bnlg1144** |
| | | 1054 | 78.5 | *umc1886** |
| | | 1063 | 78.5 | *bnlg1325* |
| | | 1069 | 78.5 | *csu230* |
| | | 1102 | 78.51 | *bnlg1523* |
| | | 1127 | 78.51 | *umc1814* |
| | | 1351 | 78.53 | *me3* |
| | | 1400 | 95.4 | *AY109549** |
| | | 1443 | 98.42 | *cko1** |
| | 112 | 26 | 103.3 | *bnlg1647** |
| 3.03 | | 87 | 109 | ***asg24a(gts)**** |
| | | 353 | 127.8 | *umc2369* |
| | | 353 | 127.8 | *umc2258** |
| | | 359 | 131.7 | *umc2259** |
| | | 436 | 129.4 | *bnlg1447** |
| | | 447 | 132.59 | *bnlg1904* |
| | 113 | | 131 | unpublished |
| 3.04 | 114 | 20 | 152.7 | ***asg48**** |
| | | 137 | 153.75 | *csu242* |
| | | 297 | 157.3 | *uaz159b** |
| | | 375 | 159 | *umc59e** |
| | | 375 | 159 | *umc1030** |
| | | 448 | 163.5 | *umc1772** |
| | | 452 | 163.5 | *umc1729* |
| | | 685 | 165 | *umc1425** |
| | | 819 | 166.9 | *umc2000** |
| | | 972 | 168.01 | *tpi4* |
| | | 980 | 168.02 | *bnlg2136* |
| | 114 | 1005 | 168.02 | *umc1965* |
| | 115 | 180 | 177.4 | *umc1495** |
| | | 181 | 176.6 | *umc2158** |
| | | 194 | 177.4 | *umc1351* |
| | | 543 | 181.7 | *umc2033** |
| | | 605 | 181.1 | *umc1392** |
| | 116 | 45 | 189 | *umc1742** |
| | | 258 | 189.03 | *rz543a* |

Chromosome 3

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | | 481 | 190.2 | *umc2117** |
| | | 548 | 191.1 | *umc1655** |
| | | 548 | 190.6 | *bnlg1019a** |
| | | 559 | 190.8 | *bnlg1452** |
| | 117 | 24 | 191.97 | *ocl1* |
| | | 152 | 191.98 | *umc1087* |
| | | 152 | 190.8 | *bnlg1113** |
| | | 179 | 190.8 | *umc1717** |
| | | 792 | 192.04 | *bnlg2047* |
| | | 956 | 192.05 | *umc2260* |
| | | 1017 | 192.06 | *AY107193* |
| | | 1287 | 208.6 | *mmc0132** |
| | | 1476 | | *umc1810* |
| | | 1687 | 210.4 | *umc2261** |
| | | 2111 | 212.7 | *mmc0312** |
| | | 2111 | 213.6 | *umc1908** |
| | | 2390 | 213.63 | *PCO107756* |
| | | 2476 | 214.7 | *umc2262** |
| | | 3684 | 214.82 | *npi220b* |
| | | 3737 | 214.83 | *umc1347* |
| | 118 | 489 | 227.8 | *umc2263** |
| | | 681 | 337.23 | *te1* |
| | | 1812 | 318.2 | *umc2020** |
| | 119 | 297 | 228.2 | *PCO068796* |
| | | 362 | 228.2 | *umc1504** |
| | | 869 | 228.5 | *mmp29** |
| | 120 | 244 | 238.1 | *AY110403** |
| | | 636 | 244.7 | *AY110297** |
| | | 661 | 266 | *umc1683** |
| | | 694 | 266 | *PCO141323* |
| | | 2956 | 266.03 | *bnlg1957* |
| | 121 | 975 | 254.6 | *AY110151** |
| | | 1391 | 254.64 | *AY111333* |
| | | 2034 | 261.1 | *umc2264** |
| | | 2300 | 261.11 | *bnlg602* |
| | | 2766 | 261.12 | *umc1750* |
| | | 2776 | 262.9 | *mmp9** |
| | | 2782 | 269.4 | *umc1449** |
| | 122 | 70 | 283.89 | *cdo1160b(kri)* |
| | 123 | 231 | 279.3 | *umc1527** |
| | | 432 | 279.32 | *umc1616* |
| | | 525 | 279.33 | *bnlg1628* |
| | | 543 | 280.4 | *umc1773** |
| | | 1344 | 290.6 | *umc2002** |
| | | 1489 | 290.62 | *gpm14* |
| 3.05 | 124 | 268 | 297.9 | ***umc102a**** |
| | | 337 | 299.2 | *umc1174** |
| | | 337 | 301 | *umc1600** |
| | | 704 | 301.03 | *AI714716* |
| | | 876 | 301.04 | *umc1300* |
| | | 1514 | 306.06 | *phys2** |
| | | 1870 | 306.09 | *abp1* |
| | | 1934 | 306.1 | *bnlg1601** |
| | 125 | 89 | 312.77 | *chr109b* |
| | | 310 | 312.8 | *umc1102** |
| | | 310 | 313.4 | *bnlg1035** |
| | | 408 | 315.4 | *AY110352** |
| | | 595 | 315.42 | *csu439(trm)* |
| | 126 | 43 | 318.14 | *atp1* |
| | | 398 | 319.2 | *umc1167** |
| | | 680 | 318.2 | *umc2020** |

Chromosome 3

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | | 696 | 318.2 | mmc0022* |
| | | 696 | 318.2 | umc2020* |
| | | 1099 | 319.26 | umc2155 |
| | | 1116 | 319.26 | umc2127 |
| | 127 | 54 | 326.2 | AY112215* |
| | | 514 | 326.25 | csu706 |
| | 128 | 305 | 331.3 | AY111507* |
| | | 476 | 334.6 | AY111541* |
| | | 1033 | 334.66 | bnlg1117 |
| | 129 | 491 | 343.78 | ldp1 |
| | 130 | 73 | 345.77 | umc1954 |
| | 131 | 142 | 346.8 | myb2* |
| | | 388 | 346.83 | cdo109 |
| | | 411 | 346.83 | umc1839 |
| | | 440 | 346.83 | si618046E03 |
| | | 745 | 354 | umc2265* |
| | | 821 | 361.1 | csu636* |
| | | 882 | 358.3 | sps2* |
| | 132 | 876 | 371.4 | umc1973* |
| | | 947 | 384.9 | AY111296* |
| | | 1142 | 384.92 | umc1400 |
| | | 1168 | 384.92 | umc2166 |
| | | 1192 | 388.1 | AI770873* |
| 3.06 | | 1317 | 391.4 | **bnl5.37a*** |
| | | 1339 | 390.3 | umc1539* |
| | | 1499 | 391.41 | umc1593b |
| | | 1702 | 394.8 | umc1311* |
| | | 1723 | 394.8 | bnlg1449 |
| | | 1963 | 398.4 | umc1730* |
| | | 2096 | 401.2 | umc1027* |
| | 133 | 141 | 402.94 | npi268b |
| | 134 | 85 | 411.6 | bnlg1063a |
| | | 128 | 411.6 | umc1266* |
| | | 240 | 411.61 | npi432 |
| | | 277 | 411.62 | bnlg1798 |
| | 135 | 171 | 434.3 | umc2266* |
| | | 370 | 434.33 | bnlg1047a |
| | 136 | | 445 | unpublished |
| | 137 | 197 | 452.7 | umc60* |
| | | 213 | 452.7 | umc2408 |
| | | 236 | 452.7 | umc1951 |
| | 138 | 84 | 461.1 | umc2268* |
| | | 613 | 461.15 | csu351 |
| | | 630 | 461.15 | umc2076 |
| | | 700 | 482.3 | umc2269* |
| | | 716 | 481.6 | bnlg1951* |
| | | 1002 | 482.33 | umc1985 |
| | | 1037 | 482.33 | bnlg1931 |
| | | 1049 | 488 | csu191* |
| | | 1245 | 491.4 | bnlg1160* |
| | | 1306 | 491.41 | csu264 |
| | | 1306 | 491.41 | umc2381 |
| | | 1338 | 491.41 | csu180 |
| | | 1338 | 491.41 | umc2169 |
| | | 1437 | 494 | umc2270* |
| | | 1438 | 494 | umc2271* |
| | | 1682 | 494.02 | CL13054_1 |
| | | 1732 | 503 | lim424* |
| | | 1880 | 507.2 | AY111125* |
| | 139 | 177 | 511.5 | dupssr17 |
| | | 177 | 511.5 | bnlg197* |

Chromosome 3

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | | 542 | 512.7 | AI770795* |
| | | 614 | 512.71 | si618016E09 |
| 3.07 | 140 | 348 | 540.2 | umc1135* |
| | | 348 | 538.2 | umc2050* |
| | 141 | 25 | 544.18 | umc1690 |
| | | 101 | 544.19 | si605077F08 |
| | | 228 | 544.2 | umc2272* |
| | | 383 | 544.4 | umc1528* |
| | | 452 | 544.6 | umc1399* |
| | | 459 | 552.67 | csu567(ces) |
| | | 501 | 544.6 | bnlg1605* |
| | | 775 | 544.63 | umc1659 |
| | 142 | 297 | 562.1 | AY104511* |
| | | 371 | 567.6 | umc1489* |
| | | 380 | 568 | umc2273* |
| | | 417 | 568.3 | umc1404* |
| | | 457 | 578.05 | cdo1160c(kri) |
| | 143 | 84 | 570.14 | umc1286 |
| | | 291 | 575.18 | nfc101 |
| | 144 | 43 | 579.49 | AY106518 |
| | | 129 | 579.5 | umc1825* |
| 3.08 | 145 | 28 | 597.53 | AW258116 |
| | | 741 | 597.6 | AY105849* |
| | | 766 | 597.6 | gpm3 |
| | | 813 | 597.61 | bnlg1779 |
| | | 900 | 609.2 | umc1140* |
| | | 913 | 610.2 | umc2275* |
| | 146 | 124 | 617.5 | umc1915* |
| | | 137 | 618.6 | bnlg1108* |
| | | 591 | 618.65 | sdg115 |
| | | 682 | 633.8 | umc1320* |
| | | 688 | 638.3 | AY109934* |
| | | 689 | 652.4 | umc2276* |
| | | 718 | 634.8 | umc1273* |
| | | 763 | 652.41 | si946021A07 |
| | 147 | 195 | 653.81 | csu397(cah) |
| 3.09 | 148 | 77 | 699.2 | csu303* |
| | | 112 | 699.2 | sh2 |
| | | 189 | 702.2 | csu845* |
| | 149 | 50 | 702.19 | AY111254 |
| | | 196 | 702.2 | bnlg1257 |
| | | 264 | 702.21 | bnlg1182 |
| | | 506 | 738.7 | umc2152* |
| | | 570 | 747 | umc2008* |
| | | 672 | 748.5 | umc1813* |
| | | 710 | 747.5 | umc2277* |
| | | 711 | 747.5 | cdo665a |
| | 150 | 487 | 759.89 | mmc0001 |
| | | 496 | 759.89 | csu58a |
| | | 567 | 759.9 | npi425a* |
| | | 589 | 760.9 | bnlg1496* |
| | | 769 | 769 | AY110567* |
| | 151 | 135 | 806.9 | umc1361 |
| | | 139 | 806.9 | umc1052 |
| | | 184 | 806.9 | umc1641* |
| | | 617 | 806.94 | nph1 |
| | | 721 | 806.95 | umc255b |
| | | 833 | 806.97 | umc2048 |
| | | 895 | 826.71 | umc1136 |
| | | 895 | 806.97 | umc1639 |
| | 152 | 62 | 826.9 | bnlg1098 |

Chromosome 3

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | | 290 | 826.93 | *csu728a* |
| | | 307 | 826.93 | *plt2** |
| | 153 | 14 | 828.9 | *umc1594** |
| | | 60 | 828.9 | *cyp1* |

Chromosome 4

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| 4.01 | 155 | 93 | 15.8 | _bnlg1370_ |
| | | 147 | 15.8 | _msf1*_ |
| | | 211 | 23.4 | _umc1228*_ |
| | | 216 | 23.4 | _umc2148_ |
| | | 220 | 22.9 | _umc2279*_ |
| | | 240 | 24.6 | _umc123*_ |
| | | 312 | 24.61 | _cyp3_ |
| | | 315 | 37.5 | _bx4*_ |
| | | 329 | 37.5 | _umc1276_ |
| | | 385 | 46.6 | _cyp5*_ |
| | 156 | 138 | 81 | _bnlg1318_ |
| | | 161 | 81 | _umc1759*_ |
| | | 165 | 81 | _umc1758_ |
| | | 165 | 81 | _umc1757*_ |
| 4.02 | | 165 | 81 | __*phi295450**__ |
| | | 188 | 71.87 | _umc2409_ |
| | | 213 | 81 | _umc2150_ |
| | | 248 | 101.1 | _umc1943*_ |
| | | 251 | 101.1 | _umc1509_ |
| | | 445 | 101.12 | _PCO146629_ |
| | 157 | 616 | 116.15 | _umc1288_ |
| | | 616 | 116.15 | _umc1294_ |
| 4.03 | 158 | 19 | 135.1 | __*umc31a**__ |
| | | 19 | 135.7 | _AY110398*_ |
| | | 123 | 141.6 | _umc2082*_ |
| | | 330 | 143.4 | _csu235*_ |
| | | 411 | 147.21 | _adh2*_ |
| | 159 | 157 | 152.9 | _AY110253*_ |
| | | 240 | 152.91 | _pdi1_ |
| | 160 | 246 | 158.8 | _umc2280*_ |
| | | 246 | 158.6 | _umc2281*_ |
| | | 341 | 181.4 | _umc1902*_ |
| | | 458 | 196.4 | _umc2039*_ |
| | | 489 | 196.4 | _umc2211_ |
| | | 539 | 200.3 | _pgd3*_ |
| | | 539 | 214.53 | _umc1821_ |
| | | 944 | 205 | _wip2*_ |
| 4.04 | | 1132 | 210.83 | __*npi386a(eks)**__ |
| | | 1186 | 210.83 | _umc49d_ |
| | 161 | | 213 | unpublished |
| | 162 | 182 | 218.48 | _uaz246a(mbf)_ |
| | | 343 | 218.5 | _umc1117*_ |
| | | 513 | 223.6 | _lim415*_ |
| | | 560 | 228.4 | _umc1652*_ |
| | | 740 | 228.42 | _psb3_ |
| | 163 | 328 | 232.13 | _ocl5a_ |
| | | 511 | 232.15 | _zp1*_ |
| | | 511 | 736.7 | _cat3*_ |
| | | 804 | 237.8 | _bnlg490*_ |
| 4.05 | 164 | 143 | 250.75 | _bm3_ |
| | | 240 | 250.76 | _umc2206_ |
| | | 609 | 250.8 | _umc2061*_ |
| | | 757 | 250.82 | _umc1662_ |
| | | 766 | 250.82 | _AY107128_ |
| | | 968 | 254.9 | _umc2282*_ |
| | | 1109 | 252.15 | _gpc1*_ |
| | | 1141 | 253.9 | _csu474(rpS14)_ |
| | | 1428 | 253.93 | _bnlg1937_ |
| | | 1859 | 253.97 | _umc1382_ |
| | | 2236 | 254.01 | _bnlg1217_ |
| | | 2266 | 271.4 | _umc1964*_ |
| | | 2272 | 270.3 | _umc1303*_ |
| | | 2449 | 268.4 | _bnlg1265*_ |
| | | 2521 | 698.9 | _umc1180*_ |
| | | 2774 | 271.41 | _bnlg252_ |
| | | 2881 | 271.41 | _umc1390_ |
| | | 3322 | 274.7 | _AY110290*_ |
| | 165 | 271 | 279.79 | _chr112a_ |
| | | 1051 | 279.87 | _csu661_ |
| | | 1283 | 279.9 | _csu509*_ |
| | 166 | 745 | 287.3 | _umc1175*_ |
| | | 746 | 287.3 | _akh1_ |
| | 167 | 278 | 289.26 | _bnlg1729_ |
| | 168 | 61 | 295.2 | _umc1511*_ |
| | 169 | 117 | 298.1 | _umc1791*_ |
| | | 481 | 298.11 | _umc1851_ |
| | 170 | | 298.5 | unpublished |
| | 171 | 966 | 299.9 | _bnlg1755*_ |
| | | 1182 | 298.9 | _mmp140*_ |
| | 172 | 498 | 294.3 | _umc1953*_ |
| | | 503 | 294.4 | _umc2283*_ |
| | | 1051 | 294.45 | _umc1451_ |
| | | 1090 | 294.45 | _umc1548_ |
| | | 1209 | 294.46 | _umc1317_ |
| | | 1371 | 294.47 | _umc1896_ |
| | | 1676 | 294.5 | _umc1895_ |
| | | 1704 | 294.5 | _pep7_ |
| | 173 | | 300 | unpublished |
| | 174 | 149 | 300.72 | _umc1362_ |
| | | 161 | 300.72 | _umc2054_ |
| | 175 | | 301 | unpublished |
| | 176 | 69 | 302.49 | _csu34b(rpS8)_ |
| | | 230 | 302.5 | _umc1142*_ |
| | 177 | 137 | 303.4 | _csu39_ |
| | 178 | 299 | 304.31 | *CL65845_1* |
| | 179 | 112 | 305.2 | _umc1702*_ |
| | | 456 | 326.5 | _AY110355*_ |
| | | 611 | 320.4 | _AY110562*_ |
| 4.06 | | 1110 | 331.3 | _mmc0371*_ |
| | | 1228 | 333.2 | _umc1945*_ |
| | | 1248 | 332.4 | _umc2284*_ |
| | 180 | | 335 | unpublished |
| | 181 | 441 | 362.34 | _umc2391_ |
| | | 934 | 362.39 | _bnlg1621a_ |
| | | 1060 | 362.4 | _AY110310*_ |
| | | 1454 | 362.44 | _umc1299_ |
| | 182 | 173 | 373.3 | _rz567b(klc)*_ |
| | | 293 | 373.31 | _umc2070_ |
| | | 372 | 373.32 | _umc1869_ |
| | | 1234 | 373.4 | _umc1329_ |
| | | 2046 | 392.2 | _bnlg2291*_ |
| | | 2082 | 392.4 | _bnlg1137*_ |
| | | 2331 | 392.42 | _bnlg1784_ |
| 4.07 | | 2756 | 411.3 | _umc2038*_ |
| | | 2843 | 411.31 | _umc1651_ |
| | | 2859 | 414.2 | _umc19*_ |
| | | 3174 | 414.23 | _umc1994_ |
| | | 3220 | 414.24 | _umc1620_ |
| | | 3222 | 414.24 | _umc1847_ |
| | | 3545 | 428 | _bnlg1189*_ |
| | | 3791 | 428.02 | _PCO119336_ |
| | | 3854 | 428.03 | _csu672b_ |

Chromosome 4

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| 4.08 | | 4044 | 443.2 | *umc1775** |
| | | 4071 | 443.2 | *uaz171* |
| | | 4185 | 443.21 | *mmc0341* |
| | | 4186 | 443.21 | *umc2009* |
| | | 4359 | 452.1 | *AY109534** |
| | | 4381 | 455.9 | *mmp3** |
| | | 4466 | 455.91 | *umc1043* |
| | | 4466 | 455.91 | *umc1871* |
| | 183 | 321 | 462.1 | *umc1476** |
| | 184 | 16 | 463.3 | *gol1** |
| | | 202 | 463.32 | *pdh1* |
| | | 434 | 463.34 | *bnl8.45b* |
| | | 445 | 463.34 | *umc2404* |
| | | 580 | 467.1 | *bnlg2244** |
| | | 583 | 467.1 | *umc2384* |
| | | 632 | 467.1 | *bnlg1927* |
| | | 655 | 467.11 | *umc1418* |
| | | 696 | 470.6 | *umc1899** |
| | | 741 | 470.6 | *PCO129009* |
| | | 766 | 475.7 | *bnlg2162** |
| | | 844 | 475.71 | *umc2365* |
| | | 905 | 475.71 | *umc2041* |
| | | 946 | 475.72 | *zrp4* |
| | 185 | 19 | 514.89 | *umc1612* |
| | | 138 | 514.9 | *umc2285** |
| | 186 | 33 | 515.91 | *umc1086* |
| | 187 | 344 | 522.06 | *ssu1** |
| | 188 | 12 | 532.23 | *mmc0321* |
| | | 134 | 532.24 | *cdo365(pet)* |
| | | 136 | 532.24 | *csu166a* |
| | | 307 | 532.26 | *umc1051* |
| | | 400 | 531.7 | *umc2187** |
| | | 636 | 532.29 | *CL12681_1* |
| | | 1039 | 536.9 | *AY110989** |
| | | 1043 | 536.9 | *PCO136722* |
| | | 1074 | 535.4 | *AY109980** |
| | | 1115 | 535.4 | *umc1371* |
| | | 1379 | 536.3 | *AY105971** |
| | | 1428 | 535.5 | *umc1856* |
| | | 1494 | 535.5 | *umc1132** |
| | | 1634 | 535.5 | *umc2153* |
| | 189 | 118 | 562.75 | *umc1313* |
| | 190 | | 536.7 | unpublished |
| | 191 | 177 | 553.7 | *umc2286** |
| | | 188 | 554.1 | *umc2188** |
| 4.09 | 192 | 142 | 561.46 | *umc1559* |
| | 193 | 396 | 561.5 | *AY110170** |
| | | 495 | 559 | *umc52** |
| | | 744 | 561.52 | *umc1039* |
| | 194 | 49 | 565.38 | *umc1834* |
| | | 123 | 565.39 | *csu704* |
| | | 307 | 565.4 | *lim446** |
| | | 437 | 565.41 | *umc2200* |
| | 195 | 241 | 574.8 | *umc2139** |
| | 196 | 292 | 574.81 | *ensl002b* |
| | | 497 | 574.83 | *PCO104784* |
| | | 646 | 574.84 | *umc1939* |
| | | 646 | 581.8 | *umc1940** |
| | | 652 | 581.8 | *AY111962* |
| | 197 | | 612 | unpublished |
| | 198 | 21 | 616.7 | *AY110064** |

Chromosome 4

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | | 31 | 619.4 | *umc2287** |
| | | 32 | 618.1 | *umc1328** |
| | 199 | 345 | 601.34 | *bnlg1023a* |
| | | 845 | 601.39 | *AY107200* |
| | | 940 | 601.4 | *rz599b** |
| | | 1141 | 601.42 | *umc1631* |
| | | 1150 | 601.42 | *rpd3* |
| | | 1175 | 601.42 | *umc1820* |
| | 200 | 19 | 635.16 | *umc1740* |
| | | 224 | 635.18 | *umc2360* |
| | | 376 | 635.19 | *umc2138* |
| | | 386 | 635.2 | *umc2137* |
| | | 388 | 635.2 | *umc2382* |
| | | 430 | 635.2 | *AY110231** |
| | | 587 | 635.21 | *sbp2** |
| | 201 | 83 | 657 | *umc2046** |
| | | 140 | 657.01 | *PCO088312* |
| | | 153 | 655 | *umc1101** |
| | | 207 | 657.01 | *AY107910* |
| 4.10 | | 283 | 669.8 | ***php20608a**** |
| | | 288 | 670.2 | *bnlg589** |
| | | 301 | 670.2 | *csu758* |
| | | 314 | 670.2 | *umc1503* |
| | | 493 | 670.22 | *umc1720* |
| | | 596 | 670.23 | *umc1699* |
| | | 610 | 687.8 | *umc1109** |
| | | 641 | 687.8 | *umc2044* |
| | | 641 | 692.1 | *umc2288** |
| | 202 | 84 | 707.79 | *PCO109372* |
| | | 139 | 707.8 | *umc2289** |
| | | 139 | 715.5 | *AY109611** |
| | | 164 | 708.5 | *AY109859** |
| | | 165 | 716.21 | *bnlg1337* |
| | | 182 | 716.21 | *AY111822* |
| | | 198 | 716.21 | *umc1719* |
| | | 198 | 728.5 | *umc169** |
| | | 208 | 730.34 | *wee1* |
| | | 296 | 730.34 | *umc1716* |
| | | 323 | 736.7 | *bip2** |
| | | 327 | 736.7 | *cat3** |
| | | 372 | 740.7 | *mmp182** |
| | | 372 | 739.3 | *umc1649** |
| | 203 | 55 | 748.3 | *umc1707** |

Chromosome 5

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| 5.01 | 205 | 49 | 115.56 | *bnlg1836a* |
| | | 82 | 115.56 | *bnlg143* |
| | 206 | 13 | 124.69 | *umc1766* |
| | | 99 | 124.69 | *umc1365* |
| | | 183 | 124.7 | *umc1781* |
| | | 227 | 124.7 | *umc2036** |
| 5.02 | 207 | 13 | 147.5 | ***umc90*** |
| | | 71 | 147.6 | *umc66c(lcr)* |
| | | 100 | 150.9 | *bnlg565** |
| | 208 | 80 | 147.5 | *tua4** |
| | | 218 | 156.9 | *umc1587** |
| | | 363 | 160.2 | *umc107b(croc)** |
| | | 364 | 160.2 | *umc1894* |
| | | 453 | 160.21 | *cdo542* |
| | 209 | 128 | 189.77 | *ole3* |
| | | 142 | 189.77 | *umc2115* |
| | | 261 | 189.78 | *bnlg1660* |
| | | 375 | 189.79 | *AY110835* |
| | | 396 | 189.79 | *bnlg105* |
| | | 435 | 189.8 | *umc1761* |
| | | 466 | 189.8 | *bnlg1879** |
| | 210 | 54 | 196.89 | *umc2167* |
| | | 132 | 196.9 | *umc2293** |
| | | 160 | 196.9 | *tbp2* |
| | | 231 | 196.91 | *rps15* |
| 5.03 | | 347 | 203.3 | *csu164b** |
| | | 375 | 203.3 | *umc2060* |
| | 211 | 39 | 216.29 | *umc2388* |
| | | 93 | 216.01 | *umc2113a* |
| | | 134 | 216.3 | *bnlg1046** |
| | | 294 | 216.32 | *umc1852* |
| | | 300 | 217.85 | *umc27a* |
| | | 352 | 217.8 | *umc1597** |
| | 212 | 63 | 230.35 | *umc1468* |
| | | 492 | 230.39 | *bnlg557* |
| | | 500 | 230.39 | *PCO135705* |
| | | 571 | 230.4 | *umc2159* |
| | | 583 | 230.4 | *mmc0351** |
| | 213 | | 231.5 | unpublished |
| | 214 | | 232 | unpublished |
| | 215 | 23 | 235.6 | *AY111142** |
| | | 201 | 235.62 | *umc83b* |
| | | 397 | 235.64 | *cpn1* |
| | 216 | 86 | 242.6 | *umc1048** |
| | | 16 | 242.59 | *px13* |
| | | 285 | 242.62 | *bnlg1700* |
| | | 342 | 247.6 | *umc1447** |
| | | 348 | 245.5 | *umc2294** |
| | | 579 | 247.62 | *umc1163* |
| | | 749 | 254 | *lim175** |
| | | 1231 | 257.8 | *umc2295** |
| | 218 | 874 | 260.2 | *umc1315** |
| | | 1257 | 260.24 | *umc1151* |
| | 219 | 696 | 267.5 | *umc2296** |
| | | 1008 | 267.7 | *umc1935** |
| | | 1300 | 267.73 | *umc1475* |
| | | 1550 | 271.5 | *umc1692** |
| | | 1612 | 271.5 | *umc1850* |
| | 220 | 634 | 275.9 | *gpm5* |
| | | 642 | 279.1 | *umc2297** |
| | | 646 | 279.1 | *umc1212* |
| | | 696 | 275.9 | *umc1609** |
| | | 768 | 279.11 | *umc2073* |
| | | 781 | 279.11 | *umc1784* |
| | | 840 | 279.12 | *AY107414* |
| | | 899 | 281.2 | *umc1355** |
| | | 964 | 281.21 | *umc1274* |
| | 221 | 173 | 285.49 | *cat1* |
| | | 262 | 285.5 | *umc1870** |
| | 222 | 160 | 286 | *umc1226* |
| | 223 | 79 | 286.5 | *umc1389** |
| | | 79 | 286.6 | *umc1429** |
| | | 88 | 286.6 | *umc1731* |
| | | 89 | 286.6 | *umc1373* |
| | | 257 | 286.62 | *a2* |
| | | 394 | 286.64 | *umc2140* |
| | | 981 | 286.71 | *gtc102* |
| | 224 | 329 | 294.94 | *cdo456c* |
| | | 762 | 294.99 | *umc2400* |
| | | 838 | 295 | *mmp58** |
| | 225 | 539 | 297.5 | *bnlg1902** |
| 5.04 | | 606 | 301.6 | ***bnl4.36**** |
| | | 893 | 301.63 | *umc2373* |
| | | 895 | 301.63 | *umc1815* |
| | | 1410 | 307 | *umc2298** |
| | | 1414 | 307 | *umc1110* |
| | | 1418 | 307 | *csu670* |
| | | 1487 | 307.01 | *bnlg653* |
| | | 1532 | 307.01 | *csu774(lhcb)* |
| | | 1980 | 310 | *umc2299** |
| | 226 | 160 | 309.82 | *uaz275* |
| | 227 | 180 | 309.82 | *umc1629* |
| | | 221 | 314.1 | *umc1591** |
| | | 646 | 314.14 | *umc1224* |
| | | 912 | 315.2 | *umc2300** |
| | 228 | | 314.4 | unpublished |
| | 229 | 171 | 315.72 | *umc1563* |
| | 230 | | 315 | unpublished |
| | 231 | 92 | 316.26 | *bnlg1287* |
| | 232 | 66 | 316.53 | *umc1860* |
| | | 476 | 316.54 | *umc1283* |
| | | 934 | 313.3 | *bnlg1892c** |
| | 233 | 54 | 316.8 | *umc2302** |
| | | 63 | 316.8 | *umc2406* |
| | | 162 | 316.81 | *umc1162* |
| | 234 | 1247 | 317.6 | *umc1060** |
| | 235 | 102 | 320.1 | *BE639933** |
| | | 678 | 318.79 | *nfd108* |
| | | 1171 | 318.85 | *dupssr10* |
| | 236 | 154 | 336.39 | *npi285d(cac)* |
| | | 733 | 336.47 | *AY105205* |
| | | 1003 | 336.5 | *AY110906** |
| | 237 | 281 | 338 | *AY105029** |
| | | 380 | 338.01 | *umc1092* |
| | 238 | 30 | 346.45 | *umc1192* |
| | | 183 | 346.46 | *PCO103687* |
| | | 600 | 346.5 | *umc1348* |
| | | 600 | 346.5 | *umc1349** |
| | | 1014 | 351.2 | *AY109532** |
| | | 1053 | 371.2 | *csu308** |
| | | 1053 | 368.4 | *umc1221** |
| | | 1146 | 377 | *csu600** |

Chromosome 5

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | | 1151 | 377.9 | *umc1966** |
| | | 1193 | 377.9 | *incw1** |
| | | 1334 | 377.91 | *umc2111* |
| 5.05 | | 1758 | 389.9 | *mmc0081** |
| | 239 | 46 | 394.4 | *phi333597** |
| | 240 | 174 | 392.7 | *AY109682** |
| | | 190 | 397 | *umc2026** |
| | | 349 | 397.02 | *mmc0282* |
| | | 357 | 397.02 | *umc1800* |
| | | 376 | 402.2 | *mmp47** |
| | | 403 | 404.9 | *umc1264** |
| | | 494 | 427.92 | *serk2** |
| | | 644 | 427.93 | *umc2386* |
| | | 778 | 427.94 | *PCO060271* |
| | 241 | 18 | 408.8 | *PCO078116* |
| | | 18 | 408.8 | *umc2303** |
| | 242 | 84 | 410.8 | *umc1155** |
| | | 138 | 410.8 | *umc1687* |
| | | 189 | 410.81 | *AY111089* |
| | | 209 | 410.81 | *CL11475_1* |
| | | 217 | 410.81 | *umc1502* |
| | | 323 | 413.8 | *nbp35** |
| | | 324 | 413.8 | *umc2086* |
| | | 324 | 413.6 | *csu173** |
| | | 520 | 413.82 | *PCO099796* |
| | 243 | 25 | 415.78 | *AY107329* |
| | | 27 | 415.78 | *CL16923_1* |
| | 244 | 368 | 435.96 | *bnlg1847* |
| | | 407 | 435.96 | *umc1853* |
| | 245 | 27 | 467.14 | *umc1722* |
| | | 260 | 467.17 | *cdo400a* |
| | | 601 | 467.2 | *AY110063** |
| 5.06 | 246 | 330 | 479.47 | ***umc126a**** |
| | | 331 | 469.39 | *umc156b* |
| | 247 | 31 | 470.1 | *AY109938** |
| | | 258 | 470.12 | *umc2072* |
| | | 346 | 476.6 | *mmc0481** |
| | | 462 | 481.2 | *umc54** |
| | | 566 | 479.7 | *umc2305** |
| | 248 | 25 | 488.4 | *csu604b(trh)* |
| | | 31 | 488.4 | *umc1752** |
| | 249 | 309 | 493.5 | *umc1524** |
| | 250 | 52 | 493.5 | *umc1680** |
| | | 87 | 492.7 | *umc1941** |
| | | 121 | 493.7 | *umc51a** |
| | | 463 | 493.73 | *csu615a* |
| | | 536 | 500.7 | *bnlg609** |
| | | 540 | 500.1 | *umc2306** |
| | | 922 | 511.3 | *rz567a(klc)** |
| | | 967 | 511.3 | *PCO111982* |
| | | 1208 | 511.33 | *umc2216* |
| | | 1240 | 516.3 | *mmp169** |
| | | 1533 | 516.33 | *umc49m* |
| | 251 | 68 | 528.83 | *umc2201* |
| | | 79 | 528.83 | *gln4** |
| | | 252 | 528.84 | *umc2198* |
| | | 407 | 528.86 | *bnlg1346* |
| | | 439 | 538.49 | *umc1537* |
| | | 575 | 528.88 | *umc1646* |
| | | 591 | 528.88 | *umc1375* |
| | | 681 | 528.89 | *umc2013* |

Chromosome 5

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | | 687 | 528.89 | *bnlg2305* |
| 5.07 | 252 | 27 | 536.6 | ***umc108**** |
| | 253 | 331 | 590.39 | *csu672a* |
| | | 369 | 590.4 | *lhcb4* |
| | | 408 | 590.4 | *bnlg1118** |
| | | 549 | 600 | *umc1072** |
| | | 574 | 600.4 | *AY110369** |
| | | 595 | 600.4 | *bnl7.49d* |
| 5.08 | | 721 | 609.4 | *bnlg118** |
| | | 884 | 625.8 | *umc1792** |
| | 254 | 15 | 643.6 | *AY110182** |
| | | 158 | 643.61 | *umc2143* |
| | | 217 | 656.7 | *AY105910** |
| | | 255 | 656.7 | *umc2136* |
| | | 359 | 664.3 | *AW065811** |
| 5.09 | | 441 | 669.4 | ***php10017**** |
| | | 497 | 669.41 | *bnlg1695* |
| | | 497 | 669.41 | *bnlg1711* |
| | | 574 | 669.41 | *umc2209* |
| | | 697 | 676.7 | *umc1153** |

Chromosome 6

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| 6.00 | 256 |  | 5 | unpublished |
|  | 256 | 75 | 27.8 | _bnlg1043_ |
|  |  | 88 | 27.8 | _umc2309*_ |
|  |  | 141 | 27.8 | _umc2208_ |
|  |  | 142 | 27.6 | _umc2310*_ |
|  |  |  | 17.5 | unpublished |
|  | 257 | 50 | 37.56 | _umc2068_ |
|  |  | 280 | 48.9 | _umc1143*_ |
|  |  | 311 | 37.57 | _csu782_ |
|  | 258 |  | 30 | unpublished |
|  | 259 | 29 | 60.87 | _umc1883_ |
|  | 260 | 159 | 63.58 | _bnlg2243_ |
| 6.01 |  | 368 | 66.4 | **_umc85a*_** |
|  |  | 458 | 63.6 | _AY110100*_ |
|  |  | 601 | 69.2 | _umc1606*_ |
|  | 261 | 524 | 71.8 | _mmp163*_ |
|  | 262 | 141 | 71.5 | _umc2311*_ |
|  |  | 396 | 72.68 | _umc1753_ |
|  |  | 577 | 72.7 | _bnlg1371*_ |
|  |  | 601 | 72.7 | _bnlg426_ |
|  |  | 602 | 72.7 | _bnlg1165_ |
|  |  | 904 | 75.8 | _umc2312*_ |
|  |  | 1218 | 75.84 | _bnlg1432_ |
|  |  | 1218 | 75.84 | _bnlg1600_ |
|  |  | 1283 | 78.3 | _bnlg1867*_ |
|  |  | 1299 | 78.3 | _gpm8_ |
|  |  | 1823 | 80.7 | _umc1229*_ |
|  | 263 | 241 | 81 | _umc1625_ |
|  | 264 | 581 | 82.46 | _umc2196_ |
|  | 265 | 466 | 96 | _uck1*_ |
|  |  | 666 | 98.4 | _umc1444*_ |
|  |  | 951 | 98.4 | _bnlg391_ |
|  |  | 1308 | 98.4 | _bnlg1433_ |
|  |  | 1484 | 98.4 | _AY107121_ |
|  | 266 | 124 | 98.4 | _bnlg1641*_ |
|  | 267 | 1731 | 98.43 | _umc1498_ |
|  |  | 1797 | 98.43 | _csu243_ |
|  |  | 1797 | 99 | _umc2056*_ |
|  | 268 | 15 | 100.3 | _uaz232b(sci)*_ |
|  |  | 112 | 100.31 | _csu680e_ |
|  |  | 270 | 99.3 | _umc2314*_ |
|  |  | 548 | 110.4 | _mmp10*_ |
|  | 269 | 60 | 98.6 | _umc1133*_ |
|  |  | 726 | 98.4 | _AY110213*_ |
|  |  | 1064 |  | _rDNA5.8S_ |
|  |  | 1209 | 112.38 | _bnlg1538_ |
|  |  | 1860 | 91.9 | _umc2313*_ |
|  |  | 2013 | 98 | _umc2074*_ |
|  |  | 2209 | 112.48 | _bnlg1188_ |
|  |  | 2326 | 314.6 | _bnlg1174*_ |
|  | 270 | 501 | 116.16 | _umc1195_ |
|  |  | 648 | 116.17 | _mez1_ |
|  |  | 933 | 116.2 | _mmp4*_ |
|  |  | 1226 | 120.5 | _y1*_ |
|  |  | 1326 | 121.13 | _cyc3_ |
|  |  | 1388 | 121.14 | _bnlg1139_ |
|  |  | 1388 | 121.14 | _csu146a(cdc48)_ |
|  |  | 1664 | 121.16 | _bnlg1422_ |
| 6.02 | 271 | 225 | 124.94 | **_umc59a_** |
|  |  | 225 | 124.94 | _umc1517_ |
|  |  | 382 | 124.95 | _saur1_ |

Chromosome 6

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
|  |  | 635 | 124.98 | _umc1376_ |
|  |  | 872 | 125 | _umc1006*_ |
|  |  | 910 | 127.8 | _umc1083*_ |
|  |  | 929 | 126.91 | _mir2_ |
|  |  | 930 | 127.8 | _csu395a_ |
|  |  | 982 | 133.4 | _umc1656*_ |
|  |  | 1422 | 133.44 | _bnlg2151_ |
|  |  | 1439 | 145.7 | _umc1257*_ |
|  |  | 1790 | 148.7 | _bnlg2191*_ |
|  | 272 | 18 | 153.54 | _umc1723_ |
|  |  | 311 | 153.56 | _sbp3*_ |
|  | 273 | 115 | 154.55 | _umc2010_ |
| 6.03 | 274 |  | 166 | unpublished |
|  | 275 | 329 | 166.6 | _umc2316*_ |
|  |  | 361 | 167.6 | _AY104775*_ |
|  |  | 409 | 166.8 | _umc1887*_ |
| 6.04 | 276 | 142 | 181.9 | **_umc65a*_** |
|  |  | 153 | 189.9 | _umc1918*_ |
|  |  | 492 | 199 | _umc1105*_ |
|  |  | 512 | 200.3 | _umc1979*_ |
|  |  | 599 | 200.31 | _si606044D05_ |
|  | 277 | 42 | 203.2 | _umc1857*_ |
|  | 278 | 34 | 204.1 | _AY108825_ |
|  |  | 57 | 204.1 | _AY109804_ |
|  | 279 |  | 205 | unpublished |
|  | 280 | 311 | 211.3 | _pl1*_ |
|  |  | 520 | 211.32 | _agrr37a_ |
|  | 281 | 299 | 228.89 | _rz144b_ |
|  |  | 383 | 228.9 | _umc2006*_ |
|  |  | 1261 | 235.8 | _umc2317*_ |
|  |  | 1330 | 235.81 | _umc1614_ |
|  |  | 1430 | 235.82 | _bnlg1617_ |
|  |  | 1659 | 235.84 | _AY107053_ |
|  |  | 1687 | 235.84 | _tm20_ |
|  |  | 1807 | 235.85 | _bnlg1922_ |
|  |  | 2084 | 235.88 | _PCO152525_ |
|  |  | 2089 | 235.88 | _umc1795_ |
| 6.05 |  | 2393 | 244.9 | _umc2319*_ |
|  |  | 2469 | 244.91 | _AY105479_ |
|  |  | 2474 | 244.7 | _umc2318*_ |
|  |  | 2487 | 244.91 | _AY107517_ |
|  |  | 3234 | 253 | _bnlg1154*_ |
|  |  | 3350 | 254.5 | _umc1250*_ |
|  |  | 3458 | 254.51 | _csu382a(cld)_ |
|  |  | 3499 | 254.52 | _PCO146525_ |
|  |  | 3533 | 254.52 | _umc1751_ |
|  |  | 3551 | 254.52 | _cesa2_ |
|  | 282 |  | 269.8 | unpublished |
|  | 283 | 18 | 277.09 | _umc2055_ |
|  |  | 140 | 277.1 | _umc1413*_ |
|  |  | 487 | 277.13 | _PCO134814_ |
|  |  | 489 | 278 | _bnlg2249*_ |
|  |  | 591 | 295.4 | _umc2141*_ |
|  |  | 604 | 290.6 | _AY110542*_ |
|  |  | 711 | 284.3 | _umc1314*_ |
|  |  | 969 | 281.45 | _csu360(elf1A)_ |
|  |  | 1037 | 296.3 | _AY110435*_ |
|  |  | 1060 | 296.3 | _dhn1_ |
|  |  | 1321 | 297.1 | _umc1379*_ |
|  |  | 1475 | 297.12 | _csu16b_ |
|  | 284 | 286 | 302 | _umc1388*_ |

Chromosome 6

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | 285 | 102 | 310.68 | _umc2065_ |
| | | 223 | 310.69 | _umc2040_ |
| | | 229 | 312 | _npi252*_ |
| | | 307 | 310.7 | _AY110260*_ |
| | | 430 | 314.8 | _AY109873*_ |
| | | 625 | 316.83 | _mmc0241_ |
| | | 715 | 317.77 | _csu158b(eno)_ |
| | | 718 | 317.8 | _pdk1*_ |
| | | 719 | 317.81 | _bcd454a_ |
| | | 749 | 322.9 | _umc2320*_ |
| | | 795 | 318.6 | _AY110050*_ |
| | | 817 | 321.9 | _AY110873*_ |
| | | 1029 | 318.91 | _AY107881_ |
| | | 1095 | 319 | _umc2321*_ |
| | | 1212 | 319.16 | _umc1462_ |
| | | 1254 | 319.21 | _umc1805_ |
| | 286 | | 357.1 | unpublished |
| | 287 | 235 | 373.8 | _bnlg1732*_ |
| | | 305 | 373.81 | _si606039C09_ |
| | | 462 | 373.82 | _cdo312b_ |
| | | 596 | 373.84 | _bnlg345_ |
| | | 646 | 373.84 | _roa2_ |
| 6.06 | | 655 | 385.8 | **_umc38a*_** |
| | | 729 | 388.7 | _umc1912*_ |
| | | 751 | 391.4 | _umc1859*_ |
| | | 936 | 394.1 | _umc1762*_ |
| | | 968 | 393.9 | _umc1463*_ |
| | | 1008 | 394.11 | _CL10251_1_ |
| | | 1060 | 398.5 | _umc2162*_ |
| | | 1253 | 398.52 | _umc2389_ |
| | | 1309 | 410.3 | _AY104923*_ |
| | 288 | 100 | 420.4 | _lim379*_ |
| | | 110 | 426.4 | _AY105728*_ |
| | | 112 | 426.4 | _umc1520_ |
| | | 138 | 427.2 | _AY105785*_ |
| | | 334 | 427.22 | _umc2375_ |
| | | 378 | 435.1 | _umc2170*_ |
| | | 563 | 435.12 | _hsp101_ |
| 6.07 | | 648 | 444.2 | **_umc132a(chk)*_** |
| | | 677 | 444.2 | _hdt103_ |
| | | 799 | 450.7 | _phi299852*_ |
| | | 845 | 452.68 | _mlg3*_ |
| | | 845 | 450.7 | _umc2123_ |
| | | 877 | 466.5 | _umc1490*_ |
| | | 1052 | 483.5 | _umc2323*_ |
| | | 1177 | 501.2 | _AY104289*_ |
| | | 1178 | 498.7 | _AY109797*_ |
| | 289 | 42 | 502.9 | _umc1897_ |
| | | 42 | 502.9 | _umc2165*_ |
| | | 52 | 503.4 | _bnlg1759a*_ |
| | | 83 | 427.53 | _umc1350*_ |
| | | 111 | 504.8 | _umc1248_ |
| | | 155 | 510.6 | _bnlg1740*_ |
| | | 156 | 510.6 | _umc1779_ |
| | | 156 | 513.8 | _umc62*_ |
| | 290 | 121 | 531.62 | _umc1621_ |
| | | 122 | 531.62 | _bnlg1136*_ |
| | | 175 | 534.6 | _mmp105*_ |
| | | 175 | 534.6 | _umc1653*_ |
| | | 264 | 536.4 | _agp2*_ |
| | | 430 | 536.42 | _PCO068526_ |

Chromosome 6

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| 6.08 | 291 | 198 | 548.7 | _cdo202a(mcf)*_ |
| | | 223 | 542.7 | _umc1127_ |
| | | 238 | 542.7 | _umc2059*_ |
| | | 319 | 544.5 | _bnlg1521_ |
| | | 319 | 544.5 | _umc2324*_ |

Chromosome 7

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| 7.00 | 292 | 58 | -6.3 | umc1788 |
| | 293 | 54 | 2.7 | csu582* |
| | | 70 | -0.89 | hsp3* |
| | | 241 | 13.8 | umc1241* |
| | | 254 | 13.94 | bnlg1367 |
| | | 356 | 27.4 | umc1378* |
| | | 356 | 27.2 | umc1642* |
| | | 383 | 27.4 | umc1378* |
| | | 444 | 45 | umc1694* |
| | | 471 | 47.8 | umc1426* |
| | | 553 | 53.3 | bnlg2132* |
| 7.01 | 294 | 273 | 69.1 | AY104465* |
| | 295 | 12 | 69.07 | umc1840 |
| | 296 | 59 | 86.3 | AW308691* |
| | | 183 | 86.31 | hda110 |
| | | 325 | 86.33 | umc2364 |
| | | 363 | 92 | umc1159* |
| | | 392 | 93.41 | csu129 |
| | | 802 | 113.4 | mmp18* |
| | | 838 | 125.06 | o2* |
| | | 874 | 125.06 | umc2392 |
| | | 920 | 125.06 | dmt101 |
| | | 971 | 125.99 | his1a* |
| | | 1127 | 126.3 | umc1632* |
| | | 1359 | 126.31 | umc1428 |
| | | 1360 | 127.6 | umc2325* |
| 7.02 | | 1470 | 132 | asg34a(msd)* |
| | 297 | 161 | 151.44 | bnlg1200 |
| | | 563 | 153 | umc1401* |
| | | 569 | 153.3 | umc1986* |
| | | 812 | 151.5 | AY109536* |
| | | 826 | 153.31 | cesa9 |
| | | 968 | 154.8 | umc2326* |
| | 298 | 164 | 154.76 | sdg101 |
| | | 302 | 156.9 | umc1978* |
| | | 340 | 158 | umc2327* |
| | | 434 | 162.4 | AY105589* |
| | 299 | 221 | 170.8 | crt2* |
| | | 913 | 170.87 | umc1339 |
| | | 995 | 212.31 | cdo407 |
| | 300 | 940 | 176.8 | AY110576* |
| | 301 | 124 | 178 | AY110473* |
| | | 573 | 178.03 | umc1666 |
| | | 573 | 181.3 | mmp187* |
| | | 610 | 181.3 | cncr2 |
| | | 898 | 181.33 | nbp1 |
| | | 1363 | 181.38 | umc1409 |
| | | 1397 | 181.39 | AY109061 |
| | | 1769 | 181.43 | umc1480 |
| | | 1935 | 181.45 | AY106170 |
| | 302 | 408 | 180.5 | bnlg1094* |
| | 303 | 205 | 183.4 | umc1879* |
| | 304 | 587 | 186.3 | bnlg1247* |
| | | 872 | 186.33 | umc1433 |
| | | 966 | 188.1 | bnlg1380* |
| | | 997 | 188.1 | bnlg398 |
| | 305 | 145 | 190.38 | vef101a |
| | | 279 | 190.4 | bnlg1792* |
| | 306 | 131 | 190.6 | bnlg2203* |
| | | 229 | 190.61 | pep4 |
| | 307 | 494 | 192.5 | AY109809* |
| | | 672 | 192.72 | hag102 |
| | | 759 | 195.6 | lim333* |
| | | 1079 | 195.63 | CL4745_2 |
| | 308 | 48 | 204.8 | umc1932* |
| | 309 | 1825 | 228.7 | AY109968* |
| | | 1992 | 228.72 | umc1036 |
| | 310 | 155 | 244.3 | umc1983* |
| | | 155 | 246.3 | umc2142* |
| | | 198 | 249.1 | umc1929* |
| | | 465 | 252.4 | umc1787* |
| | 311 | | 252.6 | unpublished |
| | 312 | 188 | 252.9 | umc2092* |
| | | 502 | 252.94 | umc2057 |
| | 313 | | 255 | unpublished |
| | 314 | 217 | 258.4 | umc1393* |
| | 315 | 120 | 261.49 | umc1585 |
| | | 257 | 261.5 | umc5b* |
| | 316 | 242 | 273.8 | bnlg657 |
| | | 261 | 273.8 | bnlg1164 |
| | | 265 | 273.8 | bnlg1022a |
| | | 374 | 273.81 | umc1881 |
| | 317 | | 297 | unpublished |
| 7.03 | 318 | 20 | 298.37 | **asg49** |
| | | 87 | 298.37 | gst36 |
| | | 351 | 298.4 | umc1713* |
| | | 351 | 300.34 | php20569a* |
| | | 402 | 300.34 | umc1567 |
| | | 547 | 300.36 | bnlg1305 |
| | | 909 | 317.84 | umc1987* |
| | | 993 | 322.7 | bnlg1070* |
| | | 998 | 323.3 | bnlg434* |
| | | 1088 | 330.6 | npi394* |
| | | 1194 | 330.61 | ij1 |
| | | 1637 | 330.66 | umc1718 |
| | 319 | 171 | 343.01 | bnlg339 |
| | | 233 | 343.01 | umc1275 |
| | 320 | 339 | 347.19 | umc1333 |
| | | 414 | 347.2 | AY110374* |
| | | 461 | 347.2 | umc1481 |
| | | 656 | 351.4 | umc1660* |
| | | 983 | 365.4 | umc1408* |
| | | 1151 | 368.9 | umc1837* |
| | | 1187 | 368.9 | AY107911 |
| | | 1467 | 374 | rz404(ccp)* |
| | | 1559 | 374.01 | si614054G01 |
| | | 1616 | 374.01 | PCO101826 |
| | | 1661 | 374.02 | umc1841 |
| | | 1754 | 380.6 | umc1865* |
| | | 1798 | 381.5 | umc2328* |
| | | 1831 | 381.16 | umc1001 |
| | | 1837 | 381.2 | umc1134* |
| | | 2050 | 381.5 | AY109644* |
| | 321 | 109 | 383.8 | bnlg2271* |
| | 322 | 217 | 384.4 | umc2329* |
| | | 394 | 385.1 | umc1112* |
| | | 514 | 387.5 | umc1324* |
| | | 565 | 390.5 | umc1888* |
| | | 698 | 392.1 | bnlg1805* |
| | | 983 | 405.5 | umc1936* |
| | | 1049 | 405.5 | umc1301* |
| 7.04 | 323 | 73 | 408.4 | umc2330* |

Chromosome 7

| BIN | BAC FPC: | | Genetic | Locus |
|---|---|---|---|---|
| | Contig | CB | IBM | |
| | | 73 | 408.4 | *umc2331** |
| | | 172 | 410.5 | *umc1710** |
| | | 321 | 412.1 | *umc1251** |
| | | 344 | 412.1 | *umc2062* |
| | | 376 | 412.11 | *umc1684* |
| | | 395 | 412.11 | *uaz199* |
| | | 616 | 429.2 | *AY110023** |
| | | 683 | 430.5 | *bnlg1666** |
| | | 1115 | 444.7 | *umc1029** |
| | | 1163 | 444.7 | *umc1342* |
| | | 1175 | 444.71 | *umc1543* |
| | | 1271 | 444.71 | *umc1944* |
| | 324 | | 454 | unpublished |
| | 325 | 30 | 471.38 | *rip2* |
| | | 48 | 471.38 | *csu5a* |
| | | 64 | 472.9 | *phi328175** |
| | | 129 | 473 | *AY110439** |
| | | 176 | 481.1 | *umc1768** |
| | | 188 | 472.6 | *umc2332** |
| | | 201 | 471.4 | *umc1708** |
| | | 394 | 489.2 | *bnlg2259** |
| | | 442 | 489.2 | *AY108844* |
| | | 494 | 494.8 | *umc1295** |
| | | 524 | 495.06 | *umc1103* |
| | | 635 | 495.07 | *rpot1* |
| | | 737 | 495.08 | *csu904* |
| | | 926 | 518.9 | *umc1412** |
| | | 931 | 517.5 | *AW267377** |
| | | 988 | 530.63 | *gpm2* |
| | | 1024 | 530.63 | *PCO136133* |
| | | 1073 | 530.63 | *PCO061754* |
| | | 1077 | 530.63 | *umc1125* |
| | | 1230 | 530.64 | *AY106318* |
| | | 1346 | 530.65 | *chc101a* |
| 7.05 | | 1479 | 543.4 | *mmp25** |
| | | 1487 | 547.7 | *mmp17** |
| | | 1790 | 547.73 | *umc2368* |
| | | 1815 | 547.73 | *bnlg2328b* |
| | | 1863 | 541.11 | *csu27* |
| | | 1874 | 547.74 | *umc1671* |
| | | 1953 | 547.75 | *umc2197* |
| | | 1997 | 547.75 | *csu163a* |
| | | 2028 | 547.75 | *umc1154* |
| | | 2040 | 547.76 | *umc2222* |
| | | 2041 | 247.7 | *umc1138** |
| | | 2046 | 547.76 | *umc2379* |
| | | 2058 | 547.76 | *cdo38b(ntp)* |
| | | 2095 | 593.4 | *umc2333** |
| | | 2101 | 593.4 | *umc35a* |
| | | 2101 | 593.4 | *umc2190* |
| | | 2101 | 598.9 | *umc1406** |
| | | 2101 | 600.2 | *umc1407** |
| | | 2101 | 600.4 | *umc2334** |
| 7.06 | | 2222 | 608.2 | ***umc168**** |
| | | 2222 | 607.6 | *umc1760** |
| | | 2288 | 611.5 | *phi116** |
| | | 2335 | 611.51 | *umc1799* |
| | | 2459 | 611.52 | *umc1242* |
| | | 2509 | 618.4 | *AY109703** |
| | | 2583 | 618.41 | *oec6* |

Chromosome 8

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| 8.02 | 327 | 126 | 153.3 | *umc1872* |
| | | 151 | 153.3 | *umc1974** |
| | 328 | 36 | 159.2 | *cdo328** |
| | | 79 | 160.8 | *umc1913** |
| | 329 | 141 | 160.81 | *umc1034* |
| | | 379 | 175.9 | *csu329** |
| | | 550 | 175.92 | *nfd110* |
| 8.03 | | 553 | 175.92 | ***asg24b(gts)*** |
| | | 627 | 179.5 | *umc1530** |
| | | 668 | 179.5 | *bnlg1067* |
| | | 711 | 179.51 | *bnlg669* |
| | | 727 | 179.51 | *CL51477_1* |
| | | 917 | 179.53 | *umc1778* |
| | | 933 | 191 | *mmp120** |
| | | 1158 | 198.4 | *umc2146** |
| | | 1158 | 197.1 | *umc2147** |
| | 330 | 310 | 199.1 | *umc32b** |
| | 331 | 334 | 200.3 | *bnlg2082** |
| | | 337 | 200.3 | *umc1868* |
| | | 950 | 200.35 | *umc1236* |
| | 332 | 675 | 202 | *AW244963** |
| | 333 | 111 | 203 | *AY110450** |
| | 334 | 271 | 203 | *umc2353** |
| | 335 | 71 | 204.8 | *bnlg1834** |
| | 336 | 226 | 204.82 | *umc1360* |
| | | 293 | 206 | *umc1157** |
| | | 402 | 206.6 | *umc1904** |
| | 337 | 53 | 231.2 | *umc1470** |
| | | 84 | 232.9 | *umc2355** |
| | 338 | 404 | 240.7 | *AY103821** |
| | | 508 | 240.71 | *AW172071* |
| | | 792 | 240.73 | *umc1487* |
| | 339 | 156 | 269.66 | *umc1471* |
| | | 202 | 269.66 | *stp1* |
| | 340 | 212 | 244.79 | *csu742a(rpS7)* |
| | | 260 | 244.79 | *umc1302* |
| | | 535 | 228.6 | *umc1415** |
| | | 706 | 245.9 | *AY105457** |
| | | 750 | 246.55 | *umc2366* |
| | | 947 | 245.7 | *bnlg1863** |
| | | 1279 | 254.8 | *AY110032** |
| | | 1585 | 244.9 | *umc2075** |
| | | 1699 | 267.74 | *umc1615* |
| | | 1727 | 268.6 | *AY109740** |
| | | 1816 | 268.6 | *umc1427* |
| | 341 | 111 | 273.8 | *rps28* |
| | 342 | 125 | 274.02 | *umc1802* |
| | 343 | 568 | 274.24 | *AY110113* |
| | | 740 | 274.25 | *umc1377* |
| | 344 | 480 | 274.46 | *umc1617* |
| | | 509 | 274.46 | *oec23* |
| | 345 | 39 | 274.89 | *umc1473* |
| | | 703 | 274.9 | *phi100175** |
| | | 809 | 279.9 | *umc1735** |
| | | 912 | 282.7 | *AY109626** |
| | | 931 | 284.6 | *umc1457** |
| | 346 | | 285 | unpublished |
| | 347 | 53 | 289.8 | *phi121** |
| | | 172 | 282.11 | *tub2* |
| | 348 | 27 | 295.25 | *bcd454b* |
| | | 34 | 295.25 | *mbd101a* |
| | | 277 | 295.28 | *bnlg1446* |
| | | 461 | 295.3 | *rip1* |
| | | 474 | 295.3 | *umc2154** |
| | 349 | 257 | 304.2 | *umc1460** |
| | | 464 | 307.59 | *PCO147505* |
| | | 551 | 309.02 | *csu9a(trf)* |
| | | 625 | 312.4 | *umc1858** |
| | | 635 | 310.4 | *AY110056** |
| 8.04 | | 1281 | 312.42 | *AY107079* |
| | 350 | 84 | 315.2 | *umc1765* |
| | | 136 | 315.2 | *bnlg2046** |
| | 351 | 26 | 316.2 | *pdc1* |
| | | 27 | 316.2 | *pdc1* |
| | | 27 | 316.2 | *cdo312a* |
| | | 158 | 316.22 | *umc38b* |
| 8.05 | 352 | 212 | 329.4 | ***bnl2.369**** |
| | 353 | 61 | 337.12 | *rop7* |
| | | 74 | 337.13 | *umc2367* |
| | | 229 | 337.14 | *hox1** |
| | | 463 | 342 | *AY104566** |
| | 354 | 78 | 353.3 | *umc1562** |
| | | 80 | 348.2 | *mmp15** |
| | | 253 | 348.22 | *umc1882* |
| | | 410 | 352.2 | *umc1959** |
| | | 549 | 353.9 | *umc1263** |
| | | 642 | 353.91 | *mrp1* |
| | | 964 | 353.94 | *umc1864* |
| | | 1087 | 357.9 | *umc1846** |
| | | 1646 | 357.95 | *umc2c* |
| | | 1738 | 367 | *bnlg162** |
| | | 1738 | 367 | *bnlg666** |
| | | 1738 | 366.8 | *bnlg2181** |
| | | 1781 | 368.43 | *bnlg1599* |
| | | 1784 | 368.53 | *umc2378* |
| | | 1838 | 370.32 | *csu829* |
| | | 1887 | 374.9 | *umc1889** |
| | | 1907 | 372.6 | *umc12a** |
| | | 1931 | 372.6 | *umc1712* |
| | | 1931 | 372.6 | *umc2401* |
| | | 1947 | 374.5 | *bnlg1651** |
| | | 2215 | 377.7 | *umc1340** |
| | | 2239 | 377.7 | *hdt102* |
| | | 2804 | 377.76 | *bnlg1812* |
| | 355 | 27 | 381.68 | *umc1670* |
| | | 30 | 382.9 | *umc1777** |
| | | 176 | 381.7 | *umc1316** |
| | 356 | | 382 | unpublished |
| | 357 | 244 | 215.6 | *cdo1160a(kri)** |
| | 358 | 127 | 388.71 | *umc1121* |
| | | 748 | 388.77 | *umc2175* |
| | | 794 | 388.78 | *csu31a* |
| | | 1337 | 388.83 | *umc2199* |
| | | 1528 | 388.85 | *bnlg2289* |
| | | 1813 | 388.87 | *umc1665* |
| | | 1945 | 388.89 | *umc2210* |
| | | 2053 | 388.9 | *umc17b* |
| | 359 | | 390 | unpublished |
| | 360 | 46 | 410.95 | *bnlg1782* |
| | | 316 | 410.97 | *umc1828* |
| 8.06 | 361 | 57 | 412.88 | *umc1141* |
| | | 173 | 412.89 | *umc2031* |

Chromosome 8

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | | 225 | 412.9 | *umc1161* |
| | | 225 | 412.9 | *umc2212* |
| | | 253 | 413.2 | *umc1960** |
| | | 253 | 412.9 | *umc2356** |
| | | 255 | 413.2 | *sdg118* |
| | | 255 | 413.9 | *umc1149** |
| | | 255 | 414.1 | *bnlg1152** |
| | | 288 | 416 | *mmp32** |
| | | 289 | 416 | *bnlg240* |
| | 362 | 81 | 432.37 | *csu382b(cld)* |
| | 362 | 143 | 432.37 | *PCO079694* |
| | | 164 | 432.38 | *sbe3* |
| | | 356 | 432.4 | *umc2037* |
| | | 396 | 432.4 | *umc1728** |
| | | 405 | 432.4 | *umc2361* |
| | | 593 | 432.42 | *umc2395* |
| | | 623 | 432.42 | *mmc0181* |
| | | 646 | 439.6 | *umc1905** |
| | 363 | 145 | 455.1 | *bnlg1031** |
| | | 170 | 456.17 | *umc1724* |
| 8.07 | | 222 | 459.2 | ***npi268a**** |
| | | 222 | 460.8 | *bnlg1065** |
| | | 226 | 460.8 | *CL9311_1* |
| | | 325 | 466.5 | *umc1607** |
| | | 612 | 483.4 | *bnlg1823** |
| | | 718 | 489.7 | *psy2** |
| | | 718 | 486.9 | *AY110569** |
| | | 848 | 494.7 | *umc1268** |
| | | 963 | 494.71 | *umc1384* |
| 8.08 | | 978 | 509.8 | ***npi414a**** |
| | 364 | 30 | 515 | *mmp64** |
| | | 39 | 515 | *umc1032* |
| | | 168 | 515.01 | *umc2218* |
| | | 317 | 515.03 | *umc2052* |
| | | 317 | 540.3 | *umc1933** |
| | 365 | 19 | 550.4 | *AY110053** |
| | | 26 | 550.4 | *bnlg1056* |
| | 366 | 195 | 572.18 | *gst1** |
| | | 195 | 580.1 | *agrr21** |
| | | 245 | 596.4 | *AY110127** |
| | | 327 | 609.1 | *phi233376** |
| | | 333 | 608.1 | *umc1663** |
| | | 364 | 621.6 | *umc1638** |
| | | 654 | 632 | *AY109853** |

Chromosome 9

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| 9.00 | 367 | | 0.1 | unpublished |
| | 368 | 98 | 4.87 | *AY112355* |
| | | 118 | 4.88 | *umc1279* |
| 9.01 | | 534 | 5 | *umc109** |
| | | 537 | 0 | *umc1957** |
| | | 726 | 11.8 | *bnlg1724** |
| | | 753 | 17.7 | *umc1370** |
| | | 755 | 17.7 | *umc2084* |
| | | 829 | 21.2 | *umc1040** |
| | | 831 | 21.3 | *bnlg2122** |
| | | 875 | 21.3 | *umc2393* |
| | | 877 | 24.3 | *umc1867** |
| | | 948 | 24.31 | *bnlg1288* |
| | | 1118 | 41.68 | *csu95a* |
| | 369 | 17 | 62.3 | *bnlg1583** |
| | | 17 | 62.3 | *bnlg1810** |
| | 370 | 134 | 64.7 | *c1** |
| | 371 | 105 | 74.8 | *umc2335** |
| | | 201 | 80.3 | *sh1** |
| | | 205 | 80.3 | *umc2362* |
| | | 234 | 84.3 | *umc1967** |
| | | 245 | 84.3 | *stc1* |
| 9.02 | | 248 | 90.1 | *bz1** |
| | | 309 | 90.11 | *AY107496* |
| | | 370 | 90.11 | *umc1958* |
| | | 373 | 95.8 | *AY104252** |
| | | 375 | 95.8 | *umc2078* |
| | 372 | 43 | 101.1 | *umc1764* |
| | | 72 | 101.1 | *umc1170** |
| | 373 | 68 | 101.1 | *umc1430* |
| | | 131 | 101.11 | *bnlg1372* |
| | | 286 | 101.12 | *umc2130* |
| | | 286 | 101.12 | *umc2219* |
| | | 383 | 125.7 | *umc2336** |
| | | 562 | 131.1 | *umc1636** |
| | | 816 | 131.12 | *ss1* |
| | | 934 | 142.6 | *bnlg244** |
| | | 1044 | 147.5 | *bnlg1401** |
| | | 1359 | 164.15 | *mgs3* |
| | | 1384 | 162.5 | *mmp30** |
| | | 1386 | 162.5 | *umc1037* |
| | | 1389 | 162.5 | *umc1893* |
| | | 1390 | 162.5 | *umc1033* |
| | | 1734 | 162.54 | *AY105451* |
| | | 1757 | 162.54 | *umc2213* |
| 9.03 | | 1962 | 192.17 | *wx1** |
| | | 2016 | 193.2 | *umc1634** |
| | | 2036 | 195.7 | *umc1258** |
| | | 2082 | 196.4 | *AY109570** |
| | | 2381 | 199.7 | *umc1586** |
| | | 2468 | 199.91 | *umc2128* |
| | | 2486 | 199.95 | *gpm6* |
| | | 2508 | 202.3 | *lim101** |
| | | 2509 | 202.3 | *PCO061815* |
| | | 2676 | 200.4 | *AY109816** |
| | | 2703 | 202.32 | *d3* |
| | | 3009 | 219.4 | *umc2338** |
| | | 3025 | 220.1 | *umc2337** |
| | 374 | 248 | 226.28 | *csu321* |
| | 375 | 447 | 226.3 | *umc81** |
| | | 583 | 226.31 | *bnlg127* |

Chromosome 9

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | 377 | 75 | 230.95 | *php20075b(ext)* |
| | | 260 | 230.96 | *umc1420* |
| | 378 | 413 | 241.55 | *bnlg430* |
| | | 620 | 241.57 | *umc2370* |
| | 376 | 439 | 230.1 | *umc1599** |
| | | 1109 | 230.16 | *bnlg1626* |
| | | 1109 | 232.8 | *umc1191** |
| | | 1339 | 240.5 | *umc1271** |
| | | 1339 | 238.9 | *umc2339** |
| | | 1345 | 238.4 | *umc2340** |
| | | 1598 | 238.41 | *AY107743* |
| | | 1598 | 238.41 | *BE518809* |
| | | 2089 | 238.44 | *gtd101* |
| | | 2206 | 238.44 | *bnlg1688* |
| | | 2532 | 238.46 | *si605086B11* |
| | | 2593 | 238.46 | *gl15* |
| | | 2593 | 247.6 | *umc1688** |
| | | 2593 | 244.1 | *umc1691** |
| | | 2943 | 249.75 | *cdo78* |
| | | 3272 | 252.3 | *umc2087** |
| | | 3273 | 254.3 | *umc114** |
| | | 3277 | 251.8 | *umc1700** |
| | | 3349 | 254.6 | *AY103770** |
| | | 3392 | 254 | *umc1743** |
| | | 3610 | 253.7 | *AW257883** |
| | | 3630 | 256.4 | *csu147* |
| | | 3979 | 257.6 | *umc1267** |
| | | 4497 | 257.66 | *umc2394* |
| 9.04 | 379 | 192 | 260.55 | *bnlg1687* |
| | 380 | 19 | 266.15 | *sbp4** |
| | | 81 | 268.4 | *lim166** |
| | | 343 | 268.43 | *csu56d(ohp)* |
| | | 430 | 273.2 | *bnlg1209** |
| | 381 | 160 | 273.17 | *umc1522* |
| | 382 | 190 | 287 | *bnlg1159b** |
| | | 342 | 298 | *bnlg1012** |
| | | 788 | 298.04 | *rz672b(cgs)* |
| | | 816 | 298.05 | *umc1878* |
| | | 1015 | 308 | *umc1492** |
| | | 1158 | 308.01 | *AY110782* |
| | 384 | 17 | -86.18 | *umc1120** |
| | | 129 | 311.9 | *sus1** |
| | | 131 | 311.9 | *AY109764** |
| | | 191 | 312.5 | *mmp96** |
| | 385 | 271 | 314.3 | *mmp37** |
| | | 272 | 317 | *umc38c** |
| | | 323 | 315.7 | *umc2121** |
| | | 475 | 315.77 | *csu694a(uce)* |
| | | 539 | 318.87 | *bcd855f(ext)* |
| | | 861 | 318.89 | *umc1771* |
| | | 944 | 318.89 | *umc1519* |
| 9.05 | | 1092 | 322.6 | *umc1078** |
| | | 1198 | 322.61 | *umc1387* |
| | | 1239 | 322.62 | *sod9* |
| | | 1582 | 322.65 | *umc1654* |
| | | 1582 | 354.4 | *mmp179** |
| | 386 | 361 | 344.8 | *umc1657** |
| | | 388 | 344.8 | *umc1357* |
| | | 388 | 343.7 | *mmp41** |
| | | 388 | 342 | *umc1231** |
| | 387 | 25 | 373.2 | *AY110217** |

Chromosome 9

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | | 436 | 373.24 | *rgpr3235a* |
| | | 460 | 378.9 | *umc2095** |
| | | 496 | 379.69 | *umc1494* |
| | | 528 | 382.7 | *csu634** |
| | | 560 | 381.1 | *umc2341** |
| | | 604 | 384.8 | *umc2344** |
| | | 607 | 384.9 | *umc2342** |
| | | 686 | 385.2 | *si687046G05* |
| | | 713 | 385.3 | *umc2343** |
| | | 918 | 385.32 | *csu651(rpL39)* |
| | | 1085 | 385.34 | *csu59a* |
| | | 1091 | 385.34 | *umc2371* |
| | 388 | 25 | 386.22 | *umc1417* |
| | | 26 | 386.22 | *umc1417* |
| 9.06 | 389 | 50 | 421.6 | *gpm1* |
| | | 69 | 421.6 | *mmp142** |
| | | 199 | 421.61 | *umc1794* |
| | | 376 | 429.7 | *AY109550** |
| | | 697 | 429.73 | *AY107292* |
| | | 920 | 429.75 | *umc76b* |
| | | 939 | 429.76 | *bnlg1191* |
| | | 946 | 463.9 | *csu93a** |
| | | 946 | 461.6 | *umc2346** |
| | | 1006 | 491.99 | *hb1** |
| | | 1271 | 492.02 | *bnlg1525* |
| | 390 | 35 | 526 | *AY109819** |
| | | 52 | 526 | *umc1310* |
| | | 103 | 526.01 | *umc2207* |
| | | 130 | 526.01 | *bnlg292a* |
| | | 223 | 534.2 | *umc1789** |
| 9.07 | | 245 | 535.95 | ***asg12**** |
| | 391 | 20 | 536.8 | *phi448880** |
| | | 162 | 538.5 | *AY109543** |
| | | 179 | 538.5 | *umc1804* |
| | | 290 | 551.3 | *AY110382** |
| | | 325 | 554.4 | *bnlg619** |
| | | 433 | 562.7 | *umc2089** |
| | | 448 | 562.7 | *umc2359* |
| | | 472 | 562.7 | *bnlg1506* |
| | | 548 | 562.71 | *bnlg1375* |
| | | 548 | 566.8 | *umc2131** |
| | | 576 | 567.3 | *umc1714** |
| | | 618 | 578.6 | *umc2347** |
| | | 669 | 578.61 | *bnlg128* |
| | | 785 | 587.9 | *AY106323** |
| | | 1023 | 603.5 | *umc1137** |
| | | 1031 | 603.5 | *umc1942* |
| | | 1063 | 603.5 | *umc1104* |
| | | 1102 | 603.51 | *PCO127444* |
| | | 1257 | 603.52 | *dmt103a* |
| | | 1281 | 695.45 | *csu54b* |
| | | 1287 | 603.52 | *rld1* |
| | | 1317 | 603.53 | *umc1277* |
| | | 1320 | 637.1 | *AI901738** |
| | | 1362 | 624.52 | *umc1505** |
| | | 1399 | 633.2 | *umc1982** |
| | | 1670 | 633.6 | *bnlg1129** |

Chromosome 10

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| 10.00 | 392 | 225 | -34.42 | *umc2399* |
| | | 282 | 16.6 | *umc1380** |
| | | 311 | 16.6 | *umc1293* |
| 10.01 | | 347 | 34.8 | ***php20075a(gast)**** |
| | | 348 | 30.9 | *phi041** |
| | | 437 | 53 | *AW330564** |
| | | 551 | 53.01 | *rp1* |
| | | 604 | 53.02 | *umc1291* |
| | | 692 | 53.03 | *umc1319* |
| | | 705 | 53.03 | *csu577* |
| | | 705 | 53.03 | *cdo127b(pyk)* |
| | | 706 | 64.1 | *AW225120** |
| | | 712 | 76.2 | *umc2053** |
| | | 716 | 81.1 | *umc2018** |
| | | 761 | 81.1 | *bnlg1451* |
| 10.02 | | 783 | 91 | ***npi285a(cac)**** |
| | | 787 | 91.4 | *umc1152** |
| | | 874 | 104 | *AY110360** |
| | | 910 | 106.98 | *umc1432* |
| | | 937 | 97.9 | *gdcp1** |
| | | 1044 | 120.1 | *mmc0501* |
| | | 1046 | 120.1 | *umc2034** |
| | 393 | 242 | 143.3 | *umc1337** |
| | | 242 | 148.9 | *umc2114** |
| | | 269 | 136.66 | *csu103a(aba)* |
| | | 281 | 148.9 | *umc1582* |
| | | 281 | 143.5 | *phi059** |
| | | 385 | 134.8 | *AI795367** |
| | | 751 | 148.92 | *PCO062847* |
| | 394 | 452 | 160 | *umc1863* |
| 10.03 | | 482 | 160 | ***umc130**** |
| | | 691 | 160.02 | *AY105872* |
| | 395 | 236 | 168.2 | *gcsh1** |
| | | 612 | 168.23 | *umc1312* |
| | | 872 | 173.5 | *lim2** |
| | 396 | 127 | 179.66 | *umc1866* |
| | | 339 | 179.68 | *glu1* |
| | 397 | 170 | 180.7 | *umc1785* |
| | | 176 | 180.7 | *umc1962** |
| | | 455 | 183.8 | *umc1367** |
| | 398 | 81 | 183.4 | *bnlg210** |
| | | 1013 | 184.88 | *chr109a* |
| | 399 | 385 | 186.95 | *bnlg1716* |
| | | 1226 | 186.99 | *sdg108b* |
| | | 1351 | 187 | *umc1381** |
| | | 1410 | 187.01 | *gpm15* |
| | | 1699 | 187.03 | *du1* |
| | 400 | 286 | 194.5 | *umc2067** |
| | | 289 | 194.84 | *umc2017* |
| | | 294 | 195.4 | *umc2016** |
| | | 608 | 195.43 | *umc1938* |
| | | 1223 | 200.5 | *AY110248** |
| | | 1279 | 200.51 | *npi602* |
| | 401 | | 212 | unpublished |
| | 402 | 245 | 213.3 | *umc1239** |
| | | 245 | 213.1 | *bnlg1079** |
| | 403 | | 215 | unpublished |
| | 404 | 277 | 220.1 | *AY112073** |
| | | 305 | 217.8 | *bnlg1712** |
| | 405 | 211 | 225.7 | *bnlg640* |
| | | 211 | 228 | *bnlg1655** |

Chromosome 10

| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
|---|---|---|---|---|
| | 406 | 255 | 228.3 | *umc1336** |
| | | 375 | 228 | *umc1739** |
| | | 419 | 228.31 | *nac1* |
| | 407 | 177 | 227.9 | *umc2349** |
| | | 178 | 228.3 | *umc2180** |
| | | 181 | 227.9 | *csu276* |
| | 408 | | 228.5 | unpublished |
| 10.04 | 409 | 256 | 245.9 | *umc1995** |
| | | 293 | 244.6 | *umc2348** |
| | | 672 | 245.95 | *umc1589* |
| | | 1030 | 248.2 | *umc1246** |
| | | 1347 | 248.2 | *umc1246** |
| | 410 | 82 | 254.5 | *AY110514** |
| | | 162 | 254.5 | *cdo456a* |
| | 411 | 665 | 253.35 | *bnlg1526* |
| | | 761 | 253.4 | *rz69** |
| | | 1786 | 253.89 | *umc1827* |
| | | 1823 | 256.8 | *AY109920** |
| | | 2535 | 260.12 | *mgs1** |
| | | 2758 | 260.14 | *PCO086427* |
| | 412 | 52 | 271.3 | *AY110365** |
| | | 142 | 271.31 | *incw3** |
| | | 224 | 270.5 | *mmp121** |
| | | 224 | 268.1 | *mzetc34** |
| | | 539 | 280.7 | *AY109698** |
| | | 929 | 273.6 | *umc1911** |
| | | 1168 | 274.4 | *umc1453** |
| | | 1478 | 283.5 | *umc2350** |
| | 413 | 112 | 290.9 | *umc1697** |
| | | 308 | 287.9 | *umc1330** |
| | | 605 | 299.4 | *umc1272** |
| | | 605 | 299.8 | *umc1648** |
| | | 613 | 299.8 | *csu86* |
| | | 924 | 299.81 | *hag103b* |
| | | 1017 | 295.9 | *umc1115** |
| | | 1167 | 301.6 | *umc2003** |
| 10.05 | | 1215 | 319.5 | *AY110634** |
| | | 1289 | 309 | *umc259a** |
| | | 1310 | 322.77 | *umc1280* |
| | | 1425 | 322.77 | *umc1507* |
| | | 1898 | 332.1 | *bnlg1074** |
| | | 1907 | 327.3 | *mmp12** |
| | | 2001 | 334.37 | *umc2156* |
| | | 2084 | 334.37 | *PCO087182* |
| | | 2131 | 335.5 | *bnlg1250** |
| | 414 | 12 | 344.8 | *umc1506** |
| | 415 | 23 | 375.78 | *por2* |
| | | 23 | 375.78 | *tip5** |
| 10.06 | | 117 | 380.5 | *bnlg1028** |
| | | 146 | 380.5 | *r1* |
| | | 146 | 380.5 | *sn1* |
| | | 258 | 376.9 | *mmp71** |
| | | 289 | 375.8 | *umc1045** |
| | | 289 | 376.3 | *bnl10.13a** |
| | | 353 | 380.52 | *umc57a* |
| | | 394 | 380.53 | *umc44a* |
| | | 858 | 355 | *umc2043* |
| | | 880 | 380.58 | *umc2221* |
| | 416 | 234 | 399.57 | *csu615b* |
| | 417 | 182 | 410.6 | *umc1993** |
| | | 182 | 412.3 | *bnlg2190** |

| Chromosome 10 | | | | |
|---|---|---|---|---|
| BIN | BAC FPC: Contig | CB | Genetic IBM | Locus |
| | | 217 | 412.3 | *dmt102a* |
| 10.07 | | 446 | 437.6 | ***bnl7.49a(hmd)**** |
| | | 514 | 444.8 | *umc1196** |
| | | 570 | 449.3 | *bnlg1677** |
| | 418 | 56 | 450.8 | *AY110016** |
| | | 237 | 464.6 | *mmp181** |
| | | 237 | 466.4 | *bnlg1839** |
| | 419 | 17 | 483.69 | *umc1249* |
| | | 105 | 483.69 | *umc2203* |
| | | 162 | 483.7 | *umc1640* |
| | | 169 | 483.7 | *umc1877* |
| | | 169 | 483.7 | *umc2172* |
| | | 192 | 483.7 | *bnlg1450** |
| | | 212 | 483.7 | *gln1* |
| | | 468 | 505.5 | *umc2021** |
| | | 473 | 505.5 | *crr2* |
| | | 473 | 505.5 | *umc1645* |
| | | 569 | 505.51 | *bnlg1518* |
| | | 575 | 505.51 | *umc1113* |
| | | 598 | 505.52 | *bnlg1185* |
| | 420 | 194 | 525.03 | *umc1038* |
| | | 202 | 527.3 | *umc1556* |
| | 421 | 261 | 509.9 | *AY109829** |

# Press Releases-8

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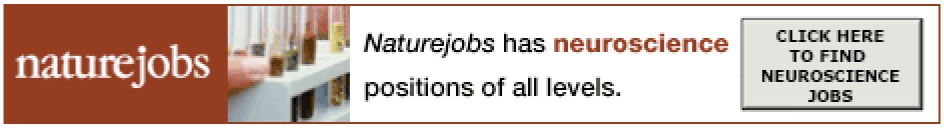
December 2003 Vol 4 No 12 HIGHLIGHTS



*Nature Reviews Genetics* **4**, 932 (2003); doi:10.1038/nrg1236

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[722K]

WEB WATCH

# Maize genetics and genomics database

Nick Campbell

http://www.maizegdb.org

MaizeGDB is undoubtedly the 'must-bookmark' one-stop shop for anyone with an interest in maize genetics.

The user-friendly web interface makes it easy to navigate through the large array of tools and resources. You can search through compilations of BACs, ESTs, probes, QTLs, phenotypes, references and so on — almost any data set you can think of that is related to maize genetics. All of these resources are provided with a layman's summary of what they are.

Tools that can be sourced through MaizeGDB include the genome browser, which provides a slick means of accessing BACs, ESTs, microsatellites and sequences from any given region of the 10 maize chromosomes, as well as a maize-specific BLAST search engine. Educational resources that are relevant to maize are also collated on the site. These resources provide some nice basic background information on maize in general, and maize genetics in particular.

It is some of the added extras on the site that show that the MaizeGDB team have gone the extra mile in an attempt to achieve their stated aim of presenting maize genetic resources "in a way that creates intuitive biological connections for the researcher with minimal effort". Examples include the online tutorial and the downloadable PowerPoint presentation for introducing new users to the database. They have also flagged their intent to make the site as responsive as possible to the community it serves through a short but pithy survey, which they encourage users to fill in, together with jobs and meetings notice boards.

Finally, if the site itself is not enough to satisfy a 'maizeophile's' thirst for information, you can also sign up for regular e-mail newsletters.

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IOWA STATE UNIVERSITY
Biotechnology Update
April 2005
Volume XIX, Issue 2
A publication of the Iowa State University Office of Biotechnology

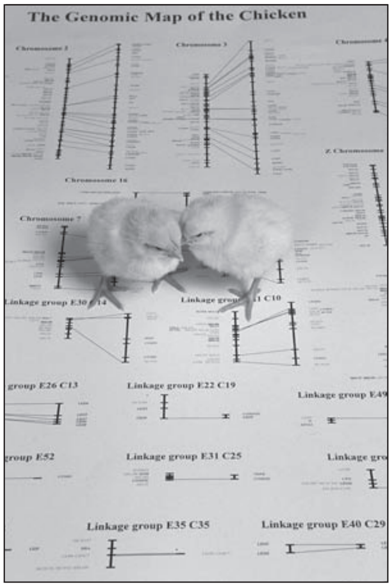
## In This Issue:

# ISU Selected as a National Resource for Agricultural Genomics

Iowa State University researchers have a long history of gathering genomic information, organizing it and making it available to other scientists. This tradition of scientific excellence and sharing is a major reason the university was chosen by the US Department of Agriculture (USDA) to lead database coordination for the National Genetics Resource Program.

James Reecy of Iowa State University has been named the USDA's US Bioinformatics Coordinator. He oversees the website that houses the six animal genome databases that are supported by the USDA's National Research Sponsored Program 8 (NRSP-8). The databases are located online at http://www.genome.iastate.edu/. The site includes genome databases for aquaculture, chicken, sheep, pigs, horses and cattle. The site has tools and tutorials for gene sequence and quantitative trait loci (QTL) studies.

"ISU already had a history of creating and maintaining databases because of Max Rothschild's pioneering work in swine. We already hosted the cattle, pig and chicken databases at ISU, so it was a logical choice for the USDA to select ISU to host the additional databases," says Reecy.



*Chicks atop a picture of a genomic map of a chicken. Photographer Peggy Greb, USDA-ARS.*

A full time programmer administers the site, constantly making updates. Early feedback indicated that researchers found the site useful, but they were interested in working with more sequences simultaneously. The site already has been expanded to fill that request.

"One of the best attributes of the databases is that the information is entirely independent. Researchers from around the world are adding information to the database and, in turn, using it in their work," Reecy says. "An unexpected benefit of the online databases has been that researchers in developing countries are able to access this information for the first time."

Key university partners with ISU in this effort include Auburn (aquaculture), Texas A&M (cattle), Kentucky (horse), Michigan State (chicken), and Utah State (sheep).

As a further result of ISU's excellence and experience with genome database technology, the USDA chose the university to house the Plant Germplasm and Information Management Unit of the Agricultural Research Service. Four new USDA positions will be filled in the next six to nine months, with appointments in agronomy and plant pathology.

The Maize (Corn) Genetics and Genomics Database (MaizeGDB located at http://www.maizegdb.org and housed at ISU) is one of the oldest genetic databases in the world. Ed Coe, with the USDA-ARS and the University of Missouri at Columbia, was the editor of the maize newsletter during the early 1990's. He also was responsible for creating a database containing the information from the newsletters. In their time, the database and its web interface were cutting edge technology, but they eventually became outdated. The original database was sent to ISU in the hope that Volker Brendel's team of biologists and computer scientists could bring the database and web interface up-to-date. Under Brendel's direction, a team including Trent Seigfried and Darwin Campbell made MaizeGDB the successful and useful resource that it is today.

*(cont. on page 2)*

(cont. from page 1)

Carolyn Lawrence is the current lead scientist on the MaizeGDB project. "The database we have today is the result of a community of maize geneticists working together over decades. It is a composite of everybody's work, rather than that of a single group."

There are many plant databases developing independently at ISU. BarleyBase is a plant microarray data resource that supports 11 plant microarray platforms. BarleyBase houses gene expression data along with experiment information. The database is led by Julie Dickerson and Roger Wise and located online at http://www.barleybase.org/.

SoyBase is the central repository for data about soybean genetics, genomics, pathology and almost all other research topics concerning soybean. The genetic maps are the central organizing theme of the database, with the rest of the data organized by subject. The SoyBase project is led by Randy Shoemaker and is located online at http://www.soybase.org/.

PlantGDB, led by Brendel and managed by staff scientist Qunfeng Dong, is located at http://www.plantgdb.org. PlantGDB is an NSF-funded project to develop plant species-specific databases, to provide web-accessible tools and inter-species query capabilities and to provide genome browsing and annotation capabilities.

The ARS Plant Germplasm and Information Management Unit of the USDA-ARS will bring these and other plant databases together in one center. Central organization through the Plant Germplasm and Information Unit will allow researchers, hardware specialists and programmers to learn database techniques from each other to more efficiently improve and advance the databases.

## Biotechnology News

### *New Website Resource for ISU-Industry Partnerships*

Iowa State University has a wealth of resources to help biotechnology businesses through all phases of development. The university offers, among others, business and technical assistance, business incubators and physical space, instrumentation and service facilities and a research park. Now, information for all of these services is found in one place – the Industry Relations website, online at www.industry.iastate.edu.

The site is the result of a six-month project by the Industry Coordination Effort (ICE). The focus of the site is to provide access to all of the university's business resources in one user-friendly interface. Each of the Systems for Innovation links on the left side of the page has a facilitator who can be contacted for further information.

There are links for R & D agreements, strategic partnering, philanthropy, research, faculty and staff expertise, success stories, events, newsletters, tip sheets, recruitment and more.

### *Iowa State Agricultural Research Among Most Cited Worldwide*

*Based on a news release by Ed Adcock, ISU Agriculture Communications*

Over the past decade, Iowa State University was the 10th most-cited institution in the world in agricultural sciences, according to In-Cites, a web site that tracks the use of scientific information that is mentioned in research papers worldwide.

From January 1, 1994, to June 30, 2004, Iowa State ranked 10th among all institutions and fifth among the world's universities. Among American universities, ISU ranked fourth, preceded by the University of California-Davis, the University of Wisconsin and Cornell University. According to In-Cites, scientists cited 1,196 agricultural science papers created at Iowa State 8,340 times over the decade.

"The fact that researchers are citing Iowa State agricultural research results to such a degree speaks volumes on the quality of our science and that it is in areas of vital concern," said Catherine Woteki, dean of the College of Agriculture and director of the Iowa Agriculture and Home Economics Experiment Station. The Experiment Station administers faculty research programs that support Iowa's agriculture, natural resources, family and consumer programs at Iowa State.

In-Cites is an editorial component of Essential Science Indicators, a web resource that helps researchers analyze research and track trends in science worldwide. The top 20 institutions listed were chosen from among 298 government agencies and universities. The report can be found at: http://in-cites.com/institutions/agr_1994-2004.htm

## Upcoming Events

**May 18** — Biotech Mixer
11:00 a.m. - 4:30 p.m. HNI Corporation, Muscatine
Registration information available at
www.industry.iastate.edu/biotechmixer/biotechmixerVIII.html

**July 13** — Economic Development Open House
9:00 a.m. - 3:30 p.m. Iowa State University. For more information contact Lora Bierbaum, lora@iastate.edu

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# News & Events

## Here's One A-MAIZE-ing Website

The Maize Genetics and Genomics Database offers loads of information on traits, gene sequences and other features of this diverse and crucial plant species.

By Luis Pons
December 15, 2005

Need some detailed data on the genetics and genomics of maize? Then the Agricultural Research Service (ARS) and Iowa State University (ISU) have just the website for you.

The Maize Genetics and Genomics Database, also known as the MaizeGDB, offers loads of information on the traits, genetic sequences and other related features of maize (*Zea mays* L. ssp. *mays*), including those aspects having to do with breeding and crop improvement.

The site is a portal to cutting-edge research on this staple crop, as well as to landmark work done decades ago. It also provides contact information for more than 2,400 cooperative researchers, along with web-based tools for ordering items such as maize stocks and cloned sequences.

MaizeGDB was developed by geneticist Carolyn Lawrence and information technology specialists Trent Seigfried and Darwin Campbell at ARS' Corn Insects and Crop Genetics Research Unit in Ames, Iowa, in collaboration with ISU researcher Volker Brendel in Ames and geneticist Mary Schaeffer of ARS' Plant Genetics Research Unit in Columbia, Mo.

According to Lawrence, the site presents maize information in a way that clearly summarizes biological relationships, and features easy-to-use computational tools. With it, a researcher can connect how a plant looks to the genetic sequences responsible for causing its phenotype.

Lawrence explained that maize is much more than a source of food for both people and livestock worldwide. It's also used in the manufacture of diverse commodities including glue, paint, insecticides, toothpaste, rubber tires, rayon and molded plastics. It is also the nation's major source of ethanol.

MaizeGDB is the successor to, and encapsulates the data from, two pioneer databases devoted to maize research: the Maize Database (MaizeDB), started by former ARS geneticist Ed Coe in 1991, and ZmDB, which was launched by the National Science Foundation-funded Maize Gene Discovery Project (MGDP).

The MaizeGDB website can be accessed at http://www.maizegdb.org/.

ARS is the U.S. Department of Agriculture's chief in-house scientific research agency.

[Top]
Last Modified: 12/15/2005

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U.S. Department of Agriculture Agricultural Research Service July 2006

# Agricultural Research

Solving Problems for the Growing World

## Phytase Reinvented, p. 14

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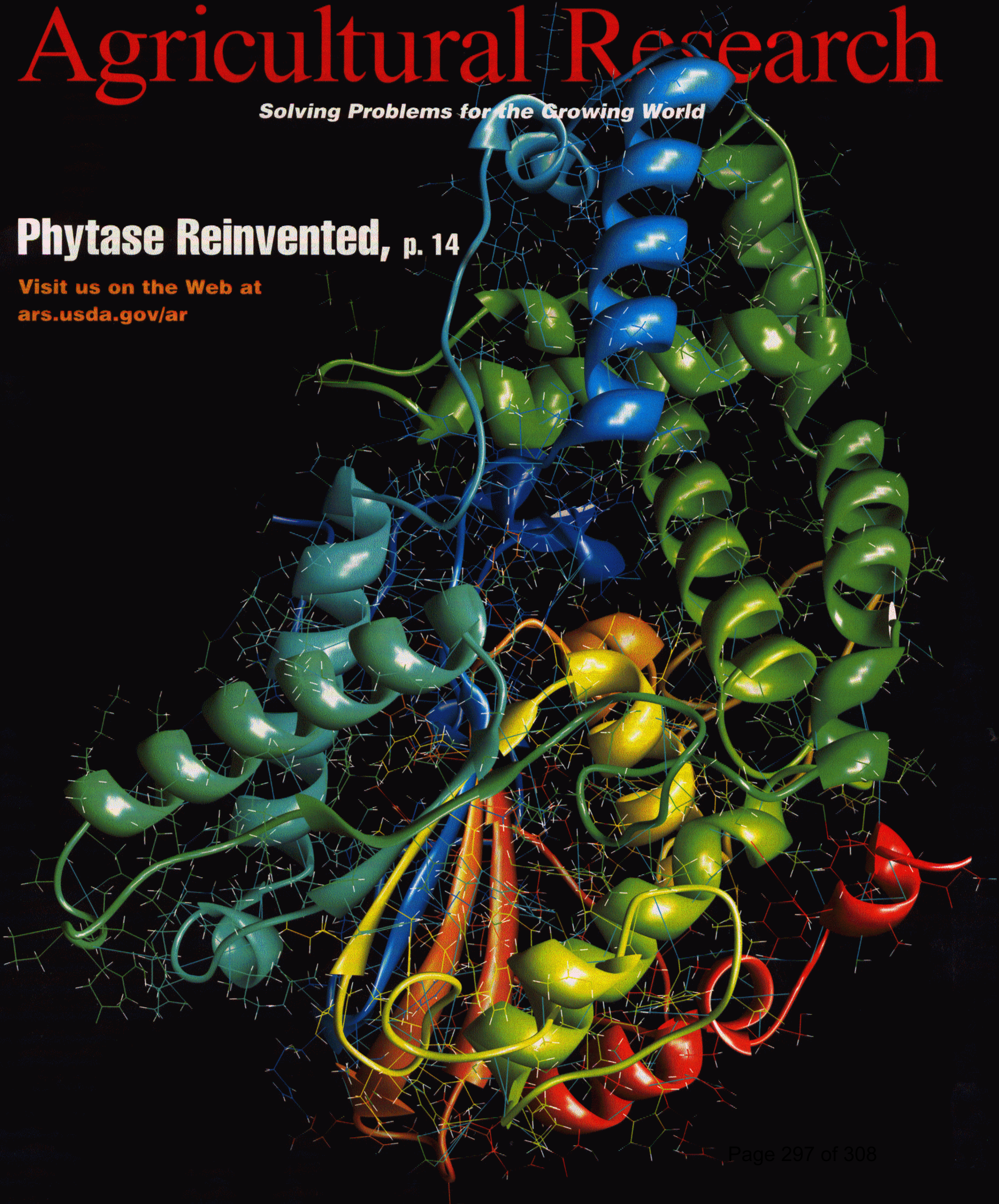

# Science Update

## Fresh Strawberries for Winter Holidays!

It's now possible for growers in the mid-Atlantic area to harvest in early winter, and again in spring, from June-bearing strawberries. And the berries that ripen into December will bring premium prices!

This new production method requires rooting runner tips collected from mother plants in early July and planting them as 8-week-old transplants in early September. These new plantlets will flower and fruit during autumn, yielding ripe berries for fresh-market sales into December, and possibly beyond. In those places where freezing might be a danger, inexpensive plastic tunnels are used to protect the fruit, which also speeds the harvest of spring-season berries. *Fumiomi Takeda, USDA-ARS Appalachian Fruit Research Station, Kearneysville, West Virginia; phone (304) 725-3451, ext. 212, e-mail ftakeda@afrs.ars.usda.gov.*

## An Amazing Corn-Based Website

Here's a one-point source to tap to find everything there is to know about maize—that is, *Zea mays* ssp. *mays,* the Latin name for today's corn. The Maize Genetics and Genomics Database, or MaizeGDB, offers information on traits, genetic sequences, and other features of this valuable staple crop, including those related to its breeding and improvement. Few realize that, in addition to corn's extensive food and feed use, research has facilitated its use in products as diverse as glue, paint, insecticides, toothpaste, rubber tires, rayon, and molded plastics. It's also the major feedstock for domestic ethanol production.

Developed in collaboration with Iowa State University-Ames, MaizeGDB gives free access to an amazing array of information in a way that summarizes biological relationships, and it features easy-to-use computational tools. To access MaizeGDB, go to www.maizegdb.org. *Carolyn J. Lawrence, USDA-ARS Corn Insects and Crop Genetics Research Unit, Ames, Iowa; phone (515) 294-7380, e-mail triffid@iastate.edu.*

## Boosting Ethanol Production—With Shiitakes?

The ability of shiitake mushrooms to dissolve the fallen logs that they call home may one day speed conversion of farm-based feedstocks into ethanol for fuel. That's because scientists have found and copied a shiitake gene, called *Xyn11A,* that lets the mushroom produce an enzyme known as xylanase. This enzyme helps convert decaying wood into sugars that shiitakes use for food.

In the laboratory, researchers successfully transferred the gene into a yeast, which was then able to produce xylanase—something it can't normally do. Next they'll try to modify the *Xyn11A* gene so it enables the yeast—or some other organism—to make more of the xylanase enzyme in less time. Such a boost in efficiency might one day help make production of plant-based fuels an even more practical alternative to petroleum products. *Charles C. Lee, USDA-ARS Bioproduct Chemistry and Engineering Research Unit, Albany, California; phone (510) 559-5858, e-mail clee@pw.usda.gov.*

KEITH WELLER (K3024-19)

**Shiitake mushrooms.**

## Honey Bees Get a New Antibiotic

Pity the poor honey bee. It works so hard—pollinating the trillions of blossoms that eventually develop into billions of dollars worth of U.S. farm crops. Yet this tireless worker is vulnerable to some pests and diseases that have made its future—and agricultural economics—somewhat perilous. One of these perils is American foulbrood, a widespread and devastating bacterial disease of honey bees. It kills young bee larvae and turns their remains into dark, shriveled corpses, or "scales," that contain billions of spores that easily spread. While the disease poses no human danger, severe outbreaks can weaken or kill entire bee colonies.

The bacterium responsible for this bee carnage, *Paenibacillus larvae,* has developed resistance against the one antibiotic that's been effective against American foulbrood. Recently, however, a new one, tylosin tartrate (TYLAN Soluble), produced by Elanco Animal Health of Greenfield, Indiana, was approved for use by the U.S. Food and Drug Administration after research demonstrated its field efficacy and safety for both honey bees and humans. *Mark F. Feldlaufer, USDA-ARS Chemicals Affecting Insect Behavior Laboratory, Beltsville, Maryland; phone (301) 504-8637, e-mail feldlaum@ba.ars.usda.gov.*

## Reducing High Harvest Costs

While modern combines efficiently harvest, thresh, separate, and clean grains, the expensive mechanisms for performing these operations can bring the total purchase cost to $250,000 per combine. Now there's an alternative that relies on a simple, low-cost harvesting unit and a stationary thresher. The system components are much less expensive, and one thresher could significantly lower overall production costs by serving several farms.

This harvester strips wheat heads and stores them in a bulk tank while a flail mower chops standing residue into small pieces to facilitate later field operations. The thresher separates wheat from chaff. An assessment is under way to determine the feasibility of using a fluidized bed to segregate the harvested material by density. Early studies suggest that this method could improve grain quality consistency, especially with soft white wheat. *Mark C. Siemens, USDA-ARS Columbia Plateau Conservation Research Center, Pendleton, Oregon; phone (541) 278-4403, e-mail markc.siemens@oregonstate.edu.*

***What's New***

Colletti named senior associate dean

Donations fund new wells in Uganda

More news ...

Adventures in summer science

New Student Application Information ▾

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Ed Adcock, Web site editor

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# *Adventures in summer science*

**By Brandon Scott, Ag Communications Intern**

**Previous features:**
Research propels student toward goal

Student researches auto-steering

Making gas from grass

Increasing the swine bottomline

## Native American interns' research projects go beyond science

Delbert Thompson isn’t your typical summer science intern. He’s 47 years old, married, has five children and he hopes one outcome of his research will be a lasting effect on his religion.

***Delbert Thompson***

“I am Lakota, of the Minneconjou band from the plains of South Dakota, I was attending Haskell Indian Nation University in Lawrence, Kan., studying environmental science and one of my professors handed me an application for Iowa State’s George Washington Carver Summer Internship Program,” Thompson said. “I had just taken a genetics class, which I really enjoyed, and the program sounded interesting.”

The George Washington Carver (GWC) Summer Intern Program is designed to give students, especially under-represented populations, the opportunity to conduct scientific research. The program is spearheaded by the College of Agriculture, and named after Iowa State’s first African-American graduate, faculty member and one of ISU’s most famous alumni.

The George Washington Carver program has brought 39 students from various institutions across the country to Iowa State University for an eight-week program that has matched them up with Iowa State faculty mentors from various departments.

Thompson is one of six Native American students participating in the GWC Summer Internship program. The students are taking part in an ongoing study conducted by Carolyn Lawrence, a USDA collaborator and assistant professor in the departments of agronomy and genetics, development and cell biology. The program is funded by a grant from the National Science Foundation awarded to Volker Brendel, an Iowa State professor in genetics, development and cell biology.

Thompson is assisting Lawrence, director of the maize genetics and genomics database, and Von Mark Cruz, a postdoctoral student in agronomy, in researching the genetic makeup of Native American corn populations.

“We are looking for genetic sequences in an effort to keep the fifty-fifty purple-to-yellow color ratio in the corn,” Thompson said. “For American Indians, the research goes beyond science. The color is symbolic and has religious and spiritual meanings. ”

Alexandra Volker agrees. Volker is a senior at Iowa State with a double major in biology and history and a minor in French. She also is researching southwestern maize. Like Thompson, Volker, in addition to the quest for knowledge, has another motive for taking part in the research.

***Alexandra Volker***

“I am one-eighth Cherokee,” Volker said. “There is a story among the Cherokee of a type of maize called Sacred Eagle corn that had white kernels crowned with purple spots, that strain of maize no longer exists.

My grandmother told me the year the settlers appeared the eagle flew away and only white kernels were left behind. I would like to help bring our purple corn back."

The research Thompson and Volker are conducting is part of an effort by the U.S. Department of Agriculture's Agricultural Research Service (USDA-ARS) to maintain genetic diversity of plants and enter germplasm information into a public database. The research focuses on a genetic abnormality that threatens the genetic diversity of southwestern maize, which would affect various phenotypes, including kernel color.

Cruz explains that by using genetic markers the researchers plan to develop a means to identify the Abnormal Chromosome 10 (Ab10) in maize.

“This is a component of the project that aims to ultimately get molecular fingerprints of the maize germplasm donated by Native American Indian tribes to the U.S. National Plant Germplasm System,” Cruz said. “Once these fingerprints are generated, it will be possible for tribe members to submit inviable kernels of corn for similar analyses. By matching the fingerprints from the inviable kernels to those of the seeds in the National Plant Germplasm System, plants once lost from the tribes' collections can be restored.”

“Part of our goal is to determine if there are molecular markers that are associated with the Abnormal Chromosome 10,” Cruz said. “Then its impact on the diversity of southwest maize collections held by the North Central Regional Plant Introduction Station here at Iowa State can be evaluated.”

The National Plant Germplasm System hopes to maintain diversity not only for cultural purposes, but also to protect the world's crops. The world's food supply relies on genetic uniformity, but this uniformity increases plant susceptibility to pests and disease.

“Data generated, as well as information describing cultural practices involving those plants, are stored and made accessible through a website created by two other summer interns,” Lawrence said. “Students are working with Candice Gardner, Mark Widrlechner and other USDA-ARS and North Central Regional Plant Introduction station scientists and staff, which consists of both ARS and Iowa State personnel, to learn about the principles of plant genetic conservation, to grow and propagate the plants, evaluate and characterize specific traits and collect and preserve plant material. The students also are using molecular markers in the lab to characterize the southwest maize accessions (germplasm).”

The researchers are working with tribal elders to log the genetic information of their maize, much like a plant encyclopedia.

“An advisory council made up of tribal elders has been involved in this process, and each elder traveled to Ames to work with the students,” Lawrence said. “In this manner, the elders' hopes for the students have been conveyed alongside the outcomes anticipated by the students' research mentors."

When his internship is over, Thompson plans to return home to Overland Park, Kan., and continue his education at Haskell Indian Nation University, and possibly take it a step further.

"The George Washington Carver program has caused me to think about agriculture, genetics and possibly graduate school here at Iowa State," Thompson said. "I have been impressed with the school and the program. Without the opportunity the program offered, and the support of my wonderful wife, Cynthia, I would not have had the venue to make those decisions."

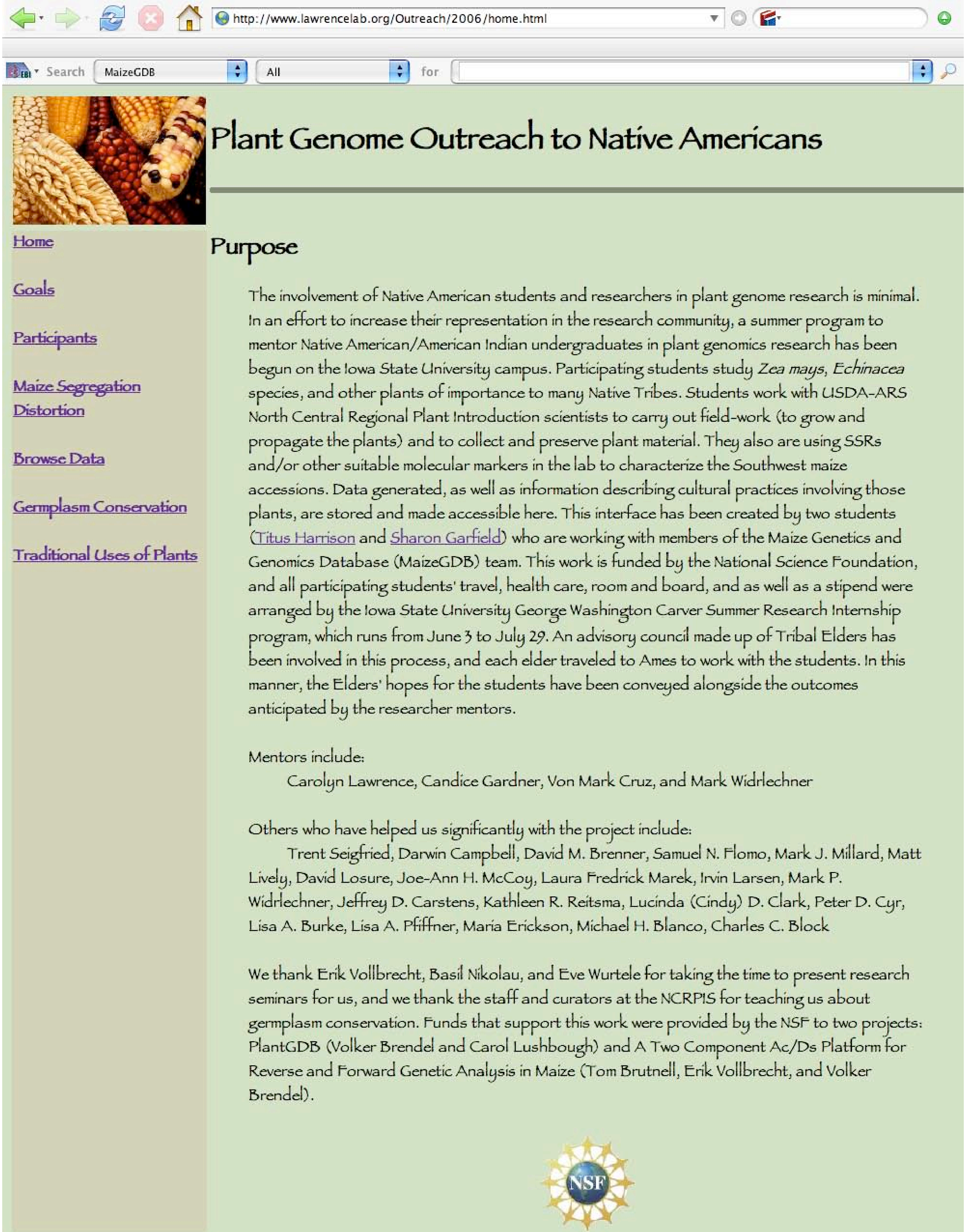
Volker will continue with classes at Iowa State and pursue further education after her graduation next spring.

"I'm looking forward to Chinese and Russian history in the coming year," Volker said. "But when shopping for a graduate school, I will be looking at genetics and infectious disease programs."

They may have entered from different walks of life, but both interns say they have enjoyed their summer in Ames and at Iowa State, participating in the George Washington Carver Internship program. Whether in the fields getting samples or in the lab running tests, both said they would remember the experience and make use of what they have learned.

To read more about the project and browse student generated data, visit its website.

Learn more about the George Washington Carver Summer Internship program.



# Plant Genome Outreach to Native Americans

## Purpose

The involvement of Native American students and researchers in plant genome research is minimal. In an effort to increase their representation in the research community, a summer program to mentor Native American/American Indian undergraduates in plant genomics research has been begun on the Iowa State University campus. Participating students study *Zea mays*, *Echinacea* species, and other plants of importance to many Native Tribes. Students work with USDA-ARS North Central Regional Plant Introduction scientists to carry out field-work (to grow and propagate the plants) and to collect and preserve plant material. They also are using SSRs and/or other suitable molecular markers in the lab to characterize the Southwest maize accessions. Data generated, as well as information describing cultural practices involving those plants, are stored and made accessible here. This interface has been created by two students (Titus Harrison and Sharon Garfield) who are working with members of the Maize Genetics and Genomics Database (MaizeGDB) team. This work is funded by the National Science Foundation, and all participating students' travel, health care, room and board, and as well as a stipend were arranged by the Iowa State University George Washington Carver Summer Research Internship program, which runs from June 3 to July 29. An advisory council made up of Tribal Elders has been involved in this process, and each elder traveled to Ames to work with the students. In this manner, the Elders' hopes for the students have been conveyed alongside the outcomes anticipated by the researcher mentors.

Mentors include:
Carolyn Lawrence, Candice Gardner, Von Mark Cruz, and Mark Widrlechner

Others who have helped us significantly with the project include:
Trent Seigfried, Darwin Campbell, David M. Brenner, Samuel N. Flomo, Mark J. Millard, Matt Lively, David Losure, Joe-Ann H. McCoy, Laura Fredrick Marek, Irvin Larsen, Mark P. Widrlechner, Jeffrey D. Carstens, Kathleen R. Reitsma, Lucinda (Cindy) D. Clark, Peter D. Cyr, Lisa A. Burke, Lisa A. Pfiffner, Maria Erickson, Michael H. Blanco, Charles C. Block

We thank Erik Vollbrecht, Basil Nikolau, and Eve Wurtele for taking the time to present research seminars for us, and we thank the staff and curators at the NCRPIS for teaching us about germplasm conservation. Funds that support this work were provided by the NSF to two projects: PlantGDB (Volker Brendel and Carol Lushbough) and A Two Component Ac/Ds Platform for Reverse and Forward Genetic Analysis in Maize (Tom Brutnell, Erik Vollbrecht, and Volker Brendel).

# Questions-9

## A few questions to get the Working Group started on the creation of the guidance document:

1. How often should the Working Group meet?
2. Where should the Working Group meet?
3. When and how should membership in the Working Group turn over?
4. Does the ARS-approved budget look appropriate given our charge?
5. Should the IT staff (Trent and Darwin) attend scientific meetings? What about the new hire at PGEC who will be a Category 3 scientist?
6. How should the POPcorn proposal be changed?
7. Should each data center's search tools have a link to an "Advanced Search" page? If so, please name persons to work with to develop example queries.
8. Should MaizeGDB create the infrastructure to store the official gene models for maize?
9. Should MaizeGDB provide training sessions for researchers? If so, when and where?
10. Should MaizeGDB be involved in the relatively new adoption of Web services for sharing data?
11. Should the MaizeGDB lead scientist be actively or tangentially involved in the ISU effort to develop a proposal for the NSF Cyberinfrastructure request for proposals?
12. How should MaizeGDB work to encourage the use of the Community Curation Tools?
13. Should MaizeGDB develop bulk upload tools and/or data templates? If so, for which data types and in what order?
14. Should the computation of the various IBM maps be continued?
15. Many researchers are confused by the various IBM maps. How should they be presented to minimize confusion?
16. The data modeling and upload of the TILLING group's first data set took up about two full weeks' time for C. Lawrence, and at least 2 days each for T. Seigfried and D. Campbell over the course of three months, and that was just for the first dataset (which did not include phenotypes). Should MaizeGDB require that contributors of large data sets make available funds for MaizeGDB? If so, how can this be handled, especially for existing projects where no funds were set aside but data are being contributed?

# Appendix-10

USDA

**United States Department of Agriculture**

Research, Education and Economics
Agricultural Research Service

August 30, 2006

SUBJECT: Permission to Drive and/or Ride in a Federal Vehicle

TO: File

FROM: Leslie C. Lewis Leslie C. Lewis
USDA, ARS, MWA
Corn Insects and Crop Genetics Research Unit

Drs. Doreen Ware, Marty Sachs, Mary Schaeffer, Kay Simmons, Steve Shafer, and Ed Buckler are employees of the USDA-ARS who will be on official travel status in Ames, Iowa. They will be in Ames to attend a MaizeGDB Working Group Meeting along with other scientists. This meeting is being hosted by the Corn Insects and Crop Genetics Research Unit (CICGRU). This document serves as notification that these USDA-ARS scientists are permitted to drive the CICGRU's federal vehicles.

This memo is to give permission for these people to drive a federal vehicle:

Drs. Doreen Ware, Marty Sachs, Mary Schaeffer, Kay Simmons, Steve Shafer, and Ed Buckler.

This memo is to give permission for these other MaizeGDB Working Group Meeting participants to ride as passengers in a federal vehicle:

Lisa Harper, Anne Sylvester, Karen Cone, Volker Brendel, Mike Freeling, Owen Hoekenga, Lukas Mueller, Pat Schnable, and Tom Slezak.

ars

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