maizeGDB
Maize Genetics and Genomics Database

MaizeGDB data types, tools, genomes and how to use them

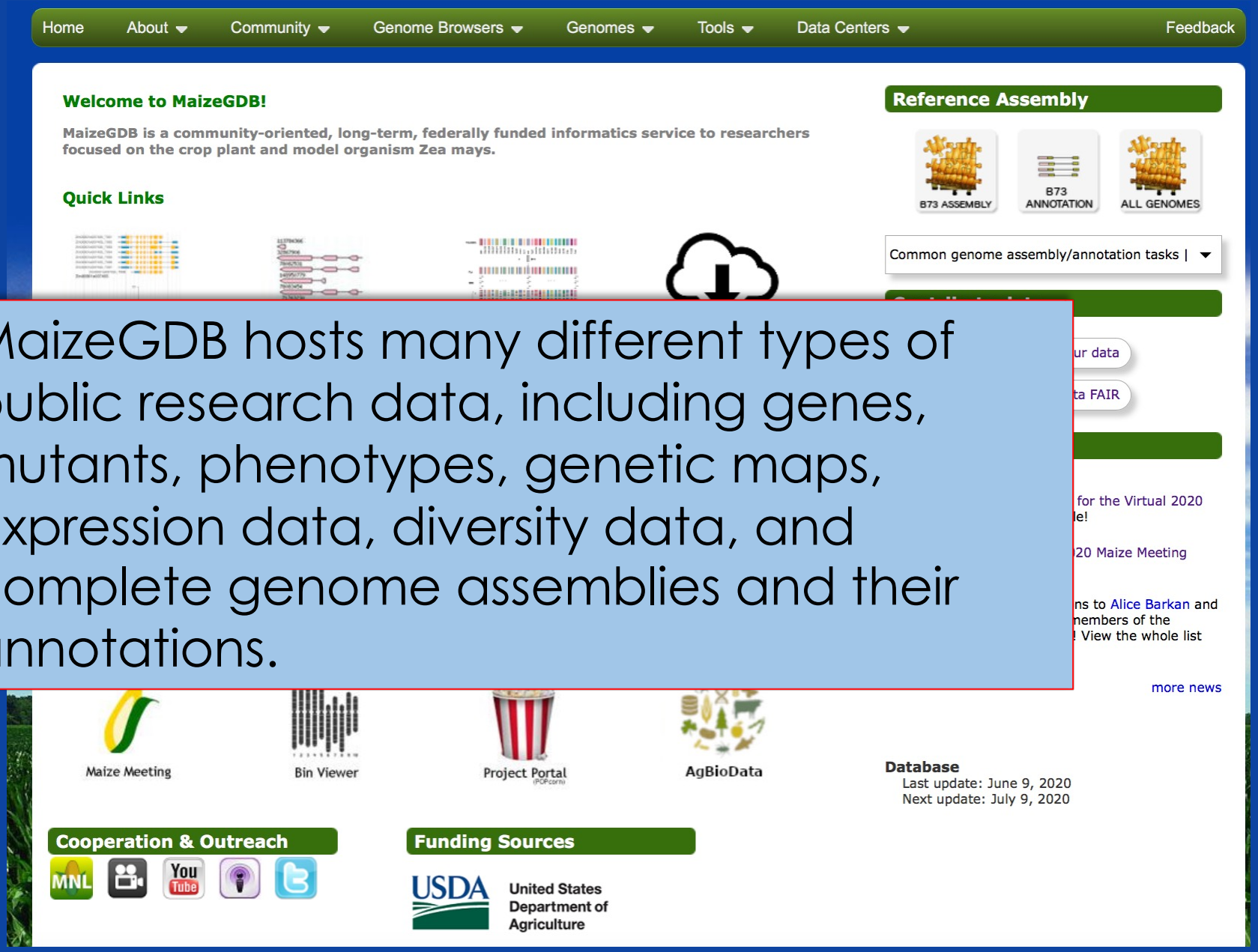
Lisa Harper, June 24, 2020

maizeGDB
Maize Genetics and Genomics Database

Outline

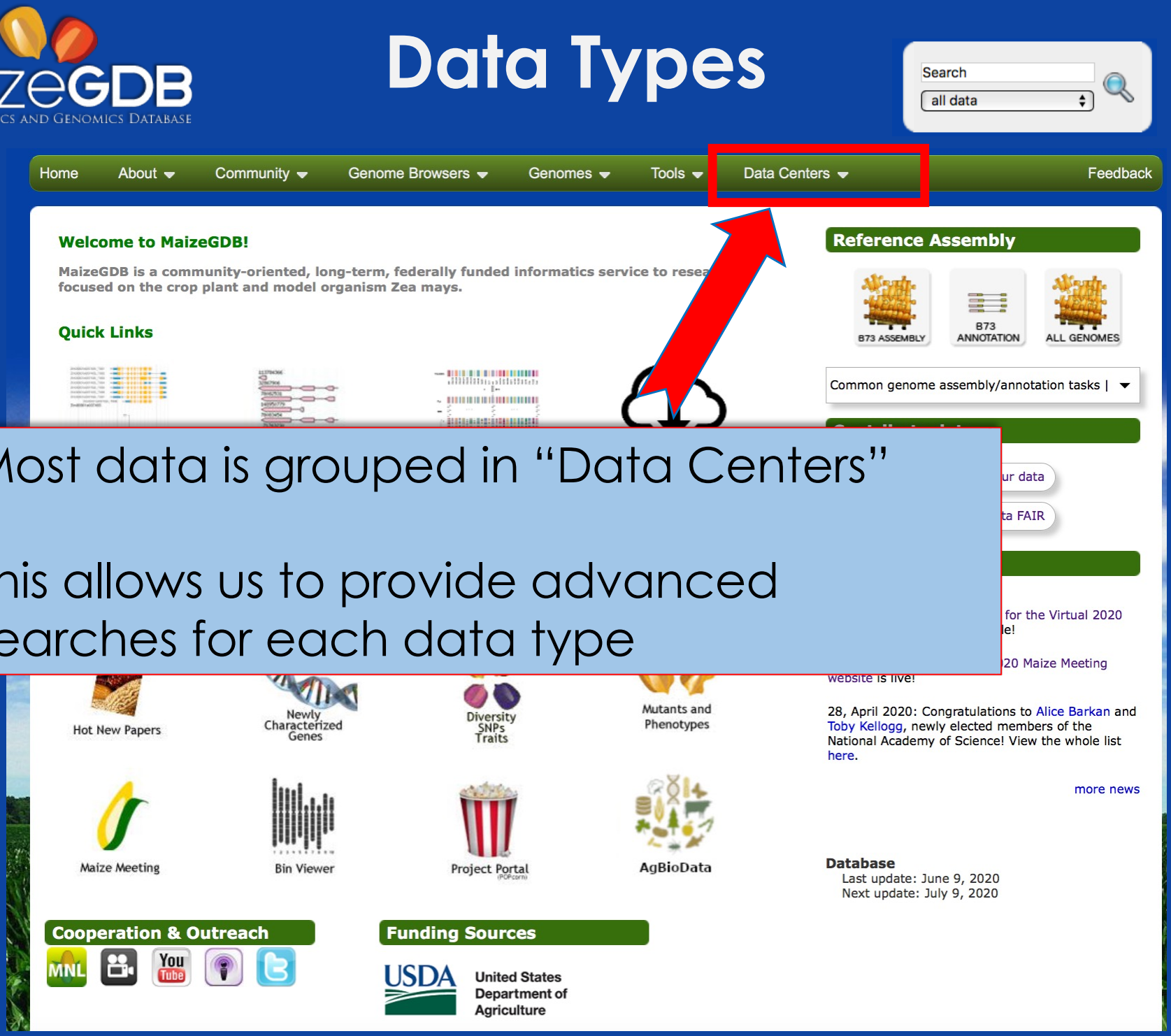
1. Data Types and how to find them
2. Tools and what they do
3. Gene and Gene Model pages
4. Genomes and JBrowse
5. Your questions answered

Data Types



MaizeGDB hosts many different types of public research data, including genes, mutants, phenotypes, genetic maps, expression data, diversity data, and complete genome assemblies and their annotations.

Data Types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MaizeGDB is a community-oriented, long-term, federally funded informatics service to resea
focused on the crop plant and model organism Zea mays.
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This allows us to provide advanced searches for each data type
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Data Centers

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Expression	Molecular Markers
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Genomes	Stocks

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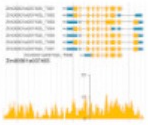
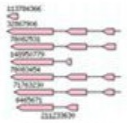
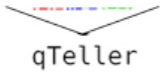

JBrowse


GBrowse

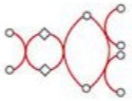

NAM Genomes


Downloads


BLAST




MaizeMine


Metabolic Pathwa


Hot New Papers


Newly Characterized Genes


Diversity SNPs Traits


Mutants and Phenotypes


Maize Meeting


Bin Viewer


Project Portal


AgBioData

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Genes/Gene Model DataCenter

Genes/Gene Model DataCenter

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Report an assembly error | Report a gene model error

Home > Gene

Gene Data In MaizeGDB

Search
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- Advanced gene/gene model search
- Search for Gene Models by sequence
- Translate Gene Model IDs

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- Download Sequence for Gene Model List
- Gene Model Annotations and Orthologs
- Gene Models with Associated Genes
- UniformMu and other insertion data sets
- Complete gene model cross references
- Older gene model downloads

Information
- About the current gene model set
- Image of Gene Model frequency
- Gene symbol list
- Top 20 genes
- NCBI B73_v4 annotation release 101
- Classical Maize Genes
- Nomenclature guidelines
- Gene Model Terms
- Gene Models With Issues

Discussion of Gene Data

Gene model FASTA | Gene model GFF | Gene proteins at GenBank | MAKER-P gene models (v3)

Note: The current B73 and NAM gene model annotations are part of a two-set release process. The first sets of models were generated from RNA-seq and refined using evidence from B73 full-length cDNAs and EST data. These represent high-quality gene models. These annotations will be augmented with a second set of gene models combining both ab-initio prediction and evidence. The second set of gene models are targeted for release in March 2020 or upon publication of the data manuscript.

Simple Search: This search form allows you to enter basic information (locus name, Gene Model ID, Transcipt ID, Translation ID, Gene symbol, Gene name), including partial names, to search for a gene and/or gene model.
Use the wildcards '%' or '' to find matches that contain your search term. '^' at the beginning of search term will find matches that start with that term. '$' at the end of search term will find matches that end with that term.*

Submit (see a sample gene model query or locus query)

Limit number of results to 100 (upper limit on results is 2,000 records)
Display 25 records per page.

More Examples: lg1, liguleless1, Zm00001d002005, GRMZM2G036297, DAA35605, Zm00001d002005_T001

Shortcuts to sections in the gene/gene model data center.

Genes/Gene Model DataCenter

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Advanced Search

Check the boxes next to the fields you want to search; if you just want to find records that have *any* value for that attribute, check the box and leave the criteria alone.

Show only genes:

- ☐ from this **gene model set:** Zm00001e.1-Zm-B73-REFERENCE-NAM-5.0
- ☐ of this **type:** All types
- ☐ on this **chromosome:** All chromosomes
- ☐ between and
- ☐ associated with a **gene locus**
- ☐ that produce this **gene product:** Any gene product
- ☐ that have this **phenotype:** Any phenotype
- ☐ that are associated with this **trait:** Any trait

Advanced Search

Submit Clear

☑ Limit number of results to 100 (upper limit on results is 2,000 records)

Genes/Gene Model DataCenter

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Search for Gene Models by Sequence

Enter sequence, Genbank IDs or gene model names (Zmdddddaddddd, ZEAMMB73_xxxx or GRMZMxx

- (•) Nucleotide
- ( ) Amino acid

Select a target dataset

Submit

BLAST against gene models

Translate Gene Model IDs - download

Enter list - 8,000 gene model limit: (Example list)

Enter gene model list here.

Translate to:

Zm00001e.1

Submit

Translate gene model ids between different assembly versions and genomes.

Alternatively, download the full gene model associations list between v3 and all other assemblies in our database

Download By Region and Gene Model Set

assembly coordinates

Gene model set: Zm00001e.1-Zm-B73-REFERENCE-NAM-5.0 Chromosome: Chromosome 1

Model type: any Data type: All Genes/Gene Models

Start position: End position:

(enter positions w/o commas or spaces, or leave both empty for entire chromosome)

marker

Start: End:

Assembly: Zm-B73-REFERENCE-NAM-5.0

Enter two markers to get gene models within the spa
on the same chromosome. Only applicable for assem
markers.

Assembly Annotation Positions

Enter List - 8,000 gene model limit (Example list)

Enter a list of Gene Models, Transcripts, and/or Proteins to retrieve their positions on a given assembly in a tab-delimited format.

Output type: Gene/gene model names only Submit

Get coordinates and associated markers for a set of gene models

Download Sequence for Gene Model List

When downloading sequence please specify which type of input you are entering. For genomic please use the g
name (e.g. GRMZM2G165390). For cDNA, CDS, and mRNA please use the transcript ID (e.g. GRMZM2G16539
protein please use the translation ID (e.g. GRMZM2G165390_P01). If you enter only the gene model ID, pleas
want to see all transcripts or only the canonical transcripts.

Enter list - 8,000 gene model limit: (Example list)

Enter gene model list here.

Input type: Gene Model ID

Output type: Sequence: genomic

Submit

Download sequence for a set of gene models.

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Reference gene model releases

Gene models for the B73 genome assembly are provided at both MaizeGDB and Gramene. Nomenclature guidelines for gene models, as agreed to by the maize research community, indicate that gene model sets are named with the associated assembly identifier. For the B73 reference genome, this is Zm0001d. Gramene, which manages these gene models uses a different versioning system.

Bold font indicates the current official gene model set.

Version	Gramene Version	Date	Changes
Zm00001e.1			
	v38/56 - v43/61	12/7/17 - 3/15/19	Changes limited to gene models outside the reference set (ENSRNA, ncRNA, and inferred organelle gene models)
	v37/55	09/21/17	3722 new non-coding gene models, using non-standard prefix, "ENSRNA"; 2318 ncRNA gene models have changed transcripts
Zm00001d.2	v36/54	06/07/17	transcripts changed for 28 miRNAs
	v35/53	04/02/17	published in Nature; transcripts changed for 547 gene models
	v34/52	12/14/16	transcripts changed for 28 miRNAs
	v33/51		174 Mt and Pt gene models added, transcripts changed for 3127 gene models
Zm00001d.1	v32/50	09/28/16	inital release

Gene Model Functional Annotations and Orthologs

Gramene.org: Functional Annotations (B73 RefGen_v2 only)
Phytozome: Functional Annotations (B73 RefGen_v3 and v4; log-in required)
Freeling Lab: Syntenic Orthologs (mapped to RefGen_v2)

Gene Models with Associated Genes

(B73 RefGen_v3 and Zm-B73-REFERENCE-GRAMENE-4.0, aka B73 RefGen_v4)

Classical Genes:	table	tab delimited
MaizeGDB curated genes:	table	tab delimited
All associated genes:	table	tab delimited

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All associated genes:	table	tab delimited

UniformMu and other insertion data sets

UniformMu
About the UniformMu project

W22 to B73 cross-reference:
Excel spreadsheet

Genomic coordinates for Zm-B73-REFERENCE-GRAMENE-4.0 (aka B73 RefGen_v4):
Release 9 Excel spreadsheet
Release 9 Excel spreadsheet with gene structure

List of gene models from the B73 RefGen_v3 Filtered Gene Set that have UniformMu insertions:
Release 8 Excel spreadsheet

List of gene models from the B73 RefGen_v2 Filtered Gene Set that have UniformMu insertions including 100 bp upstream or downstream:
Release 7 Excel spreadsheet
Release 8 Excel spreadsheet

List of gene models from the B73 RefGen_v2 Filtered Gene Set that have UniformMu insertions in exons:
Release 7 Excel spreadsheet
Release 8 Excel spreadsheet

Ac/Ds/GFP-Ds
Insertions validated by Warner et al., 2010

Zm-B73-REFERENCE-NAM-5.0/Zm00001e.1 Information

In-depth metadata for Zm-B73-REFERENCE-NAM-5.0 is available here.
See the paper for B73 RefGen_v1 here, and for Zm-B73-REFERENCE-GRAMENE-4.0 here.

Ac/Ds/GFP-Ds
Insertions validated by Warner et al., 2010

Zm-B73-REFERENCE-NAM-5.0/Zm00001e.1 Information

In-depth metadata for Zm-B73-REFERENCE-NAM-5.0 is available here.
See the paper for B73 RefGen_v1 here, and for Zm-B73-REFERENCE-GRAMENE-4.0 here.

Gene model counts are preliminary.

Counts for each chromosome.

Chromosome	Accession	Protein Coding	miRNA	Transposable Element	Low Confidence
Chromosome 1	LR618874.1	5905	14		2209
Chromosome 2	LR618875.1	4737	22		2209
Chromosome 3	LR618876.1	4737	16		1571
Chromosome 4	LR618877.1	4115	20		1826
Chromosome 5	LR618878.1	4480	24		1681
Chromosome 6	LR618879.1	3290	11		1223
Chromosome 7	LR618880.1	3108	10		1193
Chromosome 8	LR618881.1	3561	13		1288
Chromosome 9	LR618882.1	2973	7		1191
Chromosome 10	LR618883.1	2684	17		1034
Unmapped		319	0		357
Nuclear Total		39,324	154		15,516

Annotations: Zm00001e.1

Zm-B73-REFERENCE-GRAMENE-4.0/Zm00001d Stats

Gene Feature	Value
Average protein-coding transcript size	7638 bp
Average low confidence transcript size	6981 bp
Average transposable element size	*unavailable*
Average Exon size	156 bp
Average Number of exons per gene	4 exons
Maximum exons per gene	81 exons (Zm00001d040166)
Average Intron size	578 bp
Average Coding region size	207 bp

Top 20 genes

These are the most searched-for genes in 2017

1 lg1*
2 mati1
3 br2
4 vp1
5 o2
6 wx1
7 bz1
8 tb1
9 o2
10 sh2
11 lg1
12 pl1
13 sh1
14 kn1
15 ae1
16 su1
17 fea3
18 p1
19 b1
20 rap2

* lg1 is the example gene name in the gene search page

NCBI B73_v4 annotation release 101

The NCBI B73_v4 annotation release 101 was developed independently at NCBI using the NCBI Eukaryotic Genome Annotation Pipeline on B73 RefGen_v4. The final set of annotated features comprises, in order of preference, pre-existing RefSeq sequences and a subset of well-supported Gnomon-predicted models. It is built by evaluating together at each locus the known RefSeq transcripts, the features projected from curated RefSeq genomic alignments and the models predicted by Gnomon.

The NCBI B73_v3 annotation release 100 is available here.

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The NCBI B73_v3 annotation release 100 is available here.

Image of gene model frequency for Zm-B73-REFERENCE-GRAMENE-4.0 (Click image for larger view)

Gene Model Terms

Associated Genes: Associated Genes are genes that have been linked to a gene model by hand curation.

Canonical: The canonical transcript is defined as either the longest CDS, if the gene has translated transcripts, or the longest cDNA. Note: a canonical transcript is not always the first transcript (T01) or the longest transcript.

Non-canonical. All other transcripts for a gene model that are not the canonical transcript.

Evidence Type: The source of evidence to support the gene model.

Model Types:
Protein Coding A gene model with supporting evidence.
miRNA small, non-coding RNA.
TE Transposable elements.
Low Confidence A gene model with little or no supporting evidence.
WGS. (Versions 5a.59 and earlier) Working Gene Set. This set merges new annotations performed on RefGen_v2 with RefGen_v1 4a gene models mapped onto V2. New annotations were achieved by an evidence-based method (Gramene GeneBuilder) and complemented with de novo Fgenesh models performed on masked DNA.
FGS: (Versions 5b.60 and earlier) Filtered Gene Set. The filtered set was generated by screening the working set to remove pseudogenes, TE-encoded genes, and low-confidence hypothetical models.

Transcript Classes:
WH. With homology to a known non-transposable element in the NR (non-redundant) database at GenBank. Protein-coding gene.
NH. No homology in the NR (non-redundant) database at GenBank. Hypothetical gene or pseudogene.
TE. With homology to a known transposable element (TE) in the NR (non-redundant) database at GenBank. Transposable element.

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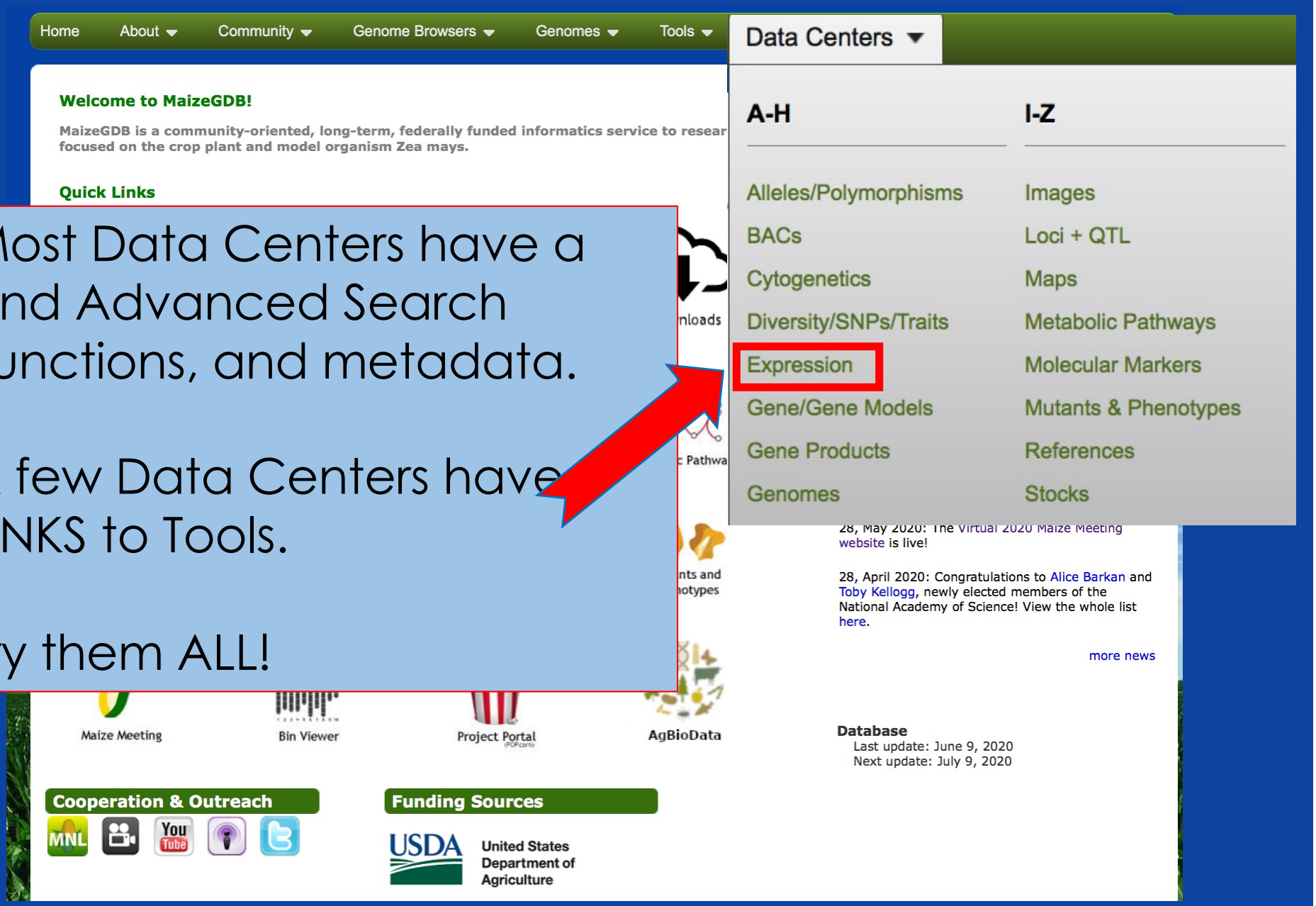
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A few Data Centers have LINKS to Tools.
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Expression Data Center

The Expression Data Center has links to useful tools to explore gene expression in a number of different ways

Expression Data at MaizeGDB

(Click 's below for more information.)

About expression data at MaizeGDB

MaizeGDB provides access to expression datasets, analysis, and a variety of visualization and analysis tools developed by partners and collaborators. Click the arrows to the left of the sections below to see more information about that class of expression data.

Tools for expression data

(Are we missing your favorite tool?)

CornCyc
Tutorial

eFP Browser
publication

MapMan
tutorial
publication
more

qTeller

Expression Datasets on the MaizeGDB Genome Browser

Below is a list of all expression tracks currently available on the MaizeGDB genome browser. You may select the tracks here, enter a feature name, then go to the genome browser to see that feature with your selected tracks displayed. Or you may go directly to the genome browser and select the tracks you wish under the 'Select Tracks' tab.

See list of tracks

NCBI SRA datasets for *Zea mays*

Raw expression data for re-analysis is available at NCBI's SRA database. There are currently **100377** series records for *Zea mays* in NCBI's SRA database. You can see all SRA data for *Zea mays* here.

BLAST your sequence against SRA datasets at NCBI.

Zea mays datasets at NCBI GEO

Raw expression data for re-analysis is available at NCBI's GEO database. There are currently **485** series records for *Zea mays* in NCBI's GEO database. You can see all GEO data for *Zea mays* here, including all samples and platforms as well as all series (experiments).

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Maize Genetics Meeting

The 63rd Annual Maize Genetics Conference will be held on **March 11-14, 2021**, at the Union Station in St. Louis, Missouri, USA.

The 62nd Annual Maize Genetics Meeting was cancelled due to COVID-19 and details about a virtual meeting will be forthcoming.

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Maize genetics community

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Maize Genetics Meeting

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The 62nd Annual Maize Genetics Meeting was cancelled due to COVID-19 and details about a virtual meeting will be forthcoming.

2017 2017
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MaizeGDB is the source for maize nomenclature information.

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Maize Genetics Meeting

The 63rd Annual Maize Genetics Conference will be held on **March 11-14, 2021**, at the Union Station in St. Louis, Missouri, USA.

The 62nd Annual Maize Genetics Meeting was cancelled due to COVID-19 and details about a virtual meeting will be forthcoming.

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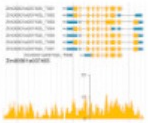
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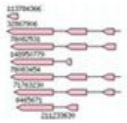
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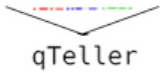
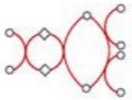



MaizeMine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Common genome assembly/annotation tasks |

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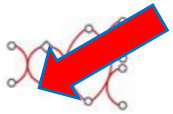
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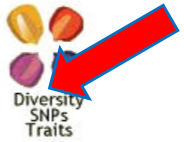
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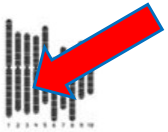
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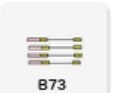
B73 ASSEMBLY


B73 ANNOTATION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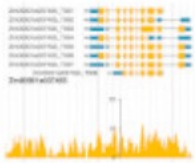
Tools: Quick links 1st row


JBrowse


GBrowse


NAM Genomes


Downloads

JBrowse: B73 v5 plus all 25 NAM founder genomes

Gbrowse: All earlier versions of B73, and all other non-NAM founder genomes, annotation sets and more

NAM Genomes: Information and links to metadata for all NAM founder line genomes

Downloads: Bulk downloads of data, including genome sequences and annotations, gene lists, etc.

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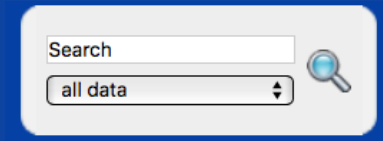
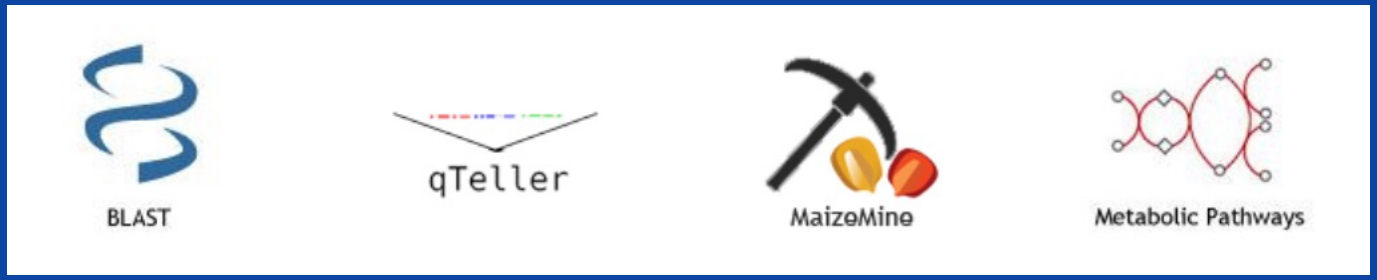
Tools: 2nd row





BLAST: All genomes and sequence sets at MaizeGDB, including annotation sets; more sequences than available at NCBI Genbank

qTeller: A tool that allows exploration of RNA expression and protein abundance for sets of genes or chromosomal regions

MaizeMine: A MINE tool that allows query of multiple types of maize data in one place

Metabolic Pathways: A tool to query the CornCyc metabolic pathway resource with gene models up to B73 v4

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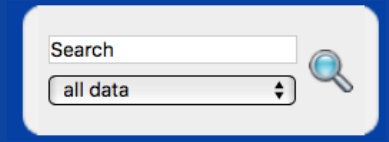
Tools: 3rd row



Hot New Papers: The MaizeGDB's Community Editorial Board's publications picks for each month

Newly Characterized Genes: new genes and new information about old genes

Diverity, SNPs, Traits: This datacenter is a portal for many tools to query the diversity of maize. Check it out!

Mutants and Phenotypes: This is a datacenter where you can search the mutant and non-mutant alleles of genes.

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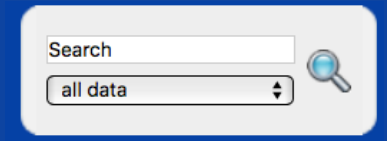
Tools: 4th row



Maize Meeting: Information about the next Maize Meeting and history of all previous meetings

Bin Viewer: View genes, QTLs and other entities based on genetic bins

Popcorn Portal: You can search Maize projects here

AgBioData: A consortium of members from >30 databases working to make biological data FAIR and consistent across databases.

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Featured tools at MaizeGDB

BLAST | MaizeMine | qTeller | CornCyc PMN (Plant Metabolic Network)

Other tools at MaizeGDB

SNPversity	Pedigree Viewer	Bin viewer
TYPSimSelector	GenomeQC	PAST

Older tools developed for B73 RefGen_v2

Incongruency	Locus lookup	Locus pair lookup

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Diversity, SNP, and Trait Data at MaizeGDB

About diversity, SNP, and trait data at MaizeGDB

MaizeGDB is working with the Schnable lab, the Panzea project, The Genome Reference Consortium, and iPlant Collaborative to create a plan for archiving, dessiminating, visualizing, and analyzing diversity data.

Please contact us if you are preparing a proposal for a project that will generate diversity data.

Search

SNPversity allows you to compare SNPs across a diverse selection of inbred lines.
Search genotype data at Panzea.
Search GBS data at Panzea.
TYPSimSelector: Sort lines from the Ames Diversity Panel based on IBS (Identity by State) score.

Types of variation data

- Single Nucleotide Polymorphisms (SNPs), including insertions and deletions.
- Copy Number Variations (CNVs).
- Presence/Absence Variations (PAVs).
- Complex alleles. (also called "alternative loci")
- Sequences which do not align to the reference genome.
- Inversion break points.
- Phenotypes.
- Germplasm via GRIN.
- Transcript assemblies and exome contigs alignments.
- Transcript assemblies and exome contigs sequences at GenBank.
- Expression data at GEO, SRA, and other repositories.
- Genetic maps.

Information for contributers

If you wish to submit diversity, SNP, or trait data to MaizeGDB, contact us.

Downloads

HapMap3 from CyVerse (Contact: Qi Sun, Cornell):
The Hapmap3 BAM files
Genotyping VCF files Raw
Genotyping VCF files Imputed
HapMap1 and HapMap2 from Panzea.

Palomero Toluqueño contigs from GenBank.
GBS v2.7 (Genotyping by Sequencing) from Panzea.
Search trait values (download all data as text)

Gene Pages

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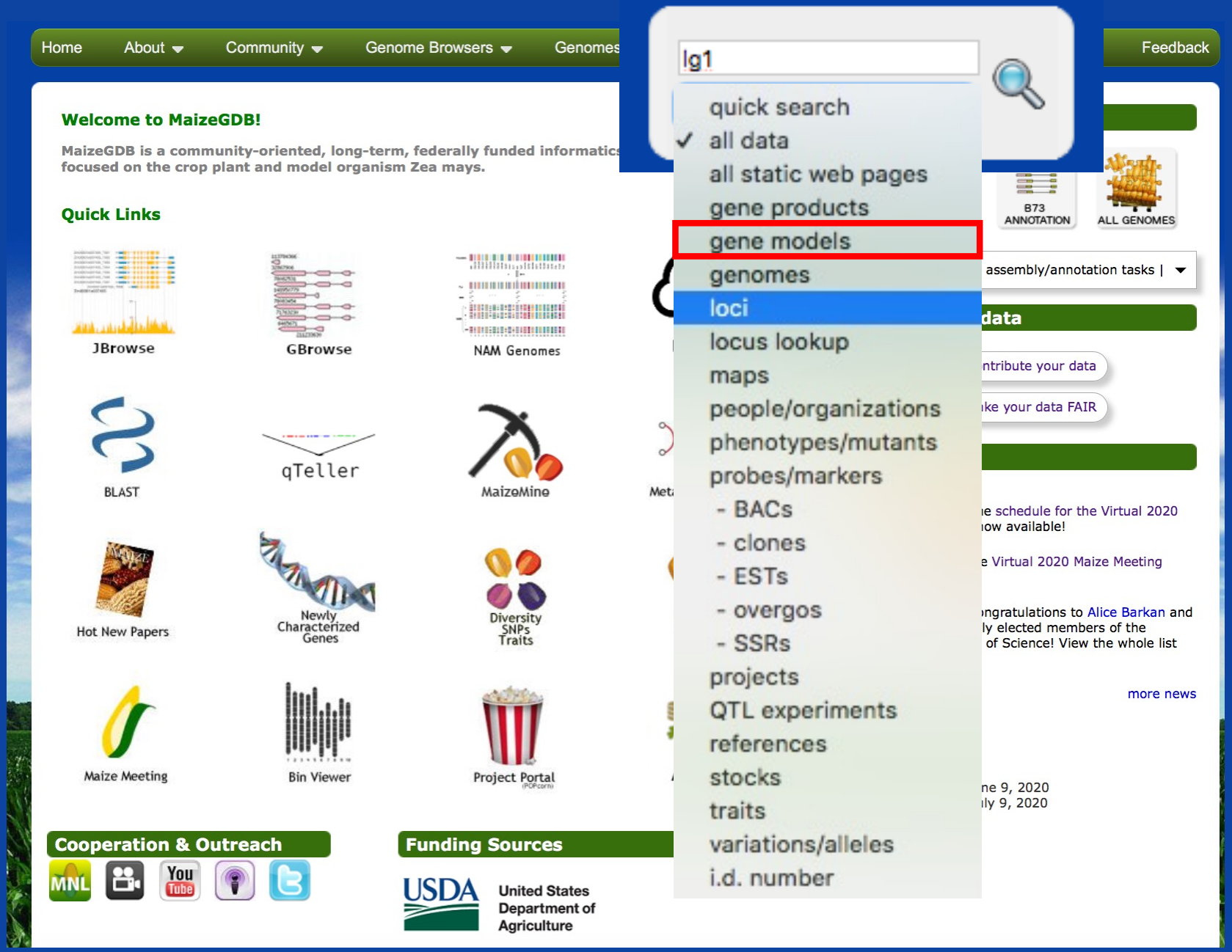
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Gene record

Report an assembly error Report a gene model error

GRMZM2G036297 (lg1 - liguleless1) [Classical Gene List]

GENE MODEL | SEQUENCE | PAN-GENE | GENETIC INFORMATION

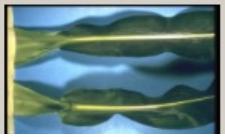
Note: A gene is a specific type of locus; the word "gene" should not be considered to be synonymous with "locus".

Gene
- Overview
- Annotations
- Map Coordinates
- Nearby Loci
- Allele/variation/polymorphism
- Genetic information
- References
- External Links

Overview
Gene name: lg1 (liguleless1)
Synonyms: ZmSBP15 (per Grassius)
Gene Products:
LG1 liguleless1 protein
SBP
UniProt accession(s):
O04003

Scroll Down

Images of expression


Captions

Allele/variation/polymorphism

lg1 (Allele)
lg1-56-3037-5 (Allele)
lg1-N2375 (Allele)
Lg1-W22 (Allele) [Links]
Lg1 (Allele)
lg1-64-4 (Allele)
lg1-PI200299 (Allele)
lg1-ZCXGRB (Allele)

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

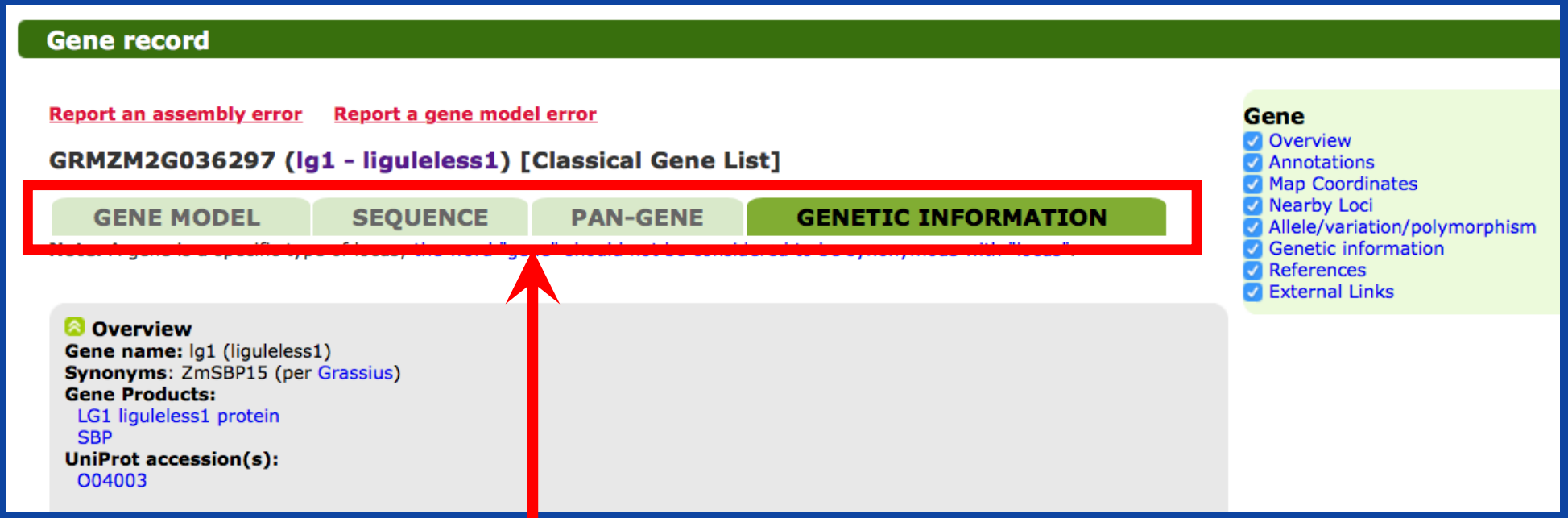
Map	Coordinate	Bin
bins 2	2.02	2.02
EBF 1935 2	0.00	2.01
Genetic 1997 2	30.00	2.01
Genetic 2 *	12.72	
Genetic 2005 2 *	13.70 +/- 1	2.02
IBM2 2005 Neighbors 2	52.11	
IBM2 2005 Neighbors Frame 2	52.11	
IBM2 2008 Neighbors 2	50.88	

Stocks:
Bold font indica
201F ws3 lg1 gl2
202A lg1-PI200299
202B lg1-PI262493
202C lg1-32TaiTaiTaSarga
202D lg1-ZCXGRB

erms

	name	qualifier	with/from	evidence	reference
GO:0003677	DNA binding		COMP		Jaiswal, P
GO:0005634	nucleus		IDA		PMID:9119226
GO:0030154	cell differentiation		IDA		PMID:25359728
GO:0040007	growth		IDA		PMID:25359728

Gene Pages



These TABs allow you to get MORE information about each gene

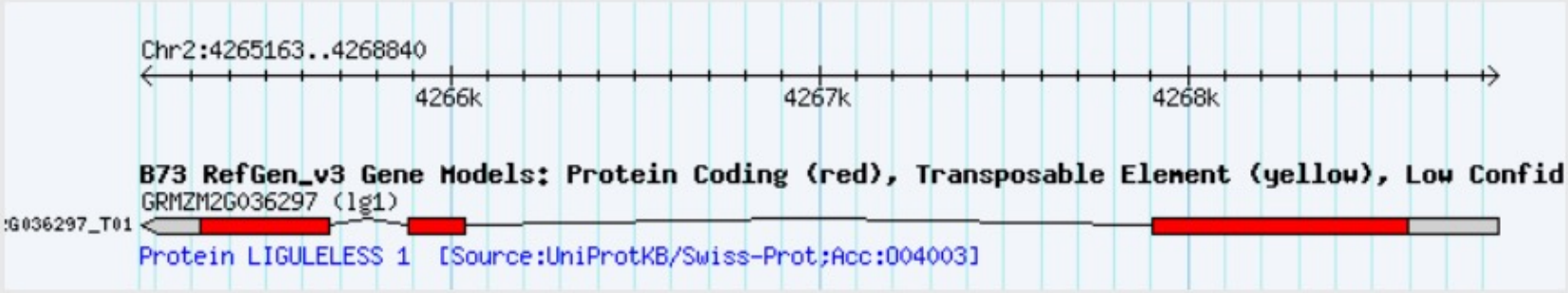
Gene Pages

GRMZM2G036297 (lg1 - liguleless1) [Classical Gene List]

GENE MODEL | SEQUENCE | PAN-GENE | GENETIC INFORMATION

Overview

Gene Model Set: , Assembly version: B73 RefGen_v3
Model Type: protein_coding
Alternative names: GenBank: ZEAMMB73_448608, ZEAMMB73_062450
NCBI Gene (Entrez Gene): 542528 ()
Line: B73
History: Introduced in gene model set 4a in assembly version RefGen_v1.
Genome Browser: (Chr2: 4263663..4270340)



Canonical Transcript: GRMZM2G036297_T01
Canonical Length: 3677bp
Canonical Protein: GRMZM2G036297_P01 (GenBank accession: DAA35605)
Metabolic Pathway: There is currently no pathway information available for this gene model.
PLAZA: GRMZM2G036297_P01 - ZM02G01890
UniProt accession(s):
GRMZM2G036297 - O04003
Orthologs (J. Schnable and M. Freeling, Schnable et al, 2012)
Sorghum bicolor (Sorghum) ortholog: Sb06g031290
Setaria italica (Foxtail millet) ortholog: Si022315m.g
Oryza sativa japonica (Rice) ortholog: LOC_Os04g56170
Brachypodium distachyon (Brachypodium) ortholog: Bradi5g24670

Gene Pages

GRMZM2G036297 (lg1 - liguleless1) [Classical Gene List]

GENE MODEL | SEQUENCE | PAN-GENE | GENETIC INFORMATION

Sequence

B73 RefGen_v3 | B73 RefGen_v2 | B73 RefGen_v1

Based on Gramene's B73 RefGen_v3 sequence

Genomic DNA for Gene Model

ID: ZEAMMB73_448608 (Gramene ID: GRMZM2G036297)

Genomic DNA

```
>GRMZM2G036297
CCACCGAGCTCTCCGCTAAGCGCTGTCCTTGCCGCCGTCCTCCCCTCCGTCCCCTACGCATCCATTTCCGTGTGCTCGTG
TGTGCGCGCGCGGGCACTCCTGCTCCTGCTCCCTCCGGCCCCTCCTCCCCTCCCAGGCTCCCAGCTAGCCGCGCCCGCCC
GCGCGACCTGCACCTGCACAGATCGGGCGGCCGGGCCGACCGATCGATCGAGATATCGTGTCAACGTGCCGGCCGGGGCG
TGGGAAGATGATGAACCTATCGGCTGCCGCCAACGGCCGCGACGAGTTCCCCCCCTACGTCGTGCCGTCCAACGCGGCCG
CTCCGCCCCCTTCCCTGCTCCCAACCATGGAGCAGCAGCAGGAGAGCAGCATCCACAGGGAGCATCATCAGCTGCTGGGC
TACAACCTCGAGGCCAACTCGCTGGCCCTCCTGCCCCCGTCCAACGCCGCCGCCGCCCACCACCACACCACCTTCGCCGG
CGGCCACAGCCCCCACGACATCCTCCACTTCTACCCTCCTCCTTCCGCCGCCTCGCACTACCTCGCCGCCGCCGGCGGCA
ACCCCTACAGCCACTTAGTCTCCGCGCCCGGGACCACCTTCCACCAGACCTCGTCGTCCTACTACCCGCCGGCGGCGGCG
GCGCAGGCCGCGCCCGAGTACTACTTCCCCACCCTCGTCAGCTCCGCCGAGGAGAACATGGCCAGCTTCGCCGCCACGCA
GCTCGGCCTCAACCTCGGCTACCGCACCTACTTCCCGCCCAGAGGAGGCTACACGTACGGCCACCACCCGCCGCGCTGCC
AGGCCGAGGGCTGCAAGGCCGACCTCTCCAGCGCCAAGAGATACCACCGTCGCCACAAGGTGTGCGAGCACCACTCCAAG
GCGCCCGTCGTCGTCACCGCCGGTGGACTGCATCAGAGGTTCTGCCAGCAGTGCAGCAGGTCAGTAGGCCACTCGGTCAT
```

BLAST DNA sequence against MaizeGDB | Download DNA sequence

Gene Pages

GRMZM2G036297 (lg1 - liguleless ... [Classical Gene List]

GENE MODEL | SEQUENCE | **PAN-GENE** | GENETIC INFORMATION

Overview

The pan-genome information displayed here is preliminary and will be replaced when the pan-genome information will be recalculated with the B73 v5 and NAM assemblies and annotations. As this is new gene model information and a new section for the gene model page, please send us comments and suggestions.

There are multiple ways to define and genera... genome annotations to group gene models b... in all annotations) and to identify orphan gen...

A **pan-gene set** is the set of gene models fr...

Datasets associated with one or more m...
MaizeGDB pan-genome, calculated by MaizeG...

Expression data is associated with one or more related genes:
Zm00001d002005

Insertion data exists for one or more related genes:
Zm00001d002005

The **NEW** "PAN-GENE" tab lists the gene models (for lg1 in this case) in other sequence assemblies

Related gene models in maize

quality	gene model(s)	set	assembly	computed by
match	**Zm00001d002005**	**Zm00001d.2**	**Zm-B73-REFERENCE-GRAMENE-4.0**	**Ware lab, Nov 2016**
syntelog	Zm00007a00011977	Zm00007a.1	Zm-B104-DRAFT-ISU_USDA-0.1	MaizeGDB, Dec 2016
syntelog	Zm00010a008419	Zm00010a.1	Zm-EP1-REFERENCE-TUM-1.0	MaizeGDB, Mar 2018
syntelog	Zm00011a008463	Zm00011a.1	Zm-F7-REFERENCE-TUM-1.0	MaizeGDB
syntelog	Zm00014a006797	Zm00014a.1	Zm-Mo17-REFERENCE-CAU-1.0	MaizeGDB, June, 2018
syntelog	Zm00009a008456	Zm00009a.1	Zm-Mo17-REFERENCE-YAN-1.0	MaizeGDB, Dec 2017
syntelog	Zm00008a006072	Zm00008a.1	Zm-PH207-REFERENCE_NS-UIUC_UMN-1.0	MaizeGDB, Dec 2016
syntelog	Zm00004b006064	Zm00004b.1	Zm-W22-REFERENCE-NRGENE-2.0	generated via SynMap by MaizeGDB

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Welcome to MaizeGDB!

MaizeGDB is a community-oriented, long-term, federally funded informa s service to researchers focused on the crop plant and model organism Zea mays.

Quick Links

JBrowse | GBrowse | NAM Genomes | Downloads

Get to the Information Page for each genome one of two ways

Hot New Papers | Newly Characterized Genes | Diversity SNPs Traits | Mutants and Phenotypes

Maize Meeting | Bin Viewer | Project Portal (POPcorn) | AgBioData

Cooperation & Outreach

Funding Sources

USDA United States Department of Agriculture

Reference Assembly

B73 ASSEMBLY | B73 ANNOTATION | ALL GENOMES

Common genome assembly/annotation tasks |

Contribute data

Contribute your data

Make your data FAIR

News

10, June 2020: The schedule for the Virtual 2020 Maize Meeting is now available!

28, May 2020: The Virtual 2020 Maize Meeting website is live!

28, April 2020: Congratulations to Alice Barkan and Toby Kellogg, newly elected members of the National Academy of Science! View the whole list here.

more news

Database
Last update: June 9, 2020
Next update: July 9, 2020

GENOMES

1. From the Genomes Data Center

GENOMES

Genome data in MaizeGDB

Genome search | Genome sets | Complete list | Nomenclature | Genomes at MaizeGDB | Definitions of terms

MaizeGDB hosts 44 genomes. To learn how to contribute your genome to MaizeGDB, click here.
The representative maize genome is **B73** and its current version is **Zm-B73-REFERENCE-NAM-5.0**.

This search form allow
for a genome assembl
Use the wildcards '%'
matches that start wit

IMPORTANT: Lists of genomes are collapsed by default. Click "+" to expand

Submit (see a sample genome query)

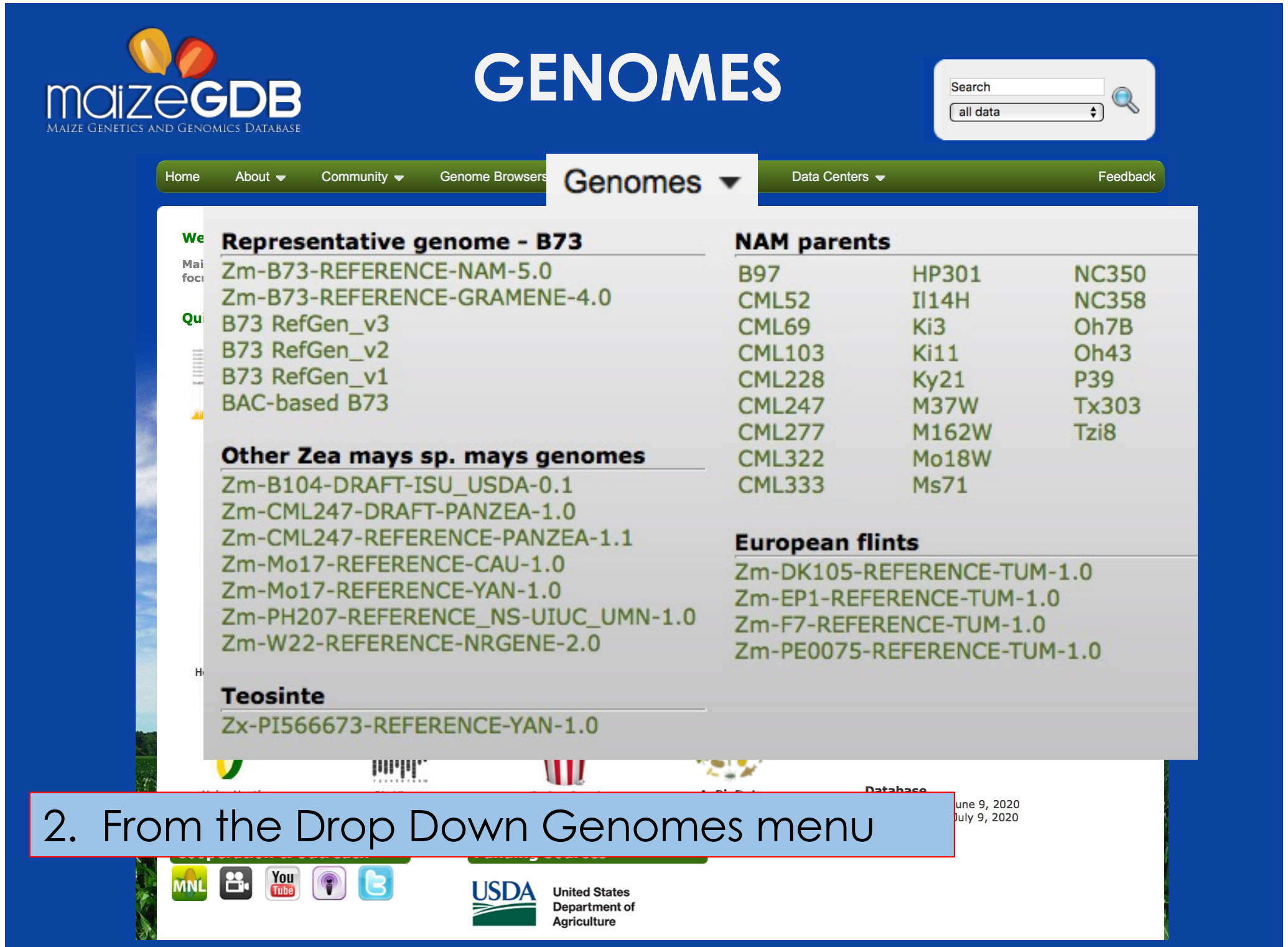
Limit number of results to 100 (upper limit on results is 2,000 records)

Genome sets
+ B73 representative reference genome (More information is available here.)
+ European flint lines, developed as part of the MAZE project
+ NAM founders, developed by the Whole-genome assembly of the NAM founders project

All genomes
+ Complete table of 44 genomes.

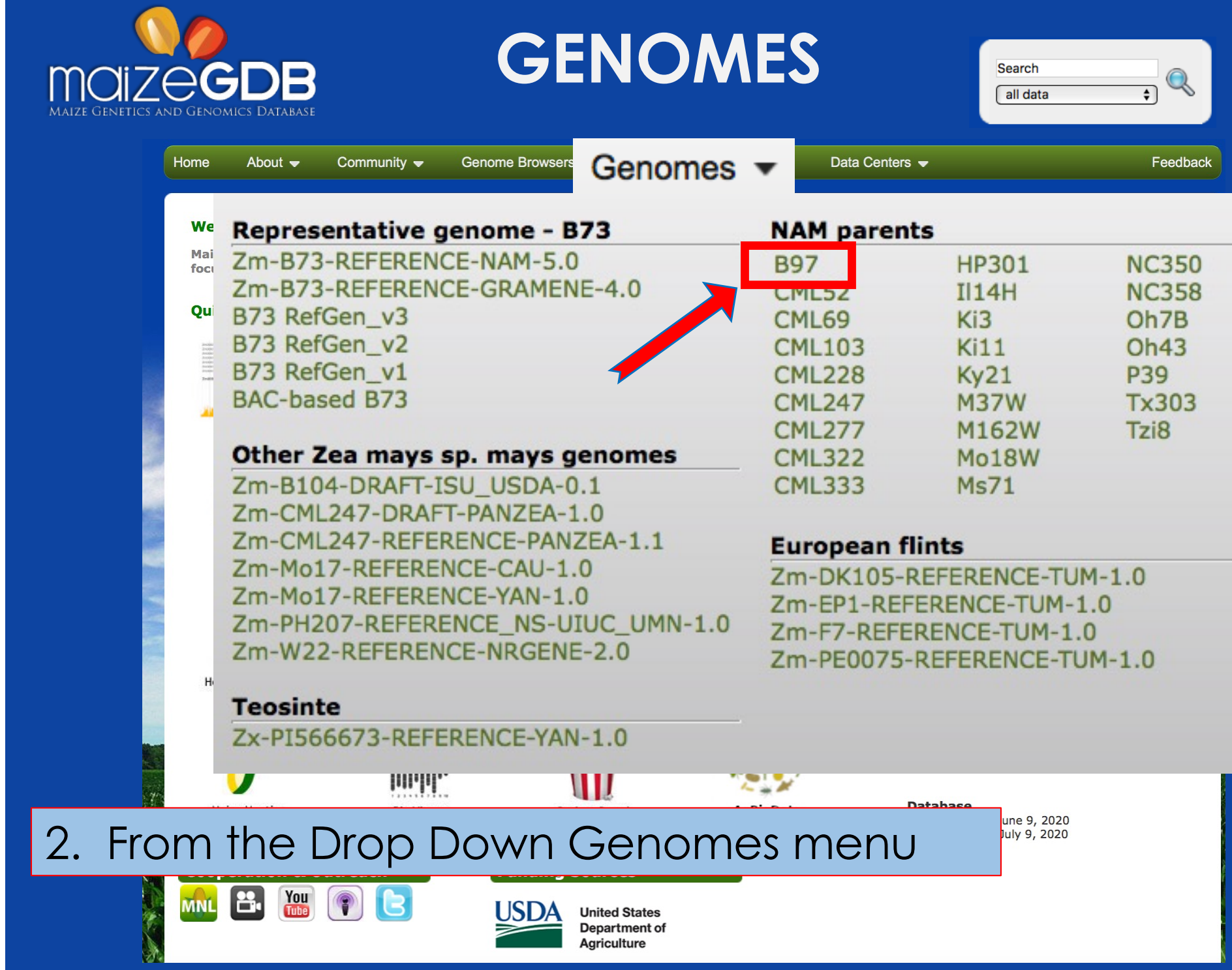
Genome assembly nomenclature
Genome assemblies are named according to the following formula:
[species abbreviation]-[cultivar or accession]-[quality]-[provider].[version]

GENOMES



2. From the Drop Down Genomes menu

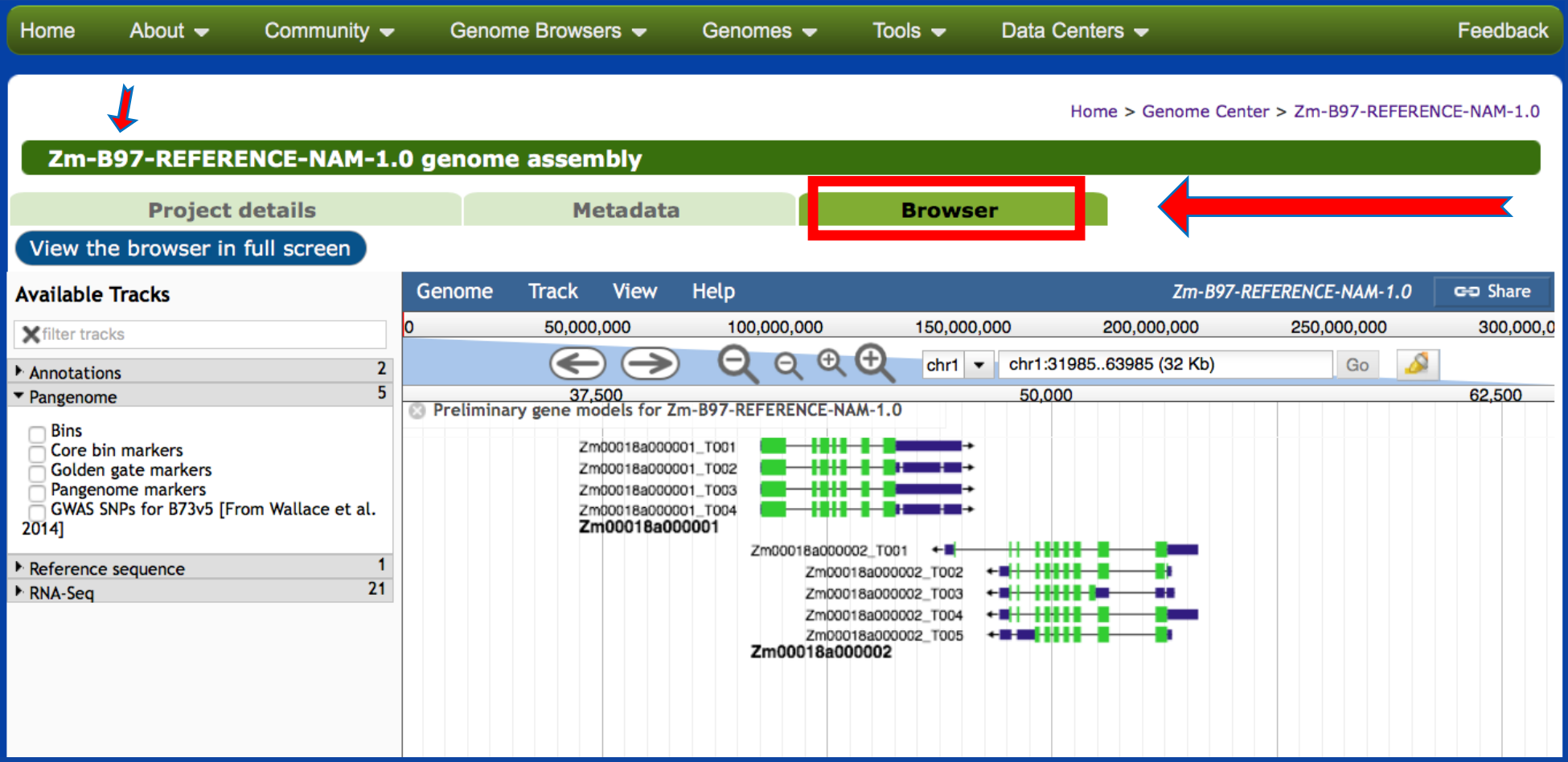
GENOMES



2. From the Drop Down Genomes menu

GENOMES

A Genome Data Page- Note Tabs!



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GENOMES

A Genome Data Page- Note Tabs!

Zm-B97-REFERENCE-NAM-1.0 genome assembly

Project Details | **Metadata** | Browser

Information about assembly Zm-B97-REFERENCE-NAM-1.0

Report an assembly error

Click here to learn about maize genome and gene model nomenclature rules.

Genome Sequencing Project Information

The sequencing and assembly of the maize Nested Association Mapping (NAM) founder lines, selected to represent a broad cross-section of maize diversity.

GenBank BioProject PRJEB31061
Project PI Kelly Dawe

Zm-B97-REFERENCE-NAM-1.0 genome assembly

Project Details | Metadata | Browser

The NAM parents sequencing project

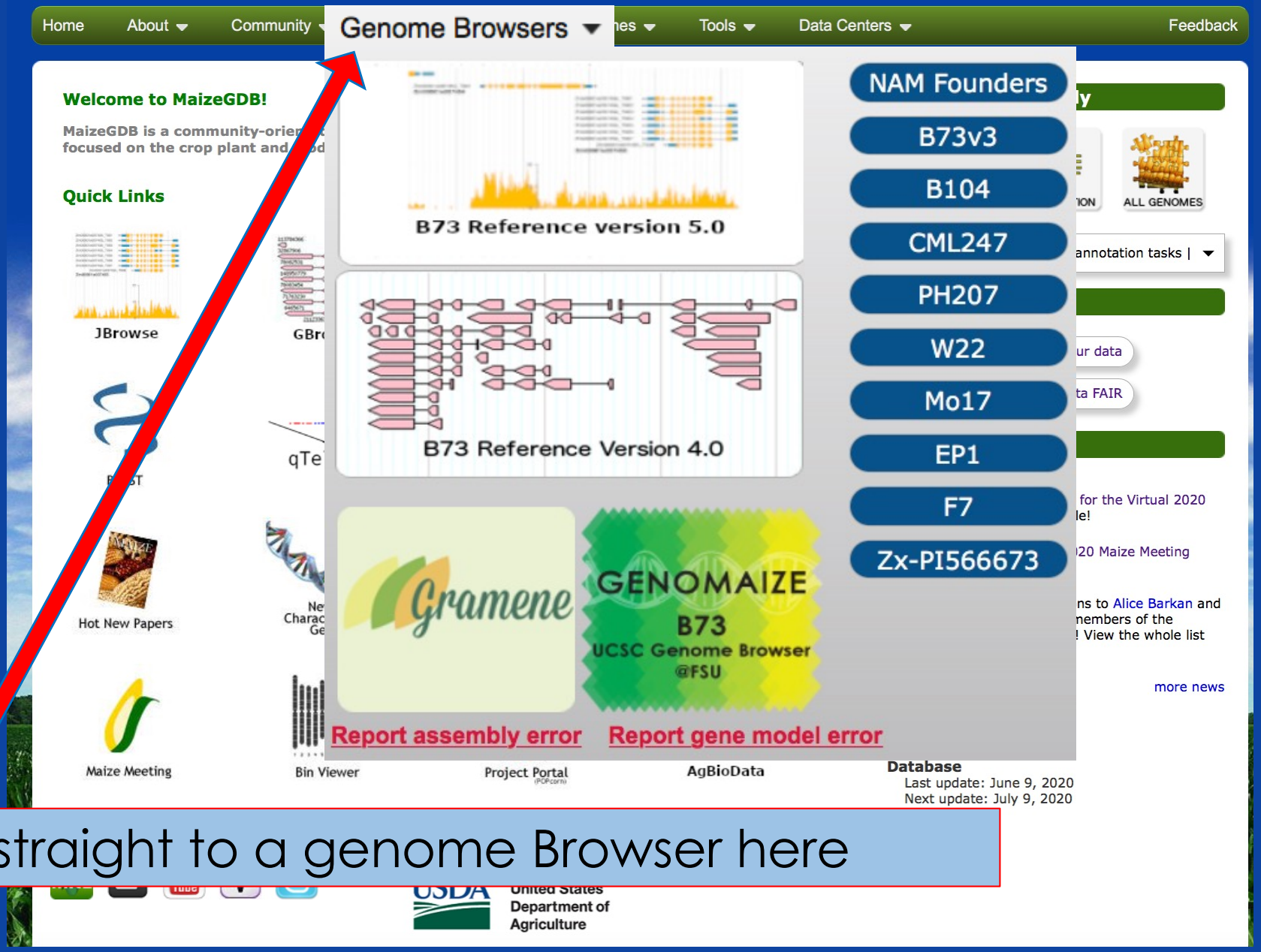
Report an assembly error Report a gene model error

NAM Consortium website: https://nam-genomes.org/

Note: These current gene model annotations are part of a two-set release process. The first set of models were generated using accession-specific RNA-seq from 10 tissues and the models obtained from these tissues were refined using evidence from B73 full-length cDNAs and EST data. These represent high-quality gene models expressed in the 10 tissues. These annotations will be augmented with a second set of gene models combining both ab-initio prediction and evidence. The second set of gene models are targeted for release in March 2020 or upon publication of the data manuscript.

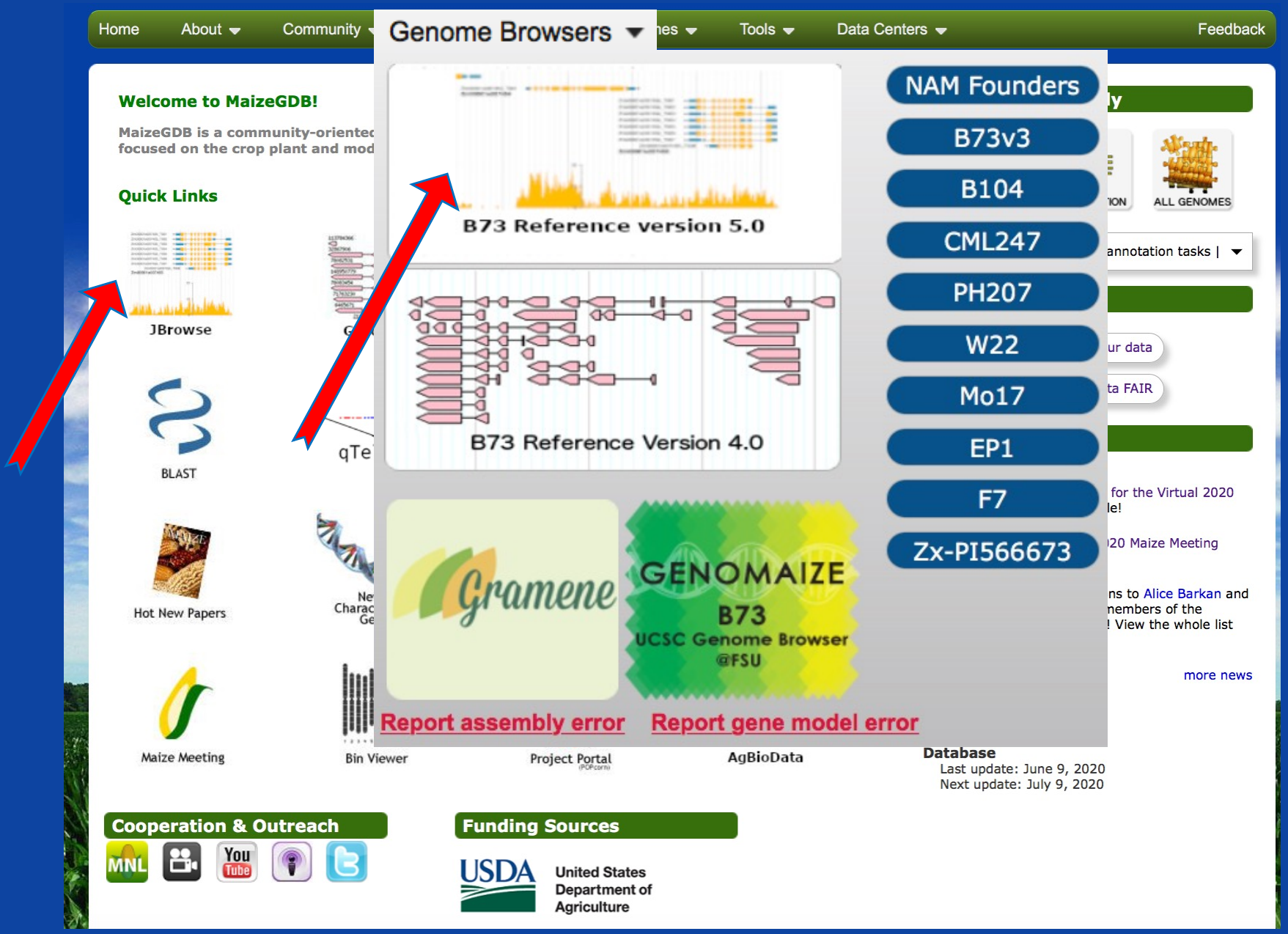
Currently, many or most forms of sequence analyses are referenced to the single B73 inbred. Beyond B73, some of the most extensively researched maize lines are the core set of 25 inbreds known as the NAM founder lines, which represent a broad cross-

GENOMES



Go straight to a genome Browser here

JBrowse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MaizeGDB is a community-oriented
focused on the crop plant and mod
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ALL GENOMES
annotation tasks |
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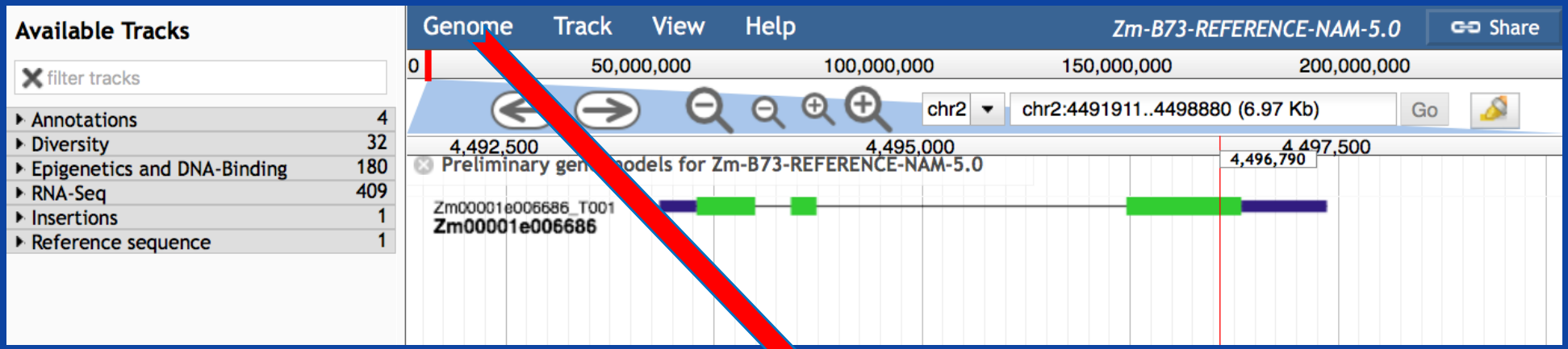
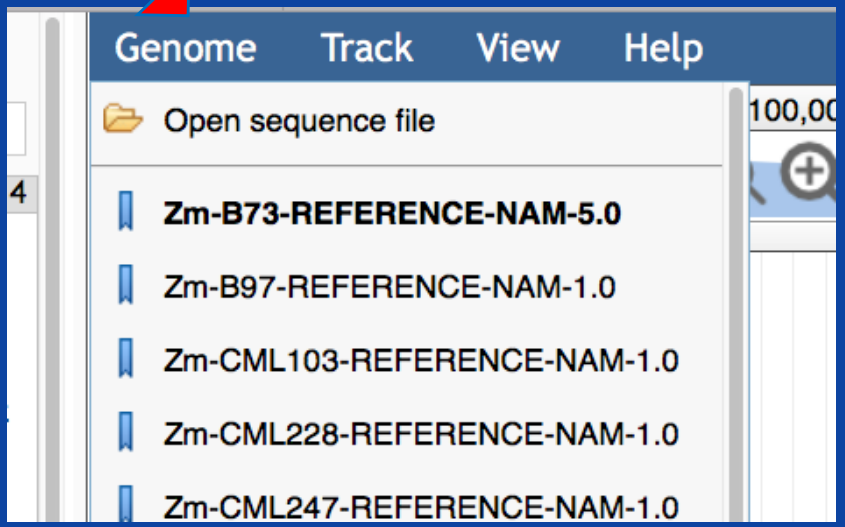
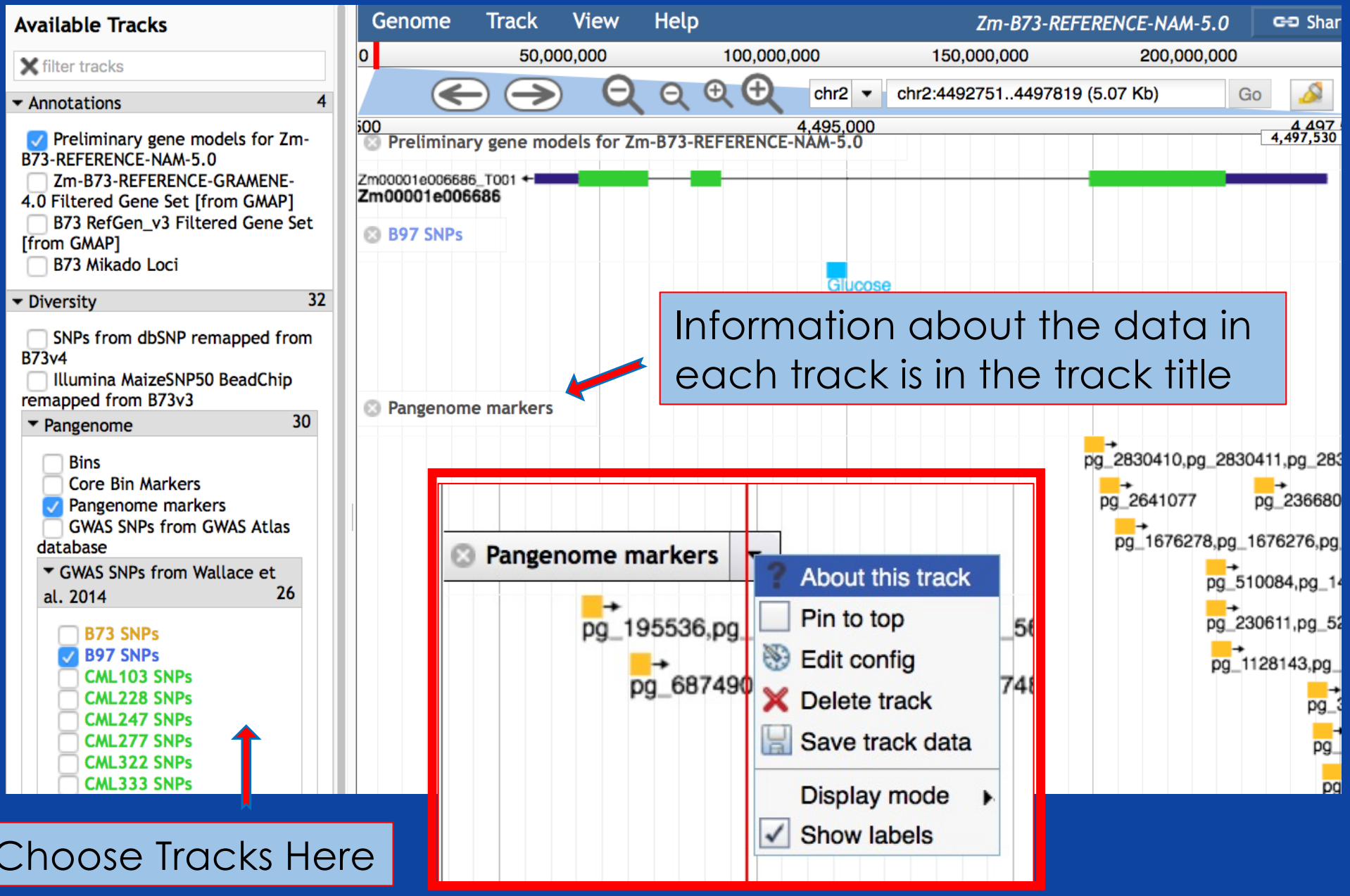


627 Tracks on B73 v5!!



JBrowse


Available Tracks
filter tracks
Annotations 4
Preliminary gene models for Zm-B73-REFERENCE-NAM-5.0
Zm-B73-REFERENCE-GRAMENE-4.0 Filtered Gene Set [from GMAP]
B73 RefGen_v3 Filtered Gene Set [from GMAP]
B73 Mikado Loci
Diversity 32
SNPs from dbSNP remapped from B73v4
Illumina MaizeSNP50 BeadChip remapped from B73v3
Pangenome 30
Bins
Core Bin Markers
Pangenome markers
GWAS SNPs from GWAS Atlas database
GWAS SNPs from Wallace et al. 2014 26
B73 SNPs
B97 SNPs
CML103 SNPs
CML228 SNPs
CML247 SNPs
CML277 SNPs
CML322 SNPs
CML333 SNPs
Genome Track View Help
Zm-B73-REFERENCE-NAM-5.0
0 50,000,000 100,000,000 150,000,000 200,000,000
chr2
chr2:4492751..4497819 (5.07 Kb)
Go
4,495,000
4,497,530
Preliminary gene models for Zm-B73-REFERENCE-NAM-5.0
Zm00001e006686_T001
Zm00001e006686
B97 SNPs
Glucose
Pangenome markers
Information about the data in each track is in the track title
pg_2830410,pg_2830411,pg_283
pg_2641077
pg_236680
pg_1676278,pg_1676276,pg
pg_510084,pg_1
pg_230611,pg_52
pg_1128143,pg
Pangenome markers
About this track
Pin to top
Edit config
Delete track
Save track data
Display mode
Show labels
pg_195536,pg
pg_687490
Choose Tracks Here

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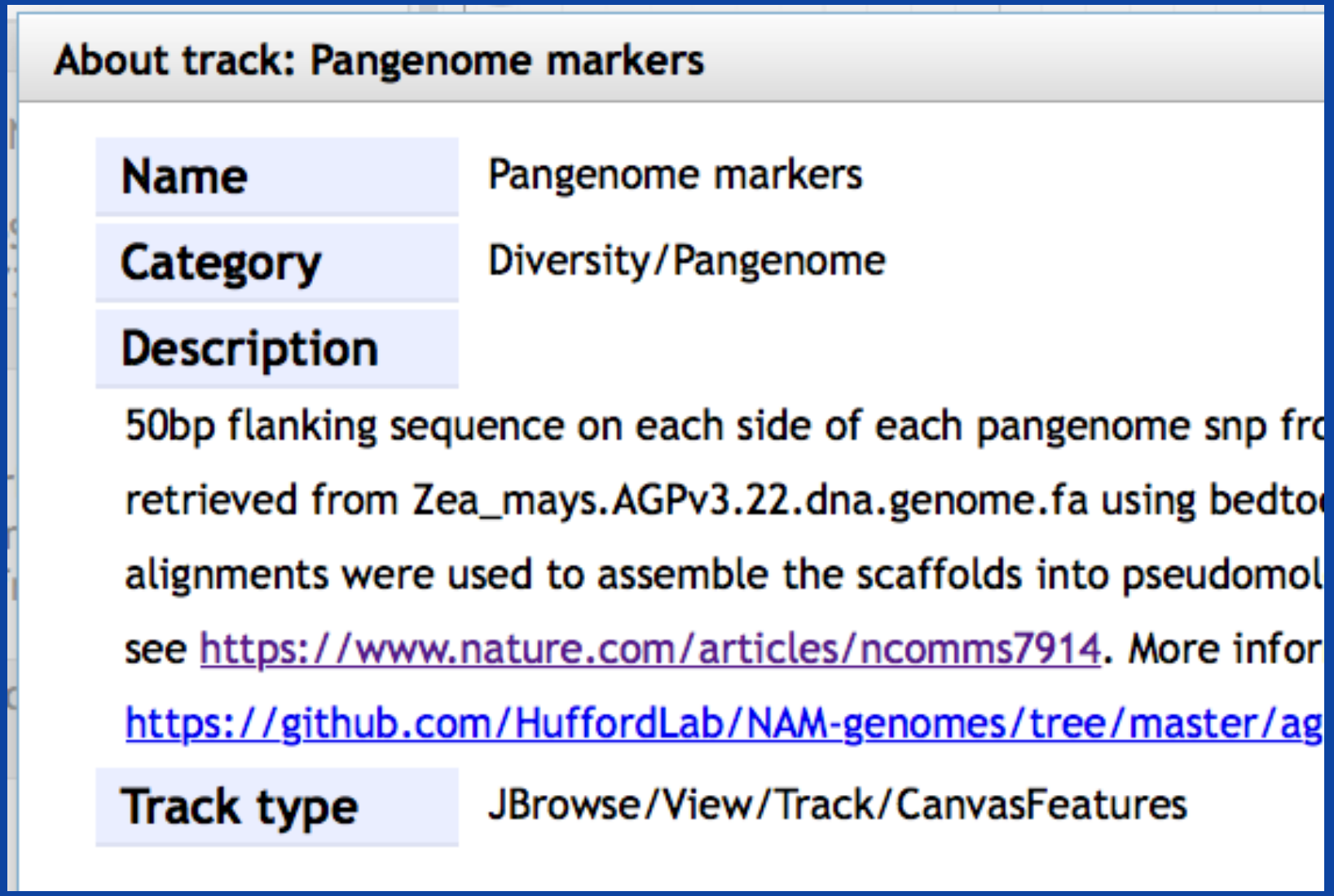

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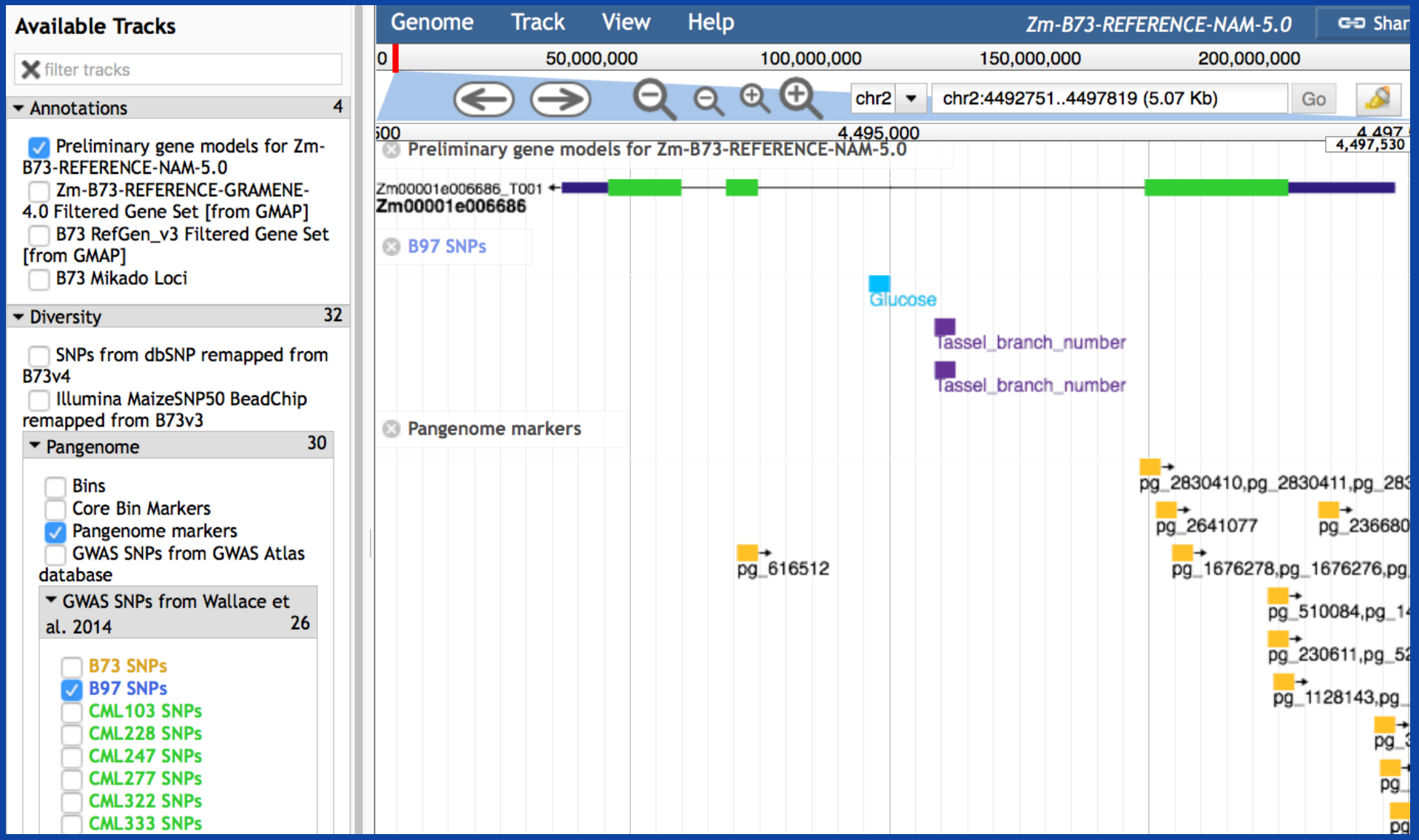
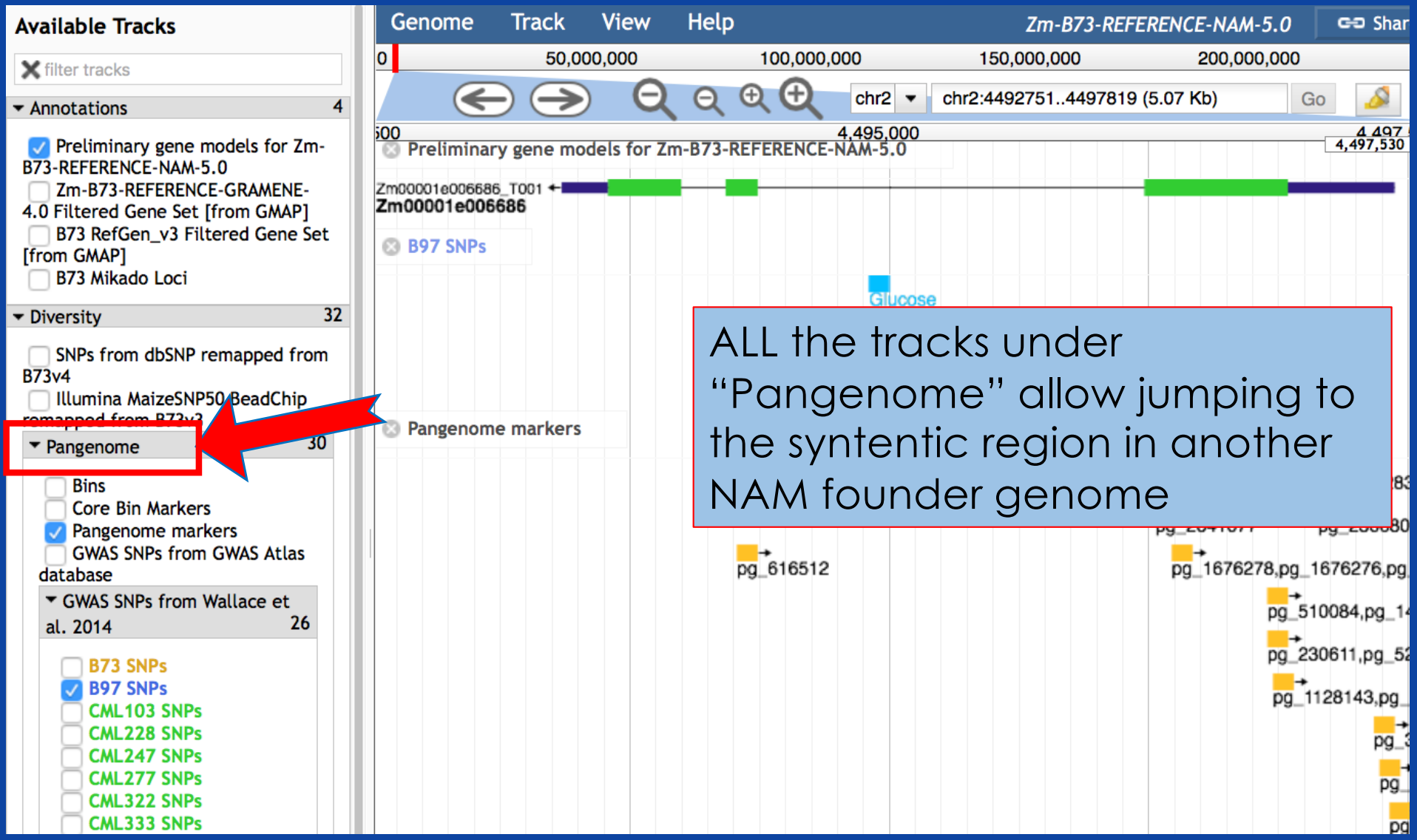
MAIZE GENETICS AND GENOMICS DATABASE

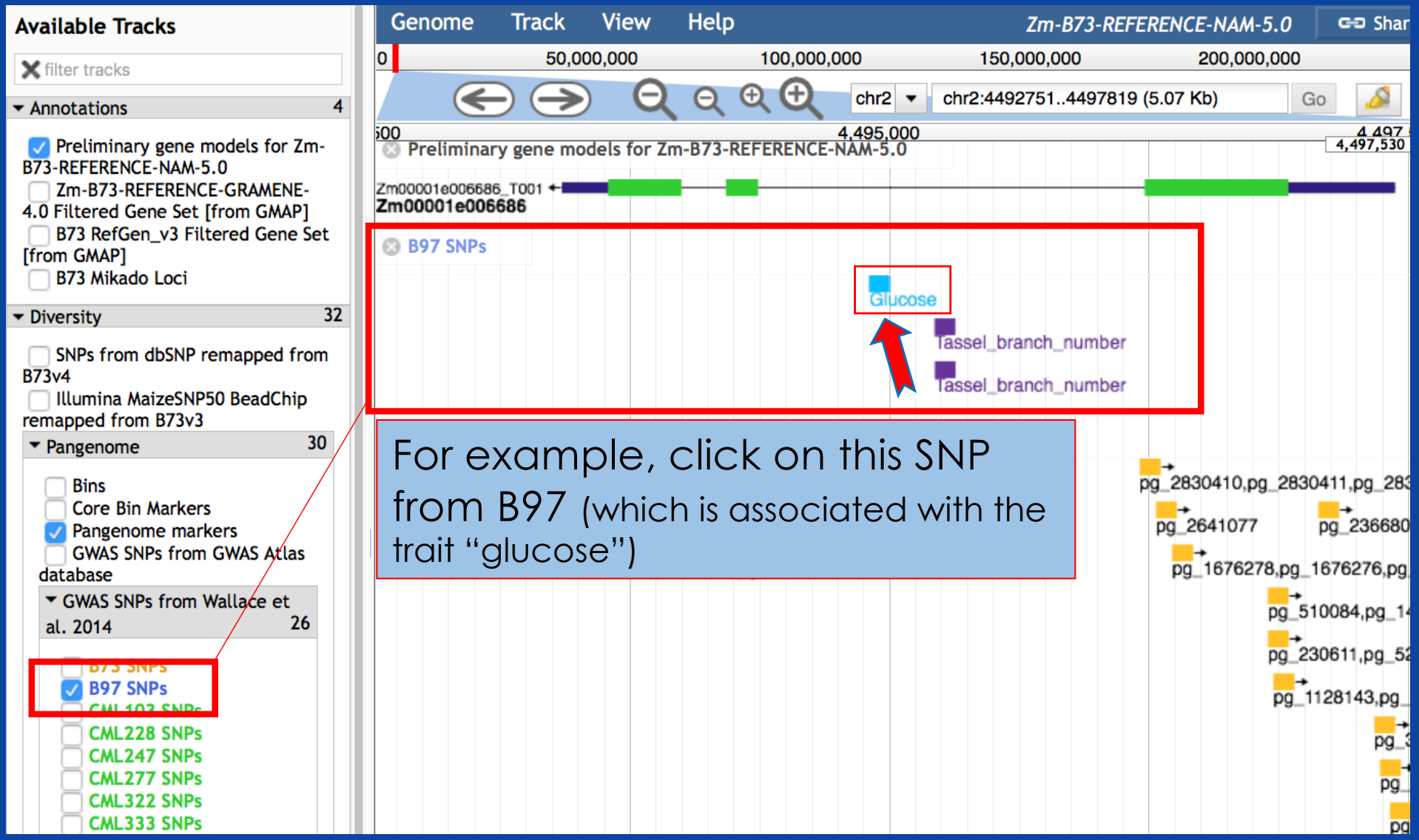
JBrowse



JBrowse JUMP between NAM genomes



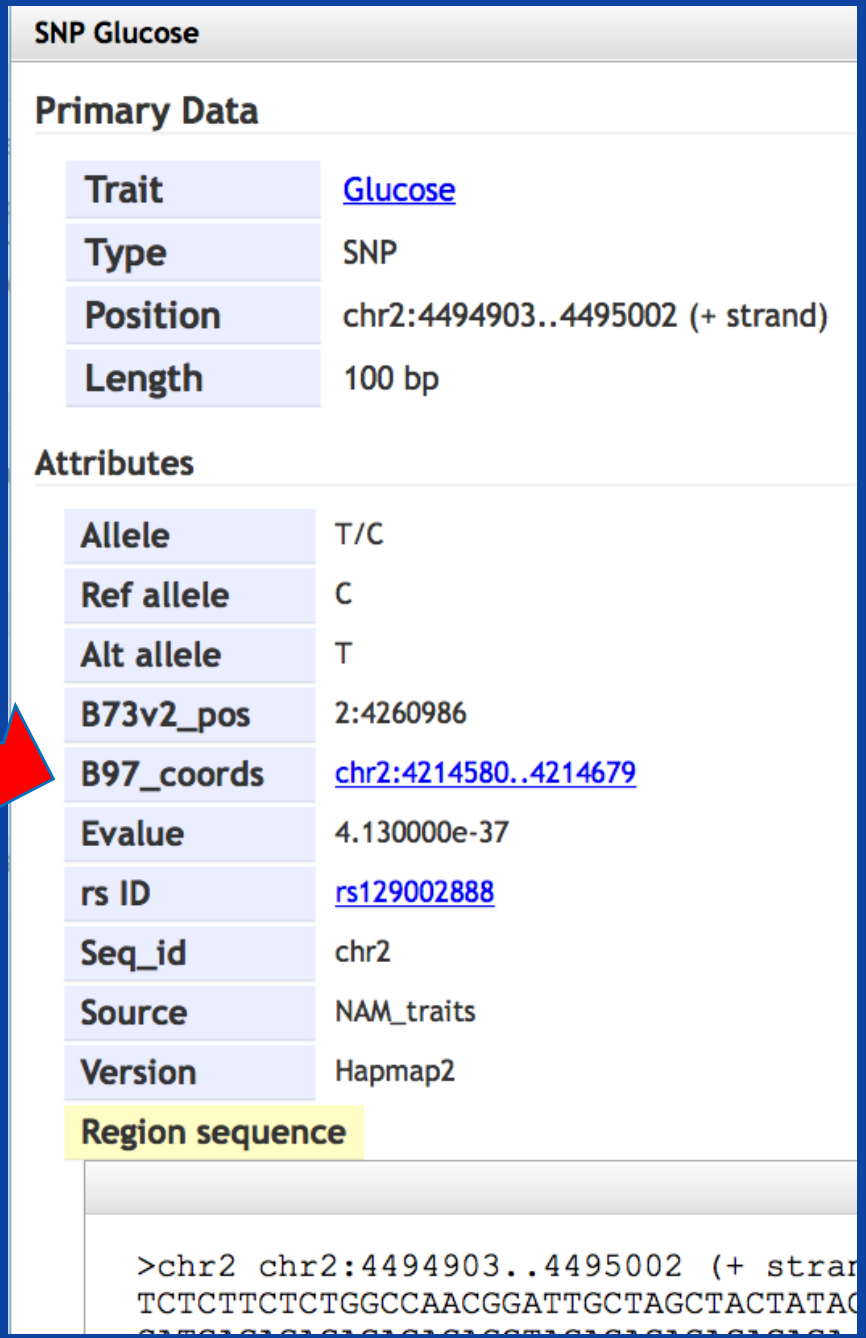
JBrowse JUMP between NAM genomes



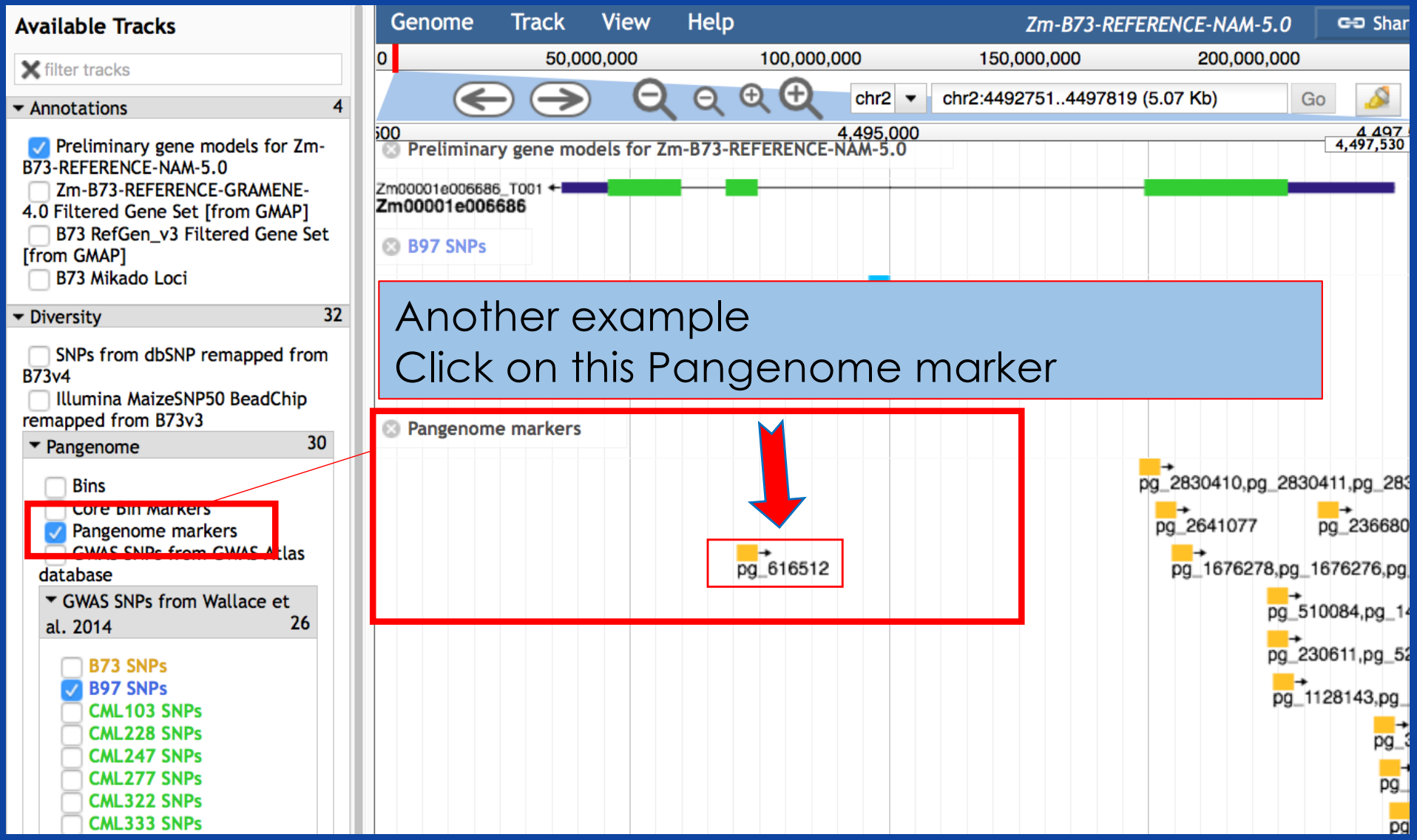
JBrowse

Information about this SNP will pop up

To see this SNP in the B97 (NAM founder) genome, Click here



JBrowse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CML333 SNPs
Genome
Track
View
Help
Zm-B73-REFERENCE-NAM-5.0
0
50,000,000
100,000,000
150,000,000
200,000,000
chr2
chr2:4492751..4497819 (5.07 Kb)
Go
4,495,000
4,497,530
Preliminary gene models for Zm-B73-REFERENCE-NAM-5.0
Zm00001e006686_T001
Zm00001e006686
B97 SNPs
Another example
Click on this Pangenome marker
Pangenome markers
pg_616512
pg_2830410,pg_2830411,pg_283
pg_2641077
pg_236680
pg_1676278,pg_1676276,pg
pg_510084,pg_1
pg_230611,pg_52
pg_1128143,pg

JBrowse

Information will pop up

To see this marker any other NAM founder genome, select from the drop down menu

SNP

Primary Data

Markers	pg_616512
Type	SNP
Score	60
Position	chr2:4494268..4494368 (+ strand)
Length	101 bp

Attributes

Pangenome	View pg_616512 on the B73v5 browser GO!!!
Genetic_distance	42.6594
Linkage_group	2
Seq_id	chr2
Source	pangenome

Region sequence

FASTA

```
>chr2 chr2:4494268..4494368 (+ strand) class=SNP length=101
CAGCATCCGATGGCTTTGACTTCCGGCGGCGGCGGTTGTGGTCCGCTAGGCGTTTCCTGCAGCTC
TTCTTAGCATCGTCGAACTCATCCAGCAGATGGAAT
```

OK

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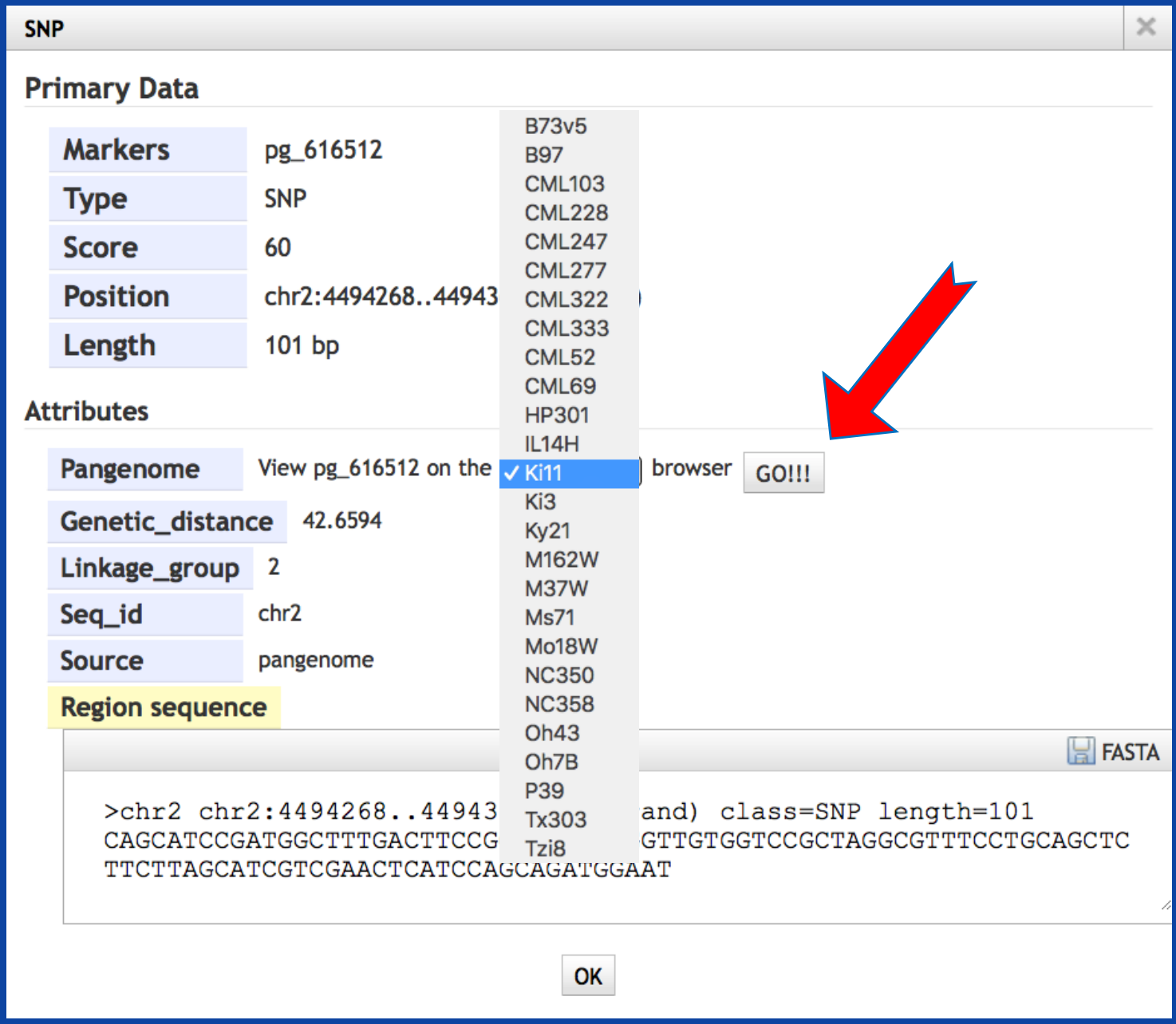
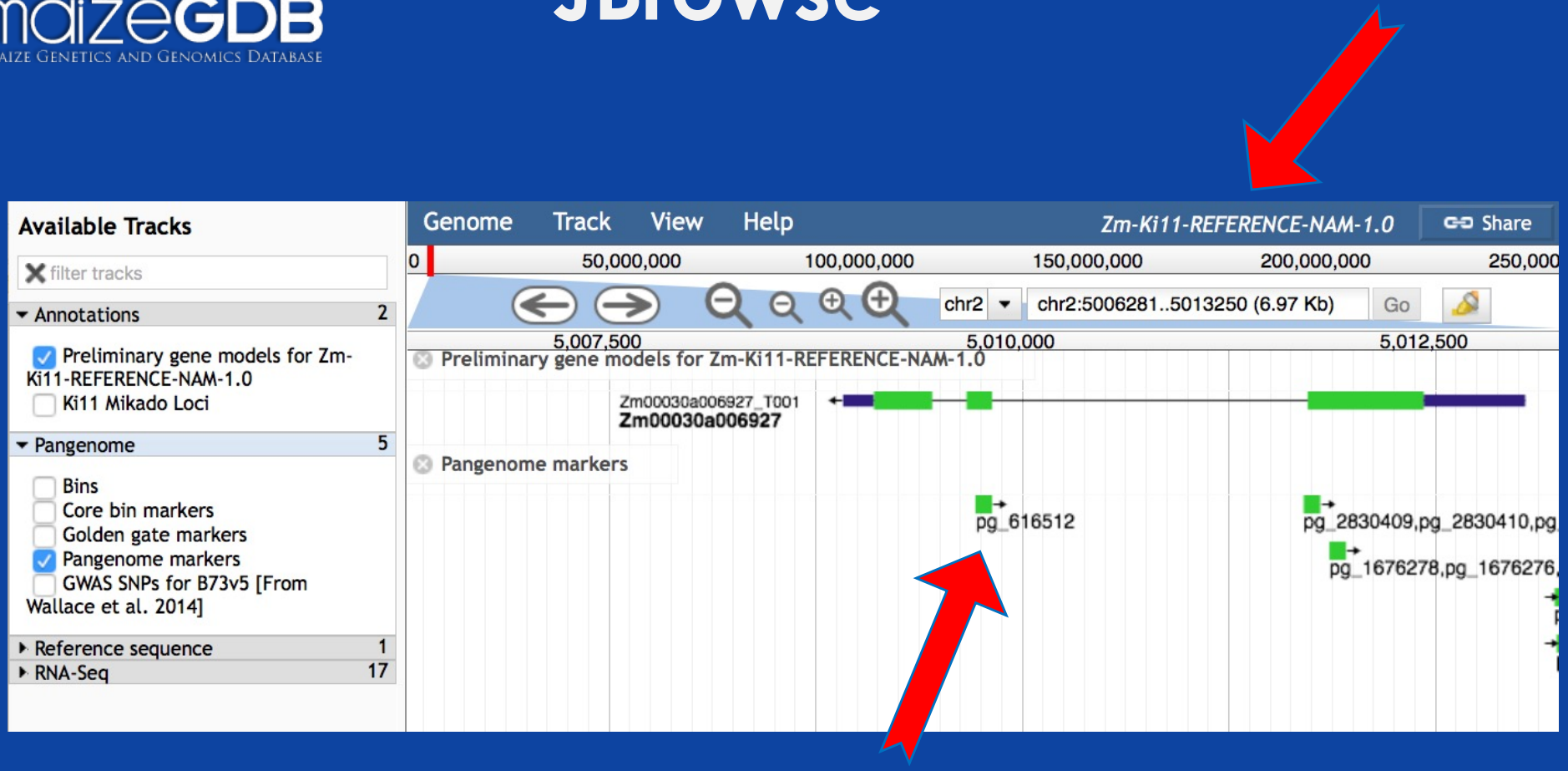


JBrowse



Now we are in the Ki11 genome right at that marker!

Note that currently only the B73 v5 Jbrowse has over 600 tracks

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Your Questions!

This is not the only time you can ask questions! Contact any of the MaizeGDB team, and we will do our best to help you!