Utilizing the *G. raimondii* Genome Sequence for Mapping RKN Resistance

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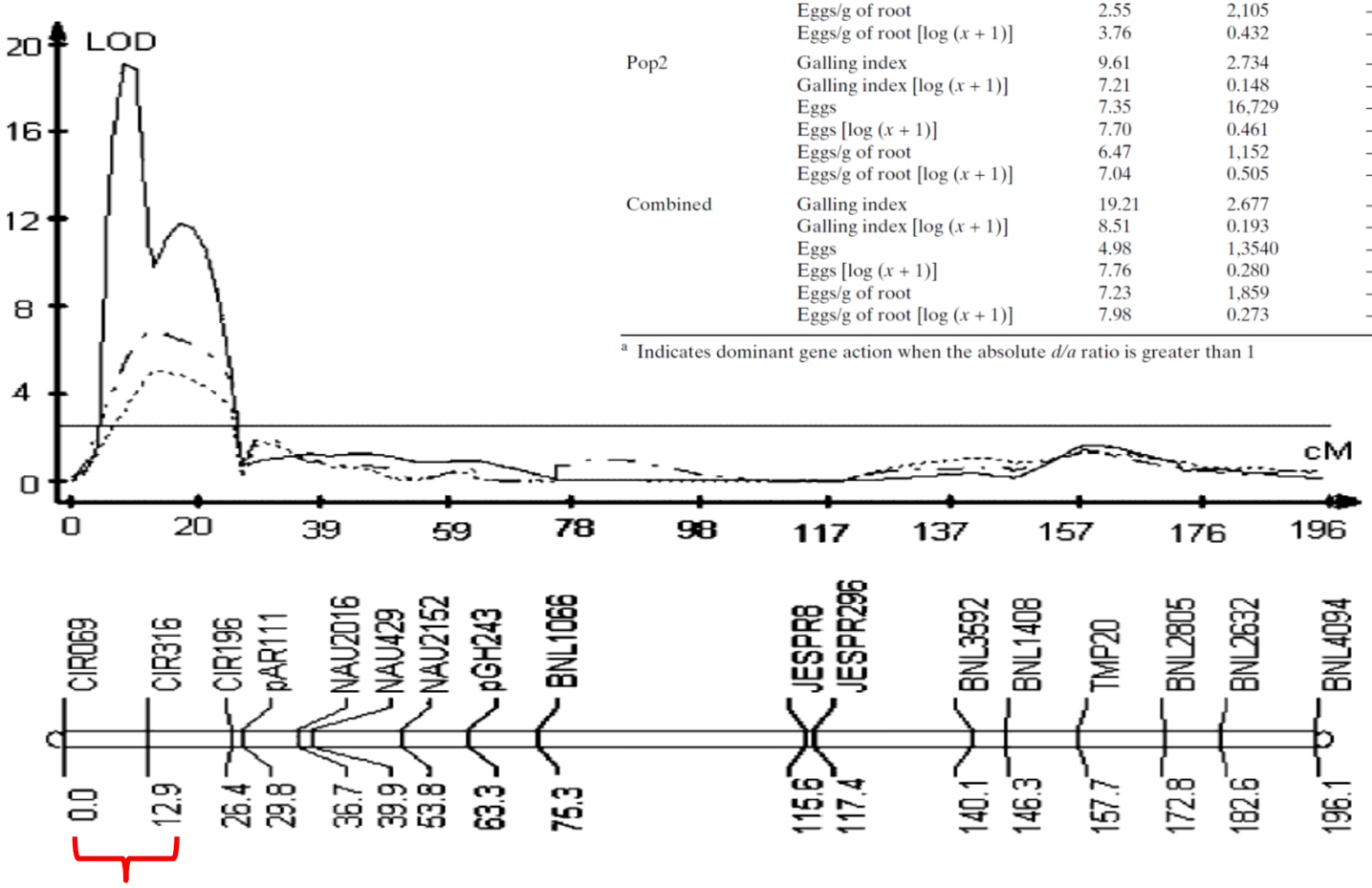
Breeding Cotton for Resistance to Fusarium and Nematodes
Dallas, Texas April 3, 2012

Chromosome (interval)		LOD	Add	Dom	*d*/*a*[a]	PV (%)
Chr. 11 (CIR069-CIR316)						
Pop1	Galling index	9.69	2.463	−2.521	1.02	52.6
	Galling index [log (*x* + 1)]	9.68	0.221	−0.269	1.20	34.4
	Eggs [log (*x* + 1)]	3.32	0.391	−0.376	0.96	11.0
	Eggs/g of root	2.55	2,105	−1,539	0.73	12.9
	Eggs/g of root [log (*x* + 1)]	3.76	0.432	−0.353	0.82	15.84
Pop2	Galling index	9.61	2.734	−2.831	1.04	65.6
	Galling index [log (*x* + 1)]	7.21	0.148	−0.184	1.24	31.7
	Eggs	7.35	16,729	−21,862	1.31	23.3
	Eggs [log (*x* + 1)]	7.70	0.461	−0.655	1.42	33.8
	Eggs/g of root	6.47	1,152	−1,800	1.56	18.9
	Eggs/g of root [log (*x* + 1)]	7.04	0.505	−0.545	1.08	25.4
Combined	Galling index	19.21	2.677	−2.896	−1.08	63.7
	Galling index [log (*x* + 1)]	8.51	0.193	−0.208	−1.08	35.8
	Eggs	4.98	1,3540	−14,346	−1.06	8.9
	Eggs [log (*x* + 1)]	7.76	0.280	−0.434	−1.54	14.4
	Eggs/g of root	7.23	1,859	−2,155	−1.16	16.1
	Eggs/g of root [log (*x* + 1)]	7.98	0.273	−0.444	−1.63	15.0

[a] Indicates dominant gene action when the absolute *d*/*a* ratio is greater than 1



RKN resistance QTL

Shen et al 2006 TAG

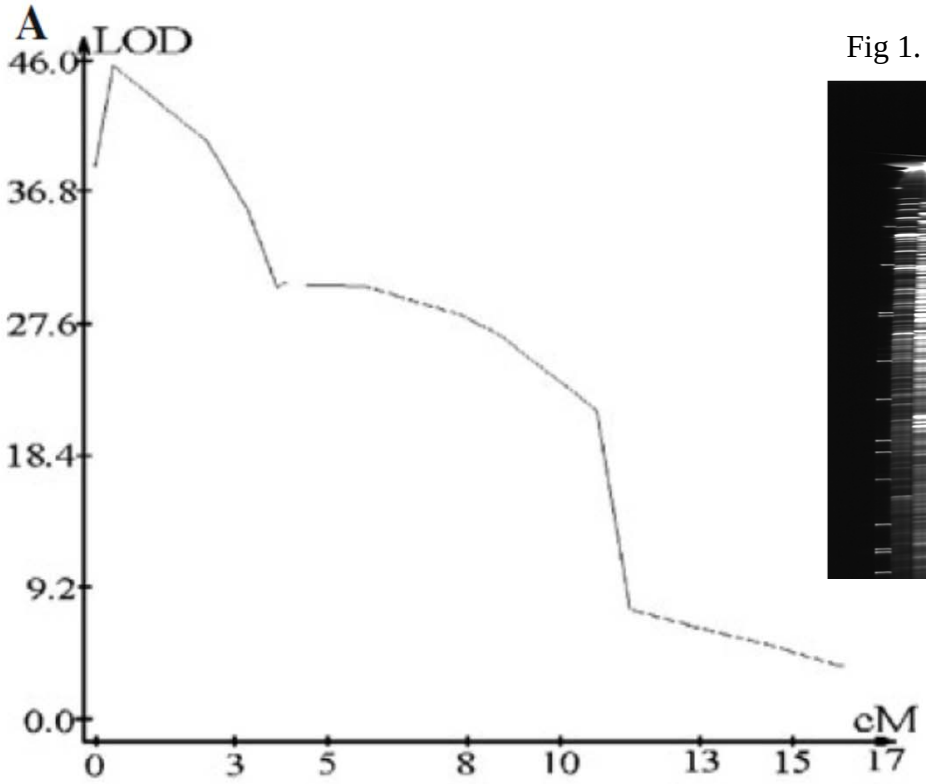
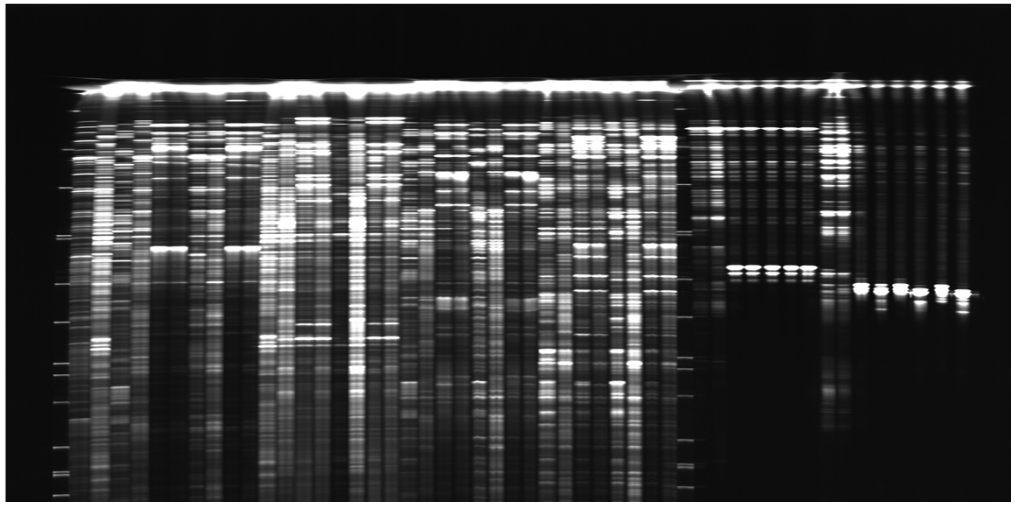
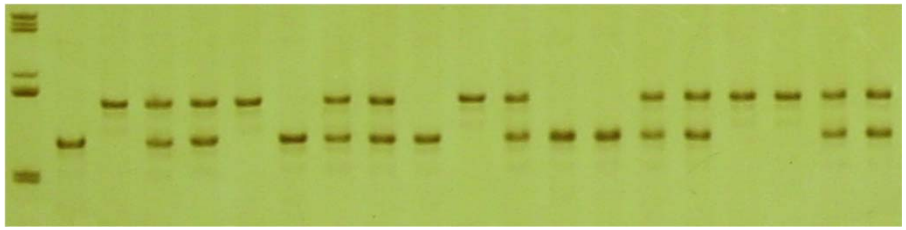


Fig 1. Polymorphisms analysis using AFLP markers

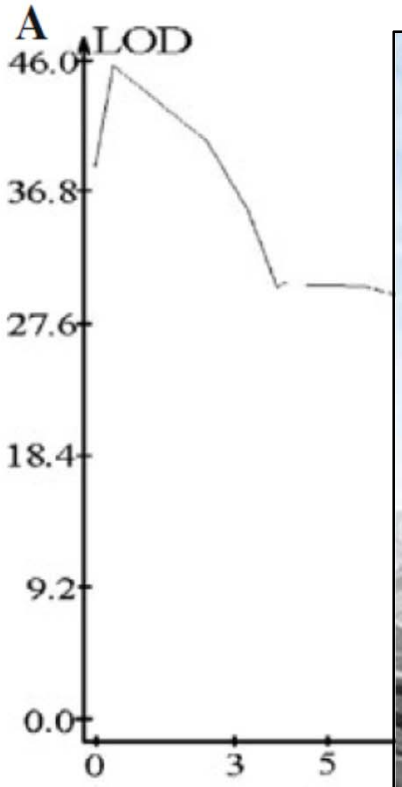


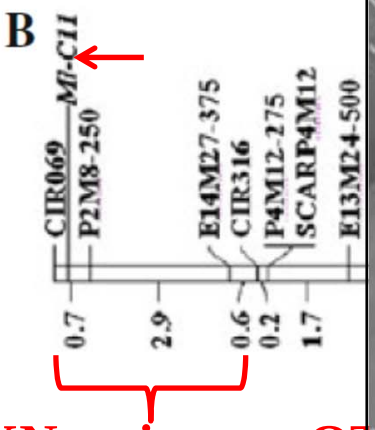
RKN resistance QTL

Fig 3. Polymorphisms analysis of SCAR marker P4M12 in mapping parents and individuals.

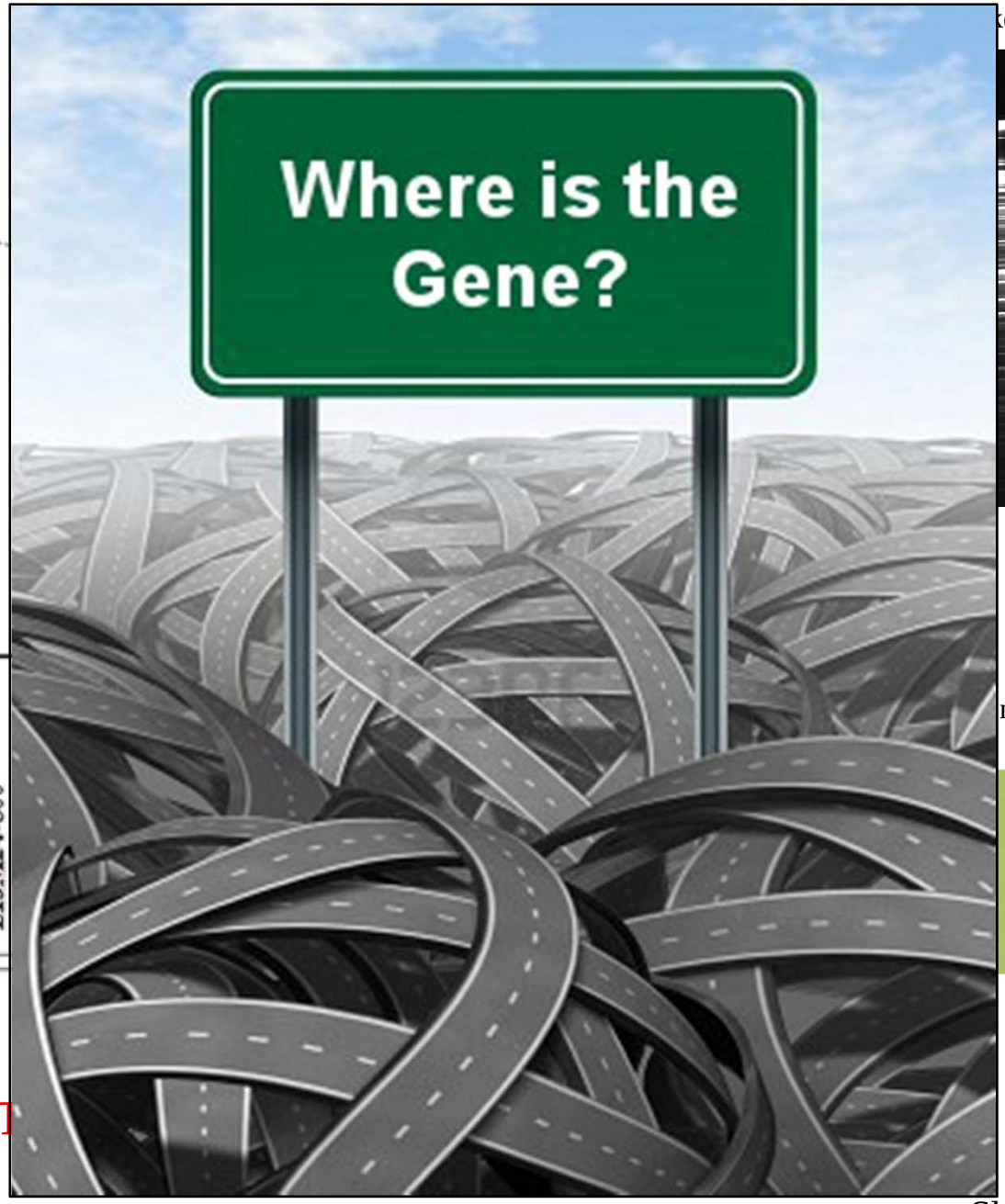


Shen et al 2010 TAG





RKN resistance QT



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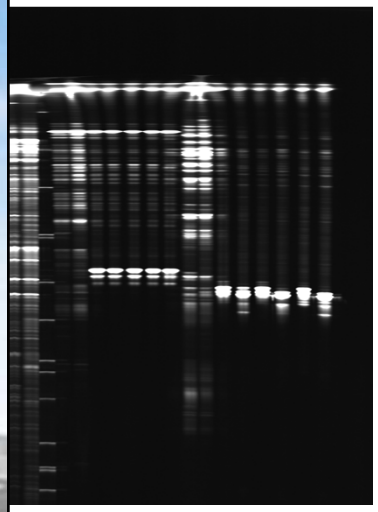
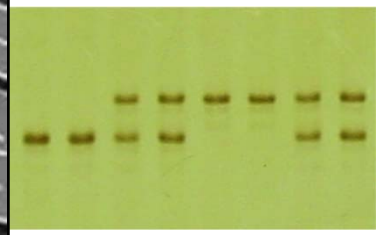


marker P4M12 in mapping



Shen et al 2010 TAG

PRESSROOM

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'Gold-Standard' Cotton Genome Sequence Will Advance Fiber, Fuel, and Food Applications

Thursday January 05, 2012

New York, NY
An international consortium, led by Professor Andrew Paterson of the University of Georgia, has made publicly available the first 'gold-standard' genome sequence for cotton. Cotton was among the first plants studied at the molecular level, and the sequence obtained by Paterson and his team is the culmination of a 20-plus year effort in the analysis of cotton genes and genomic DNA. This critical sequence will be invaluable to better understanding and optimizing the production and sustainability of the cotton plant.

The research effort of Paterson and others gained momentum in 2007 when a proposal from 22 leading cotton scientists representing the world's seven largest cotton-producing nations was approved by the United States Department of Energy (DOE) Joint Genome Institute (JGI) Community Sequencing Program. The study established the strategy that was used for 'gold-standard' sequencing of the New World cotton progenitor, *Gossypium raimondii*; which was chosen by the worldwide cotton community to be the first of 50 cotton species to be sequenced. "This achievement, and the ongoing research community annotations of our cotton genome, will speed continued improvement of cotton production and help sustain one of the world's largest industries," said Professor Paterson.

The cotton sequence is among the highest-quality flowering plant sequences yet produced. A novel strategy integrating "next-generation" and conventional sequencing methods was used. Critical to the effort was information about the cotton hereditary blueprint, which had been accumulated over more than 20 years of research funded by the U.S. National Science Foundation, the U.S. Department of Agriculture, Cotton Incorporated, and other public and private agencies.

JGI Home Project List Login

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Plant Genomics Program

Capturing Light to Fuel Our Future

plants

Announcements

- Jan 16, 2012

Phytozome v8.0 has been released!

- Oct 07, 2011

Release of Thellungiella halophila genome and Biomart sequence issue fixed.

Releases

- December 22, 2011

Asterochloris sp. Cgr/DA1pho v1.0

- August 22, 2011

Micromonas pusilla CCMP1545 v3.0

- January 8, 2010

Cucumis sativus v1.0

- January 8, 2010

Mimulus guttatus v1.0

- December 18, 2009

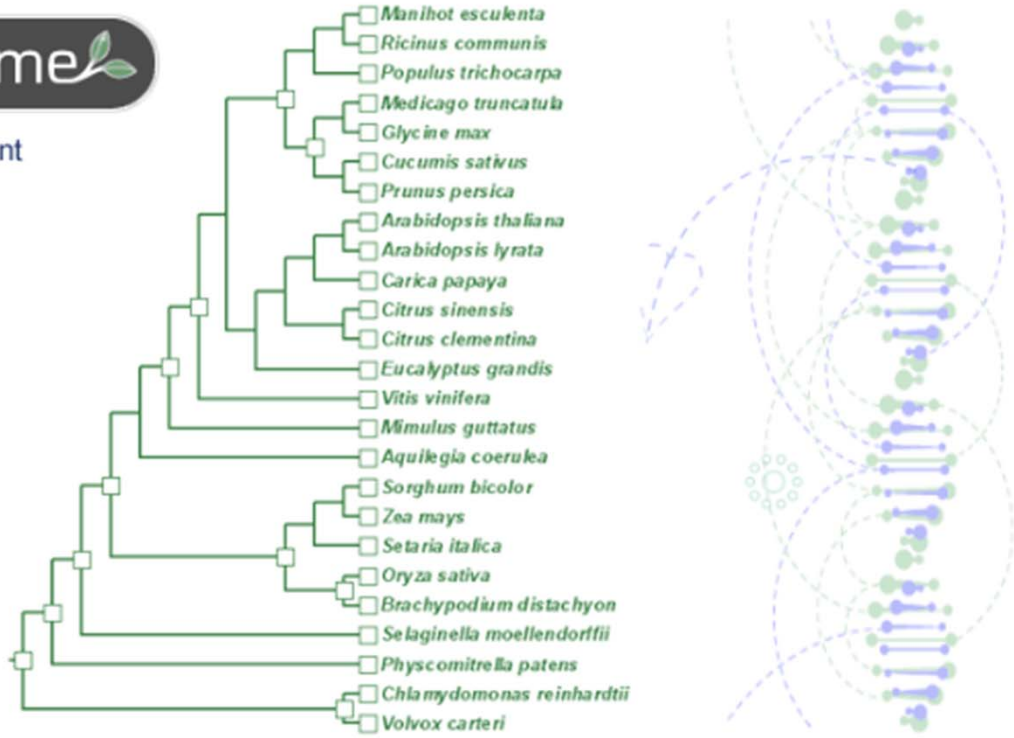
Coccomyxa sp. C-169 v2.0

more »

by Keyword Search Genome

phytozome

a tool for green plant comparative genomics



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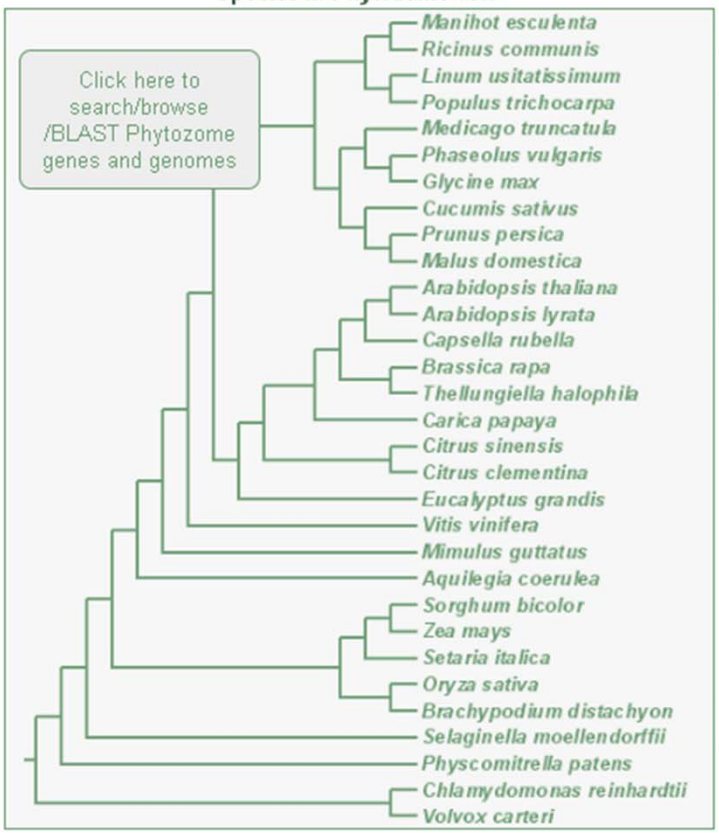
Genome Portal version:6.0.263.15068 content:15068 clustering:3405 synteny:3405 gp-edge2.jgi-psf.org 28-Mar-2012 07:52:35.289 PST

U.S. DEPARTMENT OF ENERGY | Office of Science

Species in Phytozome v8.0



Welcome to Phytozome!

Phytozome is a joint project of the Department of Energy's Joint Genome Institute and the Center for Integrative Genomics to facilitate comparative genomic studies amongst green plants. Families of orthologous and paralogous genes that represent the modern descendents of ancestral gene sets are constructed at key phylogenetic nodes. These families allow easy access to clade specific orthology/paralogy relationships as well as clade specific genes and gene expansions. As of release v8.0, Phytozome provides access to thirty-one sequenced and annotated green plant genomes which have been clustered into gene families at eleven evolutionarily significant nodes. Where possible, each gene has been annotated with PFAM, KOG, KEGG, and PANTHER assignments, and publicly available annotations from RefSeq, UniProt, TAIR, JGI are hyper-linked and searchable.

Using Phytozome: video tutorials

Announcements

[14 Feb 2012] **A service outage for filesystem maintenance is currently scheduled for Wednesday, February 15th, 2012 from approximately 7 AM to 2 PM Pacific Standard Time.**

[16 Jan 2012] **Phytozome v8.0 has been released!**

[12 Dec 2011] **A service outage for filesystem maintenance is currently scheduled for Tuesday, December 13th, 2011 from approximately 12 AM to 3 PM Pacific Standard Time.**

News

[16 Jan 2012] **Phytozome v8.0 has been released!**
The lastest version of Phytozome has been released. Version 8 includes 21 genomes assembled and/or annotated at the JGI, and 9

[12 Dec 2011] **Service Outage Tuesday, December 13th, 2011**
A service outage for filesystem maintenance is currently scheduled for Tuesday, December 13th, 2011 from approximately 12 AM to 3 PM

[07 Oct 2011] **Release of Thellungiella halophila genome and Biomart sequence issue fixed.**
The version 1.0 genome annotation and assembly of Thellungiella

[05 Aug 2011] **Service Outage Tuesday, August 9th, 2011**
A service outage for filesystem maintenance is currently scheduled for Tuesday, August 9th, 2011 from approximately 7 AM to 5 PM Pacific

:: Go to the news page to view all the news ::

Early release genomes

- Panicum virgatum
- Gossypium raimondii

Info

- Release notes
- Plant Genomics resources

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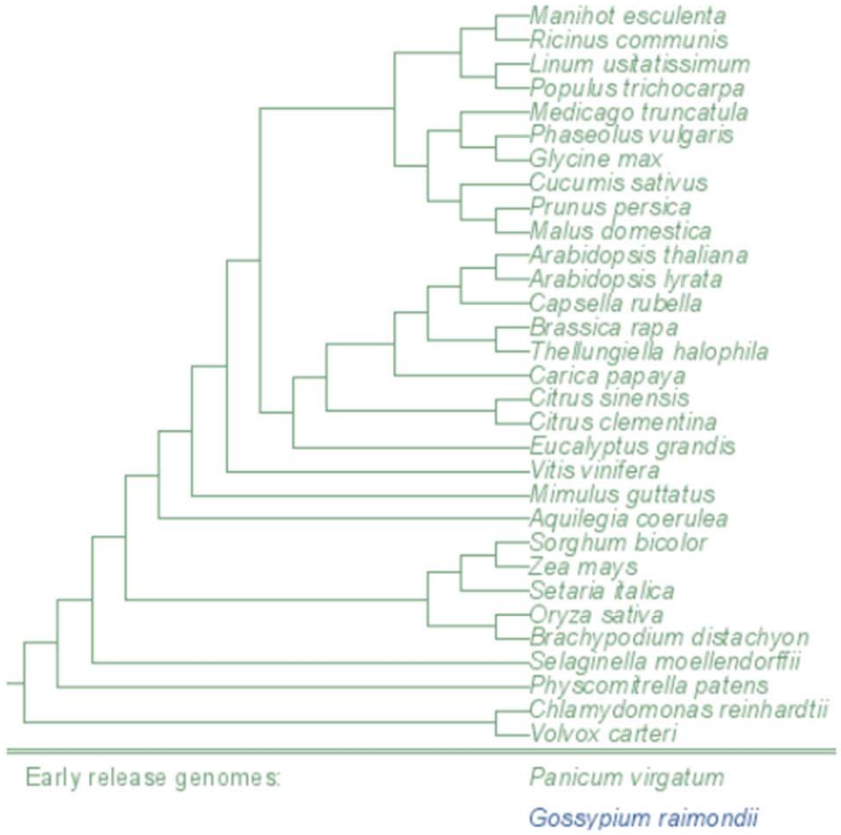
Gossypium raimondii (cotton)

Browse Genome | BLAST Genome | Download data

About the genome:

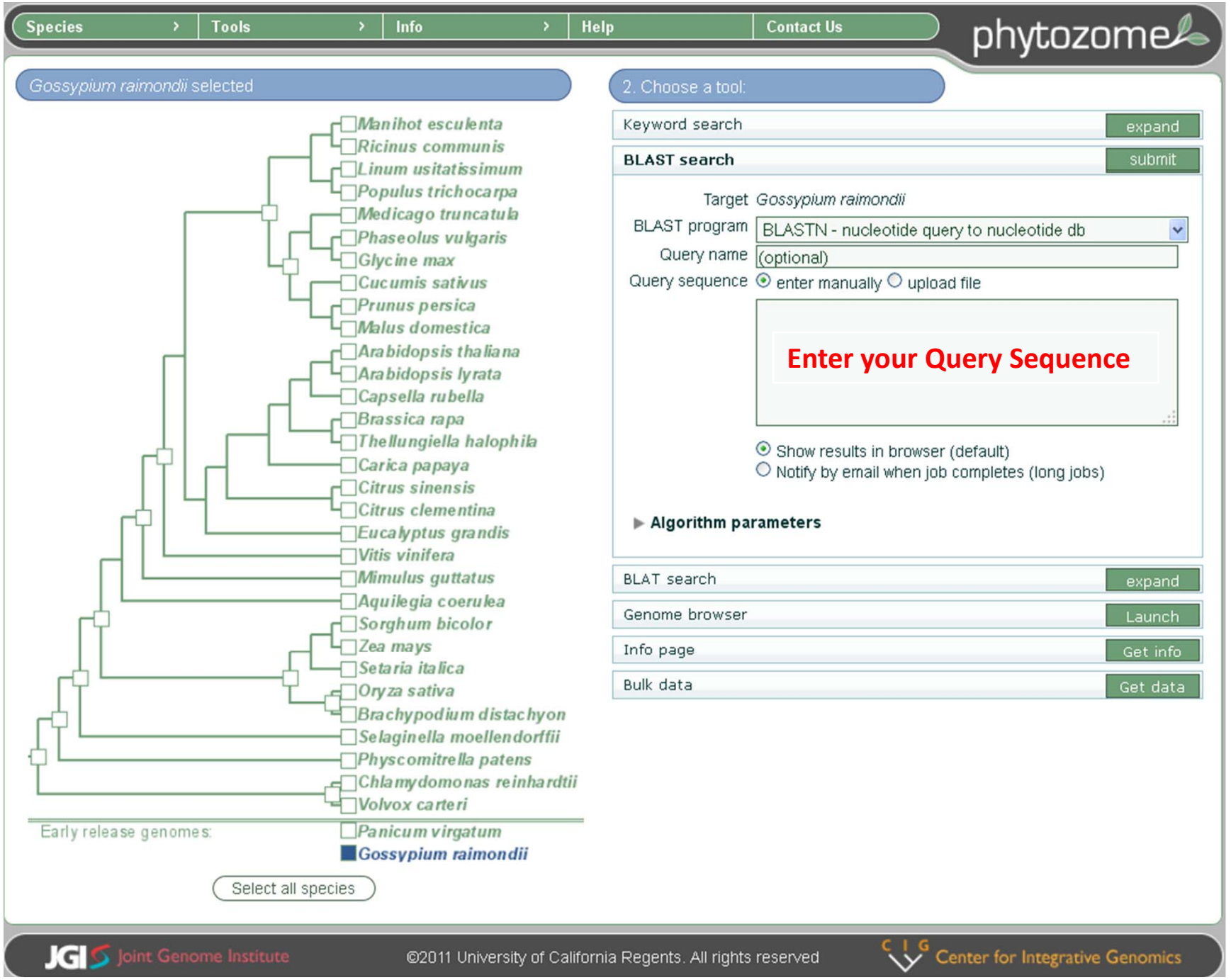
- **Statistics**
- **FAQ**
  - What can I do with the *Gossypium raimondii* dataset?



Statistics

This is release of assembly version v1.0 of the Cotton D genome.

Genome
Scaffold total: 1,448
Contig total: 28,582
Scaffold sequence total: 763.8 Mb
Contig sequence total: 749.4 Mb (-> 1.9% gap)
Scaffold N50 (L50) = 6 (62.2 Mb)
Contig N50 (L50) = 1,596 (135.1kb)
35 scaffolds are > 50kb in size, representing approximately 98.3% of the genome


Species
Tools
Info
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phytozome
Gossypium raimondii selected
Manihot esculenta
Ricinus communis
Linum usitatissimum
Populus trichocarpa
Medicago truncatula
Phaseolus vulgaris
Glycine max
Cucumis sativus
Prunus persica
Malus domestica
Arabidopsis thaliana
Arabidopsis lyrata
Capsella rubella
Brassica rapa
Thellungiella halophila
Carica papaya
Citrus sinensis
Citrus clementina
Eucalyptus grandis
Vitis vinifera
Mimulus guttatus
Aquilegia coerulea
Sorghum bicolor
Zea mays
Setaria italica
Oryza sativa
Brachypodium distachyon
Selaginella moellendorffii
Physcomitrella patens
Chlamydomonas reinhardtii
Volvox carteri
Early release genomes:
Panicum virgatum
Gossypium raimondii
Select all species
2. Choose a tool:
Keyword search
expand
BLAST search
submit
Target Gossypium raimondii
BLAST program
BLASTN - nucleotide query to nucleotide db
Query name
(optional)
Query sequence
enter manually
upload file
Enter your Query Sequence
Show results in browser (default)
Notify by email when job completes (long jobs)
Algorithm parameters
BLAT search
expand
Genome browser
Launch
Info page
Get info
Bulk data
Get data
JGI Joint Genome Institute
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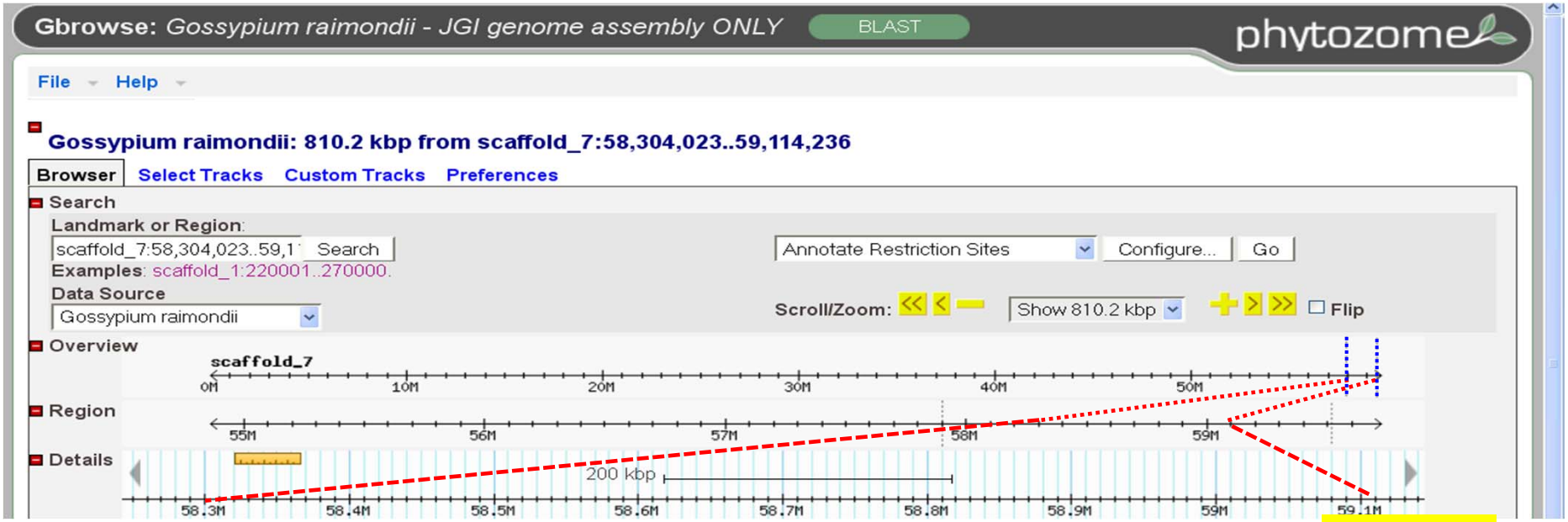
CIG Center for Integrative Genomics

BLAST results- sequences of CIR316 and CIR069

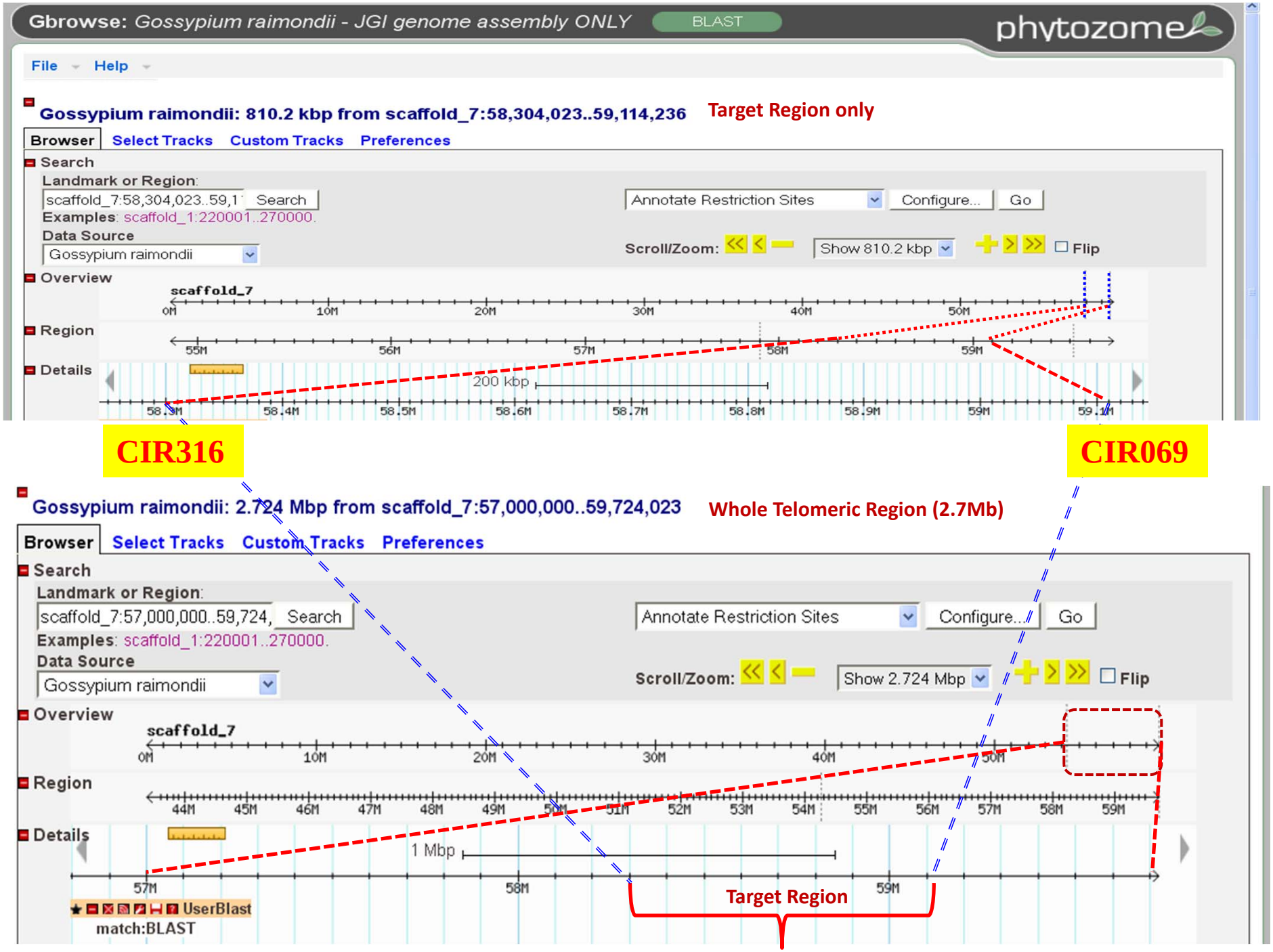
Chromosome 11 = Scaffold-7 of *Gossypium raimondii* (59.7Mb)



CIR316

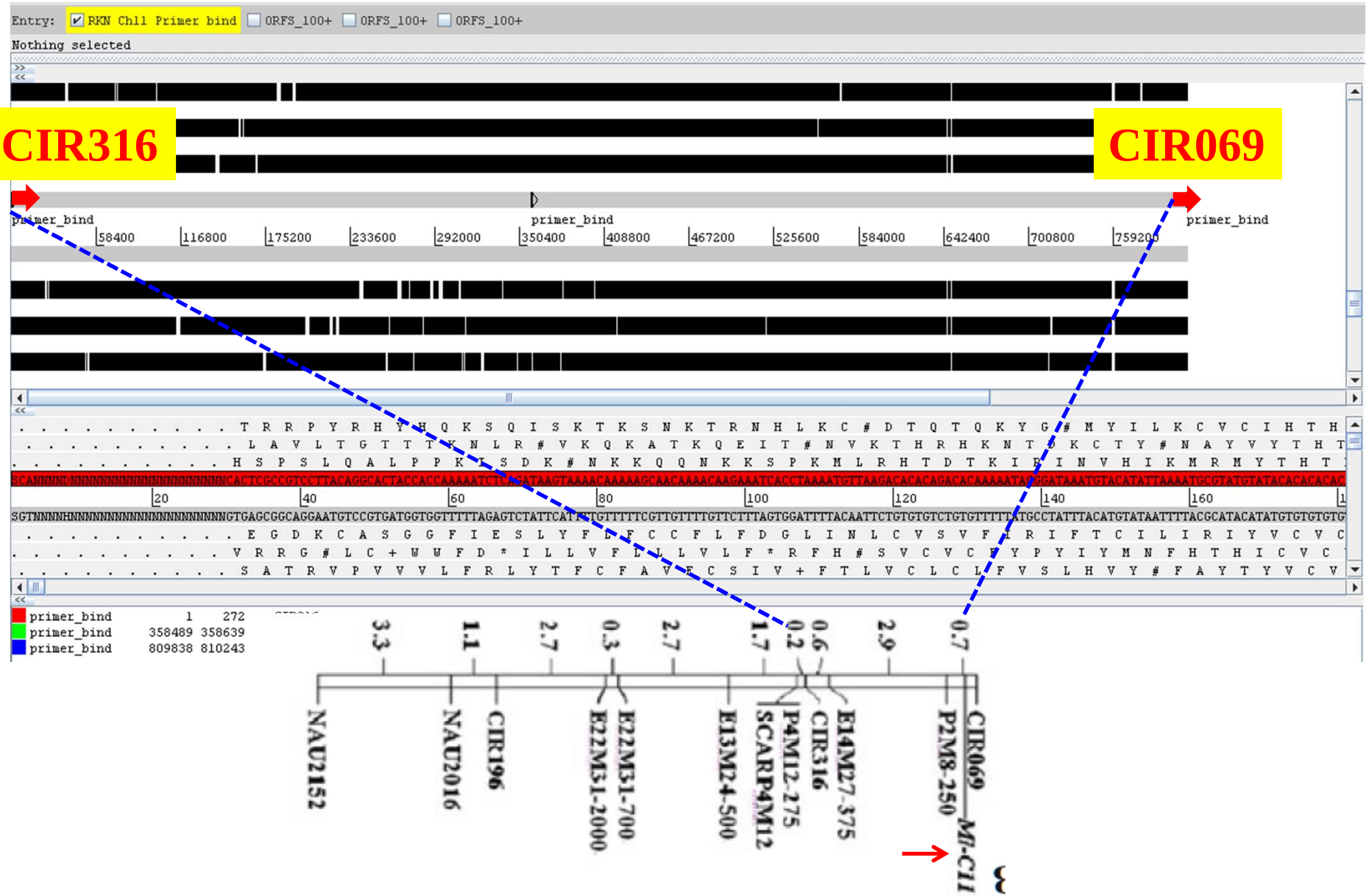
CIR069

810 Kbp


Gbrowse: Gossypium raimondii - JGI genome assembly ONLY
BLAST
phytozome
File
Help
Gossypium raimondii: 810.2 kbp from scaffold_7:58,304,023..59,114,236
Target Region only
Browser
Select Tracks
Custom Tracks
Preferences
Search
Landmark or Region:
scaffold_7:58,304,023..59,1
Search
Examples: scaffold_1:220001..270000.
Data Source
Gossypium raimondii
Annotate Restriction Sites
Configure...
Go
Scroll/Zoom:
Show 810.2 kbp
Flip
Overview
scaffold_7
Region
Details
200 kbp
CIR316
CIR069
Gossypium raimondii: 2.724 Mbp from scaffold_7:57,000,000..59,724,023
Whole Telomeric Region (2.7Mb)
scaffold_7:57,000,000..59,724,
Show 2.724 Mbp
1 Mbp
UserBlast
match:BLAST
Target Region

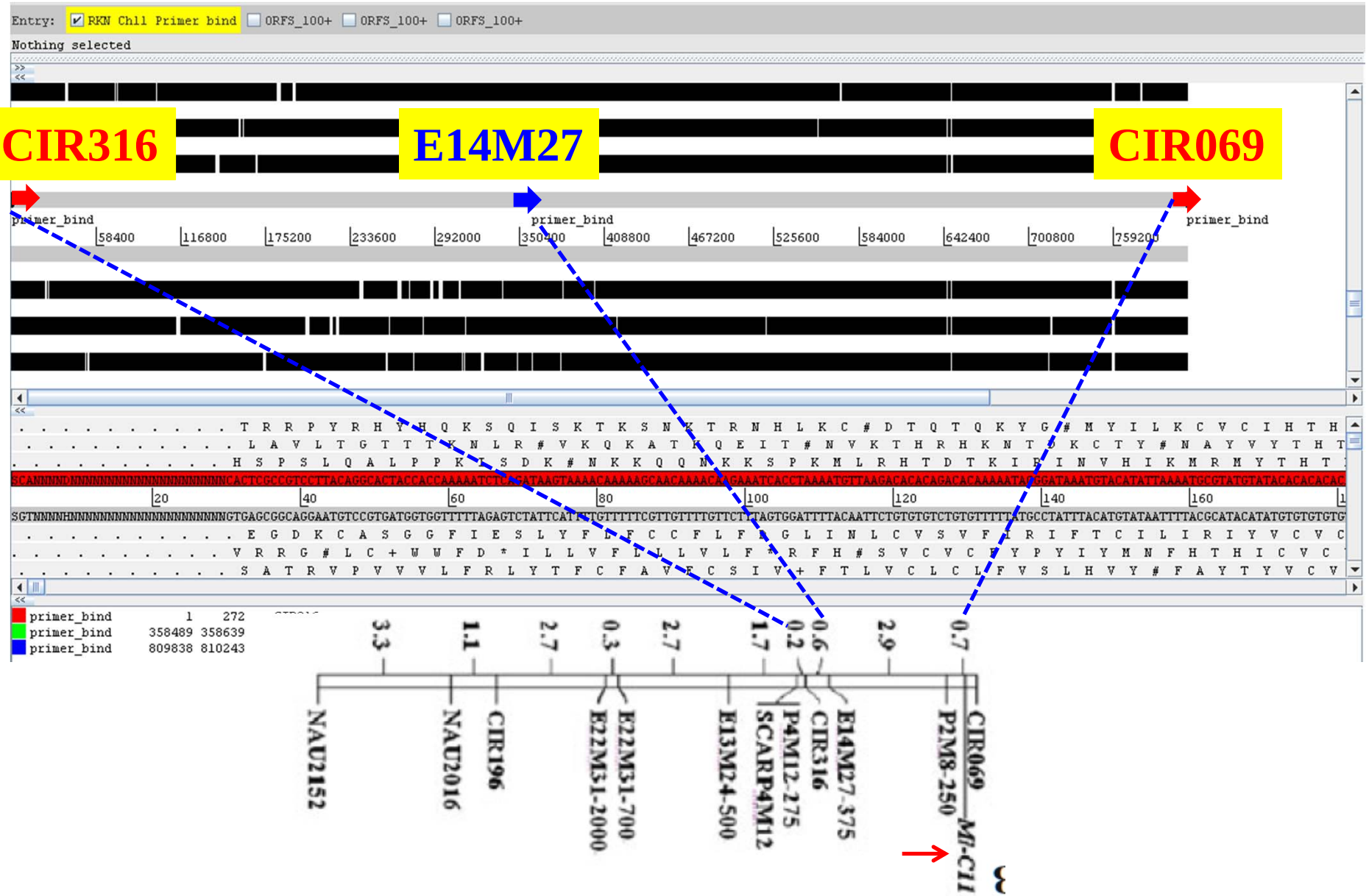
Artemis Genome viewer

Sequence location of the AFLP marker (E14M27)



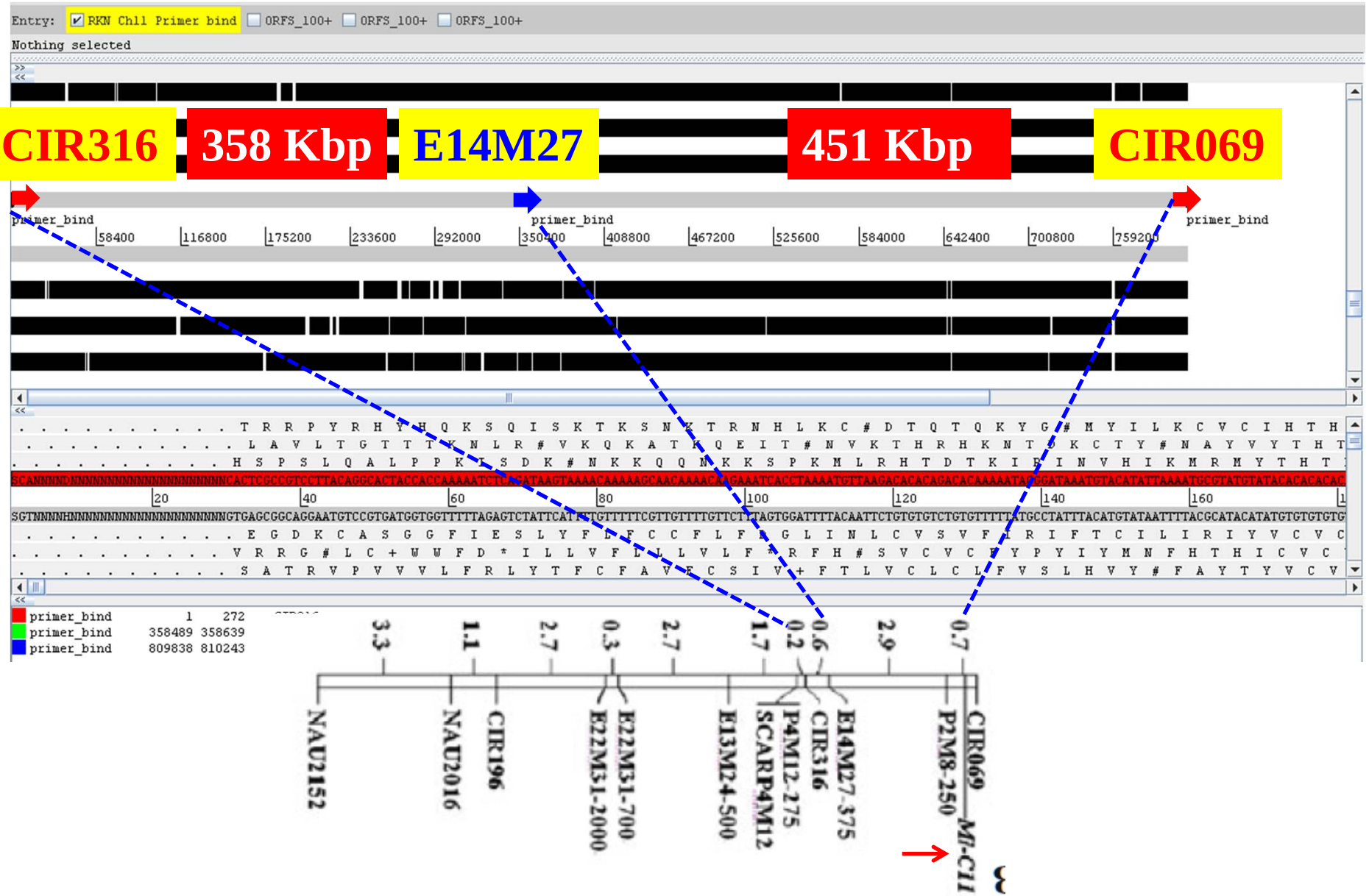
Artemis Genome viewer

Sequence location of the new AFLP marker (E14M27)

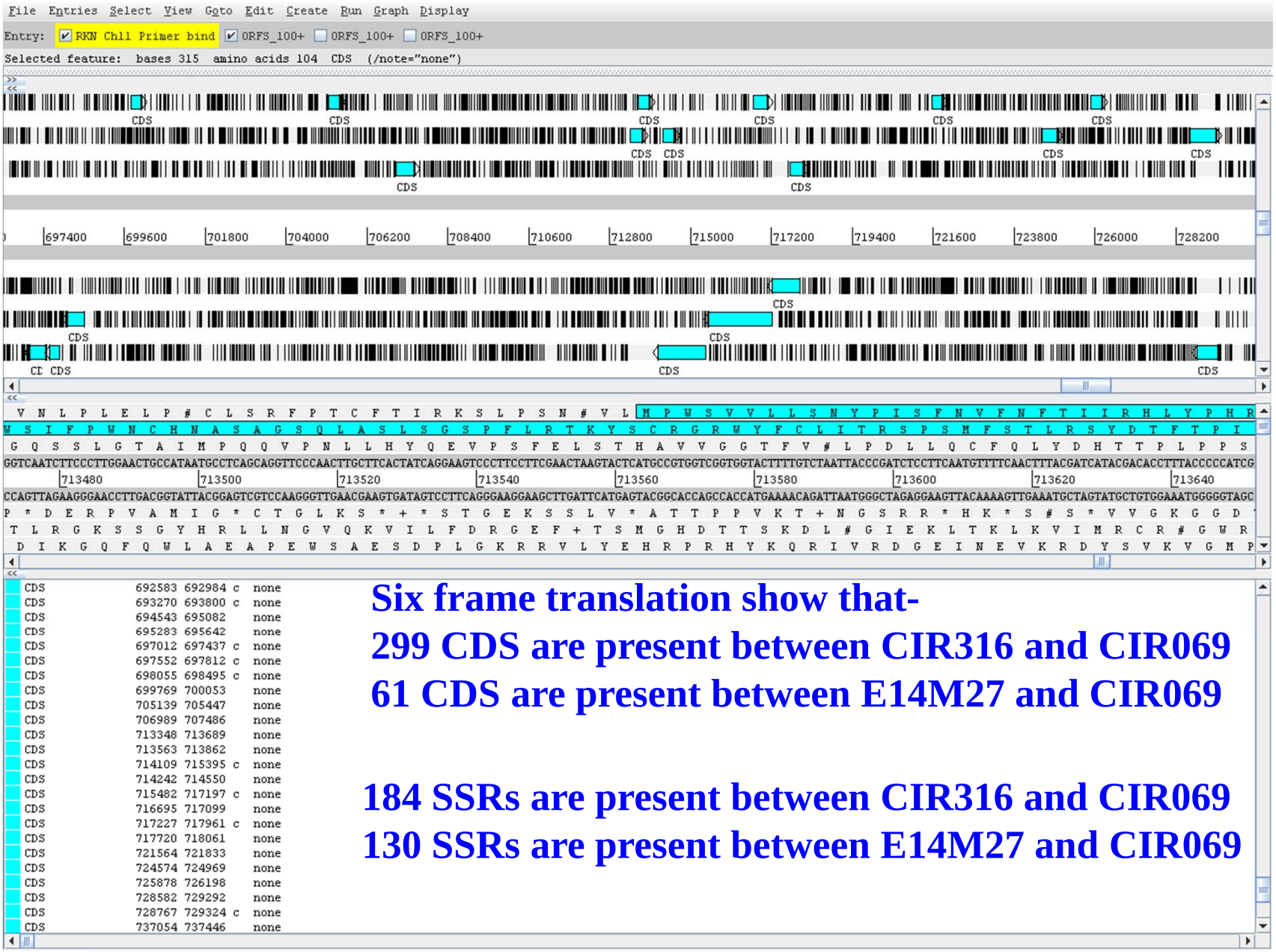


Artemis Genome viewer

Sequence location of the new AFLP marker (E14M27)



CDS (Coding DNA Sequences) or the ORF (Open Reading Frames) in this region



Six frame translation show that-

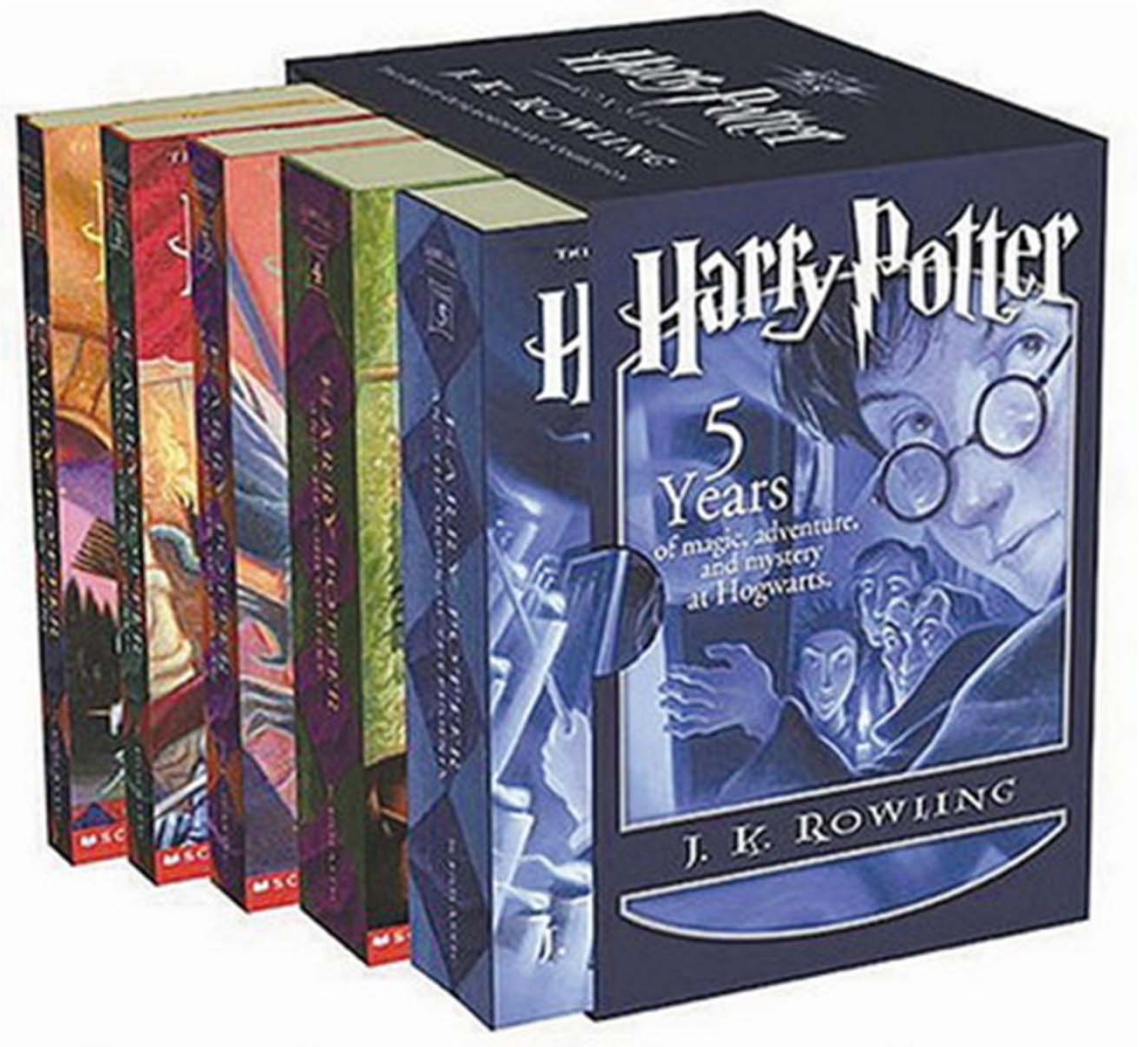
299 CDS are present between CIR316 and CIR069

61 CDS are present between E14M27 and CIR069

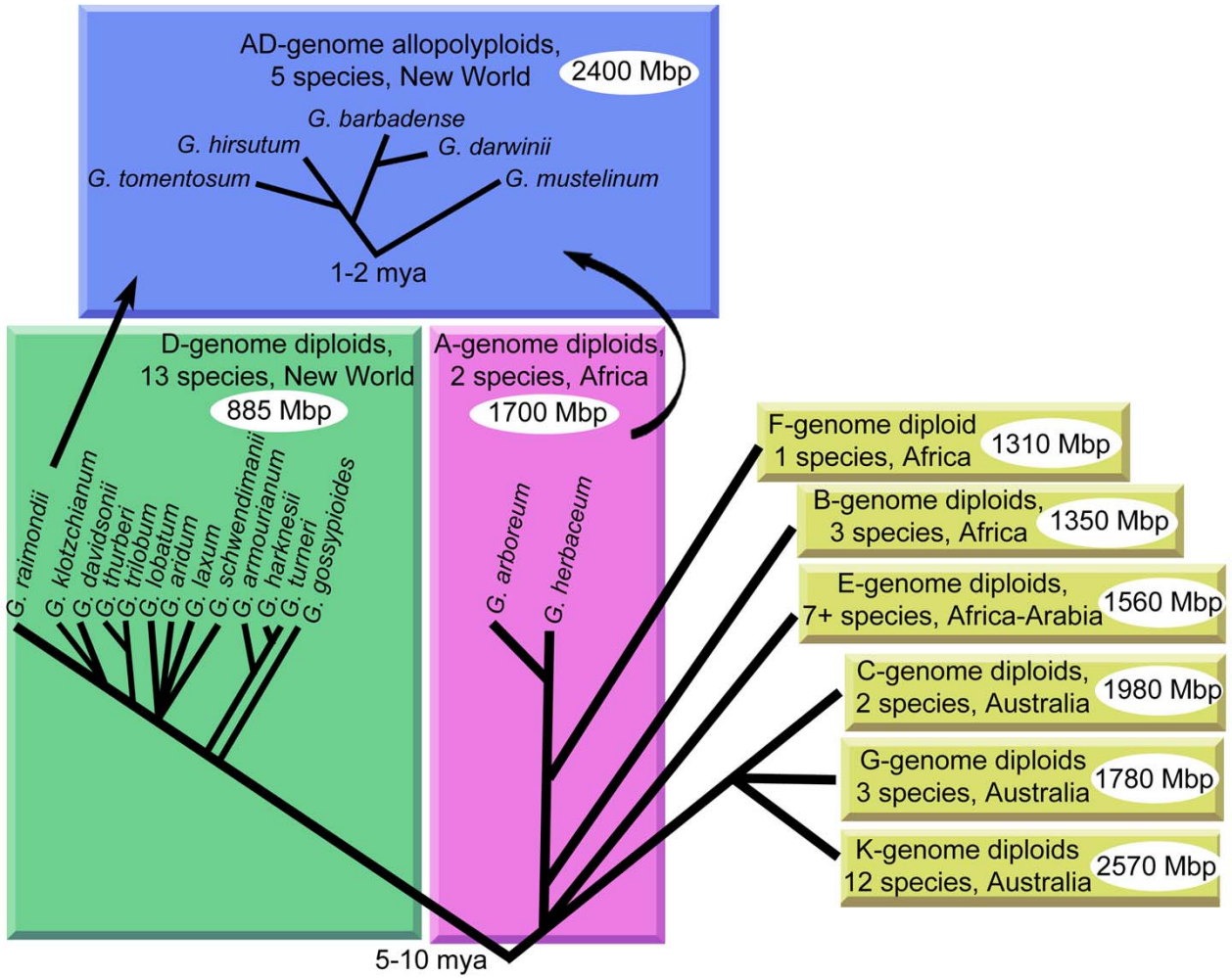
184 SSRs are present between CIR316 and CIR069

130 SSRs are present between E14M27 and CIR069

Challenges: 810 Kbp between flanking markers

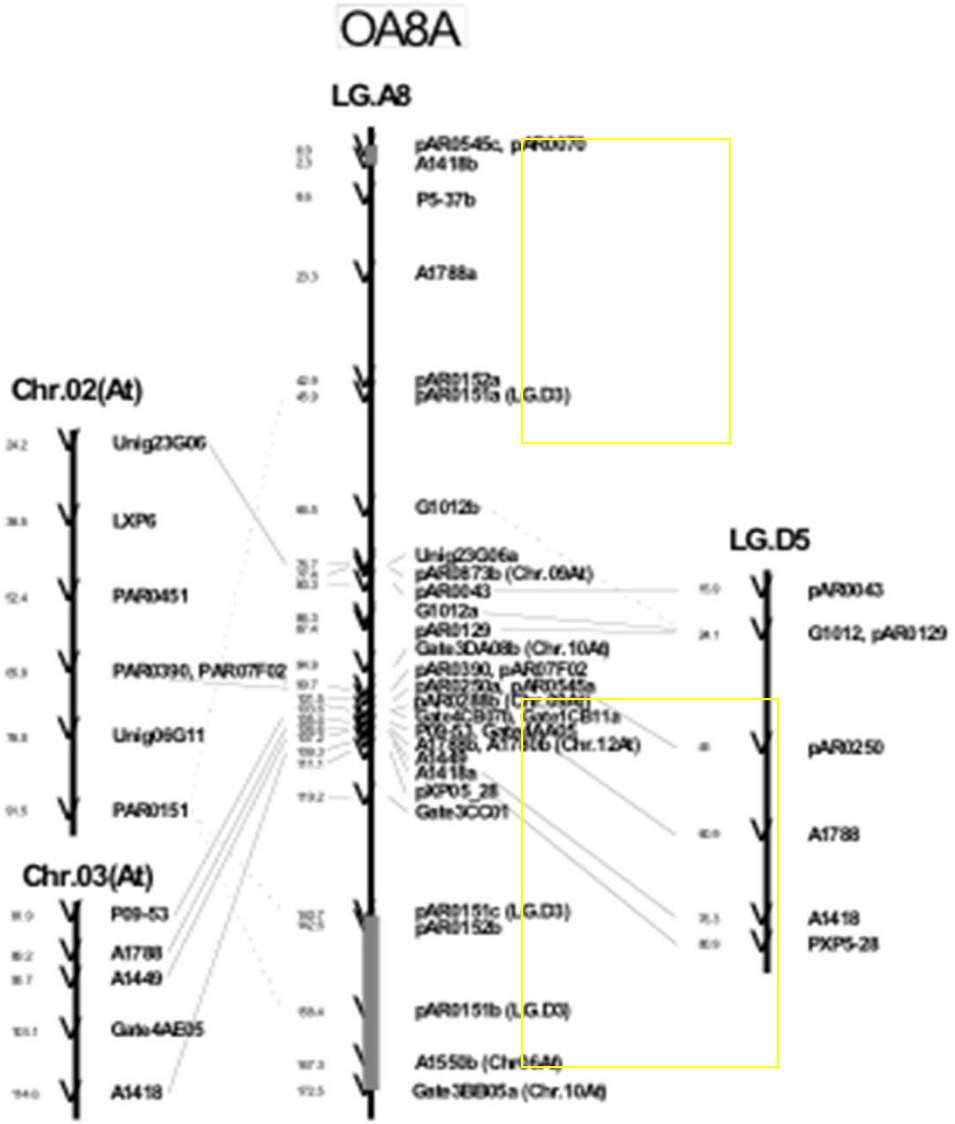


Challenges: A genome (1.75Gb) is about twice the size of D genome (880Mb)



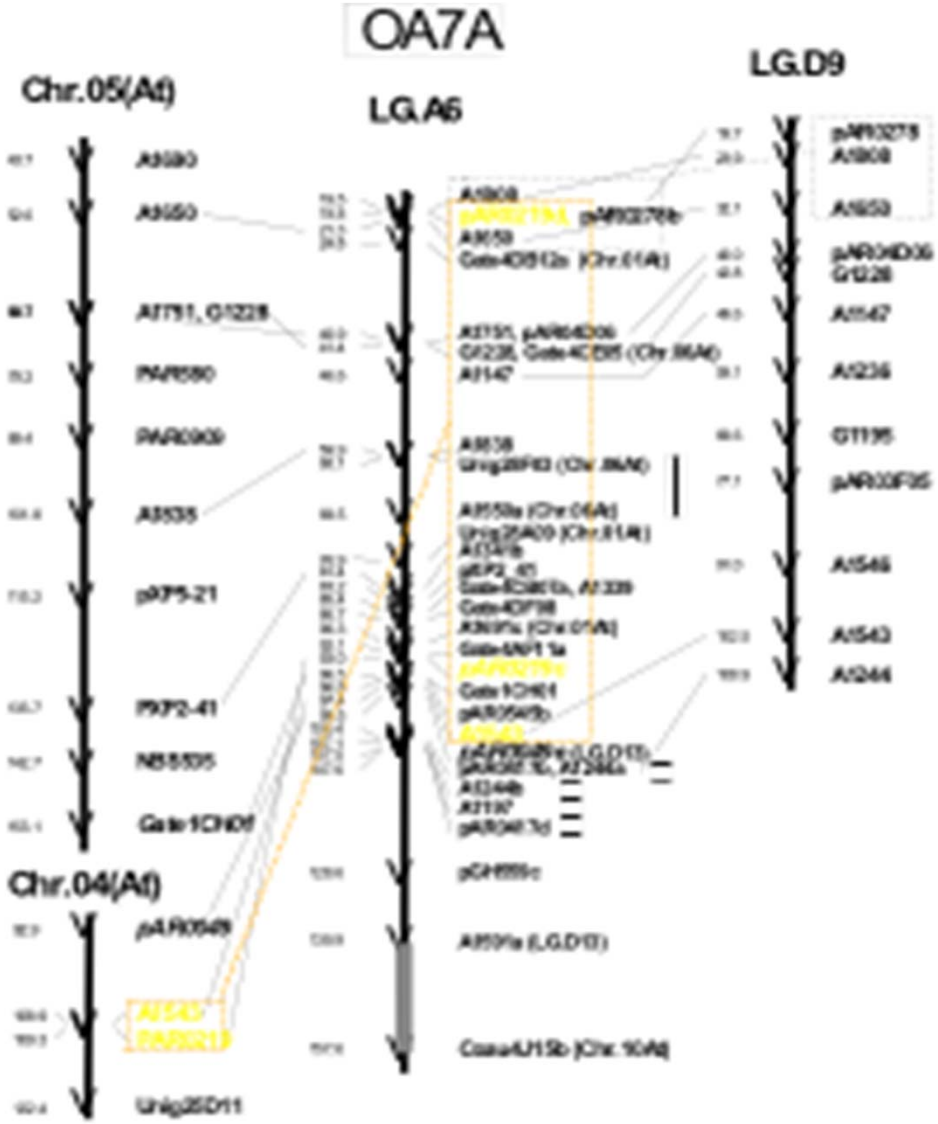
Wendel and Cronn 2002

Challenges: chromosomal structural rearrangements between D vs At genome



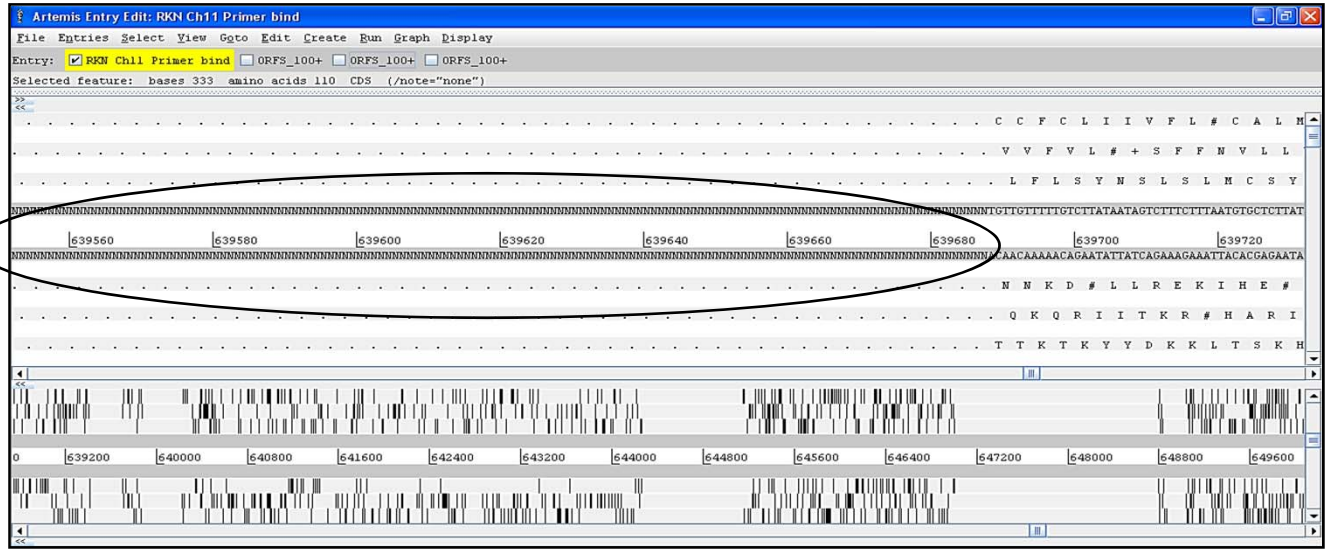
Desai et al. 2006

Challenges: chromosomal structural rearrangements between D vs At genome

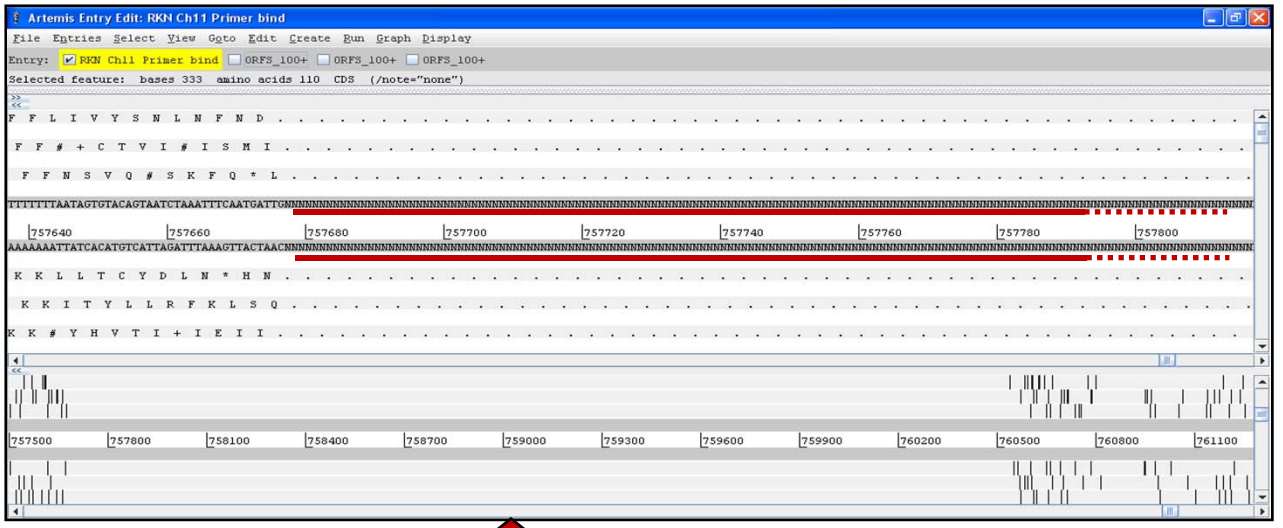


Desai et al. 2006

Challenges: no annotation and gaps in the sequence

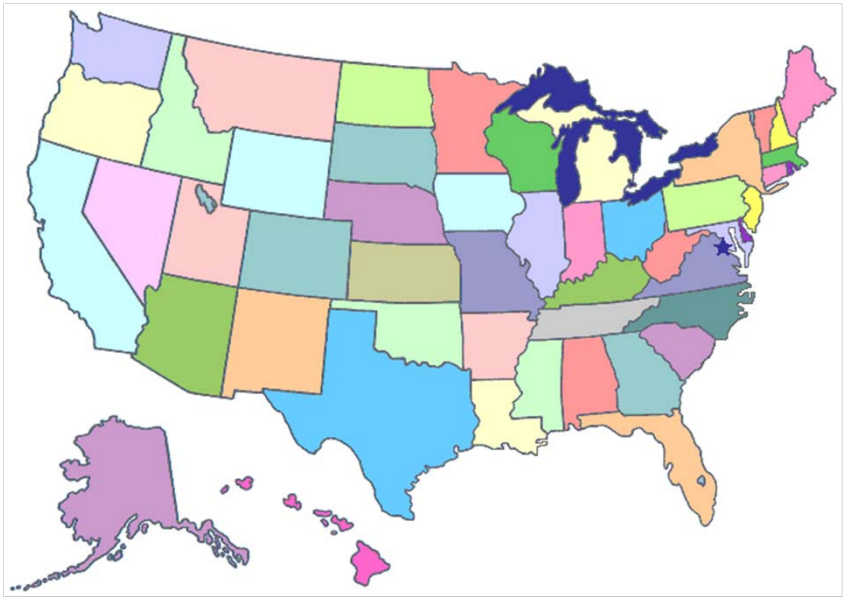


>1 Kb Gap

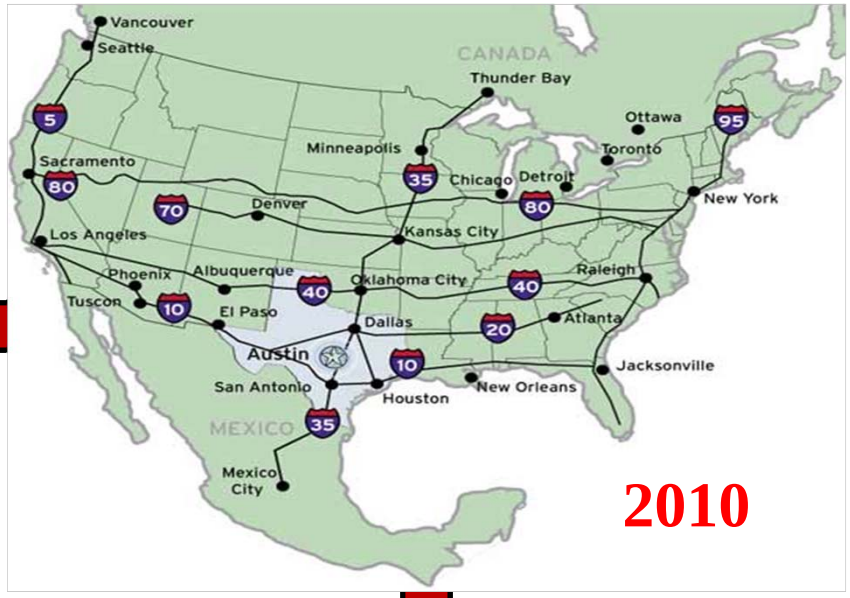


~ 3 Kb Gap

SUMMARY



START



NOW