

GBrowse Population Display and CMap

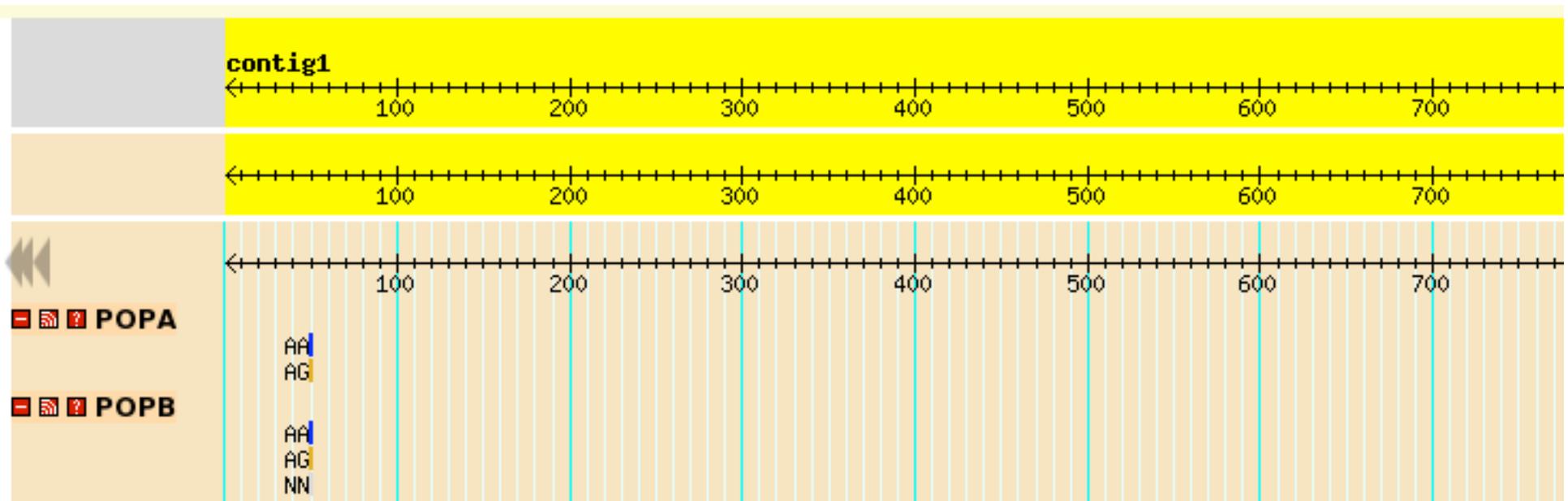
SMBE 2009
Ben Faga

Population Data in GBrowse

- Goal: Overlay population data from GBrowse on a Google Map
- PhyloGeoViz is a mash up to display population data on a Google Map
- PhyloGeoViz was a 2007 Google Summer of Code project by Yi-Hsin Erica Tsai at NESCent
- Interface between GBrowse and PhyloGeoViz
- Available in GBrowse 2 development code

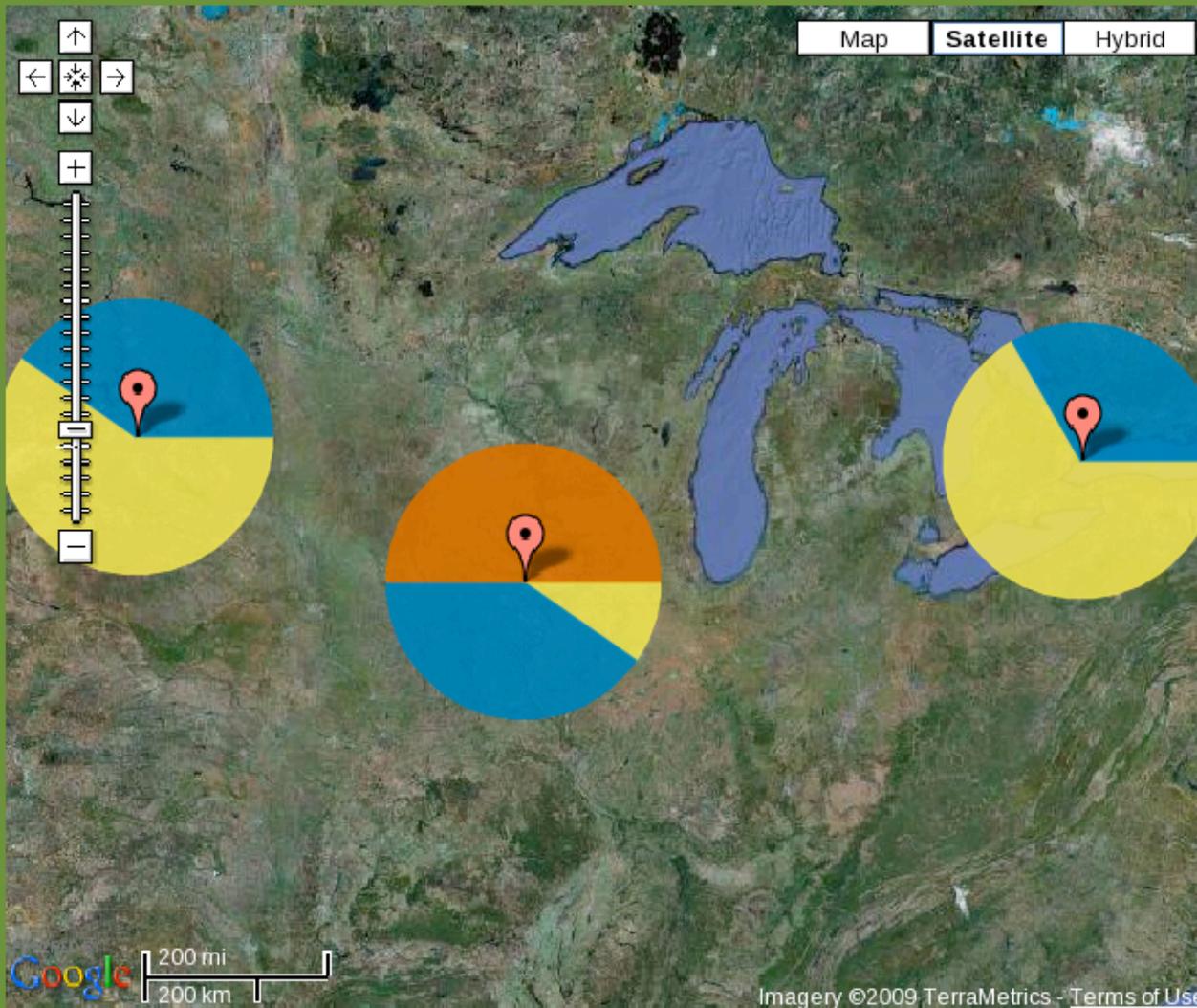
Population Demo

- http://localhost/cgi-bin/gb2/gbrowse/pop_demo
- Each population is a track with latitude and longitude values



GBrowse data in PhyloGeoViz

Your PhyloGeoViz map



Legend and Options

Click on the **+** to expand an option and edit your map.

- Haplotype colors

To edit a color, click on the appropriate colorbox. Click the **+** to expand and edit individual haplotypes.

- Haplotypes

AA

AG

NN

+ Sample sizes

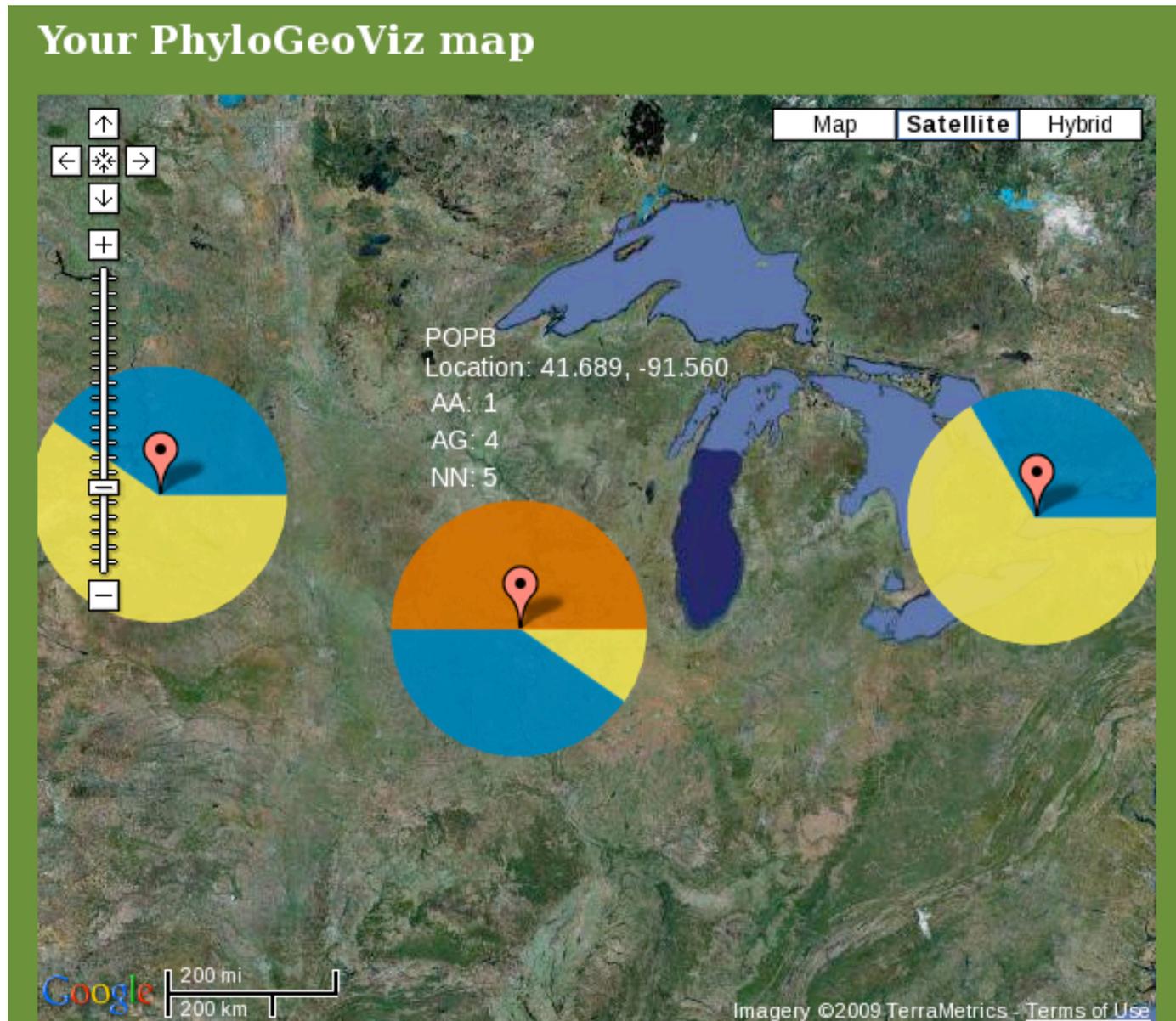
+ Pie options

+ Map options

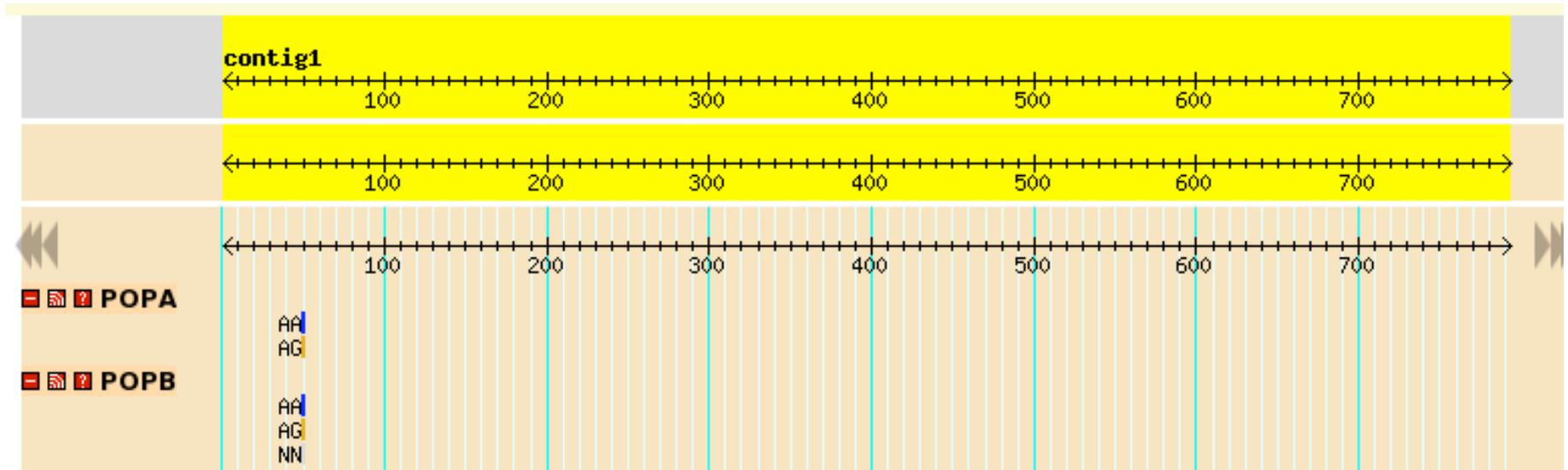
+ Export options

[Start completely over!](#)

Click Marker to Get Population Data



PhyloGeoViz in a Pop-up Balloon

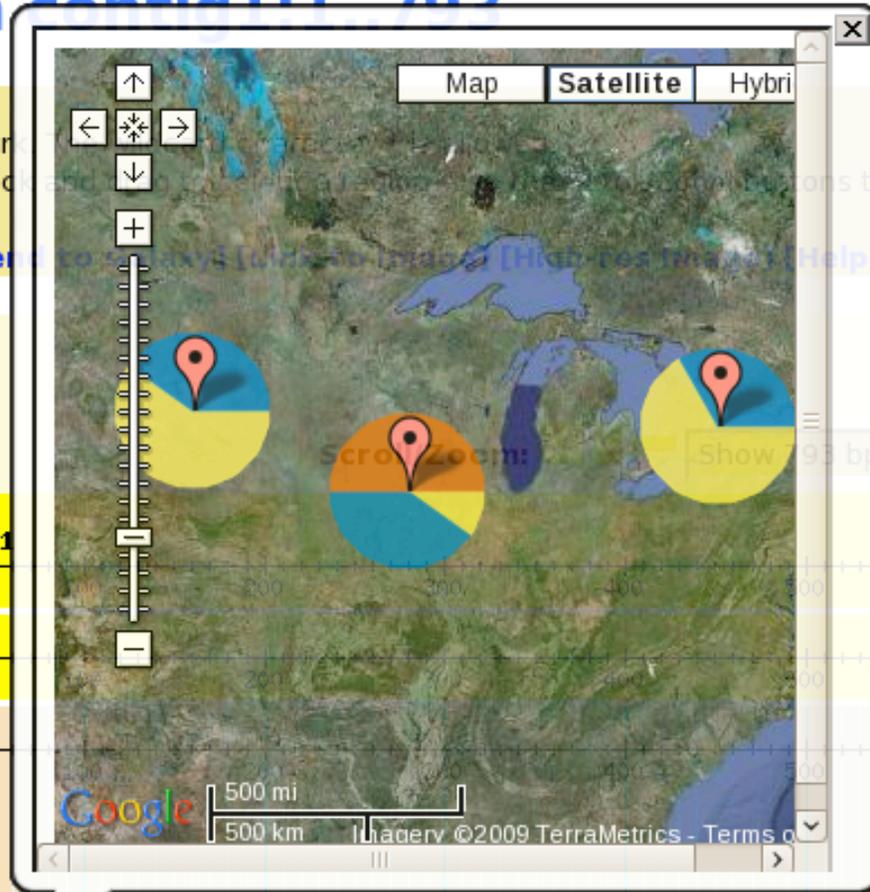


PhyloGeoViz in a Pop-up Balloon

793 bp from contig1:1-793

Name, locus, or other landmark
to center on a location, or click

[Share these tracks] [Send to Galaxy] [Link to Image] [High-res Image] [Help]



to change magnification and position.

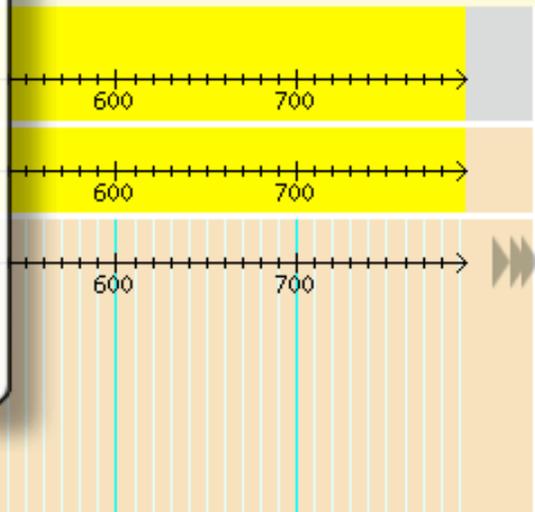
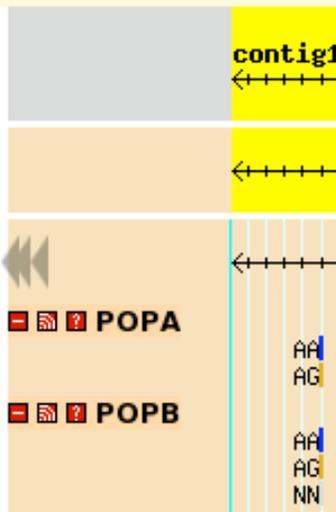
[Reset] Make an Error

+ > >> Flip

600 700

600 700

600 700



Installation Requirements

- GBrowse 2 (in development)
- PhyloGeoViz (Optional but highly recommended)
 - PHP
 - Google Maps API Key

GBrowse Data and Configuration

```
contig1 Contig scaffold 1 793 . . . Name=contig1
contig1 POPA SNP 44 44 8 . . ID=snp.POPA.contig1.44.AA;Name=AA
contig1 POPA SNP 44 44 4 . . ID=snp.POPA.contig1.44.AG;Name=AG
contig1 POPB SNP 44 44 1 . . ID=snp.POPB.contig1.44.AA;Name=AA
contig1 POPB SNP 44 44 4 . . ID=snp.POPB.contig1.44.AG;Name=AG
contig1 POPB SNP 44 44 5 . . ID=snp.POPB.contig1.44.NN;Name=NN
contig1 POPC SNP 44 44 3 . . ID=snp.POPC.contig1.44.AA;Name=AA
contig1 POPC SNP 44 44 2 . . ID=snp.POPC.contig1.44.AG;Name=AG
```

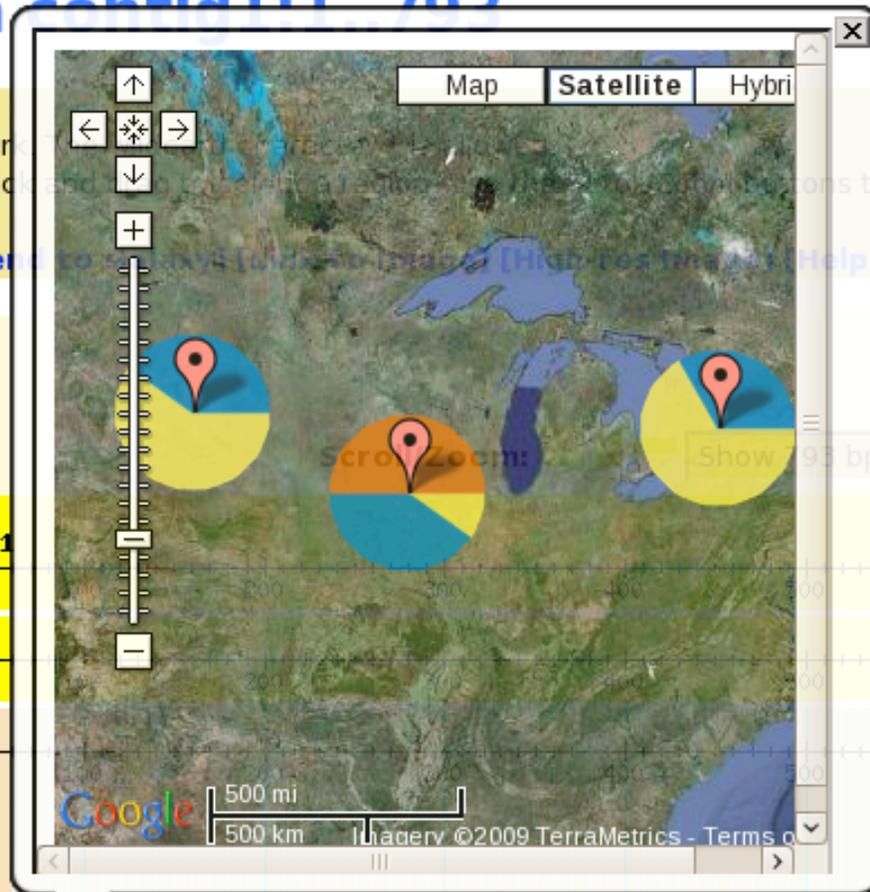
```
[POPB]
feature          = SNP:POPB
glyph            = generic
label_position  = left
fgcolor         = red
width           = 5
linewidth       = 2
category        = Variation
key             = POPB
latitude        = 41.689
longitude       = -91.560
balloon click   = /cgi-bin/gb2/gbrowse_gmap/pop_demo?balloon=1;ref=$ref;...
```

Gbrowse/PhyloGeoViz Questions?

793 bp from contig1:1-793

Name, locus, or other landmark
to center on a location, or click

[Share these tracks] [Send to Galaxy] [Link to Image] [High-res Image] [Help]



to change magnification and position.

[Reset] Make an Error

+ > >> Flip

600 700

600 700

600 700

contig1

←+++++

←+++++

←+++++

POP A

POP B

AA

AG

AA

AG

NN

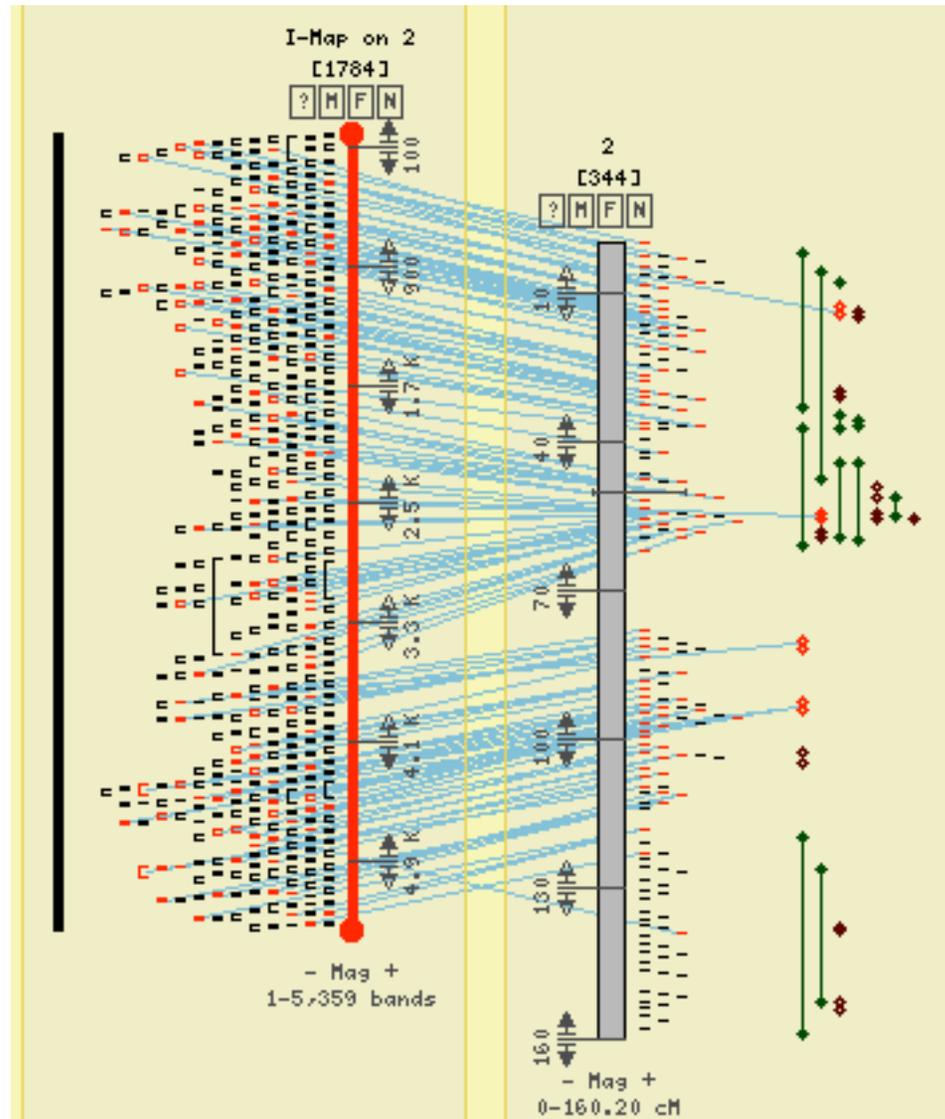
600 700

600 700

600 700

What is CMap?

CMap is a web-based, comparative map viewer



Data provided by the Gramene project (www.gramene.org)

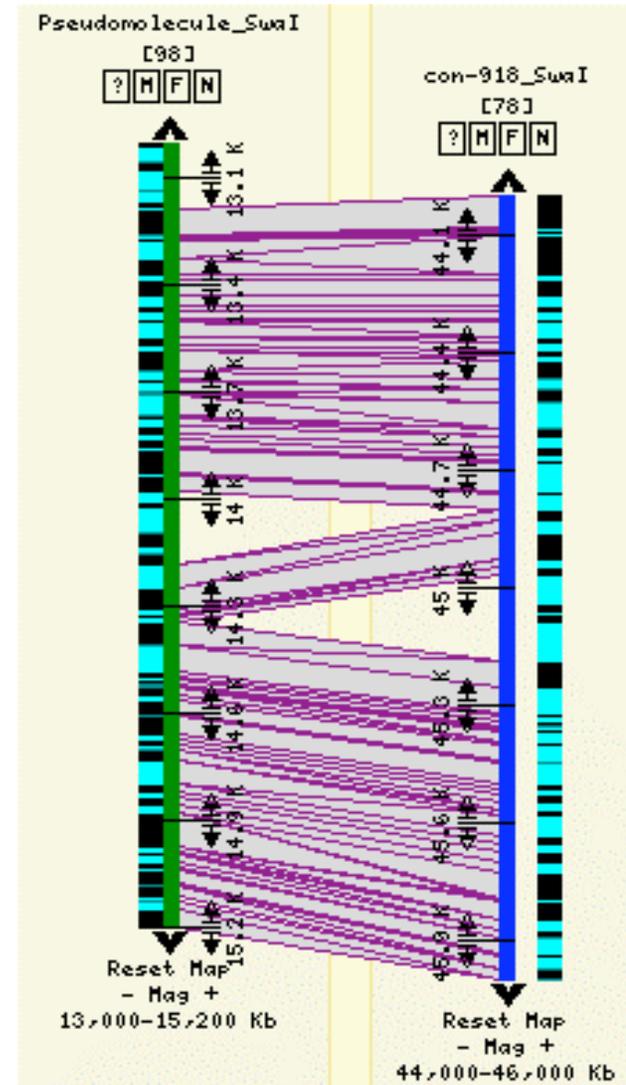
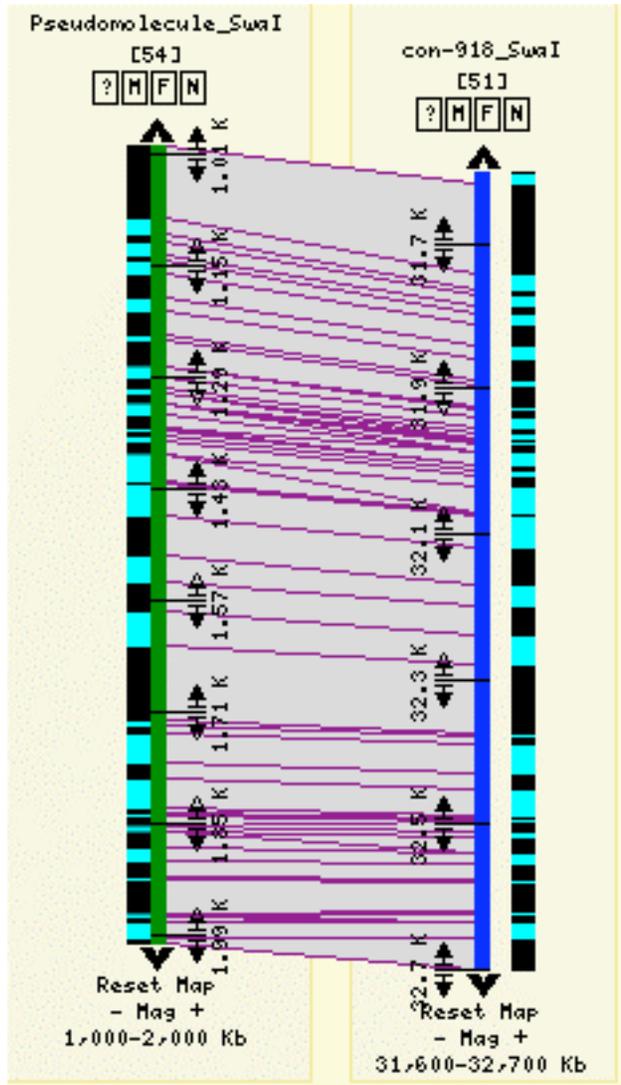
About CMap

- CMap is a web application that can be used to display data to anyone with a web browser
- CMap is a component of the GMOD project which was originally developed for Gramene
- CMap runs on a web server using Perl and is compatible most database management systems
- CMap is freely available, under the GPL or the Artistic License 2.0.

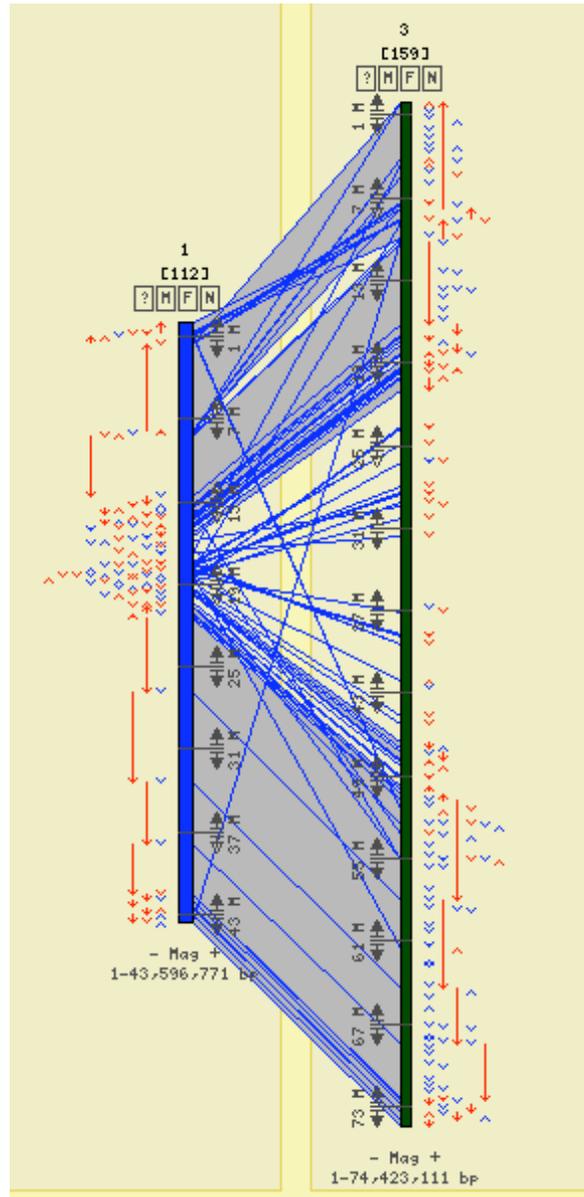
Advantages of CMap (Why Use CMap?)

- CMap is data type agnostic and can display comparisons of sequence data, physical data, genetic data, etc with each other.
- CMap can be used to compare chromosomes of different species.
- CMap can be used to display comparisons of different types of data to look for inconsistencies.
- CMap is web based which makes sharing information as easy as sending a bookmark.

Comparing Sequence Assembly Against Optical Map

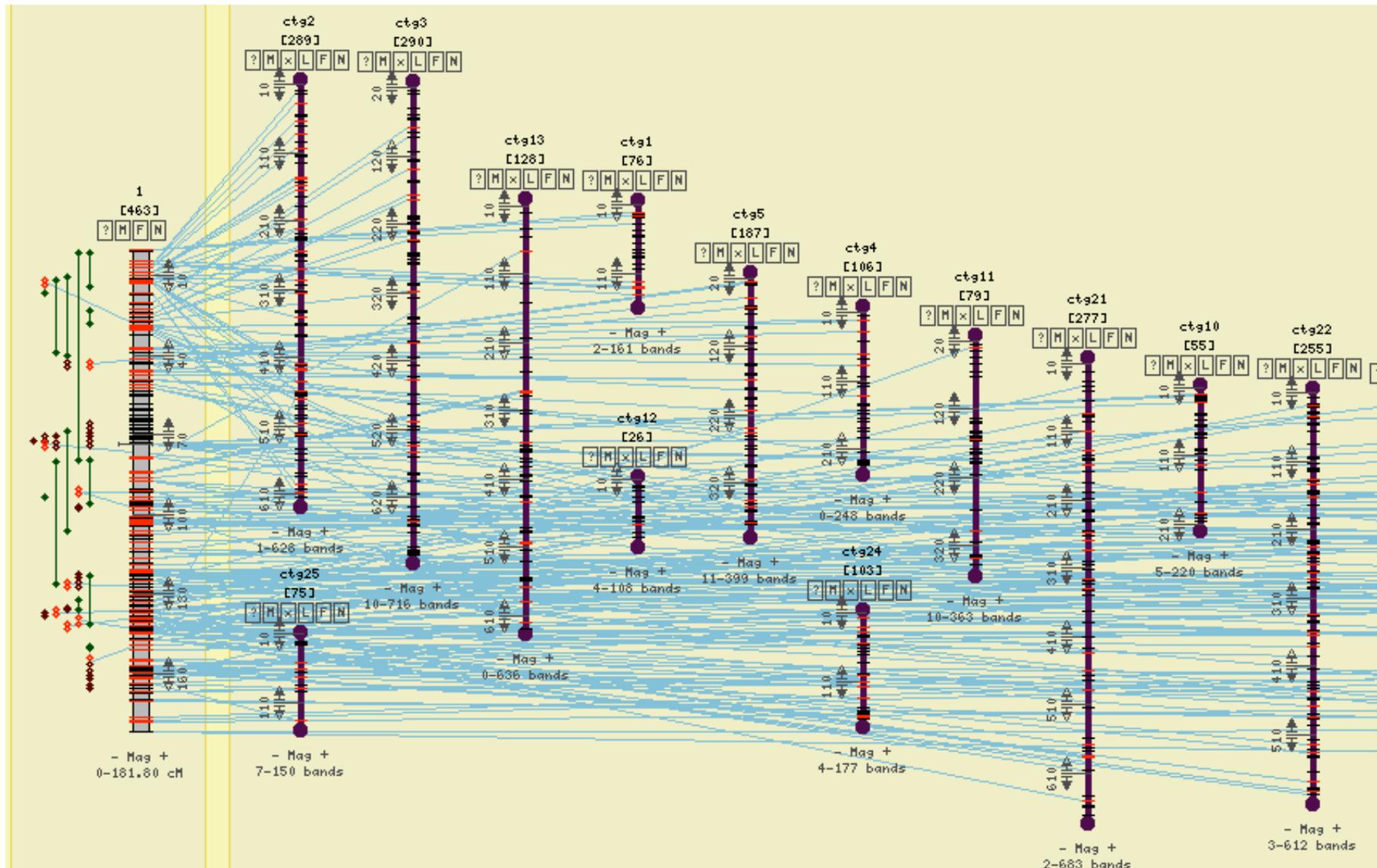


CMap Displaying Synteny



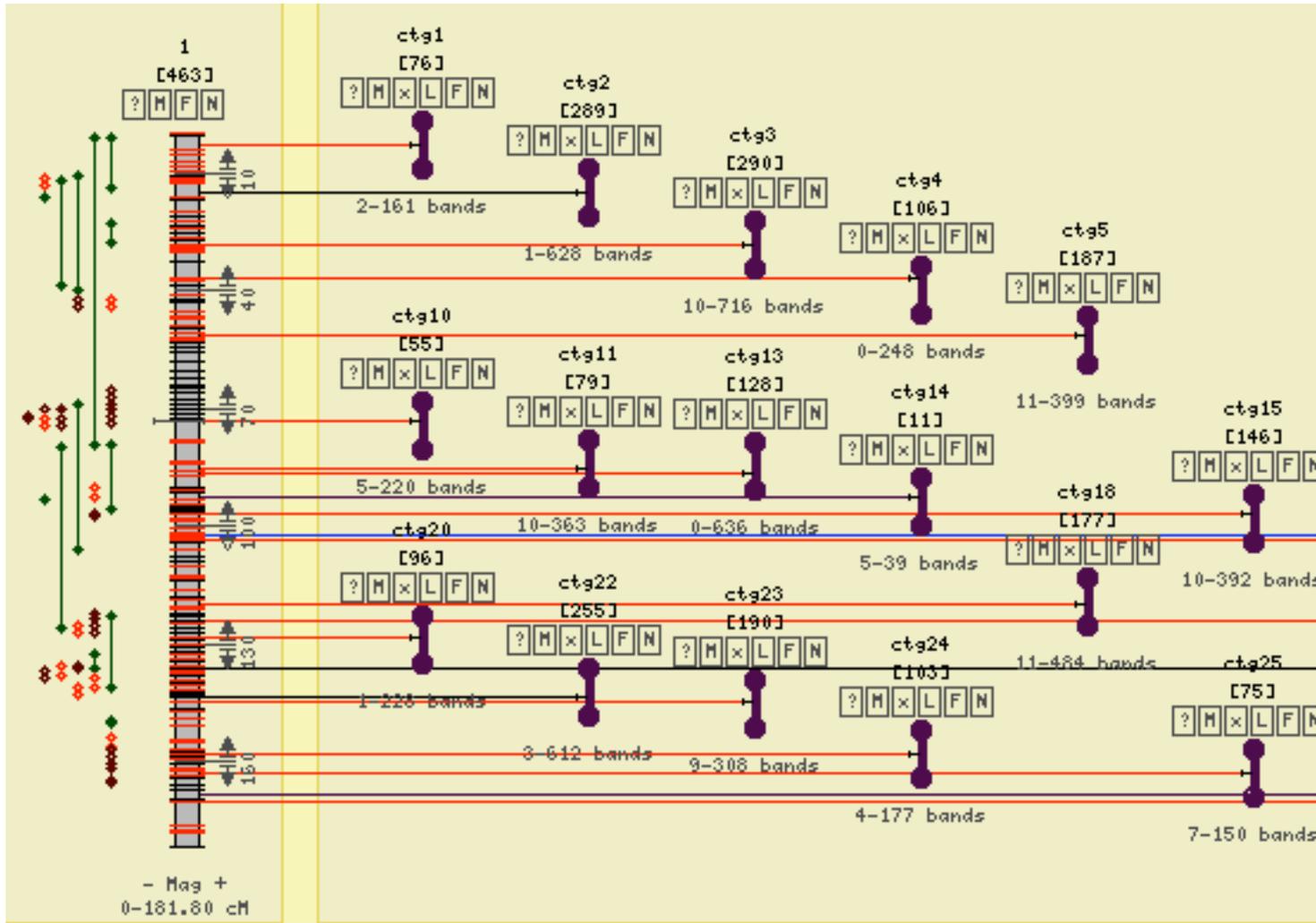
Data provided by the Gramene project (www.gramene.org)

CMap Displaying a Sequence Assembly vs a FPC Maps



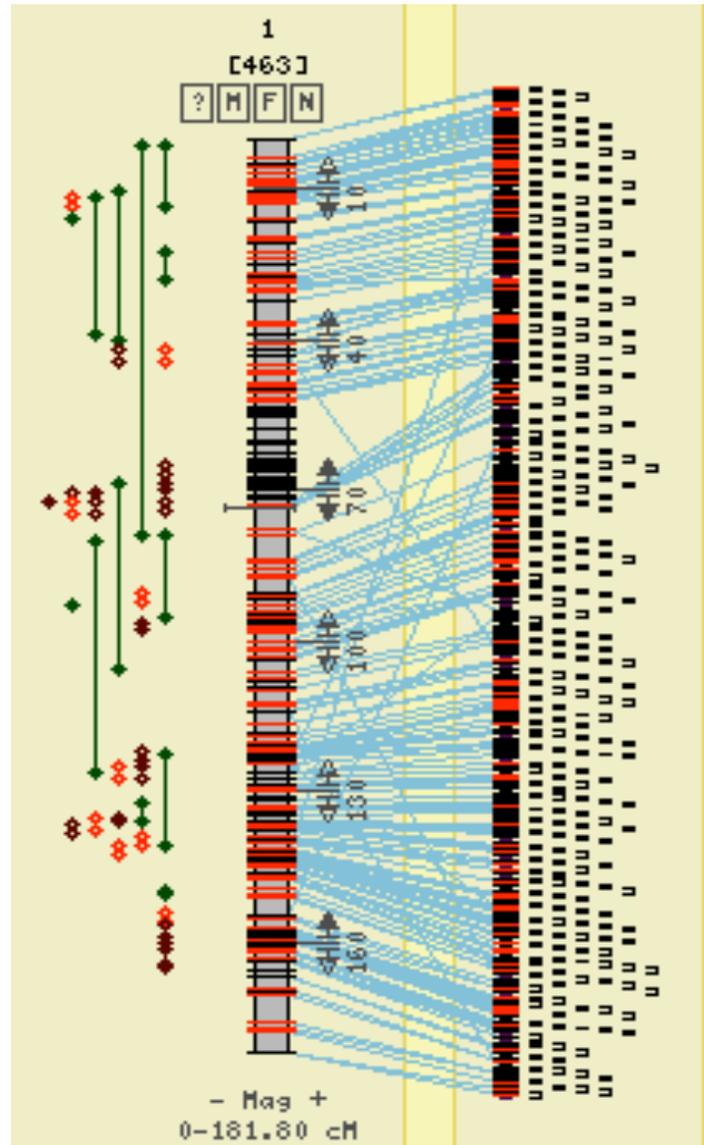
Data provided by the Gramene project (www.gramene.org)

CMap Displaying a Sequence Assembly vs a FPC Maps



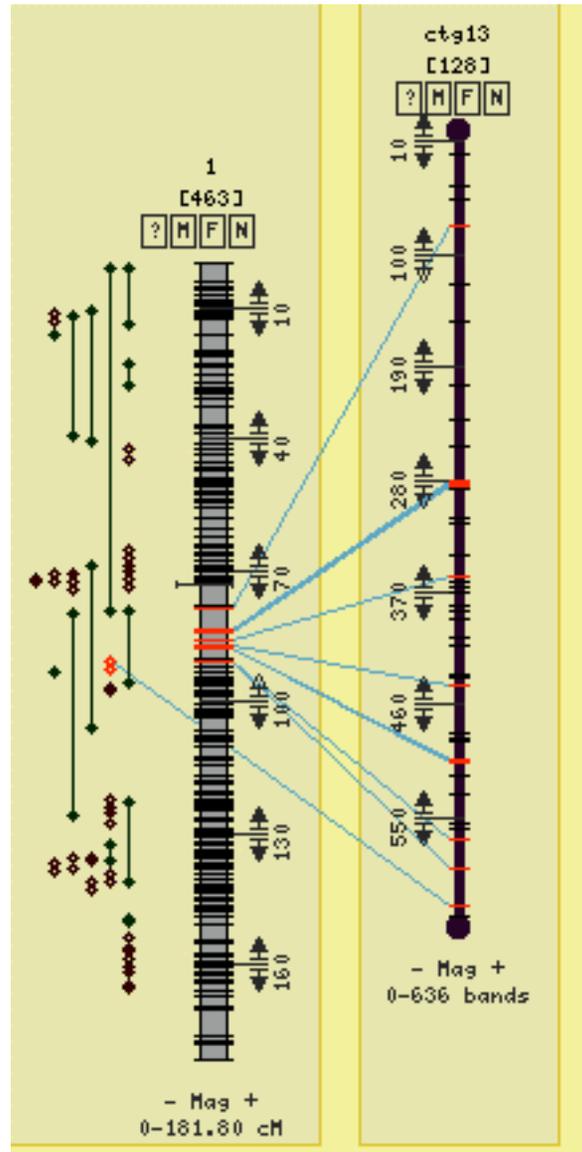
Data provided by the Gramene project (www.gramene.org)

CMap Displaying a Sequence Assembly vs a FPC Maps



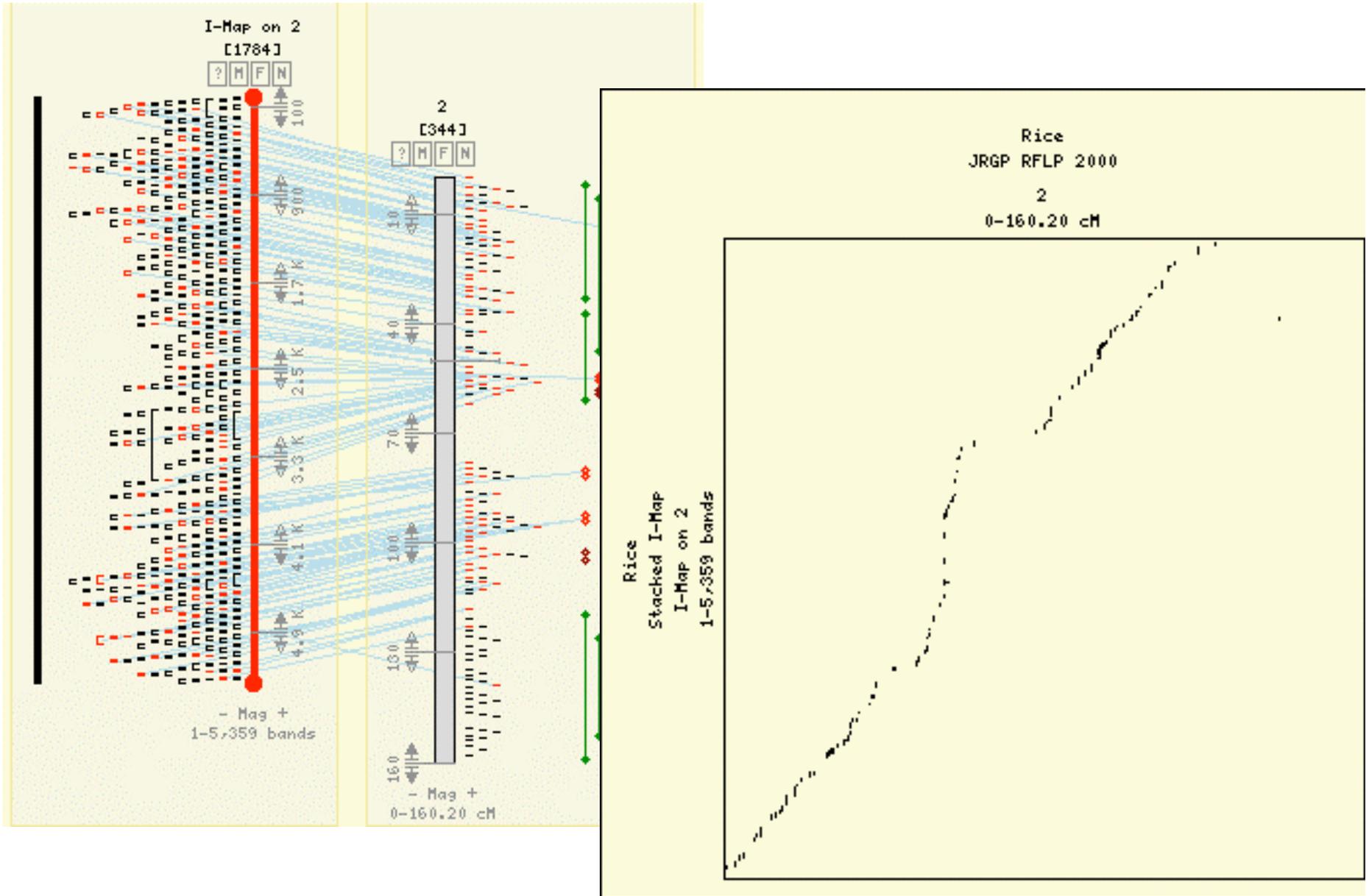
Data provided by the Gramene project (www.gramene.org)

CMap Displaying a Sequence Assembly vs a FPC Maps



Data provided by the Gramene project (www.gramene.org)

Dot Plot



What CMap is Not:

- GBrowse
- A sequence viewer (no sequence is imported)
- A tool for creating data (although it has a tool for creating correspondences between features of the same name)
- Easily googled for (use “GMOD CMap”)

Importing Data

```
tabtest1 (/usr/local/src/gmod/cmap/data) - VIM
File Edit View Terminal Tabs Help
map_name  feature name  feature_start  feature_stop  feature_type_acc  feature_aliases
T1 T1.1  0  1000  contig  T1.A,T1.AA
T1 T1.2  1000  2000  contig  T1.2,T1.B
T1 T1.3  2000  4000  contig  T1.C
T1 R1.g1  0  500  read
T1 R2.g1  450 1000  read
T1 R3.g1  1000 2000  read
T1 R4.g1  2000 2300  read
T1 R5.b1  2200 2700  read
T1 R6.b1  2650 3300  read
T1 R7.g1  3100 4000  read
T2 T2.1  0  1000  contig  T2.A
T2 R10.g1 0  500  read
T2 R11.g1 500 1000  read
T1 28 0  99  read_depth
```

- Tab Delimited
- CMap GFF3

```
test_data.gff (/usr/local/src/gmod/cmap/data) - VIM
File Edit View Terminal Tabs Help
T1 98 100 1
T1 30 200 2
T1 6 300 3
T1 72 400 4
T1 98 500 5
T1 66 600 6
T1 47 700 7
T1 38 800 8
T1 71 900 9
T1 38 1000
T1 31 1100
T1 16 1200
##gff-version 3
##cmap-gff-version 1
# This file was produced from a CMap database using Bio::GMOD::CMap::Admin::GFFProducer
# Data was created by Apurva Narechania of the Gramene Project
##cmap_species species_acc=oryza_sativa;species_common_name=0.%20sativa;species_full_name=Oryza%20sativa;display_order=1
###
##cmap_map_set map_set_name=Chromosomes;map_set_short_name=Chromosomes;map_type_acc=Seq;map_set_acc=oscl;shape=box;color=blue;width=7;published_on=2008-06-21;nit_modifier=1
##cmap_map map_name=1;map_start=1.00;map_stop=43596771.00;display_order=1
##sequence-region 1 1.00 43596771.00
1 CMap syntenic_block 272.00 770372.00 . - . ID=syntenic_block5279691;Name=sb3_272-770372;corr_by_id=syntenic_block5279692 synteny
1 CMap syntenic_block 771644.00 865909.00 . + . ID=syntenic_block5279693;Name=sb3_771644-865909;corr_by_id=syntenic_block5279694 synteny
1 CMap syntenic_block 908682.00 916533.00 . + . ID=syntenic_block5279695;Name=sb3_908682-916533;corr_by_id=syntenic_block5279696 synteny
1 CMap syntenic_block 916534.00 921969.00 . + . ID=syntenic_block5279697;Name=sb3_916534-921969;corr_by_id=syntenic_block5279698 synteny
1 CMap syntenic_block 924568.00 931238.00 . + . ID=syntenic_block5279699;Name=sb6_924568-931238;corr_by_id=syntenic_block5279700 synteny
1 CMap syntenic_block 932358.00 953538.00 . - . ID=syntenic_block5279701;Name=sb3_932358-953538;corr_by_id=syntenic_block5279702 synteny
1 CMap syntenic_block 954753.00 998110.00 . + . ID=syntenic_block5279703;Name=sb3_954753-998110;corr_by_id=syntenic_block5279704 synteny
1 CMap syntenic_block 1005103.00 1496898.00 . - . ID=syntenic_block5279705;Name=sb3_1005103-1496898;corr_by_id=syntenic_block5279706 synteny
1 CMap syntenic_block 1500876.00 1507641.00 . + . ID=syntenic_block5279707;Name=sb3_1500876-1507641;corr_by_id=syntenic_block5279708 synteny
1 CMap syntenic_block 1508867.00 7852517.00 . - . ID=syntenic_block5279709;Name=sb3_1508867-7852517;corr_by_id=syntenic_block5279710 synteny
1 CMap syntenic_block 7854349.00 7904439.00 . - . ID=syntenic_block5279711;Name=sb3_7854349-7904439;corr_by_id=syntenic_block5279712 synteny
1 CMap syntenic_block 8044160.00 8051670.00 . + . ID=syntenic_block5279713;Name=sb8_8044160-8051670;corr_by_id=syntenic_block5279714 synteny
1,1 T
```

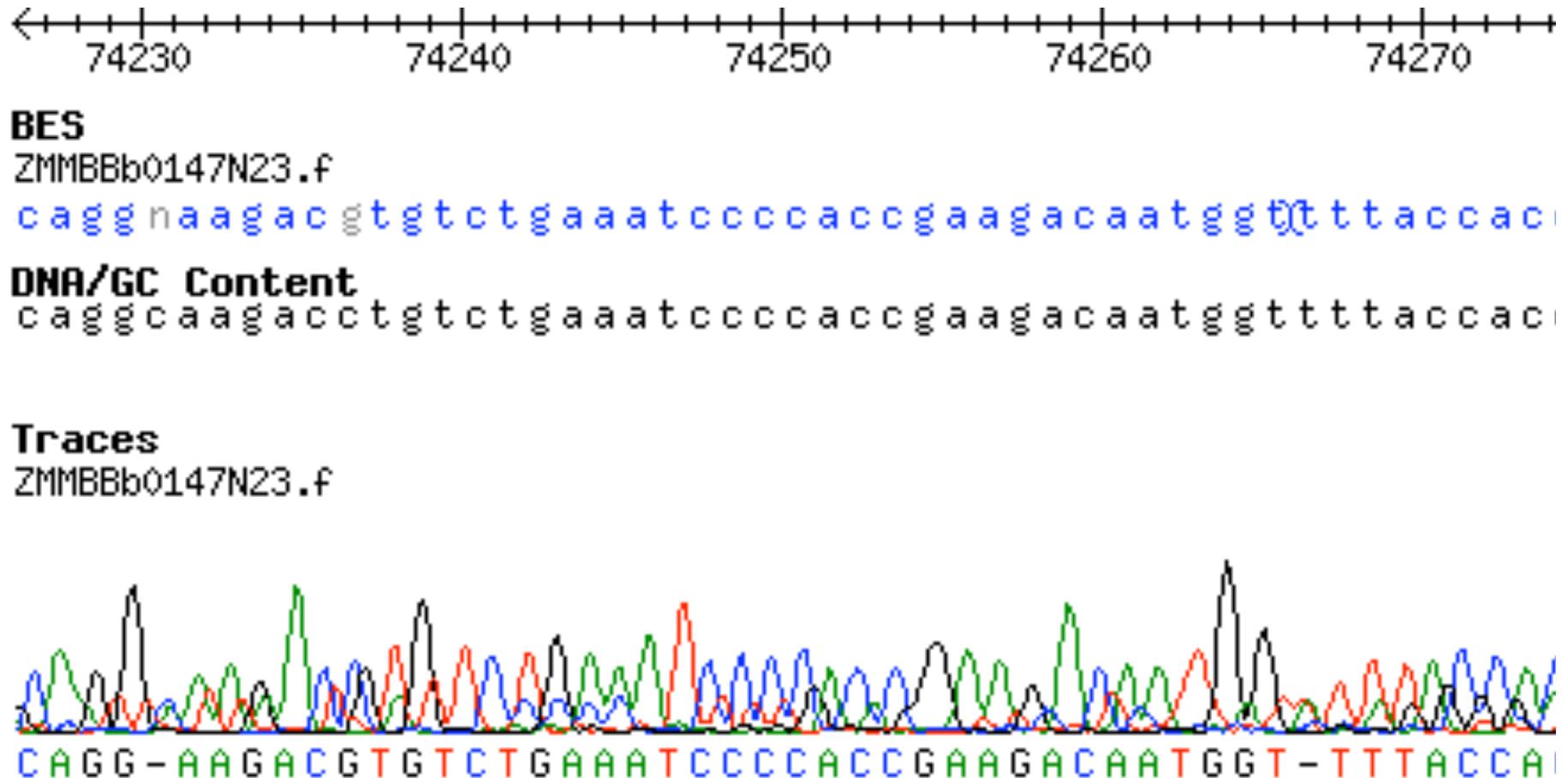
Acknowledgments

- Doreen Ware and the Ware Lab
- Lincoln Stein and the Stein Lab
- Gramene (www.gramene.org)
- GMOD (www.gmod.org)
- NESCent (www.nescent.org)
- Google (www.google.com)
- Yi-Hsin Erica Tsai (original author of PhyloGeoViz)
- Ken Clark (original author of CMap)

www.gmod.org/CMap

Live Demo
(Time and Technology Permitting)

GBrowse Alignment and Trace



Note: base differences are gray and insertions are represented by “)(“

Menu System

☐ Map Options

Map Set	Add Maps Left	Rice-JRGP RFLP 2000 (Reference Set)	Add Maps Right
Min. Correspondences			
Stack Vertically		<input type="checkbox"/>	
Maps		1	
Start		0.00	
Stop		181.80	
Magnification		Original ▼	
Flipped		<input type="checkbox"/>	

Format: Name [Total correspondences to slot, Max correspondences to single map]
hint: To save time, select the desired options before redrawing the map.

(Hide Map Menu)

- ⊕ Feature Options
- ⊕ Correspondence Options
- ⊕ Display Options
- ⊕ Advanced Options

Asynchronous Comparative Maps Menu

Comparative Maps (Right Side)

Add Map Set ▼

No Map Set Selected ▲

Min. Correspondences:

Refresh Menu

Map Set	Add Maps Left	Rice-JRGP RFLP 2000 (Reference Set)	Rice-Niigata RFLP 2000		See Menu Above
Min. Correspondences			<input type="text" value="0"/>		
Stack Vertically		<input type="checkbox"/>			
Maps		1	1 <input type="button" value="Delete"/>	2 <input type="button" value="Delete"/>	
Start		<input type="text" value="0.00"/>	<input type="text" value="0.00"/>	<input type="text" value="0.00"/>	
Stop		<input type="text" value="181.80"/>	<input type="text" value="130.30"/>	<input type="text" value="123.50"/>	
Magnification		Original ▼	Original ▼	Original ▼	

Heat Map Feature Glyph

