# 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 poplation 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

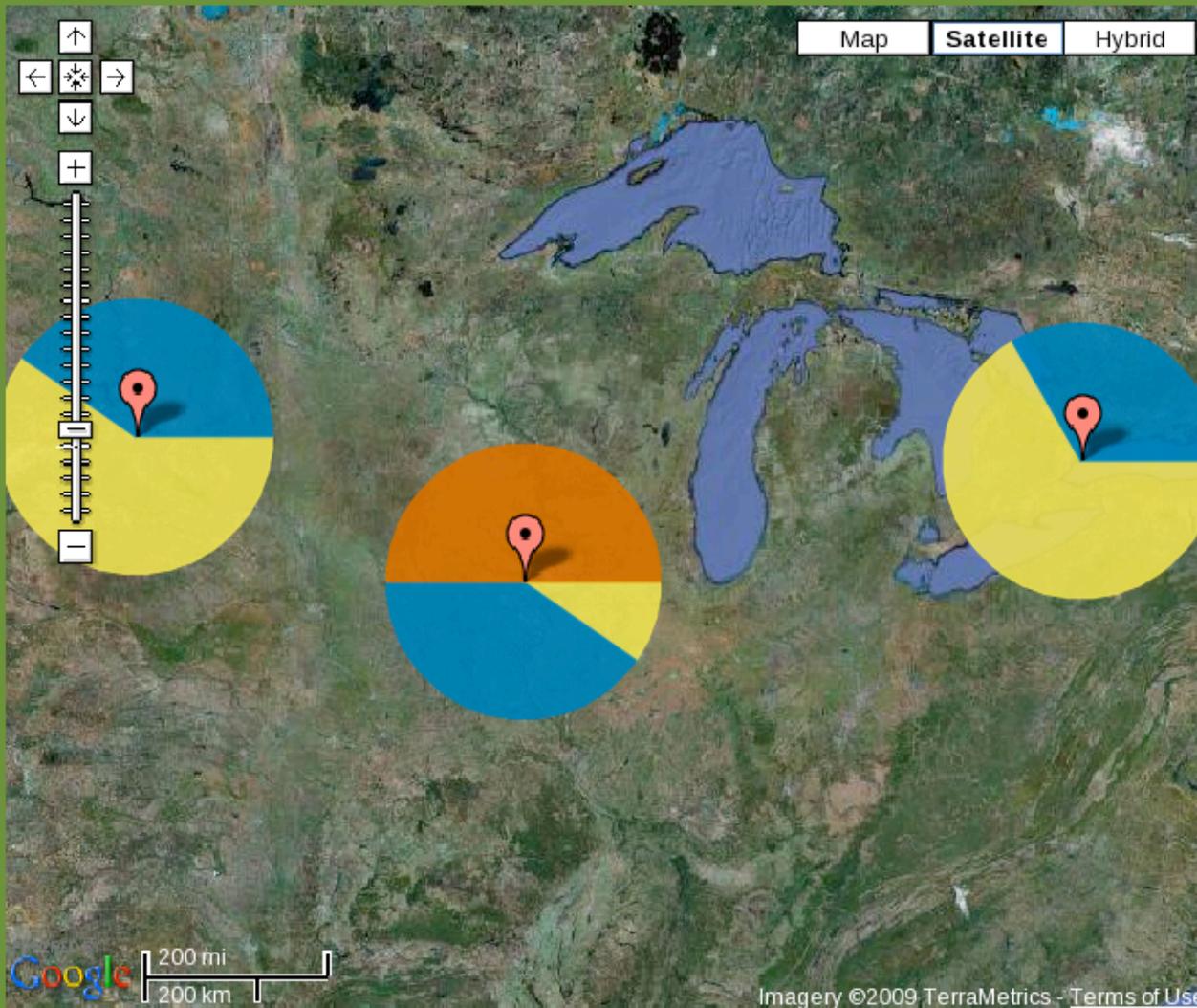- Available in GBrowse 2 development code

Population Demo

- http://localhost/cgi-bin/gb2/gbrowse/pop_demo

- Each population is a track with latitude and longitude values
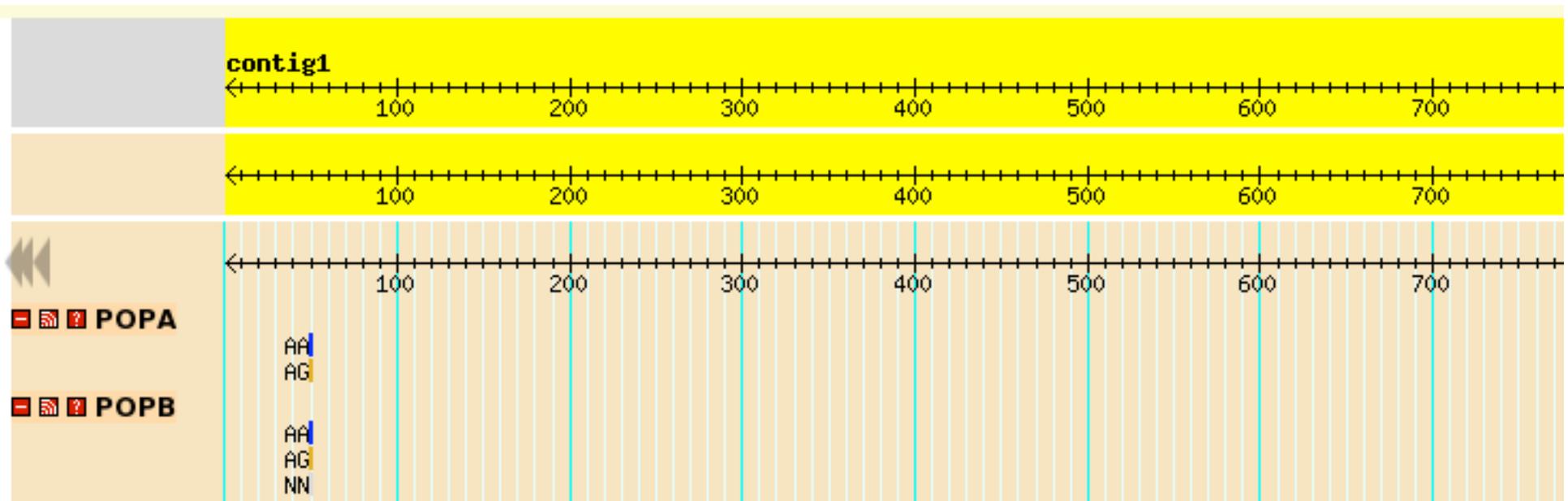
GBrowse data in PhyloGeoViz

Click Marker to Get Population Data
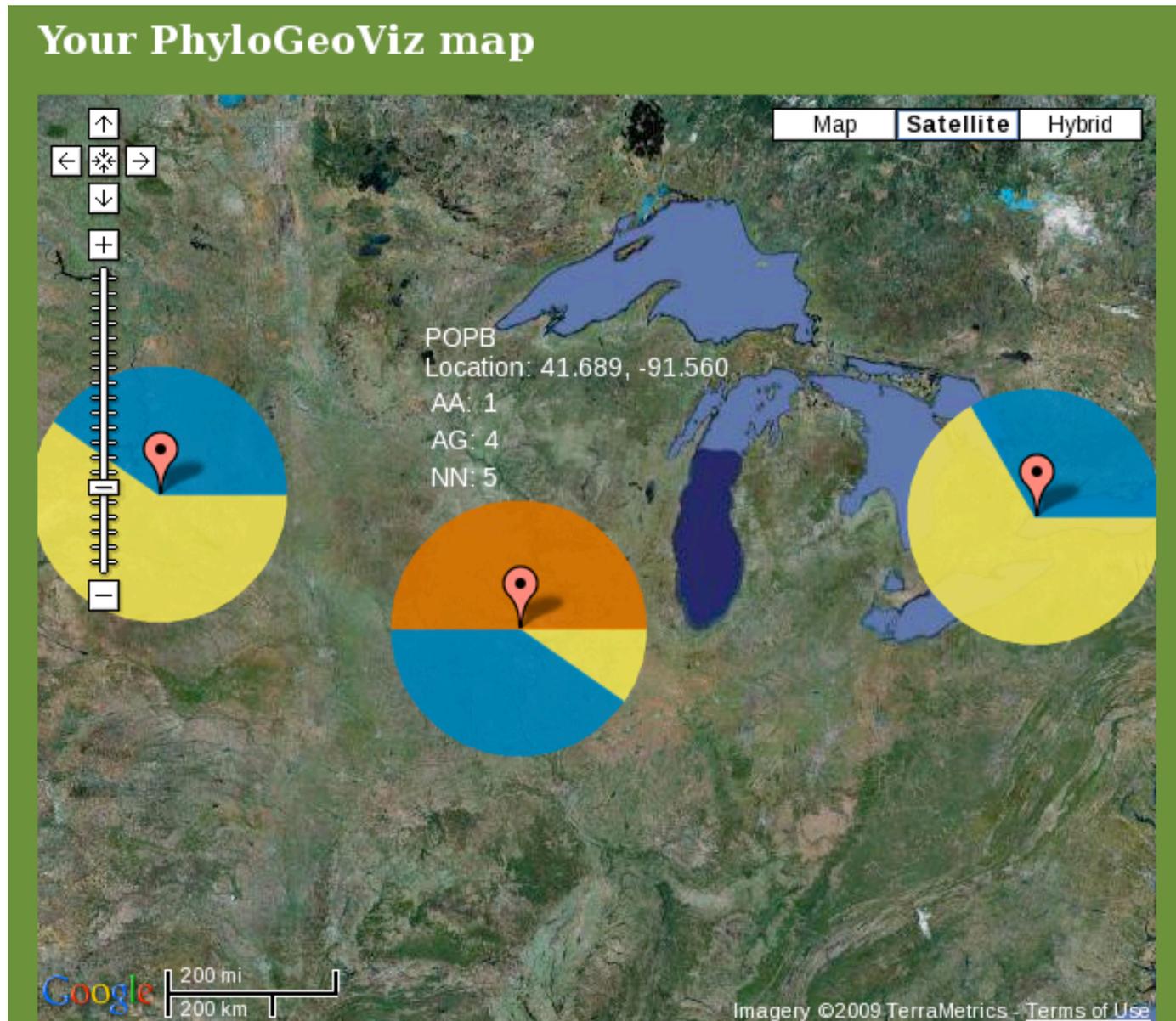
PhyloGeoViz in a Pop-up Balloon
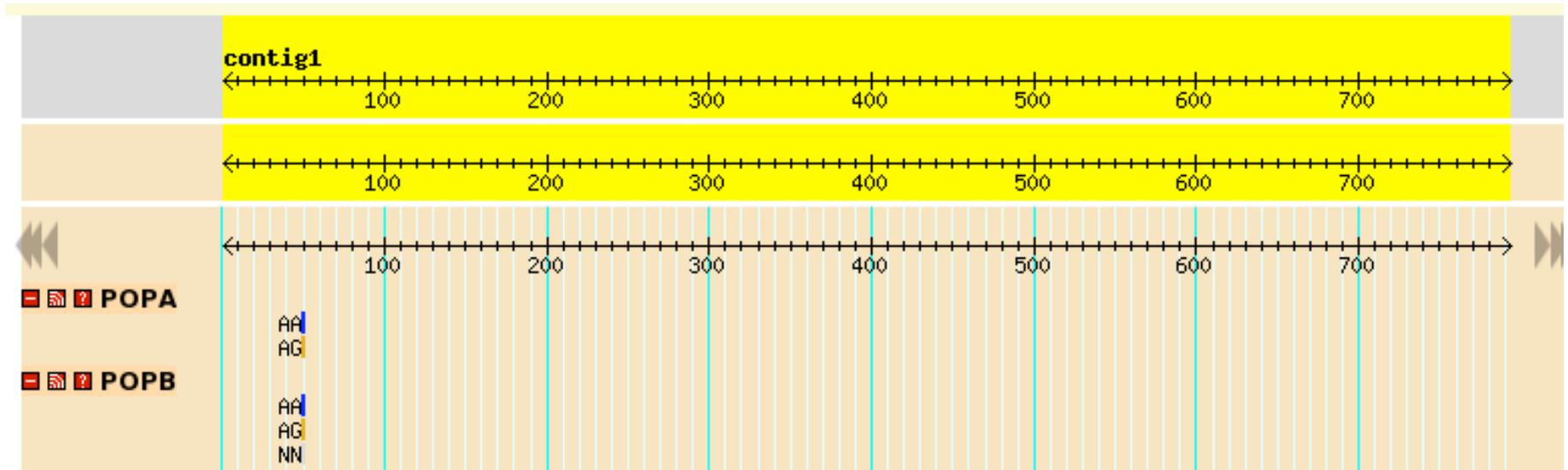
PhyloGeoViz in a Pop-up Balloon
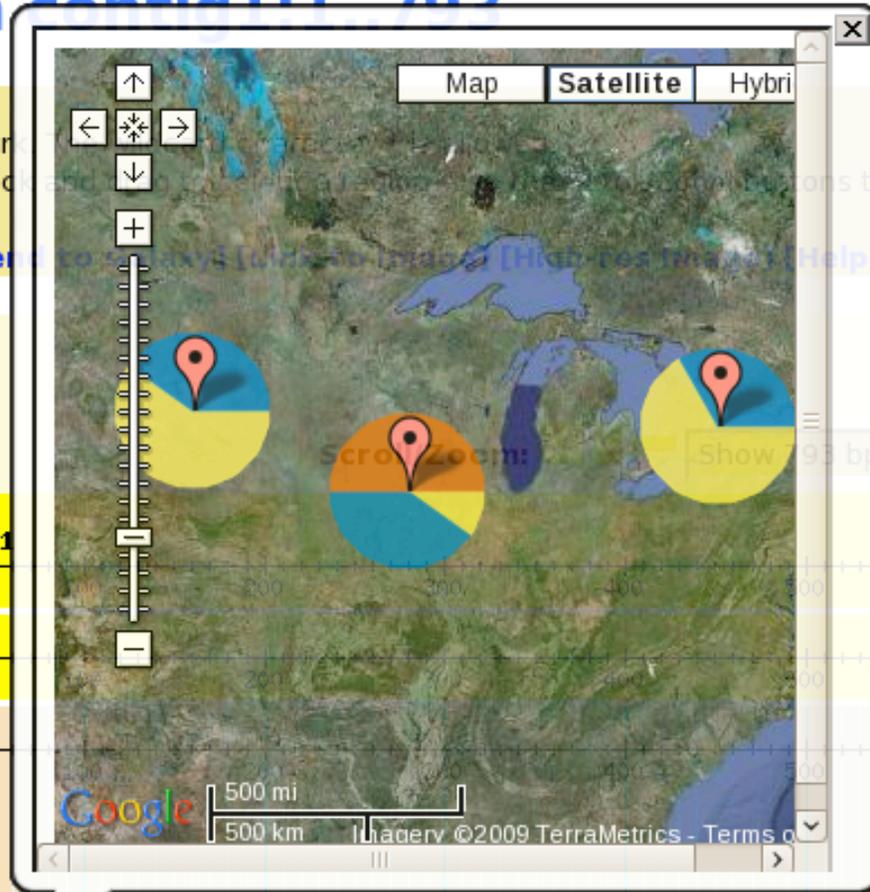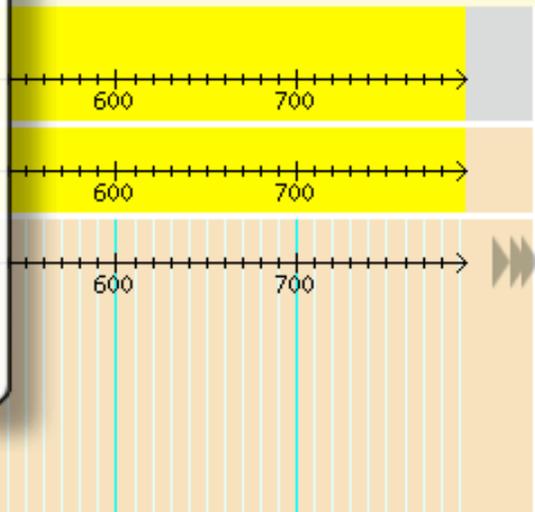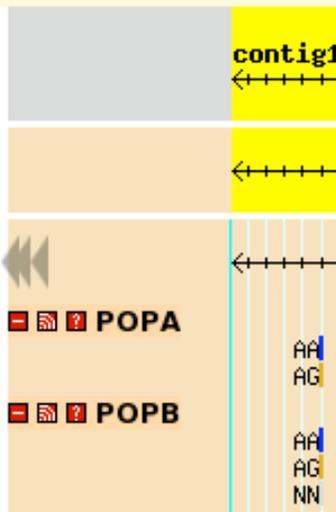
Installation Requirements

- GBrowse 2 (in development)

- PhyloGeoViz (Optional but highly recommende

  - 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;...
```
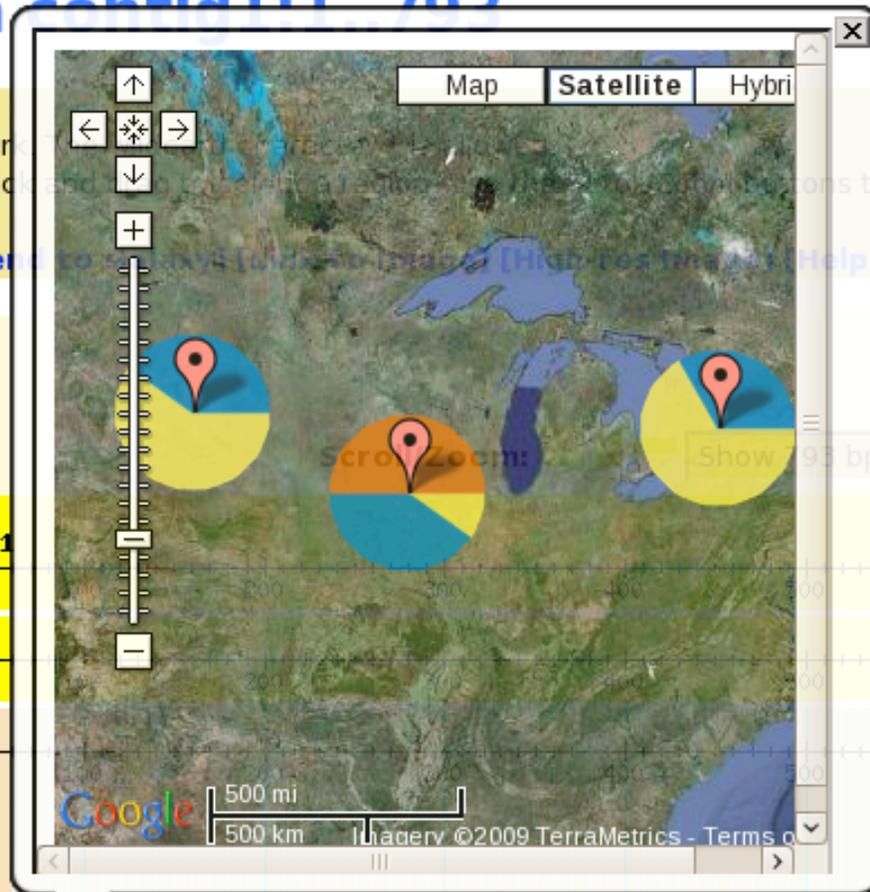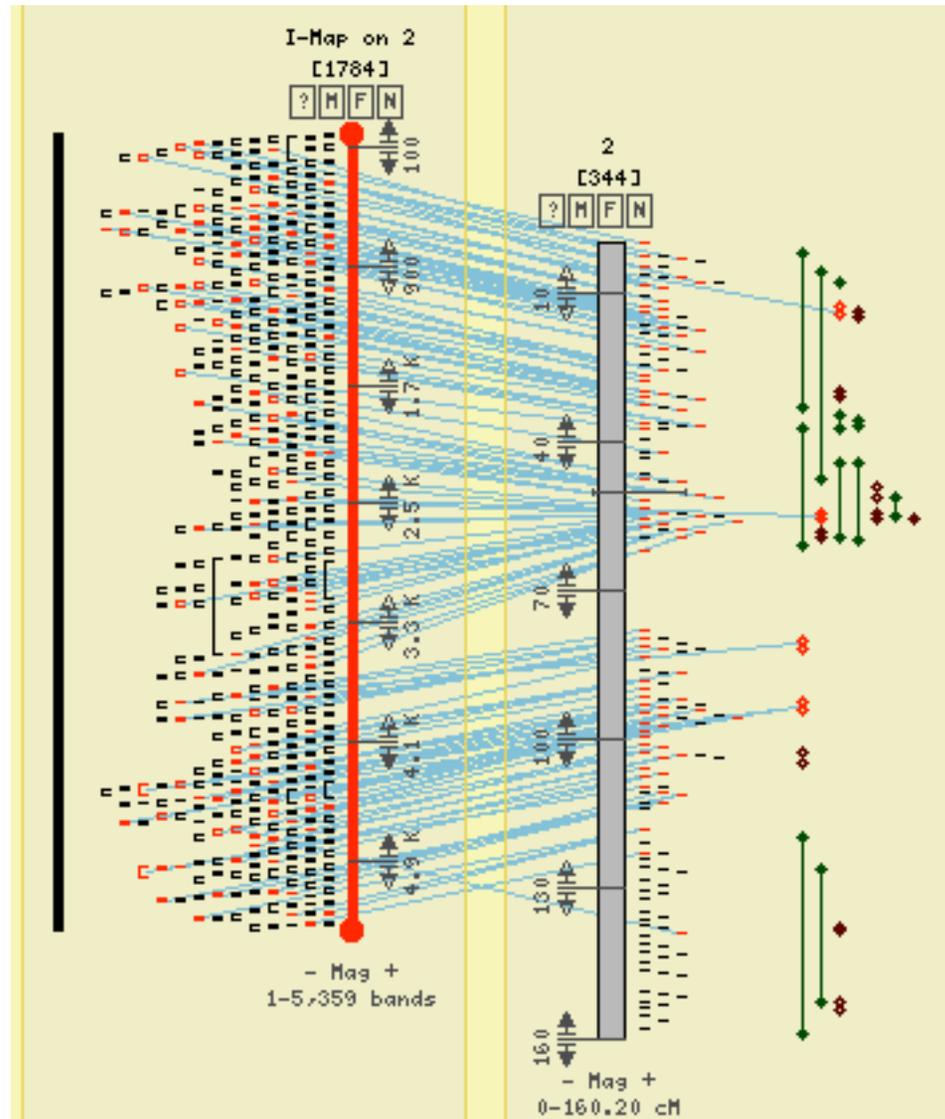
Gbrowse/PhyloGeoViz Questions?

What is CMap?

CMap is a web-based, comparative map viewer

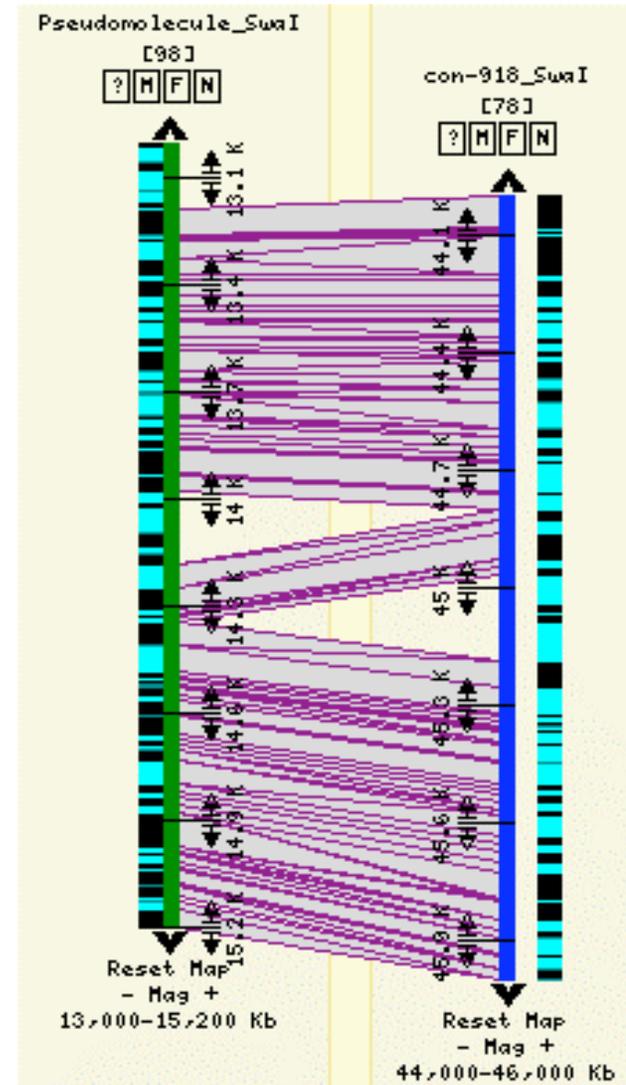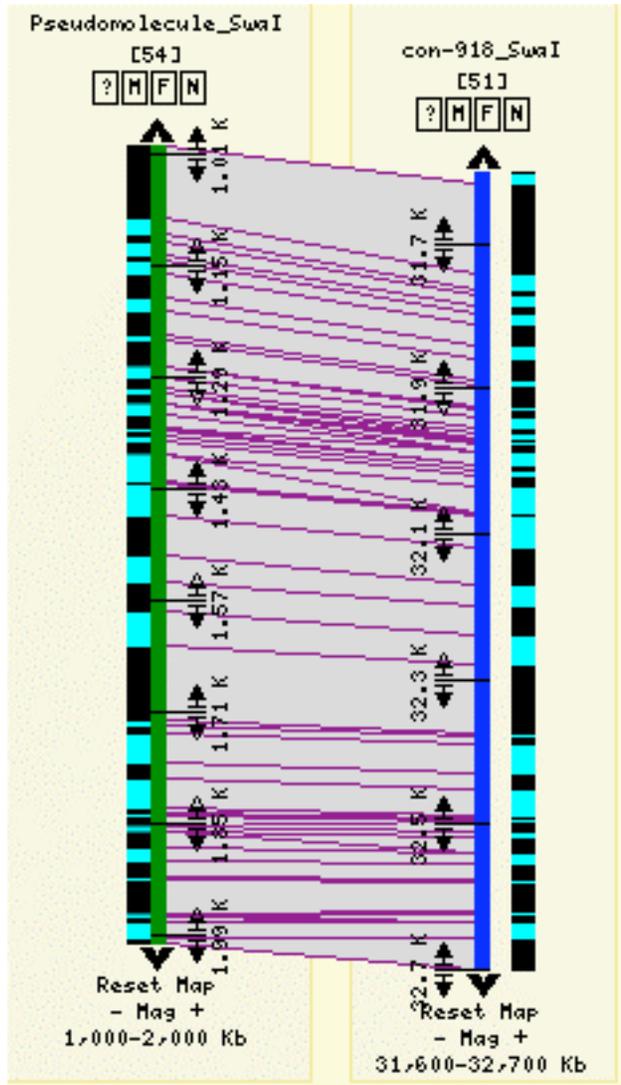Data provided by the Gramene project (www.gramene.org)

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.
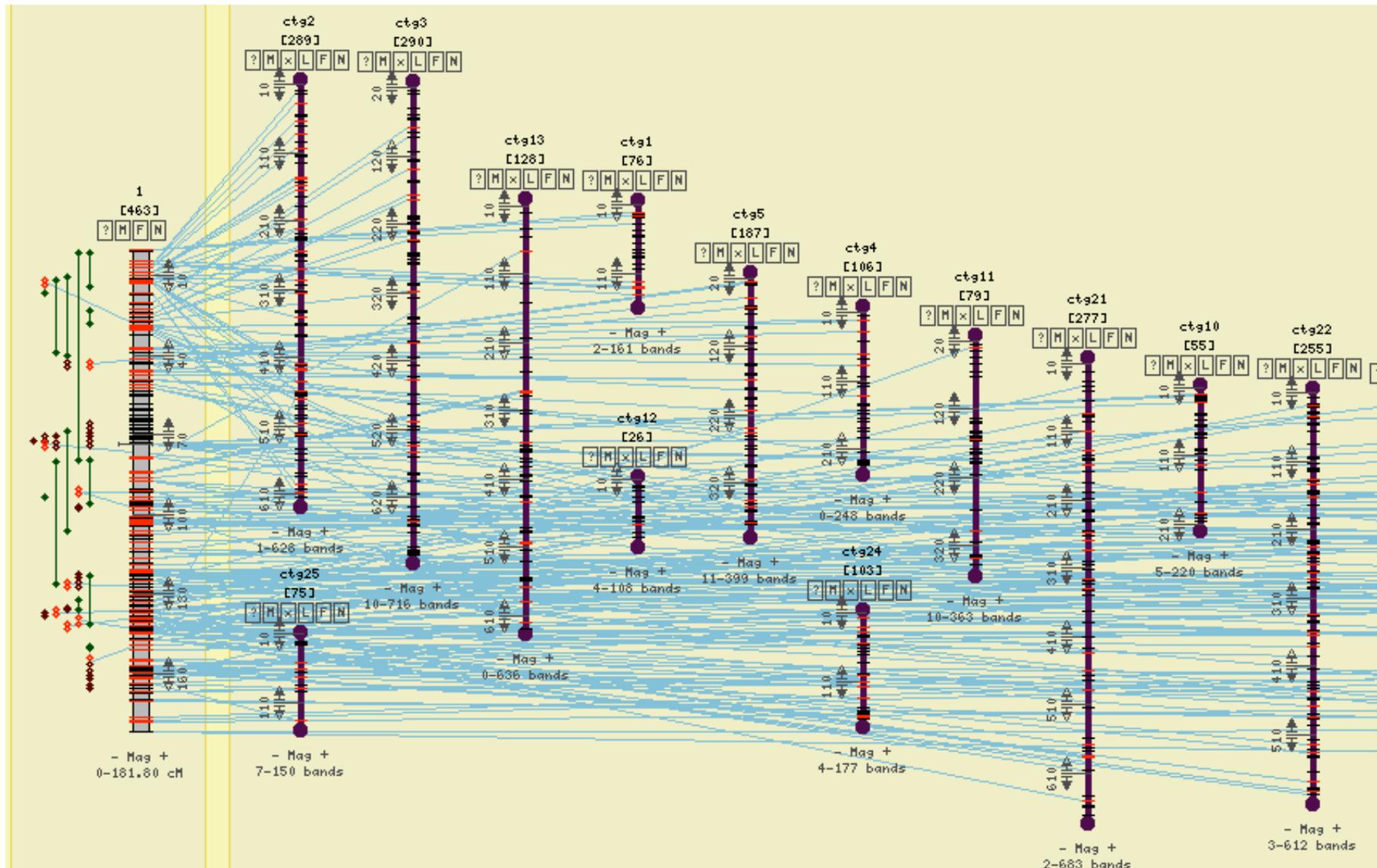
Comparing Sequence Assembly Against Optical Map
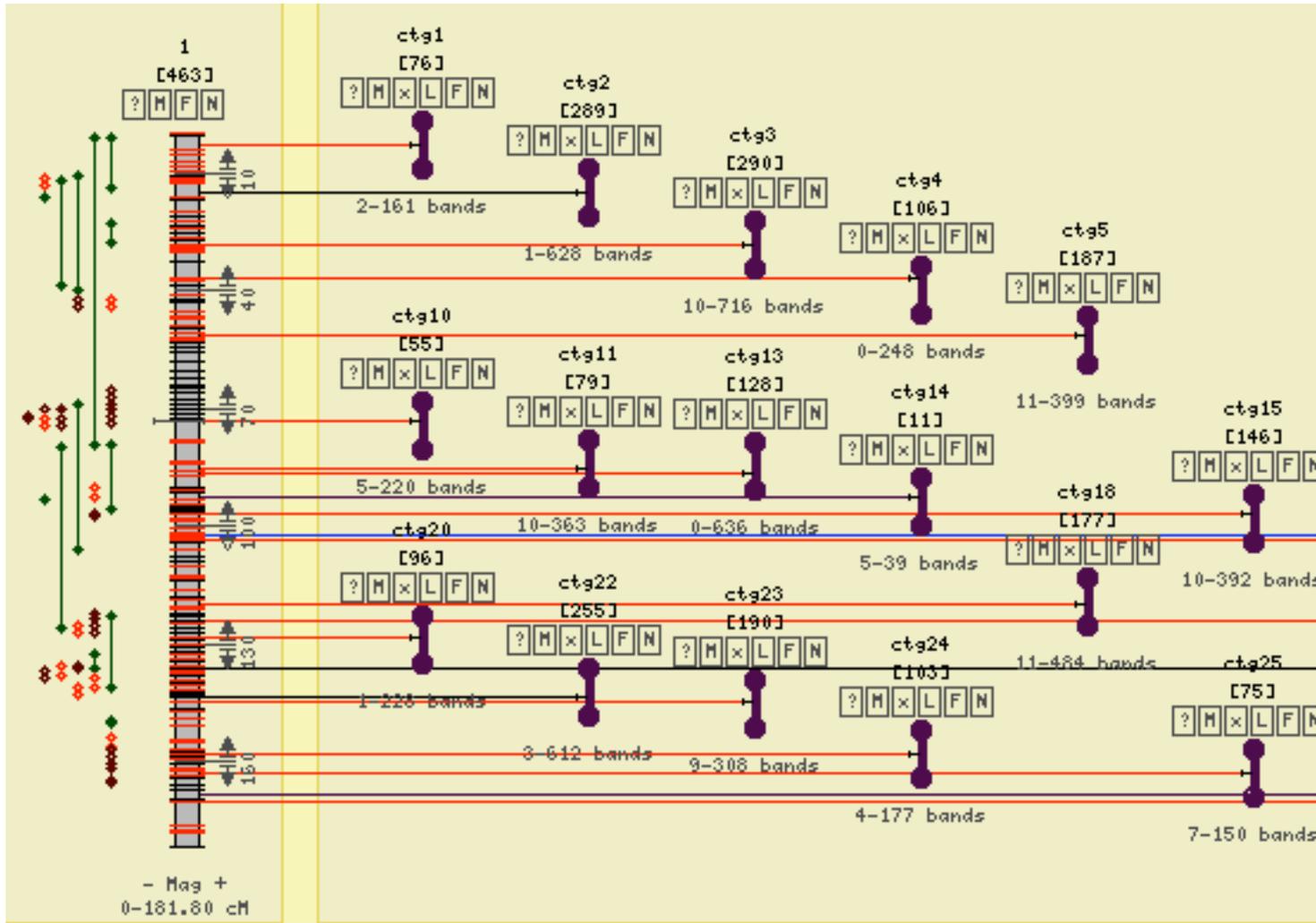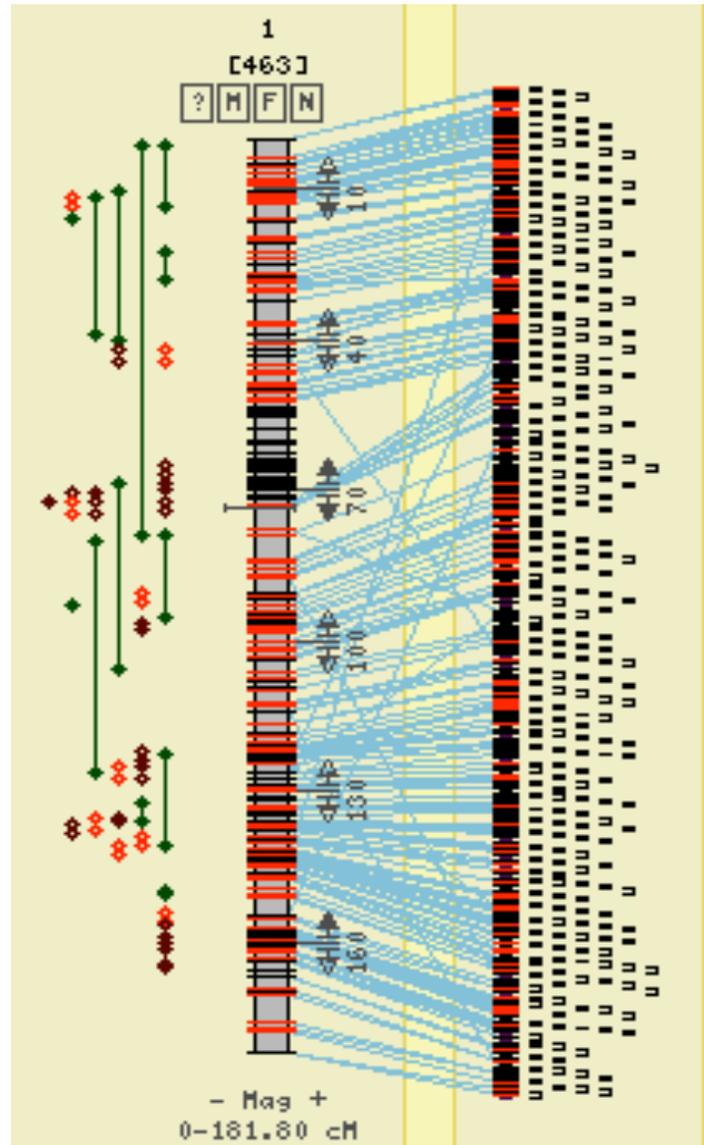
CMap Displaying Synteny
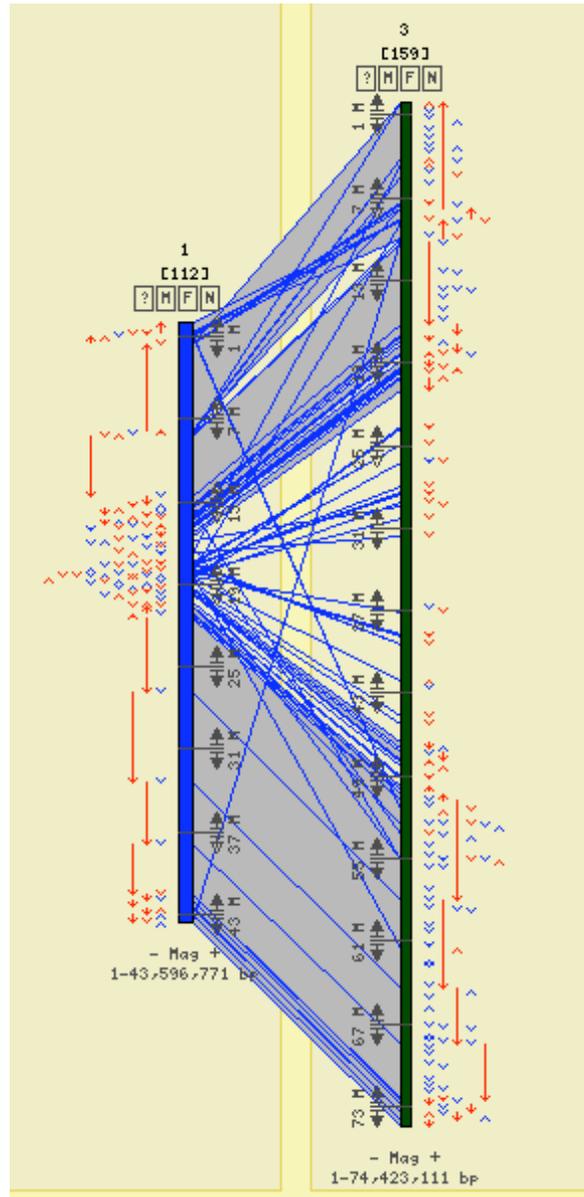
Data provided by the Gramene project (www.gramene.org)

CMap Displaying a Sequence Assembly vs a FPC Maps

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

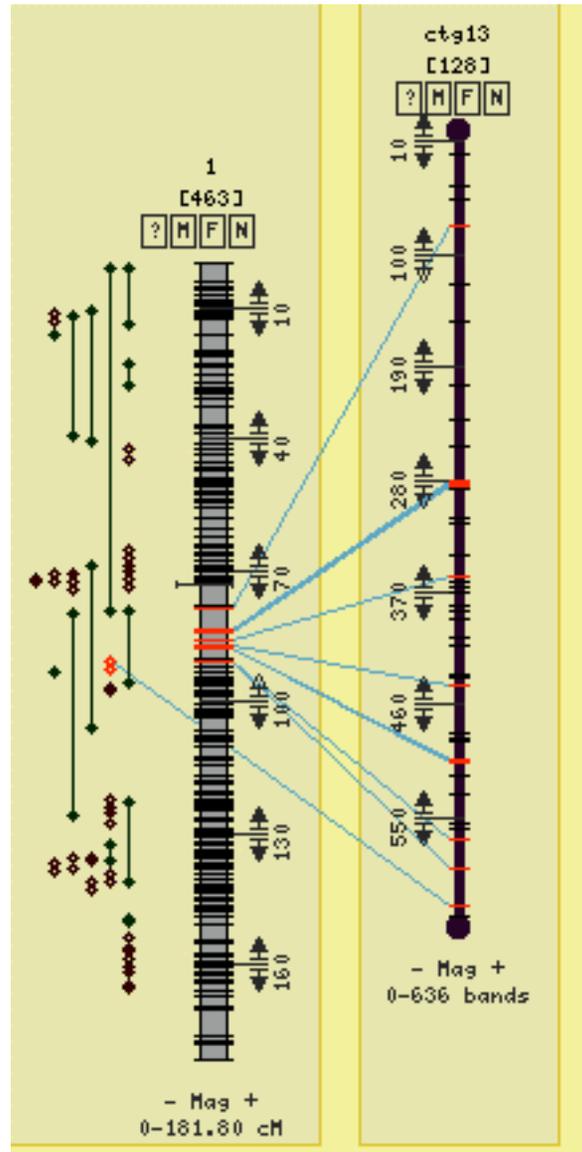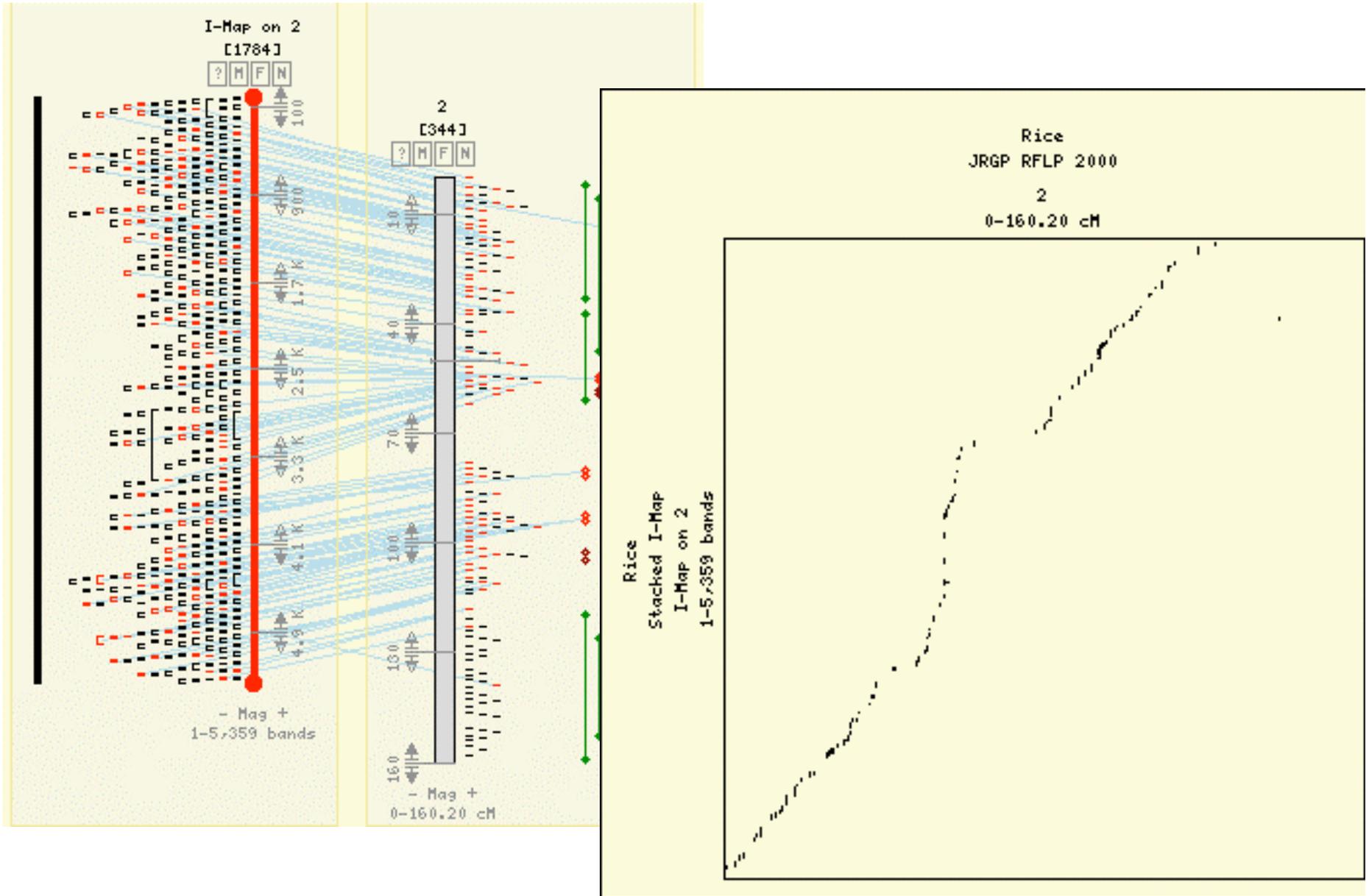# CMap Displaying a Sequence Assembly vs a FPC Maps

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

- Tab Delimited
- CMap GFF3

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

74230   74240   74250   74260   74270

BES
ZMMBBb0147N23.f

cagg n aagac g tgtctgaaatccccaccgaagacaatggt)(tttaccac

DNA/GC Content
caggcaagacctgtctgaaatccccaccgaagacaatggttttaccac

Traces
ZMMBBb0147N23.f

CAGG-AAGACGTGTCTGAAATCCCCACCGAAGACAATGGT-TTTACCA
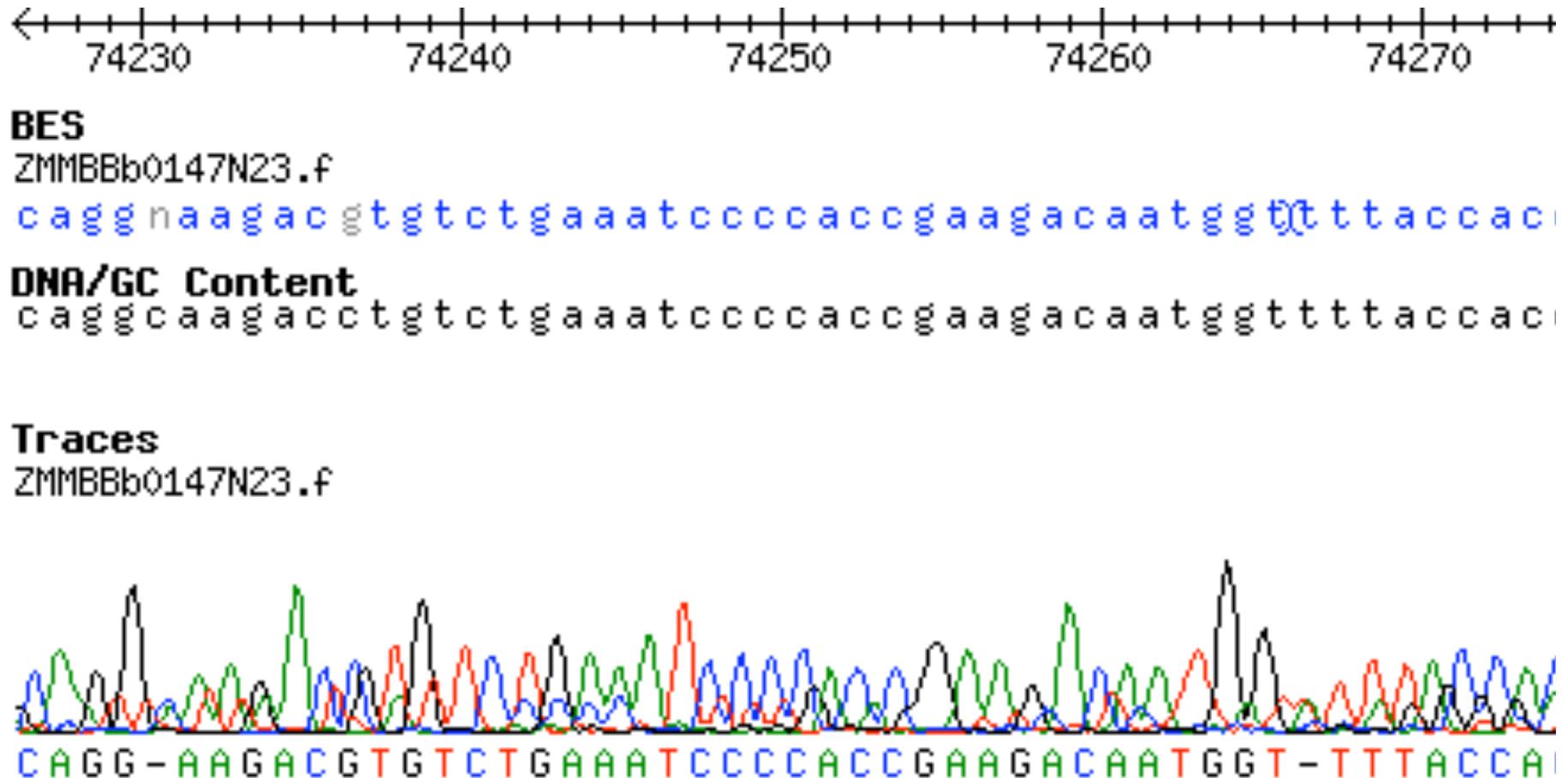
Note: base differences are gray and insertions are represented by ")("

Menu System

☐ **Map Options** [Redraw] [Reset]

Map Set	Add Maps Left	Rice-JRGP RFLP 2000 (Reference Set)	Add Maps Right
Min. Correspondences			
Stack Vertically		☐	
Maps		1	
Start		0.00	
Stop		181.80	
Magnification		Original ▼	
Flipped		☐	

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

[New Reference Maps]

[Redraw] [Reset] **(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: 0

| Refresh Menu | Redraw Image |

Map Set	Add Maps Left	Rice-JRGP RFLP 2000 (Reference Set)	Rice-Niigata RFLP 2000 Delete Set		See Menu Above
Min. Correspondences			0		
Stack Vertically		☐			
Maps		1	1 Delete	2 Delete	
Start		0.00	0.00	0.00	
Stop		181.80	130.30	123.50	
Magnification		Original ▼	Original ▼	Original ▼	

Heat Map Feature Glyph