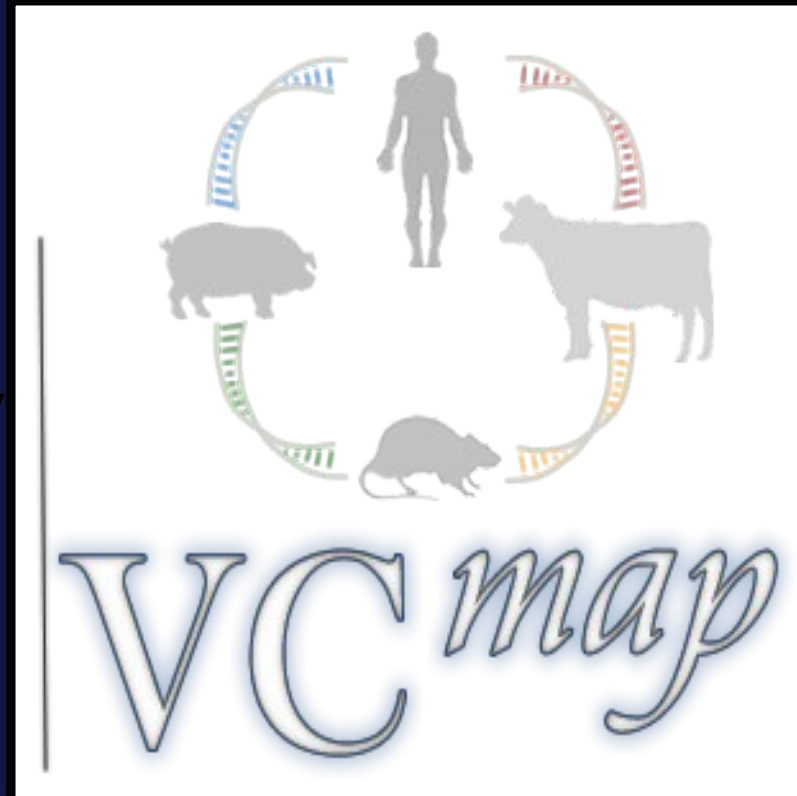


VMap: A Comparative Genomics Viewer and Database Designed to Facilitate Genomic Discovery

J.E. Koltes^{1*}, S.G. Davis^{2*}, Z-L Hu¹, M. Shimomoya^{3,4}, M. Dwinell^{3,4}, A.E. Kwitek⁵, and J.M. Reecy¹

¹Iowa State University, Ames, IA, USA; ²Bio::Neos, Inc, Coralville, IA, USA; ³Medical College of Wisconsin, Milwaukee, WI, USA; ⁴Rat Genome Database;

⁵University of Iowa, Iowa City, IA, USA



IOWA STATE UNIVERSITY



Bio::Neos



OBJECTIVES

- VMap is a comparative genomics visualization tool.
- Species currently supported include: chicken, cattle, mouse, pig, rat, and human genomes.
- Comparative maps include: genetic, genomic sequence and radiation hybrid data.
- GOALS:** Facilitate integrated comparative genetics discovery by blending map data, annotation, and other genomic data that will facilitate discovery of major genes responsible for trait variation.
- Allow seamless user data uploads and export of cross- species data and images.

APPLICATION & DATABASE

- VMap is written in Java is launched via Java Web Start for complete platform independence.
- VMap accesses a MySQL based relational database back-end.
- The VMap database contains:
 - 1) Gene and pseudo gene annotations
 - 2) Genetic and genomic map from NCBI, UCSC, and Ensembl (1,2,3)
 - 3) Radiation hybrid map data from Iowa State and the Evolution Highway at the University of Illinois (4)
 - 4) QTL annotation data from the Iowa State University's Animal QTLdb and the Rat Genome Database for each species (5,6)

SUPPORTED DATA FORMATS

- VMap supports private user datasets in a variety of formats including: GFF3, BED, BAM, SAM, and more.
- Users can easily view private Genome-Wide Association Studies, SNP locations, DNA or RNA Next-Generation sequencing data, or custom annotations data.

PLANNED FUTURE UPDATES

- Inclusion of new tracks**, including: gene expression, cross-species phenotype ontologies, SNP chip annotations.
- Addition of more species.**
- Increase User flexibility to add custom data.**
- Expand use to facilitate visualization of Recombinant Inbred Lines.**

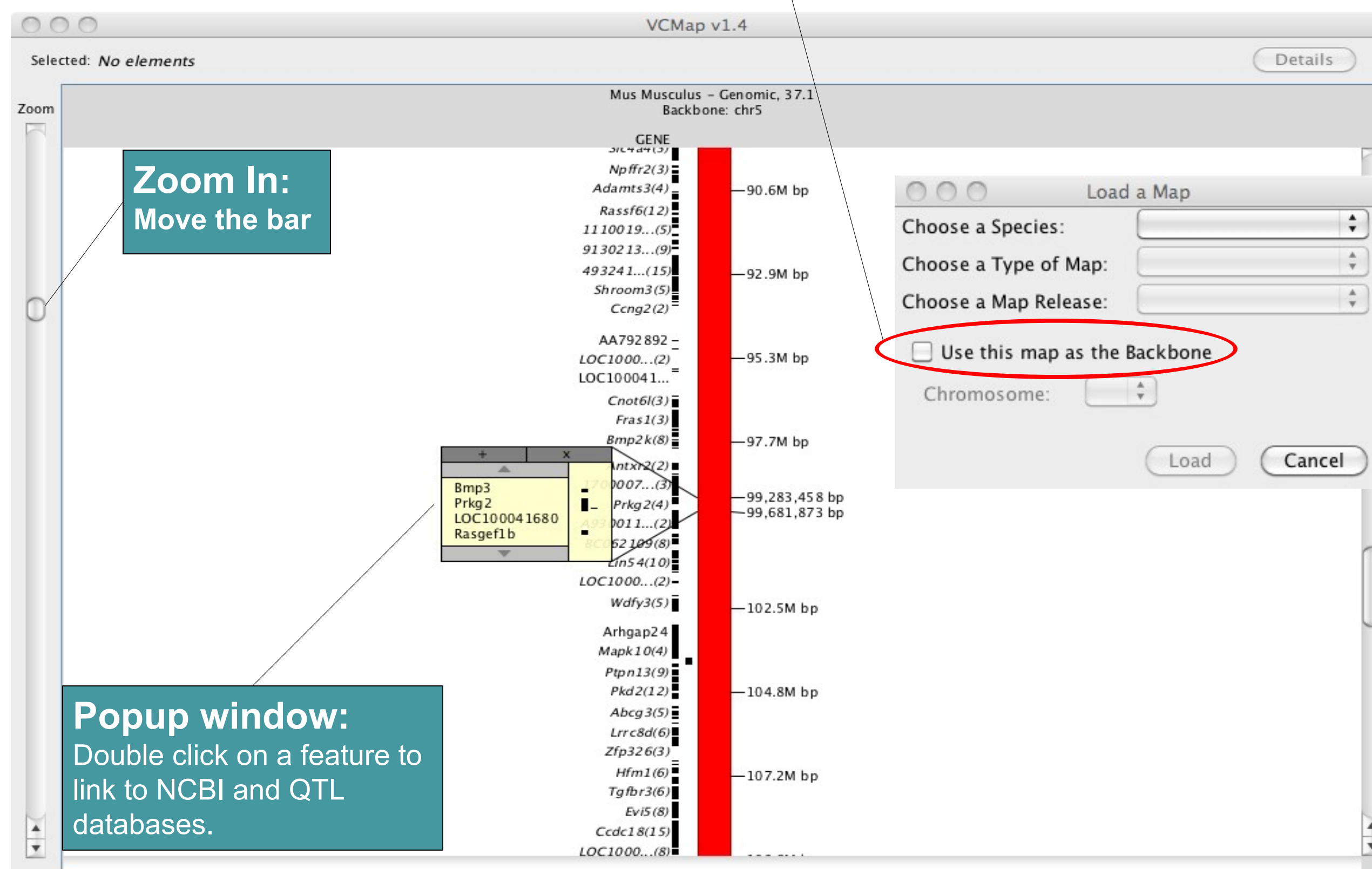
REFERENCES

1. NCBI Gene database; <http://www.ncbi.nlm.nih.gov/gene/>.
2. UCSC genome browser; <http://genome.ucsc.edu/>.
3. ENSEMBL genome browser; <http://uswest.ensembl.org/index.html>
4. Murphy et al., 2005. Science 309: 613-617.
5. Hu et al., 2007. Nucleic Acids Research 35: D604-609.
6. Rat Genome Database; <http://rgd.mcw.edu/>

see: vcmap.bioneos.com or www.animalgenome.org

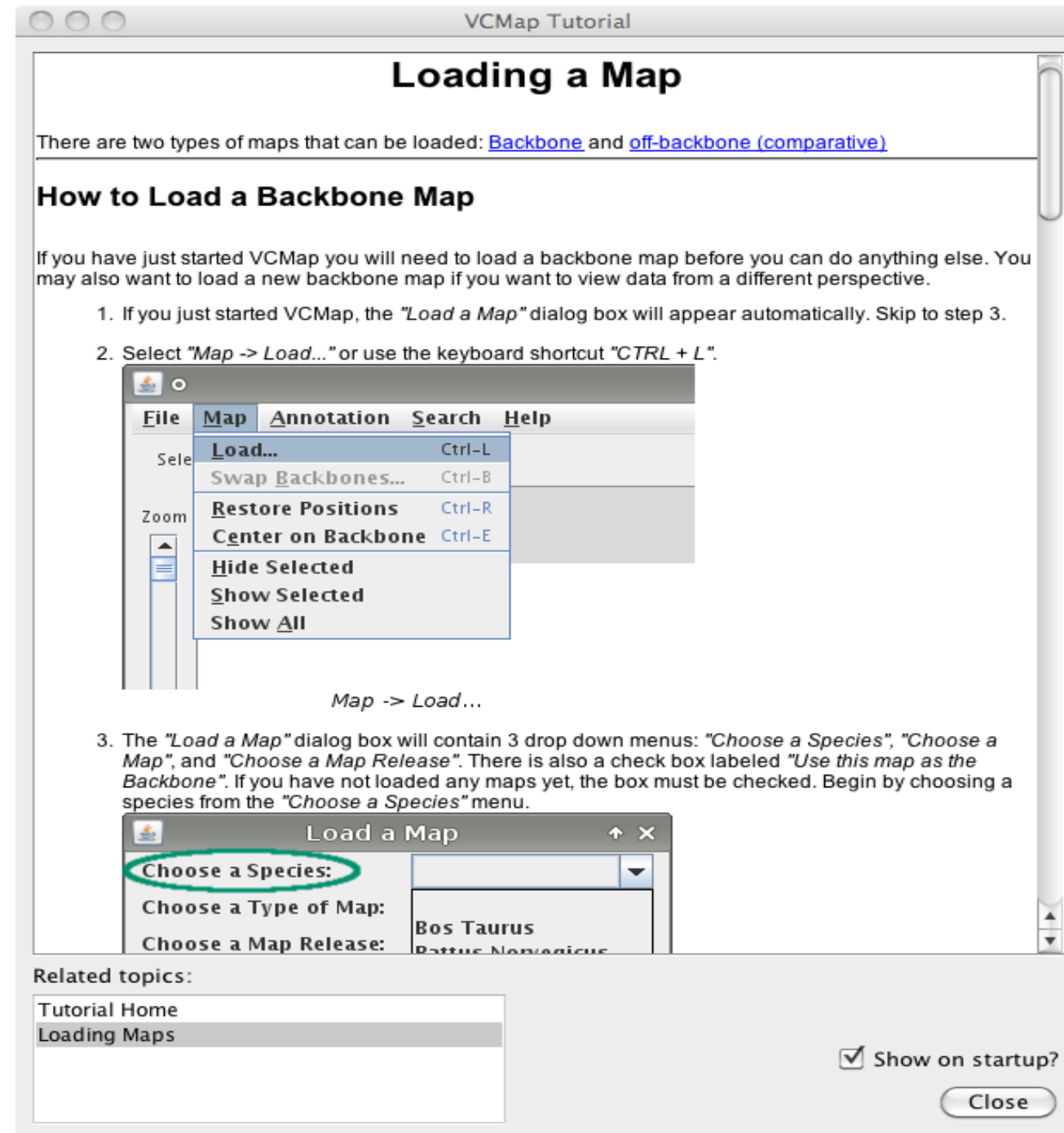
1) Navigating the maps- loading the backbone

Select Map, Load from the Menu & Choose the backbone



2) Follow the interactive tutorial

Opens automatically with the software

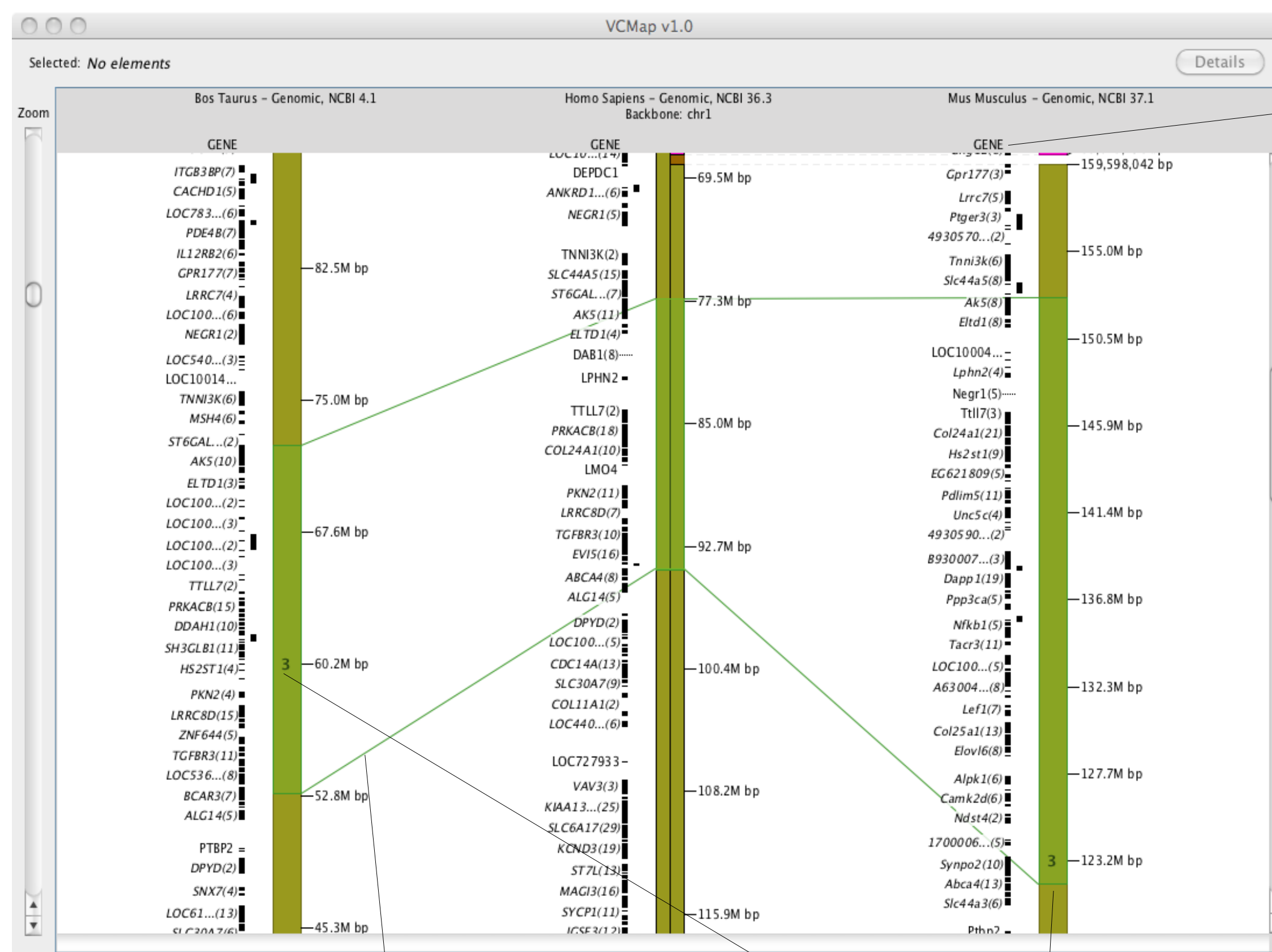


3) Compare cross-species annotation

Select Map, Load from Menu, NOT as backbone

Load Annotation:

Add gene names, QTL, etc.



Connecting lines:

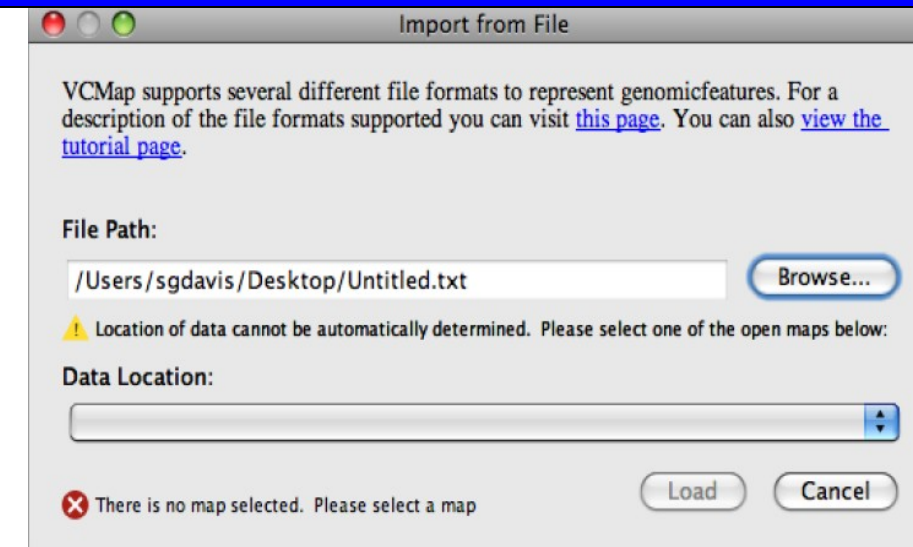
The lines represents homologous regions and features. Green connecting lines represent approximate homologous regions. Gray connecting lines represent homologous annotation, and turn blue when selected.

Visualize Synteny:

VMap aligns homologous chromosome blocks.

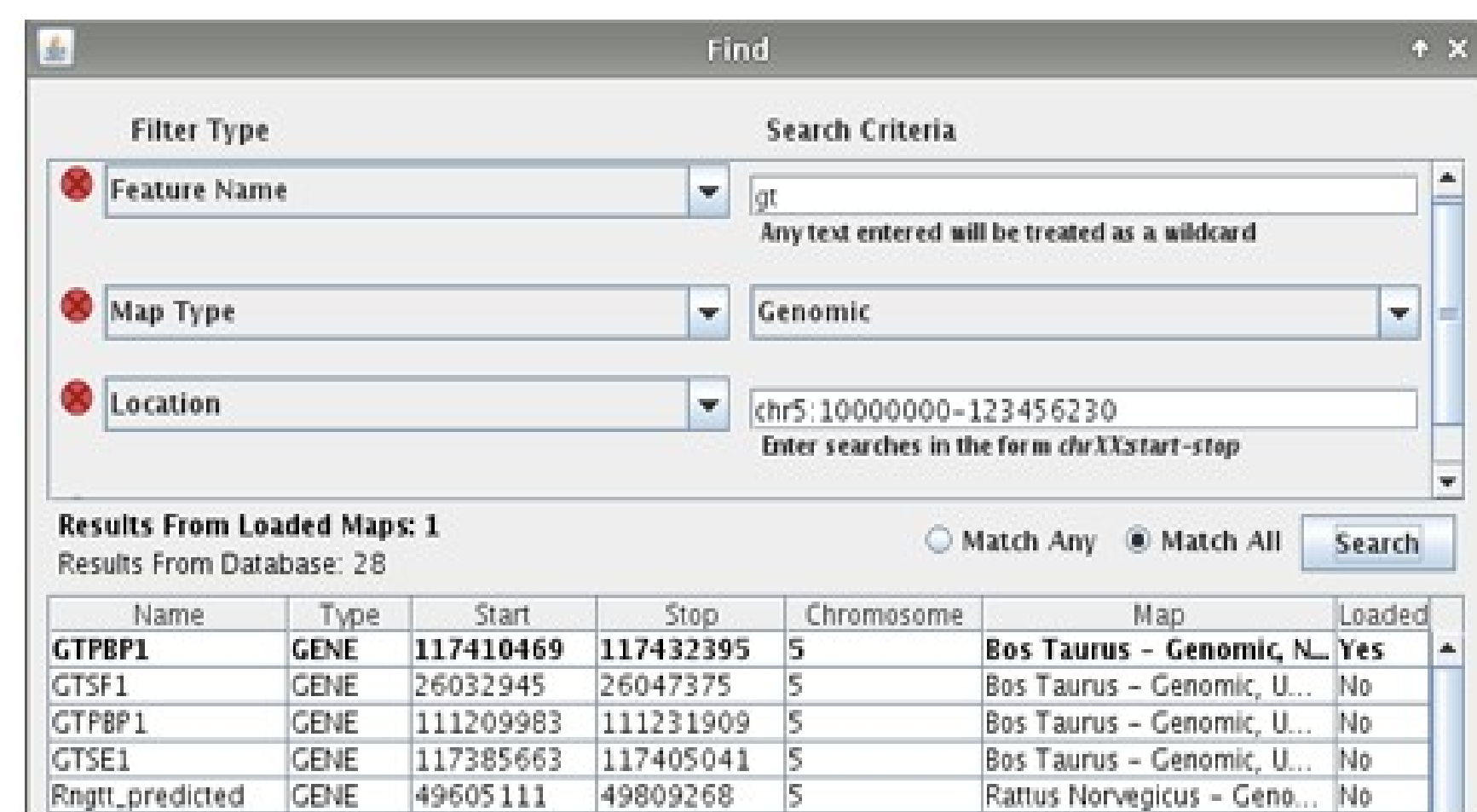
4) Load & visualize custom data

Select Annotation, Import from File



5) Search for annotation of interest

Select Search, Find



Find annotation for your species of interest:

VMap can help you view cross-species annotation when annotation is sparse in a species of interest.

View Evolutionary Rearrangements.

6) Export & save for publication

Select File, Export Image

