
Module 2: Maps and Genome Sequence (ZFIN)

iii - ZFIN Map Viewer

Aims

- Introduce ZFIN Map Viewer
- Suggest starting points for various queries

Introduction

ZFIN's map viewer provides an integrated view of the zebrafish mapping panels (HS, MGH, T51, LN54, GAT, MOP) to assist with identification of candidate loci and conserved chromosome segments. An integrated map, designed by John Postlethwait et al. is also available. <http://zfin.org/cgi-bin/webdriver?Mlval=aa-crossview.apg&OID=ZDB-REFCROSS-010114-1>.

Framework markers are used to link panels. Genes, ESTs, anonymous markers and SNPs are displayed. Detailed information for a gene or marker may be found by clicking on the symbols displayed on the map.

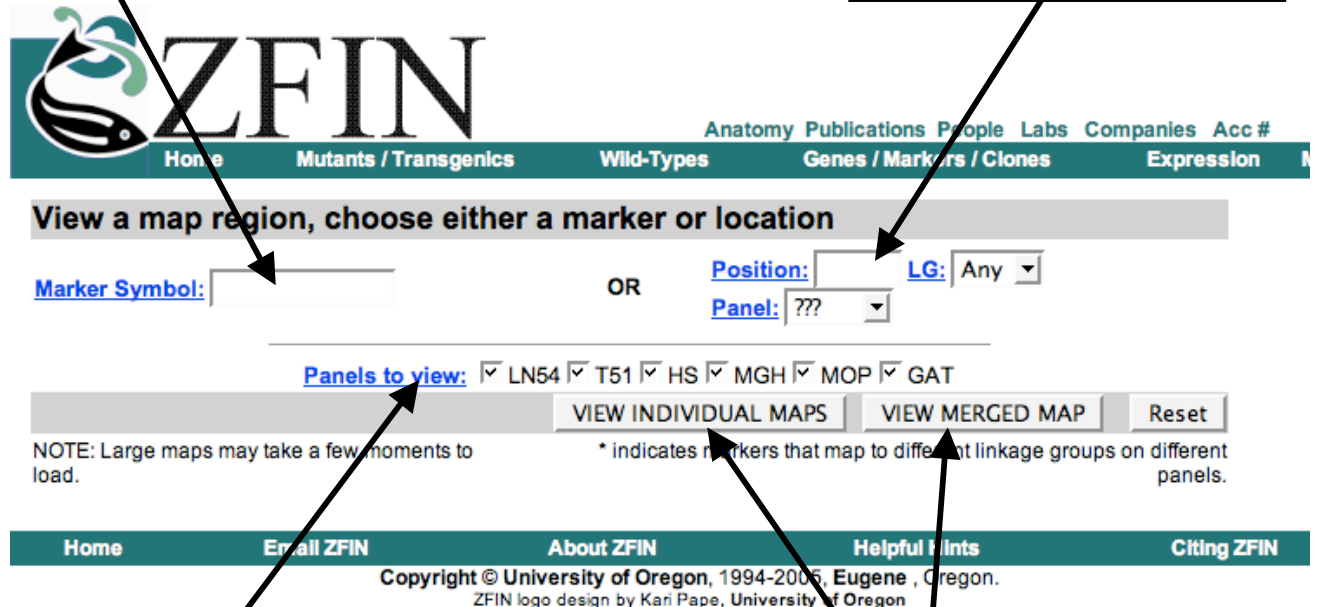
Maps may be generated by specifying a gene or marker name or by specifying a location on a linkage group.

To generate an integrated view of mapping panel data, click on the ‘Genetic Maps’ link present on ZFIN’s home page.

Generate a map for a specific Gene or Marker

-----OR-----

Generate a map for a specific location by specifying a position, LG and panel

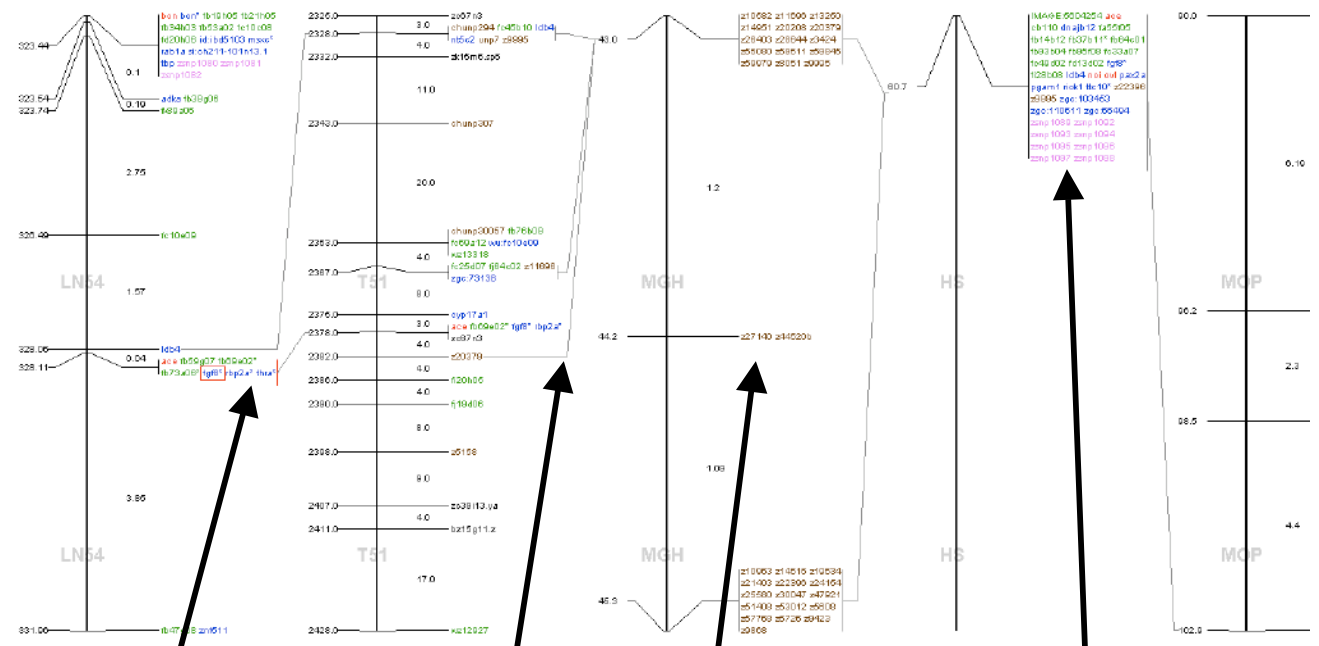


Specify panels to be included

Request a map

- individual panels
- merged map

Comparison of LN54, HS and T51 panels for marker *fgf8*



Red lines link requested markers

Dark lines link Framework markers

Different colors represent different marker types

Click on symbol for details

View of Merged (Consolidated) Map for fgf8



Exercises

1. Use the ZFIN Map Viewer to generate a map for a specified position on a linkage group.
2. Use the ZFIN Map Viewer to generate a merged (consolidated) map for a gene of your choice.