**Module 2: Maps and Genome Sequence (NCBI)**

**iii - Map Viewer Genome Browser**

**Aims**

- Introduce NCBI's Map Viewer Genome Browser
- Suggest alternative search strategies
- Provide examples of text queries
- Show examples of display options

**Introduction**


You can submit a text based query against the whole genome, a subset of chromosomes, or a single chromosome. Query by a gene symbol, gene name, accession number, or a wild card search using an asterisk (*) to view placement in the genomic context. Text searches can be submitted from the search bar on Map Viewer’s home page, the genome view or map view pages or on the Advanced Search form. Regions of interest can also be retrieved by sequence alignment with a BLAST search.

You may also look for gene information by its position relative to other mapped markers, genes, clones, SNPs or gene models.

MapViewer enables you to identify genes within a candidate region, members of a gene family, genes associated with SNPs or disease related genes between two markers.

**Exercises**
To explore a region of a particular chromosome or the placement of an object, try one of the following:

- Submit a text search of a gene or marker
- Limit your search by chromosome, the type of mapped object or map name by clicking on the "Advanced Search" button
- Review the hits on the available maps
- Choose one or more hits and view results in the graphical viewer
- Scroll up or down the chromosome from your mapped gene to see neighboring mapped objects
- Zoom in or out to change the level of visible detail
- View connections between maps
- Change the visible maps by clicking on "Maps and Options"
- Examine the transcript evidence support the placement of a gene on the genome

Choose among these options and explore the Zebrafish genome in NCBI's MapViewer (http://www.ncbi.nlm.nih.gov/mapview).
Advanced Search:
Submit a query against Chromosomes 8 and 17 for all zgc mapped genes on the Ab initio, estDr, MGH and T51 maps.

Try adding another term to your query with “AND” to further restrict your query.
View the results of the query: zgc* AND transcription, restricted to Chromosomes 8 and 17. Click on the red tick marks to go to see the placement of the objects on Chromosome 8.

- Click on the gene symbol or map name to view the placement of the objects on chromosome 8.

- View the placement of nkx2.7 on Chromosome 8.
- Follow links to ZFIN or UniSTS (sts).
- View placement information by clicking on the “Go To” blue arrow.
- Click on the chromosome or the zoom box to zoom in our out.
- Click on “Maps & Options” to change the maps displayed and other display options.
Mouse over the chromosome, click and open this box. Choose an option to change your view.

And click on 'go' to jump to the placement of nkh2.y on the other maps.
Another option is to view one of the genes in the results set: gad45bl

- Click on maps and options
- Select from the Available Maps, click Add, to add these maps to the Maps Displayed list
- Click Apply to make these changes in the display

View the transcript evidence in the Dr ESTs map or the Gnomon models representing supported alternative transcripts in the Model map (http://tinyurl.com/dogvo).
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Contig NW_634497

Gnomon models

RefSeq: NM_001012386

or in zoomed in a bit …