GDR GBrowse

The generic Genome Browser (GBrowse)

• A combination database and interactive web page for manipulating and displaying annotations on genomes

• Developed by GMOD (Generic Model Organism Database)

• GDR GBrowse : a customized GBrowse for the genomes in GDR
GDR GBrowse Overview

Description menus
Search
Bird’s eye view
Details
Tracks

Generic Genome Browser version 2.0. For questions about the data at this site, please contact its webmaster. For support of the browser software only, send email to gmod-gbrowse@lists.sourceforge.net or visit the GMOD Project web pages.
GDR GBrowse Search

Search by annotation ID, name, or comment

Scroll/zoom

Region displayed

Dropdown list

Hide Details
(minus-sign)

Open Details
(plus-sign)
GDR GBrowse Search
GDR GBrowse Tracks

remove track
(cross-sign)
**GDR GBrowse Tracks**

<table>
<thead>
<tr>
<th>Tracks</th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Overview</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Genetic Mapped Markers</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Region</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Genetic Mapped Markers</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Alignments</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Blat Aligned Prunus persica EST assembly V1</td>
<td></td>
<td>Genetic Marker Alignment</td>
<td>PASA Aligned ESTs</td>
</tr>
<tr>
<td>Genome Sequence</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DNA/GC Content</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Model Plant Gene Alignments</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Arabidopsis Peptide Alignment</td>
<td></td>
<td>Poplar Peptide Alignment</td>
<td>Soybean Peptide Alignment</td>
</tr>
<tr>
<td>Grape Peptide Alignment</td>
<td></td>
<td>Rice Peptide Alignment</td>
<td></td>
</tr>
<tr>
<td>RNA-seq Illumina profiles (log 10 scale)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cotyledon+Embryo, unique alignments</td>
<td></td>
<td>Fruit, all alignments</td>
<td>Root, unique alignments</td>
</tr>
<tr>
<td>Cotyledon+Embryo, all alignments</td>
<td></td>
<td>Leaf, unique alignments</td>
<td>Root, all alignments</td>
</tr>
<tr>
<td>Fruit, unique alignments</td>
<td></td>
<td>Leaf, all alignments</td>
<td></td>
</tr>
<tr>
<td>Repeats</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>20mers aligning with 0 errors (log 10 scale)</td>
<td></td>
<td>ReAS</td>
<td></td>
</tr>
<tr>
<td>LTRs</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Transcripts</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

choose tracks you want to see
GDR GBrowse Tracks
GDR GBrowse Tracks

Selecting regions with mouse
GDR GBrowse Tracks
GDR GBrowse Configuring Tracks

Customize your track views
GDR Gbrowse Preferences

“Image Width”
GDR GBrowse Preferences

Highlights the specified region and feature
GDR GBrowse Reports

- Download sequences or track data
- Display settings
GDR GBrowse Reports
GDR Gbrowse –
Adding your annotations

Upload or import your own annotation files
GDR GBrowse Tutorial

References

• http://www.openhelix.com/gbrowse
• http://gmod.org/wiki/Gbrowse

Acknowledgements

• This tutorial was based on the Open Helix Gbrowse 1.6 tutorial which was modified for the peach genome sequence and annotations implemented in GBrowse 2.0