# Term Details Page

Detailed information about the enrichment for a particular term is available by clicking on the link within the 'Term Name' column of the table on the main output page. The output is segmented into three sections, each described in detail below.

## Genomic region and gene association graphs

The first graph, "Number of associated regions per gene", is the inverse of the first graph shown on the main output page, and shows how many genomic regions are assigned as putatively regulating each gene that is associated with the ontology term of interest based on the association rule used. This information can indicate whether enriched terms are due to a spread of input regions associated with many genes or if a few genes annotated with the term receive a large number of genomic regions associated with them (suggesting possible gene-specific enrichment rather than a broader term-specific enrichment).

The distance graphs shown on the term details page are created in a similar manner to the genome-wide association graphs. However, in addition to showing the data from the entire set of genomic regions, also displayed are the subset of associations between regions and genes annotated with the ontology term of interest.

## Genomic region and gene association tables

These tables are analogous to how the genomic region and gene associations file links each input genomic region to the gene(s) it putatively regulates according to the association rule used. The difference is that only the associations that are relevant for the term of interest are included in the tables. For example, say the user provides an input set of five genomic regions which have the following associations:

```
Input.1   Gene.1 (-100)
Input.2   Gene.1 (+500), Gene.2 (-3000)
Input.3   NONE
Input.4   Gene.4 (+100000)
Input.5   Gene.5 (-500), Gene.6 (+600)
```

Furthermore, assume an ontology has a term 'Term.A', and the genes Gene.1, Gene.5, Gene.6, Gene.7, Gene.8 are annotated with Term.A. Then the term details page for Term.A would have the following region->gene association table:

```
Input.1   Gene.1 (-100)
Input.2   Gene.1 (+500)
Input.5   Gene.5 (-500), Gene.6 (+600)
```

In particular, the genomic regions Input.3 and Input.4 are not listed since they are not predicted to regulate genes involved in Term.A, and the association of Input.2 to Gene.2 is not listed since Gene.2 is not involved in Term.A.

The gene->region association table provides the identical information as the region->gene table, but grouped by gene rather than by region. So, for the example above, the gene->region table would be:

```
Gene.1   Input.1 (-100), Input.2 (+500)
Gene.5   Input.5 (-500)
Gene.6   Input.5 (+600)
```

### Region links

Each genomic region in both tables is a hyperlink. When clicked, the user is taken to the UCSC Genome Browser at the position of that region with custom tracks loaded with the user's data.

### Gene links

Each gene in both tables is also a hyperlink. When clicked, the user is taken to the UCSC Genome Browser at the position of the entire regulatory domain used to associate genomic regions to that gene given the association rule used. Additionally, the same custom tracks loaded with the user's data are provided.

## Additional ontology information

Where possible, information on the ontology term from the source website from which the ontology was curated is displayed as a frame within the page.

# Previous GREAT release term details pages

In GREAT 1.7 and below, neither the region/gene distance plots nor explicit links between regions and genes were available. Instead, a list of all implicated regions and a separate list of all implicated genes was provided. The additional ontology information was also available.