

GREAT version 4.0.4 current (08/19/2019 to now) ▼

Job Description

Job ID:

20241128-public-4.0.4-qInior

Display name:

distfilter500_DKO_K4me3_dcp.tar

Test set:

distfilter500_DKO_K4me3_dcp.target.peaks.bed (229 genomic regions)
[Show in UCSC genome browser.](#) *How do I look at my regions in the genome?*

Background:

Whole genome background

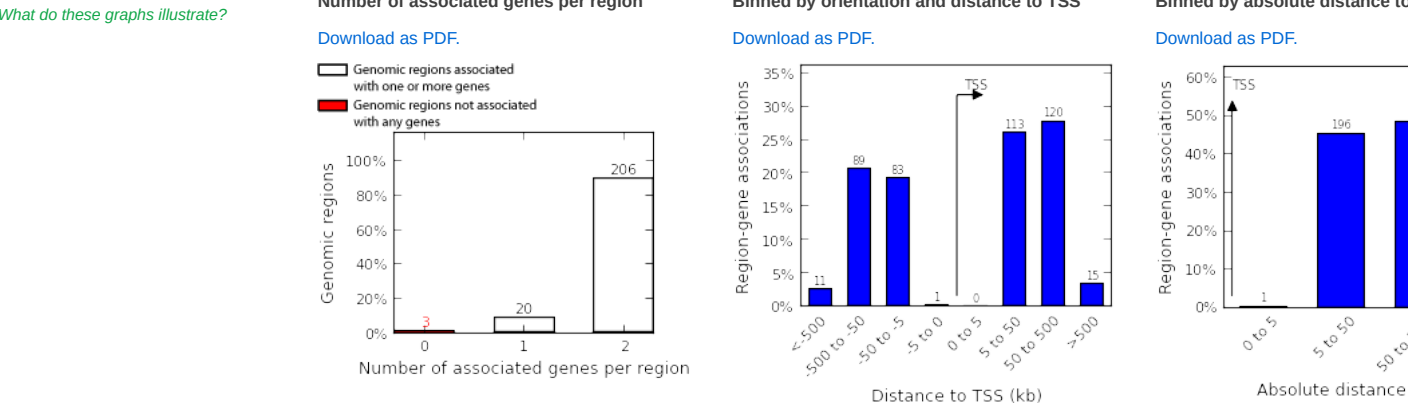
Assembly:

Mouse: NCBI build 38 ([UCSC mm10, Dec. 2011](#)) *What gene set does GREAT use?*

Associated genomic regions:

Basal+extension (constitutive 5.0 kb upstream and 1.0 kb downstream, up to 1000.0 kb max extension). Curated regulatory domains are included in 3 of all 229 genomic regions (1.3%) are not associated with any genes.
[View all genomic region-gene associations.](#) *Which genes are my regions associated with?*
[Revise the region-gene association rule.](#) *How are my regions associated with genes?*

Region-Gene Association Graphs



Global Controls

Global Export ▼

Which data is exported by each option?

Ensembl Genes (no terms)

GO Biological Process (3 terms)

Table controls:

Export ▼

Shown top rows in this table: 20 Set

Term annotation count: Min: 1 Max: Inf Set

Visualize this table: [select one]

Term Name	Binom Rank	Binom Raw P-Value	Binom FDR Q-Val	Binom Fold Enrichment	Binom Observed Region Hits	Binom Region Set Coverage	Hyper Rank	Hyper FDR Q-Val	Hyper Fold Enrichment	Other Genes
programmed cell death	3	1.0435e-5	4.5530e-2	2.1657	36	15.72%	18	8.1577e-3	2.1781	
apoptotic process	7	2.9901e-5	5.5915e-2	2.1175	34	14.85%	23	1.5286e-2	2.1457	
cell death	8	3.0246e-5	4.9489e-2	2.0597	36	15.72%	22	1.5054e-2	2.0965	

The test set of 229 genomic regions picked 417 (2%) of all 21,395 genes.
GO Biological Process has 13,090 terms covering 17,925 (84%) of all 21,395 genes, and 1,163,819 term - gene associations.
13,090 ontology terms (100%) were tested using an annotation count range of [1, Inf].

GO Cellular Component (no terms)

GO Molecular Function (no terms)

Human Phenotype (no terms)

Mouse Phenotype Single KO (no terms)

Mouse Phenotype (no terms)