

GREAT version 4.0.4

current (08/19/2019 to now)

Job Description

Job ID:20240719-public-4.0.4-nxvS8V

Display name:distfilter_DKO_K4me3_dcm.target.

Test set:distfilter_DKO_K4me3_dcm.target.peaks.bed (3,838 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?*

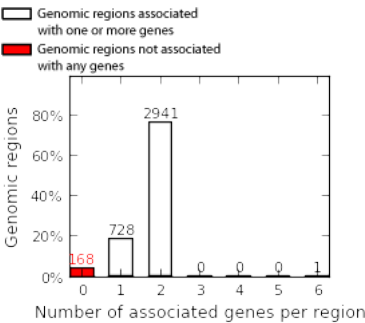
Associated genomic regions:Basal+extension (constitutive 5.0 kb upstream and 1.0 kb downstream, up to 1000.0 kb max extension). Curated regulatory domains are included for 168 of all 3,838 genomic regions (4.4%) are not associated with any genes.
[View all genomic region-gene associations.](#) *Which genes are my regions associated with?*
[Revise the region-gene association rule.](#) *How are my regions associated with genes?*

Region-Gene Association Graphs

What do these graphs illustrate?

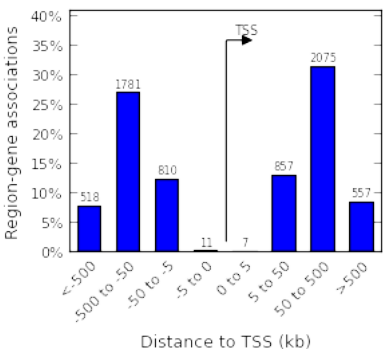
Number of associated genes per region

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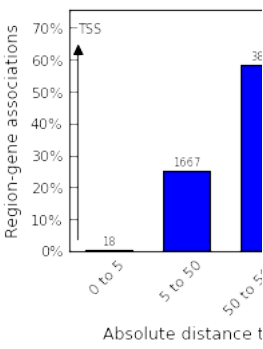
Binned by orientation and distance to TSS

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Binned by absolute distance to TSS

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Global Controls

Global Export

Which data is exported by each option?

- Ensembl Genes (no terms)
- GO Biological Process (no terms)
- GO Cellular Component (no terms)
- GO Molecular Function (no terms)
- Human Phenotype (no terms)
- Mouse Phenotype Single KO (no terms)
- Mouse Phenotype (1 term)

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	Hyper Observed Region Hits
palatal shelf hypoplasia	1	4.0634e-6	3.8907e-2	2.2696	39	1.02%	831	2.1862e-2	2.5996	38

The test set of 3,838 genomic regions picked 4,115 (19%) of all 21,395 genes.
Mouse Phenotype has 9,575 terms covering 9,654 (45%) of all 21,395 genes, and 705,265 term - gene associations.
9,575 ontology terms (100%) were tested using an annotation count range of [1, Inf].