



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

Job Description

Job ID: 20241128-public-4.0.4-JNdWfz

Display name: distfilter500_DKO_K4me3_pcm.tar

Test set: distfilter500_DKO_K4me3_pcm.target.peaks.bed (48 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?*

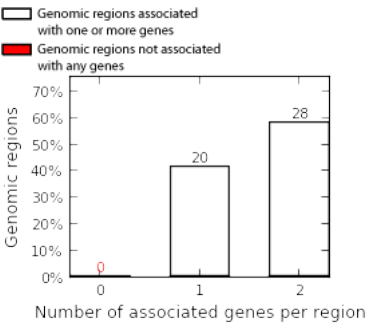
Associated genomic regions: Basal+extension (constitutive 5.0 kb upstream and 1.0 kb downstream, up to 1000.0 kb max extension). Curated regulatory domains are included. 0 of all 48 genomic regions (0%) are not associated with any genes.
[View all genomic region-gene associations.](#) *Which genes are 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?

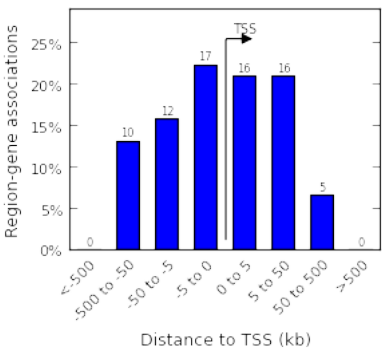
Number of associated genes per region

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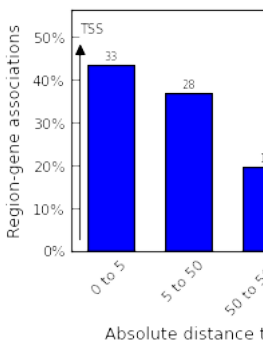
Binned by orientation and distance to TSS

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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 (no terms)

