

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

Job Description

Job ID: 20240719-public-4.0.4-Zd7s4R

Display name: `distfilter_DKO_K4me3_pcm.target.`

Test set: distfilter_DKO_K4me3_pcm.target.peaks.bed (182 genomic regions)
[Show in UCSC genome browser.](#) *How do I look at my regions in the genome?*

Background: Whole genome background

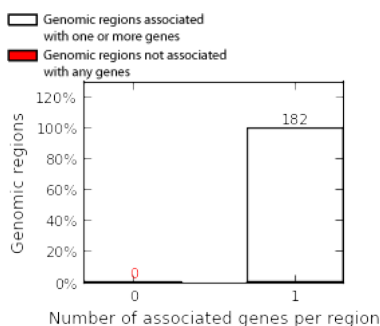
Assembly: Mouse: NCBI build 38 ([UCSC mm10, Dec. 2011](#)) *What gene set does GREAT use?*

Associated genomic regions: Single nearest gene (1000.0kb max extension). Curated regulatory domains are included.
0 of all 182 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?*

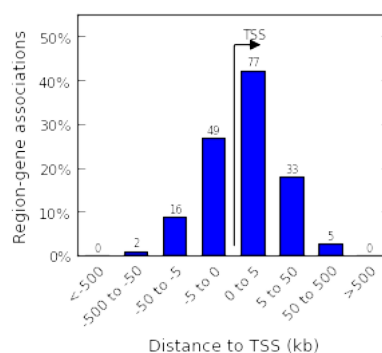
Region-Gene Association Graphs

What do these graphs illustrate?

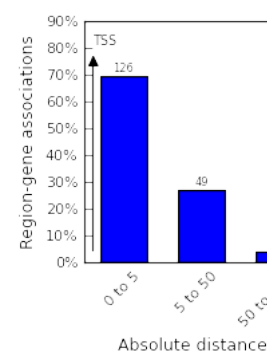
Number of associated genes per region

[Download as PDF.](#)

Binned by orientation and distance to TSS

[Download as PDF.](#)

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)



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