

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?*

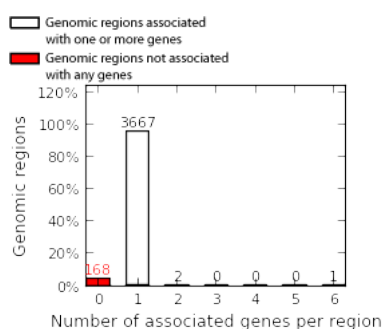
Associated genomic regions: Single nearest gene (1000.0kb max extension). Curated regulatory domains are included.  
 168 of all 3,838 genomic regions (4.4%) are not associated with any genes.  
[View all genomic region-gene associations.](#) *Which genes are my regions associated with?*  
[Revise the region-gene association rule.](#) *How are my regions associated with genes?*

## Region-Gene Association Graphs

*What do these graphs illustrate?*

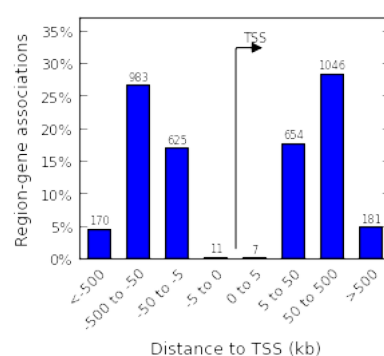
Number of associated genes per region

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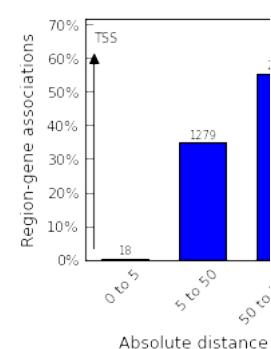
Binned by orientation and distance to TSS

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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 (no terms)



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