Overview   News   Use GREAT   Demo   Video   How to Cite   Help   Forum   Bejerano Lab

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

⊖ **Job Description**

Job ID: 20241126-public-4.0.4-hpxvmj
Display name: distfilter500_DKO_K4me3_dcm.tar
Test set: distfilter500_DKO_K4me3_dcm.target.peaks.bed (2,763 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 includ
                               161 of all 2,763 genomic regions (5.8%) are not associated with any genes.
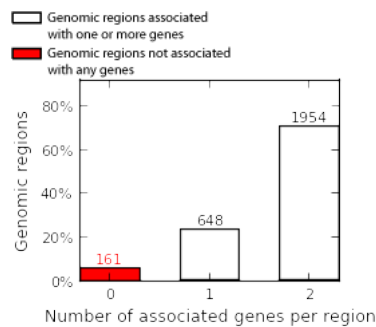   View all genomic region-gene associations.   *Which genes are my regions associated with?*
                               Revise the region-gene association rule.   *How are my regions associated with genes?*
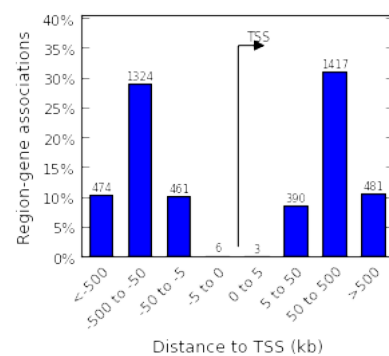
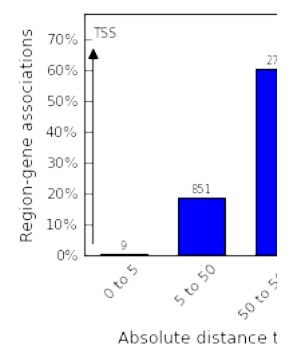⊕ **Region-Gene Association Graphs**

What do these graphs illustrate?

Number of associated genes per region

Download as PDF.

Binned by orientation and distance to TSS

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Binned by absolute distance to

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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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