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

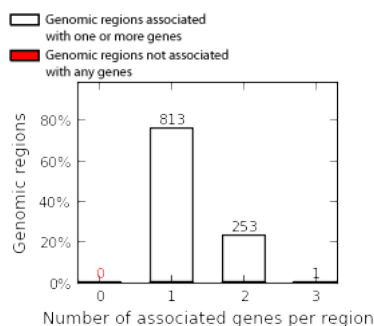|	
Job ID:	20240719-public-4.0.4-9RkkYc
Display name:	distfilter_DKO_K4me3_pcp.target.p
Test set:	distfilter_DKO_K4me3_pcp.target.peaks.bed (1,067 genomic regions)
	Show in UCSC genome browser. *How do I look at my regions in the genome?*
Background:	Whole genome background
Assembly:	Mouse: NCBI build 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
	0 of all 1,067 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
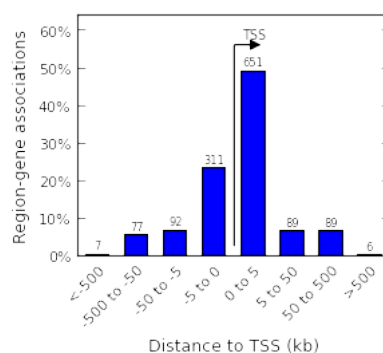
What do these graphs illustrate?

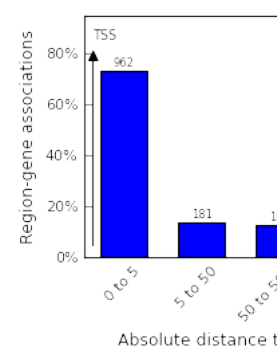**Number of associated genes per region**

Download as PDF.

Binned by orientation and distance to TSS

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Binned by absolute distance to

Download as PDF.

⊕ 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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