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

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

Warning: Your set hits a large fraction of the genes in the genome, which often does not work well with the GREAT Significant by Both view due to a saturation of the gene-based hype
See our *tips for handling large datasets* or try the Significant By Region-based Binomial view.

⊖ Job Description

|	
Job ID:	20250414-public-4.0.4-E7Jj50
Display name:	human_liver_unique_parsed.bed
Test set:	human_liver_unique_parsed.bed (89,512 genomic regions)
	Show in UCSC genome browser. *How do I look at my regions in the genome?*
Background:	Whole genome background
Assembly:	Human: GRCh38 (UCSC hg38, Dec. 2013) *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 inclu
	889 of all 89,512 genomic regions (1%) 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?*

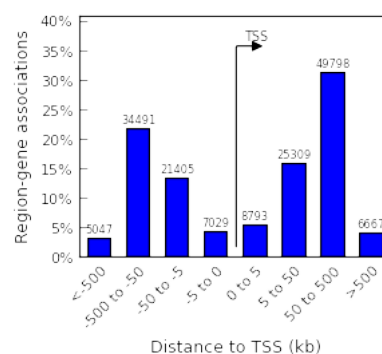## ⊕ Region-Gene Association Graphs

What do these graphs illustrate?

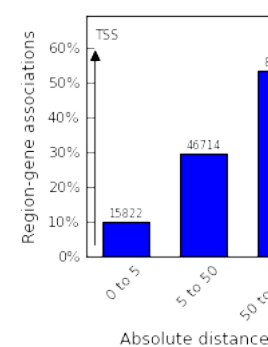**Number of associated genes per region**

Download as PDF.
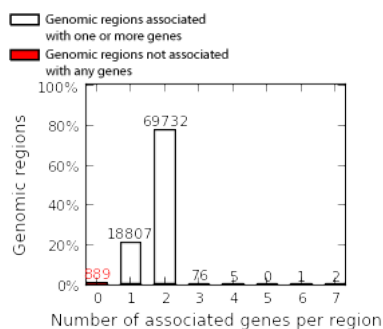
Binned by orientation and distance to TSS

Download as PDF.

Binned by absolute distance to

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)

STANFORD SCHOOL OF MEDICINE   *Bejerano Lab*   STANFORD ENGINEERING

Terms of Use   About Us   Contact Us