



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 hypothesis. See our [tips for handling large datasets](#) or try the [Significant By Region-based Binomial](#) view.

## Job Description

Job ID: 20250409-public-4.0.4-GDwpGe

Display name:

Test set: tissues\_human\_parsed.bed (75,267 genomic regions)  
[Show in UCSC genome browser.](#)    [How do I look at my regions in the genome?](#)

Background: Whole genome background

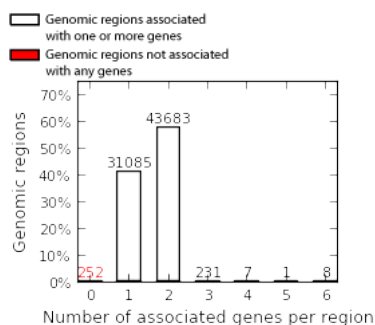
Assembly: Human: GRCh38 ([UCSC hg38, Dec. 2013](#))    [What gene set does GREAT use?](#)

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 included. 252 of all 75,267 genomic regions (0.3%) 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?](#)

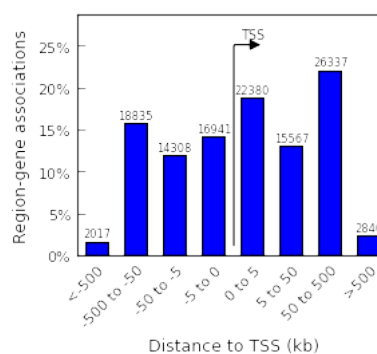
## Region-Gene Association Graphs

[What do these graphs illustrate?](#)

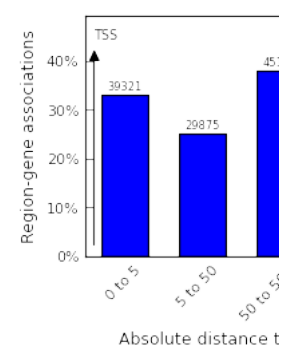
### Number of associated genes per region

[Download as PDF.](#)

### Binned by orientation and distance to TSS

[Download as PDF.](#)

### Binned by absolute distance to TSS

[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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