

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:

20250414-public-4.0.4-mDqlau

Display name:

human_pancreas_unique_parsed.t

Test set:

human_pancreas_unique_parsed.bed (94,252 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?](#)

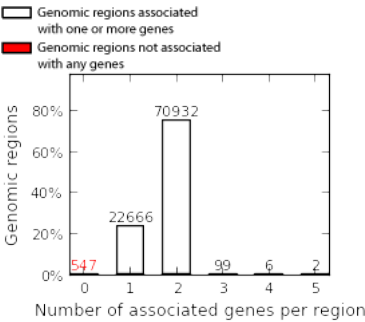
Associated genomic regions:

Basal+extension (constitutive 5.0 kb upstream and 1.0 kb downstream, up to 1000.0 kb max extension). Curated regulatory domains are included. 547 of all 94,252 genomic regions (0.6%) 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?](#)

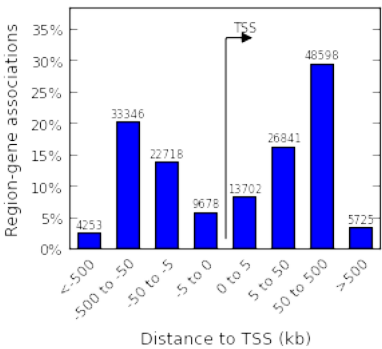
Region-Gene Association Graphs

[What do these graphs illustrate?](#)

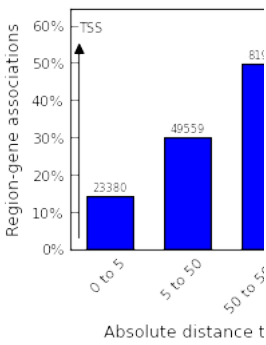
Number of associated genes per region
[Download as PDF.](#)



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)