Overview News Use GREAT Demo Video How to Cite Help Forum

Bejerano Lab, Stanford University

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

Job Description

Job ID: 20250210-public-4.0.4-piyocl

Display name: K4me3_proximal_CpG_plus_Doub

Test set: K4me3 proximal CpG plus Double KO vs F F.bed (3.125 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?

Basal+extension (constitutive 5.0 kb upstream and 1.0 kb downstream, up to 1000.0 kb max extension). Curated regulatory domains are included.

5 of all 3,125 genomic regions (0.2%) 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?

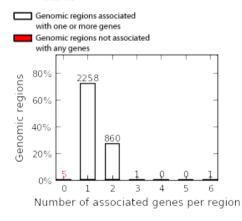
• Region-Gene Association Graphs

What do these graphs illustrate?

Associated genomic regions:

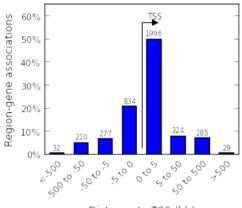
Number of associated genes per region

Download as PDF.



Binned by orientation and distance to TSS

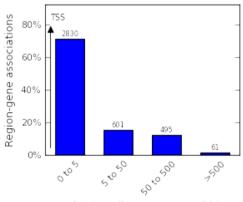
Download as PDF.



Distance to TSS (kb)

Binned by absolute distance to TSS

Download as PDF.

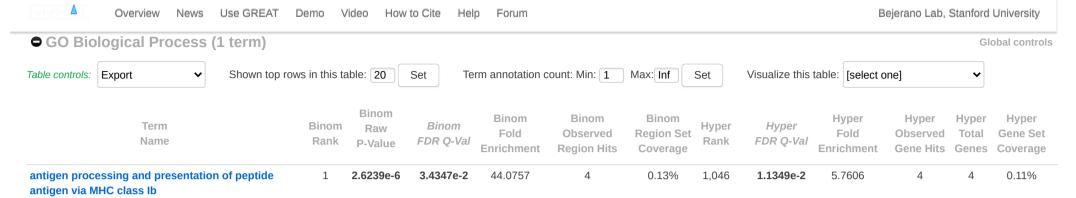


Absolute distance to TSS (kb)

• Global Controls

Global Export

Which data is exported by each option?



The test set of 3,125 genomic regions picked 3,714 (17%) of all 21,395 genes.

GO Biological Process has 13,090 terms covering 17,925 (84%) of all 21,395 genes, and 1,163,819 term - gene associations. 13,090 ontology terms (100%) were tested using an annotation count range of [1, Inf].

○ GO Cellular Component (no terms)

○ GO Molecular Function (no terms)

• Human Phenotype (no terms)

• Mouse Phenotype Single KO (no terms)

• Mouse Phenotype (no terms)

Bejerano Lab



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