

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

Job Description

Job ID:20241126-public-4.0.4-xCT3F1

Display name:proximal\_Double\_KO\_vs\_F\_F.bed

Test set:proximal\_Double\_KO\_vs\_F\_F.bed (4,788 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?*

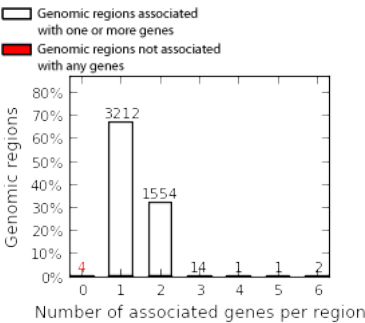
Associated genomic regions:Basal+extension (constitutive 5.0 kb upstream and 1.0 kb downstream, up to 1000.0 kb max extension). Curated regulatory domains are included in 4 of all 4,788 genomic regions (0.1%) are not associated with any genes.  
[View all genomic region-gene associations.](#)    *Which 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?*

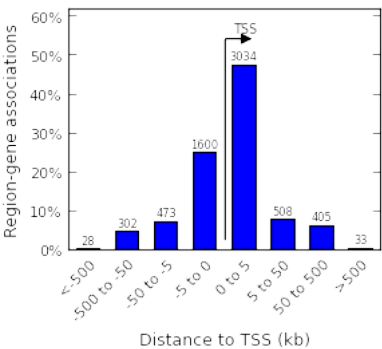
Number of associated genes per region

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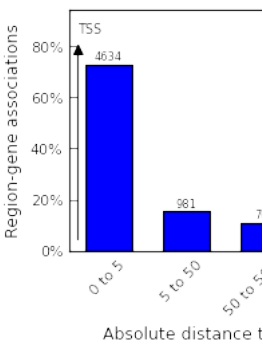
Binned by orientation and distance to TSS

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Binned by absolute distance to TSS

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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 (1 term)

Table controls: Export    Shown top rows in this table: 20    Set    Term annotation count: Min: 1    Max: Inf    Set    Visualize this table: [select one]

Term Name	Binom Rank	Binom Raw P-Value	Binom FDR Q-Val	Binom Fold Enrichment	Binom Observed Region Hits	Binom Region Set Coverage	Hyper Rank	Hyper FDR Q-Val	Hyper Fold Enrichment	Hyper Observed Region Hits
Hemolytic anemia	1	6.2732e-6	4.1397e-2	2.4555	32	0.67%	198	2.8561e-2	1.7277	198

The test set of 4,788 genomic regions picked 5,779 (27%) of all 21,395 genes.  
*Human Phenotype* has 6,599 terms covering 3,215 (15%) of all 21,395 genes, and 244,972 term - gene associations.  
6,599 ontology terms (100%) were tested using an annotation count range of [1, Inf].

Mouse Phenotype Single KO (no terms)

Mouse Phenotype (no terms)