



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

Job Description

Job ID: 20250210-public-4.0.4-VtYfqm

Display name: K4me3_proximal_CpG_minus_Do

Test set: K4me3_proximal_CpG_minus_Double_KO_vs_F_F.bed (387 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?*

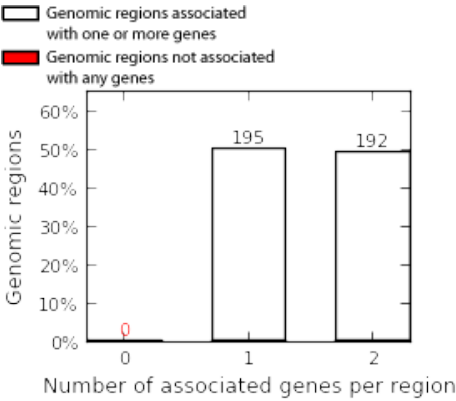
Associated genomic regions: Basal+extension (constitutive 5.0 kb upstream and 1.0 kb downstream, up to 1000.0 kb max extension). Curated regulatory domains are included.
0 of all 387 genomic regions (0%) are not associated with any genes.
[View all genomic region-gene associations.](#) *Which genes are 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?

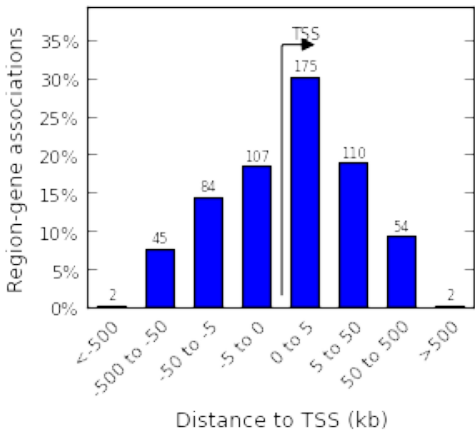
Number of associated genes per region

[Download as PDF.](#)



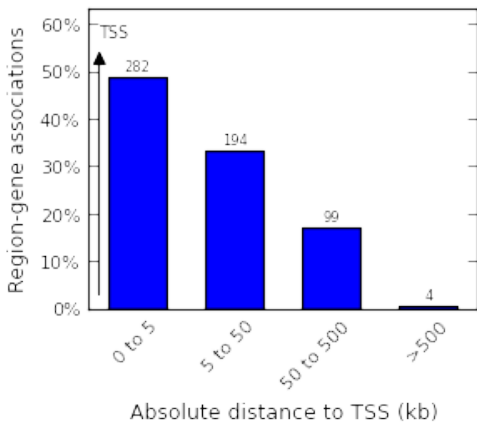
Binned by orientation and distance to TSS

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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?



GO Biological Process (1 term)

Global controls

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 Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
immune effector process	3	5.2993e-6	2.3123e-2	2.6723	27	6.98%	1	1.0105e-2	2.7291	30	417	5.32%

The test set of 387 genomic regions picked 564 (3%) 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 (2 terms)

Global controls

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 Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
polymeric cytoskeletal fiber	7	8.6856e-6	2.1019e-3	2.1674	38	9.82%	4	3.4250e-3	2.1348	39	693	6.91%
microtubule plus-end	8	4.3206e-5	9.1489e-3	9.7527	6	1.55%	5	4.7302e-2	9.4836	5	20	0.89%

The test set of 387 genomic regions picked 564 (3%) of all 21,395 genes.
GO Cellular Component has 1,694 terms covering 19,074 (89%) of all 21,395 genes, and 371,380 term - gene associations.
1,694 ontology terms (100%) were tested using an annotation count range of [1, Inf].

GO Molecular Function (no terms)

Global controls

Human Phenotype (no terms)

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Mouse Phenotype Single KO (no terms)

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Mouse Phenotype (no terms)

Global controls



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