

GREAT version 4.0.4

current (08/19/2019 to now)

Job Description

Job ID:20240719-public-4.0.4-qoHtEr

Display name:distfilter_DKO_K4me3_dcp.target.peaks.bed

Test set:distfilter_DKO_K4me3_dcp.target.peaks.bed (1,207 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?*

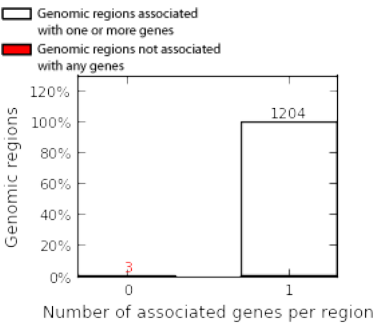
Associated genomic regions:Single nearest gene (1000.0kb max extension). Curated regulatory domains are included.
3 of all 1,207 genomic regions (0.2%) are not associated with any genes.
[View all genomic region-gene associations.](#) *Which genes are my regions associated with?*
[Revise the region-gene association rule.](#) *How are my regions associated with genes?*

Region-Gene Association Graphs

What do these graphs illustrate?

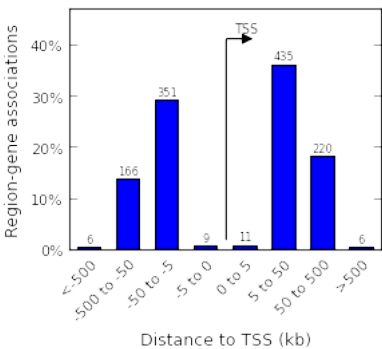
Number of associated genes per region

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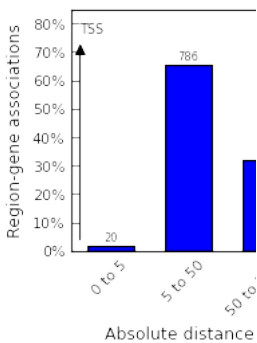
Binned by orientation and distance to TSS

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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 (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	Other Genes
dopaminergic neuron differentiation	57	2.0566e-4	4.7230e-2	3.3388	13	1.08%	213	1.5941e-2	4.5806	

The test set of 1,207 genomic regions picked 1,099 (5%) 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 (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	Other Genes
cell cortex	16	4.0880e-5	4.3281e-3	2.0996	36	2.98%	13	8.5930e-3	2.1551	

The test set of 1,207 genomic regions picked 1,099 (5%) 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)

Human Phenotype (no terms)

Mouse Phenotype Single KO (2 terms)

SRP

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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	Other Genes
decreased sensitivity to induced cell death	1	5.2682e-6	4.8309e-2	4.1910	15	1.24%	94	1.3516e-2	3.2868	
absent supraoccipital bone	4	1.2888e-5	2.9546e-2	9.4125	7	0.58%	77	8.5627e-3	9.7338	

The test set of 1,207 genomic regions picked 1,099 (5%) of all 21,395 genes.
Mouse Phenotype Single KO has 9,170 terms covering 9,466 (44%) of all 21,395 genes, and 551,620 term - gene associations.
9,170 ontology terms (100%) were tested using an annotation count range of [1, Inf].

Mouse Phenotype (3 terms)

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	Other Genes
absent supraoccipital bone	4	1.2888e-5	3.0851e-2	9.4125	7	0.58%	104	6.6197e-3	9.7338	
short scala media	7	3.5486e-5	4.8540e-2	8.0159	7	0.58%	246	4.8657e-2	11.6806	
decreased sensitivity to induced cell death	9	4.5294e-5	4.8188e-2	3.3056	16	1.33%	149	1.5628e-2	2.9625	

The test set of 1,207 genomic regions picked 1,099 (5%) of all 21,395 genes.
Mouse Phenotype has 9,575 terms covering 9,654 (45%) of all 21,395 genes, and 705,265 term - gene associations.
9,575 ontology terms (100%) were tested using an annotation count range of [1, Inf].