

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

### Job Description

Job ID: 20240719-public-4.0.4-9RkkYc

Display name: distfilter DKO K4me3 pcp.target.r

Test set: [distfilter\\_DKO\\_K4me3\\_pcp.target.peaks.bed](#) (1,067 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.kb max extension). Curated regulatory domains are included.  
0 of all 1,067 genomic regions (0%) are not associated with any genes.

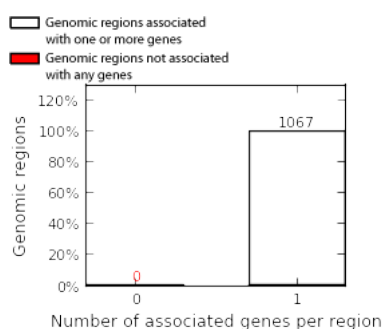
View all genomic region-gene associations. Which genes are my regions associated with?

Revise the region-gene association rule. How are my regions associated with genes?

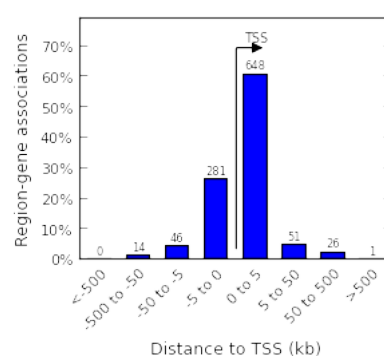
## ⊕ Region-Gene Association Graphs

What do these graphs illustrate?

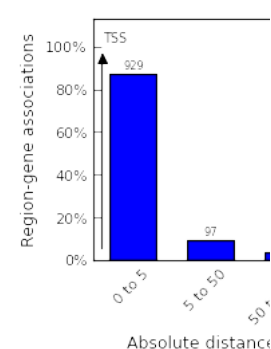
## Number of associated genes per region

[Download as PDF.](#)

**Binned by orientation and distance to TSS**

[Download as PDF](#)

## Binned by absolute distance to

[Download as PDF.](#)

**Global Controls**

Which data is exported by each option?

**⊕ Ensembl Genes (no terms)**

- GO Biological Process (5 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	Observed Region Hits
neuropeptide signaling pathway	2	1.6018e-6	1.0484e-2	3.2294	23	2.16%	7	7.7938e-7	4.6821	23
inner dynein arm assembly	3	5.8390e-6	2.5478e-2	10.6495	7	0.66%	31	5.6403e-3	7.9165	7
regulation of macrophage derived foam cell differentiation	9	1.9849e-5	2.8869e-2	6.2472	9	0.84%	18	2.0147e-4	8.7243	9
negative regulation of macrophage derived foam cell differentiation	17	6.2671e-5	4.8257e-2	12.4175	5	0.47%	40	1.8996e-2	10.1784	5
cilium movement	19	7.5140e-5	5.1768e-2	3.7035	13	1.22%	34	7.4245e-3	3.9498	13

The test set of 1,067 genomic regions picked 1,051 (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 (2 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	Observed Region Hits
axoneme	11	5.2988e-5	8.1602e-3	3.0016	18	1.69%	19	2.2654e-3	3.0283	18
inner dynein arm	16	3.5905e-4	3.8014e-2	8.4954	5	0.47%	21	4.6826e-3	10.1784	5

SRP

▲

OverviewNewsUse GREATDemoVideoHow to CiteHelpForum

Bejerano Lab

1,694 ontology terms (100%) were tested using an annotation count range of [1, Inf].

GO Molecular Function (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	Observed Region Hits
G-protein coupled peptide receptor activity	2	1.6885e-5	3.4876e-2	2.8628	22	2.06%	5	2.9376e-4	3.4450	
peptide receptor activity	3	1.9199e-5	2.6437e-2	2.8382	22	2.06%	6	3.6764e-4	3.3673	
neuropeptide receptor activity	5	2.5412e-5	2.0996e-2	3.8684	14	1.31%	2	4.9569e-5	6.1955	

The test set of 1,067 genomic regions picked 1,051 (5%) of all 21,395 genes.  
GO Molecular Function has 4,131 terms covering 17,189 (80%) of all 21,395 genes, and 227,341 term - gene associations.  
4,131 ontology terms (100%) were tested using an annotation count range of [1, Inf].

Human Phenotype (no terms)

Mouse Phenotype Single KO (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	Observed Region Hits
abnormal erythrocyte physiology	3	1.0018e-5	3.0623e-2	6.8207	9	0.84%	58	4.5559e-2	4.0714	

The test set of 1,067 genomic regions picked 1,051 (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 (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	Observed Region Hits
increased stomach pH	3	1.1713e-5	3.7385e-2	12.3893	6	0.56%	26	1.0899e-2	8.7243	

The test set of 1,067 genomic regions picked 1,051 (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].