

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

Job Description

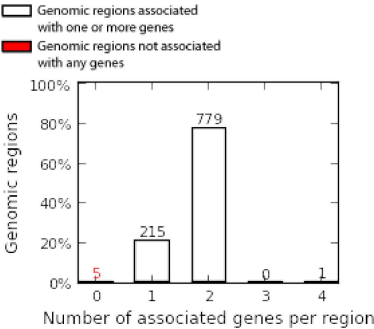
Loading...

Region-Gene Association Graphs

What do these graphs illustrate?

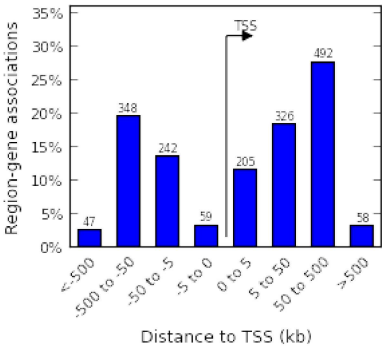
Number of associated genes per region

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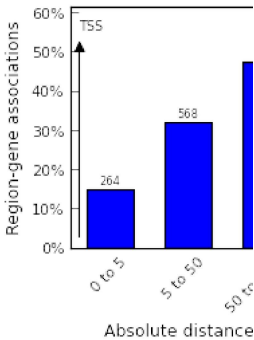
Binned by orientation and distance to TSS

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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)

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
Pcdh1	1	7.5048e-10	1.6056e-5	65.4591	6	0.60%	1	1.0000	14.8165	6
Tmem161b	2	1.3994e-9	1.4971e-5	15.9599	10	1.00%	1	1.0000	14.8165	10
Mef2c	3	3.8397e-7	2.7383e-3	12.5122	8	0.80%	1	1.0000	14.8165	8
Rhcg	4	9.1097e-7	4.8726e-3	57.6075	4	0.40%	1	1.0000	14.8165	4
Wnt7b	5	1.9340e-6	8.2756e-3	47.5859	4	0.40%	1	1.0000	14.8165	4
Polg	6	1.9614e-6	6.9941e-3	47.4159	4	0.40%	1	1.0000	14.8165	4
Ppara	7	2.1134e-6	6.4596e-3	46.5243	4	0.40%	1	1.0000	14.8165	4
Gprn1	8	2.2136e-6	5.9199e-3	125.8036	3	0.30%	1	1.0000	14.8165	3
Arap3	9	2.3553e-6	5.5991e-3	45.2594	4	0.40%	1	1.0000	14.8165	4
Tubb2b	10	3.6919e-6	7.8988e-3	105.9637	3	0.30%	1	1.0000	14.8165	3
Ddk1	11	3.9111e-6	7.6072e-3	22.2676	5	0.50%	1	1.0000	14.8165	5
Zmiz1	12	6.2010e-6	1.1056e-2	13.8737	6	0.60%	1	1.0000	14.8165	6
Slc6a17	13	6.2636e-6	1.0308e-2	88.7235	3	0.30%	1	1.0000	14.8165	3
Snph	14	7.2222e-6	1.1037e-2	84.5751	3	0.30%	1	1.0000	14.8165	3
Cstad	15	8.1759e-6	1.1662e-2	32.9410	4	0.40%	1	1.0000	14.8165	4
Fam214b	16	2.1387e-5	2.8599e-2	304.9807	2	0.20%	1	1.0000	14.8165	2
Mab21l1	17	3.4576e-5	4.3515e-2	14.0950	5	0.50%	1	1.0000	14.8165	5
Gnao1	18	3.6057e-5	4.2858e-2	22.4779	4	0.40%	1	1.0000	14.8165	4
Snca	19	4.1228e-5	4.6425e-2	219.4759	2	0.20%	1	1.0000	14.8165	2
Igsf8	20	4.5160e-5	4.8310e-2	209.6727	2	0.20%	1	1.0000	14.8165	2

The test set of 1,000 genomic regions picked 1,444 (7%) of all 21,395 genes.
Ensembl Genes has 21,395 terms covering 21,395 (100%) of all 21,395 genes, and 21,395 term - gene associations.
21,395 ontology terms (100%) were tested using an annotation count range of [1, Inf].

GO Biological Process (no 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	Hyper Observed Region Hits
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Term	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
Loading...										
The test set of 1,000 genomic regions picked 1,444 (7%) 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)

Table controls:

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Term annotation count: Min: 1Max: InfSet

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
postsynaptic density	17	2.3373e-9	2.3291e-7	2.1524	72	7.20%	7	6.5670e-13	3.4662	
postsynaptic specialization	18	3.0070e-9	2.8299e-7	2.1391	72	7.20%	8	8.5399e-13	3.4347	
asymmetric synapse	20	8.8971e-9	7.5359e-7	2.0819	72	7.20%	10	8.3117e-13	3.4192	
neuron to neuron synapse	21	1.2676e-8	1.0226e-6	2.0633	72	7.20%	11	1.1139e-12	3.3885	
nuclear transcriptional repressor complex	51	3.4950e-4	1.1609e-2	3.8699	10	1.00%	69	2.5291e-2	3.7041	

The test set of 1,000 genomic regions picked 1,444 (7%) 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)

Table controls:

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Term annotation count: Min: 1Max: InfSet

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
mRNA binding	11	2.1306e-6	8.0013e-4	2.4128	36	3.60%	35	3.5115e-2	2.0515	
transcription corepressor activity	20	1.1319e-5	2.3379e-3	2.0821	42	4.20%	7	2.8256e-4	2.6195	

The test set of 1,000 genomic regions picked 1,444 (7%) 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)

Table controls:

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Term annotation count: Min: 1Max: InfSet

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
Loading...										
The test set of 1,000 genomic regions picked 1,444 (7%) 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)

Table controls:

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Term annotation count: Min: 1Max: InfSet

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
Loading...										
The test set of 1,000 genomic regions picked 1,444 (7%) 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 (no terms)

Table controls:

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Term annotation count: Min: 1Max: InfSet

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
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The test set of 1,000 genomic regions picked 1,444 (7%) 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].



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