

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

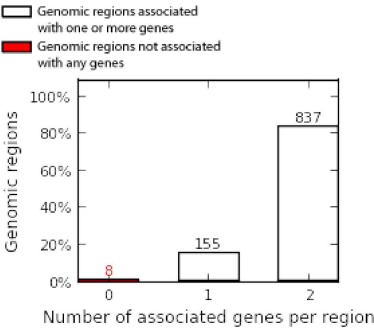
Job Description

Region-Gene Association Graphs

What do these graphs illustrate?

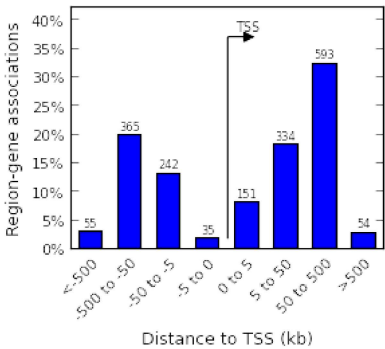
Number of associated genes per region

Download as PDF.



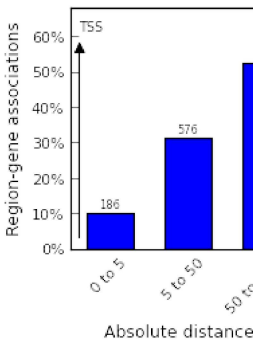
Binned by orientation and distance to TSS

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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?

Ensembl Genes (no terms)

GO Biological Process (20+ 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	Term Ob Ge
myelination	54	9.2729e-7	2.2478e-4	3.0575	26	2.60%	106	7.0803e-5	3.2695	
regulation of supramolecular fiber organization	55	9.4282e-7	2.2439e-4	2.0569	54	5.40%	191	2.9538e-3	1.9209	
regulation of synaptic plasticity	56	9.5925e-7	2.2422e-4	2.1451	49	4.90%	57	1.8440e-7	3.0439	
axon ensheathment	61	1.4357e-6	3.0810e-4	2.9109	27	2.70%	95	3.4441e-5	3.3113	
small GTPase mediated signal transduction	83	8.2753e-6	1.3051e-3	2.0121	47	4.70%	146	9.6877e-4	2.1008	
regulation of protein polymerization	93	1.1930e-5	1.6792e-3	2.3590	32	3.20%	277	1.3664e-2	2.0504	
plasma membrane organization	94	1.2153e-5	1.6924e-3	2.0757	42	4.20%	144	8.7243e-4	2.1889	
cell-cell junction organization	103	1.9160e-5	2.4350e-3	2.3775	30	3.00%	139	7.3852e-4	2.6176	
cell junction assembly	105	2.0379e-5	2.5406e-3	2.5054	27	2.70%	127	3.6852e-4	2.9521	
positive regulation of protein polymerization	129	5.8245e-5	5.9102e-3	2.8746	19	1.90%	241	6.6087e-3	2.6466	
protein localization to cell periphery	144	9.9342e-5	9.0305e-3	2.0772	33	3.30%	265	9.8828e-3	2.0965	
actin filament organization	148	1.2533e-4	1.1085e-2	2.0016	35	3.50%	128	3.6870e-4	2.3510	
cell junction organization	154	1.5482e-4	1.3160e-2	2.1102	30	3.00%	205	3.3575e-3	2.3505	
Ras protein signal transduction	156	1.5934e-4	1.3370e-2	2.2090	27	2.70%	294	2.0658e-2	2.2156	
protein localization to plasma membrane	157	1.6344e-4	1.3627e-2	2.0739	31	3.10%	274	1.3603e-2	2.1198	
regulation of microtubule polymerization or depolymerization	160	1.7106e-4	1.3994e-2	2.9369	16	1.60%	339	4.0342e-2	2.6423	
Type I pneumocyte differentiation	174	2.2288e-4	1.6767e-2	5.1051	8	0.80%	322	3.2519e-2	7.8977	
cortical cytoskeleton organization	180	2.7273e-4	1.9834e-2	3.6844	11	1.10%	355	4.6799e-2	3.2734	
positive regulation of supramolecular fiber organization	182	2.8067e-4	2.0186e-2	2.1296	27	2.70%	302	2.2539e-2	2.0732	
regulation of neuronal synaptic plasticity	209	4.2506e-4	2.6622e-2	2.6058	17	1.70%	229	5.4358e-3	3.3273	

The test set of 1,000 genomic regions picked 1,548 (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 (11 terms)

Table controls:

Export

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Set

Term annotation count: Min:

1

 Max:

Inf

Set

Visualize this table:

[select one]

Name	Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment	Ge
postsynaptic density	12	7.6998e-11	1.0870e-8	2.2720	76	7.60%	7	1.3609e-13	3.4236	
postsynaptic specialization	15	1.0159e-10	1.1473e-8	2.2579	76	7.60%	9	1.6142e-13	3.3924	
asymmetric synapse	18	3.3562e-10	3.1586e-8	2.1976	76	7.60%	10	1.7901e-13	3.3771	
neuron to neuron synapse	20	4.9596e-10	4.2008e-8	2.1779	76	7.60%	12	2.2550e-13	3.3468	
myelin sheath	43	1.2106e-6	4.7693e-5	2.5134	35	3.50%	58	2.3867e-3	2.0799	
Z disc	67	4.3251e-4	1.0935e-2	2.0694	27	2.70%	49	1.0003e-3	2.5431	
I band	69	5.0575e-4	1.2417e-2	2.0172	28	2.80%	57	2.1566e-3	2.3525	
paranode region of axon	71	6.5188e-4	1.5553e-2	4.9487	7	0.70%	76	1.3465e-2	5.1829	
main axon	72	7.8513e-4	1.8472e-2	2.1681	22	2.20%	40	3.4770e-5	3.7131	
axon initial segment	73	9.3619e-4	2.1725e-2	4.6473	7	0.70%	53	1.5276e-3	7.5388	
protein serine/threonine phosphatase complex	82	2.1226e-3	4.3850e-2	2.8497	11	1.10%	98	4.7022e-2	2.7642	

The test set of 1,000 genomic regions picked 1,548 (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 (5 terms)

Table controls: Export

Shown top rows in this table: 20Set

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	Hyper Observed Region Hits
tubulin binding	8	8.5889e-7	4.4351e-4	2.0320	56	5.60%	20	2.9802e-3	1.9744	
microtubule binding	9	1.2893e-6	5.9181e-4	2.2542	43	4.30%	12	1.0387e-3	2.2720	
phosphatase regulator activity	21	5.4844e-5	1.0789e-2	2.7958	20	2.00%	49	3.8584e-2	2.5418	
binding, bridging	25	9.2070e-5	1.5214e-2	2.2101	29	2.90%	15	2.4795e-3	2.5979	
protein binding, bridging	28	1.3503e-4	1.9921e-2	2.2731	26	2.60%	24	3.9393e-3	2.6440	

The test set of 1,000 genomic regions picked 1,548 (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 (1 term)

Table controls: Export

Shown top rows in this table: 20Set

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	Hyper Observed Region Hits
Abnormal peripheral myelination	2	9.0069e-6	2.9718e-2	3.4440	18	1.80%	3	1.3195e-2	3.4052	

The test set of 1,000 genomic regions picked 1,548 (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 (8 terms)

Table controls: Export

Shown top rows in this table: 20Set

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	Hyper Observed Region Hits
abnormal axon morphology	6	2.5459e-7	3.8909e-4	2.4962	40	4.00%	47	2.2067e-4	2.6544	
abnormal sebaceous gland morphology	22	8.5679e-6	3.5713e-3	3.3188	19	1.90%	171	3.5901e-2	2.7642	
eye inflammation	24	1.4098e-5	5.3867e-3	3.1998	19	1.90%	85	5.1732e-3	3.1895	
decreased nerve conduction velocity	29	3.1868e-5	1.0077e-2	3.7862	14	1.40%	128	1.7805e-2	4.0126	
abnormal oligodendrocyte morphology	38	6.1226e-5	1.4775e-2	3.2174	16	1.60%	62	9.8380e-4	4.4825	
abnormal eosinophil cell number	42	7.5267e-5	1.6433e-2	2.4081	25	2.50%	182	3.9768e-2	2.1765	
abnormal myelination	68	3.5602e-4	4.8011e-2	2.0340	29	2.90%	136	2.2618e-2	2.2194	
increased gland tumor incidence	70	3.8184e-4	5.0021e-2	2.1213	26	2.60%	116	1.3774e-2	2.3211	

9,717 ontology terms (100%) were tested using an annotation count range of [1, Inf].

Mouse Phenotype (16 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
abnormal axon morphology	18	2.0389e-7	1.0846e-4	2.1127	57	5.70%	41	6.6546e-7	2.6650	57
increased insulin sensitivity	56	2.7163e-5	4.6444e-3	2.0660	39	3.90%	147	7.1105e-3	2.1381	39
abnormal endocrine pancreas development	59	3.2167e-5	5.2203e-3	3.4012	16	1.60%	229	1.9708e-2	4.0951	16
abnormal liver cholesterol level	65	4.7768e-5	7.0366e-3	3.2875	16	1.60%	265	3.2927e-2	2.8111	16
abnormal axon initial segment morphology	67	5.3261e-5	7.6116e-3	9.4199	6	0.60%	153	8.0512e-3	11.0569	6
decreased nerve conduction velocity	74	8.2806e-5	1.0714e-2	3.0056	17	1.70%	223	1.8100e-2	3.2347	17
abnormal cellular glucose import	75	8.8934e-5	1.1354e-2	2.4333	24	2.40%	278	4.1417e-2	2.4106	24
abnormal muscle cell glucose uptake	76	9.0276e-5	1.1374e-2	2.4869	23	2.30%	269	3.5544e-2	2.5460	23
abnormal pancreatic beta cell differentiation	118	2.9069e-4	2.3588e-2	3.4134	12	1.20%	280	4.2237e-2	4.6070	12
abnormal pancreatic alpha cell morphology	121	3.4901e-4	2.7618e-2	2.3081	22	2.20%	198	1.3001e-2	3.1895	22
abnormal nerve conduction	128	3.9014e-4	2.9184e-2	2.3422	21	2.10%	183	1.0179e-2	2.8399	21
abnormal oligodendrocyte morphology	133	4.2542e-4	3.0627e-2	2.6056	17	1.70%	194	1.2216e-2	3.0453	17
sebaceous gland hyperplasia	144	5.9825e-4	3.9779e-2	5.9801	6	0.60%	143	6.1384e-3	8.6382	6
reduced AMPA-mediated synaptic currents	149	6.2753e-4	4.0326e-2	3.5843	10	1.00%	91	1.0438e-3	6.5040	10
ductus venosus stenosis	153	6.8442e-4	4.2832e-2	10.3336	4	0.40%	293	4.9286e-2	6.9105	4
abnormal AMPA-mediated synaptic currents	158	7.2864e-4	4.4157e-2	2.9102	13	1.30%	80	7.1824e-4	4.9042	13

The test set of 1,000 genomic regions picked 1,548 (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].