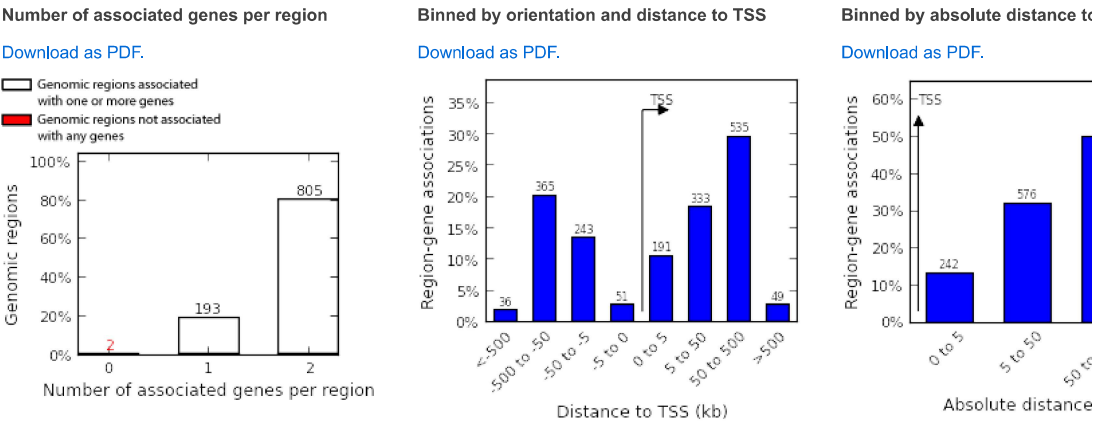


GREAT version 4.0.4 current (08/19/2019 to now)

Job Description

Region-Gene Association Graphs

What do these graphs illustrate?



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	Other
regulation of synaptic plasticity	16	7.5160e-10	6.1490e-7	2.4953	57	5.70%	74	3.4713e-6	2.8694	
regulation of dendritic spine morphogenesis	18	2.7090e-9	1.9700e-6	4.8650	22	2.20%	247	7.2961e-3	3.9384	
protein localization to cell periphery	28	2.7831e-8	1.3011e-5	2.6437	42	4.20%	185	1.3989e-3	2.3099	
protein localization to plasma membrane	31	4.3294e-8	1.8281e-5	2.6760	40	4.00%	199	1.8341e-3	2.3485	
regulation of transporter activity	37	1.1827e-7	4.1841e-5	2.2230	53	5.30%	58	2.9782e-7	2.7339	
protein localization to membrane	44	3.1624e-7	9.4082e-5	2.0678	58	5.80%	208	2.5697e-3	1.8934	
plasma membrane organization	46	4.4139e-7	1.2561e-4	2.2734	46	4.60%	349	3.4130e-2	1.8605	
regulation of dendrite morphogenesis	47	4.4701e-7	1.2450e-4	2.8886	30	3.00%	299	1.6011e-2	2.6921	
regulation of dendritic spine development	49	5.0195e-7	1.3409e-4	3.0050	28	2.80%	254	8.7563e-3	3.0075	
regulation of ion transmembrane transporter activity	52	5.8438e-7	1.4711e-4	2.2048	48	4.80%	72	2.3643e-6	2.6842	
regulation of dendrite development	64	1.9694e-6	4.0281e-4	2.2163	43	4.30%	156	4.8528e-4	2.6651	
regulation of transmembrane transporter activity	65	2.0270e-6	4.0820e-4	2.1058	48	4.80%	75	5.1560e-6	2.6083	
brain-derived neurotrophic factor receptor signaling pathway	77	4.1428e-6	7.0428e-4	7.6259	9	0.90%	378	4.5949e-2	10.6337	
neuromuscular process controlling balance	81	5.2488e-6	8.4823e-4	2.9160	24	2.40%	168	7.9064e-4	3.4372	
regulation of calcium ion transmembrane transporter activity	93	1.1970e-5	1.6849e-3	2.8456	23	2.30%	158	5.0577e-4	3.2719	
regulation of neuronal synaptic plasticity	99	1.5510e-5	2.0507e-3	3.0656	20	2.00%	176	1.1757e-3	3.6758	
phagocytosis, recognition	117	3.5937e-5	4.0207e-3	6.6747	8	0.80%	315	2.1892e-2	5.3168	
regulation of sequestering of calcium ion	120	3.9402e-5	4.2981e-3	2.3641	28	2.80%	120	1.1430e-4	3.0764	
negative regulation of homeostatic process	129	5.3658e-5	5.4449e-3	2.2101	31	3.10%	302	1.7145e-2	2.1135	
regulation of calcium ion transmembrane transport	132	6.5505e-5	6.4959e-3	2.1855	31	3.10%	182	1.2983e-3	2.5585	

The test set of 1,000 genomic regions picked 1,509 (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 (20+ terms)

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	7	1.1583e-13	2.8030e-11	2.4813	83	8.30%	9	3.5692e-14	3.5120	
postsynaptic specialization	8	1.5976e-13	3.3828e-11	2.4659	83	8.30%	11	4.4704e-14	3.4801	
asymmetric synapse	10	6.4051e-13	1.0850e-10	2.4000	83	8.30%	12	5.0590e-14	3.4644	
neuron to neuron synapse	11	1.0092e-12	1.5542e-10	2.3785	83	8.30%	13	7.0863e-14	3.4333	
neuron spine	26	7.8074e-9	5.0868e-7	2.5895	47	4.70%	22	2.0584e-9	3.7134	
dendritic spine	28	1.4570e-8	8.8149e-7	2.5668	46	4.60%	23	4.7436e-9	3.6887	
myelin sheath	30	1.9837e-8	1.1201e-6	2.8006	39	3.90%	70	6.8835e-3	1.9960	
cation channel complex	38	7.5688e-7	3.3741e-5	2.0892	53	5.30%	21	5.4790e-10	3.3029	
calcium channel complex	49	4.8986e-5	1.6935e-3	3.0195	18	1.80%	39	2.4358e-5	4.2010	
actomyosin	54	6.6801e-5	2.0956e-3	2.9453	18	1.80%	69	5.7737e-3	2.7983	
voltage-gated potassium channel complex	62	1.1002e-4	3.0062e-3	2.1221	31	3.10%	31	7.4197e-7	3.8365	
I band	68	2.3225e-4	5.7858e-3	2.0893	29	2.90%	65	3.5161e-3	2.3128	
presynaptic active zone	69	2.5714e-4	6.3129e-3	3.0911	14	1.40%	43	7.2736e-5	5.0041	
ruffle	73	3.1915e-4	7.4061e-3	2.1117	27	2.70%	76	1.0599e-2	2.0876	
sarcoplasm	79	5.3791e-4	1.1535e-2	2.4017	19	1.90%	87	2.1326e-2	2.6331	
stress fiber	82	5.9684e-4	1.2330e-2	2.8350	14	1.40%	96	3.1252e-2	2.6175	
apical dendrite	90	1.0143e-3	1.9091e-2	4.5825	7	0.70%	83	1.8417e-2	5.9076	
actin filament bundle	92	1.1966e-3	2.2032e-2	2.5310	15	1.50%	93	2.9791e-2	2.5249	
neuronal cell body membrane	99	1.3968e-3	2.3901e-2	3.2176	10	1.00%	58	2.2927e-3	5.1557	
cell body membrane	102	1.5488e-3	2.5722e-2	3.1721	10	1.00%	62	3.0860e-3	4.9316	

The test set of 1,000 genomic regions picked 1,509 (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 (2 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	Observed Region Hits
phosphoprotein binding	14	1.6264e-5	4.7990e-3	2.7897	23	2.30%	21	4.2503e-3	3.0025	
ion channel binding	18	6.2288e-5	1.4295e-2	2.3007	28	2.80%	7	5.4762e-4	3.0113	

The test set of 1,000 genomic regions picked 1,509 (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)

Mouse Phenotype Single KO (9 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	Observed Region Hits
abnormal long term potentiation	1	1.4942e-7	1.3702e-3	2.0423	63	6.30%	7	5.7642e-10	3.3905	
reduced long term potentiation	2	5.6063e-7	2.5705e-3	2.2775	45	4.50%	10	6.5562e-9	3.9799	
increased susceptibility to age-related hearing loss	4	5.0973e-6	1.1685e-2	4.8186	13	1.30%	124	3.0520e-2	4.7261	
abnormal susceptibility to hearing loss	12	2.8694e-5	2.1927e-2	3.4345	16	1.60%	84	8.8270e-3	4.1701	
abnormal AMPA-mediated synaptic currents	18	4.9234e-5	2.5082e-2	4.1454	12	1.20%	76	6.4237e-3	5.4012	
abnormal object recognition memory	19	5.0115e-5	2.4187e-2	2.8146	20	2.00%	90	1.0201e-2	3.1507	
abnormal miniature excitatory postsynaptic currents	23	8.6438e-5	3.4462e-2	2.2556	28	2.80%	37	1.8339e-4	3.4581	
increased susceptibility to noise-induced hearing loss	29	1.4011e-4	4.4304e-2	4.3479	10	1.00%	98	1.2701e-2	6.5438	

Name	Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment	Ge
abnormal long term depression	30	1.4186e-4	4.3363e-2	2.2254	27	2.70%	55	1.6092e-3	3.3018	

The test set of 1,000 genomic regions picked 1,509 (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 (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	Other Genes
abnormal long term potentiation	1	7.3435e-10	7.0314e-6	2.1203	79	7.90%	7	1.2412e-12	3.3083	
reduced long term potentiation	3	5.3200e-8	1.6980e-4	2.2605	54	5.40%	14	3.8831e-10	3.6123	
small cerebellum	8	3.1322e-6	3.7489e-3	2.0533	49	4.90%	60	2.1632e-4	2.6357	
enhanced paired-pulse facilitation	9	4.3876e-6	4.6679e-3	3.3499	20	2.00%	90	3.0320e-3	3.9567	
abnormal miniature excitatory postsynaptic currents	11	7.0820e-6	6.1646e-3	2.2825	36	3.60%	37	7.1632e-6	3.3820	
increased susceptibility to age-related hearing loss	12	7.2925e-6	5.8188e-3	4.0723	15	1.50%	97	4.3268e-3	4.9079	
abnormal object recognition memory	13	7.8661e-6	5.7937e-3	2.7074	26	2.60%	85	2.0523e-3	3.0382	
abnormal glutamate-mediated receptor currents	14	7.9863e-6	5.4620e-3	2.9204	23	2.30%	59	1.7614e-4	3.8259	
abnormal hippocampus layer morphology	18	1.5068e-5	8.0154e-3	2.3684	31	3.10%	223	3.9616e-2	2.2585	
abnormal skeletal muscle fiber type ratio	19	2.0764e-5	1.0464e-2	3.7178	15	1.50%	174	1.9502e-2	3.5446	
abnormal susceptibility to hearing loss	21	2.4494e-5	1.1168e-2	3.1891	18	1.80%	77	1.1765e-3	4.3625	
abnormal long term depression	27	5.1151e-5	1.8140e-2	2.0980	35	3.50%	42	1.5352e-5	3.4372	
abnormal synaptic vesicle recycling	28	5.8731e-5	2.0084e-2	5.4190	9	0.90%	162	1.7311e-2	4.9624	
abnormal AMPA-mediated synaptic currents	29	6.4527e-5	2.1305e-2	3.3579	15	1.50%	68	6.6057e-4	5.0310	
abnormal excitatory postsynaptic potential	37	1.0443e-4	2.7026e-2	2.0212	35	3.50%	28	5.8235e-7	3.6090	
abnormal cochlear nerve morphology	38	1.1062e-4	2.7873e-2	4.0980	11	1.10%	220	3.9273e-2	5.9076	
increased susceptibility to noise-induced hearing loss	47	1.4011e-4	2.8544e-2	4.3479	10	1.00%	133	9.7716e-3	6.5438	
abnormal paired-pulse facilitation	57	2.0820e-4	3.4975e-2	2.2957	24	2.40%	155	1.6883e-2	2.7620	
decreased circulating adrenocorticotropin level	66	3.0219e-4	4.3841e-2	4.8753	8	0.80%	109	6.8282e-3	7.0891	
abnormal synaptic plasticity	73	3.6704e-4	4.8143e-2	2.2503	23	2.30%	183	2.3072e-2	2.7569	

The test set of 1,000 genomic regions picked 1,509 (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].