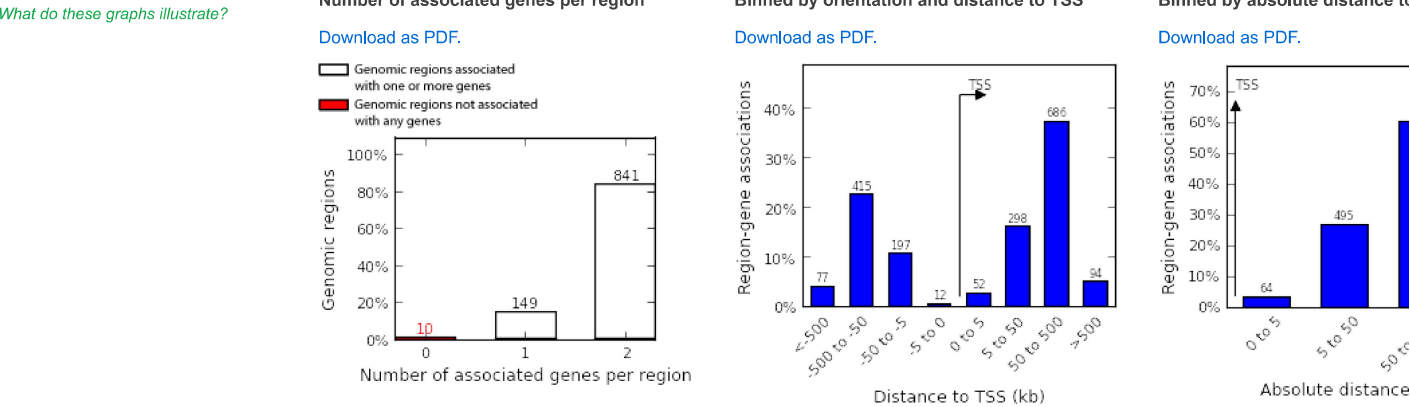


GREAT version 4.0.4 current (08/19/2019 to now)

Job Description

Region-Gene Association Graphs



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
postsynapse	4	1.5570e-17	6.5939e-15	2.1429	143	14.30%	2	3.6806e-27	3.5035	143
synaptic membrane	10	1.1004e-15	1.8641e-13	2.2758	113	11.30%	4	5.9873e-25	3.9849	113
postsynaptic membrane	14	8.2359e-14	9.9655e-12	2.3217	95	9.50%	5	2.0672e-22	4.2913	95
postsynaptic density	15	1.1583e-13	1.3081e-11	2.4813	83	8.30%	14	4.5731e-13	3.4377	83
postsynaptic specialization	16	1.5976e-13	1.6914e-11	2.4659	83	8.30%	16	5.9400e-13	3.4064	83
asymmetric synapse	17	6.4051e-13	6.3825e-11	2.4000	83	8.30%	17	6.7975e-13	3.3910	83
neuron to neuron synapse	18	1.0092e-12	9.4977e-11	2.3785	83	8.30%	18	9.4527e-13	3.3606	83
dendritic spine	37	2.6034e-7	1.1919e-5	2.3994	43	4.30%	32	6.0066e-7	3.3451	43
neuron spine	38	3.6242e-7	1.6156e-5	2.3691	43	4.30%	34	9.9160e-7	3.2654	43
myofibril	39	4.3936e-7	1.9084e-5	2.2985	45	4.50%	59	1.0084e-3	2.1471	45
sarcomere	43	1.0291e-6	4.0542e-5	2.3010	42	4.20%	57	7.4245e-4	2.2491	42
contractile fiber	45	1.5309e-6	5.7630e-5	2.1914	45	4.50%	64	2.0539e-3	2.0624	45
contractile fiber part	50	3.3279e-6	1.1275e-4	2.1931	42	4.20%	63	2.0852e-3	2.1194	42
GABA receptor complex	52	3.4653e-6	1.1289e-4	5.4466	12	1.20%	38	2.0079e-5	7.7794	12
Z disc	59	1.4180e-5	4.0712e-4	2.3760	31	3.10%	68	2.5737e-3	2.4687	31
I band	60	1.8543e-5	5.2354e-4	2.3054	32	3.20%	70	5.2536e-3	2.2927	32
caveola	61	2.0693e-5	5.7465e-4	2.6137	25	2.50%	45	7.0771e-5	3.4048	25
plasma membrane raft	64	2.8747e-5	7.6088e-4	2.4549	27	2.70%	54	3.5101e-4	2.9389	27
GABA-A receptor complex	69	5.5702e-5	1.3675e-3	4.8740	10	1.00%	49	1.2253e-4	7.3472	10
excitatory synapse	84	3.2350e-4	6.5239e-3	3.1797	13	1.30%	47	9.4502e-5	5.8777	13

The test set of 1,000 genomic regions picked 1,456 (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 (11 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
divalent inorganic cation transmembrane transporter activity	25	4.0301e-5	6.6593e-3	2.0279	39	3.90%	39	1.3392e-2	2.1957	39
ligand-gated ion channel activity	26	4.4602e-5	7.0865e-3	2.1128	35	3.50%	7	1.9039e-8	3.7921	35
postsynaptic neurotransmitter receptor activity	28	9.5209e-5	1.4047e-2	4.5627	10	1.00%	49	3.8601e-2	4.6755	10
GABA receptor activity	29	1.0117e-4	1.4411e-2	3.8366	12	1.20%	14	1.8488e-4	6.6793	12
syntaxin-1 binding	39	2.4059e-4	2.5484e-2	4.4783	9	0.90%	42	2.3091e-2	5.1430	9
Ras guanyl-nucleotide exchange factor activity	41	2.6061e-4	2.6258e-2	2.1400	27	2.70%	47	2.8742e-2	2.3324	27
calmodulin-dependent protein kinase activity	43	2.6641e-4	2.5594e-2	4.0076	10	1.00%	48	3.5275e-2	4.1984	10
ligand-gated cation channel activity	57	5.8105e-4	4.2111e-2	2.3246	20	2.00%	10	7.0100e-5	3.9323	20
extracellular ligand-gated ion channel activity	61	5.9252e-4	4.0126e-2	2.1714	23	2.30%	8	4.5476e-7	4.5532	23
calcium channel activity	62	6.1554e-4	4.1013e-2	2.0206	27	2.70%	32	5.3873e-3	2.6962	27
GABA-A receptor activity	67	7.8105e-4	4.8157e-2	3.4814	10	1.00%	21	2.9714e-4	6.9605	10

The test set of 1,000 genomic regions picked 1,456 (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 (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	Hyper Observed Region Hits
abnormal long term potentiation	8	6.0711e-9	6.9590e-6	2.1719	67	6.70%	9	1.2737e-12	3.7535	67

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Name	Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment	Ge
reduced long term potentiation	11	1.4233e-8	1.1865e-5	2.4799	49	4.90%	15	9.2037e-9	3.9958	
decreased prepulse inhibition	18	8.2661e-7	4.2111e-4	2.4445	38	3.80%	187	4.7085e-2	2.1984	
abnormal contextual conditioning behavior	23	1.0974e-6	4.3754e-4	2.1971	46	4.60%	20	1.1061e-7	3.6153	
abnormal temporal memory	24	1.3314e-6	5.0870e-4	2.1008	50	5.00%	21	1.2865e-7	3.3531	
abnormal spatial working memory	27	2.1304e-6	7.2355e-4	2.9186	26	2.60%	81	3.5483e-3	3.4868	
abnormal dendrite morphology	28	2.2177e-6	7.2629e-4	2.1823	44	4.40%	35	7.9271e-6	3.0613	
abnormal synaptic plasticity	31	4.6070e-6	1.3628e-3	2.9393	24	2.40%	33	3.1336e-6	4.8091	
abnormal excitatory postsynaptic currents	32	7.0083e-6	2.0083e-3	2.2535	37	3.70%	28	5.8876e-7	3.9501	
abnormal T cell selection	34	7.0976e-6	1.9143e-3	4.3474	14	1.40%	109	1.0420e-2	4.8981	
abnormal hippocampus pyramidal cell morphology	35	7.1234e-6	1.8663e-3	3.3636	19	1.90%	137	2.0284e-2	3.3675	
decreased exploration in new environment	37	7.2376e-6	1.7938e-3	2.4615	31	3.10%	47	5.1291e-5	3.5469	
lymph node hyperplasia	41	9.3372e-6	2.0884e-3	4.5484	13	1.30%	127	1.6809e-2	4.5213	
impaired synaptic plasticity	47	2.1611e-5	4.2165e-3	3.3584	17	1.70%	60	2.7622e-4	5.0381	
abnormal glutamate-mediated receptor currents	49	2.7263e-5	5.1020e-3	3.1625	18	1.80%	90	4.2650e-3	3.8333	
abnormal parturition	58	5.5457e-5	8.7680e-3	4.0932	12	1.20%	158	2.6573e-2	4.6755	
abnormal positive T cell selection	59	5.7292e-5	8.9045e-3	4.4201	11	1.10%	120	1.4016e-2	6.2976	
increased lean body mass	64	7.6996e-5	1.1032e-2	2.2715	28	2.80%	184	4.4903e-2	2.1136	
abnormal hippocampus pyramidal cell layer	66	8.1898e-5	1.1379e-2	2.7129	20	2.00%	164	2.9600e-2	2.9887	
weakness	76	1.5268e-4	1.8422e-2	2.1120	30	3.00%	135	1.8608e-2	2.4953	

The test set of 1,000 genomic regions picked 1,456 (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

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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 Ot Ge
abnormal excitatory postsynaptic currents	7	7.2584e-11	9.9285e-8	2.5826	60	6.00%	17	4.4164e-12	4.0818	
impaired synaptic plasticity	17	1.6878e-8	9.5064e-6	3.9086	25	2.50%	65	1.1214e-5	4.7982	
reduced long term potentiation	18	2.2106e-8	1.1759e-5	2.3023	55	5.50%	27	1.4139e-9	3.5566	
abnormal contextual conditioning behavior	19	2.2182e-8	1.1178e-5	2.2619	57	5.70%	24	1.0423e-9	3.6025	
abnormal synaptic plasticity	20	3.1717e-8	1.5185e-5	3.1308	32	3.20%	42	2.7066e-7	4.4899	
abnormal dendrite morphology	22	4.1499e-8	1.8061e-5	2.1838	59	5.90%	33	3.8986e-8	2.9815	
abnormal temporal memory	25	4.9134e-8	1.8818e-5	2.1399	61	6.10%	25	1.1204e-9	3.3360	
decreased exploration in new environment	35	8.7746e-7	2.4005e-4	2.5503	35	3.50%	63	9.6435e-6	3.4575	
abnormal T cell selection	37	1.8195e-6	4.7085e-4	3.7071	19	1.90%	232	1.5147e-2	3.2987	
lymph node hyperplasia	41	3.1463e-6	7.3477e-4	4.1223	16	1.60%	260	2.2335e-2	3.3396	
abnormal synaptic depression	49	5.4522e-6	1.0654e-3	2.0643	46	4.60%	37	9.0040e-8	3.4831	
abnormal hippocampus pyramidal cell morphology	51	7.5895e-6	1.4249e-3	2.9298	23	2.30%	200	9.2031e-3	2.9815	
abnormal spatial working memory	53	8.9392e-6	1.6150e-3	2.4345	31	3.10%	101	4.2656e-4	3.3481	
abnormal hippocampus layer morphology	55	1.5068e-5	2.6232e-3	2.3684	31	3.10%	165	4.1159e-3	2.6008	
abnormal hippocampus pyramidal cell layer	56	1.7099e-5	2.9236e-3	2.5856	26	2.60%	171	4.4233e-3	2.8387	
abnormal long term depression	58	2.2775e-5	3.7598e-3	2.1580	36	3.60%	68	2.1444e-5	3.4138	
abnormal glutamate-mediated receptor currents	59	2.4138e-5	3.9173e-3	2.7934	22	2.20%	124	1.2181e-3	3.4987	
abnormal miniature excitatory postsynaptic currents	68	3.8799e-5	5.4632e-3	2.1557	34	3.40%	78	1.1653e-4	3.1006	
abnormal excitatory postsynaptic potential	74	4.8232e-5	6.2408e-3	2.0789	36	3.60%	29	9.7369e-9	4.0076	
abnormal head shape	81	7.4455e-5	8.8013e-3	2.3171	27	2.70%	212	1.1951e-2	2.6717	

The test set of 1,000 genomic regions picked 1,456 (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].

