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

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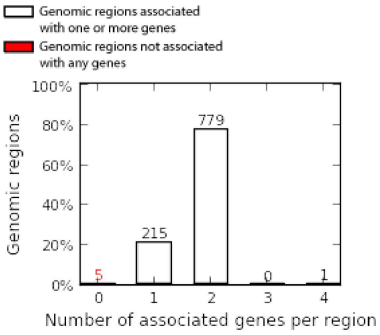

Binned by orientation and distance to TSS

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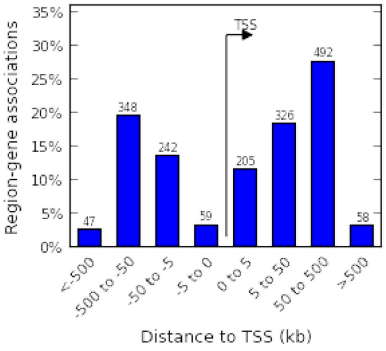

Binned by absolute distance to

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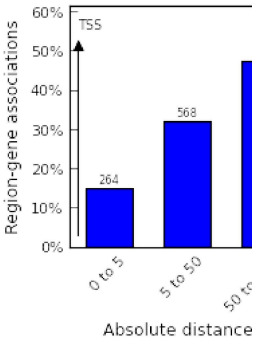

Global Controls

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	H Ob Ge
regulation of neurotransmitter secretion	92	**6.4067e-7**	**9.1157e-5**	3.6637	21	2.10%	381	**2.0211e-2**	3.1343	
transepithelial transport	101	**1.1215e-6**	**1.4535e-4**	6.0889	12	1.20%	243	**1.3756e-3**	5.9266	
regulation of ion transmembrane transporter activity	120	**3.0241e-6**	**3.2988e-4**	2.1129	46	4.60%	204	**5.4226e-4**	2.3016	
regulation of synaptic plasticity	132	**4.7045e-6**	**4.6653e-4**	2.0575	47	4.70%	128	**8.3334e-6**	2.8222	
regulation of transmembrane transporter activity	150	**9.5742e-6**	**8.3551e-4**	2.0181	46	4.60%	218	**9.2531e-4**	2.2365	
cell proliferation in forebrain	160	**1.5020e-5**	**1.2288e-3**	3.3122	18	1.80%	329	**9.8840e-3**	4.0409	
regulation of neurotransmitter levels	166	**2.6587e-5**	**2.0965e-3**	2.1416	36	3.60%	363	**1.4278e-2**	2.1166	
metanephric nephron tubule development	174	**3.2592e-5**	**2.4519e-3**	4.3303	12	1.20%	255	**2.1471e-3**	6.4822	
3'-UTR-mediated mRNA destabilization	175	**3.2955e-5**	**2.4650e-3**	5.8474	9	0.90%	437	**3.3906e-2**	5.6986	
phagocytosis, recognition	179	**3.5937e-5**	**2.6280e-3**	6.6747	8	0.80%	365	**1.4902e-2**	5.5562	
positive regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	180	**3.6701e-5**	**2.6690e-3**	5.7655	9	0.90%	266	**3.2952e-3**	6.1009	
synapse maturation	185	**4.5173e-5**	**3.1963e-3**	7.7082	7	0.70%	443	**3.4289e-2**	7.4082	
chemoattraction of axon	191	**5.4547e-5**	**3.7384e-3**	9.3788	6	0.60%	346	**1.1609e-2**	14.8165	
metanephric tubule development	192	**5.5937e-5**	**3.8136e-3**	4.0894	12	1.20%	306	**6.5833e-3**	5.4587	
positive regulation of mRNA catabolic process	195	**6.0038e-5**	**4.0302e-3**	4.8295	10	1.00%	322	**8.9394e-3**	4.5589	
axon ensheathment	210	**9.4170e-5**	**5.8699e-3**	2.4797	23	2.30%	498	**4.9592e-2**	2.3151	
forebrain ventricular zone progenitor cell division	216	**1.0570e-4**	**6.4054e-3**	5.0098	9	0.90%	338	**1.0750e-2**	9.8777	
negative regulation of ossification	229	**1.3184e-4**	**7.5360e-3**	2.3693	24	2.40%	220	**9.8548e-4**	3.1884	
regulation of cation channel activity	230	**1.3640e-4**	**7.7628e-3**	2.0959	31	3.10%	345	**1.1144e-2**	2.3518	
metanephric nephron epithelium development	236	**1.4973e-4**	**8.3050e-3**	3.6755	12	1.20%	323	**9.0378e-3**	5.1858	

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 (5 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	Ob Ge
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 (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	Ob Ge
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 (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	Ob Ge
Hypoplasia of the corpus callosum	3	1.7092e-7	3.7596e-4	2.4691	42	4.20%	6	2.0271e-2	2.3226	

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 (18 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	Ob Ge
abnormal limbic system morphology	4	2.4210e-10	5.5501e-7	2.0595	89	8.90%	12	1.3501e-11	2.9732	
abnormal temporal lobe morphology	6	1.3684e-9	2.0913e-6	2.0789	80	8.00%	9	1.4163e-12	3.2482	
abnormal hippocampus morphology	8	8.3504e-9	9.5716e-6	2.0258	77	7.70%	11	6.3953e-12	3.2083	
abnormal axon morphology	18	2.5459e-7	1.2970e-4	2.4962	40	4.00%	199	9.2874e-3	2.2568	
abnormal Ammon gyrus morphology	20	7.2572e-7	3.3274e-4	3.0991	26	2.60%	38	3.1949e-6	5.0376	
abnormal hippocampus region morphology	23	1.3191e-6	5.2590e-4	3.0790	25	2.50%	39	3.9895e-6	5.2681	
abnormal hippocampus layer morphology	38	2.3854e-5	5.7562e-3	2.6526	24	2.40%	63	1.3799e-4	3.7041	
abnormal corpus callosum morphology	49	4.2550e-5	7.9630e-3	2.1745	33	3.30%	220	1.1694e-2	2.5702	
abnormal dorsal telencephalic commissure morphology	51	5.5956e-5	1.0061e-2	2.1429	33	3.30%	239	1.5547e-2	2.4939	
increased cochlear inner hair cell number	53	6.1902e-5	1.0710e-2	4.3812	11	1.10%	169	5.7621e-3	6.8384	
abnormal seizure response to electrical stimulation	56	8.1825e-5	1.3399e-2	3.2856	15	1.50%	203	9.9334e-3	4.5589	
increased cochlear hair cell number	61	1.0349e-4	1.5558e-2	3.8271	12	1.20%	184	7.6696e-3	5.4587	
abnormal hippocampus CA3 region morphology	76	1.9599e-4	2.3648e-2	3.5676	12	1.20%	164	5.7702e-3	5.7620	
pale yolk sac	82	2.2221e-4	2.4849e-2	2.2853	24	2.40%	317	4.0661e-2	2.4694	
abnormal susceptibility to hearing loss	115	3.3950e-4	2.7071e-2	3.0051	14	1.40%	318	4.5459e-2	3.4862	

Name	Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment	Ge
abnormal hippocampus CA1 region morphology	117	3.7367e-4	2.9287e-2	3.1308	13	1.30%	101	1.9534e-3	5.3339	
abnormal hippocampus pyramidal cell layer	138	6.1770e-4	4.1046e-2	2.4416	18	1.80%	172	6.6183e-3	3.2646	
abnormal vein development	140	6.8675e-4	4.4982e-2	2.3521	19	1.90%	163	5.7995e-3	3.3209	

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 (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	H Ob Ge
dilated dorsal aorta	9	2.2683e-9	2.4132e-6	5.7611	19	1.90%	580	4.5036e-2	4.0409	
decreased urine ammonia level	22	2.8965e-7	1.2606e-4	16.8483	7	0.70%	322	8.2544e-3	9.8777	
abnormal brain ventricle size	25	6.3155e-7	2.4189e-4	2.1777	49	4.90%	141	4.6854e-4	2.4414	
tonic-clonic seizures	26	6.9769e-7	2.5694e-4	2.8872	29	2.90%	88	2.0824e-5	3.7510	
abnormal urine ammonia level	27	1.0244e-6	3.6330e-4	13.9153	7	0.70%	526	3.5994e-2	6.5851	
abnormal skeletal muscle fiber type ratio	29	1.1727e-6	3.8719e-4	4.2135	17	1.70%	314	7.5782e-3	3.7041	
abnormal paired-pulse facilitation	32	1.5182e-6	4.5428e-4	2.7740	29	2.90%	161	6.8747e-4	3.2712	
enlarged brain ventricles	33	1.7229e-6	4.9991e-4	2.1595	46	4.60%	181	1.0626e-3	2.3955	
convulsive seizures	34	1.7453e-6	4.9150e-4	2.1376	47	4.70%	72	4.6301e-6	2.8143	
abnormal hippocampus layer morphology	40	2.2684e-6	5.4299e-4	2.5212	33	3.30%	115	1.3301e-4	3.0157	
abnormal cerebellum development	42	2.5359e-6	5.7813e-4	2.0349	51	5.10%	87	2.0992e-5	2.8312	
failure of endochondral bone ossification	47	4.1411e-6	8.4364e-4	5.3504	12	1.20%	319	7.8952e-3	7.4082	
enhanced paired-pulse facilitation	49	4.3876e-6	8.5738e-4	3.3499	20	2.00%	371	1.2055e-2	3.4457	
abnormal stratification in cerebral cortex	51	4.9421e-6	9.2786e-4	3.0104	23	2.30%	502	3.1034e-2	2.9633	
intestinal/bowel diverticulum	55	8.1917e-6	1.4261e-3	19.0890	5	0.50%	584	4.5363e-2	8.8899	
absent corpus callosum	57	1.1335e-5	1.9041e-3	2.8556	23	2.30%	306	7.2421e-3	3.4677	
abnormal cerebellum lobule morphology	60	1.3652e-5	2.1787e-3	2.0448	43	4.30%	145	5.1092e-4	2.8345	
decreased type I pneumocyte number	64	1.6588e-5	2.4817e-3	5.0786	11	1.10%	291	5.7656e-3	6.3499	
abnormal Ammon gyrus morphology	71	2.8386e-5	3.8281e-3	2.4567	27	2.70%	104	6.9831e-5	3.7563	
trabecula carnea hypoplasia	78	4.0291e-5	4.9459e-3	2.7742	21	2.10%	409	1.8409e-2	2.8677	

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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