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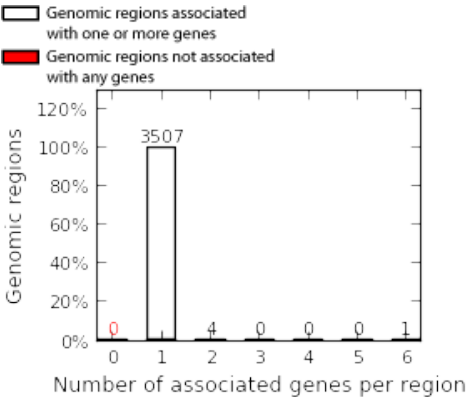
GREAT version 4.0.4   current (08/19/2019 to now) ▾

⊕ **Job Description**

⊕ **Region-Gene Association Graphs**
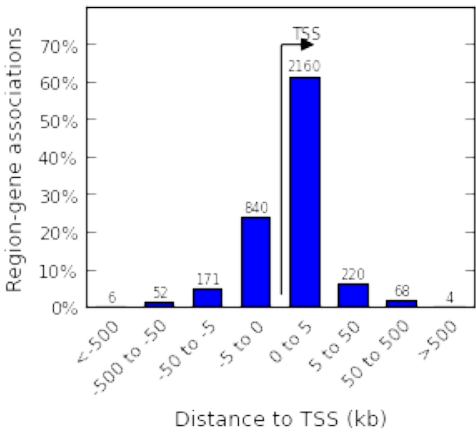
What do these graphs illustrate?

Number of associated genes per region
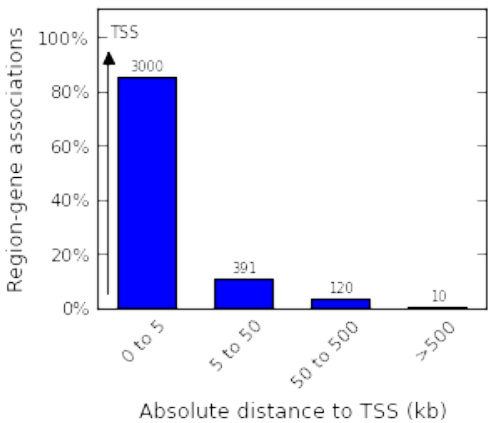
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⊕ **Global Controls**   Global Export ▾   *Which data is exported by each option?*

⊕ **Ensembl Genes (no terms)**   *Global controls*

⊖ **GO Biological Process (20+ terms)**   *Global controls*

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 Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
synaptic vesicle cycle	32	1.9024e-7	7.7822e-5	2.4499	43	1.22%	358	1.3218e-6	2.4443	38	98	1.12%

Name	Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment	Gene Hits	Genes	Coverage
antigen processing and presentation of peptide antigen via MHC class Ib	41	7.8908e-7	2.5193e-4	59.8060	4	0.11%	961	8.6133e-3	6.3038	4	4	0.12%
positive regulation of cyclic nucleotide biosynthetic process	42	8.5044e-7	2.6505e-4	2.3961	40	1.14%	243	6.7541e-9	2.8861	38	83	1.12%
positive regulation of cAMP biosynthetic process	46	1.2273e-6	3.4924e-4	2.4920	36	1.03%	222	2.0186e-9	3.1989	34	67	1.00%
regulation of cyclic nucleotide biosynthetic process	49	1.6796e-6	4.4868e-4	2.0066	56	1.59%	145	1.3033e-11	2.7675	54	123	1.59%
neurotransmitter transport	53	2.5733e-6	6.3557e-4	2.1055	48	1.37%	326	3.8848e-7	2.3198	46	125	1.36%
regulation of cAMP biosynthetic process	54	2.5818e-6	6.2584e-4	2.0362	52	1.48%	126	2.3549e-12	3.0018	50	105	1.47%
piRNA metabolic process	55	2.6954e-6	6.4151e-4	8.0675	9	0.26%	998	1.0190e-2	3.1519	9	18	0.27%
positive regulation of cyclic nucleotide metabolic process	63	4.6398e-6	9.6405e-4	2.1801	42	1.20%	266	1.4201e-8	2.7408	40	92	1.18%
positive regulation of cAMP metabolic process	65	4.9060e-6	9.8799e-4	2.3074	37	1.05%	260	1.1056e-8	2.9815	35	74	1.03%
synaptic vesicle transport	68	5.6837e-6	1.0941e-3	2.1614	42	1.20%	518	1.0457e-4	2.1013	37	111	1.09%
synaptic vesicle localization	70	8.3498e-6	1.5614e-3	2.1260	42	1.20%	543	1.5948e-4	2.0641	37	113	1.09%
antigen processing and presentation of endogenous peptide antigen via MHC class Ib	73	9.4613e-6	1.6966e-3	77.2841	3	0.09%	1,350	3.8680e-2	6.3038	3	3	0.09%
positive regulation of purine nucleotide biosynthetic process	79	1.8155e-5	3.0082e-3	2.0973	40	1.14%	290	4.5788e-8	2.7221	38	88	1.12%
antigen processing and presentation of exogenous protein antigen via MHC class Ib, TAP-dependent	86	2.2771e-5	3.4660e-3	57.4774	3	0.09%	1,350	3.8680e-2	6.3038	3	3	0.09%
antigen processing and presentation of endogenous antigen	94	3.6149e-5	5.0340e-3	8.0034	7	0.20%	914	6.5615e-3	4.0115	7	11	0.21%
calcium ion regulated exocytosis	100	5.1715e-5	6.7695e-3	2.3391	28	0.80%	546	1.6228e-4	2.4103	26	68	0.77%
negative regulation of high voltage-gated calcium channel activity	101	5.2835e-5	6.8476e-3	20.3758	4	0.11%	961	8.6133e-3	6.3038	4	4	0.12%
regulation of circadian sleep/wake cycle, sleep	103	5.5433e-5	7.0448e-3	4.8890	10	0.28%	1,082	1.5355e-2	2.9860	9	19	0.27%
synaptic vesicle exocytosis	105	6.2076e-5	7.7387e-3	2.4011	26	0.74%	537	1.4841e-4	2.5215	24	60	0.71%

The test set of 3,512 genomic regions picked 3,394 (16%) 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].

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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 Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
P granule	15	2.1326e-6	2.4085e-4	8.3065	9	0.26%	97	2.2166e-2	2.9860	9	19	0.27%
pi-body	25	5.4650e-5	3.7031e-3	12.8018	5	0.14%	103	2.6092e-2	4.5027	5	7	0.15%
extrinsic component of cytoplasmic side of plasma membrane	29	8.5465e-5	4.9923e-3	2.0803	34	0.97%	98	2.3244e-2	1.7350	30	109	0.88%
chromatoid body	41	4.5380e-4	1.8750e-2	5.2747	7	0.20%	112	4.6365e-2	3.1519	7	14	0.21%
synaptic vesicle membrane	48	6.4830e-4	2.2880e-2	2.0542	26	0.74%	89	1.2682e-2	1.9219	25	82	0.74%

The test set of 3,512 genomic regions picked 3,394 (16%) 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 (14 terms)   Global controls

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 Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
peptide receptor activity	8	5.2219e-7	2.6965e-4	2.1031	55	1.57%	38	6.9609e-10	2.5594	54	133	1.59%
G-protein coupled peptide receptor activity	15	1.8755e-6	5.1652e-4	2.0438	53	1.51%	42	3.0012e-9	2.5215	52	130	1.53%
clathrin binding	27	7.6460e-5	1.1698e-2	2.4175	25	0.71%	71	2.2497e-4	2.6361	23	55	0.68%
syntaxin binding	28	7.7439e-5	1.1425e-2	2.3676	26	0.74%	115	1.5871e-2	1.9699	25	80	0.74%
oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	30	8.8354e-5	1.2166e-2	4.2172	11	0.31%	151	4.7132e-2	2.5682	11	27	0.32%
hyaluronic acid binding	36	1.8583e-4	2.1324e-2	3.8663	11	0.31%	137	3.0676e-2	2.8654	10	22	0.29%
water channel activity	37	2.0278e-4	2.2640e-2	6.0412	7	0.20%	116	1.6316e-2	4.0115	7	11	0.21%
catecholamine binding	39	2.0466e-4	2.1678e-2	3.5602	12	0.34%	80	9.2207e-4	3.6022	12	21	0.35%
neuropeptide receptor activity	44	2.5903e-4	2.4319e-2	2.1513	27	0.77%	44	4.0430e-9	3.7000	27	46	0.80%
water transmembrane transporter activity	46	3.3319e-4	2.9922e-2	5.5586	7	0.20%	132	2.9693e-2	3.6772	7	12	0.21%

Name	Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment	Gene Hits	Genes	Coverage
carbonate dehydratase activity	54	5.5002e-4	4.2077e-2	3.9968	9	0.26%	85	2.8531e-3	4.0524	9	14	0.27%
structural constituent of myelin sheath	55	6.0532e-4	4.5465e-2	5.9750	6	0.17%	155	4.9727e-2	3.7823	6	10	0.18%
neuropeptide receptor binding	56	6.0543e-4	4.4662e-2	2.6195	16	0.46%	69	1.4407e-4	3.3620	16	30	0.47%
neuropeptide binding	58	6.3413e-4	4.5165e-2	2.7083	15	0.43%	53	1.5989e-6	4.5027	15	21	0.44%

The test set of 3,512 genomic regions picked 3,394 (16%) 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 Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
decreased inflammatory response	9	1.9046e-8	1.9406e-5	2.1340	67	1.91%	397	2.4140e-4	1.6880	64	239	1.89%
abnormal circulating interferon level	11	6.0168e-8	5.0158e-5	3.2831	29	0.83%	771	8.7469e-3	1.8839	26	87	0.77%
abnormal interferon level	13	2.4010e-7	1.6936e-4	2.9349	31	0.88%	998	2.4932e-2	1.6972	28	104	0.82%
arrest of spermatogenesis	18	1.8665e-6	9.5090e-4	2.0769	51	1.45%	498	9.6896e-4	1.7223	50	183	1.47%
abnormal male germ cell apoptosis	20	2.5381e-6	1.1637e-3	2.2881	40	1.14%	442	4.7617e-4	1.9102	40	132	1.18%
abnormal erythrocyte physiology	22	3.2642e-6	1.3606e-3	3.9142	17	0.48%	1,021	2.6406e-2	2.1013	15	45	0.44%
decreased interferon-alpha secretion	26	4.8378e-6	1.7063e-3	5.8246	11	0.31%	959	2.1768e-2	2.6266	10	24	0.29%
abnormal male meiosis	30	8.7816e-6	2.6842e-3	2.1921	39	1.11%	865	1.4948e-2	1.6185	38	148	1.12%
abnormal meiosis	31	9.0664e-6	2.6819e-3	2.0770	44	1.25%	914	1.8365e-2	1.5489	43	175	1.27%
decreased acute inflammation	36	1.3966e-5	3.5574e-3	2.0032	46	1.31%	526	1.1785e-3	1.7619	45	161	1.33%
arrest of male meiosis	38	1.5761e-5	3.8033e-3	2.3398	32	0.91%	772	8.7373e-3	1.7765	31	110	0.91%
abnormal sebaceous gland morphology	41	1.7362e-5	3.8832e-3	2.5432	27	0.77%	553	1.5504e-3	2.2306	23	65	0.68%
abnormal urine potassium level	51	2.5617e-5	4.6060e-3	3.8774	14	0.40%	418	3.4882e-4	3.2686	14	27	0.41%
abnormal circulating interferon-gamma level	53	3.2747e-5	5.6659e-3	2.9170	20	0.57%	1,070	3.0190e-2	1.8540	20	68	0.59%
abnormal interferon-alpha secretion	59	4.9182e-5	7.6441e-3	4.5096	11	0.31%	1,041	2.8721e-2	2.5215	10	25	0.29%

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Name	Rank	P-Value	FDR Q-Val	Enrichment	Region Hits	Coverage	Rank	FDR Q-Val	Enrichment	Gene Hits	Genes	Coverage
joint inflammation	61	4.9378e-5	7.4229e-3	2.1152	35	1.00%	930	1.8634e-2	1.6846	31	116	0.91%
increased brown adipose tissue amount	65	5.2890e-5	7.4615e-3	3.4312	15	0.43%	824	1.1209e-2	2.3852	14	37	0.41%
increased male germ cell apoptosis	77	7.9617e-5	9.4817e-3	8.7628	6	0.17%	790	1.0008e-2	4.2025	6	9	0.18%
arthritis	87	1.3970e-4	1.4725e-2	2.0765	32	0.91%	1,180	3.7583e-2	1.6343	28	108	0.82%
abnormal cone electrophysiology	90	1.4785e-4	1.5064e-2	2.1594	29	0.83%	367	1.3060e-4	2.3534	28	75	0.82%

The test set of 3,512 genomic regions picked 3,394 (16%) 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)**   **Global controls**

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 Gene Hits	Hyper Total Genes	Hyper Gene Set Coverage
decreased inflammatory response	2	1.6821e-8	8.0533e-5	2.0304	76	2.16%	594	6.9766e-4	1.5652	73	294	2.15%
abnormal circulating interferon level	8	1.1286e-7	1.3508e-4	2.8646	34	0.97%	826	3.5339e-3	1.8611	31	105	0.91%
abnormal urine potassium level	9	9.1612e-7	9.7465e-4	3.5992	21	0.60%	261	1.8749e-6	3.3943	21	39	0.62%
abnormal interferon level	11	1.4457e-6	1.2584e-3	2.4737	36	1.03%	1,220	1.7833e-2	1.6380	33	127	0.97%
decreased interferon-alpha secretion	12	2.3804e-6	1.8994e-3	5.6720	12	0.34%	1,138	1.4496e-2	2.5682	11	27	0.32%
abnormal male germ cell apoptosis	17	1.2036e-5	6.7790e-3	2.0719	43	1.22%	698	1.5242e-3	1.7651	42	150	1.24%
abnormal circulating interferon-gamma level	21	1.6442e-5	7.4969e-3	2.8016	23	0.65%	1,448	2.7924e-2	1.7468	23	83	0.68%
increased circulating interferon-gamma level	24	1.8078e-5	7.2122e-3	3.5848	16	0.46%	1,356	2.4371e-2	2.0172	16	50	0.47%
abnormal interferon-alpha secretion	28	2.5131e-5	8.5939e-3	4.4632	12	0.34%	1,342	2.4027e-2	2.3911	11	29	0.32%
decreased prostaglandin level	37	5.0816e-5	1.3150e-2	4.9413	10	0.28%	715	1.6995e-3	3.5021	10	18	0.29%
abnormal prostaglandin level	40	6.7915e-5	1.6257e-2	3.1999	16	0.46%	479	1.4455e-4	3.1519	16	32	0.47%
increased male germ cell apoptosis	43	7.9617e-5	1.7729e-2	8.7628	6	0.17%	983	8.3985e-3	4.2025	6	9	0.18%
iris stroma hypoplasia	49	1.1043e-4	2.1579e-2	5.6797	8	0.23%	1,638	4.2315e-2	4.2025	4	6	0.12%
abnormal rib development	50	1.1177e-4	2.1404e-2	3.2027	15	0.43%	1,254	1.9018e-2	2.3639	12	32	0.35%
brachypodia	51	1.1834e-4	2.2217e-2	4.9450	9	0.26%	1,113	1.3648e-2	4.5027	5	7	0.15%

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impaired behavioral response to addictive substance	59	1.5847e-4	2.5719e-2	2.5203	21	0.60%	580	5.8892e-4	2.5215	20	50	0.59%
arrest of male meiosis	61	1.7174e-4	2.6958e-2	2.0023	34	0.97%	1,300	2.1924e-2	1.6126	33	129	0.97%
abnormal circadian temperature homeostasis	62	1.7675e-4	2.7296e-2	4.2326	10	0.28%	798	2.9694e-3	3.5459	9	16	0.27%
abnormal cone electrophysiology	65	1.8287e-4	2.6938e-2	2.0445	32	0.91%	444	8.4940e-5	2.2723	31	86	0.91%
abnormal vitamin A level	68	1.8851e-4	2.6544e-2	5.2454	8	0.23%	1,100	1.3389e-2	3.1519	8	16	0.24%

The test set of 3,512 genomic regions picked 3,394 (16%) 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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