

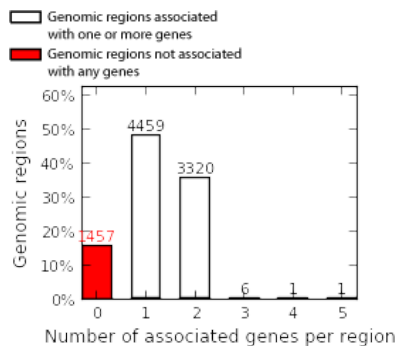
⊕ Job Description

⊕ Region-Gene Association Graphs

What do these graphs illustrate?

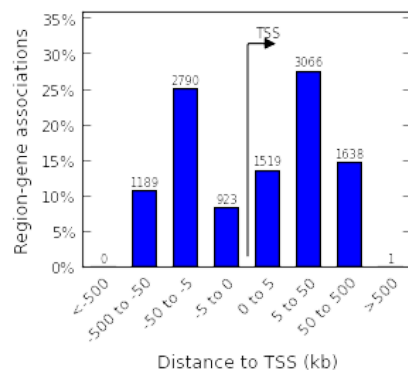
Number of associated genes per region

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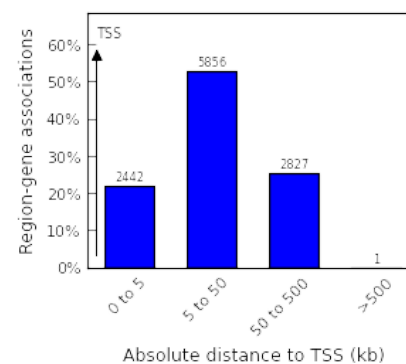
Binned by orientation and distance to TSS

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Binned by absolute distance to TSS

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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:

Shown top rows in this table:

Term annotation count: Min: Max:

Visualize this table:

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
anion transport	229	1.2952e-32	7.4037e-31	2.0061	352	3.81%	160	4.0300e-8	1.3834	233	470	3.04%
small molecule biosynthetic process	313	1.7909e-23	7.4898e-22	2.0334	241	2.61%	394	2.1154e-4	1.3193	165	349	2.15%
regulation of myeloid cell differentiation	354	5.7643e-21	2.1315e-19	2.2096	176	1.90%	262	1.2219e-5	1.4829	110	207	1.43%
carboxylic acid transport	365	3.6501e-20	1.3090e-18	2.1414	181	1.96%	320	5.9435e-5	1.4330	114	222	1.49%
organic acid transport	373	8.7233e-20	3.0613e-18	2.0884	188	2.03%	343	8.9741e-5	1.4132	118	233	1.54%
neuromuscular process	398	2.9900e-18	9.8339e-17	2.3672	131	1.42%	237	3.1939e-6	1.6743	72	120	0.94%
plasma membrane organization	416	1.1338e-17	3.5676e-16	2.0258	179	1.94%	332	8.3201e-5	1.4268	113	221	1.47%
developmental maturation	418	1.4534e-17	4.5513e-16	2.0294	177	1.91%	253	8.7497e-6	1.4700	118	224	1.54%
anion transmembrane transport	442	1.6416e-16	4.8615e-15	2.0515	161	1.74%	295	3.7937e-5	1.4548	110	211	1.43%
regulation of innate immune response	443	2.2220e-16	6.5657e-15	2.0290	164	1.77%	560	2.1729e-3	1.3316	115	241	1.50%
monocarboxylic acid transport	466	2.8150e-15	7.9073e-14	2.4322	102	1.10%	397	2.1997e-4	1.5946	60	105	0.78%

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
regulation of cysteine-type endopeptidase activity involved in apoptotic process	468	2.8891e-15	8.0810e-14	2.0218	153	1.66%	622	4.1771e-3	1.3411	99	206	1.29%
carboxylic acid biosynthetic process	474	3.3060e-15	9.1297e-14	2.0029	156	1.69%	674	5.8735e-3	1.3192	104	220	1.36%
regulation of mitochondrion organization	491	9.9366e-15	2.6491e-13	2.0809	137	1.48%	988	3.0452e-2	1.2733	94	206	1.23%
neurotransmitter transport	492	1.5164e-14	4.0344e-13	2.2243	116	1.25%	317	5.5781e-5	1.5850	71	125	0.93%
monocarboxylic acid biosynthetic process	512	4.0888e-14	1.0454e-12	2.2166	113	1.22%	701	6.7699e-3	1.3953	71	142	0.93%
regulation of purine nucleotide biosynthetic process	527	6.8593e-14	1.7038e-12	2.1645	117	1.27%	191	4.0532e-7	1.6958	79	130	1.03%
regulation of cyclic nucleotide biosynthetic process	528	6.9966e-14	1.7346e-12	2.1977	113	1.22%	211	7.1584e-7	1.7015	75	123	0.98%
regulation of cyclic nucleotide metabolic process	532	7.8414e-14	1.9294e-12	2.0922	126	1.36%	227	1.7020e-6	1.6278	84	144	1.10%
neuromuscular process controlling balance	546	2.0705e-13	4.9639e-12	2.5961	78	0.84%	361	1.4241e-4	1.7758	42	66	0.55%

The test set of 9,244 genomic regions picked 7,667 (36%) 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)

Global controls

Table controls: Shown top rows in this table: Term annotation count: Min: Max: Visualize this table:

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
microtubule	78	9.2038e-27	1.9989e-25	2.0243	280	3.03%	78	1.9137e-4	1.2956	182	392	2.37%
myelin sheath	87	3.9348e-21	7.6615e-20	2.3275	159	1.72%	111	5.1290e-3	1.3275	98	206	1.28%
late endosome	106	7.9624e-18	1.2725e-16	2.1610	155	1.68%	69	9.7930e-5	1.4213	109	214	1.42%
anchored component of membrane	130	1.4745e-13	1.9215e-12	2.1155	120	1.30%	89	7.7627e-4	1.4297	83	162	1.08%
synaptic vesicle	142	2.4720e-12	2.9490e-11	2.0585	115	1.24%	125	1.7660e-2	1.3402	73	152	0.95%
transport vesicle membrane	149	1.8462e-11	2.0989e-10	2.0253	110	1.19%	146	3.6723e-2	1.3178	68	144	0.89%
melanosome	153	3.5290e-11	3.9072e-10	2.2346	85	0.92%	109	3.8660e-3	1.4742	56	106	0.73%
extrinsic component of cytoplasmic side of plasma membrane	158	1.2353e-10	1.3245e-9	2.1029	92	1.00%	110	4.8049e-3	1.4593	57	109	0.74%
caveola	171	1.3267e-9	1.3143e-8	2.1201	80	0.87%	62	2.8465e-5	1.7356	51	82	0.67%
multivesicular body	173	1.6339e-9	1.5999e-8	3.1688	38	0.41%	101	1.3123e-3	1.9449	23	33	0.30%
ruffle membrane	177	2.3035e-9	2.2046e-8	2.1911	72	0.78%	118	1.0271e-2	1.4974	44	82	0.57%

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
presynaptic membrane	185	7.5145e-9	6.8809e-8	2.1266	72	0.78%	119	1.0985e-2	1.5328	39	71	0.51%
transcriptional repressor complex	186	1.1172e-8	1.0175e-7	2.0694	75	0.81%	114	5.8112e-3	1.5075	47	87	0.61%
cytoplasmic microtubule	187	1.2982e-8	1.1760e-7	2.5199	49	0.53%	150	4.6441e-2	1.4883	32	60	0.42%
intrinsic component of synaptic vesicle membrane	196	5.4874e-8	4.7427e-7	3.5866	26	0.28%	124	1.3260e-2	1.9932	15	21	0.20%
sperm flagellum	207	1.8675e-7	1.5283e-6	2.0078	67	0.72%	148	4.0983e-2	1.3812	49	99	0.64%
cortical actin cytoskeleton	213	6.9926e-7	5.5613e-6	2.1207	53	0.57%	147	3.9482e-2	1.4825	34	64	0.44%
integral component of synaptic vesicle membrane	230	4.4891e-6	3.3063e-5	3.6485	18	0.19%	128	1.8289e-2	2.1926	11	14	0.14%
nuclear transcriptional repressor complex	232	5.3078e-6	3.8756e-5	2.5213	31	0.34%	133	2.4346e-2	1.7441	20	32	0.26%
dendritic shaft	239	7.9700e-6	5.6491e-5	2.2601	37	0.40%	143	3.3915e-2	1.6592	22	37	0.29%

The test set of 9,244 genomic regions picked 7,667 (36%) 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 (20+ terms)

Global controls

Table controls: Shown top rows in this table: Term annotation count: Min: Max: Visualize this table:

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
core promoter proximal region sequence-specific DNA binding	52	4.9084e-37	3.8993e-35	2.1038	358	3.87%	31	1.4803e-9	1.4538	211	405	2.75%
core promoter proximal region DNA binding	53	4.3128e-36	3.3615e-34	2.0800	358	3.87%	35	3.1962e-9	1.4431	211	408	2.75%
RNA polymerase II core promoter proximal region sequence-specific DNA binding	54	2.1988e-35	1.6820e-33	2.0948	345	3.73%	32	1.7918e-9	1.4593	205	392	2.67%
transcription factor activity, RNA polymerase II core promoter proximal region sequence-specific binding	55	9.6292e-35	7.2324e-33	2.0165	371	4.01%	26	2.7054e-10	1.4611	222	424	2.90%
transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding	56	2.3556e-34	1.7377e-32	2.0136	368	3.98%	6	3.2009e-14	1.5555	233	418	3.04%
transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	66	3.6541e-28	2.2871e-26	2.1150	266	2.88%	28	5.8326e-10	1.5568	159	285	2.07%
symporter activity	104	1.2071e-15	4.7946e-14	2.2150	127	1.37%	75	3.0600e-4	1.4969	81	151	1.06%
enhancer binding	105	1.3214e-15	5.1987e-14	2.3911	108	1.17%	65	8.5003e-5	1.6195	65	112	0.85%

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
enhancer sequence-specific DNA binding	111	1.3775e-14	5.1265e-13	2.4176	98	1.06%	80	3.9578e-4	1.6025	58	101	0.76%
RNA polymerase II distal enhancer sequence-specific DNA binding	113	3.2125e-14	1.1744e-12	2.6962	78	0.84%	72	1.9033e-4	1.7172	48	78	0.63%
lyase activity	115	2.1315e-13	7.6568e-12	2.0544	127	1.37%	135	2.5300e-2	1.3311	83	174	1.08%
channel regulator activity	116	2.8420e-13	1.0121e-11	2.2204	105	1.14%	53	2.7978e-5	1.6203	72	124	0.94%
carboxylic acid transmembrane transporter activity	118	3.8298e-13	1.3408e-11	2.1904	107	1.16%	104	2.9760e-3	1.4734	66	125	0.86%
organic acid transmembrane transporter activity	119	1.2745e-12	4.4242e-11	2.0887	114	1.23%	112	6.4481e-3	1.4258	70	137	0.91%
solute:cation symporter activity	127	4.0499e-11	1.3173e-9	2.2529	83	0.90%	88	8.1264e-4	1.5714	58	103	0.76%
phosphatidylserine binding	129	6.9842e-11	2.2366e-9	2.7958	54	0.58%	77	3.0693e-4	1.9738	29	41	0.38%
monocarboxylic acid transmembrane transporter activity	130	8.2294e-11	2.6151e-9	2.9970	48	0.52%	157	4.1274e-2	1.6743	24	40	0.31%
SNARE binding	131	8.4224e-11	2.6560e-9	2.1499	89	0.96%	131	2.3909e-2	1.4202	57	112	0.74%
ion channel regulator activity	132	1.1073e-10	3.4653e-9	2.2691	78	0.84%	46	1.6575e-5	1.7728	54	85	0.70%
dioxygenase activity	138	7.1353e-10	2.1359e-8	2.2410	73	0.79%	137	2.5188e-2	1.4755	46	87	0.60%

The test set of 9,244 genomic regions picked 7,667 (36%) 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 (5 terms)

Global controls

Table controls: Shown top rows in this table: Term annotation count: Min: Max: Visualize this table:

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
Abnormal larynx morphology	232	1.8204e-8	5.1779e-7	2.3278	56	0.61%	24	3.5371e-2	1.6943	34	56	0.44%
Hypotelorism	276	1.7403e-7	4.1610e-6	2.3543	47	0.51%	8	8.7007e-3	1.9827	27	38	0.35%
Abnormality of the phalanges of the toes	301	4.3211e-7	9.4733e-6	2.4072	42	0.45%	25	4.2184e-2	1.8877	23	34	0.30%
Adrenal overactivity	397	7.5549e-6	1.2558e-4	2.8703	24	0.26%	17	3.4348e-2	2.1563	17	22	0.22%
Abnormality of the gingiva	404	8.5219e-6	1.3920e-4	2.0307	47	0.51%	31	4.7144e-2	1.6743	33	55	0.43%

The test set of 9,244 genomic regions picked 7,667 (36%) 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 (20+ terms)

Global controls

Table controls: Export Showed 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
abnormal digestive system physiology	107	2.2104e-34	1.8943e-32	2.0210	365	3.95%	93	8.9588e-11	1.4391	246	477	3.21%
abnormal immunoglobulin level	116	7.9157e-32	6.2575e-30	2.0333	332	3.59%	165	2.0060e-7	1.3733	219	445	2.86%
decreased inflammatory response	127	1.0075e-30	7.2743e-29	2.4935	207	2.24%	150	3.8586e-8	1.5412	132	239	1.72%
abnormal acute inflammation	132	3.8851e-29	2.6989e-27	2.3170	226	2.44%	243	1.2453e-5	1.4051	143	284	1.87%
abnormal blood vessel physiology	147	1.8589e-27	1.1596e-25	2.0497	279	3.02%	68	1.4713e-12	1.5776	186	329	2.43%
abnormal circulating triglyceride level	180	9.2423e-25	4.7085e-23	2.0468	251	2.72%	407	3.5120e-4	1.3117	157	334	2.05%
abnormal macrophage physiology	181	1.0048e-24	5.0905e-23	2.0134	261	2.82%	269	2.0663e-5	1.3520	172	355	2.24%
increased or absent threshold for auditory brainstem response	187	2.5743e-24	1.2624e-22	2.0341	250	2.70%	196	1.0159e-6	1.4322	155	302	2.02%
decreased immunoglobulin level	220	1.0762e-20	4.4858e-19	2.0598	204	2.21%	343	1.0641e-4	1.3699	135	275	1.76%
decreased triglyceride level	233	6.3001e-20	2.4795e-18	2.0723	193	2.09%	528	1.3380e-3	1.3247	122	257	1.59%
abnormal posture	241	1.6437e-19	6.2541e-18	2.0752	188	2.03%	149	3.7568e-8	1.5849	117	206	1.53%
abnormal mean corpuscular volume	251	7.4184e-19	2.7102e-17	2.1600	165	1.78%	1,155	3.9467e-2	1.2446	95	213	1.24%
decreased acute inflammation	253	8.0677e-19	2.9241e-17	2.3984	132	1.43%	306	5.1056e-5	1.5079	87	161	1.13%
decreased circulating triglyceride level	282	1.3822e-17	4.4947e-16	2.1530	154	1.67%	757	9.8754e-3	1.3059	95	203	1.24%
abnormal granulocyte physiology	306	2.5652e-16	7.6872e-15	2.0618	157	1.70%	897	1.7165e-2	1.2707	102	224	1.33%
abnormal fat cell morphology	328	1.4205e-15	3.9715e-14	2.0738	147	1.59%	504	1.0829e-3	1.4032	88	175	1.15%
improved glucose tolerance	332	2.4675e-15	6.8153e-14	2.0002	158	1.71%	446	5.4012e-4	1.3953	100	200	1.30%
abnormal hypersensitivity reaction	335	3.7505e-15	1.0266e-13	2.2631	117	1.27%	636	3.9223e-3	1.3863	77	155	1.00%
abnormal intestine physiology	349	1.6798e-14	4.4137e-13	2.0188	145	1.57%	632	3.9266e-3	1.3340	98	205	1.28%
abnormal IgG1 level	354	2.8096e-14	7.2780e-13	2.0160	143	1.55%	405	3.4490e-4	1.4256	94	184	1.23%

The test set of 9,244 genomic regions picked 7,667 (36%) 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 Showed 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
abnormal acute inflammation	144	1.1868e-33	7.8912e-32	2.3075	265	2.87%	317	5.9274e-6	1.3787	166	336	2.17%

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
abnormal blood vessel physiology	153	6.6757e-33	4.1778e-31	2.0089	354	3.83%	67	9.7026e-15	1.5518	233	419	3.04%
decreased inflammatory response	168	1.5602e-30	8.8920e-29	2.3285	235	2.54%	275	2.0710e-6	1.4237	150	294	1.96%
increased or absent threshold for auditory brainstem response	219	1.3326e-25	5.8262e-24	2.0342	264	2.86%	227	3.1030e-7	1.4346	164	319	2.14%
decreased immunoglobulin level	240	3.0786e-24	1.2282e-22	2.0247	252	2.73%	356	2.2054e-5	1.3545	166	342	2.17%
abnormal posture	257	1.4785e-22	5.5082e-21	2.0023	240	2.60%	196	9.3041e-8	1.4856	148	278	1.93%
abnormal granulocyte physiology	288	2.1786e-20	7.2432e-19	2.1127	189	2.04%	875	5.9085e-3	1.2751	122	267	1.59%
decreased acute inflammation	298	3.1341e-20	1.0070e-18	2.3031	155	1.68%	534	3.9624e-4	1.4023	99	197	1.29%
abnormal mean corpuscular volume	307	2.5567e-19	7.9740e-18	2.0798	185	2.00%	1,162	1.6868e-2	1.2529	110	245	1.43%
increased acute inflammation	349	2.0853e-17	5.7211e-16	2.3706	124	1.34%	1,001	9.9203e-3	1.3491	73	151	0.95%
decreased circulating triglyceride level	351	2.3441e-17	6.3944e-16	2.0375	173	1.87%	996	9.8828e-3	1.2737	110	241	1.43%
decreased susceptibility to weight gain	365	7.5067e-17	1.9692e-15	2.2292	136	1.47%	293	3.0090e-6	1.5893	86	151	1.12%
decreased circulating HDL cholesterol level	384	4.1991e-16	1.0470e-14	2.2161	131	1.42%	647	1.2563e-3	1.4226	78	153	1.02%
abnormal hypersensitivity reaction	391	4.9521e-16	1.2127e-14	2.2189	130	1.41%	844	5.0132e-3	1.3477	85	176	1.11%
increased susceptibility to injury	418	4.7656e-15	1.0916e-13	2.1357	132	1.43%	355	2.1759e-5	1.5441	83	150	1.08%
increased energy expenditure	429	1.5809e-14	3.5284e-13	2.0676	137	1.48%	308	4.7149e-6	1.5599	90	161	1.17%
paralysis	431	1.7537e-14	3.8960e-13	2.1105	130	1.41%	927	7.7386e-3	1.3585	74	152	0.97%
decreased susceptibility to diet-induced obesity	456	5.8854e-14	1.2358e-12	2.2038	113	1.22%	447	1.0074e-4	1.5503	70	126	0.91%
abnormal interleukin-6 secretion	464	1.1591e-13	2.3919e-12	2.0470	131	1.42%	799	3.6968e-3	1.3498	89	184	1.16%
cardiomyopathy	479	1.8721e-13	3.7422e-12	2.0203	133	1.44%	298	3.3072e-6	1.5697	90	160	1.17%

The test set of 9,244 genomic regions picked 7,667 (36%) 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].