Job Description

Region-Gene Association Graphs

What do these graphs illustrate?

Number of associated genes per region

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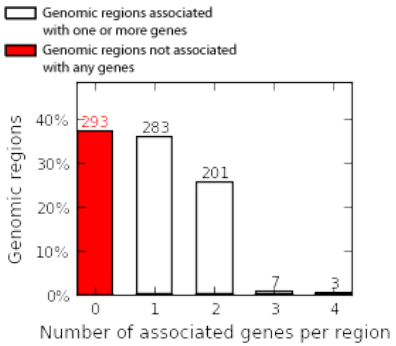

Binned by orientation and distance to TSS

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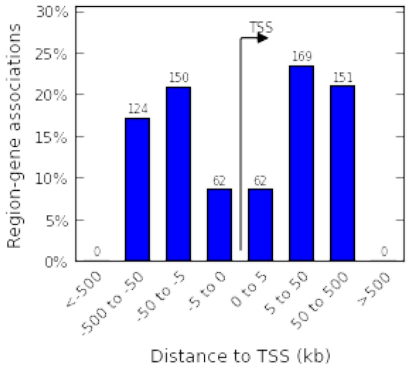

Binned by absolute distance to TSS

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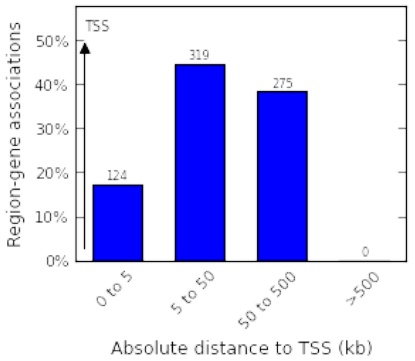

Global Controls

Global Export

Which data is exported by each option?

Ensembl Genes (no terms)

Global controls

GO Biological Process (20+ terms)

Global controls

Table controls: 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
regulation of protein binding	11	**3.3774e-49**	**4.0191e-46**	10.7800	72	9.15%	164	**9.1956e-4**	3.4144	17	198	3.16%
pattern specification process	12	**4.6653e-48**	**5.0891e-45**	6.3134	101	12.83%	19	**1.7294e-9**	3.6152	40	440	7.43%
regulation of binding	23	**4.6367e-40**	**2.6389e-37**	6.7453	80	10.17%	187	**1.9099e-3**	2.6283	23	348	4.28%
brain development	33	**2.1480e-27**	**8.5206e-25**	3.5578	100	12.71%	150	**4.0043e-4**	2.1613	40	736	7.43%
central nervous system development	35	**7.4253e-27**	**2.7771e-24**	3.2194	111	14.10%	118	**7.4670e-5**	2.1181	49	920	9.11%
head development	36	**1.1628e-26**	**4.2282e-24**	3.4224	102	12.96%	142	**3.1632e-4**	2.1386	42	781	7.81%
locomotion	39	**2.6540e-24**	**8.9080e-22**	2.9700	112	14.23%	296	**2.3415e-2**	1.6740	45	1,069	8.36%
nervous system development	48	**4.6297e-21**	**1.2626e-18**	2.1614	164	20.84%	76	**2.6415e-6**	1.7711	97	2,178	18.03%
regulation of anatomical structure morphogenesis	49	**7.7588e-21**	**2.0727e-18**	2.9249	98	12.45%	141	**2.8664e-4**	2.0427	47	915	8.74%
cell projection organization	52	**2.5787e-20**	**6.4914e-18**	2.8343	100	12.71%	279	**1.5997e-2**	1.7343	43	986	7.99%

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
DNA replication-dependent nucleosome assembly	53	**4.0209e-20**	**9.9308e-18**	54.8546	14	1.78%	72	**9.3054e-7**	12.0508	10	33	1.86%
regulation of developmental process	56	**1.3150e-19**	**3.0738e-17**	2.0635	168	21.35%	22	**1.8492e-9**	1.9191	115	2,383	21.38%
protein heterotetramerization	58	**9.7633e-19**	**2.2035e-16**	22.6602	18	2.29%	21	**1.7387e-9**	12.3722	14	45	2.60%
chromatin silencing at rDNA	76	**5.1014e-14**	**8.7864e-12**	19.5040	14	1.78%	107	**4.7332e-5**	7.9535	10	50	1.86%
innate immune response in mucosa	82	**1.5673e-13**	**2.5020e-11**	40.9740	10	1.27%	115	**5.9591e-5**	13.2559	7	21	1.30%
protein heterooligomerization	94	**1.3399e-11**	**1.8660e-9**	6.8756	21	2.67%	74	**1.5359e-6**	5.6338	17	120	3.16%
negative regulation of transcription, DNA-templated	98	**2.4885e-11**	**3.3239e-9**	2.1766	86	10.93%	42	**5.4079e-8**	2.2468	70	1,239	13.01%
nucleosome assembly	100	**4.4017e-11**	**5.7619e-9**	8.5597	17	2.16%	23	**2.6306e-9**	7.1653	20	111	3.72%
protein tetramerization	101	**5.7845e-11**	**7.4969e-9**	5.9953	22	2.80%	97	**1.6537e-5**	4.7276	17	143	3.16%
negative regulation of nucleic acid-templated transcription	102	**6.0915e-11**	**7.8174e-9**	2.1375	86	10.93%	47	**1.5556e-7**	2.1868	70	1,273	13.01%

The test set of 787 genomic regions picked 538 (3%) 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 (9 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
nuclear nucleosome	23	**2.6968e-15**	**1.9863e-13**	24.2849	14	1.78%	12	**7.3036e-6**	9.6994	10	41	1.86%
nucleosome	25	**1.9105e-12**	**1.2946e-10**	10.5013	17	2.16%	1	**9.6018e-19**	10.1104	30	118	5.58%
DNA packaging complex	28	**1.3103e-11**	**7.9273e-10**	9.2680	17	2.16%	2	**3.7732e-18**	9.4685	30	126	5.58%
nuclear chromatin	48	**2.4684e-7**	**8.7114e-6**	3.1089	28	3.56%	27	**3.6489e-3**	2.5657	22	341	4.09%
chromatin	49	**4.0390e-7**	**1.3963e-5**	2.6327	35	4.45%	4	**6.0265e-11**	3.5179	46	520	8.55%
protein-DNA complex	51	**7.4228e-7**	**2.4655e-5**	4.1302	18	2.29%	3	**1.2662e-12**	5.8426	31	211	5.76%
extracellular matrix	56	**1.1946e-5**	**3.6136e-4**	2.1654	38	4.83%	25	**2.6720e-3**	2.2341	30	534	5.58%
basement membrane	72	**1.6216e-3**	**3.8153e-2**	2.9492	11	1.40%	33	**3.0857e-2**	3.8075	9	94	1.67%
cell-cell adherens junction	73	**1.8493e-3**	**4.2914e-2**	2.8992	11	1.40%	31	**9.8123e-3**	4.0579	10	98	1.86%

The test set of 787 genomic regions picked 538 (3%) 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 (7 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
frizzled binding	22	**4.7801e-9**	**8.9757e-7**	8.9784	13	1.65%	22	**7.3648e-3**	7.3256	7	38	1.30%
G-protein coupled receptor binding	24	**1.0489e-8**	**1.8055e-6**	3.6336	28	3.56%	26	**3.5468e-2**	2.6934	17	251	3.16%
chromatin DNA binding	25	**1.2979e-8**	**2.1447e-6**	5.8248	17	2.16%	23	**1.5759e-2**	4.0504	11	108	2.04%
chromatin binding	26	**1.5735e-8**	**2.5001e-6**	2.5503	46	5.84%	10	**1.4270e-5**	2.6985	38	560	7.06%
sequence-specific DNA binding	27	**3.0690e-8**	**4.6956e-6**	2.0067	72	9.15%	9	**3.4330e-7**	2.3086	62	1,068	11.52%
transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding	30	**2.9998e-7**	**4.1307e-5**	2.5066	39	4.96%	13	**9.5919e-5**	2.8541	30	418	5.58%
protein heterodimerization activity	54	**3.0945e-5**	**2.3673e-3**	2.1202	36	4.57%	4	**1.5900e-9**	3.2901	46	556	8.55%

The test set of 787 genomic regions picked 538 (3%) 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 (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
Recurrent upper respiratory tract infections	11	**5.9186e-65**	**3.5506e-62**	30.9501	58	7.37%	255	**4.8293e-2**	3.9768	7	70	1.30%
Abnormality of the nasopharynx	16	**1.8390e-59**	**7.5847e-57**	22.7873	60	7.62%	120	**9.8230e-3**	4.4739	9	80	1.67%
Abnormality of the pharynx	18	**2.8977e-57**	**1.0623e-54**	20.8675	60	7.62%	162	**1.7760e-2**	3.9768	9	90	1.67%
Conductive hearing impairment	19	**1.2727e-56**	**4.4204e-54**	20.3359	60	7.62%	195	**2.5720e-2**	4.0787	8	78	1.49%
Functional abnormality of the middle ear	20	**1.0032e-55**	**3.3099e-53**	19.6158	60	7.62%	205	**3.1434e-2**	3.9277	8	81	1.49%
Abnormality of the middle ear	21	**4.2467e-48**	**1.3345e-45**	13.1214	63	8.01%	226	**4.5449e-2**	2.8970	11	151	2.04%
Abnormality of the upper respiratory tract	23	**4.8568e-47**	**1.3935e-44**	11.5820	66	8.39%	116	**8.6702e-3**	3.1633	14	176	2.60%
Abnormality of the nose	27	**1.1965e-34**	**2.9244e-32**	4.4136	100	12.71%	19	**3.9342e-4**	2.2888	40	695	7.43%
Hearing impairment	30	**4.0454e-33**	**8.8986e-31**	4.9860	85	10.80%	140	**1.3498e-2**	2.0544	28	542	5.20%
Hearing abnormality	31	**6.1047e-33**	**1.2995e-30**	4.9566	85	10.80%	149	**1.4271e-2**	2.0394	28	546	5.20%
Abnormality of the ear	33	**5.3954e-31**	**1.0789e-28**	3.6724	109	13.85%	48	**1.4405e-3**	1.9670	46	930	8.55%
Abnormality of the face	35	**3.2887e-29**	**6.2006e-27**	3.0068	132	16.77%	2	**3.3248e-4**	1.9469	68	1,389	12.64%

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
Abnormality of the head	39	**1.1600e-26**	**1.9627e-24**	2.7511	137	17.41%	8	**2.4106e-4**	1.8312	74	1,607	13.75%
Abnormality of head or neck	40	**3.2823e-26**	**5.4151e-24**	2.7206	137	17.41%	11	**3.0947e-4**	1.8043	74	1,631	13.75%
Abnormality of the periorbital region	42	**2.6820e-9**	**4.2140e-7**	3.5644	31	3.94%	1	**4.8351e-4**	3.7181	23	246	4.28%
Abnormality of skin adnexa morphology	43	**7.9423e-9**	**1.2189e-6**	2.5174	49	6.23%	6	**2.3365e-4**	2.5144	38	601	7.06%
Abnormality of the urethra	44	**9.9646e-9**	**1.4945e-6**	4.5086	22	2.80%	30	**7.1423e-4**	4.4540	14	125	2.60%
Abnormality of the eyebrow	45	**2.3899e-8**	**3.5046e-6**	3.7052	26	3.30%	15	**3.1887e-4**	3.7969	19	199	3.53%
Abnormality of the hand	46	**3.2637e-8**	**4.6820e-6**	2.4032	49	6.23%	3	**2.6289e-4**	2.5342	39	612	7.25%
Cleft lip	47	**4.4126e-8**	**6.1954e-6**	4.7559	19	2.41%	42	**1.1262e-3**	4.8203	12	99	2.23%

The test set of 787 genomic regions picked 538 (3%) 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 | 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
abnormal trachea morphology	13	**3.7820e-58**	**2.6678e-55**	20.8210	61	7.75%	111	**4.6035e-3**	5.1871	9	69	1.67%
abnormal digestive system morphology	19	**1.9968e-32**	**9.6373e-30**	3.7591	111	14.10%	21	**2.4122e-5**	2.3279	48	820	8.92%
digestive/alimentary phenotype	22	**3.4243e-31**	**1.4273e-28**	3.3585	122	15.50%	20	**2.3333e-5**	2.1445	57	1,057	10.59%
postnatal lethality, incomplete penetrance	24	**6.1193e-29**	**2.3381e-26**	4.1024	90	11.44%	69	**6.3329e-4**	2.3352	34	579	6.32%
abnormal brain development	26	**1.7542e-27**	**6.1868e-25**	3.9904	88	11.18%	158	**1.4155e-2**	2.0153	30	592	5.58%
lethality during fetal growth through weaning	28	**4.3656e-27**	**1.4297e-24**	2.5019	161	20.46%	7	**2.4442e-9**	2.1240	94	1,760	17.47%
abnormal respiratory system morphology	29	**2.4420e-26**	**7.7217e-24**	3.6251	94	11.94%	80	**1.0637e-3**	2.1217	39	731	7.25%
abnormal nervous system development	30	**6.9579e-25**	**2.1268e-22**	3.0816	109	13.85%	67	**6.1322e-4**	1.9967	48	956	8.92%
postnatal lethality	31	**1.7867e-23**	**5.2851e-21**	2.9933	107	13.60%	55	**3.5407e-4**	2.0340	49	958	9.11%
respiratory system phenotype	34	**1.9534e-22**	**5.2686e-20**	2.8097	112	14.23%	61	**4.3644e-4**	1.9186	55	1,140	10.22%
abnormal craniofacial morphology	45	**4.8215e-12**	**9.8251e-10**	2.3042	82	10.42%	1	**8.5832e-11**	2.8257	68	957	12.64%
craniofacial phenotype	46	**5.4121e-12**	**1.0789e-9**	2.2988	82	10.42%	2	**5.2573e-11**	2.8139	68	961	12.64%
abnormal palate morphology	47	**5.8652e-12**	**1.1443e-9**	3.8249	38	4.83%	8	**1.3741e-8**	4.6983	28	237	5.20%
abnormal head morphology	48	**1.0399e-11**	**1.9866e-9**	2.4677	70	8.89%	3	**9.4308e-11**	3.0713	58	751	10.78%
abnormal facial morphology	52	**3.3636e-10**	**5.9315e-8**	2.5148	58	7.37%	9	**2.0495e-8**	3.0539	46	599	8.55%
abnormal cranium morphology	54	**8.8416e-10**	**1.5014e-7**	2.4722	57	7.24%	12	**3.0486e-8**	3.0383	45	589	8.36%

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 craniofacial bone morphology	56	**1.8483e-9**	**3.0266e-7**	2.4212	57	7.24%	11	**1.9860e-8**	3.0387	46	602	8.55%
abnormal axial skeleton morphology	57	**2.8223e-9**	**4.5405e-7**	2.0114	82	10.42%	10	**2.0437e-8**	2.3716	69	1,157	12.83%
abnormal mouth morphology	58	**3.8257e-9**	**6.0485e-7**	2.6751	46	5.84%	13	**3.1437e-7**	3.2911	36	435	6.69%
abnormal esophageal smooth muscle morphology	59	**2.8613e-8**	**4.4471e-6**	35.2635	6	0.76%	41	**8.8457e-5**	39.7677	4	4	0.74%

The test set of 787 genomic regions picked 538 (3%) 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
abnormal trachea morphology	14	**9.6276e-51**	**6.5846e-48**	15.5092	61	7.75%	242	**1.5873e-2**	4.0214	9	89	1.67%
abnormal digestive system morphology	18	**4.8410e-33**	**2.5751e-30**	3.3387	130	16.52%	17	**2.3039e-7**	2.3054	64	1,104	11.90%
digestive/alimentary phenotype	20	**3.8211e-31**	**1.8294e-28**	2.9982	141	17.92%	18	**8.2531e-7**	2.0930	73	1,387	13.57%
lethality during fetal growth through weaning	22	**2.1712e-29**	**9.4496e-27**	2.3459	193	24.52%	5	**2.6591e-13**	2.1310	124	2,314	23.05%
abnormal brain development	25	**1.6297e-28**	**6.2418e-26**	3.5322	105	13.34%	77	**1.6180e-4**	2.1736	44	805	8.18%
abnormal respiratory system morphology	29	**4.7671e-25**	**1.5740e-22**	3.1848	105	13.34%	65	**8.6502e-5**	2.1086	50	943	9.29%
postnatal lethality, incomplete penetrance	30	**1.2501e-24**	**3.9898e-22**	3.3154	98	12.45%	123	**1.2382e-3**	2.0280	41	804	7.62%
abnormal nervous system development	31	**1.1887e-23**	**3.6716e-21**	2.7189	124	15.76%	53	**4.3969e-5**	1.9741	62	1,249	11.52%
respiratory system phenotype	32	**1.3662e-23**	**4.0880e-21**	2.6326	130	16.52%	43	**1.4269e-5**	1.9467	70	1,430	13.01%
postnatal lethality	35	**4.0381e-22**	**1.1047e-19**	2.5671	127	16.14%	58	**5.3420e-5**	1.9088	66	1,375	12.27%
abnormal respiratory system physiology	36	**7.6612e-20**	**2.0377e-17**	2.8871	95	12.07%	319	**3.0685e-2**	1.6913	39	917	7.25%
abnormal brain morphology	40	**2.6930e-16**	**6.4464e-14**	2.1337	131	16.65%	199	**6.3061e-3**	1.5722	68	1,720	12.64%
abnormal head morphology	43	**8.1410e-15**	**1.8128e-12**	2.5195	87	11.05%	2	**2.7389e-13**	3.0328	71	931	13.20%
abnormal facial morphology	45	**3.8650e-13**	**8.2238e-11**	2.5691	74	9.40%	9	**5.7930e-11**	3.0309	58	761	10.78%
abnormal craniofacial morphology	46	**1.1567e-12**	**2.4076e-10**	2.2098	94	11.94%	6	**7.0677e-12**	2.6466	77	1,157	14.31%
craniofacial phenotype	47	**1.2888e-12**	**2.6256e-10**	2.2054	94	11.94%	7	**7.2856e-12**	2.6375	77	1,161	14.31%
abnormal palate morphology	48	**1.5346e-12**	**3.0612e-10**	3.4207	46	5.84%	11	**1.3958e-8**	3.9889	33	329	6.13%
abnormal mouth morphology	53	**6.6388e-10**	**1.1994e-7**	2.5430	55	6.99%	16	**1.6467e-7**	2.9986	42	557	7.81%
abnormal autopod morphology	56	**3.3224e-9**	**5.6807e-7**	2.8444	42	5.34%	32	**6.8015e-6**	3.1369	31	393	5.76%

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 cranium morphology	58	**5.0886e-9**	**8.4006e-7**	2.2537	62	7.88%	12	**1.8607e-8**	2.8366	51	715	9.48%

The test set of 787 genomic regions picked 538 (3%) 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].