Job Description

Job ID: 20201106-public-4.0.4-pOiBTG

Display name: cluster_1_galaxy.bed

Test set: cluster_1_galaxy.bed (10,363 genomic regions)
Show in UCSC genome browser. *How do I look at my regions in the genome?*

Background: Whole genome background

Assembly: Mouse: NCBI build 38 (UCSC mm10, Dec. 2011) *What gene set does GREAT use?*

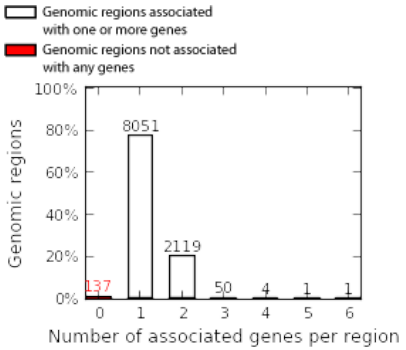
Associated genomic regions: Basal+extension (constitutive 5.0 kb upstream and 1.0 kb downstream, up to 100.0 kb max extension). Curated regulatory domains are included.
137 of all 10,363 genomic regions (1.3%) are not associated with any genes.
View all genomic region-gene associations. *Which genes are my regions associated with?*
Revise the region-gene association rule. *How are my regions associated with genes?*

Region-Gene Association Graphs

What do these graphs illustrate?

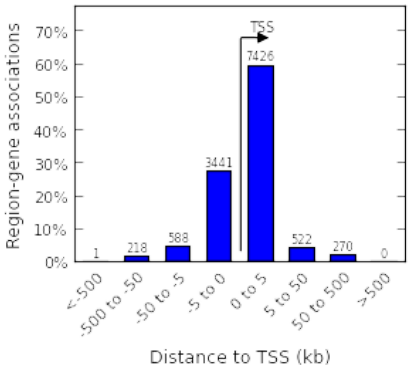
Number of associated genes per region

Download as PDF.



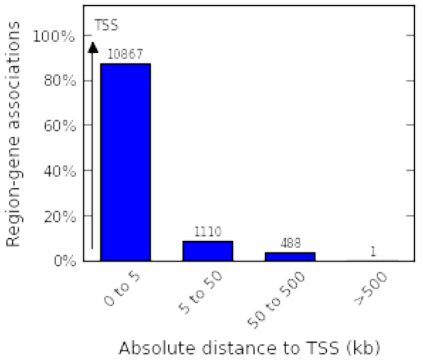
Binned by orientation and distance to TSS

Download as PDF.



Binned by absolute distance to TSS

Download as PDF.



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
cellular metabolic process	1	**0.0000**	**0.0000**	2.1754	5,642	54.44%	1	**0.0000**	1.3744	5,299	7,645	49.11%
cellular macromolecule metabolic process	1	**0.0000**	**0.0000**	2.2797	4,758	45.91%	1	**0.0000**	1.4471	4,341	5,948	40.23%
primary metabolic process	1	**0.0000**	**0.0000**	2.1537	5,656	54.58%	3	**4.1172e-315**	1.3374	5,288	7,840	49.01%
organic substance metabolic process	1	**0.0000**	**0.0000**	2.1356	5,863	56.58%	4	**7.1684e-314**	1.3241	5,495	8,229	50.93%

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
metabolic process	1	**0.0000**	**0.0000**	2.1144	6,062	58.50%	5	**2.9869e-311**	1.3088	5,732	8,684	53.12%
macromolecule metabolic process	1	**0.0000**	**0.0000**	2.2024	5,026	48.50%	6	**5.5768e-311**	1.3802	4,601	6,610	42.64%
cellular nitrogen compound metabolic process	1	**0.0000**	**0.0000**	2.3494	3,605	34.79%	7	**1.2216e-260**	1.4552	3,224	4,393	29.88%
nitrogen compound metabolic process	1	**0.0000**	**0.0000**	2.2888	3,792	36.59%	8	**1.6901e-252**	1.4286	3,405	4,726	31.56%
nucleobase-containing compound metabolic process	1	**0.0000**	**0.0000**	2.3600	3,203	30.91%	9	**5.2295e-240**	1.4771	2,827	3,795	26.20%
heterocycle metabolic process	1	**0.0000**	**0.0000**	2.3443	3,277	31.62%	10	**1.5912e-235**	1.4635	2,897	3,925	26.85%
nucleic acid metabolic process	1	**0.0000**	**0.0000**	2.4180	2,898	27.96%	11	**6.6600e-231**	1.5060	2,517	3,314	23.33%
cellular aromatic compound metabolic process	1	**0.0000**	**0.0000**	2.3173	3,293	31.78%	12	**1.2004e-228**	1.4537	2,912	3,972	26.99%
organic cyclic compound metabolic process	1	**0.0000**	**0.0000**	2.2870	3,389	32.70%	13	**2.9937e-220**	1.4337	3,005	4,156	27.85%
cellular component organization or biogenesis	1	**0.0000**	**0.0000**	2.0322	3,781	36.49%	14	**2.9067e-195**	1.3650	3,440	4,997	31.88%
gene expression	1	**0.0000**	**0.0000**	2.3642	2,742	26.46%	15	**2.5992e-192**	1.4760	2,353	3,161	21.81%
cellular protein metabolic process	1	**0.0000**	**0.0000**	2.2199	2,577	24.87%	16	**3.7990e-183**	1.4649	2,336	3,162	21.65%
cellular biosynthetic process	1	**0.0000**	**0.0000**	2.1863	2,993	28.88%	17	**1.9868e-173**	1.4149	2,628	3,683	24.36%
RNA metabolic process	1	**0.0000**	**0.0000**	2.3580	2,498	24.10%	18	**1.2928e-171**	1.4766	2,129	2,859	19.73%
organic substance biosynthetic process	1	**0.0000**	**0.0000**	2.1791	3,035	29.29%	19	**1.8193e-170**	1.4070	2,661	3,750	24.66%
biosynthetic process	1	**0.0000**	**0.0000**	2.1688	3,078	29.70%	20	**3.1964e-169**	1.4004	2,707	3,833	25.09%

The test set of 10,363 genomic regions picked 10,790 (50%) 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: 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
intracellular	1	**0.0000**	**0.0000**	2.1073	8,920	86.08%	1	**0.0000**	1.2738	8,917	13,881	82.64%
nucleus	1	**0.0000**	**0.0000**	2.2418	5,293	51.08%	1	**0.0000**	1.4167	4,857	6,798	45.01%
cytoplasm	1	**0.0000**	**0.0000**	2.0990	7,091	68.43%	1	**0.0000**	1.3167	6,928	10,433	64.21%
organelle	1	**0.0000**	**0.0000**	2.1049	8,418	81.23%	1	**0.0000**	1.2831	8,323	12,862	77.14%
membrane-bounded organelle	1	**0.0000**	**0.0000**	2.1348	7,982	77.02%	1	**0.0000**	1.3091	7,793	11,804	72.22%
intracellular organelle	1	**0.0000**	**0.0000**	2.1677	8,052	77.70%	1	**0.0000**	1.3272	7,899	11,801	73.21%
intracellular membrane-bounded organelle	1	**0.0000**	**0.0000**	2.2281	7,308	70.52%	1	**0.0000**	1.3825	7,069	10,139	65.51%

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
organelle lumen	1	**0.0000**	**0.0000**	2.4688	3,544	34.20%	1	**0.0000**	1.5641	3,205	4,063	29.70%
organelle part	1	**0.0000**	**0.0000**	2.2681	6,055	58.43%	1	**0.0000**	1.4123	5,790	8,129	53.66%
intracellular part	1	**0.0000**	**0.0000**	2.1227	8,758	84.51%	1	**0.0000**	1.2885	8,738	13,447	80.98%
nuclear part	1	**0.0000**	**0.0000**	2.4301	3,502	33.79%	1	**0.0000**	1.5512	3,141	4,015	29.11%
cytoplasmic part	1	**0.0000**	**0.0000**	2.1439	5,750	55.49%	1	**0.0000**	1.3627	5,511	8,019	51.08%
intracellular organelle part	1	**0.0000**	**0.0000**	2.3042	5,979	57.70%	1	**0.0000**	1.4314	5,703	7,900	52.85%
intracellular organelle lumen	1	**0.0000**	**0.0000**	2.4720	3,543	34.19%	1	**0.0000**	1.5648	3,204	4,060	29.69%
nuclear lumen	1	**0.0000**	**0.0000**	2.4464	3,166	30.55%	15	**5.6226e-318**	1.5634	2,818	3,574	26.12%
nucleoplasm	1	**0.0000**	**0.0000**	2.5392	2,492	24.05%	16	**5.3197e-280**	1.6201	2,193	2,684	20.32%
macromolecular complex	1	**0.0000**	**0.0000**	2.2565	3,964	38.25%	17	**4.8913e-276**	1.4257	3,667	5,100	33.99%
cytosol	1	**0.0000**	**0.0000**	2.2801	2,807	27.09%	18	**1.6815e-214**	1.4842	2,509	3,352	23.25%
protein complex	1	**0.0000**	**0.0000**	2.3392	2,665	25.72%	19	**1.7751e-193**	1.4738	2,371	3,190	21.97%
intracellular non-membrane-bounded organelle	1	**0.0000**	**0.0000**	2.2206	3,222	31.09%	20	**1.0608e-179**	1.3930	2,905	4,135	26.92%

The test set of 10,363 genomic regions picked 10,790 (50%) 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: 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
heterocyclic compound binding	1	**0.0000**	**0.0000**	2.1803	4,445	42.89%	1	**1.1660e-203**	1.3331	3,993	5,939	37.01%
organic cyclic compound binding	1	**0.0000**	**0.0000**	2.1609	4,474	43.17%	2	**1.4474e-192**	1.3205	4,017	6,032	37.23%
nucleic acid binding	1	**0.0000**	**0.0000**	2.3833	3,267	31.53%	3	**1.1318e-187**	1.4118	2,836	3,983	26.28%
RNA binding	8	**2.8284e-298**	**1.4605e-295**	2.8352	1,584	15.29%	4	**9.8560e-177**	1.6399	1,382	1,671	12.81%
transferase activity	11	**4.2811e-186**	**1.6078e-183**	2.0565	1,812	17.49%	8	**2.3413e-94**	1.3992	1,647	2,334	15.26%
DNA binding	12	**3.8927e-177**	**1.3401e-174**	2.0867	1,680	16.21%	25	**6.8530e-44**	1.2896	1,371	2,108	12.71%
enzyme binding	13	**7.0419e-166**	**2.2377e-163**	2.1008	1,560	15.05%	9	**2.7784e-84**	1.4196	1,376	1,922	12.75%
hydrolase activity, acting on acid anhydrides	33	**1.4043e-63**	**1.7579e-61**	2.0538	656	6.33%	41	**1.9260e-26**	1.3631	585	851	5.42%
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	34	**1.6013e-63**	**1.9456e-61**	2.0543	655	6.32%	40	**1.6960e-26**	1.3639	584	849	5.41%
pyrophosphatase activity	35	**2.9674e-63**	**3.5024e-61**	2.0534	653	6.30%	42	**3.1041e-26**	1.3625	582	847	5.39%

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
transcription factor binding	36	**5.7220e-63**	**6.5660e-61**	2.2333	539	5.20%	30	**5.0014e-34**	1.5057	426	561	3.95%
kinase binding	37	**1.8289e-60**	**2.0419e-58**	2.1551	559	5.39%	35	**8.3316e-31**	1.4502	471	644	4.37%
chromatin binding	38	**2.7096e-59**	**2.9456e-57**	2.2020	523	5.05%	36	**1.6717e-30**	1.4801	418	560	3.87%
nucleoside-triphosphatase activity	39	**8.5414e-59**	**9.0473e-57**	2.0438	614	5.92%	49	**2.2088e-23**	1.3515	548	804	5.08%
protein kinase binding	43	**6.5958e-52**	**6.3365e-50**	2.1325	491	4.74%	39	**5.7872e-27**	1.4481	417	571	3.86%
ubiquitin-like protein transferase activity	44	**5.3931e-51**	**5.0634e-49**	2.2971	411	3.97%	31	**2.1725e-33**	1.5518	360	460	3.34%
ubiquitin-protein transferase activity	46	**1.1365e-49**	**1.0206e-47**	2.3060	397	3.83%	32	**4.9046e-33**	1.5602	347	441	3.22%
transcription factor activity, protein binding	47	**4.7643e-49**	**4.1875e-47**	2.1159	472	4.55%	48	**1.0574e-23**	1.4397	379	522	3.51%
transcription factor activity, transcription factor binding	48	**3.1485e-47**	**2.7097e-45**	2.1024	461	4.45%	53	**1.9132e-22**	1.4312	371	514	3.44%
transcription cofactor activity	52	**3.8286e-43**	**3.0415e-41**	2.1441	402	3.88%	56	**5.8032e-20**	1.4380	322	444	2.98%

The test set of 10,363 genomic regions picked 10,790 (50%) 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
Abnormality of the nervous system	1	**7.7393e-171**	**5.1072e-167**	2.0426	1,702	16.42%	14	**2.1253e-90**	1.4187	1,471	2,056	13.63%
Abnormality of nervous system physiology	2	**1.7719e-163**	**5.8465e-160**	2.0832	1,567	15.12%	10	**2.9540e-93**	1.4483	1,360	1,862	12.60%
Abnormality of nervous system morphology	3	**2.3863e-151**	**5.2491e-148**	2.1703	1,339	12.92%	6	**1.4349e-98**	1.5105	1,164	1,528	10.79%
Morphological abnormality of the central nervous system	4	**5.4701e-149**	**9.0242e-146**	2.2360	1,242	11.98%	2	**5.0716e-105**	1.5565	1,077	1,372	9.98%
Abnormality of the musculature	5	**1.0415e-147**	**1.3746e-144**	2.2306	1,238	11.95%	16	**2.2242e-89**	1.5046	1,079	1,422	10.00%
Abnormality of skeletal morphology	6	**1.2557e-146**	**1.3810e-143**	2.1283	1,354	13.07%	17	**9.1054e-86**	1.4710	1,161	1,565	10.76%
Neurodevelopmental abnormality	7	**2.4964e-146**	**2.3534e-143**	2.2280	1,230	11.87%	3	**6.5618e-102**	1.5538	1,054	1,345	9.77%
Abnormality of brain morphology	8	**4.0281e-143**	**3.3226e-140**	2.2747	1,156	11.16%	1	**3.4825e-108**	1.5907	1,006	1,254	9.32%
Abnormality of the skeletal system	9	**5.6923e-142**	**4.1738e-139**	2.0823	1,377	13.29%	20	**9.3095e-79**	1.4430	1,184	1,627	10.97%
Abnormality of head or neck	10	**1.0100e-140**	**6.6649e-138**	2.0752	1,376	13.28%	23	**1.0168e-77**	1.4394	1,184	1,631	10.97%
Abnormality of the head	11	**3.4607e-140**	**2.0761e-137**	2.0801	1,364	13.16%	21	**1.9749e-78**	1.4449	1,171	1,607	10.85%
Abnormality of the eye	12	**1.2155e-134**	**6.6843e-132**	2.0871	1,304	12.58%	24	**2.1388e-75**	1.4457	1,125	1,543	10.43%

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 axial skeleton morphology	13	**1.5110e-133**	**7.6701e-131**	2.2080	1,149	11.09%	15	**6.9730e-90**	1.5336	990	1,280	9.18%
Abnormality of muscle physiology	14	**4.8357e-131**	**2.2793e-128**	2.2747	1,063	10.26%	19	**4.0202e-84**	1.5313	936	1,212	8.67%
Neurodevelopmental delay	15	**2.3076e-126**	**1.0152e-123**	2.3535	961	9.27%	13	**9.9819e-91**	1.6040	813	1,005	7.53%
Abnormal muscle tone	16	**4.9795e-125**	**2.0537e-122**	2.3818	930	8.97%	12	**1.4414e-91**	1.6055	817	1,009	7.57%
Abnormality of the skull	17	**4.7307e-124**	**1.8364e-121**	2.2871	998	9.63%	11	**7.0335e-93**	1.5922	860	1,071	7.97%
Global developmental delay	18	**1.5712e-123**	**5.7603e-121**	2.5634	805	7.77%	8	**9.1349e-96**	1.6904	682	800	6.32%
Abnormality of the cerebrum	20	**3.2719e-120**	**1.0796e-117**	2.3923	888	8.57%	4	**4.3467e-101**	1.6658	767	913	7.11%
Abnormality of forebrain morphology	21	**6.8040e-120**	**2.1381e-117**	2.3876	889	8.58%	5	**6.4452e-101**	1.6643	768	915	7.12%

The test set of 10,363 genomic regions picked 10,790 (50%) 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
preweaning lethality	1	**0.0000**	**0.0000**	2.0809	3,096	29.88%	1	**1.1384e-241**	1.4963	2,697	3,574	25.00%
abnormal survival	1	**0.0000**	**0.0000**	2.0402	3,376	32.58%	2	**7.5098e-241**	1.4632	2,959	4,010	27.42%
prenatal lethality	4	**2.0302e-257**	**4.6542e-254**	2.3251	1,908	18.41%	3	**3.4866e-218**	1.6448	1,659	2,000	15.38%
embryonic lethality	5	**8.7049e-219**	**1.5965e-215**	2.4369	1,514	14.61%	5	**2.2779e-200**	1.7055	1,322	1,537	12.25%
embryo phenotype	9	**5.1922e-150**	**5.2903e-147**	2.1021	1,420	13.70%	7	**5.9988e-119**	1.5549	1,210	1,543	11.21%
embryonic lethality prior to tooth bud stage	11	**6.1674e-128**	**5.1414e-125**	2.6749	775	7.48%	6	**1.2608e-126**	1.8009	683	752	6.33%
embryonic lethality prior to organogenesis	13	**6.8683e-121**	**4.8448e-118**	2.7423	704	6.79%	8	**1.3044e-117**	1.8108	621	680	5.76%
abnormal embryo morphology	14	**9.9529e-117**	**6.5192e-114**	2.1108	1,112	10.73%	10	**5.5429e-98**	1.5815	934	1,171	8.66%
abnormal prenatal growth/weight/body size	17	**1.1297e-104**	**6.0938e-102**	2.1446	968	9.34%	9	**5.1160e-100**	1.6367	818	991	7.58%
preweaning lethality, complete penetrance	18	**1.7663e-103**	**8.9986e-101**	2.4273	747	7.21%	11	**5.1414e-94**	1.6916	668	783	6.19%
abnormal embryo development	19	**5.4444e-103**	**2.6276e-100**	2.2575	856	8.26%	13	**4.9705e-90**	1.6444	724	873	6.71%
abnormal embryonic growth/weight/body size	22	**9.1130e-90**	**3.7985e-87**	2.1755	809	7.81%	12	**5.3138e-90**	1.6649	686	817	6.36%
abnormal prenatal body size	34	**2.4610e-75**	**6.6375e-73**	2.1097	729	7.03%	16	**2.4187e-74**	1.6356	617	748	5.72%
abnormal cell morphology	35	**3.2559e-75**	**8.5305e-73**	2.0077	817	7.88%	31	**1.1448e-37**	1.3970	713	1,012	6.61%
abnormal embryonic tissue morphology	36	**5.0065e-75**	**1.2753e-72**	2.0308	793	7.65%	22	**2.0910e-59**	1.5407	655	843	6.07%
embryonic lethality during organogenesis	37	**9.6278e-75**	**2.3861e-72**	2.1234	713	6.88%	19	**3.8086e-64**	1.5959	598	743	5.54%

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
prenatal growth retardation	46	**1.1013e-64**	**2.1954e-62**	2.2463	547	5.28%	20	**9.2828e-64**	1.6896	461	541	4.27%
abnormal embryo size	48	**3.3977e-64**	**6.4910e-62**	2.1333	607	5.86%	17	**3.0571e-67**	1.6664	516	614	4.78%
embryonic lethality during organogenesis, complete penetrance	49	**1.0243e-61**	**1.9169e-59**	2.1493	574	5.54%	23	**3.6147e-56**	1.6276	481	586	4.46%
embryonic lethality between implantation and placentation	51	**6.2623e-61**	**1.1260e-58**	2.5153	413	3.99%	21	**7.6007e-61**	1.7741	357	399	3.31%

The test set of 10,363 genomic regions picked 10,790 (50%) 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
preweaning lethality	1	**0.0000**	**0.0000**	2.0374	3,410	32.91%	1	**5.2831e-243**	1.4628	2,987	4,049	27.68%
prenatal lethality	4	**4.4271e-291**	**1.0597e-287**	2.2713	2,219	21.41%	3	**6.8570e-228**	1.6039	1,913	2,365	17.73%
embryonic lethality	5	**3.3330e-253**	**6.3827e-250**	2.4105	1,764	17.02%	4	**2.3486e-215**	1.6759	1,518	1,796	14.07%
embryo phenotype	9	**9.0263e-174**	**9.6030e-171**	2.0945	1,638	15.81%	6	**1.6400e-129**	1.5346	1,390	1,796	12.88%
abnormal embryo morphology	13	**7.8477e-143**	**5.7802e-140**	2.1285	1,321	12.75%	10	**1.4175e-110**	1.5644	1,099	1,393	10.19%
embryonic lethality prior to tooth bud stage	16	**7.2705e-134**	**4.3510e-131**	2.6359	830	8.01%	7	**6.8197e-128**	1.7777	728	812	6.75%
abnormal prenatal growth/weight/body size	19	**9.8239e-128**	**4.9507e-125**	2.1546	1,159	11.18%	9	**1.1021e-113**	1.6187	969	1,187	8.98%
embryonic lethality prior to organogenesis	20	**1.3045e-125**	**6.2451e-123**	2.6905	754	7.28%	8	**6.0252e-119**	1.7884	662	734	6.14%
abnormal embryo development	22	**1.6141e-118**	**7.0250e-116**	2.2310	1,004	9.69%	12	**3.0130e-98**	1.6194	842	1,031	7.80%
abnormal embryonic growth/weight/body size	25	**2.8873e-114**	**1.1059e-111**	2.2008	997	9.62%	11	**3.6862e-107**	1.6557	830	994	7.69%
preweaning lethality, complete penetrance	31	**6.6396e-105**	**2.0508e-102**	2.3988	774	7.47%	14	**2.6805e-93**	1.6763	689	815	6.39%
embryonic lethality during organogenesis	33	**2.1034e-103**	**6.1030e-101**	2.1721	931	8.98%	17	**5.6879e-82**	1.5917	765	953	7.09%
abnormal prenatal body size	40	**1.0951e-94**	**2.6214e-92**	2.1500	874	8.43%	16	**2.8525e-87**	1.6300	730	888	6.77%
abnormal embryonic tissue morphology	42	**2.8190e-94**	**6.4266e-92**	2.0501	968	9.34%	23	**2.2771e-66**	1.5155	788	1,031	7.30%
abnormal cell morphology	44	**2.0349e-92**	**4.4283e-90**	2.0243	978	9.44%	31	**2.9209e-48**	1.4102	852	1,198	7.90%
embryonic lethality during organogenesis, complete penetrance	50	**5.8681e-85**	**1.1237e-82**	2.1898	756	7.30%	20	**2.9784e-71**	1.6181	621	761	5.76%
abnormal embryo size	52	**1.1754e-82**	**2.1643e-80**	2.1869	738	7.12%	18	**6.8221e-82**	1.6709	616	731	5.71%
prenatal growth retardation	60	**1.3664e-75**	**2.1805e-73**	2.2067	663	6.40%	21	**2.2047e-70**	1.6564	553	662	5.13%

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 embryo size	70	**9.2257e-69**	**1.2619e-66**	2.1557	635	6.13%	22	**3.8289e-69**	1.6688	526	625	4.87%
embryonic growth retardation	76	**1.2484e-65**	**1.5729e-63**	2.2125	573	5.53%	24	**1.2880e-62**	1.6687	478	568	4.43%

The test set of 10,363 genomic regions picked 10,790 (50%) 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].