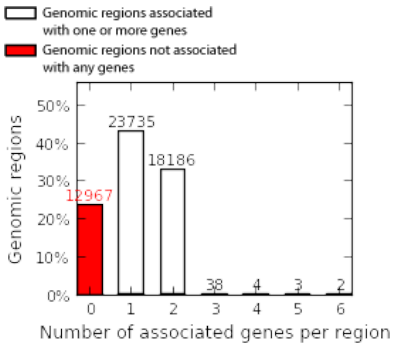
Job Description

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

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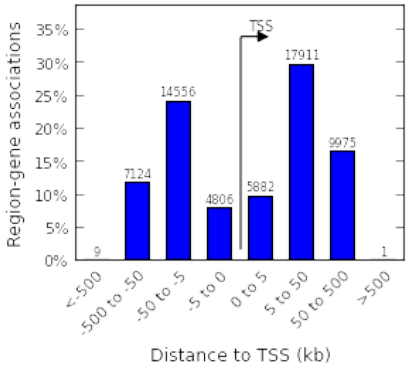

Binned by absolute distance to TSS

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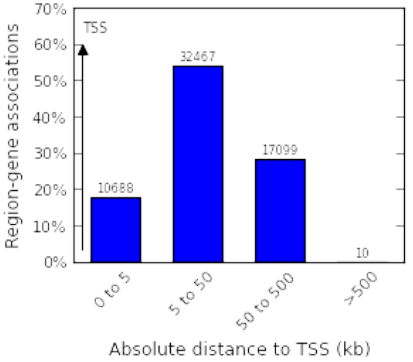

Global Controls

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
animal organ morphogenesis	1	**0.0000**	**0.0000**	2.0393	5,190	9.45%	43	**2.1062e-47**	1.2648	874	962	5.69%
anatomical structure formation involved in morphogenesis	1	**0.0000**	**0.0000**	2.0189	4,594	8.36%	51	**5.7786e-44**	1.2662	804	884	5.23%
epithelium development	1	**0.0000**	**0.0000**	2.0296	5,328	9.70%	72	**4.5403e-39**	1.2344	923	1,041	6.01%
embryo development	1	**0.0000**	**0.0000**	2.0091	5,309	9.66%	94	**3.9094e-34**	1.2167	943	1,079	6.14%
tissue morphogenesis	1	**0.0000**	**0.0000**	2.1463	3,472	6.32%	96	**8.9745e-34**	1.2800	559	608	3.64%
embryonic morphogenesis	1	**0.0000**	**0.0000**	2.1460	3,479	6.33%	98	**2.8486e-33**	1.2745	574	627	3.74%
tube development	1	**0.0000**	**0.0000**	2.1484	3,840	6.99%	111	**2.1421e-31**	1.2625	594	655	3.87%
pattern specification process	1	**0.0000**	**0.0000**	2.3480	2,622	4.77%	187	**1.4361e-21**	1.2656	400	440	2.60%
negative regulation of transcription from RNA polymerase II promoter	1	**0.0000**	**0.0000**	2.0807	4,129	7.52%	242	**1.7075e-17**	1.1790	708	836	4.61%

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
embryo development ending in birth or egg hatching	166	**6.9169e-323**	**5.4545e-321**	2.0366	3,497	6.37%	274	**8.9678e-16**	1.1826	615	724	4.00%
chordate embryonic development	167	**1.2712e-320**	**9.9643e-319**	2.0376	3,469	6.31%	271	**7.1148e-16**	1.1841	609	716	3.96%
morphogenesis of an epithelium	173	**3.8931e-309**	**2.9457e-307**	2.1689	2,902	5.28%	136	**4.8958e-27**	1.2776	457	498	2.97%
regionalization	177	**5.2691e-293**	**3.8968e-291**	2.4473	2,153	3.92%	206	**3.7245e-20**	1.2870	318	344	2.07%
transcription from RNA polymerase II promoter	178	**2.0853e-292**	**1.5335e-290**	2.1043	2,942	5.36%	171	**1.2477e-23**	1.2450	516	577	3.36%
embryonic organ development	179	**6.4136e-292**	**4.6902e-290**	2.1729	2,733	4.97%	167	**2.8454e-24**	1.2669	445	489	2.90%
tube morphogenesis	184	**2.5089e-288**	**1.7849e-286**	2.2562	2,491	4.53%	176	**4.6166e-23**	1.2864	365	395	2.38%
skeletal system development	191	**5.2037e-266**	**3.5663e-264**	2.1594	2,530	4.61%	165	**1.7510e-24**	1.2747	423	462	2.75%
cell morphogenesis involved in differentiation	196	**3.9151e-260**	**2.6147e-258**	2.0324	2,849	5.19%	95	**4.6168e-34**	1.3073	462	492	3.01%
gland development	204	**2.3350e-251**	**1.4983e-249**	2.0904	2,577	4.69%	211	**7.3255e-20**	1.2506	415	462	2.70%
epithelial cell differentiation	206	**4.3925e-248**	**2.7912e-246**	2.0361	2,708	4.93%	223	**1.6409e-18**	1.2255	478	543	3.11%

The test set of 54,935 genomic regions picked 15,368 (72%) 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 (19 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
cell-cell adherens junction	95	**1.3105e-74**	**2.3367e-73**	2.3108	612	1.11%	121	**2.6806e-6**	1.2927	91	98	0.59%
ruffle membrane	120	**2.5686e-50**	**3.6260e-49**	2.2378	437	0.80%	172	**1.4474e-3**	1.2394	73	82	0.48%
stress fiber	124	**6.0020e-49**	**8.1995e-48**	2.4040	366	0.67%	176	**1.7118e-3**	1.2637	59	65	0.38%
actin filament bundle	126	**7.2958e-49**	**9.8088e-48**	2.3022	399	0.73%	159	**2.6547e-4**	1.2778	67	73	0.44%
actomyosin	138	**1.2346e-45**	**1.5156e-44**	2.2171	403	0.73%	152	**1.3036e-4**	1.2823	70	76	0.46%
transcriptional repressor complex	152	**1.2464e-41**	**1.3891e-40**	2.0476	441	0.80%	218	**2.1950e-2**	1.1842	74	87	0.48%
cortical cytoskeleton	157	**2.0625e-39**	**2.2254e-38**	2.0142	434	0.79%	162	**5.3778e-4**	1.2409	82	92	0.53%
cortical actin cytoskeleton	176	**9.2662e-34**	**8.9187e-33**	2.1411	318	0.58%	199	**6.6614e-3**	1.2399	57	64	0.37%
MHC protein complex	192	**1.8324e-26**	**1.6167e-25**	4.2324	83	0.15%	220	**2.8428e-2**	1.3342	23	24	0.15%
PcG protein complex	210	**2.9334e-23**	**2.3663e-22**	2.1438	213	0.39%	203	**1.0055e-2**	1.2711	42	46	0.27%
dendritic shaft	219	**5.8754e-22**	**4.5447e-21**	2.1174	206	0.37%	166	**7.5573e-4**	1.3546	36	37	0.23%
excitatory synapse	238	**1.0714e-17**	**7.6257e-17**	2.1930	150	0.27%	217	**2.1474e-2**	1.3365	24	25	0.16%

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
desmosome	239	**1.5025e-17**	**1.0649e-16**	2.2459	141	0.26%	201	**9.5157e-3**	1.3425	27	28	0.18%
compact myelin	266	**1.3256e-14**	**8.4419e-14**	2.4128	99	0.18%	224	**3.7896e-2**	1.3922	16	16	0.10%
costamere	267	**1.4936e-14**	**9.4761e-14**	2.1505	126	0.23%	205	**1.1009e-2**	1.3922	20	20	0.13%
lamellipodium membrane	274	**5.2168e-14**	**3.2253e-13**	2.1481	121	0.22%	222	**3.7757e-2**	1.3316	22	23	0.14%
paranode region of axon	279	**8.4665e-14**	**5.1406e-13**	2.3370	99	0.18%	224	**3.7896e-2**	1.3922	16	16	0.10%
myosin II complex	313	**1.0454e-10**	**5.6577e-10**	2.0349	101	0.18%	236	**4.7527e-2**	1.3289	21	22	0.14%
Golgi medial cisterna	343	**2.2340e-9**	**1.1033e-8**	2.5061	55	0.10%	224	**3.7896e-2**	1.3922	16	16	0.10%

The test set of 54,935 genomic regions picked 15,368 (72%) 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
transcription regulatory region sequence-specific DNA binding	1	**0.0000**	**0.0000**	2.1823	3,941	7.17%	4	**9.3706e-35**	1.2625	672	741	4.37%
RNA polymerase II transcription factor activity, sequence-specific DNA binding	1	**0.0000**	**0.0000**	2.1573	4,143	7.54%	5	**1.5525e-34**	1.2577	692	766	4.50%
regulatory region DNA binding	1	**0.0000**	**0.0000**	2.1434	4,611	8.39%	6	**2.1077e-34**	1.2396	796	894	5.18%
transcription regulatory region DNA binding	1	**0.0000**	**0.0000**	2.1427	4,604	8.38%	7	**2.8375e-34**	1.2392	794	892	5.17%
sequence-specific DNA binding	1	**0.0000**	**0.0000**	2.1553	5,398	9.83%	8	**5.0528e-33**	1.2162	933	1,068	6.07%
RNA polymerase II regulatory region sequence-specific DNA binding	1	**0.0000**	**0.0000**	2.2198	3,572	6.50%	9	**9.8904e-33**	1.2691	598	656	3.89%
RNA polymerase II regulatory region DNA binding	1	**0.0000**	**0.0000**	2.2113	3,579	6.51%	10	**1.7536e-32**	1.2675	600	659	3.90%
sequence-specific double-stranded DNA binding	1	**0.0000**	**0.0000**	2.1497	4,025	7.33%	11	**8.2288e-31**	1.2431	692	775	4.50%
double-stranded DNA binding	1	**0.0000**	**0.0000**	2.0995	4,183	7.61%	13	**1.5865e-27**	1.2216	745	849	4.85%
transcription factor activity, RNA polymerase II core promoter proximal region sequence-specific binding	24	**7.0261e-282**	**1.2094e-279**	2.2472	2,457	4.47%	18	**8.9338e-24**	1.2838	391	424	2.54%
transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding	25	**1.4297e-281**	**2.3625e-279**	2.2513	2,445	4.45%	12	**1.4588e-29**	1.3122	394	418	2.56%

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 DNA binding	27	**6.2579e-255**	**9.5746e-253**	2.2242	2,275	4.14%	32	**1.4474e-18**	1.2591	369	408	2.40%
core promoter proximal region sequence-specific DNA binding	30	**7.9636e-251**	**1.0966e-248**	2.2210	2,246	4.09%	33	**2.8502e-18**	1.2581	366	405	2.38%
RNA polymerase II core promoter proximal region sequence-specific DNA binding	31	**9.8930e-248**	**1.3183e-245**	2.2355	2,188	3.98%	35	**4.0785e-18**	1.2608	355	392	2.31%
transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	37	**2.8795e-192**	**3.2149e-190**	2.2491	1,681	3.06%	34	**3.9241e-18**	1.2994	266	285	1.73%
transcriptional repressor activity, RNA polymerase II transcription regulatory region sequence-specific binding	61	**1.9347e-122**	**1.3102e-120**	2.1029	1,245	2.27%	72	**9.3818e-10**	1.2494	210	234	1.37%
transcriptional repressor activity, RNA polymerase II core promoter proximal region sequence-specific binding	71	**7.0170e-96**	**4.0827e-94**	2.2276	854	1.55%	107	**4.8310e-6**	1.2447	135	151	0.88%
enhancer binding	84	**5.3362e-69**	**2.6243e-67**	2.2427	602	1.10%	96	**1.0661e-6**	1.2927	104	112	0.68%
enhancer sequence-specific DNA binding	94	**7.6663e-59**	**3.3691e-57**	2.2042	531	0.97%	104	**3.4657e-6**	1.2957	94	101	0.61%
transcription factor activity, RNA polymerase II distal enhancer sequence-specific binding	102	**1.7629e-55**	**7.1399e-54**	2.0675	580	1.06%	89	**3.2191e-7**	1.3119	98	104	0.64%

The test set of 54,935 genomic regions picked 15,368 (72%) 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
Abnormal vascular morphology	55	**5.3009e-123**	**6.3602e-121**	2.0158	1,386	2.52%	46	**5.6904e-6**	1.1852	252	296	1.64%
Oral cleft	60	**2.4385e-118**	**2.6819e-116**	2.0856	1,227	2.23%	160	**2.4463e-3**	1.1532	193	233	1.26%
Abnormality of the nail	64	**1.0185e-112**	**1.0502e-110**	2.2776	959	1.75%	52	**7.9629e-6**	1.2217	172	196	1.12%
Cleft palate	66	**6.1184e-112**	**6.1175e-110**	2.1098	1,129	2.06%	173	**3.3837e-3**	1.1548	180	217	1.17%
Abnormality of the hard palate	68	**4.6439e-110**	**4.5067e-108**	2.0681	1,164	2.12%	152	**2.0881e-3**	1.1591	184	221	1.20%
Abnormality of the periorbital region	69	**1.1720e-109**	**1.1208e-107**	2.0211	1,227	2.23%	93	**2.6769e-4**	1.1715	207	246	1.35%
Abnormal morphology of the great vessels	72	**1.1794e-108**	**1.0810e-106**	2.1375	1,063	1.94%	59	**1.3121e-5**	1.2115	181	208	1.18%
Cleft lip	91	**1.4960e-93**	**1.0848e-91**	2.4528	684	1.25%	350	**3.2943e-2**	1.1812	84	99	0.55%
Abnormality of upper limb joint	92	**1.7149e-93**	**1.2301e-91**	2.0359	1,026	1.87%	138	**1.8211e-3**	1.1623	182	218	1.18%

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
Cleft upper lip	102	**8.0710e-86**	**5.2216e-84**	2.4203	643	1.17%	301	**2.0478e-2**	1.1976	80	93	0.52%
Aplasia/Hypoplasia of the nails	105	**1.3364e-85**	**8.3990e-84**	2.8127	490	0.89%	115	**8.6456e-4**	1.2808	69	75	0.45%
Abnormality of the stomach	112	**1.5387e-81**	**9.0659e-80**	2.1774	762	1.39%	119	**9.2706e-4**	1.2040	128	148	0.83%
Limb joint contracture	117	**1.1233e-78**	**6.3359e-77**	2.2069	713	1.30%	202	**6.0732e-3**	1.1773	126	149	0.82%
Abnormal systemic arterial morphology	150	**5.2098e-69**	**2.2920e-67**	2.0578	734	1.34%	190	**5.1071e-3**	1.1766	131	155	0.85%
Congenital malformation of the great arteries	154	**3.2310e-68**	**1.3845e-66**	2.0570	726	1.32%	136	**1.7357e-3**	1.1988	124	144	0.81%
Clinodactyly	166	**6.0109e-67**	**2.3895e-65**	2.0147	750	1.37%	262	**1.3949e-2**	1.1649	123	147	0.80%
Aplasia/Hypoplasia involving bones of the thorax	175	**1.1970e-65**	**4.5136e-64**	2.2824	551	1.00%	271	**1.5531e-2**	1.2017	82	95	0.53%
Patent ductus arteriosus	180	**1.1966e-64**	**4.3867e-63**	2.1777	601	1.09%	117	**8.6948e-4**	1.2375	96	108	0.62%
Regional abnormality of skin	186	**7.9654e-62**	**2.8260e-60**	2.0082	697	1.27%	316	**2.3408e-2**	1.1554	122	147	0.79%
Flexion contracture of digit	192	**2.1325e-60**	**7.3294e-59**	2.2161	539	0.98%	254	**1.3234e-2**	1.1992	87	101	0.57%

The test set of 54,935 genomic regions picked 15,368 (72%) 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
neonatal lethality, complete penetrance	83	**3.9095e-229**	**4.3193e-227**	2	2,618	4.77%	172	**5.3002e-15**	1.2174	418	478	2.72%
abnormal craniofacial development	105	**2.1899e-202**	**1.9125e-200**	2.1813	1,890	3.44%	198	**1.7458e-13**	1.2525	278	309	1.81%
abnormal cartilage morphology	132	**1.1321e-171**	**7.8643e-170**	2.1299	1,694	3.08%	133	**3.7952e-18**	1.2987	264	283	1.72%
abnormal neurocranium morphology	151	**1.2367e-163**	**7.5106e-162**	2.2707	1,403	2.55%	337	**2.4650e-9**	1.2473	198	221	1.29%
perinatal lethality, complete penetrance	157	**1.0899e-158**	**6.3659e-157**	2.2563	1,379	2.51%	377	**1.5142e-8**	1.2361	198	223	1.29%
abnormal eye development	158	**1.2594e-158**	**7.3092e-157**	2.2139	1,436	2.61%	359	**6.3708e-9**	1.2318	215	243	1.40%
abnormal eyelid morphology	175	**1.5027e-144**	**7.8740e-143**	2.3014	1,205	2.19%	341	**2.8320e-9**	1.2656	170	187	1.11%
abnormal autopod morphology	187	**1.6359e-136**	**8.0219e-135**	2.0005	1,568	2.85%	321	**1.4531e-9**	1.2153	268	307	1.74%
abnormal joint morphology	189	**6.6141e-136**	**3.2091e-134**	2.0706	1,434	2.61%	226	**1.8871e-12**	1.2560	249	276	1.62%
abnormal lens morphology	216	**7.1003e-115**	**3.0143e-113**	2.0037	1,314	2.39%	309	**9.6103e-10**	1.2334	233	263	1.52%
abnormal eye size	219	**3.0325e-114**	**1.2698e-112**	2.2321	1,015	1.85%	718	**5.9884e-5**	1.1977	154	179	1.00%
abnormal pectoral girdle bone morphology	225	**9.5613e-112**	**3.8968e-110**	2.1043	1,134	2.06%	303	**8.2954e-10**	1.2625	185	204	1.20%

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
embryonic lethality during organogenesis, incomplete penetrance	226	**1.5266e-111**	**6.1943e-110**	2.0149	1,258	2.29%	650	**1.9651e-5**	1.1816	202	238	1.31%
microphthalmia	234	**8.3082e-108**	**3.2558e-106**	2.2303	959	1.75%	702	**4.4846e-5**	1.2077	144	166	0.94%
exencephaly	241	**1.7946e-103**	**6.8283e-102**	2.1256	1,025	1.87%	928	**5.4674e-4**	1.1686	162	193	1.05%
abnormal tooth morphology	242	**1.2199e-102**	**4.6225e-101**	2.1111	1,033	1.88%	432	**2.9205e-7**	1.2427	158	177	1.03%
abnormal cornea morphology	247	**7.2808e-101**	**2.7030e-99**	2.2119	913	1.66%	438	**3.7754e-7**	1.2487	148	165	0.96%
abnormal epidermal layer morphology	248	**9.2816e-101**	**3.4320e-99**	2.0386	1,103	2.01%	386	**2.0311e-8**	1.2302	205	232	1.33%
lethality throughout fetal growth and development, incomplete penetrance	253	**7.7269e-100**	**2.8006e-98**	2.1080	1,008	1.83%	784	**1.1026e-4**	1.1911	154	180	1.00%
abnormal renal glomerulus morphology	266	**5.1081e-98**	**1.7609e-96**	2.0123	1,108	2.02%	353	**5.4280e-9**	1.2395	203	228	1.32%

The test set of 54,935 genomic regions picked 15,368 (72%) 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 craniofacial development	104	**3.5940e-262**	**3.3089e-260**	2.1989	2,397	4.36%	198	**2.1192e-18**	1.2604	354	391	2.30%
abnormal eye development	137	**3.1929e-224**	**2.2315e-222**	2.2484	1,959	3.57%	301	**1.6482e-13**	1.2461	290	324	1.89%
abnormal cartilage morphology	151	**1.0504e-214**	**6.6607e-213**	2.0711	2,256	4.11%	120	**8.8151e-26**	1.3003	368	394	2.39%
perinatal lethality, complete penetrance	158	**2.3018e-208**	**1.3949e-206**	2.1959	1,917	3.49%	312	**3.9051e-13**	1.2443	286	320	1.86%
abnormal angiogenesis	167	**1.5490e-196**	**8.8811e-195**	2.0013	2,248	4.09%	137	**1.6146e-23**	1.2838	379	411	2.47%
abnormal autopod morphology	174	**2.4197e-188**	**1.3315e-186**	2.0268	2,089	3.80%	314	**4.1843e-13**	1.2221	345	393	2.24%
abnormal neurocranium morphology	179	**3.2132e-186**	**1.7188e-184**	2.2005	1,707	3.11%	360	**1.2193e-11**	1.2464	248	277	1.61%
abnormal tail morphology	186	**5.3958e-182**	**2.7777e-180**	2.0082	2,066	3.76%	239	**8.5275e-16**	1.2371	367	413	2.39%
abnormal joint morphology	189	**8.5176e-181**	**4.3151e-179**	2.1142	1,814	3.30%	214	**4.5683e-17**	1.2686	308	338	2.00%
abnormal palate morphology	196	**3.2595e-177**	**1.5923e-175**	2.0465	1,921	3.50%	405	**1.0878e-10**	1.2187	288	329	1.87%
abnormal neural tube closure	198	**6.5162e-177**	**3.1511e-175**	2.0368	1,940	3.53%	396	**8.7964e-11**	1.2041	333	385	2.17%
abnormal eyelid morphology	204	**1.5765e-171**	**7.3997e-170**	2.1930	1,585	2.89%	289	**9.6899e-14**	1.2739	237	259	1.54%
abnormal spinal cord morphology	215	**5.9663e-163**	**2.6571e-161**	2.0183	1,829	3.33%	223	**2.6228e-16**	1.2619	310	342	2.02%
abnormal forebrain development	218	**1.3470e-161**	**5.9163e-160**	2.1687	1,531	2.79%	409	**1.3220e-10**	1.2448	228	255	1.48%

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 epidermal layer morphology	235	**1.2759e-150**	**5.1988e-149**	2.0175	1,693	3.08%	320	**6.3471e-13**	1.2298	318	360	2.07%
abnormal pectoral girdle bone morphology	244	**7.9106e-148**	**3.1042e-146**	2.0856	1,533	2.79%	313	**4.1338e-13**	1.2633	245	270	1.59%
exencephaly	281	**1.1637e-127**	**3.9652e-126**	2.0543	1,373	2.50%	788	**4.0465e-6**	1.1820	225	265	1.46%
abnormal spinal cord grey matter morphology	283	**5.3482e-127**	**1.8095e-125**	2.0836	1,320	2.40%	316	**4.2156e-13**	1.2796	216	235	1.41%
abnormal brainstem morphology	285	**1.2911e-125**	**4.3378e-124**	2.0493	1,359	2.47%	311	**3.2870e-13**	1.2771	222	242	1.44%
abnormal eye size	286	**1.3919e-125**	**4.6600e-124**	2.1194	1,254	2.28%	643	**2.9082e-7**	1.2166	194	222	1.26%

The test set of 54,935 genomic regions picked 15,368 (72%) 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].