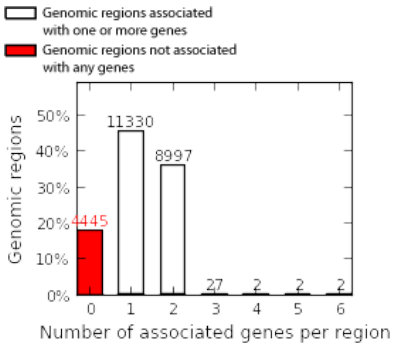
Job Description

Region-Gene Association Graphs

What do these graphs illustrate?

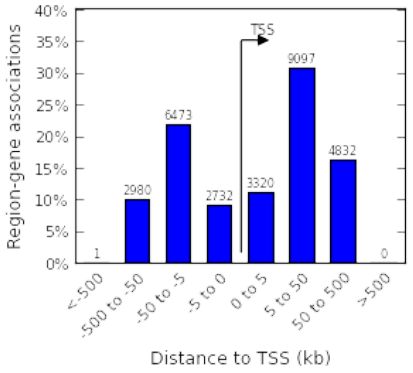
Number of associated genes per region

Download as PDF.



Binned by orientation and distance to TSS

Download as PDF.



Binned by absolute distance to TSS

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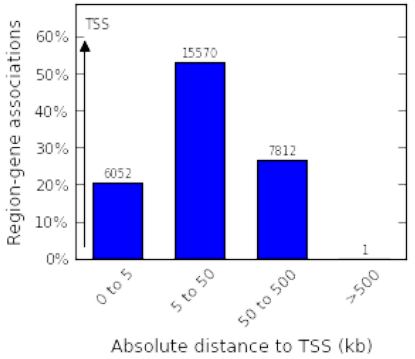

Global Controls

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
single-multicellular organism process	1	**0.0000**	**0.0000**	2.0001	10,420	42.01%	1	**2.4473e-139**	1.3017	3,475	5,396	32.83%
multicellular organism development	1	**0.0000**	**0.0000**	2.0657	9,621	38.79%	2	**9.0450e-127**	1.3137	3,069	4,722	28.99%
anatomical structure development	1	**0.0000**	**0.0000**	2.0346	9,980	40.23%	3	**2.8168e-124**	1.2978	3,236	5,040	30.57%
single-organism developmental process	1	**0.0000**	**0.0000**	2.0032	10,305	41.54%	4	**1.8629e-122**	1.2843	3,398	5,348	32.10%
system development	1	**0.0000**	**0.0000**	2.0974	8,766	35.34%	7	**3.6754e-113**	1.3200	2,722	4,168	25.72%
anatomical structure morphogenesis	1	**0.0000**	**0.0000**	2.3402	5,498	22.16%	8	**2.6350e-105**	1.4590	1,500	2,078	14.17%
cell differentiation	1	**0.0000**	**0.0000**	2.1221	7,523	30.33%	10	**1.1261e-95**	1.3273	2,297	3,498	21.70%
regulation of multicellular organismal process	1	**0.0000**	**0.0000**	2.0663	5,943	23.96%	11	**1.5412e-95**	1.3783	1,850	2,713	17.48%
cellular developmental process	1	**0.0000**	**0.0000**	2.1090	7,635	30.78%	12	**7.9571e-94**	1.3195	2,339	3,583	22.10%
animal organ development	1	**0.0000**	**0.0000**	2.1695	6,916	27.88%	14	**2.5174e-90**	1.3410	2,058	3,102	19.44%

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
tissue development	1	**0.0000**	**0.0000**	2.4020	4,330	17.46%	15	**1.3586e-79**	1.4565	1,171	1,625	11.06%
nervous system development	1	**0.0000**	**0.0000**	2.2183	5,305	21.39%	16	**1.6188e-77**	1.3856	1,493	2,178	14.10%
regulation of developmental process	1	**0.0000**	**0.0000**	2.1940	5,630	22.70%	17	**1.1891e-73**	1.3580	1,601	2,383	15.13%
neurogenesis	1	**0.0000**	**0.0000**	2.2714	4,027	16.23%	18	**1.5015e-73**	1.4522	1,105	1,538	10.44%
regulation of signaling	1	**0.0000**	**0.0000**	2.0223	6,271	25.28%	19	**1.3925e-72**	1.3059	2,008	3,108	18.97%
regulation of cell communication	1	**0.0000**	**0.0000**	2.0176	6,220	25.08%	20	**3.0463e-72**	1.3064	1,994	3,085	18.84%
regulation of multicellular organismal development	1	**0.0000**	**0.0000**	2.2143	4,417	17.81%	21	**4.3188e-72**	1.4129	1,254	1,794	11.85%
positive regulation of metabolic process	1	**0.0000**	**0.0000**	2.0810	6,355	25.62%	23	**1.9676e-67**	1.2950	1,990	3,106	18.80%
generation of neurons	1	**0.0000**	**0.0000**	2.2925	3,805	15.34%	24	**6.1038e-67**	1.4507	1,017	1,417	9.61%
animal organ morphogenesis	1	**0.0000**	**0.0000**	2.6123	3,002	12.10%	26	**6.7155e-66**	1.5443	735	962	6.94%

The test set of 24,805 genomic regions picked 10,585 (49%) 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
anchoring junction	44	**1.1968e-173**	**4.6077e-172**	2.3923	1,316	5.31%	30	**4.3661e-22**	1.4327	370	522	3.50%
adherens junction	46	**3.8450e-162**	**1.4160e-160**	2.3630	1,260	5.08%	32	**7.0055e-20**	1.4185	353	503	3.33%
transcription factor complex	48	**7.2550e-142**	**2.5604e-140**	2.4867	1,002	4.04%	72	**7.8103e-11**	1.3566	249	371	2.35%
cell-cell junction	51	**1.2686e-134**	**4.2137e-133**	2.2404	1,169	4.71%	31	**2.6072e-21**	1.4532	330	459	3.12%
actin cytoskeleton	59	**1.0631e-124**	**3.0523e-123**	2.2776	1,047	4.22%	33	**1.3543e-19**	1.4386	321	451	3.03%
focal adhesion	60	**2.4568e-122**	**6.9363e-121**	2.3881	934	3.77%	62	**3.4409e-12**	1.3719	262	386	2.48%
cell-substrate adherens junction	63	**7.6843e-121**	**2.0662e-119**	2.3706	936	3.77%	66	**6.6771e-12**	1.3647	264	391	2.49%
cell-substrate junction	64	**1.6481e-119**	**4.3623e-118**	2.3486	943	3.80%	65	**6.3816e-12**	1.3628	267	396	2.52%
cell body	70	**3.1652e-100**	**7.6597e-99**	2.0183	1,107	4.46%	49	**8.4962e-16**	1.3671	349	516	3.30%
extracellular matrix	71	**9.1001e-99**	**2.1712e-97**	2.0050	1,109	4.47%	50	**1.2318e-15**	1.3589	359	534	3.39%
cell leading edge	72	**2.8389e-95**	**6.6792e-94**	2.1694	889	3.58%	67	**7.5375e-12**	1.3771	248	364	2.34%
neuronal cell body	76	**1.8748e-88**	**4.1788e-87**	2.0213	974	3.93%	53	**1.0770e-13**	1.3688	300	443	2.83%
axon	77	**8.3800e-88**	**1.8436e-86**	2.0045	987	3.98%	34	**1.4595e-19**	1.4471	310	433	2.93%

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
cell projection membrane	83	**1.9502e-74**	**3.9803e-73**	2.2394	647	2.61%	106	**1.7782e-7**	1.3378	184	278	1.74%
membrane raft	88	**2.2844e-68**	**4.3974e-67**	2.0767	704	2.84%	46	**2.7629e-17**	1.4963	228	308	2.15%
cytoplasmic region	89	**3.2257e-68**	**6.1397e-67**	2.0674	710	2.86%	102	**1.2621e-7**	1.3129	215	331	2.03%
cell cortex	91	**5.2806e-67**	**9.8300e-66**	2.1655	626	2.52%	121	**2.3952e-6**	1.3127	176	271	1.66%
extrinsic component of membrane	98	**1.2844e-60**	**2.2201e-59**	2.1254	590	2.38%	73	**1.3188e-10**	1.4119	190	272	1.79%
ruffle	99	**1.9145e-59**	**3.2760e-58**	2.4261	437	1.76%	148	**4.7796e-4**	1.3144	106	163	1.00%
apical plasma membrane	100	**2.0046e-59**	**3.3957e-58**	2.0117	660	2.66%	57	**6.0984e-13**	1.4351	213	300	2.01%

The test set of 24,805 genomic regions picked 10,585 (49%) 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
sequence-specific DNA binding	1	**0.0000**	**0.0000**	2.7571	3,118	12.57%	3	**3.3153e-49**	1.4516	767	1,068	7.25%
RNA polymerase II transcription factor activity, sequence-specific DNA binding	1	**0.0000**	**0.0000**	2.7562	2,390	9.64%	4	**3.2749e-48**	1.5278	579	766	5.47%
transcription regulatory region DNA binding	1	**0.0000**	**0.0000**	2.7293	2,648	10.68%	5	**2.5564e-46**	1.4797	653	892	6.17%
regulatory region DNA binding	1	**0.0000**	**0.0000**	2.7281	2,650	10.68%	6	**2.7101e-46**	1.4786	654	894	6.18%
RNA polymerase II regulatory region DNA binding	1	**0.0000**	**0.0000**	2.8352	2,072	8.35%	7	**4.6393e-46**	1.5550	507	659	4.79%
RNA polymerase II regulatory region sequence-specific DNA binding	1	**0.0000**	**0.0000**	2.8489	2,070	8.35%	8	**4.5715e-46**	1.5560	505	656	4.77%
transcription regulatory region sequence-specific DNA binding	1	**0.0000**	**0.0000**	2.7753	2,263	9.12%	9	**2.6241e-45**	1.5194	557	741	5.26%
sequence-specific double-stranded DNA binding	1	**0.0000**	**0.0000**	2.7241	2,303	9.28%	10	**2.0639e-41**	1.4866	570	775	5.38%
double-stranded DNA binding	1	**0.0000**	**0.0000**	2.6378	2,373	9.57%	12	**1.3160e-36**	1.4380	604	849	5.71%
transcription factor activity, sequence-specific DNA binding	1	**0.0000**	**0.0000**	2.4487	2,905	11.71%	18	**1.7001e-26**	1.3190	755	1,157	7.13%
enzyme binding	1	**0.0000**	**0.0000**	2.0282	3,605	14.53%	19	**1.9478e-26**	1.2430	1,182	1,922	11.17%
DNA binding	1	**0.0000**	**0.0000**	2.2651	4,365	17.60%	22	**1.0928e-23**	1.2187	1,271	2,108	12.01%
macromolecular complex binding	19	**2.7995e-315**	**6.0866e-313**	2.1242	2,971	11.98%	27	**5.5151e-19**	1.2373	906	1,480	8.56%

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
transcription factor activity, RNA polymerase II core promoter proximal region sequence-specific binding	23	**2.6800e-264**	**4.8136e-262**	2.8965	1,430	5.76%	13	**8.0953e-35**	1.6018	336	424	3.17%
transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding	24	**2.9772e-245**	**5.1245e-243**	2.8222	1,384	5.58%	11	**3.6409e-37**	1.6247	336	418	3.17%
core promoter proximal region DNA binding	26	**3.5868e-222**	**5.6989e-220**	2.7823	1,285	5.18%	15	**3.5019e-28**	1.5556	314	408	2.97%
core promoter proximal region sequence-specific DNA binding	27	**1.2043e-216**	**1.8426e-214**	2.7681	1,264	5.10%	16	**1.2785e-27**	1.5521	311	405	2.94%
RNA polymerase II core promoter proximal region sequence-specific DNA binding	28	**2.7077e-216**	**3.9948e-214**	2.8013	1,238	4.99%	14	**7.8696e-29**	1.5727	305	392	2.88%
protein domain specific binding	33	**3.7764e-196**	**4.7274e-194**	2.2821	1,627	6.56%	25	**7.3318e-20**	1.3551	478	713	4.52%
transcription factor binding	34	**1.7449e-190**	**2.1201e-188**	2.4270	1,402	5.65%	34	**1.5462e-14**	1.3439	373	561	3.52%

The test set of 24,805 genomic regions picked 10,585 (49%) 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
Autosomal dominant inheritance	1	**2.8691e-313**	**1.8933e-309**	2.1284	2,941	11.86%	1	**5.8139e-42**	1.3812	889	1,301	8.40%
Abnormality of the integument	9	**6.5918e-202**	**4.8333e-199**	2.0164	2,195	8.85%	10	**5.1793e-15**	1.2523	684	1,104	6.46%
Abnormality of the mouth	11	**4.4709e-190**	**2.6822e-187**	2.0715	1,945	7.84%	9	**1.8223e-15**	1.2852	571	898	5.39%
Abnormality of the oral cavity	16	**3.6164e-175**	**1.4915e-172**	2.1466	1,659	6.69%	11	**1.3645e-14**	1.3079	473	731	4.47%
Abnormality of the orbital region	21	**2.9844e-158**	**9.3783e-156**	2.0143	1,741	7.02%	15	**4.9969e-12**	1.2639	514	822	4.86%
Abnormal appendicular skeleton morphology	26	**1.2439e-140**	**3.1571e-138**	2.0014	1,577	6.36%	22	**3.3669e-10**	1.2518	475	767	4.49%
Abnormality of cardiovascular system morphology	27	**1.2376e-131**	**3.0249e-129**	2.0330	1,423	5.74%	46	**3.5994e-8**	1.2307	439	721	4.15%
Abnormality of the nose	31	**2.9773e-130**	**6.3379e-128**	2.0151	1,439	5.80%	51	**7.4452e-8**	1.2302	423	695	4.00%
Abnormality of digit	34	**1.1253e-123**	**2.1840e-121**	2.0481	1,315	5.30%	27	**2.4949e-9**	1.2725	379	602	3.58%
Abnormality of skin adnexa morphology	35	**3.5042e-121**	**6.6070e-119**	2.0636	1,266	5.10%	56	**2.0062e-7**	1.2410	369	601	3.49%
Abnormality of the palate	36	**1.3281e-119**	**2.4345e-117**	2.2716	1,010	4.07%	25	**1.5270e-9**	1.3344	272	412	2.57%

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
Aplasia/hypoplasia affecting bones of the axial skeleton	40	**2.2350e-117**	**3.6871e-115**	2.3967	890	3.59%	47	**4.1593e-8**	1.3270	237	361	2.24%
Abnormal morphology of the ocular adnexa	41	**3.2782e-116**	**5.2763e-114**	2.0391	1,250	5.04%	30	**3.3823e-9**	1.2732	371	589	3.50%
Abnormal heart morphology	43	**7.2568e-116**	**1.1137e-113**	2.0588	1,218	4.91%	74	**9.4583e-7**	1.2259	373	615	3.52%
Abnormality of the dentition	45	**2.5972e-115**	**3.8086e-113**	2.2898	958	3.86%	62	**4.4710e-7**	1.3017	237	368	2.24%
Abnormality of the gastrointestinal tract	46	**3.8034e-115**	**5.4562e-113**	2.0715	1,193	4.81%	34	**6.5531e-9**	1.2770	350	554	3.31%
Abnormality of connective tissue	47	**7.4816e-115**	**1.0504e-112**	2.0804	1,178	4.75%	23	**4.6271e-10**	1.2935	359	561	3.39%
Abnormality of the vasculature	50	**8.5108e-110**	**1.1233e-107**	2.0841	1,122	4.52%	40	**1.9764e-8**	1.2702	345	549	3.26%
Aplasia/hypoplasia involving the skeleton	52	**8.8742e-109**	**1.1262e-106**	2.0871	1,108	4.47%	48	**6.0122e-8**	1.2712	322	512	3.04%
Abnormal reproductive system morphology	54	**3.4735e-107**	**4.2448e-105**	2.0163	1,186	4.78%	149	**5.9925e-5**	1.2044	317	532	2.99%

The test set of 24,805 genomic regions picked 10,585 (49%) 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
nervous system phenotype	1	**0.0000**	**0.0000**	2.0198	6,250	25.20%	1	**2.4017e-99**	1.3777	1,933	2,836	18.26%
lethality during fetal growth through weaning	1	**0.0000**	**0.0000**	2.2636	4,591	18.51%	6	**4.0579e-81**	1.4424	1,256	1,760	11.87%
preweaning lethality	1	**0.0000**	**0.0000**	2.0297	7,228	29.14%	8	**8.4757e-80**	1.2957	2,291	3,574	21.64%
abnormal nervous system morphology	1	**0.0000**	**0.0000**	2.1284	5,237	21.11%	9	**7.1345e-79**	1.3841	1,527	2,230	14.43%
cardiovascular system phenotype	1	**0.0000**	**0.0000**	2.0038	4,855	19.57%	12	**5.1338e-65**	1.3469	1,506	2,260	14.23%
skeleton phenotype	1	**0.0000**	**0.0000**	2.0889	4,309	17.37%	14	**5.4533e-58**	1.3576	1,295	1,928	12.23%
abnormal skeleton morphology	1	**0.0000**	**0.0000**	2.1029	4,150	16.73%	18	**4.5641e-55**	1.3582	1,231	1,832	11.63%
perinatal lethality	1	**0.0000**	**0.0000**	2.3825	2,795	11.27%	21	**3.3852e-54**	1.4908	725	983	6.85%
abnormal brain morphology	1	**0.0000**	**0.0000**	2.1793	3,392	13.67%	27	**5.4929e-50**	1.3996	941	1,359	8.89%
abnormal cardiovascular system morphology	1	**0.0000**	**0.0000**	2.0816	3,851	15.53%	30	**1.1038e-47**	1.3459	1,138	1,709	10.75%
abnormal axial skeleton morphology	1	**0.0000**	**0.0000**	2.2849	2,936	11.84%	39	**2.1698e-41**	1.3958	799	1,157	7.55%
vision/eye phenotype	1	**0.0000**	**0.0000**	2.2103	3,254	13.12%	41	**5.1436e-41**	1.3624	916	1,359	8.65%
abnormal eye morphology	1	**0.0000**	**0.0000**	2.2631	3,093	12.47%	42	**5.3812e-39**	1.3690	848	1,252	8.01%
embryo phenotype	1	**0.0000**	**0.0000**	2.1980	3,554	14.33%	66	**1.1045e-28**	1.2838	980	1,543	9.26%

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 embryo morphology	1	**0.0000**	**0.0000**	2.2514	2,839	11.45%	98	**5.3992e-24**	1.2997	753	1,171	7.11%
craniofacial phenotype	37	**1.0672e-321**	**2.6449e-319**	2.2965	2,582	10.41%	50	**2.7947e-37**	1.4134	672	961	6.35%
abnormal craniofacial morphology	38	**6.4130e-321**	**1.5476e-318**	2.2966	2,576	10.39%	52	**4.7118e-37**	1.4130	669	957	6.32%
abnormal nervous system development	41	**4.5886e-309**	**1.0263e-306**	2.2738	2,535	10.22%	46	**1.2492e-37**	1.4166	670	956	6.33%
digestive/alimentary phenotype	42	**8.2277e-308**	**1.7964e-305**	2.2508	2,577	10.39%	53	**5.4517e-37**	1.3921	728	1,057	6.88%
integument phenotype	43	**5.2598e-304**	**1.1217e-301**	2.0038	3,270	13.18%	40	**4.1423e-41**	1.3401	1,019	1,537	9.63%

The test set of 24,805 genomic regions picked 10,585 (49%) 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
nervous system phenotype	1	**0.0000**	**0.0000**	2.0178	7,247	29.22%	1	**5.4564e-118**	1.3728	2,278	3,354	21.52%
preweaning lethality	1	**0.0000**	**0.0000**	2.0169	8,080	32.57%	6	**6.3495e-98**	1.3034	2,611	4,049	24.67%
abnormal nervous system morphology	1	**0.0000**	**0.0000**	2.1077	6,259	25.23%	7	**2.5688e-97**	1.3800	1,868	2,736	17.65%
lethality during fetal growth through weaning	1	**0.0000**	**0.0000**	2.1916	5,683	22.91%	9	**3.9913e-96**	1.4142	1,619	2,314	15.30%
cardiovascular system phenotype	1	**0.0000**	**0.0000**	2.0191	5,626	22.68%	12	**2.1219e-82**	1.3588	1,760	2,618	16.63%
skeleton phenotype	1	**0.0000**	**0.0000**	2.0935	4,916	19.82%	14	**5.7776e-73**	1.3716	1,497	2,206	14.14%
perinatal lethality	1	**0.0000**	**0.0000**	2.3141	3,636	14.66%	15	**1.0290e-70**	1.4760	980	1,342	9.26%
abnormal skeleton morphology	1	**0.0000**	**0.0000**	2.1000	4,721	19.03%	19	**1.3892e-68**	1.3707	1,420	2,094	13.42%
abnormal cardiovascular system morphology	1	**0.0000**	**0.0000**	2.1081	4,671	18.83%	22	**4.3602e-65**	1.3645	1,390	2,059	13.13%
abnormal brain morphology	1	**0.0000**	**0.0000**	2.1813	4,221	17.02%	24	**9.8089e-64**	1.3973	1,189	1,720	11.23%
muscle phenotype	1	**0.0000**	**0.0000**	2.1167	3,461	13.95%	25	**1.5579e-61**	1.4261	1,028	1,457	9.71%
abnormal neuron morphology	1	**0.0000**	**0.0000**	2.1135	3,696	14.90%	30	**5.5625e-58**	1.3999	1,077	1,555	10.17%
neonatal lethality	1	**0.0000**	**0.0000**	2.3326	2,770	11.17%	32	**5.3319e-57**	1.4996	736	992	6.95%
abnormal cardiovascular system physiology	1	**0.0000**	**0.0000**	2.0101	3,632	14.64%	34	**1.4099e-55**	1.3813	1,118	1,636	10.56%
vision/eye phenotype	1	**0.0000**	**0.0000**	2.2196	3,859	15.56%	35	**1.6325e-54**	1.3830	1,090	1,593	10.30%
abnormal eye morphology	1	**0.0000**	**0.0000**	2.2657	3,675	14.82%	37	**1.1838e-52**	1.3911	1,020	1,482	9.64%
abnormal axial skeleton morphology	1	**0.0000**	**0.0000**	2.2751	3,411	13.75%	39	**3.9310e-51**	1.4036	943	1,358	8.91%
digestive/alimentary phenotype	1	**0.0000**	**0.0000**	2.2263	3,300	13.30%	40	**2.4669e-50**	1.3961	958	1,387	9.05%

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 heart morphology	1	**0.0000**	**0.0000**	2.1154	3,401	13.71%	45	**8.8750e-49**	1.3771	1,007	1,478	9.51%
postnatal lethality	1	**0.0000**	**0.0000**	2.1099	3,290	13.26%	47	**1.5822e-48**	1.3906	946	1,375	8.94%

The test set of 24,805 genomic regions picked 10,585 (49%) 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].