Job Description

Region-Gene Association Graphs

What do these graphs illustrate?

Number of associated genes per region

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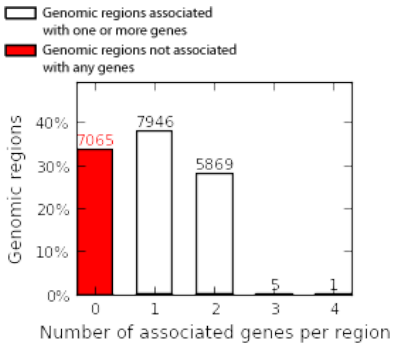
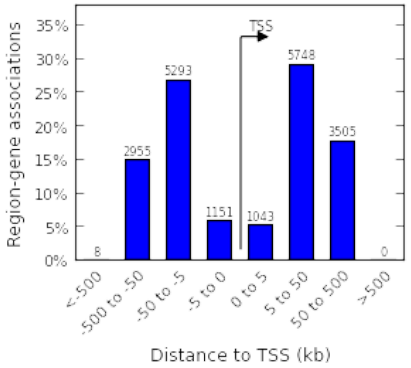


Binned by orientation and distance to TSS

Download as PDF.



Binned by absolute distance to TSS

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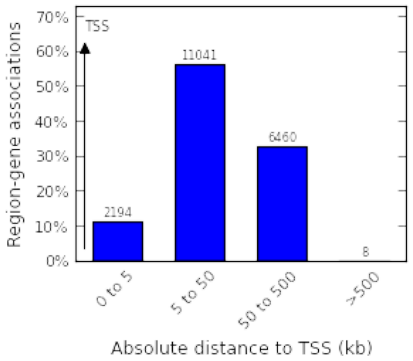

Global Controls

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
skin development	117	**3.5355e-51**	**3.9555e-49**	2.2042	456	2.18%	245	**2.6325e-10**	1.4902	162	246	1.71%
tube formation	210	**2.5797e-32**	**1.6080e-30**	2.0208	347	1.66%	307	**9.6779e-9**	1.5497	113	165	1.20%
embryonic limb morphogenesis	234	**3.5163e-30**	**1.9670e-28**	2.0205	323	1.55%	338	**2.8346e-8**	1.5714	100	144	1.06%
gland morphogenesis	244	**2.2338e-29**	**1.1984e-27**	2.0307	310	1.48%	350	**5.9832e-8**	1.5983	89	126	0.94%
hair cycle	265	**3.7487e-27**	**1.8517e-25**	2.2357	228	1.09%	432	**1.2715e-6**	1.6163	70	98	0.74%
odontogenesis	266	**3.7995e-27**	**1.8698e-25**	2.1305	254	1.22%	494	**6.3188e-6**	1.5584	73	106	0.77%
odontogenesis of dentin-containing tooth	267	**7.6039e-27**	**3.7279e-25**	2.3054	211	1.01%	551	**3.3132e-5**	1.6040	56	79	0.59%
cranial skeletal system development	281	**1.8479e-25**	**8.6084e-24**	2.4833	172	0.82%	620	**1.6814e-4**	1.6114	47	66	0.50%
somatic stem cell population maintenance	288	**6.9481e-25**	**3.1580e-23**	2.6611	148	0.71%	511	**1.0952e-5**	1.8010	39	49	0.41%
hair cycle process	297	**1.4597e-24**	**6.4336e-23**	2.2009	212	1.02%	438	**1.5526e-6**	1.6457	64	88	0.68%
hair follicle development	307	**3.8710e-24**	**1.6505e-22**	2.2109	206	0.99%	492	**6.2440e-6**	1.6239	61	85	0.65%

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
canonical Wnt signaling pathway	310	**4.5065e-24**	**1.9029e-22**	2.1574	217	1.04%	520	**1.3583e-5**	1.5721	66	95	0.70%
mesoderm development	318	**1.3298e-23**	**5.4741e-22**	2.0670	235	1.13%	356	**8.5380e-8**	1.6309	80	111	0.85%
skin epidermis development	321	**1.7286e-23**	**7.0492e-22**	2.1819	206	0.99%	532	**2.1533e-5**	1.5866	61	87	0.65%
non-canonical Wnt signaling pathway	359	**8.1133e-21**	**2.9583e-19**	2.9309	104	0.50%	938	**4.1173e-3**	1.6810	26	35	0.27%
embryonic skeletal system morphogenesis	364	**2.0555e-20**	**7.3919e-19**	2.1348	186	0.89%	1,138	**1.1970e-2**	1.3577	60	100	0.63%
keratinocyte differentiation	401	**6.8715e-19**	**2.2431e-17**	2.2360	154	0.74%	1,459	**4.6046e-2**	1.2843	63	111	0.67%
positive regulation of mesenchymal cell proliferation	413	**1.3606e-18**	**4.3123e-17**	2.3970	131	0.63%	465	**3.2924e-6**	1.9570	32	37	0.34%
embryonic hindlimb morphogenesis	419	**3.8616e-18**	**1.2064e-16**	2.4837	119	0.57%	1,016	**6.4749e-3**	1.6638	25	34	0.26%
regulation of mesenchymal cell proliferation	422	**5.2678e-18**	**1.6340e-16**	2.2509	144	0.69%	421	**8.9362e-7**	1.9108	38	45	0.40%

The test set of 20,886 genomic regions picked 9,455 (44%) 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 (5 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
actin filament bundle	72	**4.6695e-13**	**1.0986e-11**	2.0033	132	0.63%	143	**2.3533e-2**	1.3949	45	73	0.48%
desmosome	116	**8.0699e-8**	**1.1785e-6**	2.2624	54	0.26%	87	**8.4850e-4**	1.8587	23	28	0.24%
laminin complex	184	**9.1010e-5**	**8.3788e-4**	2.7912	19	0.09%	137	**1.7958e-2**	2.2628	8	8	0.08%
Golgi cis cisterna	236	**6.1781e-4**	**4.4346e-3**	2.8357	14	0.07%	137	**1.7958e-2**	2.2628	8	8	0.08%
growth cone membrane	289	**3.1616e-3**	**1.8532e-2**	2.1601	17	0.08%	156	**3.5702e-2**	2.2628	7	7	0.07%

The test set of 20,886 genomic regions picked 9,455 (44%) 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 (3 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	44	**3.5313e-17**	**3.3154e-15**	2.6284	101	0.48%	110	**2.7639e-2**	1.6078	27	38	0.29%

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
I-SMAD binding	143	**1.0660e-5**	**3.0796e-4**	2.3563	33	0.16%	80	**6.4624e-3**	2.2628	11	11	0.12%
neuropilin binding	186	**8.5861e-5**	**1.9069e-3**	2.2009	30	0.14%	101	**1.7408e-2**	2.0888	12	13	0.13%

The test set of 20,886 genomic regions picked 9,455 (44%) 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 nail	12	**3.1718e-34**	**1.7442e-31**	2.0989	336	1.61%	105	**1.8855e-3**	1.3277	115	196	1.22%
Cleft lip	18	**4.8097e-31**	**1.7633e-28**	2.3108	245	1.17%	134	**3.6532e-3**	1.4400	63	99	0.67%
Aplasia/Hypoplasia of the eyebrow	22	**8.3668e-30**	**2.5097e-27**	2.7557	169	0.81%	219	**1.7735e-2**	1.4457	46	72	0.49%
Abnormal number of teeth	25	**4.5672e-29**	**1.2056e-26**	2.1920	256	1.23%	141	**4.3276e-3**	1.4169	67	107	0.71%
Cleft upper lip	35	**1.2807e-26**	**2.4146e-24**	2.2276	225	1.08%	155	**5.9888e-3**	1.4356	59	93	0.62%
Abnormality of the eyelashes	36	**1.3291e-26**	**2.4364e-24**	2.3380	203	0.97%	109	**2.0755e-3**	1.4563	65	101	0.69%
Aplasia/Hypoplasia of the nails	39	**2.9555e-26**	**5.0009e-24**	2.5516	169	0.81%	165	**7.1203e-3**	1.4784	49	75	0.52%
Reduced number of teeth	49	**7.1761e-24**	**9.6643e-22**	2.1942	207	0.99%	226	**1.9926e-2**	1.3815	58	95	0.61%
Sparse or absent eyelashes	51	**2.4536e-23**	**3.1747e-21**	2.8953	120	0.57%	211	**1.5916e-2**	1.5557	33	48	0.35%
Anonychia	58	**1.5548e-21**	**1.7690e-19**	3.7726	76	0.36%	171	**8.5958e-3**	1.9966	15	17	0.16%
Finger syndactyly	65	**1.3284e-20**	**1.3486e-18**	2.6445	122	0.58%	9	**1.1746e-6**	2.0365	36	40	0.38%
Nail dysplasia	81	**3.7252e-18**	**3.0349e-16**	2.1215	166	0.79%	302	**4.0534e-2**	1.3528	55	92	0.58%
Abnormality of the plantar skin of foot	95	**6.0902e-17**	**4.2305e-15**	2.5247	107	0.51%	93	**1.6068e-3**	1.6536	38	52	0.40%
Plantar hyperkeratosis	97	**7.2613e-17**	**4.9399e-15**	3.1214	75	0.36%	246	**2.2752e-2**	1.6457	24	33	0.25%
Hypodontia	100	**1.0258e-16**	**6.7690e-15**	2.2326	135	0.65%	312	**4.5947e-2**	1.4331	38	60	0.40%
Abnormality of hair texture	133	**3.8755e-14**	**1.9229e-12**	2.0227	141	0.68%	139	**4.2749e-3**	1.4512	59	92	0.62%
Abnormality of epidermal morphology	139	**9.3992e-14**	**4.4622e-12**	2.5868	81	0.39%	314	**4.6472e-2**	1.5482	26	38	0.27%
Abnormal blistering of the skin	156	**9.2997e-13**	**3.9339e-11**	4.0533	39	0.19%	297	**3.9322e-2**	1.9396	12	14	0.13%
Cutaneous syndactyly	197	**2.8941e-11**	**9.6944e-10**	2.3409	78	0.37%	17	**2.8645e-5**	2.1012	26	28	0.27%
Fragile nails	198	**3.1876e-11**	**1.0624e-9**	3.3935	42	0.20%	142	**4.4170e-3**	2.1120	14	15	0.15%

The test set of 20,886 genomic regions picked 9,455 (44%) 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 vibrissa morphology	112	**9.2927e-24**	**7.6084e-22**	2.2036	204	0.98%	256	**6.1663e-7**	1.6435	69	95	0.73%
abnormal cardiac outflow tract development	127	**3.6388e-22**	**2.6274e-20**	2.0047	237	1.13%	213	**8.9432e-8**	1.6191	83	116	0.88%
abnormal sphenoid bone morphology	139	**2.2335e-21**	**1.4735e-19**	2.1928	184	0.88%	168	**6.5612e-9**	1.8162	61	76	0.65%
abnormal tongue morphology	142	**5.2565e-21**	**3.3945e-19**	2.1295	193	0.92%	419	**3.5544e-5**	1.5685	61	88	0.65%
abnormal epidermis stratum spinosum morphology	165	**1.4210e-19**	**7.8972e-18**	2.6110	118	0.56%	1,182	**1.5900e-2**	1.4435	37	58	0.39%
abnormal hair shaft morphology	178	**5.7720e-19**	**2.9735e-17**	2.3610	138	0.66%	606	**5.9133e-4**	1.5666	45	65	0.48%
abnormal epidermis stratum basale morphology	198	**2.5862e-17**	**1.1977e-15**	2.8083	91	0.44%	1,292	**2.2070e-2**	1.5517	24	35	0.25%
abnormal merocrine gland morphology	200	**3.0943e-17**	**1.4187e-15**	2.0319	174	0.83%	281	**1.1339e-6**	1.7124	56	74	0.59%
abnormal basicranium morphology	206	**5.1547e-17**	**2.2946e-15**	2.1129	156	0.75%	259	**6.7392e-7**	1.7456	54	70	0.57%
abnormal frontal bone morphology	221	**4.9979e-16**	**2.0738e-14**	2.0344	160	0.77%	391	**2.1212e-5**	1.6881	47	63	0.50%
abnormal epidermis stratum granulosum morphology	222	**5.2441e-16**	**2.1662e-14**	2.2625	125	0.60%	1,220	**1.7223e-2**	1.4234	39	62	0.41%
abnormal tooth development	223	**5.3293e-16**	**2.1915e-14**	2.1110	146	0.70%	892	**4.9023e-3**	1.4743	43	66	0.45%
eyelids open at birth	224	**6.5007e-16**	**2.6612e-14**	2.1117	145	0.69%	388	**2.0636e-5**	1.7505	41	53	0.43%
abnormal midface morphology	232	**2.8103e-15**	**1.1108e-13**	3.9015	50	0.24%	1,360	**2.6061e-2**	2.0365	9	10	0.10%
abnormal hair follicle orientation	233	**2.8687e-15**	**1.1290e-13**	2.9275	74	0.35%	1,260	**2.0580e-2**	1.8385	13	16	0.14%
abnormal keratinocyte morphology	234	**2.9348e-15**	**1.1501e-13**	2.3992	105	0.50%	752	**2.0697e-3**	1.6028	34	48	0.36%
abnormal basisphenoid bone morphology	246	**1.7587e-14**	**6.5557e-13**	2.3091	107	0.51%	254	**5.5474e-7**	1.9471	37	43	0.39%
abnormal nasal septum morphology	265	**7.4468e-14**	**2.5769e-12**	2.4013	94	0.45%	297	**1.7198e-6**	2.0042	31	35	0.33%
epidermis stratum spinosum hyperplasia	266	**8.9135e-14**	**3.0728e-12**	2.5720	82	0.39%	1,400	**2.7643e-2**	1.4902	27	41	0.29%
abnormal keratinocyte physiology	270	**1.0351e-13**	**3.5156e-12**	2.1236	121	0.58%	1,102	**1.3031e-2**	1.4367	40	63	0.42%

The test set of 20,886 genomic regions picked 9,455 (44%) 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 epidermis stratum basale morphology	106	**7.3426e-35**	**6.6326e-33**	3.0588	169	0.81%	977	**1.3292e-3**	1.5463	41	60	0.43%
curly tail	160	**5.2672e-28**	**3.1521e-26**	2.6337	171	0.82%	906	**8.3646e-4**	1.5307	46	68	0.49%
abnormal epidermis stratum corneum morphology	171	**6.2889e-27**	**3.5214e-25**	2.0355	281	1.35%	690	**1.2073e-4**	1.3734	105	173	1.11%
abnormal ectoderm morphology	179	**2.7606e-26**	**1.4767e-24**	2.7650	147	0.70%	542	**1.6859e-5**	1.8103	36	45	0.38%
blistering	197	**4.3473e-25**	**2.1130e-23**	3.3876	103	0.49%	866	**5.8924e-4**	1.7828	26	33	0.27%
abnormal vibrissa morphology	199	**4.8834e-25**	**2.3497e-23**	2.0483	256	1.23%	314	**4.6668e-8**	1.6163	85	119	0.90%
abnormal apical ectodermal ridge morphology	211	**3.1159e-24**	**1.4139e-22**	2.8122	131	0.63%	565	**2.3039e-5**	1.8567	32	39	0.34%
abnormal tongue morphology	214	**6.5298e-24**	**2.9216e-22**	2.0208	252	1.21%	439	**1.6496e-6**	1.5463	82	120	0.87%
thick epidermis	230	**1.2159e-22**	**5.0617e-21**	2.0547	228	1.09%	677	**1.0459e-4**	1.4574	76	118	0.80%
abnormal epidermis stratum spinosum morphology	231	**1.2962e-22**	**5.3728e-21**	2.4288	158	0.76%	968	**1.2697e-3**	1.4795	51	78	0.54%
abnormal sphenoid bone morphology	246	**1.8676e-21**	**7.2692e-20**	2.0361	220	1.05%	260	**5.6636e-9**	1.7143	75	99	0.79%
decreased intestinal adenoma incidence	253	**5.8296e-21**	**2.2063e-19**	5.6889	48	0.23%	1,697	**1.8551e-2**	2.2628	7	7	0.07%
abnormal basicranium morphology	255	**6.6410e-21**	**2.4936e-19**	2.0885	201	0.96%	366	**2.1703e-7**	1.6610	69	94	0.73%
impaired skin barrier function	264	**1.6921e-20**	**6.1370e-19**	2.2203	171	0.82%	920	**9.3715e-4**	1.4512	59	92	0.62%
abnormal keratinocyte morphology	267	**1.8422e-20**	**6.6065e-19**	2.2009	174	0.83%	632	**6.9824e-5**	1.5428	60	88	0.63%
abnormal dendritic cell number	271	**2.1323e-20**	**7.5338e-19**	2.0572	203	0.97%	657	**8.3913e-5**	1.4534	79	123	0.84%
abnormal hair shaft morphology	277	**3.2789e-20**	**1.1334e-18**	2.1877	174	0.83%	755	**2.4211e-4**	1.5085	58	87	0.61%
decreased organ/body region tumor incidence	280	**3.7680e-20**	**1.2885e-18**	2.5194	130	0.62%	1,203	**4.0506e-3**	1.5557	33	48	0.35%
abnormal substantia nigra morphology	283	**6.1182e-20**	**2.0700e-18**	3.2254	86	0.41%	1,492	**1.0271e-2**	1.6762	20	27	0.21%
oligodactyly	285	**8.3295e-20**	**2.7984e-18**	2.1503	177	0.85%	382	**2.7015e-7**	1.7529	55	71	0.58%

The test set of 20,886 genomic regions picked 9,455 (44%) 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].