

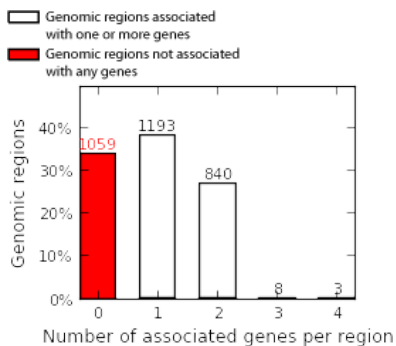
⊕ Job Description

⊕ Region-Gene Association Graphs

What do these graphs illustrate?

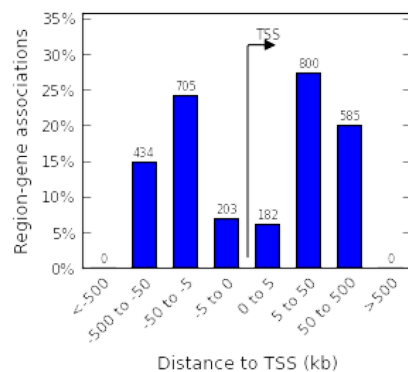
Number of associated genes per region

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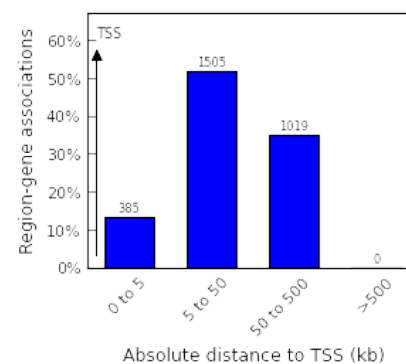
Binned by orientation and distance to TSS

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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:

Shown top rows in this table:

Term annotation count: Min:  Max:

Visualize this table:

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
<a href="#">pattern specification process</a>	23	2.2839e-32	1.2998e-29	2.7903	176	5.67%	48	9.5937e-11	2.1198	98	440	4.36%
<a href="#">regulation of protein binding</a>	31	3.9155e-30	1.6534e-27	3.9113	103	3.32%	371	1.3204e-3	1.9227	40	198	1.78%
<a href="#">regulation of binding</a>	45	7.0139e-27	2.0403e-24	2.9083	136	4.38%	261	7.2776e-5	1.8050	66	348	2.94%
<a href="#">central nervous system development</a>	47	2.9169e-26	8.1238e-24	2.0008	272	8.77%	128	8.0532e-8	1.6138	156	920	6.94%
<a href="#">brain development</a>	53	2.8999e-25	7.1622e-23	2.1025	233	7.51%	192	4.4645e-6	1.6035	124	736	5.52%
<a href="#">head development</a>	64	1.0367e-23	2.1204e-21	2.0254	238	7.67%	205	7.2470e-6	1.5720	129	781	5.74%
<a href="#">Ras protein signal transduction</a>	66	2.0442e-23	4.0543e-21	4.1349	74	2.38%	750	3.9994e-2	1.8163	25	131	1.11%
<a href="#">small GTPase mediated signal transduction</a>	113	3.4680e-18	4.0174e-16	2.8415	93	3.00%	681	2.8701e-2	1.5989	42	250	1.87%
<a href="#">positive regulation of intracellular transport</a>	134	8.6727e-17	8.4720e-15	2.5838	100	3.22%	585	1.6448e-2	1.5810	50	301	2.22%
<a href="#">regulation of cell morphogenesis</a>	140	1.7814e-16	1.6656e-14	2.1938	135	4.35%	417	2.6842e-3	1.5678	71	431	3.16%
<a href="#">gland development</a>	141	1.8120e-16	1.6822e-14	2.1111	147	4.74%	113	2.4797e-8	1.9364	94	462	4.18%

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
<a href="#">defense response to virus</a>	147	<b>9.4252e-16</b>	<b>8.3929e-14</b>	3.6380	56	1.80%	504	<b>8.7262e-3</b>	1.8203	35	183	1.56%
<a href="#">metencephalon development</a>	151	<b>3.3094e-15</b>	<b>2.8689e-13</b>	3.3490	60	1.93%	782	<b>4.7604e-2</b>	1.8128	24	126	1.07%
<a href="#">regulation of cellular protein localization</a>	156	<b>4.2193e-15</b>	<b>3.5405e-13</b>	2.0339	146	4.71%	495	<b>7.2730e-3</b>	1.4450	87	573	3.87%
<a href="#">actin cytoskeleton organization</a>	163	<b>6.6548e-15</b>	<b>5.3443e-13</b>	2.1692	124	4.00%	589	<b>1.7238e-2</b>	1.4835	65	417	2.89%
<a href="#">protein heterotetramerization</a>	166	<b>7.3753e-15</b>	<b>5.8158e-13</b>	7.9822	25	0.81%	155	<b>4.9257e-7</b>	4.2299	20	45	0.89%
<a href="#">hindbrain development</a>	178	<b>1.8311e-14</b>	<b>1.3466e-12</b>	2.8239	73	2.35%	443	<b>4.4376e-3</b>	1.9147	34	169	1.51%
<a href="#">muscle structure development</a>	188	<b>5.3888e-14</b>	<b>3.7521e-12</b>	2.0113	138	4.45%	127	<b>8.0596e-8</b>	1.8914	94	473	4.18%
<a href="#">response to virus</a>	189	<b>5.5440e-14</b>	<b>3.8397e-12</b>	2.8832	68	2.19%	451	<b>4.8427e-3</b>	1.7236	46	254	2.05%
<a href="#">adult walking behavior</a>	190	<b>5.6152e-14</b>	<b>3.8686e-12</b>	5.2353	33	1.06%	588	<b>1.6819e-2</b>	2.7856	12	41	0.53%

The test set of 3,103 genomic regions picked 2,248 (11%) 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 (8 terms)

Global controls

Table controls:  Shown top rows in this table:   Term annotation count: Min:  Max:   Visualize this table:

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
<a href="#">anchoring junction</a>	23	<b>1.2121e-18</b>	<b>8.9277e-17</b>	2.2088	152	4.90%	27	<b>5.7414e-4</b>	1.5862	87	522	3.87%
<a href="#">adherens junction</a>	24	<b>1.2430e-17</b>	<b>8.7734e-16</b>	2.1888	146	4.71%	31	<b>3.4431e-3</b>	1.5326	81	503	3.60%
<a href="#">endoplasmic reticulum lumen</a>	50	<b>5.4844e-11</b>	<b>1.8581e-9</b>	3.3789	41	1.32%	33	<b>5.7393e-3</b>	2.2031	25	108	1.11%
<a href="#">nuclear nucleosome</a>	56	<b>3.6967e-10</b>	<b>1.1182e-8</b>	7.4791	17	0.55%	48	<b>2.6663e-2</b>	2.7856	12	41	0.53%
<a href="#">nucleosome</a>	69	<b>1.0227e-6</b>	<b>2.5109e-5</b>	3.4468	22	0.71%	9	<b>5.3360e-6</b>	2.7423	34	118	1.51%
<a href="#">cell-cell adherens junction</a>	70	<b>1.0369e-6</b>	<b>2.5093e-5</b>	2.4733	37	1.19%	15	<b>6.3112e-5</b>	2.7192	28	98	1.25%
<a href="#">DNA packaging complex</a>	72	<b>7.2118e-6</b>	<b>1.6968e-4</b>	3.0419	22	0.71%	11	<b>2.5357e-5</b>	2.5682	34	126	1.51%
<a href="#">basement membrane</a>	86	<b>1.3524e-4</b>	<b>2.6640e-3</b>	2.1080	31	1.00%	26	<b>5.8999e-4</b>	2.5312	25	94	1.11%

The test set of 3,103 genomic regions picked 2,248 (11%) 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 (4 terms)

Global controls

Table controls:  Shown top rows in this table:   Term annotation count: Min:  Max:   Visualize this table:

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
<a href="#">type I interferon receptor binding</a>	13	<b>3.3247e-15</b>	<b>1.0565e-12</b>	20.5527	15	0.48%	11	<b>3.3779e-4</b>	4.2982	14	31	0.62%
<a href="#">frizzled binding</a>	48	<b>1.6529e-7</b>	<b>1.4225e-5</b>	3.8536	22	0.71%	14	<b>4.7547e-3</b>	3.5064	14	38	0.62%
<a href="#">S100 protein binding</a>	86	<b>6.5131e-5</b>	<b>3.1286e-3</b>	5.3566	9	0.29%	22	<b>2.5432e-2</b>	5.1247	7	13	0.31%
<a href="#">beta-catenin binding</a>	88	<b>7.6381e-5</b>	<b>3.5856e-3</b>	2.2841	28	0.90%	18	<b>1.3020e-2</b>	2.4983	21	80	0.93%

The test set of 3,103 genomic regions picked 2,248 (11%) 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:  Shown top rows in this table:   Term annotation count: Min:  Max:   Visualize this table:

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
<a href="#">Functional abnormality of the middle ear</a>	17	<b>1.1778e-33</b>	<b>4.5718e-31</b>	6.1359	74	2.38%	97	<b>4.0674e-2</b>	2.2325	19	81	0.85%
<a href="#">Limited elbow movement</a>	46	<b>4.9100e-11</b>	<b>7.0437e-9</b>	4.0397	33	1.06%	69	<b>2.8787e-2</b>	2.4128	18	71	0.80%
<a href="#">Sparse hair</a>	52	<b>1.4130e-10</b>	<b>1.7932e-8</b>	2.8990	49	1.58%	13	<b>3.9849e-3</b>	2.2560	32	135	1.42%
<a href="#">Abnormality of hair density</a>	54	<b>3.3501e-10</b>	<b>4.0939e-8</b>	2.8231	49	1.58%	19	<b>5.1740e-3</b>	2.1910	32	139	1.42%
<a href="#">Cleft lip</a>	59	<b>1.2060e-9</b>	<b>1.3489e-7</b>	2.8569	45	1.45%	1	<b>1.2962e-3</b>	2.7879	29	99	1.29%
<a href="#">Limitation of joint mobility</a>	63	<b>5.3272e-9</b>	<b>5.5800e-7</b>	2.8759	41	1.32%	74	<b>3.2566e-2</b>	2.0512	25	116	1.11%
<a href="#">Aplasia/Hypoplasia of the eyebrow</a>	65	<b>9.6810e-9</b>	<b>9.8285e-7</b>	3.4023	31	1.00%	45	<b>1.7114e-2</b>	2.5115	19	72	0.85%
<a href="#">Syndactyly</a>	66	<b>1.1190e-8</b>	<b>1.1189e-6</b>	2.5244	49	1.58%	17	<b>4.2162e-3</b>	2.2230	32	137	1.42%
<a href="#">Regional abnormality of skin</a>	69	<b>1.5129e-8</b>	<b>1.4469e-6</b>	2.4994	49	1.58%	47	<b>1.6571e-2</b>	2.0071	31	147	1.38%
<a href="#">Cleft upper lip</a>	73	<b>2.1284e-8</b>	<b>1.9240e-6</b>	2.7322	41	1.32%	7	<b>2.0747e-3</b>	2.6608	26	93	1.16%
<a href="#">Cleft palate</a>	75	<b>2.2795e-8</b>	<b>2.0056e-6</b>	2.1505	65	2.09%	10	<b>4.1233e-3</b>	1.9736	45	217	2.00%
<a href="#">Oral cleft</a>	76	<b>3.2068e-8</b>	<b>2.7844e-6</b>	2.0763	69	2.22%	6	<b>1.7865e-3</b>	2.0015	49	233	2.18%
<a href="#">Abnormality of the hard palate</a>	81	<b>6.3399e-8</b>	<b>5.1651e-6</b>	2.0760	66	2.13%	9	<b>3.2742e-3</b>	1.9810	46	221	2.05%
<a href="#">Aplasia/Hypoplasia affecting the eye</a>	86	<b>9.1991e-8</b>	<b>7.0587e-6</b>	2.2063	56	1.80%	23	<b>5.6627e-3</b>	2.0355	37	173	1.65%
<a href="#">Abnormality of thumb phalanx</a>	88	<b>1.2509e-7</b>	<b>9.3801e-6</b>	3.0258	31	1.00%	33	<b>1.2469e-2</b>	2.6207	19	69	0.85%
<a href="#">Clinodactyly</a>	94	<b>2.8547e-7</b>	<b>2.0041e-5</b>	2.2828	48	1.55%	65	<b>2.8012e-2</b>	1.9423	30	147	1.33%
<a href="#">Microphthalmia</a>	97	<b>3.1997e-7</b>	<b>2.1768e-5</b>	2.3725	44	1.42%	12	<b>3.7257e-3</b>	2.3050	31	128	1.38%
<a href="#">Finger syndactyly</a>	109	<b>9.1930e-7</b>	<b>5.5655e-5</b>	3.3557	23	0.74%	3	<b>2.4568e-3</b>	3.8069	16	40	0.71%
<a href="#">Triangular shaped phalanges of the hand</a>	111	<b>1.0230e-6</b>	<b>6.0820e-5</b>	2.7346	31	1.00%	58	<b>2.3789e-2</b>	2.4111	19	75	0.85%

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
<a href="#">Abnormal morphology of bones of the upper limbs</a>	112	<b>1.1005e-6</b>	<b>6.4839e-5</b>	2.1937	47	1.51%	35	<b>1.2072e-2</b>	2.0440	32	149	1.42%

The test set of 3,103 genomic regions picked 2,248 (11%) 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:  Shown top rows in this table:  Set Term annotation count: Min:  Max:  Set Visualize this table:

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
<a href="#">abnormal trachea morphology</a>	17	<b>1.3432e-31</b>	<b>7.2452e-29</b>	6.0599	70	2.26%	526	<b>3.1097e-2</b>	2.2069	16	69	0.71%
<a href="#">abnormal brain ventricular system morphology</a>	28	<b>1.3143e-19</b>	<b>4.3044e-17</b>	2.7250	108	3.48%	645	<b>4.7009e-2</b>	1.5173	44	276	1.96%
<a href="#">postnatal lethality, incomplete penetrance</a>	31	<b>5.9181e-19</b>	<b>1.7506e-16</b>	2.0694	179	5.77%	86	<b>2.1858e-5</b>	1.6602	101	579	4.49%
<a href="#">abnormal erythrocyte morphology</a>	35	<b>1.2254e-18</b>	<b>3.2106e-16</b>	2.0537	179	5.77%	329	<b>8.9542e-3</b>	1.3902	104	712	4.63%
<a href="#">abnormal brain development</a>	37	<b>4.4079e-18</b>	<b>1.0925e-15</b>	2.0357	177	5.70%	104	<b>5.2967e-5</b>	1.6237	101	592	4.49%
<a href="#">abnormal esophageal smooth muscle morphology</a>	80	<b>2.7347e-9</b>	<b>3.1347e-7</b>	14.9062	10	0.32%	258	<b>4.3216e-3</b>	9.5173	4	4	0.18%
<a href="#">abnormal renal glomerulus basement membrane morphology</a>	97	<b>5.9975e-8</b>	<b>5.6698e-6</b>	4.0934	22	0.71%	125	<b>1.4487e-4</b>	3.8584	15	37	0.67%
<a href="#">abnormal hair growth</a>	109	<b>2.4744e-7</b>	<b>2.0817e-5</b>	2.1053	58	1.87%	90	<b>3.0880e-5</b>	2.1506	47	208	2.09%
<a href="#">abnormal esophagus development</a>	122	<b>7.5993e-7</b>	<b>5.7120e-5</b>	9.4344	9	0.29%	164	<b>7.1321e-4</b>	9.5173	5	5	0.22%
<a href="#">abnormal cornea morphology</a>	126	<b>9.6236e-7</b>	<b>7.0038e-5</b>	2.1445	50	1.61%	80	<b>1.3037e-5</b>	2.3649	41	165	1.82%
<a href="#">abnormal incisor morphology</a>	129	<b>1.0342e-6</b>	<b>7.3513e-5</b>	2.5492	35	1.13%	178	<b>9.5195e-4</b>	2.5453	23	86	1.02%
<a href="#">abnormal keratinocyte morphology</a>	134	<b>1.3741e-6</b>	<b>9.4035e-5</b>	3.3836	22	0.71%	222	<b>3.1107e-3</b>	2.9742	15	48	0.67%
<a href="#">abnormal renal glomerulus basement membrane thickness</a>	139	<b>1.8537e-6</b>	<b>1.2229e-4</b>	4.3169	16	0.52%	224	<b>3.2176e-3</b>	3.9656	10	24	0.44%
<a href="#">alopecia</a>	141	<b>1.8843e-6</b>	<b>1.2254e-4</b>	2.5189	34	1.10%	102	<b>5.0241e-5</b>	2.7192	28	98	1.25%
<a href="#">abnormal eye size</a>	147	<b>2.9844e-6</b>	<b>1.8617e-4</b>	2.0245	52	1.68%	115	<b>9.2589e-5</b>	2.1800	41	179	1.82%
<a href="#">abnormal cranial suture morphology</a>	152	<b>4.0612e-6</b>	<b>2.4501e-4</b>	2.8994	25	0.81%	103	<b>5.2780e-5</b>	3.4775	19	52	0.85%
<a href="#">microphthalmia</a>	161	<b>6.1808e-6</b>	<b>3.5204e-4</b>	2.0174	49	1.58%	112	<b>8.7548e-5</b>	2.2360	39	166	1.73%
<a href="#">thick epidermis</a>	171	<b>1.1351e-5</b>	<b>6.0872e-4</b>	2.6634	26	0.84%	157	<b>5.7890e-4</b>	2.7759	21	72	0.93%
<a href="#">abnormal palatine bone horizontal plate morphology</a>	173	<b>1.2354e-5</b>	<b>6.5482e-4</b>	3.5259	17	0.55%	198	<b>2.0482e-3</b>	3.8774	11	27	0.49%

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
<a href="#">abnormal outer ear morphology</a>	175	1.4051e-5	7.3629e-4	2.2236	36	1.16%	188	1.3991e-3	2.3344	26	106	1.16%

The test set of 3,103 genomic regions picked 2,248 (11%) 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:  Shown top rows in this table:   Term annotation count: Min:  Max:   Visualize this table:

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
<a href="#">abnormal digestive system morphology</a>	18	6.6267e-30	3.5251e-27	2.0062	308	9.93%	59	1.4257e-9	1.6207	188	1,104	8.36%
<a href="#">abnormal trachea morphology</a>	19	4.0448e-29	2.0384e-26	4.9653	77	2.48%	329	9.7812e-4	2.4595	23	89	1.02%
<a href="#">abnormal mean corpuscular volume</a>	40	3.3527e-21	8.0256e-19	3.1482	94	3.03%	893	3.4596e-2	1.5539	40	245	1.78%
<a href="#">abnormal blood urea nitrogen level</a>	43	3.2717e-20	7.2852e-18	2.9968	96	3.09%	654	1.3867e-2	1.6465	41	237	1.82%
<a href="#">abnormal brain ventricular system morphology</a>	54	4.0917e-18	7.2552e-16	2.3295	132	4.25%	599	9.7321e-3	1.5130	62	390	2.76%
<a href="#">abnormal respiratory epithelium morphology</a>	59	1.7901e-17	2.9051e-15	2.6339	101	3.25%	517	6.0016e-3	1.6861	45	254	2.00%
<a href="#">abnormal tail morphology</a>	85	2.0432e-14	2.3016e-12	2.1339	124	4.00%	138	1.3824e-5	1.7975	78	413	3.47%
<a href="#">curly tail</a>	88	4.8934e-14	5.3243e-12	4.2504	41	1.32%	574	8.7165e-3	2.3793	17	68	0.76%
<a href="#">increased regulatory T cell number</a>	92	7.4708e-14	7.7753e-12	4.4985	38	1.22%	672	1.5378e-2	2.3072	16	66	0.71%
<a href="#">abnormal brainstem morphology</a>	101	4.0140e-13	3.8053e-11	2.3760	89	2.87%	135	1.1412e-5	2.0844	53	242	2.36%
<a href="#">abnormal midbrain morphology</a>	112	2.0878e-12	1.7849e-10	2.6795	67	2.16%	244	1.9432e-4	2.1823	36	157	1.60%
<a href="#">abnormal regulatory T cell number</a>	113	2.2854e-12	1.9365e-10	2.9883	56	1.80%	427	2.6466e-3	2.0071	31	147	1.38%
<a href="#">abnormal regulatory T cell morphology</a>	121	6.1611e-12	4.8754e-10	2.9108	56	1.80%	461	3.6095e-3	1.9669	31	150	1.38%
<a href="#">hair follicle degeneration</a>	122	6.1648e-12	4.8384e-10	6.1226	24	0.77%	148	2.0863e-5	4.5946	14	29	0.62%
<a href="#">decreased bone marrow cell number</a>	134	2.5847e-11	1.8469e-9	2.7704	57	1.84%	622	1.0812e-2	1.8421	30	155	1.33%
<a href="#">abnormal circulating amino acid level</a>	136	4.3498e-11	3.0624e-9	2.3833	73	2.35%	937	3.5475e-2	1.5475	40	246	1.78%
<a href="#">abnormal amino acid level</a>	144	1.3331e-10	8.8645e-9	2.1738	84	2.71%	952	3.7798e-2	1.4784	48	309	2.14%
<a href="#">increased cell proliferation</a>	151	1.8315e-10	1.1614e-8	2.2201	79	2.55%	334	1.0599e-3	1.8057	48	253	2.14%
<a href="#">abnormal hair growth</a>	153	2.0547e-10	1.2859e-8	2.1103	88	2.84%	105	8.8795e-7	2.0528	66	306	2.94%
<a href="#">small hair follicles</a>	168	7.3622e-10	4.1960e-8	7.7448	16	0.52%	774	2.3534e-2	4.0789	6	14	0.27%

The test set of 3,103 genomic regions picked 2,248 (11%) 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].