

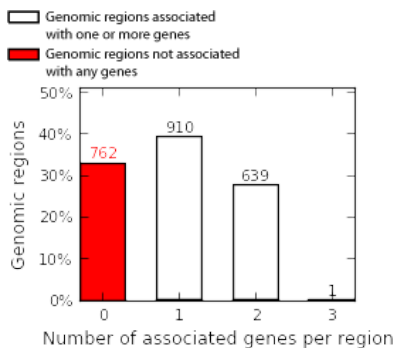
⊕ Job Description

⊕ Region-Gene Association Graphs

What do these graphs illustrate?

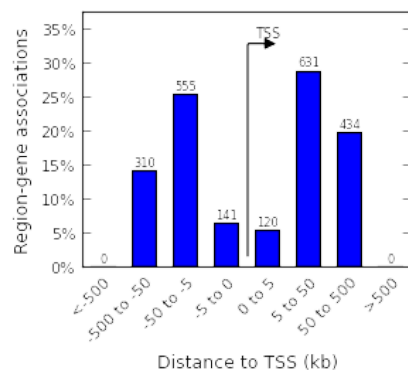
Number of associated genes per region

Download as PDF.



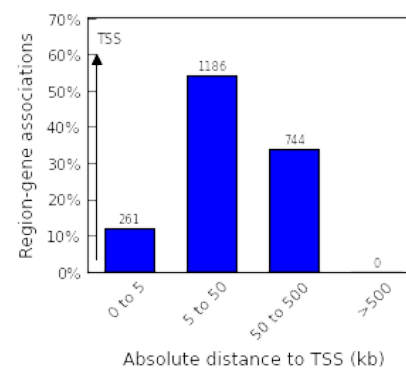
Binned by orientation and distance to TSS

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

Term annotation count: Min: 1  Max: Inf

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 |
|---|------------|-------------------|-----------------|-----------------------|----------------------------|---------------------------|------------|-----------------|-----------------------|--------------------------|-------------------|-------------------------|
| <a href="#">defense response to virus</a>                         | 50         | 6.3478e-20        | 1.6618e-17      | 4.7083                | 54                         | 2.34%                     | 231        | 1.9948e-3       | 2.0991                | 33                       | 183               | 1.80%                   |
| <a href="#">response to virus</a>                                 | 64         | 1.9447e-18        | 3.9775e-16      | 3.6989                | 65                         | 2.81%                     | 201        | 8.5003e-4       | 1.9706                | 43                       | 254               | 2.34%                   |
| <a href="#">negative regulation of lipid biosynthetic process</a> | 82         | 3.6241e-16        | 5.7853e-14      | 5.8598                | 35                         | 1.51%                     | 376        | 1.5700e-2       | 2.7161                | 14                       | 60                | 0.76%                   |
| <a href="#">liver development</a>                                 | 87         | 6.6572e-16        | 1.0016e-13      | 3.7143                | 55                         | 2.38%                     | 461        | 2.8844e-2       | 1.9674                | 24                       | 142               | 1.31%                   |
| <a href="#">hepaticobiliary system development</a>                | 92         | 1.7900e-15        | 2.5469e-13      | 3.6250                | 55                         | 2.38%                     | 494        | 3.6248e-2       | 1.9267                | 24                       | 145               | 1.31%                   |
| <a href="#">adult walking behavior</a>                            | 96         | 5.0391e-15        | 6.8710e-13      | 6.3877                | 30                         | 1.30%                     | 534        | 4.9346e-2       | 2.8391                | 10                       | 41                | 0.54%                   |
| <a href="#">regulation of lipid biosynthetic process</a>          | 97         | 6.1487e-15        | 8.2975e-13      | 3.7329                | 51                         | 2.21%                     | 230        | 1.9070e-3       | 2.2634                | 28                       | 144               | 1.52%                   |
| <a href="#">immune effector process</a>                           | 101        | 1.4329e-14        | 1.8571e-12      | 2.6208                | 83                         | 3.59%                     | 321        | 7.2370e-3       | 1.6190                | 58                       | 417               | 3.16%                   |
| <a href="#">gland development</a>                                 | 116        | 6.5626e-14        | 7.4056e-12      | 2.1780                | 113                        | 4.89%                     | 114        | 2.9502e-5       | 1.8393                | 73                       | 462               | 3.97%                   |
| <a href="#">regulation of autophagy</a>                           | 126        | 3.4782e-13        | 3.6134e-11      | 3.0576                | 58                         | 2.51%                     | 375        | 1.5728e-2       | 1.8238                | 34                       | 217               | 1.85%                   |
| <a href="#">response to other organism</a>                        | 134        | 8.2929e-13        | 8.1011e-11      | 2.0455                | 119                        | 5.15%                     | 522        | 4.4609e-2       | 1.3498                | 93                       | 802               | 5.06%                   |

| 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="#">striated muscle tissue development</a>                                     | 149        | <b>3.2438e-12</b> | <b>2.8498e-10</b> | 2.3707                | 82                         | 3.55%                     | 168        | <b>4.2732e-4</b> | 1.9089                | 51                       | 311               | 2.77%                   |
| <a href="#">natural killer cell activation involved in immune response</a>             | 153        | <b>4.9574e-12</b> | <b>4.2414e-10</b> | 13.8653               | 14                         | 0.61%                     | 174        | <b>4.9830e-4</b> | 4.0899                | 13                       | 37                | 0.71%                   |
| <a href="#">regulation of lipid metabolic process</a>                                  | 161        | <b>1.2273e-11</b> | <b>9.9786e-10</b> | 2.4652                | 72                         | 3.11%                     | 316        | <b>6.4589e-3</b> | 1.7519                | 45                       | 299               | 2.45%                   |
| <a href="#">muscle structure development</a>   | 163        | <b>1.4794e-11</b> | <b>1.1880e-9</b>  | 2.0539                | 105                        | 4.54%                     | 111        | <b>1.8046e-5</b> | 1.8457                | 75                       | 473               | 4.08%                   |
| <a href="#">positive regulation of peptidyl-serine phosphorylation of STAT protein</a> | 166        | <b>1.8209e-11</b> | <b>1.4359e-9</b>  | 12.5467               | 14                         | 0.61%                     | 159        | <b>2.6610e-4</b> | 4.3236                | 13                       | 35                | 0.71%                   |
| <a href="#">muscle tissue development</a>  | 186        | <b>8.8044e-11</b> | <b>6.1962e-9</b>  | 2.2120                | 82                         | 3.55%                     | 223        | <b>1.5694e-3</b> | 1.8044                | 51                       | 329               | 2.77%                   |
| <a href="#">regulation of peptidyl-serine phosphorylation of STAT protein</a>          | 188        | <b>1.0504e-10</b> | <b>7.3139e-9</b>  | 10.9525               | 14                         | 0.61%                     | 174        | <b>4.9830e-4</b> | 4.0899                | 13                       | 37                | 0.71%                   |
| <a href="#">muscle cell differentiation</a>  | 190        | <b>1.1610e-10</b> | <b>7.9989e-9</b>  | 2.3244                | 73                         | 3.16%                     | 206        | <b>1.0305e-3</b> | 1.9055                | 46                       | 281               | 2.50%                   |
| <a href="#">developmental growth</a>   | 197        | <b>1.5658e-10</b> | <b>1.0404e-8</b>  | 2.0672                | 93                         | 4.02%                     | 48         | <b>2.2512e-7</b> | 2.1033                | 73                       | 404               | 3.97%                   |

The test set of 2,312 genomic regions picked 1,838 (9%) 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 (3 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="#">endoplasmic reticulum lumen</a> | 19         | <b>3.8820e-11</b> | <b>3.4611e-9</b> | 3.8713                | 35                         | 1.51%                     | 13         | <b>4.8844e-3</b> | 2.4790                | 23                       | 108               | 1.25%                   |
| <a href="#">cell-cell adherens junction</a> | 59         | <b>9.6164e-5</b>  | <b>2.7610e-3</b> | 2.3327                | 26                         | 1.12%                     | 20         | <b>1.8338e-2</b> | 2.3756                | 20                       | 98                | 1.09%                   |
| <a href="#">dynein complex</a>              | 60         | <b>9.6318e-5</b>  | <b>2.7194e-3</b> | 2.9761                | 17                         | 0.74%                     | 32         | <b>3.9765e-2</b> | 2.7022                | 13                       | 56                | 0.71%                   |

The test set of 2,312 genomic regions picked 1,838 (9%) 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 (1 term)

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> | 6          | <b>1.3170e-15</b> | <b>9.0676e-13</b> | 25.7455               | 14                         | 0.61%                     | 3          | <b>8.6258e-4</b> | 4.8814                | 13                       | 31                | 0.71%                   |

The test set of 2,312 genomic regions picked 1,838 (9%) 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 (1 term)**

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 |
|------------------|------------|-------------------|------------------|-----------------------|----------------------------|---------------------------|------------|------------------|-----------------------|--------------------------|-------------------|-------------------------|
| <b>Cleft lip</b> | 85         | <b>2.1187e-4</b>  | <b>1.6449e-2</b> | 2.2154                | 26                         | 1.12%                     | 1          | <b>1.5987e-2</b> | 2.8219                | 24                       | 99                | 1.31%                   |

The test set of 2,312 genomic regions picked 1,838 (9%) 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:   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 |
|---|------------|-------------------|------------------|-----------------------|----------------------------|---------------------------|------------|------------------|-----------------------|--------------------------|-------------------|-------------------------|
| <b>decreased triglyceride level</b>                           | 71         | <b>4.2967e-6</b>  | <b>5.5494e-4</b> | 2.0607                | 48                         | 2.08%                     | 117        | <b>3.0291e-3</b> | 1.9023                | 42                       | 257               | 2.29%                   |
| <b>dilated capillary</b>                                      | 113        | <b>5.2157e-5</b>  | <b>4.2326e-3</b> | 6.3357                | 8                          | 0.35%                     | 95         | <b>1.7719e-3</b> | 6.7902                | 7                        | 12                | 0.38%                   |
| <b>abnormal renal glomerulus basement membrane morphology</b> | 121        | <b>7.5670e-5</b>  | <b>5.7346e-3</b> | 3.4961                | 14                         | 0.61%                     | 77         | <b>7.8882e-4</b> | 4.0899                | 13                       | 37                | 0.71%                   |
| <b>increased energy expenditure</b>                           | 134        | <b>9.8587e-5</b>  | <b>6.7466e-3</b> | 2.1767                | 30                         | 1.30%                     | 159        | <b>7.7384e-3</b> | 2.2046                | 25                       | 132               | 1.36%                   |
| <b>abnormal vitreous body morphology</b>                      | 138        | <b>1.0392e-4</b>  | <b>6.9052e-3</b> | 2.5321                | 22                         | 0.95%                     | 47         | <b>7.6026e-5</b> | 3.3951                | 21                       | 72                | 1.14%                   |
| <b>decreased heart rate</b>                                   | 140        | <b>1.1955e-4</b>  | <b>7.8307e-3</b> | 2.1851                | 29                         | 1.25%                     | 121        | <b>3.3115e-3</b> | 2.4562                | 23                       | 109               | 1.25%                   |
| <b>abnormal cornea morphology</b>                             | 142        | <b>1.2133e-4</b>  | <b>7.8355e-3</b> | 2.0147                | 35                         | 1.51%                     | 84         | <b>1.0998e-3</b> | 2.2575                | 32                       | 165               | 1.74%                   |
| <b>abnormal cranial suture morphology</b>                     | 145        | <b>1.2788e-4</b>  | <b>8.0875e-3</b> | 2.8018                | 18                         | 0.78%                     | 48         | <b>1.5940e-4</b> | 3.8055                | 17                       | 52                | 0.92%                   |
| <b>abnormal Harderian gland morphology</b>                    | 149        | <b>1.4167e-4</b>  | <b>8.7191e-3</b> | 4.8236                | 9                          | 0.39%                     | 115        | <b>2.9353e-3</b> | 6.2679                | 7                        | 13                | 0.38%                   |
| <b>cataract</b>   | 172        | <b>2.4368e-4</b>  | <b>1.2992e-2</b> | 2.0916                | 29                         | 1.25%                     | 175        | <b>1.0164e-2</b> | 2.1556                | 25                       | 135               | 1.36%                   |
| <b>increased mean systemic arterial blood pressure</b>        | 182        | <b>3.2917e-4</b>  | <b>1.6585e-2</b> | 3.0218                | 14                         | 0.61%                     | 133        | <b>4.6648e-3</b> | 3.5817                | 12                       | 39                | 0.65%                   |
| <b>abnormal aortic valve morphology</b>                       | 192        | <b>3.8090e-4</b>  | <b>1.8192e-2</b> | 2.7354                | 16                         | 0.69%                     | 256        | <b>2.2398e-2</b> | 2.7514                | 13                       | 55                | 0.71%                   |
| <b>abnormal bronchiole morphology</b>                         | 196        | <b>4.0788e-4</b>  | <b>1.9083e-2</b> | 3.5165                | 11                         | 0.48%                     | 172        | <b>9.3771e-3</b> | 3.7550                | 10                       | 31                | 0.54%                   |
| <b>cachexia</b>   | 213        | <b>5.4542e-4</b>  | <b>2.3481e-2</b> | 2.1506                | 24                         | 1.04%                     | 180        | <b>1.0439e-2</b> | 2.3281                | 21                       | 105               | 1.14%                   |
| <b>thick epidermis</b>  | 215        | <b>5.4711e-4</b>  | <b>2.3335e-2</b> | 2.4748                | 18                         | 0.78%                     | 107        | <b>2.3473e-3</b> | 2.9101                | 18                       | 72                | 0.98%                   |
| <b>abnormal mammary gland lobule morphology</b>               | 227        | <b>6.1783e-4</b>  | <b>2.4958e-2</b> | 3.5981                | 10                         | 0.43%                     | 224        | <b>1.8089e-2</b> | 4.0488                | 8                        | 23                | 0.44%                   |

| 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 |
|-------------------------------|------------|-------------------|-----------------|-----------------------|----------------------------|---------------------------|------------|-----------------|-----------------------|--------------------------|-------------------|-------------------------|
| increased fatty acid level    | 229        | 6.2289e-4         | 2.4943e-2       | 2.2148                | 22                         | 0.95%                     | 264        | 2.2044e-2       | 2.1963                | 20                       | 106               | 1.09%                   |
| abnormal vein development     | 235        | 6.5484e-4         | 2.5553e-2       | 2.5116                | 17                         | 0.74%                     | 204        | 1.3946e-2       | 2.8097                | 14                       | 58                | 0.76%                   |
| decreased ventral retina size | 237        | 6.6314e-4         | 2.5658e-2       | 10.4300               | 4                          | 0.17%                     | 257        | 2.2589e-2       | 11.6404               | 3                        | 3                 | 0.16%                   |
| dilated vasculature           | 240        | 6.7314e-4         | 2.5720e-2       | 3.3063                | 11                         | 0.48%                     | 318        | 4.1559e-2       | 3.1746                | 9                        | 33                | 0.49%                   |

The test set of 2,312 genomic regions picked 1,838 (9%) 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 |
|---------------------------------------|------------|-------------------|-----------------|-----------------------|----------------------------|---------------------------|------------|-----------------|-----------------------|--------------------------|-------------------|-------------------------|
| increased regulatory T cell number    | 30         | 1.6666e-15        | 5.3191e-13      | 5.5609                | 35                         | 1.51%                     | 360        | 1.0307e-2       | 2.6455                | 15                       | 66                | 0.82%                   |
| curly tail                            | 33         | 2.7617e-15        | 8.0132e-13      | 5.1480                | 37                         | 1.60%                     | 283        | 5.5265e-3       | 2.7389                | 16                       | 68                | 0.87%                   |
| increased T cell number               | 51         | 1.0786e-13        | 2.0250e-11      | 2.1969                | 109                        | 4.71%                     | 274        | 5.2424e-3       | 1.5520                | 70                       | 525               | 3.81%                   |
| abnormal regulatory T cell number     | 54         | 1.9140e-13        | 3.3939e-11      | 3.5094                | 49                         | 2.12%                     | 262        | 4.6308e-3       | 2.1380                | 27                       | 147               | 1.47%                   |
| decreased bone marrow cell number     | 63         | 4.4227e-13        | 6.7219e-11      | 3.3268                | 51                         | 2.21%                     | 548        | 2.7943e-2       | 1.8775                | 25                       | 155               | 1.36%                   |
| abnormal regulatory T cell morphology | 64         | 4.8605e-13        | 7.2717e-11      | 3.4183                | 49                         | 2.12%                     | 293        | 5.8651e-3       | 2.0953                | 27                       | 150               | 1.47%                   |
| abnormal brainstem morphology         | 71         | 1.6188e-12        | 2.1831e-10      | 2.5798                | 72                         | 3.11%                     | 91         | 6.4357e-5       | 2.1645                | 45                       | 242               | 2.45%                   |
| increased astrocyte number            | 72         | 1.6201e-12        | 2.1546e-10      | 3.6492                | 43                         | 1.86%                     | 403        | 1.4262e-2       | 2.0754                | 23                       | 129               | 1.25%                   |
| abnormal circulating amino acid level | 75         | 2.5385e-12        | 3.2408e-10      | 2.7605                | 63                         | 2.72%                     | 589        | 3.4803e-2       | 1.6562                | 35                       | 246               | 1.90%                   |
| abnormal astrocyte number             | 76         | 3.4342e-12        | 4.3267e-10      | 3.5635                | 43                         | 1.86%                     | 455        | 1.7569e-2       | 2.0282                | 23                       | 132               | 1.25%                   |
| astrocytosis                          | 77         | 3.6121e-12        | 4.4916e-10      | 3.6243                | 42                         | 1.82%                     | 468        | 1.9101e-2       | 2.0487                | 22                       | 125               | 1.20%                   |
| hair follicle degeneration            | 84         | 6.7679e-12        | 7.7146e-10      | 7.1901                | 21                         | 0.91%                     | 168        | 8.3775e-4       | 4.4153                | 11                       | 29                | 0.60%                   |
| abnormal midbrain morphology          | 87         | 1.5788e-11        | 1.7376e-9       | 2.8984                | 54                         | 2.34%                     | 153        | 5.9117e-4       | 2.2984                | 31                       | 157               | 1.69%                   |
| abnormal bone marrow cell number      | 105        | 6.6438e-11        | 6.0585e-9       | 2.6678                | 58                         | 2.51%                     | 586        | 3.4553e-2       | 1.7009                | 32                       | 219               | 1.74%                   |
| abnormal amino acid level             | 114        | 1.0618e-10        | 8.9178e-9       | 2.3965                | 69                         | 2.98%                     | 705        | 4.7832e-2       | 1.5445                | 41                       | 309               | 2.23%                   |
| increased cell proliferation          | 116        | 1.4946e-10        | 1.2337e-8       | 2.4516                | 65                         | 2.81%                     | 321        | 7.5403e-3       | 1.7944                | 39                       | 253               | 2.12%                   |
| decreased B cell number               | 120        | 1.8557e-10        | 1.4807e-8       | 2.0331                | 96                         | 4.15%                     | 248        | 3.8275e-3       | 1.5972                | 66                       | 481               | 3.59%                   |
| abnormal tail morphology              | 130        | 5.0542e-10        | 3.7226e-8       | 2.0556                | 89                         | 3.85%                     | 158        | 6.5438e-4       | 1.7475                | 62                       | 413               | 3.37%                   |
| small hair follicles                  | 142        | 1.1134e-9         | 7.5075e-8       | 9.0952                | 14                         | 0.61%                     | 416        | 1.5040e-2       | 4.9887                | 6                        | 14                | 0.33%                   |
| neuron degeneration                   | 147        | 1.7857e-9         | 1.1631e-7       | 2.0803                | 81                         | 3.50%                     | 282        | 5.3582e-3       | 1.6501                | 55                       | 388               | 2.99%                   |

The test set of 2,312 genomic regions picked 1,838 (9%) 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].