

(a)

| Ontology              | # 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 |
|-----------------------|--------------------------------------------------------------|------------|-------------------|-----------------|-----------------------|----------------------------|---------------------------|------------|-----------------|-----------------------|--------------------------|-------------------|-------------------------|
| GO Biological Process | translational elongation                                     | 23         | 2.66872e-12       | 1.01655e-9      | 2.3947                | 82                         | 1.46%                     | 310        | 3.30618e-2      | 1.3909                | 60                       | 123               | 0.98%                   |
|                       | translational termination                                    | 26         | 2.15818e-11       | 7.27225e-9      | 2.6314                | 63                         | 1.12%                     | 208        | 7.65965e-3      | 1.5353                | 49                       | 91                | 0.79%                   |
|                       | cellular macromolecular complex disassembly                  | 31         | 1.11011e-10       | 3.13730e-8      | 2.1239                | 90                         | 1.60%                     | 148        | 1.04368e-3      | 1.5300                | 66                       | 123               | 1.06%                   |
|                       | macromolecular complex disassembly                           | 34         | 1.49849e-10       | 3.86126e-8      | 2.1109                | 90                         | 1.60%                     | 153        | 1.42384e-3      | 1.5177                | 66                       | 124               | 1.06%                   |
|                       | viral transcription                                          | 39         | 6.20059e-10       | 1.39291e-7      | 2.5445                | 57                         | 1.01%                     | 300        | 3.00110e-2      | 1.4748                | 45                       | 87                | 0.72%                   |
|                       | positive regulation of viral transcription                   | 50         | 4.92860e-9        | 8.63589e-7      | 2.5694                | 50                         | 0.89%                     | 251        | 1.33387e-2      | 1.6590                | 32                       | 55                | 0.51%                   |
|                       | cellular protein complex disassembly                         | 52         | 8.66704e-9        | 1.46023e-6      | 2.1161                | 72                         | 1.28%                     | 201        | 6.86532e-3      | 1.5095                | 54                       | 102               | 0.87%                   |
|                       | protein complex disassembly                                  | 53         | 1.16800e-8        | 1.93073e-6      | 2.1000                | 72                         | 1.28%                     | 223        | 8.60413e-3      | 1.4949                | 54                       | 103               | 0.87%                   |
|                       | nuclear export                                               | 62         | 5.29089e-8        | 7.47637e-6      | 2.1193                | 64                         | 1.14%                     | 281        | 2.10698e-2      | 1.4905                | 46                       | 88                | 0.74%                   |
|                       | regulation of interferon-gamma-mediated signaling pathway    | 68         | 8.97852e-8        | 1.15678e-5      | 3.0129                | 32                         | 0.57%                     | 155        | 1.61958e-3      | 2.2315                | 18                       | 23                | 0.29%                   |
|                       | RNA export from nucleus                                      | 78         | 2.23949e-7        | 2.51541e-5      | 2.2844                | 49                         | 0.87%                     | 311        | 3.35599e-2      | 1.5290                | 37                       | 69                | 0.59%                   |
|                       | positive regulation by host of viral transcription           | 161        | 1.67836e-5        | 9.13301e-4      | 3.8039                | 15                         | 0.27%                     | 318        | 3.89584e-2      | 2.5345                | 8                        | 9                 | 0.13%                   |
|                       | myofibril assembly                                           | 166        | 2.16836e-5        | 1.14440e-3      | 2.1049                | 39                         | 0.69%                     | 317        | 3.89576e-2      | 1.7821                | 20                       | 32                | 0.32%                   |
|                       | regulation of transcription from RNA polymerase III promoter | 217        | 7.51976e-5        | 3.03597e-3      | 2.5320                | 23                         | 0.41%                     | 216        | 8.43560e-3      | 2.3167                | 13                       | 16                | 0.21%                   |
|                       | blood vessel endothelial cell migration                      | 256        | 1.45418e-4        | 4.97660e-3      | 2.0472                | 33                         | 0.59%                     | 283        | 2.12165e-2      | 2.1010                | 14                       | 19                | 0.22%                   |
|                       | negative regulation of endocytosis                           | 386        | 9.66704e-4        | 2.19412e-2      | 2.2925                | 19                         | 0.34%                     | 322        | 4.20793e-2      | 1.9960                | 14                       | 20                | 0.22%                   |

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| The test set of 5,632 genomic regions picked 6,223 genes (35%) of all 17,744 genes.                                                    |                                                                                      |
| GO Biological Process has 8,761 terms covering 14,760 (83%) of all 17,744 genes.                                                       | 8,761 ontology terms were tested (100%) using an annotation count range of [1, Inf]. |
| GREAT version 2.0.2                                                                                                                    |                                                                                      |
| Species assembly: hg19                                                                                                                 |                                                                                      |
| Association rule: Basal+extension: 5000 bp upstream, 1000 bp downstream, 1000000 bp max extension, curated regulatory domains included |                                                                                      |

(b)

| Ontology              | # 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 |
|-----------------------|---------------------------------------------------------------------------------------------|------------|-------------------|-----------------|-----------------------|----------------------------|---------------------------|------------|-----------------|-----------------------|--------------------------|-------------------|-------------------------|
| GO Biological Process | actin filament organization                                                                 | 17         | 3.82004e-11       | 1.96967e-8      | 2.3301                | 77                         | 2.06%                     | 285        | 1.36055e-2      | 1.6009                | 42                       | 101               | 0.91%                   |
|                       | myofibril assembly                                                                          | 69         | 2.45459e-7        | 3.11662e-5      | 2.7678                | 34                         | 0.91%                     | 163        | 7.82467e-4      | 2.4062                | 20                       | 32                | 0.43%                   |
|                       | ruffle organization                                                                         | 87         | 1.48668e-6        | 1.49710e-4      | 3.7778                | 19                         | 0.51%                     | 330        | 2.90859e-2      | 2.5666                | 10                       | 15                | 0.22%                   |
|                       | regulation of smooth muscle cell migration                                                  | 105        | 5.31593e-6        | 4.43551e-4      | 2.3980                | 34                         | 0.91%                     | 217        | 2.84570e-3      | 2.4639                | 16                       | 25                | 0.35%                   |
|                       | actomyosin structure organization                                                           | 117        | 7.22585e-5        | 5.41074e-4      | 2.2386                | 38                         | 1.02%                     | 190        | 1.42758e-3      | 2.1488                | 24                       | 43                | 0.52%                   |
|                       | platelet-derived growth factor receptor signaling pathway                                   | 152        | 2.03264e-5        | 1.17158e-3      | 2.2132                | 35                         | 0.94%                     | 135        | 1.23653e-4      | 2.7719                | 18                       | 25                | 0.39%                   |
|                       | regulation of metanephros development                                                       | 185        | 6.79416e-6        | 3.21749e-3      | 2.4365                | 25                         | 0.67%                     | 318        | 2.43415e-2      | 2.4911                | 11                       | 17                | 0.24%                   |
|                       | regulation of interferon-gamma-mediated signaling pathway                                   | 219        | 1.37295e-4        | 5.49241e-3      | 2.6982                | 19                         | 0.51%                     | 382        | 4.14633e-2      | 2.1760                | 13                       | 23                | 0.28%                   |
|                       | negative regulation of endocytosis                                                          | 242        | 1.95406e-4        | 7.07419e-3      | 2.9118                | 16                         | 0.43%                     | 352        | 3.33837e-2      | 2.3099                | 12                       | 20                | 0.26%                   |
|                       | blood vessel endothelial cell migration                                                     | 264        | 3.03812e-4        | 1.00822e-2      | 2.2457                | 24                         | 0.64%                     | 172        | 9.34513e-4      | 2.8367                | 14                       | 19                | 0.30%                   |
|                       | regulation of transcription from RNA polymerase II promoter in response to oxidative stress | 299        | 4.24146e-4        | 1.24279e-2      | 4.1468                | 9                          | 0.24%                     | 339        | 3.05093e-2      | 3.8499                | 5                        | 5                 | 0.11%                   |
|                       | SMAD protein signal transduction                                                            | 360        | 8.35367e-4        | 2.03296e-2      | 2.2126                | 21                         | 0.56%                     | 281        | 1.27079e-2      | 2.6468                | 11                       | 16                | 0.24%                   |
|                       | epithelial-mesenchymal cell signaling                                                       | 449        | 1.81253e-3        | 3.53665e-2      | 2.6306                | 13                         | 0.35%                     | 371        | 3.93824e-2      | 3.2999                | 6                        | 7                 | 0.13%                   |

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| The test set of 3,734 genomic regions picked 4,609 genes (26%) of all 17,744 genes.                                                    |                                                                                      |
| GO Biological Process has 8,761 terms covering 14,760 (83%) of all 17,744 genes.                                                       | 8,761 ontology terms were tested (100%) using an annotation count range of [1, Inf]. |
| GREAT version 2.0.2                                                                                                                    |                                                                                      |
| Species assembly: hg19                                                                                                                 |                                                                                      |
| Association rule: Basal+extension: 5000 bp upstream, 1000 bp downstream, 1000000 bp max extension, curated regulatory domains included |                                                                                      |

(c)

| Ontology              | # 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 |
|-----------------------|---------------------------------------------------|------------|-------------------|-----------------|-----------------------|----------------------------|---------------------------|------------|-----------------|-----------------------|--------------------------|-------------------|-------------------------|
| GO Molecular Function | structural constituent of ribosome                | 1          | 1.21925e-10       | 4.14667e-7      | 2.8300                | 51                         | 2.69%                     | 6          | 7.40712e-5      | 2.1442                | 48                       | 164               | 1.98%                   |
|                       | translation factor activity, nucleic acid binding | 4          | 1.66816e-7        | 1.41836e-4      | 2.7125                | 36                         | 1.90%                     | 7          | 3.60032e-4      | 2.3311                | 35                       | 110               | 1.45%                   |
|                       | translation elongation factor activity            | 7          | 2.04625e-6        | 9.94185e-4      | 5.2614                | 13                         | 0.68%                     | 11         | 3.17815e-2      | 3.0723                | 13                       | 31                | 0.54%                   |
|                       | RNA methyltransferase activity                    | 8          | 9.83230e-6        | 4.17796e-3      | 4.5357                | 13                         | 0.68%                     | 10         | 1.50071e-2      | 3.2841                | 13                       | 29                | 0.54%                   |

|                                                                                                                                        |                                                                                      |
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| The test set of 1,898 genomic regions picked 2,422 genes (14%) of all 17,744 genes.                                                    |                                                                                      |
| GO Molecular Function has 3,401 terms covering 14,912 (84%) of all 17,744 genes.                                                       | 3,401 ontology terms were tested (100%) using an annotation count range of [1, Inf]. |
| GREAT version 2.0.2                                                                                                                    |                                                                                      |
| Species assembly: hg19                                                                                                                 |                                                                                      |
| Association rule: Basal+extension: 5000 bp upstream, 1000 bp downstream, 1000000 bp max extension, curated regulatory domains included |                                                                                      |