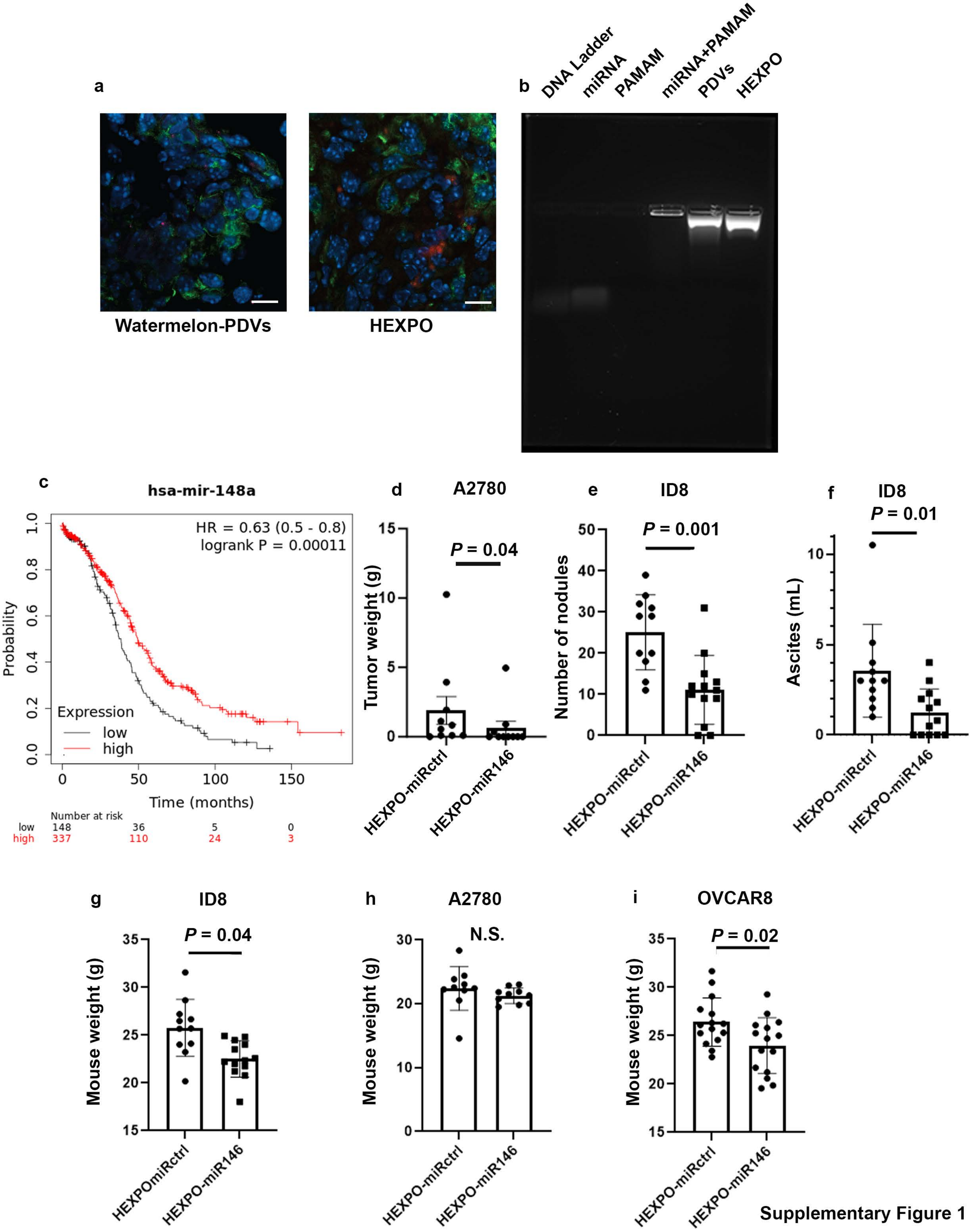
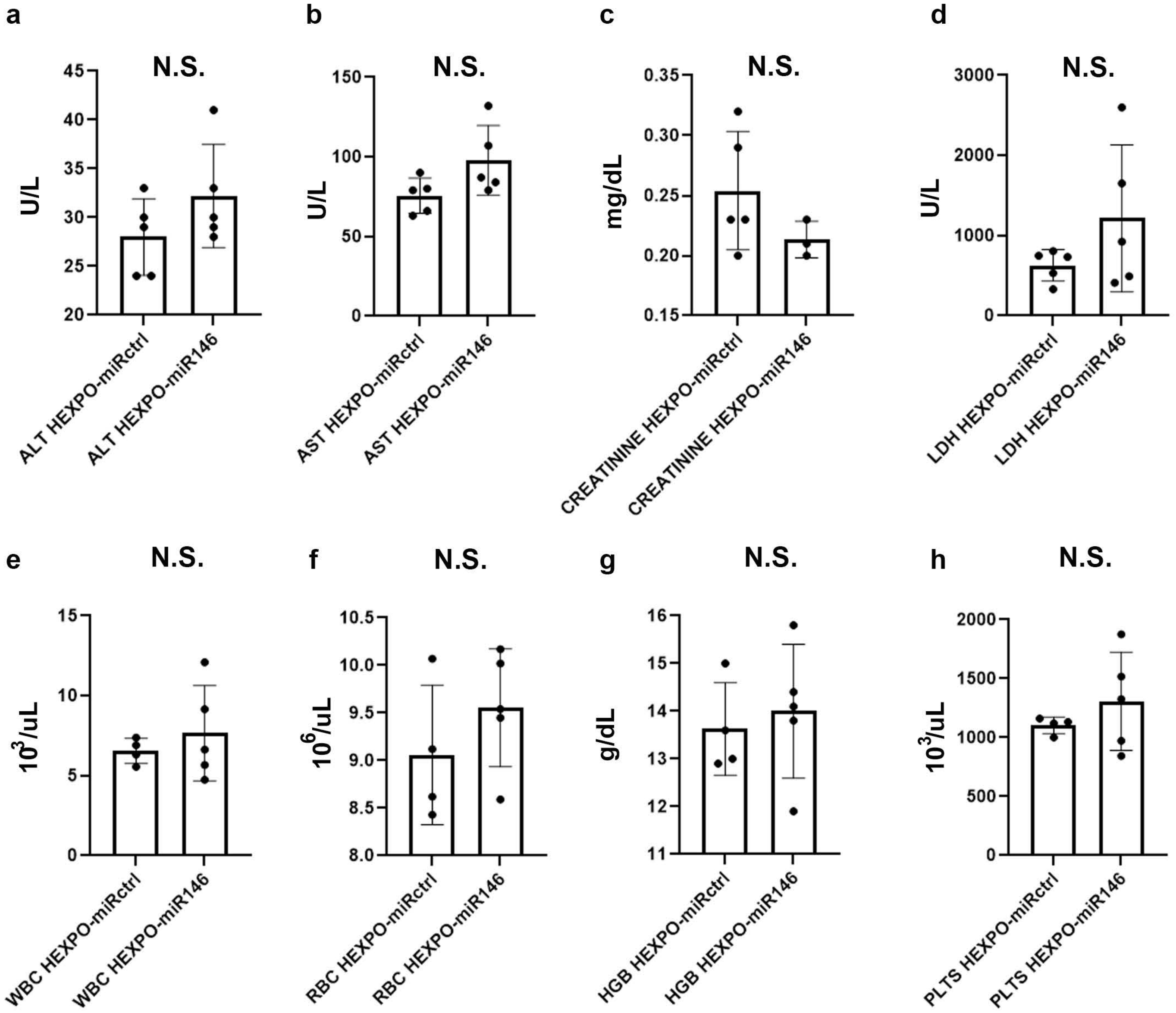


Supplementary Figure 1

**Supplementary Figure 1**: A) Watermelon-PDVs (fuchsia) and HEXPO (red) uptake from cytokeratin positive (green) tumor cells in ID8 tumor nodules. Scale bar= 10 μm. B) Electrophoresis retardation assay; C) Kaplan Meier curve representing survival in ovarian cancer patients with high and low tumor expression of miR148a (kmplotter.com); D) Quantification of tumor weight from the A2780 *in vivo* model treated with hybrid exosomal polymeric control microRNA (HEXPO-miRctrl) and hybrid exosomal polymeric miR146a (HEXPO-miR-146), without outliers exclusion (dots represent each sample, bars represent means, and whiskers the standard error of the mean) E) Quantification of tumor nodules from the ID8 *in vivo* model treated with hybrid exosomal polymeric control microRNA (HEXPO-miRctrl) and hybrid exosomal polymeric miR146a (HEXPO-miR-146); F) Quantification of ascites from the ID8 in vivo model; G) Quantification of body weight from the ID8 in vivo model; H) Quantification of body weight from the A2780 in vivo model in mice treated with HEXPO-ctrl *versus* HEXPO-miR146; I) Quantification of body weight from the OVCAR8 in vivo model in mice treated with HEXPO-ctrl *versus* HEXPO-miR146.

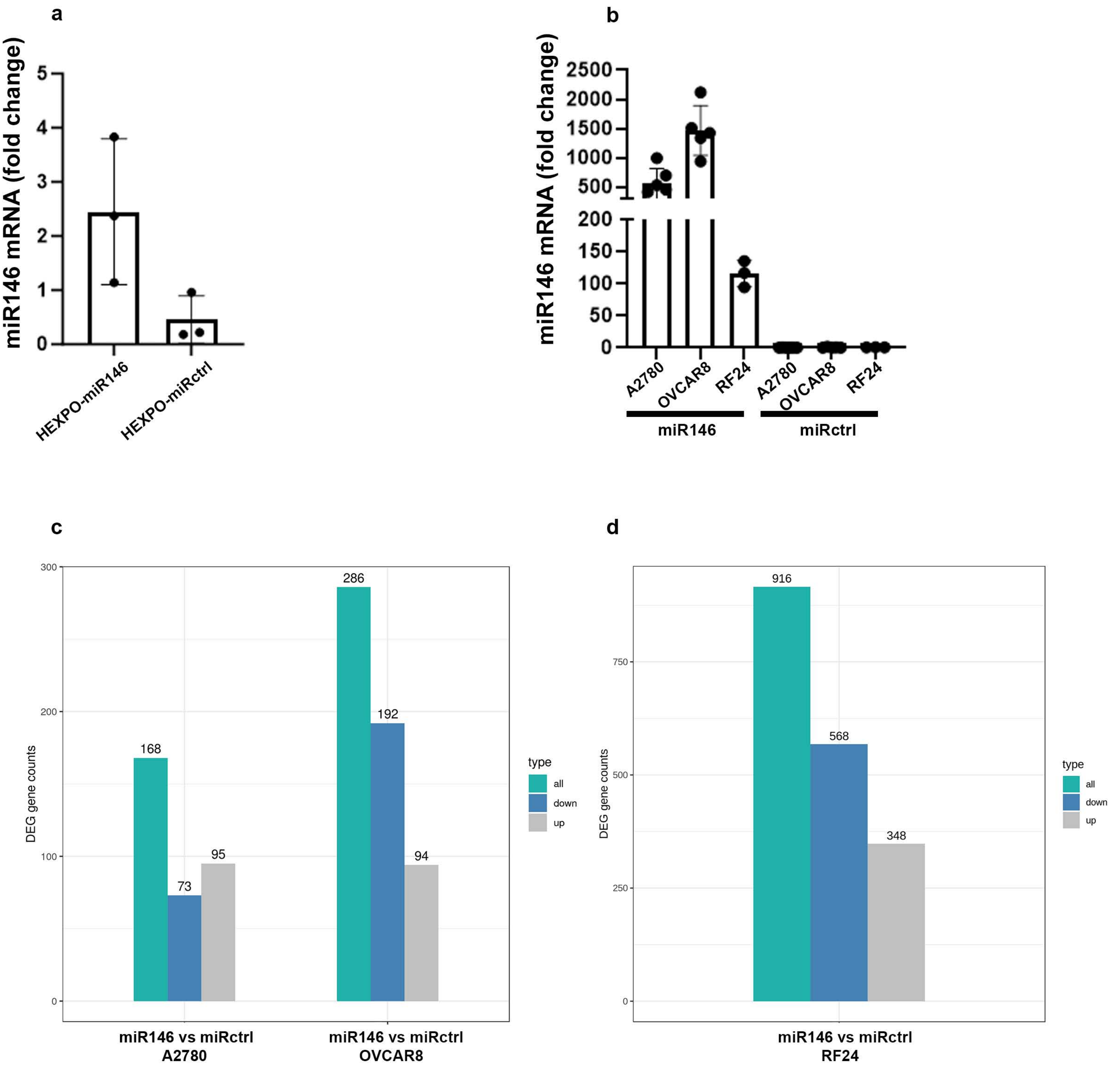
ABBREVIATIONS: miRctrl = mirna negative control; miR146 = mirna 146a.



**Supplementary Figure 2**

**Supplementary Figure 2**: Serum levels of ALT (A), AST (B), creatinine (C), LDH (D), WBC (E ), RBC (F), HBG (G), PLTS (H) in mouse treated with HEXPO-ctrl *versus* HEXPO-miR146 in the OVCAR8 in vivo model.

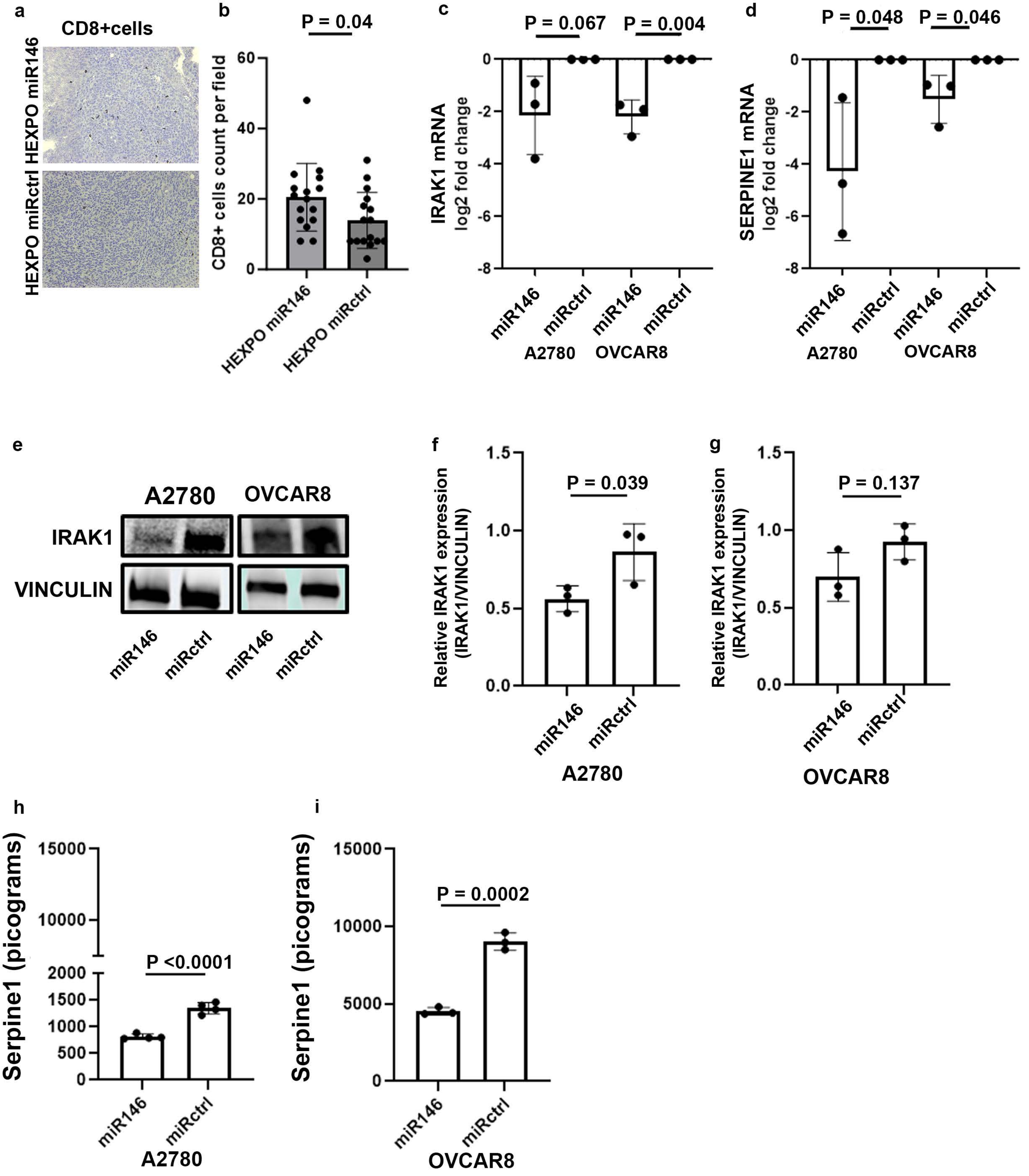
ABBREVIATIONS: miRctrl = mirna negative control; miR146 = mirna 146a; ALT = serum alanine transaminase; AST = Serum aspartate transaminase; LDH = lactate dehydrogenase; WBC = white blood cells; RBC = red blood cells; HBG = hemoglobin; PLTS = platelets.



**Supplementary figure 3**

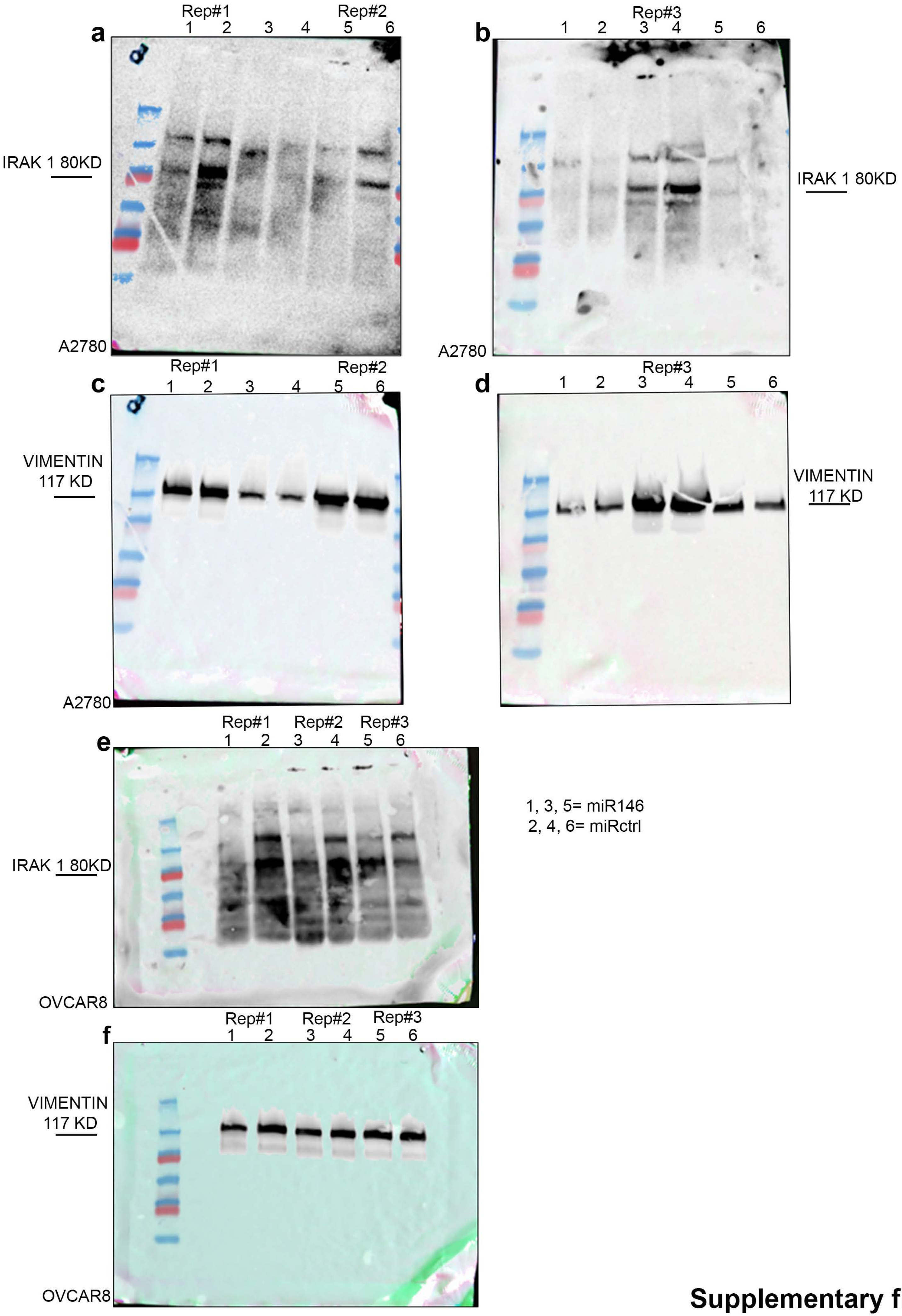
**Supplementary Figure 3**: A) miR146 expression in tumors from ID8 mice treated with HEXPO-miRctrl or HEXPO-miR146; B) miR146 expression in A2780, OVCAR8 and RF24 cells transfected with miR146 or miRctrl; C) DEG counts of all, downregulated and upregulated genes in A2780 and OVCAR8 cells transfected with miR146 versus A2780 and OVCAR8 cells transfected with miRctrl; D) DEG counts of all, downregulated and upregulated genes in RF24 cells transfected with miR146 versus RF24 cells transfected with miRctrl. MiR146 expression is calculated as fold change over housekeeping gene. Bars in histograms represent mean values and whiskers represent standard deviation from the mean.

ABBREVIATIONS: miRctrl = mirna negative control; miR146 = mirna 146a, DEG= differentially expressed genes.



**Supplementary Figure 4**

**Supplementary Figure 4:** A) representative pictures from 20X magnification quadrants of tumor sections from the ID8 mouse model treated with HEXPO-ctrl and HEXPO-miR146 stained with anti-CD8 antibody, and quantification of CD8-positive cells in B); C) IRAK1 mRNA differential expression in $\log_2$ fold change between miR146 and miRctrl treated A2780 and OVCAR8 cells; D) SERPINE1 mRNA differential expression in log2 fold change between miR146 and miRctrl treated A2780 and OVCAR8 cells; E, F, and G) Western blot with quantification showing IRAK1 protein expression in miR146 and miRctrl treated A2780 and OVCAR8 cells normalized to vimentin (the pale blue background is an artifact from the imaging software); H and I) Quantification of ELISA assay showing SERPINE1 protein expression in the supernatant from miR146 and miRctrl treated A2780 and OVCAR8 cells.



1, 3, 5= miR146
2, 4, 6= miRctrl

**Supplementary figure 5**

**Supplementary Figure 5:** Original acquired blots from Western Blot analysis (three experimental triplicates) of IRAK1 protein expression in A2780 cells (A and B), and OVCAR8 cells ( E), and VINCULIN as housekeeping protein (C, D and F). Rep= replicate

| **Database** | **Pathway** | **Evidence** | **Hits** | **Expected hits** | **P value** |
|---|---|---|---|---|---|
| Gene Ontology - Biological Process | RNA metabolic process | predicted (intersection) | 963 | 814.2 | 3.90e-8 |
| Gene Ontology - Biological Process | RNA metabolic process | predicted (intersection) | 810 | 670.2 | 3.90e-8 |
| Gene Ontology - Biological Process | regulation of gene expression | predicted (intersection) | 936 | 785.7 | 3.90e-8 |
| Gene Ontology - Biological Process | transcription, DNA-templated | predicted (intersection) | 788 | 650.5 | 3.90e-8 |
| Gene Ontology - Biological Process | transcription by RNA polymerase II | predicted (intersection) | 627 | 505.4 | 9.25e-8 |
| Gene Ontology - Biological Process | RNA biosynthetic process | predicted (intersection) | 798 | 663.9 | 1.02e-7 |
| Gene Ontology - Biological Process | transcription, DNA-templated | predicted (intersection) | 745 | 616.3 | 1.50e-7 |
| Gene Ontology - Biological Process | RNA biosynthetic process | predicted (intersection) | 758 | 632.1 | 3.54e-7 |
| Gene Ontology - Biological Process | nucleic acid-templated transcription | predicted (intersection) | 757 | 630.6 | 3.54e-7 |
| Gene Ontology - Biological Process | transcription by RNA polymerase II | predicted (intersection) | 589 | 476.3 | 3.54e-7 |
| Gene Ontology - Biological Process | regulation of cellular metabolic | predicted (intersection) | 679 | 562 | 9.12e-7 |
| Gene Ontology - Biological Process | positive regulation of metabolic process | predicted (intersection) | 732 | 615.3 | 2.96e-6 |
| Gene Ontology - Biological Process | positive regulation of transcription, DNA-templated | predicted (intersection) | 337 | 260.4 | 1.93e-5 |
| Gene Ontology - Biological Process | anatomical structure morphogenesis | predicted (union) | 989 | 867.6 | 2.30e-5 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of RNA biosynthetic process | predicted (union) | 627 | 530.2 | 2.30e-5 |
| Gene Ontology - Biological Process | positive regulation of nucleic acid-templated transcription | predicted (union) | 627 | 529.8 | 2.30e-5 |
| Gene Ontology - Biological Process | positive regulation of transcription, DNA-templated | predicted (union) | 589 | 493.6 | 2.30e-5 |
| Gene Ontology - Biological Process | nervous system development | predicted (union) | 897 | 784.5 | 2.35e-5 |
| Gene Ontology - Biological Process | positive regulation of gene expression | predicted (union) | 745 | 641 | 2.35e-5 |
| Gene Ontology - Biological Process | positive regulation of macromolecule biosynthetic process | predicted (union) | 719 | 617.6 | 2.35e-5 |
| Gene Ontology - Biological Process | positive regulation of transcription by RNA polymerase II | predicted (union) | 454 | 372.8 | 2.35e-5 |
| Gene Ontology - Biological Process | positive regulation of gene expression | predicted (intersection) | 423 | 338.1 | 2.52e-5 |
| Gene Ontology - Biological Process | negative regulation of transcription by RNA polymerase II | predicted (union) | 336 | 267.5 | 2.52e-5 |
| Gene Ontology - Biological Process | regulation of cell differentiation | predicted (union) | 706 | 606.5 | 2.54e-5 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of cellular metabolic process | predicted (intersection) | 524 | 430.8 | 2.78e-5 |
| Gene Ontology - Biological Process | positive regulation of RNA biosynthetic process | predicted (intersection) | 357 | 279.7 | 2.78e-5 |
| Gene Ontology - Biological Process | positive regulation of nucleic acid-templated transcription | predicted (intersection) | 357 | 279.4 | 2.78e-5 |
| Gene Ontology - Biological Process | positive regulation of transcription by RNA polymerase II | predicted (intersection) | 262 | 196.6 | 3.63e-5 |
| Gene Ontology - Biological Process | positive regulation of cellular biosynthetic process | predicted (union) | 747 | 646.2 | 3.66e-5 |
| Gene Ontology - Biological Process | positive regulation of macromolecule biosynthetic process | predicted (intersection) | 407 | 325.8 | 4.01e-5 |
| Gene Ontology - Biological Process | anatomical structure morphogenesis | predicted (intersection) | 551 | 457.6 | 4.25e-5 |
| Gene Ontology - Biological Process | positive regulation of cellular biosynthetic process | predicted (intersection) | 421 | 340.9 | 8.64e-5 |
| Gene Ontology - Biological Process | cellular protein modification process | predicted (intersection) | 824 | 717.2 | 9.49e-5 |
| Gene Ontology - Biological Process | nervous system development | predicted (intersection) | 500 | 413.8 | 9.49e-5 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | protein modification process | predicted (intersection) | 824 | 717.2 | 9.49e-5 |
| Gene Ontology - Biological Process | urogenital system development | predicted (intersection) | 99 | 62.26 | 9.49e-5 |
| Gene Ontology - Biological Process | tube development | predicted (union) | 432 | 358.1 | 1.08e-4 |
| Gene Ontology - Biological Process | negative regulation of cellular metabolic process | predicted (union) | 920 | 816.7 | 2.49e-4 |
| Gene Ontology - Biological Process | tube morphogenesis | predicted (union) | 352 | 289.3 | 4.82e-4 |
| Gene Ontology - Biological Process | intracellular signal transduction | predicted (union) | 985 | 882.7 | 5.97e-4 |
| Gene Ontology - Biological Process | enzyme linked receptor protein signaling pathway | predicted (intersection) | 233 | 178.2 | 5.98e-4 |
| Gene Ontology - Biological Process | regulation of cell differentiation | predicted (intersection) | 388 | 319.9 | 0.001 |
| Gene Ontology - Biological Process | tube development | predicted (intersection) | 243 | 188.9 | 0.001 |
| Gene Ontology - Biological Process | enzyme linked receptor protein signaling pathway | predicted (union) | 402 | 337.8 | 0.001 |
| Gene Ontology - Biological Process | heart development | predicted (union) | 240 | 191.2 | 0.001 |
| Gene Ontology - Biological Process | negative regulation of nucleic acid-templated transcription | predicted (union) | 463 | 394.6 | 0.001 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of transcription, DNA-templated | predicted (union) | 441 | 373.6 | 0.001 |
| Gene Ontology - Biological Process | cellular protein metabolic process | predicted (intersection) | 988 | 888.4 | 0.002 |
| Gene Ontology - Biological Process | response to growth factor | predicted (intersection) | 169 | 125.2 | 0.002 |
| Gene Ontology - Biological Process | muscle structure development | predicted (union) | 266 | 216.6 | 0.002 |
| Gene Ontology - Biological Process | negative regulation of RNA biosynthetic process | predicted (union) | 463 | 395.4 | 0.002 |
| Gene Ontology - Biological Process | negative regulation of biosynthetic process | predicted (union) | 571 | 496 | 0.002 |
| Gene Ontology - Biological Process | protein phosphorylation | predicted (union) | 732 | 649.4 | 0.002 |
| Gene Ontology - Biological Process | regulation of cellular component organization | predicted (union) | 893 | 802.4 | 0.002 |
| Gene Ontology - Biological Process | regulation of neurogenesis | predicted (union) | 322 | 267.1 | 0.002 |
| Gene Ontology - Biological Process | head development | predicted (intersection) | 184 | 139.6 | 0.003 |
| Gene Ontology - Biological Process | regulation of cellular component organization | predicted (intersection) | 497 | 423.3 | 0.003 |
| Gene Ontology - Biological Process | renal system development | predicted (intersection) | 85 | 55.76 | 0.003 |
| Gene Ontology - Biological Process | cell development | predicted (union) | 770 | 687.1 | 0.003 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | brain development | predicted (intersection) | 174 | 131.7 | 0.004 |
| Gene Ontology - Biological Process | cell development | predicted (intersection) | 429 | 362.5 | 0.004 |
| Gene Ontology - Biological Process | cell migration | predicted (intersection) | 296 | 240.7 | 0.004 |
| Gene Ontology - Biological Process | kidney development | predicted (intersection) | 81 | 53.04 | 0.004 |
| Gene Ontology - Biological Process | negative regulation of transcription by RNA polymerase II | predicted (intersection) | 185 | 141.1 | 0.004 |
| Gene Ontology - Biological Process | tube morphogenesis | predicted (intersection) | 198 | 152.6 | 0.004 |
| Gene Ontology - Biological Process | negative regulation of gene expression | predicted (union) | 668 | 591.4 | 0.004 |
| Gene Ontology - Biological Process | negative regulation of gene expression | predicted (intersection) | 373 | 311.9 | 0.005 |
| Gene Ontology - Biological Process | phosphate-containing compound metabolic process | predicted (intersection) | 650 | 571.5 | 0.005 |
| Gene Ontology - Biological Process | dephosphorylation | predicted (union) | 205 | 163.7 | 0.005 |
| Gene Ontology - Biological Process | cellular response to growth factor stimulus | predicted (intersection) | 159 | 119.7 | 0.006 |
| Gene Ontology - Biological Process | neurogenesis | predicted (union) | 596 | 525.4 | 0.006 |
| Gene Ontology - Biological Process | negative regulation of biosynthetic process | predicted (intersection) | 317 | 261.6 | 0.007 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | generation of neurons | predicted (union) | 561 | 493.6 | 0.007 |
| Gene Ontology - Biological Process | phosphorylation | predicted (union) | 875 | 791.7 | 0.007 |
| Gene Ontology - Biological Process | positive regulation of autophagy | predicted (union) | 62 | 41.33 | 0.007 |
| Gene Ontology - Biological Process | positive regulation of cell differentiation | predicted (union) | 385 | 328.7 | 0.007 |
| Gene Ontology - Biological Process | protein modification by small protein conjugation | predicted (union) | 363 | 308.8 | 0.007 |
| Gene Ontology - Biological Process | stem cell population maintenance | predicted (union) | 82 | 57.63 | 0.007 |
| Gene Ontology - Biological Process | regulation of phosphorus metabolic process | predicted (union) | 645 | 573.9 | 0.008 |
| Gene+2:81 Ontology - Biological Process | central nervous system development | predicted (intersection) | 222 | 176.7 | 0.010 |
| Gene Ontology - Biological Process | circadian rhythm | predicted (intersection) | 60 | 37.94 | 0.011 |
| Gene Ontology - Biological Process | muscle structure development | predicted (intersection) | 151 | 114.3 | 0.011 |
| Gene Ontology - Biological Process | immune system development | predicted (union) | 379 | 325.5 | 0.011 |
| Gene Ontology - Biological Process | regulation of chromatin organization | predicted (union) | 84 | 60.01 | 0.011 |
| Gene Ontology - Biological Process | regulation of muscle organ development | predicted (union) | 68 | 46.9 | 0.011 |
| Gene Ontology - Biological Process | vasculature development | predicted (union) | 292 | 245.2 | 0.011 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | cell migration | predicted (union) | 518 | 456.2 | 0.012 |
| Gene Ontology - Biological Process | regulation of cellular protein metabolic process | predicted (union) | 927 | 845.7 | 0.012 |
| Gene Ontology - Biological Process | response to growth factor | predicted (union) | 283 | 237.3 | 0.012 |
| Gene Ontology - Biological Process | protein phosphorylation | predicted (intersection) | 402 | 342.5 | 0.013 |
| Gene Ontology - Biological Process | cellular response to growth factor stimulus | predicted (union) | 271 | 226.9 | 0.014 |
| Gene Ontology - Biological Process | organophosphate metabolic process | predicted (union) | 394 | 340.6 | 0.014 |
| Gene Ontology - Biological Process | protein K48-linked ubiquitination | predicted (union) | 34 | 20.27 | 0.014 |
| Gene Ontology - Biological Process | cell surface receptor signaling pathway | predicted (intersection) | 586 | 516.1 | 0.015 |
| Gene Ontology - Biological Process | blood vessel development | predicted (union) | 280 | 235.7 | 0.015 |
| Gene Ontology - Biological Process | cardiovascular system development | predicted (union) | 294 | 248.4 | 0.015 |
| Gene Ontology - Biological Process | urogenital system development | predicted (union) | 150 | 118 | 0.015 |
| Gene Ontology - Biological Process | blood vessel morphogenesis | predicted (union) | 248 | 206.7 | 0.016 |
| Gene Ontology - Biological Process | cell projection morphogenesis | predicted (union) | 242 | 201.1 | 0.016 |
| Gene Ontology - Biological Process | lipid phosphorylation | predicted (union) | 57 | 38.55 | 0.016 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | locomotion | predicted (union) | 650 | 583.4 | 0.016 |
| Gene Ontology - Biological Process | regulation of cellular response to stress | predicted (union) | 293 | 248 | 0.016 |
| Gene Ontology - Biological Process | regulation of intracellular signal transduction | predicted (union) | 675 | 607.3 | 0.016 |
| Gene Ontology - Biological Process | positive regulation of neuron apoptotic process | predicted (intersection) | 23 | 10.9 | 0.017 |
| Gene Ontology - Biological Process | regulation of neurogenesis | predicted (intersection) | 180 | 140.9 | 0.017 |
| Gene Ontology - Biological Process | coenzyme biosynthetic process | predicted (union) | 66 | 46.1 | 0.018 |
| Gene Ontology - Biological Process | anatomical structure formation involved in morphogenesis | predicted (intersection) | 242 | 197.1 | 0.019 |
| Gene Ontology - Biological Process | negative regulation of transcription, DNA-templated | predicted (intersection) | 242 | 197.1 | 0.019 |
| Gene Ontology - Biological Process | regulation of chromatin organization | predicted (intersection) | 51 | 31.66 | 0.019 |
| Gene Ontology - Biological Process | cell adhesion | predicted (union) | 531 | 471.3 | 0.019 |
| Gene Ontology - Biological Process | proteoglycan metabolic process | predicted (intersection) | 30 | 15.93 | 0.020 |
| Gene Ontology - Biological Process | regulation of cell migration | predicted (intersection) | 187 | 147.8 | 0.020 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | transmembrane receptor protein tyrosine kinase signaling pathway | predicted (intersection) | 160 | 123.9 | 0.020 |
| Gene Ontology - Biological Process | locomotion | predicted (intersection) | 362 | 307.7 | 0.021 |
| Gene Ontology - Biological Process | postsynapse organization | predicted (intersection) | 48 | 29.56 | 0.021 |
| Gene Ontology - Biological Process | synapse assembly | predicted (intersection) | 51 | 31.86 | 0.021 |
| Gene Ontology - Biological Process | regulation of DNA-templated transcription, initiation | predicted (union) | 21 | 11.13 | 0.021 |
| Gene Ontology - Biological Process | regulation of histone modification | predicted (union) | 70 | 49.68 | 0.021 |
| Gene Ontology - Biological Process | cell part morphogenesis | predicted (union) | 247 | 207.1 | 0.022 |
| Gene Ontology - Biological Process | protein ubiquitination | predicted (union) | 325 | 279 | 0.022 |
| Gene Ontology - Biological Process | regulation of lipid metabolic process | predicted (union) | 169 | 136.3 | 0.022 |
| Gene Ontology - Biological Process | regulation of osteoclast differentiation | predicted (union) | 37 | 23.05 | 0.022 |
| Gene Ontology - Biological Process | cellular response to organonitrogen compound | predicted (intersection) | 135 | 102.5 | 0.023 |
| Gene Ontology - Biological Process | hair follicle development | predicted (intersection) | 30 | 16.14 | 0.023 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | anatomical structure formation involved in morphogenesis | predicted (union) | 426 | 373.6 | 0.023 |
| Gene Ontology - Biological Process | transmembrane receptor protein tyrosine kinase signaling pathway | predicted (union) | 277 | 234.9 | 0.023 |
| Gene Ontology - Biological Process | positive regulation of protein modification process | predicted (union) | 447 | 393.8 | 0.026 |
| Gene Ontology - Biological Process | cell motility | predicted (intersection) | 316 | 266.7 | 0.027 |
| Gene Ontology - Biological Process | regulation of cell motility | predicted (intersection) | 198 | 158.9 | 0.027 |
| Gene Ontology - Biological Process | regulation of cellular protein metabolic process | predicted (intersection) | 508 | 446.1 | 0.027 |
| Gene Ontology - Biological Process | vasculature development | predicted (intersection) | 165 | 129.3 | 0.027 |
| Gene Ontology - Biological Process | blood vessel development | predicted (intersection) | 159 | 124.3 | 0.028 |
| Gene Ontology - Biological Process | generation of neurons | predicted (intersection) | 309 | 260.4 | 0.028 |
| Gene Ontology - Biological Process | negative regulation of nucleic acid-templated transcription | predicted (intersection) | 252 | 208.2 | 0.028 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of transcription from RNA polymerase II promoter in response to stress | predicted (intersection) | 8 | 2.306 | 0.028 |
| Gene Ontology - Biological Process | neurogenesis | predicted (intersection) | 327 | 277.1 | 0.028 |
| Gene Ontology - Biological Process | regulation of cellular component movement | predicted (intersection) | 214 | 173.6 | 0.028 |
| Gene Ontology - Biological Process | regulation of protein metabolic process | predicted (union) | 978 | 901.8 | 0.028 |
| Gene Ontology - Biological Process | heart development | predicted (intersection) | 132 | 100.8 | 0.029 |
| Gene Ontology - Biological Process | negative regulation of RNA biosynthetic process | predicted (intersection) | 252 | 208.6 | 0.029 |
| Gene Ontology - Biological Process | regulation of organelle organization | predicted (intersection) | 260 | 215.9 | 0.029 |
| Gene Ontology - Biological Process | retina vasculature development in camera-type eye | predicted (intersection) | 10 | 3.354 | 0.029 |
| Gene Ontology - Biological Process | rhythmic process | predicted (intersection) | 79 | 55.34 | 0.029 |
| Gene Ontology - Biological Process | striated muscle tissue development | predicted (union) | 158 | 127.2 | 0.029 |
| Gene Ontology - Biological Process | cardiovascular system development | predicted (intersection) | 166 | 131 | 0.030 |
| Gene Ontology - Biological Process | hair cycle process | predicted (intersection) | 30 | 16.56 | 0.030 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of glycoprotein biosynthetic process | predicted (intersection) | 16 | 6.918 | 0.030 |
| Gene Ontology - Biological Process | skin epidermis development | predicted (intersection) | 30 | 16.56 | 0.030 |
| Gene Ontology - Biological Process | regulation of striated muscle tissue development | predicted (union) | 64 | 45.31 | 0.030 |
| Gene Ontology - Biological Process | cell motility | predicted (union) | 564 | 505.5 | 0.031 |
| Gene Ontology - Biological Process | muscle cell differentiation | predicted (union) | 144 | 114.9 | 0.031 |
| Gene Ontology - Biological Process | regulation of locomotion | predicted (union) | 374 | 326.3 | 0.031 |
| Gene Ontology - Biological Process | regulation of neuron apoptotic process | predicted (intersection) | 59 | 39.2 | 0.032 |
| Gene Ontology - Biological Process | covalent chromatin modification | predicted (union) | 188 | 154.6 | 0.032 |
| Gene Ontology - Biological Process | positive regulation of signal transduction | predicted (union) | 614 | 553.6 | 0.033 |
| Gene Ontology - Biological Process | muscle tissue development | predicted (union) | 163 | 132.3 | 0.034 |
| Gene Ontology - Biological Process | positive regulation of protein kinase B signaling | predicted (union) | 81 | 60.01 | 0.034 |
| Gene Ontology - Biological Process | regulation of JNK cascade | predicted (union) | 82 | 60.81 | 0.034 |
| Gene Ontology - Biological Process | regulation of phosphorylation | predicted (union) | 564 | 506.3 | 0.034 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | tissue morphogenesis | predicted (union) | 264 | 224.5 | 0.034 |
| Gene Ontology - Biological Process | phosphorylation | predicted (intersection) | 475 | 417.6 | 0.035 |
| Gene Ontology - Biological Process | positive regulation of cellular protein metabolic process | predicted (intersection) | 317 | 269.6 | 0.035 |
| Gene Ontology - Biological Process | positive regulation of glycoprotein biosynthetic process | predicted (intersection) | 11 | 3.983 | 0.035 |
| Gene Ontology - Biological Process | positive regulation of protein modification process | predicted (intersection) | 250 | 207.8 | 0.035 |
| Gene Ontology - Biological Process | regulation of locomotion | predicted (intersection) | 211 | 172.1 | 0.035 |
| Gene Ontology - Biological Process | neuron projection morphogenesis | predicted (union) | 231 | 194.3 | 0.035 |
| Gene Ontology - Biological Process | glycoprotein metabolic process | predicted (intersection) | 95 | 69.6 | 0.036 |
| Gene Ontology - Biological Process | JNK cascade | predicted (union) | 95 | 72.33 | 0.036 |
| Gene Ontology - Biological Process | cell-cell signaling | predicted (union) | 593 | 534.5 | 0.036 |
| Gene Ontology - Biological Process | macroautophagy | predicted (union) | 124 | 97.77 | 0.036 |
| Gene Ontology - Biological Process | morphogenesis of an epithelium | predicted (union) | 223 | 187.2 | 0.036 |
| Gene Ontology - Biological Process | phosphatidylinositol metabolic process | predicted (union) | 95 | 72.33 | 0.036 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of neuron differentiation | predicted (union) | 249 | 211 | 0.036 |
| Gene Ontology - Biological Process | regulation of organelle organization | predicted (union) | 461 | 409.3 | 0.036 |
| Gene Ontology - Biological Process | lung alveolus development | predicted (intersection) | 18 | 8.386 | 0.037 |
| Gene Ontology - Biological Process | neuron apoptotic process | predicted (intersection) | 65 | 44.44 | 0.037 |
| Gene Ontology - Biological Process | animal organ morphogenesis | predicted (union) | 400 | 352.1 | 0.037 |
| Gene Ontology - Biological Process | cell morphogenesis | predicted (union) | 353 | 308 | 0.037 |
| Gene Ontology - Biological Process | cellular lipid metabolic process | predicted (union) | 390 | 343 | 0.038 |
| Gene Ontology - Biological Process | regulation of cell migration | predicted (union) | 323 | 280.2 | 0.038 |
| Gene Ontology - Biological Process | regulation of dendritic spine development | predicted (union) | 36 | 23.05 | 0.038 |
| Gene Ontology - Biological Process | cell morphogenesis involved in differentiation | predicted (union) | 262 | 223.8 | 0.040 |
| Gene Ontology - Biological Process | gland development | predicted (union) | 185 | 153 | 0.040 |
| Gene Ontology - Biological Process | hippo signaling | predicted (union) | 24 | 13.91 | 0.040 |
| Gene Ontology - Biological Process | regulation of cellular component movement | predicted (union) | 375 | 329.1 | 0.040 |
| Gene Ontology - Biological Process | muscle cell proliferation | predicted (intersection) | 55 | 36.48 | 0.042 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | circadian rhythm | predicted (union) | 94 | 71.93 | 0.042 |
| Gene Ontology - Biological Process | regulation of cell motility | predicted (union) | 345 | 301.2 | 0.042 |
| Gene Ontology - Biological Process | gene silencing | predicted (intersection) | 57 | 38.15 | 0.043 |
| Gene Ontology - Biological Process | neuron development | predicted (union) | 399 | 352.1 | 0.043 |
| Gene Ontology - Biological Process | polysaccharide metabolic process | predicted (union) | 51 | 35.37 | 0.043 |
| Gene Ontology - Biological Process | regulation of transcription initiation from RNA polymerase II promoter | predicted (union) | 15 | 7.551 | 0.043 |
| Gene Ontology - Biological Process | actin filament-based process | predicted (intersection) | 154 | 121.8 | 0.044 |
| Gene Ontology - Biological Process | cell-cell signaling | predicted (intersection) | 329 | 282 | 0.045 |
| Gene Ontology - Biological Process | cell projection organization | predicted (union) | 550 | 496 | 0.045 |
| Gene Ontology - Biological Process | dendritic spine development | predicted (union) | 46 | 31.4 | 0.045 |
| Gene Ontology - Biological Process | embryonic morphogenesis | predicted (union) | 238 | 202.3 | 0.045 |
| Gene Ontology - Biological Process | glycerolipid metabolic process | predicted (union) | 180 | 149 | 0.045 |
| Gene Ontology - Biological Process | hemopoiesis | predicted (union) | 334 | 291.7 | 0.045 |
| Gene Ontology - Biological Process | kidney development | predicted (union) | 126 | 100.5 | 0.045 |
| Gene Ontology - Biological Process | neuron differentiation | predicted (union) | 491 | 439.9 | 0.045 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | neuron projection development | predicted (union) | 352 | 308.4 | 0.045 |
| Gene Ontology - Biological Process | phosphatidylinositol phosphorylation | predicted (union) | 47 | 32.19 | 0.045 |
| Gene Ontology - Biological Process | regulation of circadian rhythm | predicted (union) | 57 | 40.54 | 0.045 |
| Gene Ontology - Biological Process | regulation of neuron projection development | predicted (union) | 190 | 158.2 | 0.045 |
| Gene Ontology - Biological Process | renal system development | predicted (union) | 132 | 105.7 | 0.045 |
| Gene Ontology - Biological Process | trigeminal nerve development | predicted (union) | 10 | 4.372 | 0.045 |
| Gene Ontology - Biological Process | RNA splicing | predicted (union) | 173 | 143.1 | 0.046 |
| Gene Ontology - Biological Process | cellular response to organic substance | predicted (union) | 950 | 881.1 | 0.046 |
| Gene Ontology - Biological Process | histone modification | predicted (union) | 180 | 149.4 | 0.046 |
| Gene Ontology - Biological Process | positive regulation of dendrite development | predicted (union) | 36 | 23.45 | 0.046 |
| Gene Ontology - Biological Process | regulation of actin filament-based process | predicted (union) | 144 | 116.8 | 0.046 |
| Gene Ontology - Biological Process | regulation of developmental growth | predicted (union) | 132 | 106.1 | 0.046 |
| Gene Ontology - Biological Process | regulation of kinase activity | predicted (union) | 327 | 285.4 | 0.046 |
| Gene Ontology - Biological Process | cell projection morphogenesis | predicted (intersection) | 136 | 106.1 | 0.047 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | glomerulus development | predicted (intersection) | 22 | 11.32 | 0.047 |
| Gene Ontology - Biological Process | organelle organization | predicted (intersection) | 691 | 625.8 | 0.047 |
| Gene Ontology - Biological Process | positive regulation of smooth muscle cell proliferation | predicted (intersection) | 29 | 16.35 | 0.047 |
| Gene Ontology - Biological Process | regulation of protein metabolic process | predicted (intersection) | 534 | 475.7 | 0.047 |
| Gene Ontology - Biological Process | sensory system development | predicted (union) | 154 | 126 | 0.048 |
| Gene Ontology - Biological Process | glycoprotein biosynthetic process | predicted (intersection) | 79 | 56.81 | 0.049 |
| Gene Ontology - Biological Process | response to radiation | predicted (intersection) | 109 | 82.6 | 0.049 |
| Gene Ontology - Biological Process | sig | predicted (intersection) | 139 | 109 | 0.050 |
| Gene Ontology - Biological Process | carbohydrate derivative metabolic process | predicted (intersection) | 235 | 195.8 | 0.050 |
| Gene Ontology - Biological Process | homeostatic process | predicted (union) | 650 | 592.6 | 0.050 |
| Gene Ontology - Biological Process | peptidyl-serine phosphorylation | predicted (union) | 105 | 82.27 | 0.050 |
| Gene Ontology - Cellular Component | nucleoplasm | predicted (intersection) | 766 | 637.3 | 2.01e-7 |
| Gene Ontology - Cellular Component | chromosome | predicted (union) | 950 | 820.3 | 2.36e-7 |
| Gene Ontology - Cellular Component | nuclear chromatin | predicted (union) | 738 | 624 | 2.36e-7 |

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|---|---|---|---|---|---|
| Gene Ontology - Cellular Component | chromatin | predicted (union) | 787 | 671.3 | 3.01e-7 |
| Gene Ontology - Cellular Component | nuclear chromosome | predicted (union) | 792 | 678 | 4.60e-7 |
| Gene Ontology - Cellular Component | chromatin | predicted (intersection) | 427 | 354.1 | 7.56e-4 |
| Gene Ontology - Cellular Component | early endosome | predicted (intersection) | 94 | 61.63 | 7.56e-4 |
| Gene Ontology - Cellular Component | nuclear chromatin | predicted (intersection) | 397 | 329.1 | 7.56e-4 |
| Gene Ontology - Cellular Component | postsynapse | predicted (intersection) | 154 | 111.1 | 7.56e-4 |
| Gene Ontology - Cellular Component | postsynaptic membrane | predicted (intersection) | 88 | 57.23 | 7.56e-4 |
| Gene Ontology - Cellular Component | synapse | predicted (intersection) | 270 | 213.6 | 7.56e-4 |
| Gene Ontology - Cellular Component | synaptic membrane | predicted (intersection) | 112 | 75.89 | 7.56e-4 |
| Gene Ontology - Cellular Component | chromosome | predicted (intersection) | 505 | 432.7 | 0.002 |
| Gene Ontology - Cellular Component | postsynaptic specialization | predicted (intersection) | 88 | 59.12 | 0.002 |
| Gene Ontology - Cellular Component | Golgi membrane | predicted (union) | 301 | 249.2 | 0.002 |
| Gene Ontology - Cellular Component | integral component of synaptic membrane | predicted (intersection) | 49 | 28.72 | 0.003 |
| Gene Ontology - Cellular Component | nuclear chromosome | predicted (intersection) | 420 | 357.6 | 0.004 |
| Gene Ontology - Cellular Component | Golgi apparatus | predicted (intersection) | 326 | 271.7 | 0.005 |

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|---|---|---|---|---|---|
| Gene Ontology - Cellular Component | guanyl-nucleotide exchange factor complex | predicted (intersection) | 8 | 2.096 | 0.005 |
| Gene Ontology - Cellular Component | postsynaptic density | predicted (intersection) | 80 | 54.09 | 0.005 |
| Gene Ontology - Cellular Component | asymmetric synapse | predicted (intersection) | 80 | 54.92 | 0.007 |
| Gene Ontology - Cellular Component | cis-Golgi network | predicted (intersection) | 18 | 7.757 | 0.007 |
| Gene Ontology - Cellular Component | dendritic tree | predicted (intersection) | 127 | 95.18 | 0.008 |
| Gene Ontology - Cellular Component | nuclear body | predicted (union) | 314 | 265.5 | 0.008 |
| Gene Ontology - Cellular Component | nuclear envelope | predicted (union) | 184 | 147.4 | 0.008 |
| Gene Ontology - Cellular Component | dendrite | predicted (intersection) | 126 | 94.76 | 0.009 |
| Gene Ontology - Cellular Component | glutamatergic synapse | predicted (intersection) | 92 | 66.46 | 0.013 |
| Gene Ontology - Cellular Component | intrinsic component of membrane | predicted (intersection) | 938 | 860.8 | 0.013 |
| Gene Ontology - Cellular Component | integral component of postsynaptic membrane | predicted (intersection) | 37 | 22.01 | 0.016 |
| Gene Ontology - Cellular Component | endomembrane system | predicted (intersection) | 858 | 785.5 | 0.017 |
| Gene Ontology - Cellular Component | integral component of membrane | predicted (intersection) | 907 | 832.7 | 0.017 |
| Gene Ontology - Cellular Component | Golgi apparatus | predicted (union) | 577 | 515.1 | 0.017 |

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|---|---|---|---|---|---|
| Gene Ontology - Cellular Component | Golgi membrane | predicted (intersection) | 165 | 131.4 | 0.018 |
| Gene Ontology - Cellular Component | synapse | predicted (union) | 459 | 405 | 0.022 |
| Gene Ontology - Cellular Component | dendrite | predicted (union) | 215 | 179.6 | 0.024 |
| Gene Ontology - Cellular Component | dendritic tree | predicted (union) | 216 | 180.4 | 0.024 |
| Gene Ontology - Cellular Component | postsynapse | predicted (union) | 249 | 210.6 | 0.024 |
| Gene Ontology - Cellular Component | synaptic membrane | predicted (union) | 176 | 143.9 | 0.024 |
| Gene Ontology - Cellular Component | transcriptional repressor complex | predicted (union) | 44 | 29.01 | 0.024 |
| Gene Ontology - Cellular Component | cell junction | predicted (union) | 485 | 432 | 0.025 |
| Gene Ontology - Cellular Component | presynaptic membrane | predicted (intersection) | 42 | 26.62 | 0.027 |
| Gene Ontology - Cellular Component | cell junction | predicted (intersection) | 269 | 227.9 | 0.028 |
| Gene Ontology - Cellular Component | postsynaptic density | predicted (union) | 129 | 102.5 | 0.028 |
| Gene Ontology - Cellular Component | postsynaptic specialization | predicted (union) | 139 | 112.1 | 0.035 |
| Gene Ontology - Cellular Component | endoplasmic reticulum-Golgi intermediate compartment | predicted (intersection) | 35 | 21.8 | 0.043 |
| Gene Ontology - Cellular Component | host cell | predicted (intersection) | 24 | 13.42 | 0.043 |

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|---|---|---|---|---|---|
| Gene Ontology - Cellular Component | nucleotide-activated protein kinase complex | predicted (intersection) | 5 | 1.258 | 0.047 |
| Gene Ontology - Cellular Component | mitotic spindle | predicted (intersection) | 29 | 17.4 | 0.049 |
| Gene Ontology - Cellular Component | nuclear envelope | predicted (intersection) | 101 | 77.78 | 0.049 |
| Gene Ontology - Molecular Function | DNA-binding transcription factor activity | predicted (union) | 849 | 707.8 | 7.15e-10 |
| Gene Ontology - Molecular Function | DNA-binding transcription factor activity, RNA polymerase II-specific | predicted (union) | 681 | 566.3 | 5.96e-8 |
| Gene Ontology - Molecular Function | purine nucleotide binding | predicted (union) | 748 | 639.5 | 2.09e-6 |
| Gene Ontology - Molecular Function | purine ribonucleotide binding | predicted (union) | 745 | 637.1 | 2.09e-6 |
| Gene Ontology - Molecular Function | nucleotide binding | predicted (union) | 824 | 712.6 | 2.97e-6 |
| Gene Ontology - Molecular Function | purine ribonucleoside triphosphate binding | predicted (union) | 715 | 611.6 | 3.19e-6 |
| Gene Ontology - Molecular Function | DNA binding | predicted (union) | 889 | 776.6 | 5.16e-6 |
| Gene Ontology - Molecular Function | cation binding | predicted (intersection) | 881 | 763.3 | 2.98e-5 |
| Gene Ontology - Molecular Function | metal ion binding | predicted (intersection) | 872 | 752.4 | 2.98e-5 |
| Gene Ontology - Molecular Function | kinase activity | predicted (union) | 546 | 463.8 | 4.95e-5 |

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|---|---|---|---|---|---|
| Gene Ontology - Molecular Function | ATP binding | predicted (union) | 595 | 511.1 | 7.00e-5 |
| Gene Ontology - Molecular Function | adenyl nucleotide binding | predicted (union) | 618 | 532.2 | 7.00e-5 |
| Gene Ontology - Molecular Function | carbohydrate derivative binding | predicted (union) | 842 | 743.2 | 7.00e-5 |
| Gene Ontology - Molecular Function | DNA-binding transcription factor activity | predicted (intersection) | 454 | 373.4 | 2.59e-4 |
| Gene Ontology - Molecular Function | enzyme binding | predicted (union) | 773 | 684 | 2.91e-4 |
| Gene Ontology - Molecular Function | phosphotransferase activity, alcohol group as acceptor | predicted (union) | 499 | 426.8 | 2.91e-4 |
| Gene Ontology - Molecular Function | protein serine/threonine kinase activity | predicted (union) | 328 | 270.2 | 3.21e-4 |
| Gene Ontology - Molecular Function | enzyme binding | predicted (intersection) | 438 | 360.8 | 3.80e-4 |
| Gene Ontology - Molecular Function | protein kinase activity | predicted (union) | 458 | 390.7 | 4.17e-4 |
| Gene Ontology - Molecular Function | small molecule binding | predicted (union) | 923 | 828.6 | 4.17e-4 |
| Gene Ontology - Molecular Function | DNA-binding transcription factor activity, RNA polymerase II-specific | predicted (intersection) | 365 | 298.7 | 0.001 |
| Gene Ontology - Molecular Function | kinase activity | predicted (intersection) | 306 | 244.6 | 0.001 |
| Gene Ontology - Molecular Function | double-stranded DNA binding | predicted (union) | 319 | 265.5 | 0.001 |

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|---|---|---|---|---|---|
| Gene Ontology - Molecular Function | drug binding | predicted (union) | 658 | 583 | 0.001 |
| Gene Ontology - Molecular Function | phosphoric ester hydrolase activity | predicted (union) | 226 | 182.4 | 0.001 |
| Gene Ontology - Molecular Function | sequence-specific DNA binding | predicted (union) | 384 | 326.3 | 0.001 |
| Gene Ontology - Molecular Function | carbohydrate derivative binding | predicted (intersection) | 462 | 392 | 0.002 |
| Gene Ontology - Molecular Function | nucleotide binding | predicted (intersection) | 445 | 375.9 | 0.002 |
| Gene Ontology - Molecular Function | protein kinase activity | predicted (intersection) | 261 | 206.1 | 0.002 |
| Gene Ontology - Molecular Function | purine nucleotide binding | predicted (intersection) | 403 | 337.3 | 0.002 |
| Gene Ontology - Molecular Function | purine ribonucleotide binding | predicted (intersection) | 402 | 336 | 0.002 |
| Gene Ontology - Molecular Function | transferase activity | predicted (intersection) | 559 | 483.2 | 0.002 |
| Gene Ontology - Molecular Function | RNA polymerase II proximal promoter sequence-specific DNA binding | predicted (union) | 193 | 153.4 | 0.002 |
| Gene Ontology - Molecular Function | sequence-specific double-stranded DNA binding | predicted (union) | 290 | 241.2 | 0.002 |
| Gene Ontology - Molecular Function | transcription regulatory region sequence-specific DNA binding | predicted (union) | 276 | 228.9 | 0.002 |

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|---|---|---|---|---|---|
| Gene Ontology - Molecular Function | nucleic acid binding | predicted (intersection) | 759 | 674 | 0.003 |
| Gene Ontology - Molecular Function | phosphoric ester hydrolase activity | predicted (intersection) | 132 | 96.22 | 0.003 |
| Gene Ontology - Molecular Function | phosphotransferase activity, alcohol group as acceptor | predicted (intersection) | 278 | 225.2 | 0.003 |
| Gene Ontology - Molecular Function | RNA polymerase II regulatory region DNA binding | predicted (union) | 257 | 212.6 | 0.003 |
| Gene Ontology - Molecular Function | RNA polymerase II regulatory region sequence-specific DNA binding | predicted (union) | 257 | 212.2 | 0.003 |
| Gene Ontology - Molecular Function | transcription regulatory region DNA binding | predicted (union) | 318 | 268.7 | 0.003 |
| Gene Ontology - Molecular Function | DNA binding | predicted (intersection) | 477 | 409.6 | 0.004 |
| Gene Ontology - Molecular Function | purine ribonucleoside triphosphate binding | predicted (intersection) | 383 | 322.6 | 0.004 |
| Gene Ontology - Molecular Function | ubiquitin-like protein transferase activity | predicted (union) | 162 | 128.4 | 0.005 |
| Gene Ontology - Molecular Function | RNA polymerase II proximal promoter sequence-specific DNA binding | predicted (intersection) | 112 | 80.92 | 0.006 |

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|---|---|---|---|---|---|
| Gene Ontology - Molecular Function | proximal promoter sequence-specific DNA binding | predicted (union) | 196 | 159.4 | 0.006 |
| Gene Ontology - Molecular Function | histone acetyltransferase binding | predicted (intersection) | 14 | 5.241 | 0.008 |
| Gene Ontology - Molecular Function | transcription coregulator activity | predicted (intersection) | 129 | 96.22 | 0.008 |
| Gene Ontology - Molecular Function | proximal promoter sequence-specific DNA binding | predicted (intersection) | 114 | 84.06 | 0.011 |
| Gene Ontology - Molecular Function | protein serine/threonine kinase activity | predicted (intersection) | 180 | 142.6 | 0.014 |
| Gene Ontology - Molecular Function | transcription regulatory region DNA binding | predicted (intersection) | 179 | 141.7 | 0.014 |
| Gene Ontology - Molecular Function | protein phosphatase 1 binding | predicted (union) | 13 | 5.961 | 0.014 |
| Gene Ontology - Molecular Function | phosphatase activity | predicted (union) | 169 | 137.1 | 0.015 |
| Gene Ontology - Molecular Function | histone binding | predicted (intersection) | 51 | 32.49 | 0.016 |
| Gene Ontology - Molecular Function | adenyl nucleotide binding | predicted (intersection) | 330 | 280.7 | 0.017 |
| Gene Ontology - Molecular Function | kinase binding | predicted (intersection) | 156 | 122.2 | 0.017 |
| Gene Ontology - Molecular Function | DNA-binding transcription activator activity, RNA polymerase II-specific | predicted (union) | 173 | 141.1 | 0.017 |

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|---|---|---|---|---|---|
| Gene Ontology - Molecular Function | ubiquitin-protein transferase activity | predicted (union) | 148 | 118.8 | 0.018 |
| Gene Ontology - Molecular Function | hydrolase activity, acting on ester bonds | predicted (union) | 354 | 308.8 | 0.021 |
| Gene Ontology - Molecular Function | small molecule binding | predicted (intersection) | 495 | 437.1 | 0.024 |
| Gene Ontology - Molecular Function | RNA polymerase II regulatory region DNA binding | predicted (intersection) | 143 | 112.2 | 0.025 |
| Gene Ontology - Molecular Function | RNA polymerase II regulatory region sequence-specific DNA binding | predicted (intersection) | 143 | 111.9 | 0.025 |
| Gene Ontology - Molecular Function | SMAD binding | predicted (intersection) | 25 | 13.42 | 0.025 |
| Gene Ontology - Molecular Function | phosphoric diester hydrolase activity | predicted (intersection) | 40 | 24.53 | 0.025 |
| Gene Ontology - Molecular Function | protein serine/threonine/tyrosine kinase activity | predicted (intersection) | 32 | 18.45 | 0.025 |
| Gene Ontology - Molecular Function | transcription coactivator activity | predicted (intersection) | 79 | 56.6 | 0.025 |
| Gene Ontology - Molecular Function | transcription coregulator activity | predicted (union) | 217 | 182.4 | 0.025 |
| Gene Ontology - Molecular Function | ATP binding | predicted (intersection) | 315 | 269.6 | 0.028 |
| Gene Ontology - Molecular Function | ubiquitin conjugating enzyme binding | predicted (union) | 10 | 4.372 | 0.031 |

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|---|---|---|---|---|---|
| Gene Ontology - Molecular Function | protein domain specific binding | predicted (union) | 274 | 236.1 | 0.033 |
| Gene Ontology - Molecular Function | DNA binding, bending | predicted (union) | 13 | 6.359 | 0.038 |
| Gene Ontology - Molecular Function | transcription regulatory region sequence-specific DNA binding | predicted (intersection) | 151 | 120.8 | 0.041 |
| Gene Ontology - Molecular Function | ubiquitin protein ligase activity | predicted (union) | 74 | 55.64 | 0.046 |
| Gene Ontology - Molecular Function | enhancer binding | predicted (union) | 52 | 36.96 | 0.047 |
| KEGG | Endometrial cancer | experimental (any) | 4 | 0.284 | 0.012 |
| KEGG | Chronic myeloid leukemia | experimental (strong) | 2 | 0.139 | 0.021 |
| KEGG | ErbB signaling pathway | experimental (strong) | 2 | 0.139 | 0.021 |
| KEGG | HIF-1 signaling pathway | experimental (strong) | 2 | 0.157 | 0.021 |
| KEGG | Measles | experimental (strong) | 2 | 0.175 | 0.021 |
| KEGG | Prostate cancer | experimental (strong) | 2 | 0.162 | 0.021 |
| KEGG | Small cell lung cancer | experimental (strong) | 2 | 0.139 | 0.021 |
| KEGG | Epstein-Barr virus infection | experimental (strong) | 2 | 0.201 | 0.022 |
| KEGG | FoxO signaling pathway | experimental (strong) | 2 | 0.208 | 0.022 |
| KEGG | Circadian rhythm | predicted (union) | 20 | 10.73 | 0.024 |

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|---|---|---|---|---|---|
| KEGG | FoxO signaling pathway | predicted (union) | 66 | 46.5 | 0.024 |
| KEGG | Proteoglycans in cancer | predicted (union) | 104 | 79.88 | 0.024 |
| KEGG | Renal cell carcinoma | predicted (union) | 36 | 22.65 | 0.024 |
| KEGG | Hepatitis B | experimental (strong) | 2 | 0.237 | 0.025 |
| KEGG | Colorectal cancer | predicted (union) | 35 | 22.26 | 0.026 |
| KEGG | Ubiquitin mediated proteolysis | predicted (union) | 69 | 50.87 | 0.036 |
| KEGG | MAPK signaling pathway | predicted (union) | 115 | 91.41 | 0.038 |
| KEGG | mTOR signaling pathway | predicted (union) | 33 | 21.46 | 0.041 |
| KEGG | Transcriptional misregulation in cancer | predicted (union) | 82 | 63.19 | 0.048 |
| Reactome | Gene expression (Transcription) | predicted (union) | 639 | 517 | 1.12e-9 |
| Reactome | RNA Polymerase II Transcription | predicted (union) | 571 | 465.8 | 5.91e-8 |
| Reactome | Gene expression (Transcription) | predicted (intersection) | 358 | 272.7 | 4.01e-6 |
| Reactome | Generic Transcription Pathway | predicted (union) | 508 | 420.5 | 6.29e-6 |
| Reactome | RNA Polymerase II Transcription | predicted (intersection) | 323 | 245.7 | 1.09e-5 |
| Reactome | Generic Transcription Pathway | predicted (intersection) | 289 | 221.8 | 1.06e-4 |

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|---|---|---|---|---|---|
| Reactome | Diseases of signal transduction | predicted (union) | 185 | 138.7 | 1.24e-4 |
| Reactome | Intracellular signaling by second messengers | predicted (union) | 147 | 109.7 | 0.001 |
| Reactome | AKT phosphorylates targets in the cytosol | experimental (strong) | 2 | 0.020 | 0.004 |
| Reactome | Constitutive Signaling by AKT1 E17K in Cancer | experimental (strong) | 2 | 0.040 | 0.006 |
| Reactome | Estrogen-dependent nuclear events downstream of ESR-membrane signaling | experimental (strong) | 2 | 0.042 | 0.006 |
| Reactome | PIP3 activates AKT signaling | predicted (union) | 126 | 94.98 | 0.009 |
| Reactome | Cell Cycle, Mitotic | experimental (strong) | 3 | 0.294 | 0.009 |
| Reactome | Cyclin A:Cdk2-associated events at S phase entry | experimental (strong) | 2 | 0.064 | 0.009 |
| Reactome | Cyclin E associated events during G1/S transition | experimental (strong) | 2 | 0.062 | 0.009 |
| Reactome | Neuronal System | predicted (intersection) | 106 | 73.79 | 0.010 |
| Reactome | Cell Cycle | experimental (strong) | 3 | 0.343 | 0.011 |

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| Reactome | Extra-nuclear estrogen signaling | experimental (strong) | 2 | 0.102 | 0.011 |
| Reactome | FOXO-mediated transcription | experimental (strong) | 2 | 0.104 | 0.011 |
| Reactome | G1/S Transition | experimental (strong) | 2 | 0.106 | 0.011 |
| Reactome | S Phase | experimental (strong) | 2 | 0.108 | 0.011 |
| Reactome | Cell Cycle Checkpoints | experimental (strong) | 2 | 0.137 | 0.016 |
| Reactome | Mitotic G1-G1/S phases | experimental (strong) | 2 | 0.142 | 0.016 |
| Reactome | PI3K/AKT Signaling in Cancer | experimental (strong) | 2 | 0.150 | 0.016 |
| Reactome | Signal Transduction | experimental (strong) | 5 | 1.708 | 0.016 |
| Reactome | Activation of AKT2 | experimental (any) | 2 | 0.023 | 0.020 |
| Reactome | Constitutive Signaling by AKT1 E17K in Cancer | experimental (any) | 3 | 0.148 | 0.020 |
| Reactome | VEGFR2 mediated vascular permeability | experimental (any) | 3 | 0.153 | 0.020 |
| Reactome | SUMOylation | predicted (union) | 87 | 63.19 | 0.022 |
| Reactome | RHO GTPase Effectors | experimental (strong) | 2 | 0.192 | 0.024 |
| Reactome | Signaling by BRAF and RAF fusions | predicted (union) | 39 | 24.24 | 0.025 |
| Reactome | ESR-mediated signaling | experimental (strong) | 2 | 0.208 | 0.026 |

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| Reactome | Ligand-receptor interactions | experimental (any) | 2 | 0.045 | 0.028 |
| Reactome | Signaling by Nuclear Receptors | experimental (strong) | 2 | 0.232 | 0.030 |
| Reactome | Signaling by Rho GTPases | experimental (strong) | 2 | 0.248 | 0.032 |
| Reactome | Negative regulation of the PI3K/AKT network | predicted (union) | 59 | 40.93 | 0.038 |
| Reactome | PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling | predicted (union) | 56 | 38.55 | 0.038 |
| Reactome | Regulation of cholesterol biosynthesis by SREBP (SREBF) | predicted (union) | 32 | 19.47 | 0.038 |
| Reactome | SUMO E3 ligases SUMOylate target proteins | predicted (union) | 83 | 61.2 | 0.038 |
| Reactome | Disease | experimental (strong) | 3 | 0.739 | 0.038 |
| Reactome | PIP3 activates AKT signaling | experimental (strong) | 2 | 0.294 | 0.040 |
| Reactome | Constitutive Signaling by Aberrant PI3K in Cancer | predicted (union) | 43 | 28.22 | 0.041 |
| Reactome | Transcriptional Regulation by TP53 | experimental (strong) | 2 | 0.303 | 0.041 |
| Reactome | Generic Transcription Pathway | experimental (strong) | 3 | 0.838 | 0.044 |

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| Reactome | Intracellular signaling by second messengers | experimental (strong) | 2 | 0.325 | 0.044 |
| Reactome | RNA Polymerase II Transcription | experimental (strong) | 3 | 0.858 | 0.045 |
| WikiPathways | MECP2 and Associated Rett Syndrome | predicted (intersection) | 28 | 11.74 | 5.86e-4 |
| WikiPathways | Pathways Regulating Hippo Signaling | predicted (union) | 54 | 34.97 | 0.016 |
| WikiPathways | Brain-Derived Neurotrophic Factor (BDNF) signaling pathway | predicted (union) | 74 | 52.06 | 0.017 |
| WikiPathways | Hippo-Merlin Signaling Dysregulation | predicted (union) | 61 | 41.73 | 0.017 |
| WikiPathways | Endometrial cancer | experimental (any) | 4 | 0.346 | 0.020 |
| WikiPathways | Aryl Hydrocarbon Receptor | experimental (any) | 3 | 0.250 | 0.021 |
| WikiPathways | Integrated Cancer Pathway | experimental (any) | 3 | 0.244 | 0.021 |
| WikiPathways | Integrin-mediated Cell Adhesion | experimental (any) | 4 | 0.511 | 0.021 |
| WikiPathways | Vitamin D Receptor Pathway | experimental (any) | 5 | 0.874 | 0.021 |
| WikiPathways | Energy Metabolism | predicted (union) | 29 | 17.49 | 0.024 |

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| WikiPathways | Epithelial to mesenchymal transition in colorectal cancer | predicted (union) | 79 | 57.63 | 0.024 |
| WikiPathways | Factors and pathways affecting insulin-like growth factor (IGF1)-Akt signaling | predicted (union) | 20 | 10.73 | 0.024 |
| WikiPathways | Sterol Regulatory Element-Binding Proteins (SREBP) signalling | predicted (union) | 39 | 25.04 | 0.024 |
| WikiPathways | Synaptic signaling pathways associated with autism spectrum disorder | predicted (union) | 29 | 17.49 | 0.024 |
| WikiPathways | ErbB Signaling Pathway | experimental (strong) | 2 | 0.150 | 0.024 |
| WikiPathways | Signaling Pathways in Glioblastoma | experimental (strong) | 2 | 0.159 | 0.024 |
| WikiPathways | MECP2 and Associated Rett Syndrome | predicted (union) | 35 | 22.26 | 0.025 |
| WikiPathways | DNA Damage Response (only ATM dependent) | experimental (strong) | 2 | 0.204 | 0.026 |
| WikiPathways | Human Thyroid Stimulating Hormone (TSH) signaling pathway | predicted (intersection) | 25 | 12.37 | 0.029 |

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| WikiPathways | Pathways Regulating Hippo Signaling | predicted (intersection) | 33 | 18.45 | 0.029 |
| WikiPathways | TGF-beta Signaling Pathway | predicted (intersection) | 41 | 24.32 | 0.029 |
| WikiPathways | Human Thyroid Stimulating Hormone (TSH) signaling pathway | predicted (union) | 36 | 23.45 | 0.031 |
| WikiPathways | Leptin signaling pathway | predicted (union) | 40 | 26.63 | 0.031 |
| WikiPathways | Prolactin Signaling Pathway | predicted (union) | 41 | 27.42 | 0.031 |
| WikiPathways | Chromosomal and microsatellite instability in colorectal cancer | predicted (union) | 40 | 27.02 | 0.032 |
| WikiPathways | Endoderm Differentiation | predicted (union) | 67 | 49.68 | 0.032 |
| WikiPathways | Endometrial cancer | predicted (union) | 34 | 22.26 | 0.032 |
| WikiPathways | IL-1 signaling pathway | predicted (union) | 30 | 19.08 | 0.032 |
| WikiPathways | Interleukin-11 Signaling Pathway | predicted (union) | 26 | 15.9 | 0.032 |
| WikiPathways | TGF-beta Signaling Pathway | predicted (union) | 63 | 46.1 | 0.032 |
| WikiPathways | Association Between Physico-Chemical Features and Toxicity Associated Pathways | experimental (any) | 3 | 0.352 | 0.035 |

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|---|---|---|---|---|---|
| WikiPathways | Human Thyroid Stimulating Hormone (TSH) signaling pathway | experimental (any) | 3 | 0.369 | 0.035 |
| WikiPathways | Imatinib and Chronic Myeloid Leukemia | experimental (any) | 2 | 0.114 | 0.035 |
| WikiPathways | miRNAs involved in DNA damage response | experimental (any) | 2 | 0.096 | 0.035 |
| WikiPathways | Prion disease pathway | predicted (union) | 21 | 12.32 | 0.038 |
| WikiPathways | Chromosomal and microsatellite instability in colorectal cancer | experimental (any) | 3 | 0.409 | 0.038 |
| WikiPathways | IL-7 Signaling Pathway | experimental (any) | 2 | 0.136 | 0.038 |
| WikiPathways | ErbB Signaling Pathway | predicted (union) | 45 | 31.79 | 0.042 |
| WikiPathways | MAPK Signaling Pathway | predicted (union) | 109 | 87.43 | 0.042 |
| WikiPathways | Oncostatin M Signaling Pathway | predicted (union) | 36 | 24.24 | 0.042 |
| WikiPathways | Phosphodiesterases in neuronal function | predicted (union) | 29 | 18.68 | 0.042 |
| WikiPathways | Signaling Pathways in Glioblastoma | predicted (union) | 41 | 28.61 | 0.046 |
| WikiPathways | Signaling Pathways in Glioblastoma | experimental (any) | 3 | 0.454 | 0.046 |

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|---|---|---|---|---|---|
| WikiPathways | Sleep regulation | experimental (any) | 2 | 0.165 | 0.047 |
| WikiPathways | ERK Pathway in Huntington's Disease | predicted (intersection) | 9 | 2.935 | 0.048 |

**Supplementary Table 1a**

| **Database** | **Pathway** | **Evidence** | **Hits** | **Expected hits** | **P-value** |
|---|---|---|---|---|---|
| Ontology - Biological | response to | experimental (any) | 51 | 12 | 6.63e-16 |
| Ontology - Biological | mediated signaling | experimental (any) | 42 | 8.304 | 1.67e-15 |
| Ontology - Biological | to cytokine | experimental (any) | 51 | 12.88 | 4.51e-15 |
| Ontology - Biological | defense response | experimental (any) | 50 | 16.09 | 8.70e-11 |
| Ontology - Biological | to external biotic | experimental (any) | 47 | 14.39 | 8.70e-11 |
| Ontology - Biological | to other organism | experimental (any) | 47 | 14.38 | 8.70e-11 |
| Ontology - Biological | response to organic | experimental (any) | 69 | 28.82 | 1.88e-10 |
| Ontology - Biological | immune response | experimental (any) | 57 | 20.93 | 1.88e-10 |
| Ontology - Biological | system process | experimental (any) | 72 | 31.03 | 1.88e-10 |
| Ontology - Biological | immune response | experimental (any) | 35 | 9.221 | 1.65e-9 |
| Ontology - Biological | response to type I | experimental (any) | 13 | 0.983 | 2.31e-9 |
| Ontology - Biological | to organic substance | experimental (any) | 75 | 35.2 | 2.31e-9 |
| Ontology - Biological | interferon signaling | experimental (any) | 13 | 0.983 | 2.31e-9 |
| Ontology - Biological | of gene expressio | (intersection) | 821 | 670.6 | 3.32e-9 |
| Ontology - Biological | to type I interferon | experimental (any) | 13 | 1.023 | 3.64e-9 |
| Ontology - Biological | apoptotic process | experimental (any) | 55 | 21.68 | 5.11e-9 |
| Gene Ontology - Biological Process | cell surface receptor signaling pathway | experimental (any) | 69 | 31.41 | 5.11e-9 |
| Gene Ontology - Biological Process | positive regulation of intracellular signal transduction | experimental (any) | 37 | 10.95 | 6.62e-9 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of cellular metabolic process | experimental (any) | 73 | 34.83 | 7.28e-9 |
| Gene Ontology - Biological Process | positive regulation of signal transduction | experimental (any) | 49 | 18.12 | 7.28e-9 |
| Gene Ontology - Biological Process | response to virus | experimental (any) | 21 | 3.561 | 7.28e-9 |
| Gene Ontology - Biological Process | cell death | experimental (any) | 58 | 24.22 | 9.49e-9 |
| Gene Ontology - Biological Process | cellular response to lipopolysaccharide | experimental (any) | 16 | 2.006 | 1.61e-8 |
| Gene Ontology - Biological Process | programmed cell death | experimental (any) | 55 | 22.71 | 2.07e-8 |
| Gene Ontology - Biological Process | cellular response to molecule of bacterial origin | experimental (any) | 16 | 2.099 | 2.91e-8 |
| Gene Ontology - Biological Process | gene expression | predicted (intersection) | 947 | 798.2 | 3.88e-8 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of cellular protein metabolic process | experimental (any) | 45 | 16.69 | 4.69e-8 |
| Gene Ontology - Biological Process | regulation of intracellular signal transduction | experimental (any) | 50 | 19.96 | 4.98e-8 |
| Gene Ontology - Biological Process | regulation of RNA metabolic process | predicted (intersection) | 703 | 572 | 5.32e-8 |
| Gene Ontology - Biological Process | positive regulation of protein modification process | experimental (any) | 38 | 12.69 | 7.11e-8 |
| Gene Ontology - Biological Process | regulation of cell death | experimental (any) | 48 | 18.92 | 7.46e-8 |
| Gene Ontology - Biological Process | response to lipopolysaccharide | experimental (any) | 19 | 3.348 | 8.07e-8 |
| Gene Ontology - Biological Process | cellular macromolecule biosynthetic process | predicted (intersection) | 873 | 733.6 | 1.05e-7 |
| Gene Ontology - Biological Process | positive regulation of metabolic process | experimental (any) | 74 | 38.04 | 1.14e-7 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of cell adhesion | experimental (any) | 28 | 7.534 | 1.35e-7 |
| Gene Ontology - Biological Process | positive regulation of phosphorylation | experimental (any) | 34 | 10.76 | 1.38e-7 |
| Gene Ontology - Biological Process | positive regulation of protein phosphorylation | experimental (any) | 33 | 10.22 | 1.39e-7 |
| Gene Ontology - Biological Process | response to molecule of bacterial origin | experimental (any) | 19 | 3.494 | 1.41e-7 |
| Gene Ontology - Biological Process | intracellular signal transduction | experimental (any) | 61 | 28.59 | 1.66e-7 |
| Gene Ontology - Biological Process | leukocyte adhesion to vascular endothelial cell | experimental (any) | 8 | 0.385 | 1.71e-7 |
| Gene Ontology - Biological Process | positive regulation of protein metabolic process | experimental (any) | 45 | 17.66 | 1.89e-7 |
| Gene Ontology - Biological Process | regulation of cell population proliferation | experimental (any) | 45 | 17.67 | 1.89e-7 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of leukocyte cell-cell adhesion | experimental (any) | 16 | 2.471 | 1.99e-7 |
| Gene Ontology - Biological Process | positive regulation of NF-kappaB transcription factor activity | experimental (any) | 14 | 1.82 | 2.06e-7 |
| Gene Ontology - Biological Process | positive regulation of cell adhesion | experimental (any) | 21 | 4.531 | 2.84e-7 |
| Gene Ontology - Biological Process | regulation of immune system process | experimental (any) | 42 | 16.1 | 3.23e-7 |
| Gene Ontology - Biological Process | positive regulation of cell-cell adhesion | experimental (any) | 17 | 2.963 | 3.62e-7 |
| Gene Ontology - Biological Process | positive regulation of leukocyte adhesion to vascular endothelial cell | experimental (any) | 6 | 0.173 | 3.97e-7 |
| Gene Ontology - Biological Process | lipopolysaccharide-mediated signaling pathway | experimental (any) | 9 | 0.638 | 5.53e-7 |
| Gene Ontology - Biological Process | RNA biosynthetic process | predicted (intersection) | 686 | 566.7 | 6.21e-7 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | nucleobase-containing compound metabolic process | predicted (intersection) | 986 | 849.2 | 6.21e-7 |
| Gene Ontology - Biological Process | regulation of transcription by RNA polymerase II | predicted (intersection) | 512 | 406.5 | 6.21e-7 |
| Gene Ontology - Biological Process | transcription by RNA polymerase II | predicted (intersection) | 540 | 431.4 | 6.21e-7 |
| Gene Ontology - Biological Process | transcription, DNA-templated | predicted (intersection) | 675 | 555.2 | 6.21e-7 |
| Gene Ontology - Biological Process | regulation of viral genome replication | experimental (any) | 11 | 1.116 | 6.45e-7 |
| Gene Ontology - Biological Process | positive regulation of cellular biosynthetic process | experimental (any) | 49 | 21.33 | 7.55e-7 |
| Gene Ontology - Biological Process | negative regulation of viral genome replication | experimental (any) | 9 | 0.664 | 7.56e-7 |
| Gene Ontology - Biological Process | regulation of protein phosphorylation | experimental (any) | 39 | 14.81 | 8.41e-7 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of cytokine production | experimental (any) | 26 | 7.334 | 8.81e-7 |
| Gene Ontology - Biological Process | regulation of programmed cell death | experimental (any) | 43 | 17.47 | 9.36e-7 |
| Gene Ontology - Biological Process | response to bacterium | experimental (any) | 23 | 5.886 | 9.91e-7 |
| Gene Ontology - Biological Process | secretion | experimental (any) | 43 | 17.53 | 9.91e-7 |
| Gene Ontology - Biological Process | leukocyte cell-cell adhesion | experimental (any) | 18 | 3.627 | 9.94e-7 |
| Gene Ontology - Biological Process | negative regulation of apoptotic process | experimental (any) | 31 | 10.19 | 1.08e-6 |
| Gene Ontology - Biological Process | response to lipid | experimental (any) | 31 | 10.19 | 1.08e-6 |
| Gene Ontology - Biological Process | cytokine production | experimental (any) | 27 | 8.025 | 1.20e-6 |
| Gene Ontology - Biological Process | defense response to virus | experimental (any) | 15 | 2.525 | 1.33e-6 |
| Gene Ontology - Biological Process | RNA metabolic process | predicted (intersection) | 819 | 695 | 1.48e-6 |
| Gene Ontology - Biological Process | regulation of RNA biosynthetic process | predicted (intersection) | 653 | 539.5 | 1.48e-6 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of transcription, DNA-templated | predicted (intersection) | 639 | 526.1 | 1.48e-6 |
| Gene Ontology - Biological Process | negative regulation of programmed cell death | experimental (any) | 31 | 10.39 | 1.56e-6 |
| Gene Ontology - Biological Process | regulation of apoptotic process | experimental (any) | 42 | 17.22 | 1.56e-6 |
| Gene Ontology - Biological Process | cell population proliferation | experimental (any) | 48 | 21.3 | 1.57e-6 |
| Gene Ontology - Biological Process | I-kappaB kinase/NF-kappaB signaling | experimental (any) | 16 | 2.963 | 1.66e-6 |
| Gene Ontology - Biological Process | signal transduction | experimental (any) | 94 | 58.34 | 2.08e-6 |
| Gene Ontology - Biological Process | regulation of nucleic acid-templated transcription | predicted (intersection) | 650 | 538.2 | 2.16e-6 |
| Gene Ontology - Biological Process | response to mechanical stimulus | experimental (any) | 14 | 2.285 | 2.39e-6 |
| Gene Ontology - Biological Process | hemopoiesis | experimental (any) | 29 | 9.62 | 3.34e-6 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of phosphorylation | experimental (any) | 40 | 16.45 | 3.47e-6 |
| Gene Ontology - Biological Process | negative regulation of cell death | experimental (any) | 32 | 11.43 | 3.56e-6 |
| Gene Ontology - Biological Process | negative regulation of viral process | experimental (any) | 10 | 1.09 | 4.04e-6 |
| Gene Ontology - Biological Process | leukocyte activation | experimental (any) | 35 | 13.38 | 4.26e-6 |
| Gene Ontology - Biological Process | cellular response to lipopolysaccharide | experimental (strong) | 14 | 2.271 | 5.07e-6 |
| Gene Ontology - Biological Process | intracellular signal transduction | experimental (strong) | 45 | 21.89 | 5.07e-6 |
| Gene Ontology - Biological Process | positive regulation of cellular protein metabolic process | experimental (strong) | 37 | 14.84 | 5.07e-6 |
| Gene Ontology - Biological Process | positive regulation of phosphorylation | experimental (strong) | 30 | 10.66 | 5.07e-6 |
| Gene Ontology - Biological Process | positive regulation of protein metabolic process | experimental (strong) | 37 | 15.74 | 5.07e-6 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of protein modification process | experimental (strong) | 32 | 12.13 | 5.07e-6 |
| Gene Ontology - Biological Process | positive regulation of protein phosphorylation | experimental (strong) | 30 | 10.32 | 5.07e-6 |
| Gene Ontology - Biological Process | regulation of intracellular signal transduction | experimental (strong) | 38 | 16.29 | 5.07e-6 |
| Gene Ontology - Biological Process | viral genome replication | experimental (any) | 11 | 1.422 | 5.42e-6 |
| Gene Ontology - Biological Process | protein phosphorylation | experimental (any) | 46 | 20.95 | 5.99e-6 |
| Gene Ontology - Biological Process | regulation of cellular protein metabolic process | experimental (any) | 55 | 27.49 | 5.99e-6 |
| Gene Ontology - Biological Process | regulation of immune response | experimental (any) | 30 | 10.55 | 6.20e-6 |
| Gene Ontology - Biological Process | positive regulation of macromolecule biosynthetic process | experimental (any) | 45 | 20.32 | 6.33e-6 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | viral process | experimental (any) | 29 | 9.992 | 6.45e-6 |
| Gene Ontology - Biological Process | leukocyte differentiation | experimental (any) | 21 | 5.647 | 6.70e-6 |
| Gene Ontology - Biological Process | regulation of signal transduction | experimental (any) | 66 | 36.17 | 6.80e-6 |
| Gene Ontology - Biological Process | positive regulation of immune system process | experimental (any) | 31 | 11.24 | 6.96e-6 |
| Gene Ontology - Biological Process | cell activation | experimental (any) | 37 | 15.04 | 7.21e-6 |
| Gene Ontology - Biological Process | positive regulation of transcription, DNA-templated | experimental (any) | 39 | 16.38 | 7.41e-6 |
| Gene Ontology - Biological Process | cellular response to lipid | experimental (any) | 23 | 6.776 | 8.25e-6 |
| Gene Ontology - Biological Process | inflammatory response | experimental (any) | 23 | 6.79 | 8.44e-6 |
| Gene Ontology - Biological Process | cellular response to molecule of bacterial origin | experimental (strong) | 14 | 2.4 | 8.85e-6 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | leukocyte adhesion to vascular endothelial cell | experimental (strong) | 7 | 0.413 | 8.85e-6 |
| Gene Ontology - Biological Process | positive regulation of intracellular signal transduction | experimental (strong) | 29 | 10.51 | 8.85e-6 |
| Gene Ontology - Biological Process | positive regulation of NIK/NF-kappaB signaling | experimental (any) | 9 | 0.930 | 9.02e-6 |
| Gene Ontology - Biological Process | positive regulation of cytokine production | experimental (any) | 19 | 4.797 | 9.02e-6 |
| Gene Ontology - Biological Process | positive regulation of signal transduction | experimental (strong) | 36 | 15.62 | 9.35e-6 |
| Gene Ontology - Biological Process | lipopolysaccharide-mediated signaling pathway | experimental (strong) | 9 | 0.852 | 9.68e-6 |
| Gene Ontology - Biological Process | positive regulation of cellular metabolic process | experimental (strong) | 50 | 28.06 | 9.68e-6 |
| Gene Ontology - Biological Process | cell adhesion | experimental (any) | 36 | 14.62 | 9.72e-6 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of phosphorus metabolic process | experimental (any) | 42 | 18.66 | 9.91e-6 |
| Gene Ontology - Biological Process | cellular protein modification process | experimental (any) | 75 | 44.15 | 1.08e-5 |
| Gene Ontology - Biological Process | positive regulation of cell death | experimental (any) | 25 | 8.012 | 1.08e-5 |
| Gene Ontology - Biological Process | positive regulation of cell differentiation | experimental (any) | 30 | 10.92 | 1.08e-5 |
| Gene Ontology - Biological Process | protein modification process | experimental (any) | 75 | 44.15 | 1.08e-5 |
| Gene Ontology - Biological Process | cellular response to interleukin-1 | experimental (any) | 12 | 1.913 | 1.15e-5 |
| Gene Ontology - Biological Process | positive regulation of DNA-binding transcription factor activity | experimental (any) | 15 | 3.096 | 1.21e-5 |
| Gene Ontology - Biological Process | regulation of protein metabolic process | experimental (any) | 56 | 29.17 | 1.36e-5 |
| Gene Ontology - Biological Process | regulation of cell-cell adhesion | experimental (any) | 18 | 4.491 | 1.40e-5 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of gene expression | experimental (any) | 45 | 21.23 | 1.72e-5 |
| Gene Ontology - Biological Process | regulation of MAPK cascade | experimental (any) | 24 | 7.706 | 1.79e-5 |
| Gene Ontology - Biological Process | regulation of cell differentiation | experimental (any) | 43 | 19.9 | 1.86e-5 |
| Gene Ontology - Biological Process | regulation of viral life cycle | experimental (any) | 11 | 1.661 | 1.86e-5 |
| Gene Ontology - Biological Process | regulation of viral process | experimental (any) | 13 | 2.392 | 1.86e-5 |
| Gene Ontology - Biological Process | immune system development | experimental (any) | 29 | 10.72 | 2.07e-5 |
| Gene Ontology - Biological Process | cell communication | experimental (any) | 96 | 63.53 | 2.21e-5 |
| Gene Ontology - Biological Process | regulation of hemopoiesis | experimental (any) | 19 | 5.169 | 2.30e-5 |
| Gene Ontology - Biological Process | leukocyte activation involved in immune response | experimental (any) | 24 | 7.866 | 2.40e-5 |
| Gene Ontology - Biological Process | cell activation involved in immune response | experimental (any) | 24 | 7.919 | 2.67e-5 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of nucleic acid-templated transcription | experimental (any) | 39 | 17.49 | 2.93e-5 |
| Gene Ontology - Biological Process | positive regulation of RNA biosynthetic process | experimental (any) | 39 | 17.5 | 2.95e-5 |
| Gene Ontology - Biological Process | regulation of cell migration | experimental (any) | 26 | 9.168 | 3.07e-5 |
| Gene Ontology - Biological Process | regulation of cell motility | experimental (any) | 27 | 9.766 | 3.07e-5 |
| Gene Ontology - Biological Process | secretion by cell | experimental (any) | 37 | 16.18 | 3.07e-5 |
| Gene Ontology - Biological Process | viral life cycle | experimental (any) | 16 | 3.827 | 3.07e-5 |
| Gene Ontology - Biological Process | signaling | experimental (any) | 95 | 63.18 | 3.13e-5 |
| Gene Ontology - Biological Process | MAPK cascade | experimental (any) | 27 | 9.872 | 3.70e-5 |
| Gene Ontology - Biological Process | response to interleukin-1 | experimental (any) | 12 | 2.179 | 3.72e-5 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of cellular protein metabolic process | experimental (strong) | 42 | 21.6 | 3.84e-5 |
| Gene Ontology - Biological Process | negative regulation of cell population proliferation | experimental (any) | 23 | 7.56 | 3.87e-5 |
| Gene Ontology - Biological Process | signal transduction by protein phosphorylation | experimental (any) | 27 | 9.912 | 3.89e-5 |
| Gene Ontology - Biological Process | protein phosphorylation | experimental (strong) | 38 | 18.3 | 3.97e-5 |
| Gene Ontology - Biological Process | response to lipopolysaccharide | experimental (strong) | 16 | 3.717 | 3.97e-5 |
| Gene Ontology - Biological Process | regulation of I-kappaB kinase/NF-kappaB signaling | experimental (any) | 13 | 2.631 | 4.50e-5 |
| Gene Ontology - Biological Process | regulation of myeloid cell differentiation | experimental (any) | 13 | 2.631 | 4.50e-5 |
| Gene Ontology - Biological Process | protein metabolic process | experimental (any) | 91 | 60.11 | 4.55e-5 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of secretion | experimental (any) | 24 | 8.238 | 4.65e-5 |
| Gene Ontology - Biological Process | leukocyte activation involved in immune response | experimental (strong) | 19 | 5.343 | 4.73e-5 |
| Gene Ontology - Biological Process | positive regulation of NIK/NF-kappaB signaling | experimental (strong) | 9 | 1.058 | 4.73e-5 |
| Gene Ontology - Biological Process | positive regulation of leukocyte adhesion to vascular endothelial cell | experimental (strong) | 5 | 0.206 | 4.73e-5 |
| Gene Ontology - Biological Process | regulation of leukocyte migration | experimental (strong) | 11 | 1.704 | 4.73e-5 |
| Gene Ontology - Biological Process | cellular response to chemokine | experimental (any) | 7 | 0.624 | 4.74e-5 |
| Gene Ontology - Biological Process | regulation of signaling | experimental (any) | 68 | 40.27 | 4.82e-5 |
| Gene Ontology - Biological Process | response to stimulus | experimental (any) | 121 | 88.74 | 4.82e-5 |
| Gene Ontology - Biological Process | leukocyte migration | experimental (any) | 17 | 4.491 | 4.86e-5 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | cell activation involved in immune response | experimental (strong) | 19 | 5.395 | 4.87e-5 |
| Gene Ontology - Biological Process | response to interferon-gamma | experimental (any) | 11 | 1.873 | 4.91e-5 |
| Gene Ontology - Biological Process | cellular response to cytokine stimulus | experimental (strong) | 28 | 11.07 | 5.07e-5 |
| Gene Ontology - Biological Process | regulation of protein phosphorylation | experimental (strong) | 32 | 13.96 | 5.07e-5 |
| Gene Ontology - Biological Process | response to molecule of bacterial origin | experimental (strong) | 16 | 3.872 | 5.07e-5 |
| Gene Ontology - Biological Process | lymphocyte activation | experimental (any) | 22 | 7.162 | 5.12e-5 |
| Gene Ontology - Biological Process | MyD88-dependent toll-like receptor signaling pathway | experimental (any) | 6 | 0.425 | 5.93e-5 |
| Gene Ontology - Biological Process | positive regulation of cell activation | experimental (any) | 15 | 3.614 | 6.08e-5 |
| Gene Ontology - Biological Process | positive regulation of T cell activation | experimental (any) | 12 | 2.312 | 6.09e-5 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of RNA metabolic process | experimental (any) | 69 | 41.46 | 6.18e-5 |
| Gene Ontology - Biological Process | regulation of leukocyte migration | experimental (any) | 11 | 1.927 | 6.18e-5 |
| Gene Ontology - Biological Process | cellular macromolecule biosynthetic process | experimental (any) | 83 | 53.51 | 6.24e-5 |
| Gene Ontology - Biological Process | myeloid leukocyte activation | experimental (any) | 22 | 7.308 | 6.71e-5 |
| Gene Ontology - Biological Process | positive regulation of MAPK cascade | experimental (any) | 19 | 5.674 | 6.94e-5 |
| Gene Ontology - Biological Process | regulation of cellular component organization | predicted (intersection) | 446 | 361.3 | 6.99e-5 |
| Gene Ontology - Biological Process | cellular protein metabolic process | experimental (any) | 84 | 54.6 | 7.16e-5 |
| Gene Ontology - Biological Process | cell migration | experimental (any) | 34 | 14.99 | 8.14e-5 |
| Gene Ontology - Biological Process | leukocyte mediated immunity | experimental (any) | 24 | 8.597 | 8.14e-5 |
| Gene Ontology - Biological Process | regulation of NIK/NF-kappaB signaling | experimental (any) | 9 | 1.276 | 8.14e-5 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of extrinsic apoptotic signaling pathway via death domain receptors | experimental (any) | 7 | 0.691 | 8.14e-5 |
| Gene Ontology - Biological Process | regulation of nitrogen compound metabolic process | experimental (any) | 92 | 61.97 | 8.14e-5 |
| Gene Ontology - Biological Process | response to glucocorticoid | experimental (any) | 10 | 1.621 | 8.14e-5 |
| Gene Ontology - Biological Process | response to organic cyclic compound | experimental (any) | 27 | 10.42 | 8.14e-5 |
| Gene Ontology - Biological Process | cellular response to mechanical stimulus | experimental (any) | 8 | 0.970 | 8.22e-5 |
| Gene Ontology - Biological Process | regulation of chemotaxis | experimental (any) | 11 | 2.006 | 8.27e-5 |
| Gene Ontology - Biological Process | bone remodeling | experimental (any) | 8 | 0.983 | 8.98e-5 |
| Gene Ontology - Biological Process | positive regulation of leukocyte migration | experimental (any) | 9 | 1.302 | 9.08e-5 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | phosphorylation | experimental (strong) | 39 | 20 | 9.21e-5 |
| Gene Ontology - Biological Process | positive regulation of leukocyte migration | experimental (strong) | 9 | 1.187 | 9.71e-5 |
| Gene Ontology - Biological Process | positive regulation of metabolic process | experimental (strong) | 50 | 30.43 | 9.71e-5 |
| Gene Ontology - Biological Process | regulation of protein metabolic process | experimental (strong) | 42 | 22.74 | 9.71e-5 |
| Gene Ontology - Biological Process | positive regulation of I-kappaB kinase/NF-kappaB signaling | experimental (any) | 11 | 2.046 | 9.79e-5 |
| Gene Ontology - Biological Process | reactive oxygen species metabolic process | experimental (any) | 13 | 2.897 | 1.02e-4 |
| Gene Ontology - Biological Process | regulation of locomotion | experimental (any) | 27 | 10.58 | 1.02e-4 |
| Gene Ontology - Biological Process | regulation of cellular component movement | experimental (any) | 27 | 10.6 | 1.05e-4 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | toll-like receptor signaling pathway | experimental (any) | 10 | 1.687 | 1.07e-4 |
| Gene Ontology - Biological Process | protein secretion | experimental (any) | 19 | 5.926 | 1.13e-4 |
| Gene Ontology - Biological Process | regulation of RNA biosynthetic process | experimental (any) | 65 | 38.98 | 1.13e-4 |
| Gene Ontology - Biological Process | myeloid leukocyte activation | experimental (strong) | 17 | 4.723 | 1.20e-4 |
| Gene Ontology - Biological Process | RNA biosynthetic process | experimental (any) | 67 | 40.96 | 1.45e-4 |
| Gene Ontology - Biological Process | immune response | experimental (strong) | 31 | 13.99 | 1.49e-4 |
| Gene Ontology - Biological Process | transcription, DNA-templated | experimental (any) | 66 | 40.18 | 1.51e-4 |
| Gene Ontology - Biological Process | phosphorylation | experimental (any) | 48 | 25.76 | 1.57e-4 |
| Gene Ontology - Biological Process | regulation of DNA-binding transcription factor activity | experimental (any) | 17 | 5.009 | 1.63e-4 |
| Gene Ontology - Biological Process | regulation of cell population proliferation | experimental (strong) | 35 | 17.24 | 1.69e-4 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of signal transduction | experimental (strong) | 45 | 26.07 | 1.69e-4 |
| Gene Ontology - Biological Process | response to cytokine | experimental (strong) | 28 | 11.9 | 1.69e-4 |
| Gene Ontology - Biological Process | regulation of phosphorylation | experimental (strong) | 32 | 14.94 | 1.78e-4 |
| Gene Ontology - Biological Process | chemotaxis | experimental (any) | 19 | 6.139 | 1.80e-4 |
| Gene Ontology - Biological Process | nervous system development | predicted (union) | 883 | 770.8 | 1.81e-4 |
| Gene Ontology - Biological Process | T cell activation | experimental (any) | 17 | 5.062 | 1.84e-4 |
| Gene Ontology - Biological Process | myeloid cell differentiation | experimental (any) | 16 | 4.544 | 1.85e-4 |
| Gene Ontology - Biological Process | regulation of lymphocyte activation | experimental (any) | 16 | 4.557 | 1.90e-4 |
| Gene Ontology - Biological Process | regulation of nucleic acid-templated transcription | experimental (any) | 64 | 38.86 | 1.94e-4 |
| Gene Ontology - Biological Process | response to nitrogen compound | experimental (any) | 28 | 11.67 | 1.94e-4 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | pattern recognition receptor signaling pathway | experimental (any) | 11 | 2.232 | 2.01e-4 |
| Gene Ontology - Biological Process | regulation of transcription, DNA-templated | experimental (any) | 63 | 38.09 | 2.02e-4 |
| Gene Ontology - Biological Process | response to corticosteroid | experimental (any) | 10 | 1.834 | 2.02e-4 |
| Gene Ontology - Biological Process | peptide secretion | experimental (any) | 19 | 6.218 | 2.04e-4 |
| Gene Ontology - Biological Process | cell death | experimental (strong) | 39 | 20.86 | 2.10e-4 |
| Gene Ontology - Biological Process | cellular protein metabolic process | experimental (strong) | 51 | 32.37 | 2.10e-4 |
| Gene Ontology - Biological Process | protein metabolic process | experimental (strong) | 53 | 34.51 | 2.10e-4 |
| Gene Ontology - Biological Process | response to hypoxia | experimental (any) | 15 | 4.106 | 2.14e-4 |
| Gene Ontology - Biological Process | anatomical structure morphogenesis | predicted (union) | 965 | 852.4 | 2.16e-4 |
| Gene Ontology - Biological Process | dephosphorylation | predicted (union) | 213 | 160.9 | 2.16e-4 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of gene expression | predicted (union) | 675 | 581 | 2.16e-4 |
| Gene Ontology - Biological Process | positive regulation of apoptotic process | experimental (any) | 21 | 7.401 | 2.16e-4 |
| Gene Ontology - Biological Process | positive regulation of programmed cell death | experimental (any) | 21 | 7.454 | 2.39e-4 |
| Gene Ontology - Biological Process | leukocyte migration | experimental (strong) | 15 | 4.001 | 2.51e-4 |
| Gene Ontology - Biological Process | positive regulation of leukocyte cell-cell adhesion | experimental (strong) | 12 | 2.581 | 2.53e-4 |
| Gene Ontology - Biological Process | regulation of cell adhesion | experimental (strong) | 21 | 7.485 | 2.53e-4 |
| Gene Ontology - Biological Process | regulation of phosphorus metabolic process | experimental (strong) | 33 | 16.11 | 2.53e-4 |
| Gene Ontology - Biological Process | response to mechanical stimulus | experimental (strong) | 12 | 2.581 | 2.53e-4 |
| Gene Ontology - Biological Process | cell chemotaxis | experimental (any) | 12 | 2.777 | 2.95e-4 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | apoptotic process | experimental (strong) | 37 | 19.56 | 3.00e-4 |
| Gene Ontology - Biological Process | regulation of NIK/NF-kappaB signaling | experimental (strong) | 9 | 1.42 | 3.00e-4 |
| Gene Ontology - Biological Process | positive regulation of cell adhesion | experimental (strong) | 16 | 4.672 | 3.22e-4 |
| Gene Ontology - Biological Process | positive regulation of cell population proliferation | experimental (any) | 25 | 10.1 | 3.28e-4 |
| Gene Ontology - Biological Process | positive regulation of immune response | experimental (any) | 22 | 8.225 | 3.28e-4 |
| Gene Ontology - Biological Process | cell motility | experimental (any) | 34 | 16.2 | 3.38e-4 |
| Gene Ontology - Biological Process | cytokine biosynthetic process | experimental (any) | 8 | 1.209 | 3.46e-4 |
| Gene Ontology - Biological Process | nitric oxide metabolic process | experimental (any) | 7 | 0.890 | 3.59e-4 |
| Gene Ontology - Biological Process | tube morphogenesis | experimental (any) | 24 | 9.54 | 3.64e-4 |
| Gene Ontology - Biological Process | cytokine metabolic process | experimental (any) | 8 | 1.222 | 3.68e-4 |

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| Gene Ontology - Biological Process | response to organonitrogen compound | experimental (any) | 26 | 10.87 | 3.87e-4 |
| Gene Ontology - Biological Process | neuron differentiation | predicted (union) | 512 | 432.2 | 3.91e-4 |
| Gene Ontology - Biological Process | cytokine-mediated signaling pathway | experimental (strong) | 21 | 7.743 | 3.92e-4 |
| Gene Ontology - Biological Process | positive regulation of protein serine/threonine kinase activity | experimental (any) | 14 | 3.84 | 3.93e-4 |
| Gene Ontology - Biological Process | lymphocyte differentiation | experimental (any) | 14 | 3.853 | 4.06e-4 |
| Gene Ontology - Biological Process | regulation of protein secretion | experimental (any) | 16 | 4.903 | 4.11e-4 |
| Gene Ontology - Biological Process | heart valve morphogenesis | experimental (any) | 6 | 0.624 | 4.12e-4 |
| Gene Ontology - Biological Process | interleukin-1-mediated signaling pathway | experimental (any) | 8 | 1.249 | 4.16e-4 |
| Gene Ontology - Biological Process | programmed cell death | experimental (strong) | 37 | 19.9 | 4.32e-4 |
| Gene Ontology - Biological Process | leukocyte chemotaxis | experimental (any) | 10 | 2.033 | 4.43e-4 |

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| Gene Ontology - Biological Process | leukocyte mediated immunity | experimental (strong) | 17 | 5.395 | 4.55e-4 |
| Gene Ontology - Biological Process | positive regulation of cell-cell adhesion | experimental (strong) | 13 | 3.252 | 4.55e-4 |
| Gene Ontology - Biological Process | cell-cell adhesion | experimental (any) | 22 | 8.451 | 4.57e-4 |
| Gene Ontology - Biological Process | response to steroid hormone | experimental (any) | 15 | 4.425 | 4.58e-4 |
| Gene Ontology - Biological Process | leukocyte cell-cell adhesion | experimental (strong) | 14 | 3.768 | 4.65e-4 |
| Gene Ontology - Biological Process | cell population proliferation | experimental (strong) | 37 | 20.03 | 4.69e-4 |
| Gene Ontology - Biological Process | reactive oxygen species biosynthetic process | experimental (any) | 8 | 1.276 | 4.74e-4 |
| Gene Ontology - Biological Process | regulation of interleukin-12 biosynthetic process | experimental (any) | 3 | 0.080 | 5.11e-4 |
| Gene Ontology - Biological Process | regulation of reactive oxygen species metabolic process | experimental (any) | 10 | 2.073 | 5.11e-4 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | neurogenesis | predicted (union) | 601 | 516.2 | 5.33e-4 |
| Gene Ontology - Biological Process | immune response-regulating signaling pathway | experimental (any) | 18 | 6.165 | 5.46e-4 |
| Gene Ontology - Biological Process | activation of NF-kappaB-inducing kinase activity | experimental (any) | 4 | 0.213 | 5.48e-4 |
| Gene Ontology - Biological Process | cellular response to interferon-gamma | experimental (any) | 9 | 1.687 | 5.55e-4 |
| Gene Ontology - Biological Process | cellular response to interleukin-6 | experimental (any) | 5 | 0.412 | 5.64e-4 |
| Gene Ontology - Biological Process | positive regulation of cell migration | experimental (any) | 17 | 5.62 | 5.64e-4 |
| Gene Ontology - Biological Process | regulation of T cell activation | experimental (any) | 13 | 3.494 | 5.64e-4 |
| Gene Ontology - Biological Process | response to bacterium | experimental (strong) | 16 | 4.956 | 6.01e-4 |
| Gene Ontology - Biological Process | generation of neurons | predicted (union) | 566 | 484.9 | 6.10e-4 |
| Gene Ontology - Biological Process | regulation of cellular component organization | predicted (union) | 889 | 788.3 | 6.10e-4 |

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| Gene Ontology - Biological Process | response to growth factor | experimental (any) | 21 | 8.039 | 6.21e-4 |
| Gene Ontology - Biological Process | response to hormone | experimental (any) | 25 | 10.59 | 6.23e-4 |
| Gene Ontology - Biological Process | regulation of protein localization | experimental (any) | 26 | 11.27 | 6.36e-4 |
| Gene Ontology - Biological Process | regulation of cell death | experimental (strong) | 34 | 17.78 | 6.57e-4 |
| Gene Ontology - Biological Process | cellular response to mechanical stimulus | experimental (strong) | 8 | 1.239 | 7.17e-4 |
| Gene Ontology - Biological Process | neutrophil activation | experimental (any) | 17 | 5.767 | 7.48e-4 |
| Gene Ontology - Biological Process | positive regulation of protein kinase activity | experimental (any) | 17 | 5.767 | 7.48e-4 |
| Gene Ontology - Biological Process | response to interleukin-6 | experimental (any) | 5 | 0.438 | 7.48e-4 |
| Gene Ontology - Biological Process | cell fate commitment | experimental (any) | 11 | 2.644 | 7.58e-4 |
| Gene Ontology - Biological Process | extrinsic apoptotic signaling pathway via death domain receptors | experimental (any) | 7 | 1.023 | 7.58e-4 |

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| Gene Ontology - Biological Process | negative regulation of signal transduction | experimental (any) | 30 | 14.15 | 7.58e-4 |
| Gene Ontology - Biological Process | regulation of reactive oxygen species biosynthetic process | experimental (any) | 7 | 1.023 | 7.58e-4 |
| Gene Ontology - Biological Process | MAPK cascade | experimental (strong) | 23 | 9.524 | 7.70e-4 |
| Gene Ontology - Biological Process | positive regulation of cell motility | experimental (any) | 17 | 5.793 | 7.72e-4 |
| Gene Ontology - Biological Process | cell projection morphogenesis | predicted (union) | 250 | 197.6 | 8.06e-4 |
| Gene Ontology - Biological Process | regulation of interleukin-23 production | experimental (any) | 3 | 0.093 | 8.09e-4 |
| Gene Ontology - Biological Process | positive regulation of cellular biosynthetic process | experimental (strong) | 34 | 17.99 | 8.12e-4 |
| Gene Ontology - Biological Process | signal transduction by protein phosphorylation | experimental (strong) | 23 | 9.576 | 8.13e-4 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | nucleotide-binding oligomerization domain containing signaling pathway | experimental (any) | 5 | 0.452 | 8.26e-4 |
| Gene Ontology - Biological Process | regulation of establishment of protein localization | experimental (any) | 21 | 8.238 | 8.26e-4 |
| Gene Ontology - Biological Process | tissue development | experimental (any) | 39 | 20.81 | 8.27e-4 |
| Gene Ontology - Biological Process | response to drug | experimental (any) | 25 | 10.83 | 8.32e-4 |
| Gene Ontology - Biological Process | regulation of protein transport | experimental (any) | 20 | 7.64 | 8.46e-4 |
| Gene Ontology - Biological Process | regulation of cytokine-mediated signaling pathway | experimental (any) | 9 | 1.807 | 8.52e-4 |
| Gene Ontology - Biological Process | negative regulation of biosynthetic process | predicted (union) | 566 | 487.3 | 8.54e-4 |
| Gene Ontology - Biological Process | positive regulation of RNA biosynthetic process | predicted (union) | 602 | 520.9 | 8.54e-4 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of cell differentiation | predicted (union) | 682 | 595.8 | 8.54e-4 |
| Gene Ontology - Biological Process | negative regulation of cellular metabolic process | predicted (union) | 900 | 802.4 | 8.59e-4 |
| Gene Ontology - Biological Process | positive regulation of nucleic acid-templated transcription | predicted (union) | 601 | 520.5 | 8.59e-4 |
| Gene Ontology - Biological Process | positive regulation of immune system process | experimental (strong) | 22 | 8.931 | 8.60e-4 |
| Gene Ontology - Biological Process | cytoplasmic pattern recognition receptor signaling pathway | experimental (any) | 6 | 0.731 | 8.64e-4 |
| Gene Ontology - Biological Process | regulation of peptidyl-tyrosine phosphorylation | experimental (any) | 11 | 2.697 | 8.64e-4 |
| Gene Ontology - Biological Process | regulation of chemotaxis | experimental (strong) | 10 | 2.091 | 9.01e-4 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway | experimental (any) | 5 | 0.465 | 9.05e-4 |
| Gene Ontology - Biological Process | positive regulation of myeloid cell differentiation | experimental (any) | 7 | 1.063 | 9.05e-4 |
| Gene Ontology - Biological Process | regulation of cell activation | experimental (any) | 17 | 5.899 | 9.05e-4 |
| Gene Ontology - Biological Process | response to vitamin D | experimental (any) | 5 | 0.465 | 9.05e-4 |
| Gene Ontology - Biological Process | semi-lunar valve development | experimental (any) | 5 | 0.465 | 9.05e-4 |
| Gene Ontology - Biological Process | intracellular transport | predicted (union) | 621 | 539.6 | 9.07e-4 |
| Gene Ontology - Biological Process | locomotion | experimental (any) | 36 | 18.71 | 9.10e-4 |
| Gene Ontology - Biological Process | positive regulation of transcription by RNA polymerase II | experimental (any) | 27 | 12.28 | 9.10e-4 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | response to alcohol | experimental (any) | 11 | 2.724 | 9.10e-4 |
| Gene Ontology - Biological Process | positive regulation of cellular component movement | experimental (any) | 17 | 5.913 | 9.11e-4 |
| Gene Ontology - Biological Process | heart valve development | experimental (any) | 6 | 0.744 | 9.13e-4 |
| Gene Ontology - Biological Process | positive regulation of reactive oxygen species metabolic process | experimental (any) | 7 | 1.076 | 9.46e-4 |
| Gene Ontology - Biological Process | positive regulation of smooth muscle cell proliferation | experimental (any) | 7 | 1.076 | 9.46e-4 |
| Gene Ontology - Biological Process | response to interferon-alpha | experimental (any) | 4 | 0.252 | 9.47e-4 |
| Gene Ontology - Biological Process | monocyte chemotaxis | experimental (any) | 5 | 0.478 | 9.99e-4 |
| Gene Ontology - Biological Process | anatomical structure morphogenesis | predicted (intersection) | 467 | 390.6 | 0.001 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of gene expression | predicted (intersection) | 332 | 266.2 | 0.001 |
| Gene Ontology - Biological Process | axonogenesis | predicted (union) | 179 | 137.1 | 0.001 |
| Gene Ontology - Biological Process | cell part morphogenesis | predicted (union) | 254 | 203.4 | 0.001 |
| Gene Ontology - Biological Process | neuron projection morphogenesis | predicted (union) | 240 | 190.9 | 0.001 |
| Gene Ontology - Biological Process | positive regulation of gene expression | predicted (union) | 716 | 629.8 | 0.001 |
| Gene Ontology - Biological Process | positive regulation of transcription, DNA-templated | predicted (union) | 561 | 484.9 | 0.001 |
| Gene Ontology - Biological Process | NIK/NF-kappaB signaling | experimental (strong) | 9 | 1.729 | 0.001 |
| Gene Ontology - Biological Process | cell activation | experimental (strong) | 26 | 11.95 | 0.001 |
| Gene Ontology - Biological Process | cellular protein modification process | experimental (strong) | 45 | 28.44 | 0.001 |
| Gene Ontology - Biological Process | leukocyte activation | experimental (strong) | 24 | 10.51 | 0.001 |

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| Gene Ontology - Biological Process | neutrophil activation | experimental (strong) | 12 | 3.149 | 0.001 |
| Gene Ontology - Biological Process | positive regulation of MAPK cascade | experimental (strong) | 17 | 6.014 | 0.001 |
| Gene Ontology - Biological Process | protein modification process | experimental (strong) | 45 | 28.44 | 0.001 |
| Gene Ontology - Biological Process | regulation of immune response | experimental (strong) | 20 | 7.795 | 0.001 |
| Gene Ontology - Biological Process | regulation of signaling | experimental (strong) | 45 | 28.44 | 0.001 |
| Gene Ontology - Biological Process | response to lipid | experimental (strong) | 23 | 9.912 | 0.001 |
| Gene Ontology - Biological Process | NIK/NF-kappaB signaling | experimental (any) | 9 | 1.98 | 0.001 |
| Gene Ontology - Biological Process | T cell differentiation | experimental (any) | 11 | 2.777 | 0.001 |
| Gene Ontology - Biological Process | anatomical structure formation involved in morphogenesis | experimental (any) | 26 | 11.95 | 0.001 |
| Gene Ontology - Biological Process | blood vessel morphogenesis | experimental (any) | 18 | 6.644 | 0.001 |

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| Gene Ontology - Biological Process | cellular response to hormone stimulus | experimental (any) | 19 | 7.454 | 0.001 |
| Gene Ontology - Biological Process | chemokine-mediated signaling pathway | experimental (any) | 5 | 0.531 | 0.001 |
| Gene Ontology - Biological Process | cytokine production involved in immune response | experimental (any) | 7 | 1.183 | 0.001 |
| Gene Ontology - Biological Process | entry into host cell | experimental (any) | 8 | 1.528 | 0.001 |
| Gene Ontology - Biological Process | forebrain development | experimental (any) | 14 | 4.292 | 0.001 |
| Gene Ontology - Biological Process | innate immune response-activating signal transduction | experimental (any) | 12 | 3.362 | 0.001 |
| Gene Ontology - Biological Process | mononuclear cell migration | experimental (any) | 6 | 0.771 | 0.001 |
| Gene Ontology - Biological Process | negative regulation of cell migration | experimental (any) | 11 | 2.817 | 0.001 |
| Gene Ontology - Biological Process | negative regulation of interleukin-23 production | experimental (any) | 2 | 0.027 | 0.001 |

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| Gene Ontology - Biological Process | negative regulation of leukocyte apoptotic process | experimental (any) | 5 | 0.531 | 0.001 |
| Gene Ontology - Biological Process | nitric oxide biosynthetic process | experimental (any) | 6 | 0.824 | 0.001 |
| Gene Ontology - Biological Process | osteoclast differentiation | experimental (any) | 7 | 1.143 | 0.001 |
| Gene Ontology - Biological Process | positive regulation of T cell migration | experimental (any) | 4 | 0.292 | 0.001 |
| Gene Ontology - Biological Process | positive regulation of kinase activity | experimental (any) | 17 | 6.205 | 0.001 |
| Gene Ontology - Biological Process | positive regulation of locomotion | experimental (any) | 17 | 6.152 | 0.001 |
| Gene Ontology - Biological Process | positive regulation of secretion | experimental (any) | 14 | 4.478 | 0.001 |
| Gene Ontology - Biological Process | regulation of MAP kinase activity | experimental (any) | 13 | 3.8 | 0.001 |
| Gene Ontology - Biological Process | regulation of angiogenesis | experimental (any) | 12 | 3.282 | 0.001 |
| Gene Ontology - Biological Process | regulation of cellular process | experimental (any) | 134 | 108.2 | 0.001 |

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| Gene Ontology - Biological Process | regulation of epithelial cell proliferation | experimental (any) | 13 | 3.827 | 0.001 |
| Gene Ontology - Biological Process | regulation of innate immune response | experimental (any) | 15 | 4.929 | 0.001 |
| Gene Ontology - Biological Process | regulation of leukocyte proliferation | experimental (any) | 10 | 2.352 | 0.001 |
| Gene Ontology - Biological Process | regulation of osteoclast differentiation | experimental (any) | 6 | 0.784 | 0.001 |
| Gene Ontology - Biological Process | regulation of protein serine/threonine kinase activity | experimental (any) | 16 | 5.581 | 0.001 |
| Gene Ontology - Biological Process | regulation of type I interferon production | experimental (any) | 8 | 1.475 | 0.001 |
| Gene Ontology - Biological Process | response to estradiol | experimental (any) | 8 | 1.501 | 0.001 |
| Gene Ontology - Biological Process | response to hydroxyisoflavone | experimental (any) | 2 | 0.027 | 0.001 |
| Gene Ontology - Biological Process | response to ultrasound | experimental (any) | 2 | 0.027 | 0.001 |

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| Gene Ontology - Biological Process | response to vitamin | experimental (any) | 7 | 1.156 | 0.001 |
| Gene Ontology - Biological Process | stem cell population maintenance | experimental (any) | 9 | 1.98 | 0.001 |
| Gene Ontology - Biological Process | system development | experimental (any) | 73 | 49.77 | 0.001 |
| Gene Ontology - Biological Process | telencephalon development | experimental (any) | 11 | 2.883 | 0.001 |
| Gene Ontology - Biological Process | tissue remodeling | experimental (any) | 9 | 1.873 | 0.001 |
| Gene Ontology - Biological Process | toll-like receptor 9 signaling pathway | experimental (any) | 4 | 0.292 | 0.001 |
| Gene Ontology - Biological Process | type I interferon biosynthetic process | experimental (any) | 3 | 0.120 | 0.001 |
| Gene Ontology - Biological Process | type I interferon production | experimental (any) | 8 | 1.501 | 0.001 |
| Gene Ontology - Biological Process | nervous system development | predicted (intersection) | 426 | 353.2 | 0.002 |
| Gene Ontology - Biological Process | central nervous system neuron differentiation | predicted (union) | 91 | 62.86 | 0.002 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of organelle organization | predicted (union) | 470 | 402.2 | 0.002 |
| Gene Ontology - Biological Process | cellular response to lipid | experimental (strong) | 18 | 6.84 | 0.002 |
| Gene Ontology - Biological Process | positive regulation of cell population proliferation | experimental (strong) | 23 | 10.43 | 0.002 |
| Gene Ontology - Biological Process | positive regulation of cytokine production | experimental (strong) | 14 | 4.465 | 0.002 |
| Gene Ontology - Biological Process | reactive oxygen species metabolic process | experimental (strong) | 11 | 2.865 | 0.002 |
| Gene Ontology - Biological Process | regulation of MAPK cascade | experimental (strong) | 20 | 8.027 | 0.002 |
| Gene Ontology - Biological Process | regulation of cellular extravasation | experimental (strong) | 3 | 0.103 | 0.002 |
| Gene Ontology - Biological Process | secretion | experimental (strong) | 25 | 11.9 | 0.002 |
| Gene Ontology - Biological Process | RNA metabolic process | experimental (any) | 73 | 50.57 | 0.002 |
| Gene Ontology - Biological Process | T cell migration | experimental (any) | 5 | 0.611 | 0.002 |

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| Gene Ontology - Biological Process | activation of immune response | experimental (any) | 17 | 6.497 | 0.002 |
| Gene Ontology - Biological Process | activation of innate immune response | experimental (any) | 12 | 3.627 | 0.002 |
| Gene Ontology - Biological Process | biosynthetic process | experimental (any) | 92 | 67.59 | 0.002 |
| Gene Ontology - Biological Process | cardiac septum morphogenesis | experimental (any) | 6 | 0.943 | 0.002 |
| Gene Ontology - Biological Process | cellular response to drug | experimental (any) | 13 | 4.119 | 0.002 |
| Gene Ontology - Biological Process | cellular response to growth factor stimulus | experimental (any) | 19 | 7.706 | 0.002 |
| Gene Ontology - Biological Process | central nervous system development | experimental (any) | 24 | 10.84 | 0.002 |
| Gene Ontology - Biological Process | endoderm development | experimental (any) | 6 | 0.917 | 0.002 |
| Gene Ontology - Biological Process | extrinsic apoptotic signaling pathway | experimental (any) | 10 | 2.657 | 0.002 |
| Gene Ontology - Biological Process | glial cell differentiation | experimental (any) | 10 | 2.538 | 0.002 |
| Gene Ontology - Biological Process | immune response-activating signal transduction | experimental (any) | 16 | 5.727 | 0.002 |

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| Gene Ontology - Biological Process | interferon-alpha production | experimental (any) | 4 | 0.332 | 0.002 |
| Gene Ontology - Biological Process | negative regulation of cell motility | experimental (any) | 11 | 2.976 | 0.002 |
| Gene Ontology - Biological Process | negative regulation of signaling | experimental (any) | 30 | 15.31 | 0.002 |
| Gene Ontology - Biological Process | negative regulation of transport | experimental (any) | 15 | 5.155 | 0.002 |
| Gene Ontology - Biological Process | neutrophil mediated immunity | experimental (any) | 16 | 5.767 | 0.002 |
| Gene Ontology - Biological Process | positive regulation of MAP kinase activity | experimental (any) | 11 | 2.976 | 0.002 |
| Gene Ontology - Biological Process | positive regulation of epithelial to mesenchymal transition | experimental (any) | 5 | 0.611 | 0.002 |
| Gene Ontology - Biological Process | positive regulation of gliogenesis | experimental (any) | 6 | 0.850 | 0.002 |
| Gene Ontology - Biological Process | positive regulation of innate immune response | experimental (any) | 13 | 4.199 | 0.002 |

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| Gene Ontology - Biological Process | positive regulation of interleukin-6 production | experimental (any) | 6 | 0.890 | 0.002 |
| Gene Ontology - Biological Process | positive regulation of protein complex assembly | experimental (any) | 10 | 2.618 | 0.002 |
| Gene Ontology - Biological Process | positive regulation of reactive oxygen species biosynthetic process | experimental (any) | 5 | 0.585 | 0.002 |
| Gene Ontology - Biological Process | positive regulation of type I interferon production | experimental (any) | 6 | 0.890 | 0.002 |
| Gene Ontology - Biological Process | positive regulation of vascular endothelial growth factor production | experimental (any) | 4 | 0.332 | 0.002 |
| Gene Ontology - Biological Process | positive regulation of vasoconstriction | experimental (any) | 4 | 0.319 | 0.002 |
| Gene Ontology - Biological Process | proteolysis | experimental (any) | 33 | 17.54 | 0.002 |

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| Gene Ontology - Biological Process | regulation of ERK1 and ERK2 cascade | experimental (any) | 11 | 2.976 | 0.002 |
| Gene Ontology - Biological Process | regulation of T cell proliferation | experimental (any) | 8 | 1.674 | 0.002 |
| Gene Ontology - Biological Process | regulation of actin cytoskeleton organization | experimental (any) | 12 | 3.468 | 0.002 |
| Gene Ontology - Biological Process | regulation of calcium ion transport | experimental (any) | 10 | 2.618 | 0.002 |
| Gene Ontology - Biological Process | regulation of cytokine production involved in immune response | experimental (any) | 6 | 0.943 | 0.002 |
| Gene Ontology - Biological Process | regulation of gene expression | experimental (any) | 71 | 48.79 | 0.002 |
| Gene Ontology - Biological Process | regulation of metabolic process | experimental (any) | 95 | 70.99 | 0.002 |
| Gene Ontology - Biological Process | regulation of protein kinase activity | experimental (any) | 20 | 8.344 | 0.002 |

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| Gene Ontology - Biological Process | regulation of tissue remodeling | experimental (any) | 6 | 0.877 | 0.002 |
| Gene Ontology - Biological Process | tube development | experimental (any) | 25 | 11.64 | 0.002 |
| Gene Ontology - Biological Process | negative regulation of transcription, DNA-templated | predicted (union) | 430 | 367 | 0.003 |
| Gene Ontology - Biological Process | MyD88-dependent toll-like receptor signaling pathway | experimental (strong) | 5 | 0.516 | 0.003 |
| Gene Ontology - Biological Process | activation of NF-kappaB-inducing kinase activity | experimental (strong) | 4 | 0.310 | 0.003 |
| Gene Ontology - Biological Process | cell adhesion | experimental (strong) | 24 | 11.56 | 0.003 |
| Gene Ontology - Biological Process | cellular macromolecule biosynthetic process | experimental (strong) | 45 | 29.79 | 0.003 |
| Gene Ontology - Biological Process | cellular response to interleukin-6 | experimental (strong) | 5 | 0.568 | 0.003 |
| Gene Ontology - Biological Process | cellular response to organic substance | experimental (strong) | 40 | 24.65 | 0.003 |

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| Gene Ontology - Biological Process | macromolecule metabolic process | experimental (strong) | 62 | 48.86 | 0.003 |
| Gene Ontology - Biological Process | negative regulation of apoptotic process | experimental (strong) | 23 | 10.61 | 0.003 |
| Gene Ontology - Biological Process | negative regulation of cell death | experimental (strong) | 24 | 11.46 | 0.003 |
| Gene Ontology - Biological Process | negative regulation of programmed cell death | experimental (strong) | 23 | 10.69 | 0.003 |
| Gene Ontology - Biological Process | phosphate-containing compound metabolic process | experimental (strong) | 39 | 23.64 | 0.003 |
| Gene Ontology - Biological Process | positive regulation of NF-kappaB transcription factor activity | experimental (strong) | 9 | 2.039 | 0.003 |
| Gene Ontology - Biological Process | positive regulation of T cell migration | experimental (strong) | 4 | 0.284 | 0.003 |
| Gene Ontology - Biological Process | positive regulation of gliogenesis | experimental (strong) | 6 | 0.878 | 0.003 |

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| Gene Ontology - Biological Process | regulation of calcium ion transport | experimental (strong) | 9 | 1.962 | 0.003 |
| Gene Ontology - Biological Process | regulation of cell motility | experimental (strong) | 22 | 9.757 | 0.003 |
| Gene Ontology - Biological Process | regulation of cell-cell adhesion | experimental (strong) | 14 | 4.646 | 0.003 |
| Gene Ontology - Biological Process | regulation of immune system process | experimental (strong) | 26 | 12.83 | 0.003 |
| Gene Ontology - Biological Process | regulation of interleukin-12 biosynthetic process | experimental (strong) | 3 | 0.129 | 0.003 |
| Gene Ontology - Biological Process | regulation of nitrogen compound metabolic process | experimental (strong) | 54 | 38.77 | 0.003 |
| Gene Ontology - Biological Process | regulation of programmed cell death | experimental (strong) | 31 | 16.73 | 0.003 |
| Gene Ontology - Biological Process | ERK1 and ERK2 cascade | experimental (any) | 11 | 3.215 | 0.003 |
| Gene Ontology - Biological Process | MyD88-independent toll-like receptor signaling pathway | experimental (any) | 4 | 0.385 | 0.003 |

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| Gene Ontology - Biological Process | Ras protein signal transduction | experimental (any) | 12 | 3.84 | 0.003 |
| Gene Ontology - Biological Process | adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | experimental (any) | 10 | 2.764 | 0.003 |
| Gene Ontology - Biological Process | aortic valve morphogenesis | experimental (any) | 4 | 0.359 | 0.003 |
| Gene Ontology - Biological Process | biomineral tissue development | experimental (any) | 8 | 1.807 | 0.003 |
| Gene Ontology - Biological Process | body fluid secretion | experimental (any) | 6 | 1.023 | 0.003 |
| Gene Ontology - Biological Process | cell cycle arrest | experimental (any) | 10 | 2.737 | 0.003 |
| Gene Ontology - Biological Process | cell migration involved in sprouting angiogenesis | experimental (any) | 5 | 0.651 | 0.003 |
| Gene Ontology - Biological Process | cellular extravasation | experimental (any) | 5 | 0.624 | 0.003 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | chemokine (C-X-C motif) ligand 12 signaling pathway | experimental (any) | 2 | 0.040 | 0.003 |
| Gene Ontology - Biological Process | endothelium development | experimental (any) | 7 | 1.342 | 0.003 |
| Gene Ontology - Biological Process | epithelial cell proliferation | experimental (any) | 13 | 4.478 | 0.003 |
| Gene Ontology - Biological Process | fibroblast proliferation | experimental (any) | 6 | 1.023 | 0.003 |
| Gene Ontology - Biological Process | gliogenesis | experimental (any) | 11 | 3.348 | 0.003 |
| Gene Ontology - Biological Process | interferon-gamma-mediated signaling pathway | experimental (any) | 6 | 1.023 | 0.003 |
| Gene Ontology - Biological Process | interleukin-12 production | experimental (any) | 5 | 0.651 | 0.003 |
| Gene Ontology - Biological Process | leukocyte homeostasis | experimental (any) | 6 | 0.983 | 0.003 |
| Gene Ontology - Biological Process | lymphocyte homeostasis | experimental (any) | 5 | 0.678 | 0.003 |
| Gene Ontology - Biological Process | lymphocyte proliferation | experimental (any) | 10 | 2.764 | 0.003 |
| Gene Ontology - Biological Process | macrophage activation | experimental (any) | 6 | 0.997 | 0.003 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | maintenance of permeability of blood-brain barrier | experimental (any) | 2 | 0.040 | 0.003 |
| Gene Ontology - Biological Process | mononuclear cell proliferation | experimental (any) | 10 | 2.79 | 0.003 |
| Gene Ontology - Biological Process | muscle cell proliferation | experimental (any) | 9 | 2.299 | 0.003 |
| Gene Ontology - Biological Process | negative regulation of blood vessel endothelial cell migration | experimental (any) | 4 | 0.372 | 0.003 |
| Gene Ontology - Biological Process | negative regulation of cellular component movement | experimental (any) | 11 | 3.202 | 0.003 |
| Gene Ontology - Biological Process | negative regulation of growth rate | experimental (any) | 2 | 0.040 | 0.003 |
| Gene Ontology - Biological Process | negative regulation of locomotion | experimental (any) | 11 | 3.335 | 0.003 |
| Gene Ontology - Biological Process | negative regulation of serotonin uptake | experimental (any) | 2 | 0.040 | 0.003 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | neutrophil activation involved in immune response | experimental (any) | 15 | 5.634 | 0.003 |
| Gene Ontology - Biological Process | neutrophil degranulation | experimental (any) | 15 | 5.607 | 0.003 |
| Gene Ontology - Biological Process | nucleobase-containing compound metabolic process | experimental (any) | 84 | 61.56 | 0.003 |
| Gene Ontology - Biological Process | ossification | experimental (any) | 13 | 4.478 | 0.003 |
| Gene Ontology - Biological Process | outflow tract septum morphogenesis | experimental (any) | 4 | 0.359 | 0.003 |
| Gene Ontology - Biological Process | positive regulation of cellular response to macrophage colony-stimulating factor stimulus | experimental (any) | 2 | 0.040 | 0.003 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of cytokine production involved in immune response | experimental (any) | 5 | 0.624 | 0.003 |
| Gene Ontology - Biological Process | positive regulation of extrinsic apoptotic signaling pathway via death domain receptors | experimental (any) | 3 | 0.159 | 0.003 |
| Gene Ontology - Biological Process | positive regulation of histone acetylation | experimental (any) | 4 | 0.372 | 0.003 |
| Gene Ontology - Biological Process | positive regulation of lymphocyte migration | experimental (any) | 4 | 0.359 | 0.003 |
| Gene Ontology - Biological Process | positive regulation of lymphocyte proliferation | experimental (any) | 7 | 1.369 | 0.003 |
| Gene Ontology - Biological Process | positive regulation of mononuclear cell proliferation | experimental (any) | 7 | 1.382 | 0.003 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of nitric-oxide synthase biosynthetic process | experimental (any) | 3 | 0.159 | 0.003 |
| Gene Ontology - Biological Process | positive regulation of nucleotide-binding oligomerization domain containing 2 signaling pathway | experimental (any) | 2 | 0.040 | 0.003 |
| Gene Ontology - Biological Process | positive regulation of response to cytokine stimulus | experimental (any) | 5 | 0.638 | 0.003 |
| Gene Ontology - Biological Process | regulation of extrinsic apoptotic signaling pathway | experimental (any) | 8 | 1.847 | 0.003 |
| Gene Ontology - Biological Process | regulation of fibroblast proliferation | experimental (any) | 6 | 1.01 | 0.003 |
| Gene Ontology - Biological Process | regulation of interleukin-12 production | experimental (any) | 5 | 0.624 | 0.003 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of vascular endothelial growth factor production | experimental (any) | 4 | 0.385 | 0.003 |
| Gene Ontology - Biological Process | response to phenylpropanoid | experimental (any) | 2 | 0.040 | 0.003 |
| Gene Ontology - Biological Process | stress-activated protein kinase signaling cascade | experimental (any) | 11 | 3.255 | 0.003 |
| Gene Ontology - Biological Process | telencephalon cell migration | experimental (any) | 5 | 0.664 | 0.003 |
| Gene Ontology - Biological Process | viral entry into host cell | experimental (any) | 7 | 1.382 | 0.003 |
| Gene Ontology - Biological Process | axon development | predicted (union) | 193 | 152.3 | 0.004 |
| Gene Ontology - Biological Process | cell morphogenesis | predicted (union) | 359 | 302.6 | 0.004 |
| Gene Ontology - Biological Process | cell morphogenesis involved in neuron differentiation | predicted (union) | 215 | 171.8 | 0.004 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of nucleic acid-templated transcription | predicted (union) | 451 | 387.7 | 0.004 |
| Gene Ontology - Biological Process | neuron projection development | predicted (union) | 359 | 303 | 0.004 |
| Gene Ontology - Biological Process | cell cycle arrest | experimental (strong) | 10 | 2.607 | 0.004 |
| Gene Ontology - Biological Process | cell surface receptor signaling pathway | experimental (strong) | 39 | 24.31 | 0.004 |
| Gene Ontology - Biological Process | cellular response to interleukin-1 | experimental (strong) | 8 | 1.704 | 0.004 |
| Gene Ontology - Biological Process | immune system process | experimental (strong) | 36 | 21.68 | 0.004 |
| Gene Ontology - Biological Process | neutrophil mediated immunity | experimental (strong) | 11 | 3.149 | 0.004 |
| Gene Ontology - Biological Process | positive regulation of immune response | experimental (strong) | 16 | 6.195 | 0.004 |
| Gene Ontology - Biological Process | positive regulation of macromolecule biosynthetic process | experimental (strong) | 31 | 17.37 | 0.004 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of vasoconstriction | experimental (strong) | 4 | 0.336 | 0.004 |
| Gene Ontology - Biological Process | reactive oxygen species biosynthetic process | experimental (strong) | 7 | 1.265 | 0.004 |
| Gene Ontology - Biological Process | regulation of apoptotic process | experimental (strong) | 30 | 16.6 | 0.004 |
| Gene Ontology - Biological Process | regulation of cell migration | experimental (strong) | 21 | 9.395 | 0.004 |
| Gene Ontology - Biological Process | response to glucocorticoid | experimental (strong) | 8 | 1.678 | 0.004 |
| Gene Ontology - Biological Process | response to hypoxia | experimental (strong) | 13 | 4.31 | 0.004 |
| Gene Ontology - Biological Process | response to organonitrogen compound | experimental (strong) | 21 | 9.602 | 0.004 |
| Gene Ontology - Biological Process | viral process | experimental (strong) | 17 | 6.788 | 0.004 |
| Gene Ontology - Biological Process | SMAD protein complex assembly | experimental (any) | 3 | 0.173 | 0.004 |
| Gene Ontology - Biological Process | aortic valve development | experimental (any) | 4 | 0.412 | 0.004 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | apoptotic signaling pathway | experimental (any) | 17 | 7.029 | 0.004 |
| Gene Ontology - Biological Process | blood vessel development | experimental (any) | 18 | 7.613 | 0.004 |
| Gene Ontology - Biological Process | bone resorption | experimental (any) | 5 | 0.691 | 0.004 |
| Gene Ontology - Biological Process | cellular response to prostaglandin E stimulus | experimental (any) | 3 | 0.186 | 0.004 |
| Gene Ontology - Biological Process | forebrain cell migration | experimental (any) | 5 | 0.704 | 0.004 |
| Gene Ontology - Biological Process | myeloid cell apoptotic process | experimental (any) | 4 | 0.412 | 0.004 |
| Gene Ontology - Biological Process | negative regulation of cell migration involved in sprouting angiogenesis | experimental (any) | 3 | 0.173 | 0.004 |
| Gene Ontology - Biological Process | negative regulation of chemotaxis | experimental (any) | 4 | 0.412 | 0.004 |
| Gene Ontology - Biological Process | negative regulation of cytokine production | experimental (any) | 10 | 2.95 | 0.004 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of epithelial cell proliferation | experimental (any) | 7 | 1.462 | 0.004 |
| Gene Ontology - Biological Process | neuroinflammatory response | experimental (any) | 5 | 0.704 | 0.004 |
| Gene Ontology - Biological Process | neurotransmitter biosynthetic process | experimental (any) | 6 | 1.036 | 0.004 |
| Gene Ontology - Biological Process | positive regulation of cellular component biogenesis | experimental (any) | 15 | 5.713 | 0.004 |
| Gene Ontology - Biological Process | positive regulation of chemotaxis | experimental (any) | 7 | 1.488 | 0.004 |
| Gene Ontology - Biological Process | positive regulation of interleukin-12 production | experimental (any) | 4 | 0.412 | 0.004 |
| Gene Ontology - Biological Process | positive regulation of leukocyte proliferation | experimental (any) | 7 | 1.435 | 0.004 |
| Gene Ontology - Biological Process | positive regulation of peptidyl-lysine acetylation | experimental (any) | 4 | 0.412 | 0.004 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of peptidyl-serine phosphorylation | experimental (any) | 6 | 1.05 | 0.004 |
| Gene Ontology - Biological Process | positive regulation of small GTPase mediated signal transduction | experimental (any) | 5 | 0.718 | 0.004 |
| Gene Ontology - Biological Process | regulation of actin filament-based process | experimental (any) | 12 | 3.946 | 0.004 |
| Gene Ontology - Biological Process | regulation of cell growth | experimental (any) | 13 | 4.544 | 0.004 |
| Gene Ontology - Biological Process | regulation of epithelial to mesenchymal transition | experimental (any) | 6 | 1.036 | 0.004 |
| Gene Ontology - Biological Process | regulation of nitric oxide biosynthetic process | experimental (any) | 5 | 0.691 | 0.004 |
| Gene Ontology - Biological Process | response to toxic substance | experimental (any) | 15 | 5.727 | 0.004 |
| Gene Ontology - Biological Process | tissue morphogenesis | experimental (any) | 18 | 7.6 | 0.004 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | vascular endothelial growth factor production | experimental (any) | 4 | 0.399 | 0.004 |
| Gene Ontology - Biological Process | axon guidance | predicted (union) | 101 | 73.02 | 0.005 |
| Gene Ontology - Biological Process | negative regulation of RNA biosynthetic process | predicted (union) | 451 | 388.5 | 0.005 |
| Gene Ontology - Biological Process | I-kappaB kinase/NF-kappaB signaling | experimental (strong) | 10 | 2.762 | 0.005 |
| Gene Ontology - Biological Process | T cell migration | experimental (strong) | 5 | 0.619 | 0.005 |
| Gene Ontology - Biological Process | cellular response to chemokine | experimental (strong) | 5 | 0.645 | 0.005 |
| Gene Ontology - Biological Process | leukocyte chemotaxis | experimental (strong) | 8 | 1.781 | 0.005 |
| Gene Ontology - Biological Process | positive regulation of cell differentiation | experimental (strong) | 22 | 10.4 | 0.005 |
| Gene Ontology - Biological Process | regulation of actin cytoskeleton organization | experimental (strong) | 10 | 2.762 | 0.005 |
| Gene Ontology - Biological Process | regulation of catalytic activity | experimental (strong) | 31 | 17.68 | 0.005 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of cellular component movement | experimental (strong) | 22 | 10.4 | 0.005 |
| Gene Ontology - Biological Process | regulation of interleukin-23 production | experimental (strong) | 3 | 0.155 | 0.005 |
| Gene Ontology - Biological Process | regulation of locomotion | experimental (strong) | 22 | 10.4 | 0.005 |
| Gene Ontology - Biological Process | regulation of reactive oxygen species metabolic process | experimental (strong) | 9 | 2.271 | 0.005 |
| Gene Ontology - Biological Process | response to interleukin-6 | experimental (strong) | 5 | 0.619 | 0.005 |
| Gene Ontology - Biological Process | T cell proliferation | experimental (any) | 8 | 1.993 | 0.005 |
| Gene Ontology - Biological Process | cardiac chamber development | experimental (any) | 8 | 2.006 | 0.005 |
| Gene Ontology - Biological Process | cell differentiation | experimental (any) | 60 | 41.22 | 0.005 |
| Gene Ontology - Biological Process | cell proliferation involved in heart valve development | experimental (any) | 2 | 0.053 | 0.005 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | cellular response to organic cyclic compound | experimental (any) | 16 | 6.484 | 0.005 |
| Gene Ontology - Biological Process | developmental process | experimental (any) | 85 | 63.82 | 0.005 |
| Gene Ontology - Biological Process | endothelial cell differentiation | experimental (any) | 6 | 1.129 | 0.005 |
| Gene Ontology - Biological Process | leukocyte proliferation | experimental (any) | 10 | 3.029 | 0.005 |
| Gene Ontology - Biological Process | membrane protein intracellular domain proteolysis | experimental (any) | 3 | 0.199 | 0.005 |
| Gene Ontology - Biological Process | negative regulation of mammary gland epithelial cell proliferation | experimental (any) | 2 | 0.053 | 0.005 |
| Gene Ontology - Biological Process | neurotransmitter metabolic process | experimental (any) | 7 | 1.555 | 0.005 |
| Gene Ontology - Biological Process | positive regulation of adaptive immune response | experimental (any) | 6 | 1.116 | 0.005 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of inflammatory response | experimental (any) | 7 | 1.555 | 0.005 |
| Gene Ontology - Biological Process | positive regulation of interleukin-12 biosynthetic process | experimental (any) | 2 | 0.053 | 0.005 |
| Gene Ontology - Biological Process | positive regulation of superoxide anion generation | experimental (any) | 3 | 0.199 | 0.005 |
| Gene Ontology - Biological Process | regulation of T cell migration | experimental (any) | 4 | 0.438 | 0.005 |
| Gene Ontology - Biological Process | regulation of cytokine biosynthetic process | experimental (any) | 6 | 1.103 | 0.005 |
| Gene Ontology - Biological Process | regulation of focal adhesion assembly | experimental (any) | 5 | 0.757 | 0.005 |
| Gene Ontology - Biological Process | regulation of kinase activity | experimental (any) | 20 | 9.141 | 0.005 |
| Gene Ontology - Biological Process | regulation of mammary gland epithelial cell proliferation | experimental (any) | 3 | 0.199 | 0.005 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of translation | predicted (union) | 60 | 39.44 | 0.006 |
| Gene Ontology - Biological Process | neuron development | predicted (union) | 404 | 345.9 | 0.006 |
| Gene Ontology - Biological Process | chemotaxis | experimental (strong) | 15 | 5.833 | 0.006 |
| Gene Ontology - Biological Process | nitric oxide metabolic process | experimental (strong) | 6 | 1.032 | 0.006 |
| Gene Ontology - Biological Process | positive regulation of T cell activation | experimental (strong) | 9 | 2.349 | 0.006 |
| Gene Ontology - Biological Process | positive regulation of cell migration | experimental (strong) | 16 | 6.479 | 0.006 |
| Gene Ontology - Biological Process | positive regulation of cell motility | experimental (strong) | 16 | 6.504 | 0.006 |
| Gene Ontology - Biological Process | positive regulation of leukocyte proliferation | experimental (strong) | 7 | 1.445 | 0.006 |
| Gene Ontology - Biological Process | positive regulation of lymphocyte migration | experimental (strong) | 4 | 0.387 | 0.006 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of lymphocyte proliferation | experimental (strong) | 7 | 1.42 | 0.006 |
| Gene Ontology - Biological Process | positive regulation of mononuclear cell proliferation | experimental (strong) | 7 | 1.445 | 0.006 |
| Gene Ontology - Biological Process | regulation of T cell migration | experimental (strong) | 4 | 0.387 | 0.006 |
| Gene Ontology - Biological Process | response to corticosteroid | experimental (strong) | 8 | 1.884 | 0.006 |
| Gene Ontology - Biological Process | cardiovascular system development | experimental (any) | 18 | 8.052 | 0.006 |
| Gene Ontology - Biological Process | cell-substrate junction assembly | experimental (any) | 6 | 1.196 | 0.006 |
| Gene Ontology - Biological Process | embryonic morphogenesis | experimental (any) | 16 | 6.644 | 0.006 |
| Gene Ontology - Biological Process | heterocycle metabolic process | experimental (any) | 84 | 63.37 | 0.006 |
| Gene Ontology - Biological Process | leukocyte apoptotic process | experimental (any) | 6 | 1.183 | 0.006 |
| Gene Ontology - Biological Process | leukocyte degranulation | experimental (any) | 15 | 6.085 | 0.006 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of biosynthetic process | experimental (any) | 30 | 16.61 | 0.006 |
| Gene Ontology - Biological Process | negative regulation of extrinsic apoptotic signaling pathway via death domain receptors | experimental (any) | 4 | 0.465 | 0.006 |
| Gene Ontology - Biological Process | negative regulation of myeloid cell apoptotic process | experimental (any) | 3 | 0.213 | 0.006 |
| Gene Ontology - Biological Process | pericardium development | experimental (any) | 3 | 0.213 | 0.006 |
| Gene Ontology - Biological Process | positive regulation of ERK1 and ERK2 cascade | experimental (any) | 8 | 2.059 | 0.006 |
| Gene Ontology - Biological Process | positive regulation of T cell mediated immunity | experimental (any) | 4 | 0.478 | 0.006 |
| Gene Ontology - Biological Process | positive regulation of interleukin-8 production | experimental (any) | 4 | 0.465 | 0.006 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | pulmonary valve morphogenesis | experimental (any) | 3 | 0.213 | 0.006 |
| Gene Ontology - Biological Process | regulation of catalytic activity | experimental (any) | 39 | 23.66 | 0.006 |
| Gene Ontology - Biological Process | regulation of cell migration involved in sprouting angiogenesis | experimental (any) | 4 | 0.465 | 0.006 |
| Gene Ontology - Biological Process | regulation of immunoglobulin secretion | experimental (any) | 3 | 0.213 | 0.006 |
| Gene Ontology - Biological Process | regulation of neurogenesis | experimental (any) | 19 | 8.743 | 0.006 |
| Gene Ontology - Biological Process | regulation of smooth muscle cell proliferation | experimental (any) | 7 | 1.634 | 0.006 |
| Gene Ontology - Biological Process | vasculature development | experimental (any) | 18 | 7.946 | 0.006 |
| Gene Ontology - Biological Process | negative regulation of biosynthetic process | predicted (intersection) | 278 | 223.3 | 0.007 |
| Gene Ontology - Biological Process | regulation of cell differentiation | predicted (intersection) | 333 | 273 | 0.007 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | cell development | predicted (union) | 753 | 675.1 | 0.007 |
| Gene Ontology - Biological Process | cell morphogenesis involved in differentiation | predicted (union) | 266 | 219.8 | 0.007 |
| Gene Ontology - Biological Process | neuron projection guidance | predicted (union) | 101 | 73.8 | 0.007 |
| Gene Ontology - Biological Process | positive regulation of macromolecule biosynthetic process | predicted (union) | 680 | 606.8 | 0.007 |
| Gene Ontology - Biological Process | regulation of cellular protein localization | predicted (union) | 228 | 185.5 | 0.007 |
| Gene Ontology - Biological Process | tube morphogenesis | predicted (union) | 336 | 284.3 | 0.007 |
| Gene Ontology - Biological Process | SMAD protein complex assembly | experimental (strong) | 3 | 0.181 | 0.007 |
| Gene Ontology - Biological Process | chemokine (C-X-C motif) ligand 12 signaling pathway | experimental (strong) | 2 | 0.052 | 0.007 |
| Gene Ontology - Biological Process | defense response | experimental (strong) | 23 | 11.69 | 0.007 |

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| Gene Ontology - Biological Process | inflammatory response | experimental (strong) | 15 | 5.937 | 0.007 |
| Gene Ontology - Biological Process | maintenance of permeability of blood-brain barrier | experimental (strong) | 2 | 0.052 | 0.007 |
| Gene Ontology - Biological Process | negative regulation of calcium ion transport | experimental (strong) | 4 | 0.413 | 0.007 |
| Gene Ontology - Biological Process | negative regulation of extracellular matrix organization | experimental (strong) | 2 | 0.052 | 0.007 |
| Gene Ontology - Biological Process | negative regulation of growth rate | experimental (strong) | 2 | 0.052 | 0.007 |
| Gene Ontology - Biological Process | negative regulation of interleukin-23 production | experimental (strong) | 2 | 0.052 | 0.007 |
| Gene Ontology - Biological Process | negative regulation of signal transduction | experimental (strong) | 23 | 11.67 | 0.007 |
| Gene Ontology - Biological Process | positive regulation of cell death | experimental (strong) | 18 | 8.053 | 0.007 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of cellular component movement | experimental (strong) | 16 | 6.556 | 0.007 |
| Gene Ontology - Biological Process | positive regulation of cellular extravasation | experimental (strong) | 2 | 0.052 | 0.007 |
| Gene Ontology - Biological Process | positive regulation of chemotaxis | experimental (strong) | 7 | 1.497 | 0.007 |
| Gene Ontology - Biological Process | positive regulation of locomotion | experimental (strong) | 16 | 6.659 | 0.007 |
| Gene Ontology - Biological Process | prostaglandin biosynthetic process | experimental (strong) | 3 | 0.181 | 0.007 |
| Gene Ontology - Biological Process | regulation of T cell proliferation | experimental (strong) | 7 | 1.523 | 0.007 |
| Gene Ontology - Biological Process | regulation of cell differentiation | experimental (strong) | 30 | 17.42 | 0.007 |
| Gene Ontology - Biological Process | regulation of growth rate | experimental (strong) | 2 | 0.052 | 0.007 |
| Gene Ontology - Biological Process | regulation of leukocyte proliferation | experimental (strong) | 9 | 2.4 | 0.007 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of reactive oxygen species biosynthetic process | experimental (strong) | 6 | 1.058 | 0.007 |
| Gene Ontology - Biological Process | response to alkaloid | experimental (strong) | 6 | 1.084 | 0.007 |
| Gene Ontology - Biological Process | response to nitrogen compound | experimental (strong) | 21 | 10.04 | 0.007 |
| Gene Ontology - Biological Process | response to ultrasound | experimental (strong) | 2 | 0.052 | 0.007 |
| Gene Ontology - Biological Process | secretion by cell | experimental (strong) | 22 | 10.97 | 0.007 |
| Gene Ontology - Biological Process | signal transduction | experimental (strong) | 51 | 37.5 | 0.007 |
| Gene Ontology - Biological Process | ameboidal-type cell migration | experimental (any) | 12 | 4.332 | 0.007 |
| Gene Ontology - Biological Process | anatomical structure morphogenesis | experimental (any) | 44 | 28.05 | 0.007 |
| Gene Ontology - Biological Process | angiogenesis | experimental (any) | 14 | 5.567 | 0.007 |
| Gene Ontology - Biological Process | epithelium development | experimental (any) | 25 | 13.17 | 0.007 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | gland development | experimental (any) | 13 | 4.956 | 0.007 |
| Gene Ontology - Biological Process | mammary gland development | experimental (any) | 7 | 1.661 | 0.007 |
| Gene Ontology - Biological Process | multicellular organism development | experimental (any) | 75 | 55.29 | 0.007 |
| Gene Ontology - Biological Process | muscle tissue development | experimental (any) | 12 | 4.305 | 0.007 |
| Gene Ontology - Biological Process | positive regulation of nitric oxide biosynthetic process | experimental (any) | 4 | 0.492 | 0.007 |
| Gene Ontology - Biological Process | positive regulation of protein acetylation | experimental (any) | 4 | 0.492 | 0.007 |
| Gene Ontology - Biological Process | regulation of cytoskeleton organization | experimental (any) | 14 | 5.554 | 0.007 |
| Gene Ontology - Biological Process | regulation of growth | experimental (any) | 17 | 7.441 | 0.007 |
| Gene Ontology - Biological Process | response to alkaloid | experimental (any) | 6 | 1.209 | 0.007 |
| Gene Ontology - Biological Process | smooth muscle cell proliferation | experimental (any) | 7 | 1.648 | 0.007 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | stress-activated MAPK cascade | experimental (any) | 10 | 3.162 | 0.007 |
| Gene Ontology - Biological Process | establishment of localization in cell | predicted (union) | 746 | 670 | 0.008 |
| Gene Ontology - Biological Process | bone remodeling | experimental (strong) | 6 | 1.136 | 0.008 |
| Gene Ontology - Biological Process | neutrophil activation involved in immune response | experimental (strong) | 10 | 3.046 | 0.008 |
| Gene Ontology - Biological Process | neutrophil degranulation | experimental (strong) | 10 | 3.046 | 0.008 |
| Gene Ontology - Biological Process | nucleobase-containing compound metabolic process | experimental (strong) | 46 | 32.39 | 0.008 |
| Gene Ontology - Biological Process | positive regulation of cell activation | experimental (strong) | 11 | 3.639 | 0.008 |
| Gene Ontology - Biological Process | positive regulation of protein kinase activity | experimental (strong) | 15 | 6.066 | 0.008 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of protein serine/threonine kinase activity | experimental (strong) | 12 | 4.181 | 0.008 |
| Gene Ontology - Biological Process | regulation of cytokine production | experimental (strong) | 16 | 6.788 | 0.008 |
| Gene Ontology - Biological Process | Fc receptor signaling pathway | experimental (any) | 8 | 2.232 | 0.008 |
| Gene Ontology - Biological Process | activation of protein kinase activity | experimental (any) | 11 | 3.853 | 0.008 |
| Gene Ontology - Biological Process | animal organ regeneration | experimental (any) | 5 | 0.877 | 0.008 |
| Gene Ontology - Biological Process | cellular aromatic compound metabolic process | experimental (any) | 84 | 63.8 | 0.008 |
| Gene Ontology - Biological Process | cellular response to oxygen levels | experimental (any) | 9 | 2.75 | 0.008 |
| Gene Ontology - Biological Process | glial cell development | experimental (any) | 6 | 1.289 | 0.008 |
| Gene Ontology - Biological Process | interleukin-6-mediated signaling pathway | experimental (any) | 3 | 0.239 | 0.008 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | intracellular receptor signaling pathway | experimental (any) | 10 | 3.269 | 0.008 |
| Gene Ontology - Biological Process | mammary gland epithelium development | experimental (any) | 5 | 0.850 | 0.008 |
| Gene Ontology - Biological Process | membrane to membrane docking | experimental (any) | 2 | 0.066 | 0.008 |
| Gene Ontology - Biological Process | muscle tissue morphogenesis | experimental (any) | 5 | 0.877 | 0.008 |
| Gene Ontology - Biological Process | necroptotic signaling pathway | experimental (any) | 2 | 0.066 | 0.008 |
| Gene Ontology - Biological Process | negative regulation of apoptotic signaling pathway | experimental (any) | 9 | 2.737 | 0.008 |
| Gene Ontology - Biological Process | negative regulation of growth | experimental (any) | 9 | 2.737 | 0.008 |
| Gene Ontology - Biological Process | phosphate-containing compound metabolic process | experimental (any) | 52 | 35.18 | 0.008 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of T cell cytokine production | experimental (any) | 3 | 0.239 | 0.008 |
| Gene Ontology - Biological Process | positive regulation of cell cycle | experimental (any) | 12 | 4.398 | 0.008 |
| Gene Ontology - Biological Process | positive regulation of interferon-alpha production | experimental (any) | 3 | 0.239 | 0.008 |
| Gene Ontology - Biological Process | positive regulation of nitric oxide metabolic process | experimental (any) | 4 | 0.505 | 0.008 |
| Gene Ontology - Biological Process | regulation of adaptive immune response | experimental (any) | 7 | 1.727 | 0.008 |
| Gene Ontology - Biological Process | regulation of glial cell differentiation | experimental (any) | 5 | 0.877 | 0.008 |
| Gene Ontology - Biological Process | regulation of growth rate | experimental (any) | 2 | 0.066 | 0.008 |
| Gene Ontology - Biological Process | regulation of ossification | experimental (any) | 8 | 2.219 | 0.008 |
| Gene Ontology - Biological Process | regulation of superoxide anion generation | experimental (any) | 3 | 0.239 | 0.008 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | response to radiation | experimental (any) | 13 | 5.076 | 0.008 |
| Gene Ontology - Biological Process | response to tumor necrosis factor | experimental (any) | 10 | 3.229 | 0.008 |
| Gene Ontology - Biological Process | serotonin uptake | experimental (any) | 2 | 0.066 | 0.008 |
| Gene Ontology - Biological Process | cell morphogenesis | predicted (intersection) | 182 | 138.7 | 0.009 |
| Gene Ontology - Biological Process | response to platelet-derived growth factor | predicted (intersection) | 12 | 3.579 | 0.009 |
| Gene Ontology - Biological Process | tricuspid valve development | predicted (intersection) | 6 | 1.074 | 0.009 |
| Gene Ontology - Biological Process | cellular localization | predicted (union) | 977 | 891.8 | 0.009 |
| Gene Ontology - Biological Process | cell-cell adhesion | experimental (strong) | 16 | 6.866 | 0.009 |
| Gene Ontology - Biological Process | mononuclear cell migration | experimental (strong) | 5 | 0.774 | 0.009 |
| Gene Ontology - Biological Process | positive regulation of smooth muscle cell proliferation | experimental (strong) | 7 | 1.6 | 0.009 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of interleukin-12 production | experimental (strong) | 5 | 0.774 | 0.009 |
| Gene Ontology - Biological Process | response to external biotic stimulus | experimental (strong) | 21 | 10.43 | 0.009 |
| Gene Ontology - Biological Process | response to interleukin-1 | experimental (strong) | 8 | 2.065 | 0.009 |
| Gene Ontology - Biological Process | response to other organism | experimental (strong) | 21 | 10.43 | 0.009 |
| Gene Ontology - Biological Process | B cell activation involved in immune response | experimental (any) | 5 | 0.890 | 0.009 |
| Gene Ontology - Biological Process | positive regulation of catalytic activity | experimental (any) | 27 | 14.92 | 0.009 |
| Gene Ontology - Biological Process | positive regulation of glial cell differentiation | experimental (any) | 4 | 0.545 | 0.009 |
| Gene Ontology - Biological Process | positive regulation of protein secretion | experimental (any) | 9 | 2.764 | 0.009 |
| Gene Ontology - Biological Process | response to prostaglandin E | experimental (any) | 3 | 0.252 | 0.009 |
| Gene Ontology - Biological Process | vesicle-mediated transport | experimental (any) | 35 | 21.15 | 0.009 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | experimental (strong) | 8 | 2.117 | 0.010 |
| Gene Ontology - Biological Process | glial cell differentiation | experimental (strong) | 9 | 2.633 | 0.010 |
| Gene Ontology - Biological Process | interleukin-12 production | experimental (strong) | 5 | 0.800 | 0.010 |
| Gene Ontology - Biological Process | positive regulation of histone acetylation | experimental (strong) | 4 | 0.465 | 0.010 |
| Gene Ontology - Biological Process | positive regulation of protein complex assembly | experimental (strong) | 8 | 2.091 | 0.010 |
| Gene Ontology - Biological Process | proteolysis | experimental (strong) | 21 | 10.58 | 0.010 |
| Gene Ontology - Biological Process | regulation of RNA metabolic process | experimental (strong) | 40 | 26.87 | 0.010 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of actin filament-based process | experimental (strong) | 10 | 3.149 | 0.010 |
| Gene Ontology - Biological Process | regulation of metabolic process | experimental (strong) | 55 | 42.43 | 0.010 |
| Gene Ontology - Biological Process | toll-like receptor signaling pathway | experimental (strong) | 7 | 1.626 | 0.010 |
| Gene Ontology - Biological Process | DNA damage response, signal transduction by p53 class mediator | experimental (any) | 6 | 1.355 | 0.010 |
| Gene Ontology - Biological Process | blood vessel endothelial cell migration | experimental (any) | 6 | 1.342 | 0.010 |
| Gene Ontology - Biological Process | cellular response to prostaglandin stimulus | experimental (any) | 3 | 0.266 | 0.010 |
| Gene Ontology - Biological Process | cytokine secretion | experimental (any) | 8 | 2.325 | 0.010 |
| Gene Ontology - Biological Process | exocytosis | experimental (any) | 20 | 9.899 | 0.010 |
| Gene Ontology - Biological Process | head development | experimental (any) | 18 | 8.57 | 0.010 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | homeostasis of number of cells | experimental (any) | 9 | 2.87 | 0.010 |
| Gene Ontology - Biological Process | immunoglobulin secretion | experimental (any) | 3 | 0.266 | 0.010 |
| Gene Ontology - Biological Process | inflammatory cell apoptotic process | experimental (any) | 3 | 0.266 | 0.010 |
| Gene Ontology - Biological Process | lymphocyte migration | experimental (any) | 5 | 0.930 | 0.010 |
| Gene Ontology - Biological Process | macromolecule metabolic process | experimental (any) | 118 | 97.53 | 0.010 |
| Gene Ontology - Biological Process | necrotic cell death | experimental (any) | 4 | 0.558 | 0.010 |
| Gene Ontology - Biological Process | negative regulation of endothelial cell migration | experimental (any) | 4 | 0.558 | 0.010 |
| Gene Ontology - Biological Process | negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway | experimental (any) | 6 | 1.329 | 0.010 |
| Gene Ontology - Biological Process | peptidyl-tyrosine phosphorylation | experimental (any) | 11 | 3.973 | 0.010 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of leukocyte chemotaxis | experimental (any) | 5 | 0.917 | 0.010 |
| Gene Ontology - Biological Process | positive regulation of mononuclear cell migration | experimental (any) | 3 | 0.266 | 0.010 |
| Gene Ontology - Biological Process | prostaglandin biosynthetic process | experimental (any) | 3 | 0.266 | 0.010 |
| Gene Ontology - Biological Process | protein-containing complex assembly | experimental (any) | 32 | 18.93 | 0.010 |
| Gene Ontology - Biological Process | pulmonary valve development | experimental (any) | 3 | 0.266 | 0.010 |
| Gene Ontology - Biological Process | regulation of monocyte chemotaxis | experimental (any) | 3 | 0.266 | 0.010 |
| Gene Ontology - Biological Process | wound healing | experimental (any) | 14 | 5.82 | 0.010 |
| Gene Ontology - Biological Process | cell migration | experimental (strong) | 25 | 13.78 | 0.011 |
| Gene Ontology - Biological Process | cellular extravasation | experimental (strong) | 4 | 0.490 | 0.011 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | heterocycle metabolic process | experimental (strong) | 46 | 32.91 | 0.011 |
| Gene Ontology - Biological Process | membrane protein intracellular domain proteolysis | experimental (strong) | 3 | 0.232 | 0.011 |
| Gene Ontology - Biological Process | positive regulation of glial cell differentiation | experimental (strong) | 4 | 0.490 | 0.011 |
| Gene Ontology - Biological Process | positive regulation of peptidyl-serine phosphorylation | experimental (strong) | 6 | 1.213 | 0.011 |
| Gene Ontology - Biological Process | positive regulation of reactive oxygen species metabolic process | experimental (strong) | 6 | 1.239 | 0.011 |
| Gene Ontology - Biological Process | positive regulation of vascular endothelial growth factor production | experimental (strong) | 4 | 0.490 | 0.011 |
| Gene Ontology - Biological Process | regulation of glial cell differentiation | experimental (strong) | 5 | 0.826 | 0.011 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of immunoglobulin secretion | experimental (strong) | 3 | 0.232 | 0.011 |
| Gene Ontology - Biological Process | regulation of lymphocyte activation | experimental (strong) | 12 | 4.44 | 0.011 |
| Gene Ontology - Biological Process | regulation of monocyte chemotaxis | experimental (strong) | 3 | 0.232 | 0.011 |
| Gene Ontology - Biological Process | response to organic cyclic compound | experimental (strong) | 20 | 9.989 | 0.011 |
| Gene Ontology - Biological Process | SMAD protein signal transduction | experimental (any) | 4 | 0.585 | 0.011 |
| Gene Ontology - Biological Process | atrioventricular valve formation | experimental (any) | 2 | 0.080 | 0.011 |
| Gene Ontology - Biological Process | cardiac septum development | experimental (any) | 6 | 1.395 | 0.011 |
| Gene Ontology - Biological Process | common-partner SMAD protein phosphorylation | experimental (any) | 2 | 0.080 | 0.011 |
| Gene Ontology - Biological Process | endocardial cell differentiation | experimental (any) | 2 | 0.080 | 0.011 |
| Gene Ontology - Biological Process | endothelial cell migration | experimental (any) | 8 | 2.352 | 0.011 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | gene expression | experimental (any) | 77 | 58.17 | 0.011 |
| Gene Ontology - Biological Process | granulocyte chemotaxis | experimental (any) | 5 | 0.943 | 0.011 |
| Gene Ontology - Biological Process | heart morphogenesis | experimental (any) | 9 | 2.883 | 0.011 |
| Gene Ontology - Biological Process | lactation | experimental (any) | 4 | 0.571 | 0.011 |
| Gene Ontology - Biological Process | mesenchymal cell differentiation | experimental (any) | 8 | 2.378 | 0.011 |
| Gene Ontology - Biological Process | muscle organ morphogenesis | experimental (any) | 5 | 0.943 | 0.011 |
| Gene Ontology - Biological Process | negative regulation of extracellular matrix organization | experimental (any) | 2 | 0.080 | 0.011 |
| Gene Ontology - Biological Process | negative regulation of macrophage apoptotic process | experimental (any) | 2 | 0.080 | 0.011 |
| Gene Ontology - Biological Process | positive regulation of T-helper 2 cell cytokine production | experimental (any) | 2 | 0.080 | 0.011 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of extrinsic apoptotic signaling pathway | experimental (any) | 4 | 0.571 | 0.011 |
| Gene Ontology - Biological Process | positive regulation of lipopolysaccharide-mediated signaling pathway | experimental (any) | 2 | 0.080 | 0.011 |
| Gene Ontology - Biological Process | positive regulation of peptide secretion | experimental (any) | 9 | 2.923 | 0.011 |
| Gene Ontology - Biological Process | positive regulation of protein localization to membrane | experimental (any) | 6 | 1.395 | 0.011 |
| Gene Ontology - Biological Process | positive regulation of wound healing | experimental (any) | 4 | 0.571 | 0.011 |
| Gene Ontology - Biological Process | regulation of blood vessel diameter | experimental (any) | 6 | 1.382 | 0.011 |
| Gene Ontology - Biological Process | regulation of bone remodeling | experimental (any) | 4 | 0.571 | 0.011 |
| Gene Ontology - Biological Process | regulation of cellular extravasation | experimental (any) | 3 | 0.279 | 0.011 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of inflammatory response | experimental (any) | 10 | 3.455 | 0.011 |
| Gene Ontology - Biological Process | response to UV-A | experimental (any) | 2 | 0.080 | 0.011 |
| Gene Ontology - Biological Process | trabecula morphogenesis | experimental (any) | 4 | 0.571 | 0.011 |
| Gene Ontology - Biological Process | ventricular cardiac muscle tissue morphogenesis | experimental (any) | 4 | 0.571 | 0.011 |
| Gene Ontology - Biological Process | cellular response to hormone stimulus | predicted (intersection) | 138 | 101.3 | 0.012 |
| Gene Ontology - Biological Process | calcium ion transport | experimental (strong) | 9 | 2.736 | 0.012 |
| Gene Ontology - Biological Process | cell chemotaxis | experimental (strong) | 9 | 2.736 | 0.012 |
| Gene Ontology - Biological Process | cellular aromatic compound metabolic process | experimental (strong) | 46 | 33.14 | 0.012 |
| Gene Ontology - Biological Process | cytokine production involved in immune response | experimental (strong) | 6 | 1.265 | 0.012 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of blood vessel endothelial cell migration | experimental (strong) | 4 | 0.516 | 0.012 |
| Gene Ontology - Biological Process | positive regulation of kinase activity | experimental (strong) | 15 | 6.427 | 0.012 |
| Gene Ontology - Biological Process | protein autoubiquitination | experimental (strong) | 4 | 0.516 | 0.012 |
| Gene Ontology - Biological Process | regulation of blood vessel diameter | experimental (strong) | 6 | 1.265 | 0.012 |
| Gene Ontology - Biological Process | regulation of vascular endothelial growth factor production | experimental (strong) | 4 | 0.516 | 0.012 |
| Gene Ontology - Biological Process | response to organic substance | experimental (strong) | 41 | 28.19 | 0.012 |
| Gene Ontology - Biological Process | vascular endothelial growth factor production | experimental (strong) | 4 | 0.516 | 0.012 |
| Gene Ontology - Biological Process | cellular response to hypoxia | experimental (any) | 8 | 2.418 | 0.012 |
| Gene Ontology - Biological Process | gonad development | experimental (any) | 8 | 2.418 | 0.012 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of sprouting angiogenesis | experimental (any) | 3 | 0.292 | 0.012 |
| Gene Ontology - Biological Process | outflow tract morphogenesis | experimental (any) | 5 | 0.983 | 0.012 |
| Gene Ontology - Biological Process | positive regulation of cell growth | experimental (any) | 7 | 1.913 | 0.012 |
| Gene Ontology - Biological Process | positive regulation of chemokine production | experimental (any) | 4 | 0.598 | 0.012 |
| Gene Ontology - Biological Process | positive regulation of growth | experimental (any) | 9 | 2.936 | 0.012 |
| Gene Ontology - Biological Process | regulation of BMP signaling pathway | experimental (any) | 5 | 0.970 | 0.012 |
| Gene Ontology - Biological Process | regulation of cysteine-type endopeptidase activity involved in apoptotic process | experimental (any) | 8 | 2.392 | 0.012 |
| Gene Ontology - Biological Process | regulation of gliogenesis | experimental (any) | 6 | 1.422 | 0.012 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of interferon-beta production | experimental (any) | 4 | 0.598 | 0.012 |
| Gene Ontology - Biological Process | regulation of peptidyl-serine phosphorylation | experimental (any) | 6 | 1.422 | 0.012 |
| Gene Ontology - Biological Process | regulation of stress fiber assembly | experimental (any) | 5 | 0.970 | 0.012 |
| Gene Ontology - Biological Process | response to interferon-beta | experimental (any) | 3 | 0.292 | 0.012 |
| Gene Ontology - Biological Process | striated muscle tissue development | experimental (any) | 11 | 4.132 | 0.012 |
| Gene Ontology - Biological Process | B cell activation involved in immune response | experimental (strong) | 5 | 0.878 | 0.013 |
| Gene Ontology - Biological Process | interleukin-1-mediated signaling pathway | experimental (strong) | 5 | 0.878 | 0.013 |
| Gene Ontology - Biological Process | negative regulation of signaling | experimental (strong) | 23 | 12.47 | 0.013 |
| Gene Ontology - Biological Process | positive regulation of leukocyte chemotaxis | experimental (strong) | 5 | 0.878 | 0.013 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of transcription, DNA-templated | experimental (strong) | 26 | 14.87 | 0.013 |
| Gene Ontology - Biological Process | response to drug | experimental (strong) | 19 | 9.395 | 0.013 |
| Gene Ontology - Biological Process | Fc-epsilon receptor signaling pathway | experimental (any) | 6 | 1.462 | 0.013 |
| Gene Ontology - Biological Process | Roundabout signaling pathway | experimental (any) | 2 | 0.093 | 0.013 |
| Gene Ontology - Biological Process | brain development | experimental (any) | 17 | 8.105 | 0.013 |
| Gene Ontology - Biological Process | cellular response to tumor necrosis factor | experimental (any) | 9 | 3.003 | 0.013 |
| Gene Ontology - Biological Process | development of primary sexual characteristics | experimental (any) | 8 | 2.485 | 0.013 |
| Gene Ontology - Biological Process | endocardial cushion formation | experimental (any) | 3 | 0.306 | 0.013 |
| Gene Ontology - Biological Process | focal adhesion assembly | experimental (any) | 5 | 0.997 | 0.013 |
| Gene Ontology - Biological Process | interferon-beta production | experimental (any) | 4 | 0.624 | 0.013 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | interleukin-10 production | experimental (any) | 4 | 0.611 | 0.013 |
| Gene Ontology - Biological Process | mesenchyme development | experimental (any) | 9 | 2.99 | 0.013 |
| Gene Ontology - Biological Process | negative regulation of biomineral tissue development | experimental (any) | 3 | 0.306 | 0.013 |
| Gene Ontology - Biological Process | negative regulation of cellular metabolic process | experimental (any) | 41 | 26.79 | 0.013 |
| Gene Ontology - Biological Process | negative regulation of chemokine-mediated signaling pathway | experimental (any) | 2 | 0.093 | 0.013 |
| Gene Ontology - Biological Process | negative regulation of ion transport | experimental (any) | 6 | 1.462 | 0.013 |
| Gene Ontology - Biological Process | pericardium morphogenesis | experimental (any) | 2 | 0.093 | 0.013 |
| Gene Ontology - Biological Process | positive regulation of Ras protein signal transduction | experimental (any) | 4 | 0.624 | 0.013 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of T cell proliferation | experimental (any) | 5 | 0.997 | 0.013 |
| Gene Ontology - Biological Process | positive regulation of fibroblast proliferation | experimental (any) | 4 | 0.611 | 0.013 |
| Gene Ontology - Biological Process | receptor signaling pathway via JAK-STAT | experimental (any) | 6 | 1.448 | 0.013 |
| Gene Ontology - Biological Process | regulated exocytosis | experimental (any) | 18 | 8.823 | 0.013 |
| Gene Ontology - Biological Process | regulation of MyD88-independent toll-like receptor signaling pathway | experimental (any) | 2 | 0.093 | 0.013 |
| Gene Ontology - Biological Process | regulation of blood vessel size | experimental (any) | 6 | 1.435 | 0.013 |
| Gene Ontology - Biological Process | regulation of interleukin-6 production | experimental (any) | 6 | 1.435 | 0.013 |
| Gene Ontology - Biological Process | regulation of lymphocyte differentiation | experimental (any) | 7 | 1.927 | 0.013 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of neural precursor cell proliferation | experimental (any) | 5 | 1.01 | 0.013 |
| Gene Ontology - Biological Process | regulation of pro-B cell differentiation | experimental (any) | 2 | 0.093 | 0.013 |
| Gene Ontology - Biological Process | regulation of tube size | experimental (any) | 6 | 1.448 | 0.013 |
| Gene Ontology - Biological Process | response to fatty acid | experimental (any) | 5 | 0.997 | 0.013 |
| Gene Ontology - Biological Process | central nervous system development | predicted (union) | 382 | 329.2 | 0.014 |
| Gene Ontology - Biological Process | enzyme linked receptor protein signaling pathway | predicted (union) | 385 | 331.9 | 0.014 |
| Gene Ontology - Biological Process | positive regulation of cellular biosynthetic process | predicted (union) | 706 | 634.9 | 0.014 |
| Gene Ontology - Biological Process | RNA metabolic process | experimental (strong) | 41 | 28.47 | 0.014 |
| Gene Ontology - Biological Process | cell motility | experimental (strong) | 25 | 14.22 | 0.014 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | cytokine production | experimental (strong) | 16 | 7.33 | 0.014 |
| Gene Ontology - Biological Process | divalent metal ion transport | experimental (strong) | 9 | 2.839 | 0.014 |
| Gene Ontology - Biological Process | innate immune response | experimental (strong) | 15 | 6.582 | 0.014 |
| Gene Ontology - Biological Process | positive regulation of apoptotic process | experimental (strong) | 16 | 7.356 | 0.014 |
| Gene Ontology - Biological Process | positive regulation of cell cycle | experimental (strong) | 11 | 4.001 | 0.014 |
| Gene Ontology - Biological Process | positive regulation of epithelial to mesenchymal transition | experimental (strong) | 5 | 0.903 | 0.014 |
| Gene Ontology - Biological Process | positive regulation of mononuclear cell migration | experimental (strong) | 3 | 0.258 | 0.014 |
| Gene Ontology - Biological Process | positive regulation of peptidyl-lysine acetylation | experimental (strong) | 4 | 0.542 | 0.014 |
| Gene Ontology - Biological Process | positive regulation of type I interferon production | experimental (strong) | 5 | 0.903 | 0.014 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | prostaglandin metabolic process | experimental (strong) | 3 | 0.258 | 0.014 |
| Gene Ontology - Biological Process | regulation of ERK1 and ERK2 cascade | experimental (strong) | 10 | 3.433 | 0.014 |
| Gene Ontology - Biological Process | regulation of T cell activation | experimental (strong) | 10 | 3.407 | 0.014 |
| Gene Ontology - Biological Process | regulation of peptidyl-tyrosine phosphorylation | experimental (strong) | 9 | 2.813 | 0.014 |
| Gene Ontology - Biological Process | response to hormone | experimental (strong) | 19 | 9.55 | 0.014 |
| Gene Ontology - Biological Process | toll-like receptor 9 signaling pathway | experimental (strong) | 3 | 0.258 | 0.014 |
| Gene Ontology - Biological Process | ventricular cardiac muscle tissue morphogenesis | experimental (strong) | 4 | 0.542 | 0.014 |
| Gene Ontology - Biological Process | T cell mediated immunity | experimental (any) | 5 | 1.023 | 0.014 |
| Gene Ontology - Biological Process | aging | experimental (any) | 10 | 3.641 | 0.014 |
| Gene Ontology - Biological Process | endoderm formation | experimental (any) | 4 | 0.638 | 0.014 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | extracellular matrix assembly | experimental (any) | 3 | 0.319 | 0.014 |
| Gene Ontology - Biological Process | positive regulation of cell cycle phase transition | experimental (any) | 5 | 1.036 | 0.014 |
| Gene Ontology - Biological Process | positive regulation of focal adhesion assembly | experimental (any) | 3 | 0.319 | 0.014 |
| Gene Ontology - Biological Process | positive regulation of myeloid leukocyte differentiation | experimental (any) | 4 | 0.638 | 0.014 |
| Gene Ontology - Biological Process | regulation of intrinsic apoptotic signaling pathway | experimental (any) | 7 | 1.966 | 0.014 |
| Gene Ontology - Biological Process | regulation of lymphocyte migration | experimental (any) | 4 | 0.638 | 0.014 |
| Gene Ontology - Biological Process | regulation of supramolecular fiber organization | experimental (any) | 10 | 3.627 | 0.014 |
| Gene Ontology - Biological Process | regulation of vasoconstriction | experimental (any) | 4 | 0.638 | 0.014 |
| Gene Ontology - Biological Process | activation of protein kinase activity | experimental (strong) | 11 | 4.104 | 0.015 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | biosynthetic process | experimental (strong) | 48 | 35.88 | 0.015 |
| Gene Ontology - Biological Process | cellular nitrogen compound metabolic process | experimental (strong) | 47 | 34.74 | 0.015 |
| Gene Ontology - Biological Process | cyclooxygenase pathway | experimental (strong) | 2 | 0.077 | 0.015 |
| Gene Ontology - Biological Process | divalent inorganic cation transport | experimental (strong) | 9 | 2.891 | 0.015 |
| Gene Ontology - Biological Process | gliogenesis | experimental (strong) | 10 | 3.485 | 0.015 |
| Gene Ontology - Biological Process | lymphocyte migration | experimental (strong) | 5 | 0.929 | 0.015 |
| Gene Ontology - Biological Process | lymphocyte proliferation | experimental (strong) | 9 | 2.942 | 0.015 |
| Gene Ontology - Biological Process | monocyte chemotaxis | experimental (strong) | 4 | 0.568 | 0.015 |
| Gene Ontology - Biological Process | necrotic cell death | experimental (strong) | 4 | 0.568 | 0.015 |
| Gene Ontology - Biological Process | neurotransmitter metabolic process | experimental (strong) | 6 | 1.342 | 0.015 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | nitrogen compound metabolic process | experimental (strong) | 61 | 50.56 | 0.015 |
| Gene Ontology - Biological Process | positive regulation of DNA-binding transcription factor activity | experimental (strong) | 10 | 3.51 | 0.015 |
| Gene Ontology - Biological Process | positive regulation of ERK1 and ERK2 cascade | experimental (strong) | 8 | 2.375 | 0.015 |
| Gene Ontology - Biological Process | positive regulation of T cell proliferation | experimental (strong) | 5 | 0.929 | 0.015 |
| Gene Ontology - Biological Process | positive regulation of cellular response to macrophage colony-stimulating factor stimulus | experimental (strong) | 2 | 0.077 | 0.015 |
| Gene Ontology - Biological Process | positive regulation of interleukin-12 production | experimental (strong) | 4 | 0.568 | 0.015 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of programmed cell death | experimental (strong) | 16 | 7.434 | 0.015 |
| Gene Ontology - Biological Process | positive regulation of protein acetylation | experimental (strong) | 4 | 0.568 | 0.015 |
| Gene Ontology - Biological Process | protein-containing complex assembly | experimental (strong) | 20 | 10.45 | 0.015 |
| Gene Ontology - Biological Process | regulation of DNA replication | experimental (strong) | 5 | 0.929 | 0.015 |
| Gene Ontology - Biological Process | regulation of blood vessel size | experimental (strong) | 6 | 1.342 | 0.015 |
| Gene Ontology - Biological Process | regulation of cytoskeleton organization | experimental (strong) | 11 | 4.13 | 0.015 |
| Gene Ontology - Biological Process | regulation of pro-B cell differentiation | experimental (strong) | 2 | 0.077 | 0.015 |
| Gene Ontology - Biological Process | regulation of tube size | experimental (strong) | 6 | 1.368 | 0.015 |
| Gene Ontology - Biological Process | regulation of vasoconstriction | experimental (strong) | 4 | 0.568 | 0.015 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | response to UV-A | experimental (strong) | 2 | 0.077 | 0.015 |
| Gene Ontology - Biological Process | telencephalon cell migration | experimental (strong) | 4 | 0.568 | 0.015 |
| Gene Ontology - Biological Process | wound healing | experimental (strong) | 13 | 5.42 | 0.015 |
| Gene Ontology - Biological Process | B cell activation | experimental (any) | 8 | 2.551 | 0.015 |
| Gene Ontology - Biological Process | Notch signaling pathway | experimental (any) | 7 | 2.02 | 0.015 |
| Gene Ontology - Biological Process | T cell costimulation | experimental (any) | 4 | 0.651 | 0.015 |
| Gene Ontology - Biological Process | TRIF-dependent toll-like receptor signaling pathway | experimental (any) | 3 | 0.332 | 0.015 |
| Gene Ontology - Biological Process | cellular nitrogen compound metabolic process | experimental (any) | 87 | 68.65 | 0.015 |
| Gene Ontology - Biological Process | cellular response to decreased oxygen levels | experimental (any) | 8 | 2.538 | 0.015 |
| Gene Ontology - Biological Process | digestive tract development | experimental (any) | 6 | 1.515 | 0.015 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | heart development | experimental (any) | 14 | 6.271 | 0.015 |
| Gene Ontology - Biological Process | negative regulation of cytokine biosynthetic process | experimental (any) | 3 | 0.332 | 0.015 |
| Gene Ontology - Biological Process | neutrophil chemotaxis | experimental (any) | 4 | 0.651 | 0.015 |
| Gene Ontology - Biological Process | positive regulation of T cell differentiation | experimental (any) | 5 | 1.05 | 0.015 |
| Gene Ontology - Biological Process | positive regulation of establishment of protein localization | experimental (any) | 12 | 4.956 | 0.015 |
| Gene Ontology - Biological Process | positive regulation of peptidyl-tyrosine phosphorylation | experimental (any) | 7 | 2.02 | 0.015 |
| Gene Ontology - Biological Process | receptor signaling pathway via STAT | experimental (any) | 6 | 1.501 | 0.015 |
| Gene Ontology - Biological Process | regulation of blood vessel endothelial cell migration | experimental (any) | 5 | 1.05 | 0.015 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of fibroblast migration | experimental (any) | 3 | 0.332 | 0.015 |
| Gene Ontology - Biological Process | response to angiotensin | experimental (any) | 3 | 0.332 | 0.015 |
| Gene Ontology - Biological Process | response to morphine | experimental (any) | 3 | 0.332 | 0.015 |
| Gene Ontology - Biological Process | regulation of cell size | predicted (union) | 75 | 53.1 | 0.016 |
| Gene Ontology - Biological Process | RNA biosynthetic process | experimental (strong) | 38 | 25.99 | 0.016 |
| Gene Ontology - Biological Process | drug metabolic process | experimental (strong) | 10 | 3.562 | 0.016 |
| Gene Ontology - Biological Process | locomotion | experimental (strong) | 27 | 16.13 | 0.016 |
| Gene Ontology - Biological Process | mononuclear cell proliferation | experimental (strong) | 9 | 2.968 | 0.016 |
| Gene Ontology - Biological Process | pericardium development | experimental (strong) | 3 | 0.284 | 0.016 |
| Gene Ontology - Biological Process | regulation of extrinsic apoptotic signaling pathway via death domain receptors | experimental (strong) | 5 | 0.955 | 0.016 |
| Gene Ontology - Biological Process | T cell extravasation | experimental (any) | 2 | 0.106 | 0.016 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | defense response to bacterium | experimental (any) | 7 | 2.033 | 0.016 |
| Gene Ontology - Biological Process | extracellular matrix organization | experimental (any) | 10 | 3.734 | 0.016 |
| Gene Ontology - Biological Process | gastrulation | experimental (any) | 7 | 2.059 | 0.016 |
| Gene Ontology - Biological Process | interleukin-6 production | experimental (any) | 6 | 1.555 | 0.016 |
| Gene Ontology - Biological Process | male gonad development | experimental (any) | 6 | 1.555 | 0.016 |
| Gene Ontology - Biological Process | marginal zone B cell differentiation | experimental (any) | 2 | 0.106 | 0.016 |
| Gene Ontology - Biological Process | membrane protein proteolysis | experimental (any) | 4 | 0.664 | 0.016 |
| Gene Ontology - Biological Process | negative regulation of calcium ion transport | experimental (any) | 4 | 0.664 | 0.016 |
| Gene Ontology - Biological Process | neural tube closure | experimental (any) | 5 | 1.076 | 0.016 |
| Gene Ontology - Biological Process | positive regulation of histone H3-K9 acetylation | experimental (any) | 2 | 0.106 | 0.016 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of ossification | experimental (any) | 5 | 1.076 | 0.016 |
| Gene Ontology - Biological Process | positive regulation of transport | experimental (any) | 20 | 10.54 | 0.016 |
| Gene Ontology - Biological Process | regulation of G protein-coupled receptor signaling pathway | experimental (any) | 6 | 1.555 | 0.016 |
| Gene Ontology - Biological Process | regulation of cellular component organization | experimental (any) | 40 | 26.45 | 0.016 |
| Gene Ontology - Biological Process | regulation of extracellular matrix assembly | experimental (any) | 2 | 0.106 | 0.016 |
| Gene Ontology - Biological Process | regulation of histone acetylation | experimental (any) | 4 | 0.678 | 0.016 |
| Gene Ontology - Biological Process | regulation of macrophage activation | experimental (any) | 4 | 0.678 | 0.016 |
| Gene Ontology - Biological Process | regulation of protein localization to plasma membrane | experimental (any) | 5 | 1.076 | 0.016 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | response to nutrient | experimental (any) | 8 | 2.578 | 0.016 |
| Gene Ontology - Biological Process | transmembrane receptor protein serine/threonine kinase signaling pathway | experimental (any) | 10 | 3.734 | 0.016 |
| Gene Ontology - Biological Process | ventricular cardiac muscle tissue development | experimental (any) | 4 | 0.664 | 0.016 |
| Gene Ontology - Biological Process | cellular response to organonitrogen compound | predicted (intersection) | 121 | 87.5 | 0.017 |
| Gene Ontology - Biological Process | forebrain cell migration | experimental (strong) | 4 | 0.594 | 0.017 |
| Gene Ontology - Biological Process | leukocyte degranulation | experimental (strong) | 10 | 3.588 | 0.017 |
| Gene Ontology - Biological Process | nitric oxide biosynthetic process | experimental (strong) | 5 | 0.981 | 0.017 |
| Gene Ontology - Biological Process | positive regulation of cytokine production involved in immune response | experimental (strong) | 4 | 0.594 | 0.017 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of gene expression | experimental (strong) | 30 | 18.84 | 0.017 |
| Gene Ontology - Biological Process | regulation of G protein-coupled receptor signaling pathway | experimental (strong) | 5 | 0.981 | 0.017 |
| Gene Ontology - Biological Process | regulation of protein kinase activity | experimental (strong) | 17 | 8.311 | 0.017 |
| Gene Ontology - Biological Process | adherens junction assembly | experimental (any) | 5 | 1.103 | 0.017 |
| Gene Ontology - Biological Process | development of primary male sexual characteristics | experimental (any) | 6 | 1.568 | 0.017 |
| Gene Ontology - Biological Process | granulocyte migration | experimental (any) | 5 | 1.103 | 0.017 |
| Gene Ontology - Biological Process | mammary gland epithelial cell proliferation | experimental (any) | 3 | 0.345 | 0.017 |
| Gene Ontology - Biological Process | positive regulation of response to wounding | experimental (any) | 4 | 0.691 | 0.017 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of cysteine-type endopeptidase activity | experimental (any) | 8 | 2.618 | 0.017 |
| Gene Ontology - Biological Process | regulation of immunoglobulin production | experimental (any) | 4 | 0.691 | 0.017 |
| Gene Ontology - Biological Process | response to X-ray | experimental (any) | 3 | 0.345 | 0.017 |
| Gene Ontology - Biological Process | response to gonadotropin | experimental (any) | 3 | 0.345 | 0.017 |
| Gene Ontology - Biological Process | heart valve morphogenesis | experimental (strong) | 5 | 1.007 | 0.018 |
| Gene Ontology - Biological Process | lymphocyte activation | experimental (strong) | 15 | 6.969 | 0.018 |
| Gene Ontology - Biological Process | membrane protein proteolysis | experimental (strong) | 4 | 0.619 | 0.018 |
| Gene Ontology - Biological Process | negative regulation of leukocyte apoptotic process | experimental (strong) | 4 | 0.619 | 0.018 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway | experimental (strong) | 4 | 0.619 | 0.018 |
| Gene Ontology - Biological Process | nucleotide-binding oligomerization domain containing signaling pathway | experimental (strong) | 4 | 0.619 | 0.018 |
| Gene Ontology - Biological Process | positive regulation of RNA biosynthetic process | experimental (strong) | 26 | 15.51 | 0.018 |
| Gene Ontology - Biological Process | positive regulation of nucleic acid-templated transcription | experimental (strong) | 26 | 15.51 | 0.018 |
| Gene Ontology - Biological Process | protein secretion | experimental (strong) | 12 | 4.878 | 0.018 |
| Gene Ontology - Biological Process | regulation of lymphocyte migration | experimental (strong) | 4 | 0.619 | 0.018 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | stress-activated protein kinase signaling cascade | experimental (strong) | 10 | 3.639 | 0.018 |
| Gene Ontology - Biological Process | animal organ morphogenesis | experimental (any) | 21 | 11.48 | 0.018 |
| Gene Ontology - Biological Process | cardiocyte differentiation | experimental (any) | 6 | 1.608 | 0.018 |
| Gene Ontology - Biological Process | cellular response to dexamethasone stimulus | experimental (any) | 3 | 0.359 | 0.018 |
| Gene Ontology - Biological Process | epithelial tube morphogenesis | experimental (any) | 10 | 3.84 | 0.018 |
| Gene Ontology - Biological Process | female gonad development | experimental (any) | 5 | 1.129 | 0.018 |
| Gene Ontology - Biological Process | morphogenesis of an epithelium | experimental (any) | 14 | 6.431 | 0.018 |
| Gene Ontology - Biological Process | negative regulation of angiogenesis | experimental (any) | 5 | 1.129 | 0.018 |
| Gene Ontology - Biological Process | positive regulation of apoptotic signaling pathway | experimental (any) | 7 | 2.099 | 0.018 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of cytokine biosynthetic process | experimental (any) | 4 | 0.704 | 0.018 |
| Gene Ontology - Biological Process | positive regulation of erythrocyte differentiation | experimental (any) | 3 | 0.359 | 0.018 |
| Gene Ontology - Biological Process | positive regulation of histone modification | experimental (any) | 5 | 1.116 | 0.018 |
| Gene Ontology - Biological Process | positive regulation of interferon-beta production | experimental (any) | 3 | 0.359 | 0.018 |
| Gene Ontology - Biological Process | positive regulation of protein transport | experimental (any) | 11 | 4.478 | 0.018 |
| Gene Ontology - Biological Process | regulation of actin filament bundle assembly | experimental (any) | 5 | 1.116 | 0.018 |
| Gene Ontology - Biological Process | regulation of cell junction assembly | experimental (any) | 5 | 1.116 | 0.018 |
| Gene Ontology - Biological Process | regulation of interleukin-8 production | experimental (any) | 4 | 0.704 | 0.018 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | response to wounding | experimental (any) | 15 | 7.109 | 0.018 |
| Gene Ontology - Biological Process | stress fiber assembly | experimental (any) | 5 | 1.116 | 0.018 |
| Gene Ontology - Biological Process | superoxide anion generation | experimental (any) | 3 | 0.359 | 0.018 |
| Gene Ontology - Biological Process | ERK1 and ERK2 cascade | experimental (strong) | 10 | 3.665 | 0.019 |
| Gene Ontology - Biological Process | T cell proliferation | experimental (strong) | 7 | 1.962 | 0.019 |
| Gene Ontology - Biological Process | icosanoid biosynthetic process | experimental (strong) | 3 | 0.310 | 0.019 |
| Gene Ontology - Biological Process | immunoglobulin secretion | experimental (strong) | 3 | 0.310 | 0.019 |
| Gene Ontology - Biological Process | negative regulation of biomineral tissue development | experimental (strong) | 3 | 0.310 | 0.019 |
| Gene Ontology - Biological Process | negative regulation of cell migration involved in sprouting angiogenesis | experimental (strong) | 3 | 0.310 | 0.019 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of nitric-oxide synthase biosynthetic process | experimental (strong) | 3 | 0.310 | 0.019 |
| Gene Ontology - Biological Process | regulation of protein secretion | experimental (strong) | 11 | 4.285 | 0.019 |
| Gene Ontology - Biological Process | unsaturated fatty acid biosynthetic process | experimental (strong) | 3 | 0.310 | 0.019 |
| Gene Ontology - Biological Process | adherens junction organization | experimental (any) | 6 | 1.634 | 0.019 |
| Gene Ontology - Biological Process | cardiac atrium morphogenesis | experimental (any) | 3 | 0.372 | 0.019 |
| Gene Ontology - Biological Process | cellular response to insulin-like growth factor stimulus | experimental (any) | 2 | 0.120 | 0.019 |
| Gene Ontology - Biological Process | coronary artery morphogenesis | experimental (any) | 2 | 0.120 | 0.019 |
| Gene Ontology - Biological Process | detection of molecule of bacterial origin | experimental (any) | 2 | 0.120 | 0.019 |
| Gene Ontology - Biological Process | digestive system development | experimental (any) | 6 | 1.634 | 0.019 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | histone monoubiquitination | experimental (any) | 3 | 0.372 | 0.019 |
| Gene Ontology - Biological Process | homeostatic process | experimental (any) | 31 | 19.32 | 0.019 |
| Gene Ontology - Biological Process | interleukin-17 production | experimental (any) | 3 | 0.372 | 0.019 |
| Gene Ontology - Biological Process | lateral ventricle development | experimental (any) | 2 | 0.120 | 0.019 |
| Gene Ontology - Biological Process | negative regulation of intrinsic apoptotic signaling pathway | experimental (any) | 5 | 1.143 | 0.019 |
| Gene Ontology - Biological Process | nervous system development | experimental (any) | 38 | 25.1 | 0.019 |
| Gene Ontology - Biological Process | positive regulation of cell cycle process | experimental (any) | 9 | 3.282 | 0.019 |
| Gene Ontology - Biological Process | positive regulation of cyclin-dependent protein serine/threonine kinase activity | experimental (any) | 3 | 0.372 | 0.019 |
| Gene Ontology - Biological Process | positive regulation of neurogenesis | experimental (any) | 12 | 5.182 | 0.019 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of production of miRNAs involved in gene silencing by miRNA | experimental (any) | 2 | 0.120 | 0.019 |
| Gene Ontology - Biological Process | regulation of T cell cytokine production | experimental (any) | 3 | 0.372 | 0.019 |
| Gene Ontology - Biological Process | regulation of actin filament organization | experimental (any) | 8 | 2.697 | 0.019 |
| Gene Ontology - Biological Process | regulation of myeloid cell apoptotic process | experimental (any) | 3 | 0.372 | 0.019 |
| Gene Ontology - Biological Process | regulation of nucleotide-binding oligomerization domain containing signaling pathway | experimental (any) | 2 | 0.120 | 0.019 |
| Gene Ontology - Biological Process | regulation of superoxide metabolic process | experimental (any) | 3 | 0.372 | 0.019 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | response to temperature stimulus | experimental (any) | 8 | 2.697 | 0.019 |
| Gene Ontology - Biological Process | regulation of intracellular protein transport | predicted (union) | 109 | 82.39 | 0.020 |
| Gene Ontology - Biological Process | DNA replication | experimental (strong) | 7 | 2.013 | 0.020 |
| Gene Ontology - Biological Process | T cell activation | experimental (strong) | 12 | 5.007 | 0.020 |
| Gene Ontology - Biological Process | actin polymerization or depolymerization | experimental (strong) | 5 | 1.032 | 0.020 |
| Gene Ontology - Biological Process | icosanoid metabolic process | experimental (strong) | 4 | 0.645 | 0.020 |
| Gene Ontology - Biological Process | macrophage activation | experimental (strong) | 5 | 1.032 | 0.020 |
| Gene Ontology - Biological Process | negative regulation of endothelial cell migration | experimental (strong) | 4 | 0.645 | 0.020 |
| Gene Ontology - Biological Process | pattern recognition receptor signaling pathway | experimental (strong) | 7 | 2.013 | 0.020 |
| Gene Ontology - Biological Process | positive regulation of protein secretion | experimental (strong) | 8 | 2.555 | 0.020 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of actin filament organization | experimental (strong) | 7 | 1.987 | 0.020 |
| Gene Ontology - Biological Process | regulation of cytokine production involved in immune response | experimental (strong) | 5 | 1.032 | 0.020 |
| Gene Ontology - Biological Process | transcription, DNA-templated | experimental (strong) | 37 | 25.55 | 0.020 |
| Gene Ontology - Biological Process | activation of MAPK activity | experimental (any) | 7 | 2.166 | 0.020 |
| Gene Ontology - Biological Process | cardiac muscle tissue morphogenesis | experimental (any) | 4 | 0.731 | 0.020 |
| Gene Ontology - Biological Process | cellular component assembly | experimental (any) | 44 | 30.41 | 0.020 |
| Gene Ontology - Biological Process | cellular response to organonitrogen compound | experimental (any) | 14 | 6.551 | 0.020 |
| Gene Ontology - Biological Process | epithelial cell migration | experimental (any) | 9 | 3.335 | 0.020 |
| Gene Ontology - Biological Process | histone modification | experimental (any) | 12 | 5.222 | 0.020 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | hormone secretion | experimental (any) | 9 | 3.322 | 0.020 |
| Gene Ontology - Biological Process | liver regeneration | experimental (any) | 3 | 0.385 | 0.020 |
| Gene Ontology - Biological Process | negative regulation of cellular response to growth factor stimulus | experimental (any) | 6 | 1.648 | 0.020 |
| Gene Ontology - Biological Process | peptidyl-serine phosphorylation | experimental (any) | 8 | 2.724 | 0.020 |
| Gene Ontology - Biological Process | positive regulation of BMP signaling pathway | experimental (any) | 3 | 0.385 | 0.020 |
| Gene Ontology - Biological Process | positive regulation of epithelial cell proliferation | experimental (any) | 7 | 2.179 | 0.020 |
| Gene Ontology - Biological Process | positive regulation of interleukin-10 production | experimental (any) | 3 | 0.385 | 0.020 |
| Gene Ontology - Biological Process | positive regulation of lymphocyte differentiation | experimental (any) | 5 | 1.169 | 0.020 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of synaptic transmission | experimental (any) | 6 | 1.661 | 0.020 |
| Gene Ontology - Biological Process | regulation of T cell differentiation | experimental (any) | 6 | 1.661 | 0.020 |
| Gene Ontology - Biological Process | response to transforming growth factor beta | experimental (any) | 8 | 2.737 | 0.020 |
| Gene Ontology - Biological Process | signal transduction in response to DNA damage | experimental (any) | 6 | 1.648 | 0.020 |
| Gene Ontology - Biological Process | toll-like receptor 4 signaling pathway | experimental (any) | 3 | 0.385 | 0.020 |
| Gene Ontology - Biological Process | negative regulation of cellular metabolic process | predicted (intersection) | 430 | 367.7 | 0.021 |
| Gene Ontology - Biological Process | regulation of cytoskeleton organization | predicted (union) | 199 | 162.4 | 0.021 |
| Gene Ontology - Biological Process | regulation of dephosphorylation | predicted (union) | 93 | 68.72 | 0.021 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of adaptive immune response | experimental (strong) | 5 | 1.058 | 0.021 |
| Gene Ontology - Biological Process | regulation of RNA biosynthetic process | experimental (strong) | 37 | 25.63 | 0.021 |
| Gene Ontology - Biological Process | regulation of gliogenesis | experimental (strong) | 6 | 1.523 | 0.021 |
| Gene Ontology - Biological Process | development of primary female sexual characteristics | experimental (any) | 5 | 1.183 | 0.021 |
| Gene Ontology - Biological Process | epithelial to mesenchymal transition | experimental (any) | 6 | 1.674 | 0.021 |
| Gene Ontology - Biological Process | epithelium migration | experimental (any) | 9 | 3.362 | 0.021 |
| Gene Ontology - Biological Process | negative regulation of RNA biosynthetic process | experimental (any) | 23 | 13.25 | 0.021 |
| Gene Ontology - Biological Process | negative regulation of nucleic acid-templated transcription | experimental (any) | 23 | 13.23 | 0.021 |

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| Gene Ontology - Biological Process | negative regulation of protein metabolic process | experimental (any) | 21 | 11.68 | 0.021 |
| Gene Ontology - Biological Process | neutrophil migration | experimental (any) | 4 | 0.757 | 0.021 |
| Gene Ontology - Biological Process | regulation of toll-like receptor signaling pathway | experimental (any) | 4 | 0.757 | 0.021 |
| Gene Ontology - Biological Process | ureteric bud development | experimental (any) | 5 | 1.196 | 0.021 |
| Gene Ontology - Biological Process | cellular response to platelet-derived growth factor stimulus | predicted (intersection) | 11 | 3.4 | 0.022 |
| Gene Ontology - Biological Process | netrin-activated signaling pathway | predicted (intersection) | 8 | 1.968 | 0.022 |
| Gene Ontology - Biological Process | cell proliferation involved in heart valve development | experimental (strong) | 2 | 0.103 | 0.022 |
| Gene Ontology - Biological Process | heart valve development | experimental (strong) | 5 | 1.084 | 0.022 |
| Gene Ontology - Biological Process | interleukin-6-mediated signaling pathway | experimental (strong) | 3 | 0.336 | 0.022 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | leukocyte homeostasis | experimental (strong) | 5 | 1.084 | 0.022 |
| Gene Ontology - Biological Process | muscle cell proliferation | experimental (strong) | 9 | 3.201 | 0.022 |
| Gene Ontology - Biological Process | negative regulation of extrinsic apoptotic signaling pathway via death domain receptors | experimental (strong) | 4 | 0.671 | 0.022 |
| Gene Ontology - Biological Process | negative regulation of leukocyte migration | experimental (strong) | 3 | 0.336 | 0.022 |
| Gene Ontology - Biological Process | peptide secretion | experimental (strong) | 12 | 5.085 | 0.022 |
| Gene Ontology - Biological Process | positive regulation of histone H3-K9 acetylation | experimental (strong) | 2 | 0.103 | 0.022 |
| Gene Ontology - Biological Process | positive regulation of interleukin-12 biosynthetic process | experimental (strong) | 2 | 0.103 | 0.022 |

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| Gene Ontology - Biological Process | positive regulation of lipopolysaccharide-mediated signaling pathway | experimental (strong) | 2 | 0.103 | 0.022 |
| Gene Ontology - Biological Process | positive regulation of reactive oxygen species biosynthetic process | experimental (strong) | 4 | 0.671 | 0.022 |
| Gene Ontology - Biological Process | positive regulation of secretion | experimental (strong) | 10 | 3.794 | 0.022 |
| Gene Ontology - Biological Process | regulation of fibroblast migration | experimental (strong) | 3 | 0.336 | 0.022 |
| Gene Ontology - Biological Process | regulation of immunoglobulin production | experimental (strong) | 4 | 0.671 | 0.022 |
| Gene Ontology - Biological Process | response to estradiol | experimental (strong) | 6 | 1.549 | 0.022 |
| Gene Ontology - Biological Process | semi-lunar valve development | experimental (strong) | 4 | 0.671 | 0.022 |
| Gene Ontology - Biological Process | signaling | experimental (strong) | 51 | 39.78 | 0.022 |

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| Gene Ontology - Biological Process | ventricular cardiac muscle tissue development | experimental (strong) | 4 | 0.671 | 0.022 |
| Gene Ontology - Biological Process | cell projection morphogenesis | experimental (any) | 14 | 6.697 | 0.022 |
| Gene Ontology - Biological Process | cellular response to alkaloid | experimental (any) | 3 | 0.399 | 0.022 |
| Gene Ontology - Biological Process | cellular response to lipoteichoic acid | experimental (any) | 2 | 0.133 | 0.022 |
| Gene Ontology - Biological Process | cellular response to macrophage colony-stimulating factor stimulus | experimental (any) | 2 | 0.133 | 0.022 |
| Gene Ontology - Biological Process | cyclooxygenase pathway | experimental (any) | 2 | 0.133 | 0.022 |
| Gene Ontology - Biological Process | detection of mechanical stimulus involved in sensory perception of pain | experimental (any) | 2 | 0.133 | 0.022 |
| Gene Ontology - Biological Process | dorsal/ventral axis specification | experimental (any) | 2 | 0.133 | 0.022 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | drug metabolic process | experimental (any) | 13 | 6.006 | 0.022 |
| Gene Ontology - Biological Process | endocardium development | experimental (any) | 2 | 0.133 | 0.022 |
| Gene Ontology - Biological Process | forebrain generation of neurons | experimental (any) | 4 | 0.771 | 0.022 |
| Gene Ontology - Biological Process | hormone transport | experimental (any) | 9 | 3.415 | 0.022 |
| Gene Ontology - Biological Process | intrinsic apoptotic signaling pathway | experimental (any) | 9 | 3.401 | 0.022 |
| Gene Ontology - Biological Process | kidney epithelium development | experimental (any) | 6 | 1.687 | 0.022 |
| Gene Ontology - Biological Process | macrophage derived foam cell differentiation | experimental (any) | 3 | 0.399 | 0.022 |
| Gene Ontology - Biological Process | mesonephric epithelium development | experimental (any) | 5 | 1.209 | 0.022 |
| Gene Ontology - Biological Process | mesonephric tubule development | experimental (any) | 5 | 1.209 | 0.022 |
| Gene Ontology - Biological Process | multicellular organismal homeostasis | experimental (any) | 12 | 5.315 | 0.022 |

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| Gene Ontology - Biological Process | negative regulation of immune system process | experimental (any) | 11 | 4.664 | 0.022 |
| Gene Ontology - Biological Process | olfactory bulb interneuron differentiation | experimental (any) | 2 | 0.133 | 0.022 |
| Gene Ontology - Biological Process | pattern specification process | experimental (any) | 11 | 4.677 | 0.022 |
| Gene Ontology - Biological Process | positive regulation of adherens junction organization | experimental (any) | 3 | 0.399 | 0.022 |
| Gene Ontology - Biological Process | positive regulation of cell development | experimental (any) | 13 | 5.992 | 0.022 |
| Gene Ontology - Biological Process | regulation of macrophage apoptotic process | experimental (any) | 2 | 0.133 | 0.022 |
| Gene Ontology - Biological Process | response to gravity | experimental (any) | 2 | 0.133 | 0.022 |
| Gene Ontology - Biological Process | response to peptide hormone | experimental (any) | 11 | 4.65 | 0.022 |
| Gene Ontology - Biological Process | regulation of neuron differentiation | predicted (union) | 248 | 207.3 | 0.023 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | tube development | predicted (union) | 404 | 351.8 | 0.023 |
| Gene Ontology - Biological Process | cardiac chamber development | experimental (strong) | 7 | 2.091 | 0.023 |
| Gene Ontology - Biological Process | cellular component assembly | experimental (strong) | 27 | 16.83 | 0.023 |
| Gene Ontology - Biological Process | leukocyte proliferation | experimental (strong) | 9 | 3.226 | 0.023 |
| Gene Ontology - Biological Process | regulation of supramolecular fiber organization | experimental (strong) | 8 | 2.633 | 0.023 |
| Gene Ontology - Biological Process | cellular response to DNA damage stimulus | experimental (any) | 18 | 9.58 | 0.023 |
| Gene Ontology - Biological Process | covalent chromatin modification | experimental (any) | 12 | 5.381 | 0.023 |
| Gene Ontology - Biological Process | interleukin-8 production | experimental (any) | 4 | 0.784 | 0.023 |
| Gene Ontology - Biological Process | necroptotic process | experimental (any) | 3 | 0.412 | 0.023 |
| Gene Ontology - Biological Process | negative regulation of ERK1 and ERK2 cascade | experimental (any) | 4 | 0.784 | 0.023 |

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| Gene Ontology - Biological Process | negative regulation of epithelial cell migration | experimental (any) | 4 | 0.784 | 0.023 |
| Gene Ontology - Biological Process | negative regulation of extrinsic apoptotic signaling pathway | experimental (any) | 5 | 1.236 | 0.023 |
| Gene Ontology - Biological Process | negative regulation of transcription, DNA-templated | experimental (any) | 22 | 12.65 | 0.023 |
| Gene Ontology - Biological Process | positive regulation of cell junction assembly | experimental (any) | 3 | 0.412 | 0.023 |
| Gene Ontology - Biological Process | positive regulation of cyclin-dependent protein kinase activity | experimental (any) | 3 | 0.412 | 0.023 |
| Gene Ontology - Biological Process | regulation of DNA replication | experimental (any) | 5 | 1.236 | 0.023 |
| Gene Ontology - Biological Process | regulation of cell cycle | experimental (any) | 23 | 13.38 | 0.023 |
| Gene Ontology - Biological Process | regulation of extracellular matrix organization | experimental (any) | 3 | 0.412 | 0.023 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | response to inorganic substance | experimental (any) | 13 | 6.019 | 0.023 |
| Gene Ontology - Biological Process | central nervous system development | predicted (intersection) | 192 | 150.8 | 0.024 |
| Gene Ontology - Biological Process | organ growth | predicted (intersection) | 44 | 25.59 | 0.024 |
| Gene Ontology - Biological Process | response to hormone | predicted (intersection) | 186 | 145.5 | 0.024 |
| Gene Ontology - Biological Process | tube morphogenesis | predicted (intersection) | 169 | 130.3 | 0.024 |
| Gene Ontology - Biological Process | brain development | predicted (union) | 289 | 245.2 | 0.024 |
| Gene Ontology - Biological Process | negative regulation of transcription by RNA polymerase II | predicted (union) | 308 | 262.8 | 0.024 |
| Gene Ontology - Biological Process | animal organ regeneration | experimental (strong) | 5 | 1.11 | 0.024 |
| Gene Ontology - Biological Process | positive regulation of innate immune response | experimental (strong) | 9 | 3.252 | 0.024 |
| Gene Ontology - Biological Process | mesonephros development | experimental (any) | 5 | 1.249 | 0.024 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | neural precursor cell proliferation | experimental (any) | 6 | 1.754 | 0.024 |
| Gene Ontology - Biological Process | neural tube formation | experimental (any) | 5 | 1.249 | 0.024 |
| Gene Ontology - Biological Process | regulation of protein ubiquitination | experimental (any) | 7 | 2.285 | 0.024 |
| Gene Ontology - Biological Process | tube formation | experimental (any) | 6 | 1.754 | 0.024 |
| Gene Ontology - Biological Process | central nervous system neuron development | predicted (union) | 42 | 26.94 | 0.025 |
| Gene Ontology - Biological Process | posttranscriptional regulation of gene expression | predicted (union) | 231 | 192.1 | 0.025 |
| Gene Ontology - Biological Process | protein dephosphorylation | predicted (union) | 135 | 105.8 | 0.025 |
| Gene Ontology - Biological Process | regulation of actin filament-based process | predicted (union) | 145 | 114.8 | 0.025 |
| Gene Ontology - Biological Process | regulation of phosphatase activity | predicted (union) | 80 | 58.18 | 0.025 |
| Gene Ontology - Biological Process | central nervous system development | experimental (strong) | 17 | 8.827 | 0.025 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | detection of stimulus | experimental (strong) | 5 | 1.136 | 0.025 |
| Gene Ontology - Biological Process | innate immune response-activating signal transduction | experimental (strong) | 8 | 2.71 | 0.025 |
| Gene Ontology - Biological Process | neurotransmitter biosynthetic process | experimental (strong) | 5 | 1.136 | 0.025 |
| Gene Ontology - Biological Process | positive regulation of MAP kinase activity | experimental (strong) | 9 | 3.278 | 0.025 |
| Gene Ontology - Biological Process | positive regulation of catalytic activity | experimental (strong) | 21 | 11.98 | 0.025 |
| Gene Ontology - Biological Process | positive regulation of chemokine production | experimental (strong) | 4 | 0.697 | 0.025 |
| Gene Ontology - Biological Process | positive regulation of peptide secretion | experimental (strong) | 8 | 2.684 | 0.025 |
| Gene Ontology - Biological Process | regulation of extracellular matrix organization | experimental (strong) | 3 | 0.361 | 0.025 |

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| Gene Ontology - Biological Process | regulation of granulocyte chemotaxis | experimental (strong) | 3 | 0.361 | 0.025 |
| Gene Ontology - Biological Process | regulation of peptidyl-serine phosphorylation | experimental (strong) | 6 | 1.6 | 0.025 |
| Gene Ontology - Biological Process | regulation of protein serine/threonine kinase activity | experimental (strong) | 13 | 5.911 | 0.025 |
| Gene Ontology - Biological Process | regulation of secretion | experimental (strong) | 14 | 6.608 | 0.025 |
| Gene Ontology - Biological Process | regulation of transcription, DNA-templated | experimental (strong) | 36 | 25.04 | 0.025 |
| Gene Ontology - Biological Process | response to ammonium ion | experimental (strong) | 5 | 1.136 | 0.025 |
| Gene Ontology - Biological Process | response to angiotensin | experimental (strong) | 3 | 0.361 | 0.025 |
| Gene Ontology - Biological Process | response to stimulus | experimental (strong) | 60 | 50.41 | 0.025 |
| Gene Ontology - Biological Process | response to tumor necrosis factor | experimental (strong) | 8 | 2.684 | 0.025 |
| Gene Ontology - Biological Process | ERBB2 signaling pathway | experimental (any) | 3 | 0.425 | 0.025 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | Notch signaling involved in heart development | experimental (any) | 2 | 0.146 | 0.025 |
| Gene Ontology - Biological Process | T cell homeostasis | experimental (any) | 3 | 0.425 | 0.025 |
| Gene Ontology - Biological Process | T-helper 2 cell cytokine production | experimental (any) | 2 | 0.146 | 0.025 |
| Gene Ontology - Biological Process | bleb assembly | experimental (any) | 2 | 0.146 | 0.025 |
| Gene Ontology - Biological Process | cellular response to estradiol stimulus | experimental (any) | 3 | 0.425 | 0.025 |
| Gene Ontology - Biological Process | eyelid development in camera-type eye | experimental (any) | 2 | 0.146 | 0.025 |
| Gene Ontology - Biological Process | fibroblast migration | experimental (any) | 3 | 0.425 | 0.025 |
| Gene Ontology - Biological Process | heart valve formation | experimental (any) | 2 | 0.146 | 0.025 |
| Gene Ontology - Biological Process | macrophage apoptotic process | experimental (any) | 2 | 0.146 | 0.025 |
| Gene Ontology - Biological Process | positive regulation of DNA replication | experimental (any) | 3 | 0.425 | 0.025 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of type I interferon-mediated signaling pathway | experimental (any) | 2 | 0.146 | 0.025 |
| Gene Ontology - Biological Process | pro-B cell differentiation | experimental (any) | 2 | 0.146 | 0.025 |
| Gene Ontology - Biological Process | regulation of G1/S transition of mitotic cell cycle | experimental (any) | 6 | 1.767 | 0.025 |
| Gene Ontology - Biological Process | regulation of histone H3-K9 acetylation | experimental (any) | 2 | 0.146 | 0.025 |
| Gene Ontology - Biological Process | regulation of neuroinflammatory response | experimental (any) | 3 | 0.425 | 0.025 |
| Gene Ontology - Biological Process | regulation of response to wounding | experimental (any) | 6 | 1.767 | 0.025 |
| Gene Ontology - Biological Process | regulation of sprouting angiogenesis | experimental (any) | 4 | 0.811 | 0.025 |
| Gene Ontology - Biological Process | response to ionizing radiation | experimental (any) | 6 | 1.78 | 0.025 |
| Gene Ontology - Biological Process | small GTPase mediated signal transduction | experimental (any) | 12 | 5.421 | 0.025 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | sprouting angiogenesis | experimental (any) | 5 | 1.262 | 0.025 |
| Gene Ontology - Biological Process | response to transforming growth factor beta | predicted (intersection) | 58 | 36.68 | 0.026 |
| Gene Ontology - Biological Process | cell communication | experimental (strong) | 51 | 40.19 | 0.026 |
| Gene Ontology - Biological Process | lymphocyte homeostasis | experimental (strong) | 4 | 0.723 | 0.026 |
| Gene Ontology - Biological Process | positive regulation of small GTPase mediated signal transduction | experimental (strong) | 4 | 0.723 | 0.026 |
| Gene Ontology - Biological Process | regulation of cell migration involved in sprouting angiogenesis | experimental (strong) | 4 | 0.723 | 0.026 |
| Gene Ontology - Biological Process | response to steroid hormone | experimental (strong) | 11 | 4.594 | 0.026 |
| Gene Ontology - Biological Process | tissue remodeling | experimental (strong) | 7 | 2.168 | 0.026 |
| Gene Ontology - Biological Process | vasoconstriction | experimental (strong) | 4 | 0.723 | 0.026 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | adaptive immune response | experimental (any) | 10 | 4.159 | 0.026 |
| Gene Ontology - Biological Process | cardiac muscle tissue development | experimental (any) | 7 | 2.352 | 0.026 |
| Gene Ontology - Biological Process | cell part morphogenesis | experimental (any) | 14 | 6.883 | 0.026 |
| Gene Ontology - Biological Process | cellular process | experimental (any) | 170 | 156.4 | 0.026 |
| Gene Ontology - Biological Process | negative regulation of transcription by RNA polymerase II | experimental (any) | 17 | 9.048 | 0.026 |
| Gene Ontology - Biological Process | prostaglandin metabolic process | experimental (any) | 3 | 0.438 | 0.026 |
| Gene Ontology - Biological Process | protein monoubiquitination | experimental (any) | 4 | 0.824 | 0.026 |
| Gene Ontology - Biological Process | regulation of cell cycle arrest | experimental (any) | 5 | 1.289 | 0.026 |
| Gene Ontology - Biological Process | tissue homeostasis | experimental (any) | 7 | 2.352 | 0.026 |
| Gene Ontology - Biological Process | vasoconstriction | experimental (any) | 4 | 0.824 | 0.026 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | endothelium development | experimental (strong) | 6 | 1.652 | 0.027 |
| Gene Ontology - Biological Process | positive regulation of cell development | experimental (strong) | 12 | 5.291 | 0.027 |
| Gene Ontology - Biological Process | posttranscriptional regulation of gene expression | experimental (strong) | 10 | 3.975 | 0.027 |
| Gene Ontology - Biological Process | regulation of innate immune response | experimental (strong) | 10 | 3.975 | 0.027 |
| Gene Ontology - Biological Process | developmental growth | experimental (any) | 14 | 6.909 | 0.027 |
| Gene Ontology - Biological Process | phosphatidylinositol-mediated signaling | experimental (any) | 6 | 1.807 | 0.027 |
| Gene Ontology - Biological Process | positive regulation of B cell activation | experimental (any) | 4 | 0.837 | 0.027 |
| Gene Ontology - Biological Process | protein autoubiquitination | experimental (any) | 4 | 0.837 | 0.027 |
| Gene Ontology - Biological Process | regulation of chemokine production | experimental (any) | 4 | 0.837 | 0.027 |
| Gene Ontology - Biological Process | regulation of protein transport | experimental (strong) | 13 | 6.014 | 0.028 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | response to radiation | experimental (strong) | 10 | 4.001 | 0.028 |
| Gene Ontology - Biological Process | bone mineralization | experimental (any) | 5 | 1.315 | 0.028 |
| Gene Ontology - Biological Process | cardiac ventricle morphogenesis | experimental (any) | 4 | 0.850 | 0.028 |
| Gene Ontology - Biological Process | cell development | experimental (any) | 33 | 21.84 | 0.028 |
| Gene Ontology - Biological Process | endocardial cushion morphogenesis | experimental (any) | 3 | 0.452 | 0.028 |
| Gene Ontology - Biological Process | hydrogen peroxide metabolic process | experimental (any) | 3 | 0.452 | 0.028 |
| Gene Ontology - Biological Process | negative regulation of cell cycle | experimental (any) | 14 | 6.962 | 0.028 |
| Gene Ontology - Biological Process | negative regulation of leukocyte migration | experimental (any) | 3 | 0.452 | 0.028 |
| Gene Ontology - Biological Process | regulation of B cell activation | experimental (any) | 5 | 1.315 | 0.028 |
| Gene Ontology - Biological Process | regulation of bone mineralization | experimental (any) | 4 | 0.850 | 0.028 |
| Gene Ontology - Biological Process | reproductive structure development | experimental (any) | 11 | 4.89 | 0.028 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | response to xenobiotic stimulus | experimental (any) | 8 | 2.963 | 0.028 |
| Gene Ontology - Biological Process | cellular response to growth factor stimulus | predicted (intersection) | 136 | 102.2 | 0.029 |
| Gene Ontology - Biological Process | regulation of cellular protein localization | predicted (intersection) | 116 | 84.99 | 0.029 |
| Gene Ontology - Biological Process | tricuspid valve morphogenesis | predicted (intersection) | 5 | 0.895 | 0.029 |
| Gene Ontology - Biological Process | cardiac muscle cell differentiation | predicted (union) | 53 | 35.92 | 0.029 |
| Gene Ontology - Biological Process | cell projection organization | predicted (union) | 546 | 487.3 | 0.029 |
| Gene Ontology - Biological Process | forebrain development | predicted (union) | 163 | 131.2 | 0.029 |
| Gene Ontology - Biological Process | head development | predicted (union) | 304 | 260 | 0.029 |
| Gene Ontology - Biological Process | T cell extravasation | experimental (strong) | 2 | 0.129 | 0.029 |
| Gene Ontology - Biological Process | adaptive immune response | experimental (strong) | 8 | 2.813 | 0.029 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | atrioventricular valve formation | experimental (strong) | 2 | 0.129 | 0.029 |
| Gene Ontology - Biological Process | bone resorption | experimental (strong) | 4 | 0.749 | 0.029 |
| Gene Ontology - Biological Process | cardiac left ventricle morphogenesis | experimental (strong) | 2 | 0.129 | 0.029 |
| Gene Ontology - Biological Process | cellular response to alkaloid | experimental (strong) | 3 | 0.387 | 0.029 |
| Gene Ontology - Biological Process | cellular response to dexamethasone stimulus | experimental (strong) | 3 | 0.387 | 0.029 |
| Gene Ontology - Biological Process | cellular response to hormone stimulus | experimental (strong) | 14 | 6.814 | 0.029 |
| Gene Ontology - Biological Process | cellular response to macrophage colony-stimulating factor stimulus | experimental (strong) | 2 | 0.129 | 0.029 |
| Gene Ontology - Biological Process | common-partner SMAD protein phosphorylation | experimental (strong) | 2 | 0.129 | 0.029 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | cytoplasmic pattern recognition receptor signaling pathway | experimental (strong) | 4 | 0.749 | 0.029 |
| Gene Ontology - Biological Process | detection of mechanical stimulus involved in sensory perception of pain | experimental (strong) | 2 | 0.129 | 0.029 |
| Gene Ontology - Biological Process | detection of molecule of bacterial origin | experimental (strong) | 2 | 0.129 | 0.029 |
| Gene Ontology - Biological Process | endocardial cell differentiation | experimental (strong) | 2 | 0.129 | 0.029 |
| Gene Ontology - Biological Process | lymph node development | experimental (strong) | 2 | 0.129 | 0.029 |
| Gene Ontology - Biological Process | marginal zone B cell differentiation | experimental (strong) | 2 | 0.129 | 0.029 |
| Gene Ontology - Biological Process | membrane to membrane docking | experimental (strong) | 2 | 0.129 | 0.029 |
| Gene Ontology - Biological Process | necroptotic signaling pathway | experimental (strong) | 2 | 0.129 | 0.029 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of cell cycle | experimental (strong) | 12 | 5.42 | 0.029 |
| Gene Ontology - Biological Process | negative regulation of cell migration | experimental (strong) | 8 | 2.813 | 0.029 |
| Gene Ontology - Biological Process | negative regulation of cell population proliferation | experimental (strong) | 15 | 7.537 | 0.029 |
| Gene Ontology - Biological Process | pericardium morphogenesis | experimental (strong) | 2 | 0.129 | 0.029 |
| Gene Ontology - Biological Process | positive regulation of neurogenesis | experimental (strong) | 11 | 4.672 | 0.029 |
| Gene Ontology - Biological Process | positive regulation of peptidyl-tyrosine phosphorylation | experimental (strong) | 7 | 2.22 | 0.029 |
| Gene Ontology - Biological Process | protein modification by small protein removal | experimental (strong) | 7 | 2.22 | 0.029 |
| Gene Ontology - Biological Process | regulation of angiogenesis | experimental (strong) | 10 | 4.078 | 0.029 |
| Gene Ontology - Biological Process | regulation of cell cycle arrest | experimental (strong) | 5 | 1.187 | 0.029 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of epithelial to mesenchymal transition | experimental (strong) | 5 | 1.187 | 0.029 |
| Gene Ontology - Biological Process | regulation of extracellular matrix assembly | experimental (strong) | 2 | 0.129 | 0.029 |
| Gene Ontology - Biological Process | regulation of histone H3-K9 acetylation | experimental (strong) | 2 | 0.129 | 0.029 |
| Gene Ontology - Biological Process | regulation of kinase activity | experimental (strong) | 17 | 9.06 | 0.029 |
| Gene Ontology - Biological Process | toll-like receptor 2 signaling pathway | experimental (strong) | 2 | 0.129 | 0.029 |
| Gene Ontology - Biological Process | JNK cascade | experimental (any) | 7 | 2.405 | 0.029 |
| Gene Ontology - Biological Process | actomyosin structure organization | experimental (any) | 6 | 1.86 | 0.029 |
| Gene Ontology - Biological Process | astrocyte development | experimental (any) | 3 | 0.465 | 0.029 |
| Gene Ontology - Biological Process | cardiac left ventricle morphogenesis | experimental (any) | 2 | 0.159 | 0.029 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | detection of temperature stimulus involved in sensory perception of pain | experimental (any) | 2 | 0.159 | 0.029 |
| Gene Ontology - Biological Process | formation of primary germ layer | experimental (any) | 5 | 1.342 | 0.029 |
| Gene Ontology - Biological Process | inositol lipid-mediated signaling | experimental (any) | 6 | 1.847 | 0.029 |
| Gene Ontology - Biological Process | male sex differentiation | experimental (any) | 6 | 1.847 | 0.029 |
| Gene Ontology - Biological Process | microglial cell activation | experimental (any) | 3 | 0.465 | 0.029 |
| Gene Ontology - Biological Process | negative regulation of bone remodeling | experimental (any) | 2 | 0.159 | 0.029 |
| Gene Ontology - Biological Process | negative regulation of cell differentiation | experimental (any) | 15 | 7.706 | 0.029 |
| Gene Ontology - Biological Process | negative regulation of gene expression | experimental (any) | 31 | 20.22 | 0.029 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of intracellular steroid hormone receptor signaling pathway | experimental (any) | 3 | 0.465 | 0.029 |
| Gene Ontology - Biological Process | negative regulation of leukocyte chemotaxis | experimental (any) | 2 | 0.159 | 0.029 |
| Gene Ontology - Biological Process | neurogenesis | experimental (any) | 27 | 17.01 | 0.029 |
| Gene Ontology - Biological Process | nucleotide-binding oligomerization domain containing 2 signaling pathway | experimental (any) | 2 | 0.159 | 0.029 |
| Gene Ontology - Biological Process | positive regulation of SMAD protein signal transduction | experimental (any) | 2 | 0.159 | 0.029 |
| Gene Ontology - Biological Process | positive regulation of fibroblast migration | experimental (any) | 2 | 0.159 | 0.029 |
| Gene Ontology - Biological Process | positive regulation of hormone secretion | experimental (any) | 5 | 1.342 | 0.029 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of interleukin-17 production | experimental (any) | 2 | 0.159 | 0.029 |
| Gene Ontology - Biological Process | positive regulation of receptor signaling pathway via JAK-STAT | experimental (any) | 4 | 0.864 | 0.029 |
| Gene Ontology - Biological Process | positive regulation of tumor necrosis factor production | experimental (any) | 4 | 0.864 | 0.029 |
| Gene Ontology - Biological Process | regulation of bone resorption | experimental (any) | 3 | 0.465 | 0.029 |
| Gene Ontology - Biological Process | regulation of cell-substrate adhesion | experimental (any) | 7 | 2.405 | 0.029 |
| Gene Ontology - Biological Process | regulation of granulocyte chemotaxis | experimental (any) | 3 | 0.465 | 0.029 |
| Gene Ontology - Biological Process | regulation of heart morphogenesis | experimental (any) | 3 | 0.465 | 0.029 |
| Gene Ontology - Biological Process | regulation of neurotransmitter levels | experimental (any) | 9 | 3.627 | 0.029 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of phosphatidylinositol 3-kinase signaling | experimental (any) | 5 | 1.329 | 0.029 |
| Gene Ontology - Biological Process | reproductive system development | experimental (any) | 11 | 4.929 | 0.029 |
| Gene Ontology - Biological Process | response to estrogen | experimental (any) | 4 | 0.864 | 0.029 |
| Gene Ontology - Biological Process | response to progesterone | experimental (any) | 3 | 0.465 | 0.029 |
| Gene Ontology - Biological Process | sex differentiation | experimental (any) | 8 | 3.003 | 0.029 |
| Gene Ontology - Biological Process | response to growth factor | predicted (intersection) | 141 | 106.8 | 0.030 |
| Gene Ontology - Biological Process | activation of immune response | experimental (strong) | 11 | 4.749 | 0.030 |
| Gene Ontology - Biological Process | activation of innate immune response | experimental (strong) | 8 | 2.839 | 0.030 |
| Gene Ontology - Biological Process | cardiac muscle tissue morphogenesis | experimental (strong) | 4 | 0.774 | 0.030 |
| Gene Ontology - Biological Process | negative regulation of blood vessel diameter | experimental (strong) | 4 | 0.774 | 0.030 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of MAP kinase activity | experimental (strong) | 10 | 4.104 | 0.030 |
| Gene Ontology - Biological Process | regulation of neurogenesis | experimental (strong) | 15 | 7.588 | 0.030 |
| Gene Ontology - Biological Process | regulation of nucleic acid-templated transcription | experimental (strong) | 36 | 25.53 | 0.030 |
| Gene Ontology - Biological Process | Rho protein signal transduction | experimental (any) | 6 | 1.873 | 0.030 |
| Gene Ontology - Biological Process | positive regulation of mitotic cell cycle phase transition | experimental (any) | 4 | 0.877 | 0.030 |
| Gene Ontology - Biological Process | positive regulation of protein polymerization | experimental (any) | 5 | 1.355 | 0.030 |
| Gene Ontology - Biological Process | response to peptide | experimental (any) | 12 | 5.634 | 0.030 |
| Gene Ontology - Biological Process | cell surface receptor signaling pathway | predicted (intersection) | 504 | 440.5 | 0.031 |
| Gene Ontology - Biological Process | Golgi vesicle transport | predicted (union) | 136 | 107.4 | 0.031 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | actin cytoskeleton organization | experimental (any) | 13 | 6.391 | 0.031 |
| Gene Ontology - Biological Process | extracellular structure organization | experimental (any) | 10 | 4.318 | 0.031 |
| Gene Ontology - Biological Process | muscle organ development | experimental (any) | 10 | 4.318 | 0.031 |
| Gene Ontology - Biological Process | negative regulation of blood vessel diameter | experimental (any) | 4 | 0.890 | 0.031 |
| Gene Ontology - Biological Process | positive regulation of bone mineralization | experimental (any) | 3 | 0.478 | 0.031 |
| Gene Ontology - Biological Process | positive regulation of receptor signaling pathway via STAT | experimental (any) | 4 | 0.890 | 0.031 |
| Gene Ontology - Biological Process | programmed necrotic cell death | experimental (any) | 3 | 0.478 | 0.031 |
| Gene Ontology - Biological Process | response to dsRNA | experimental (any) | 3 | 0.478 | 0.031 |
| Gene Ontology - Biological Process | response to testosterone | experimental (any) | 3 | 0.478 | 0.031 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | somatic stem cell population maintenance | experimental (any) | 4 | 0.890 | 0.031 |
| Gene Ontology - Biological Process | MyD88-independent toll-like receptor signaling pathway | experimental (strong) | 3 | 0.413 | 0.032 |
| Gene Ontology - Biological Process | cardiac septum morphogenesis | experimental (strong) | 5 | 1.239 | 0.032 |
| Gene Ontology - Biological Process | cellular protein-containing complex assembly | experimental (strong) | 11 | 4.801 | 0.032 |
| Gene Ontology - Biological Process | fibroblast migration | experimental (strong) | 3 | 0.413 | 0.032 |
| Gene Ontology - Biological Process | hydrogen peroxide metabolic process | experimental (strong) | 3 | 0.413 | 0.032 |
| Gene Ontology - Biological Process | negative regulation of cell motility | experimental (strong) | 8 | 2.891 | 0.032 |
| Gene Ontology - Biological Process | negative regulation of ion transport | experimental (strong) | 5 | 1.239 | 0.032 |
| Gene Ontology - Biological Process | regulation of gene expression | experimental (strong) | 41 | 30.43 | 0.032 |
| Gene Ontology - Biological Process | response to gonadotropin | experimental (strong) | 3 | 0.413 | 0.032 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | response to morphine | experimental (strong) | 3 | 0.413 | 0.032 |
| Gene Ontology - Biological Process | actin filament organization | experimental (any) | 9 | 3.72 | 0.032 |
| Gene Ontology - Biological Process | endodermal cell fate commitment | experimental (any) | 2 | 0.173 | 0.032 |
| Gene Ontology - Biological Process | histone H3-K9 acetylation | experimental (any) | 2 | 0.173 | 0.032 |
| Gene Ontology - Biological Process | hyaluronan biosynthetic process | experimental (any) | 2 | 0.173 | 0.032 |
| Gene Ontology - Biological Process | positive regulation of cellular extravasation | experimental (any) | 2 | 0.173 | 0.032 |
| Gene Ontology - Biological Process | positive regulation of macrophage differentiation | experimental (any) | 2 | 0.173 | 0.032 |
| Gene Ontology - Biological Process | regulation of extracellular matrix disassembly | experimental (any) | 2 | 0.173 | 0.032 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | cellular response to transforming growth factor beta stimulus | predicted (intersection) | 56 | 35.61 | 0.033 |
| Gene Ontology - Biological Process | positive regulation of cell cycle process | experimental (strong) | 8 | 2.917 | 0.033 |
| Gene Ontology - Biological Process | positive regulation of fibroblast proliferation | experimental (strong) | 4 | 0.800 | 0.033 |
| Gene Ontology - Biological Process | positive regulation of interleukin-6 production | experimental (strong) | 4 | 0.800 | 0.033 |
| Gene Ontology - Biological Process | regulation of cell activation | experimental (strong) | 12 | 5.549 | 0.033 |
| Gene Ontology - Biological Process | regulation of histone acetylation | experimental (strong) | 4 | 0.800 | 0.033 |
| Gene Ontology - Biological Process | translation | experimental (strong) | 8 | 2.917 | 0.033 |
| Gene Ontology - Biological Process | T cell cytokine production | experimental (any) | 3 | 0.492 | 0.033 |
| Gene Ontology - Biological Process | icosanoid biosynthetic process | experimental (any) | 3 | 0.492 | 0.033 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of cell growth | experimental (any) | 6 | 1.927 | 0.033 |
| Gene Ontology - Biological Process | neuron projection morphogenesis | experimental (any) | 13 | 6.457 | 0.033 |
| Gene Ontology - Biological Process | regulation of animal organ morphogenesis | experimental (any) | 8 | 3.109 | 0.033 |
| Gene Ontology - Biological Process | regulation of cell-matrix adhesion | experimental (any) | 5 | 1.395 | 0.033 |
| Gene Ontology - Biological Process | regulation of oligodendrocyte differentiation | experimental (any) | 3 | 0.492 | 0.033 |
| Gene Ontology - Biological Process | response to ammonium ion | experimental (any) | 5 | 1.395 | 0.033 |
| Gene Ontology - Biological Process | response to dexamethasone | experimental (any) | 3 | 0.492 | 0.033 |
| Gene Ontology - Biological Process | cell-cell signaling by wnt | predicted (intersection) | 109 | 79.62 | 0.034 |
| Gene Ontology - Biological Process | phosphate-containing compound metabolic process | predicted (intersection) | 553 | 487.8 | 0.034 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | cellular response to drug | experimental (strong) | 10 | 4.207 | 0.034 |
| Gene Ontology - Biological Process | entry into host cell | experimental (strong) | 5 | 1.265 | 0.034 |
| Gene Ontology - Biological Process | immune response-regulating signaling pathway | experimental (strong) | 11 | 4.878 | 0.034 |
| Gene Ontology - Biological Process | tissue homeostasis | experimental (strong) | 6 | 1.781 | 0.034 |
| Gene Ontology - Biological Process | astrocyte differentiation | experimental (any) | 4 | 0.917 | 0.034 |
| Gene Ontology - Biological Process | positive regulation of axonogenesis | experimental (any) | 4 | 0.917 | 0.034 |
| Gene Ontology - Biological Process | positive regulation of cellular protein localization | experimental (any) | 9 | 3.76 | 0.034 |
| Gene Ontology - Biological Process | positive regulation of organelle organization | experimental (any) | 14 | 7.188 | 0.034 |
| Gene Ontology - Biological Process | Notch signaling pathway | experimental (strong) | 6 | 1.807 | 0.035 |
| Gene Ontology - Biological Process | T cell mediated immunity | experimental (strong) | 4 | 0.826 | 0.035 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | T-helper 1 type immune response | experimental (strong) | 3 | 0.439 | 0.035 |
| Gene Ontology - Biological Process | activation of MAPK activity | experimental (strong) | 7 | 2.349 | 0.035 |
| Gene Ontology - Biological Process | blood circulation | experimental (strong) | 10 | 4.259 | 0.035 |
| Gene Ontology - Biological Process | cardiac atrium morphogenesis | experimental (strong) | 3 | 0.439 | 0.035 |
| Gene Ontology - Biological Process | extrinsic apoptotic signaling pathway via death domain receptors | experimental (strong) | 5 | 1.291 | 0.035 |
| Gene Ontology - Biological Process | necroptotic process | experimental (strong) | 3 | 0.439 | 0.035 |
| Gene Ontology - Biological Process | negative regulation of chemotaxis | experimental (strong) | 3 | 0.439 | 0.035 |
| Gene Ontology - Biological Process | negative regulation of epithelial cell migration | experimental (strong) | 4 | 0.826 | 0.035 |
| Gene Ontology - Biological Process | positive regulation of BMP signaling pathway | experimental (strong) | 3 | 0.439 | 0.035 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of cytokine biosynthetic process | experimental (strong) | 4 | 0.826 | 0.035 |
| Gene Ontology - Biological Process | positive regulation of interleukin-10 production | experimental (strong) | 3 | 0.439 | 0.035 |
| Gene Ontology - Biological Process | positive regulation of interleukin-8 production | experimental (strong) | 3 | 0.439 | 0.035 |
| Gene Ontology - Biological Process | positive regulation of mitotic cell cycle phase transition | experimental (strong) | 4 | 0.826 | 0.035 |
| Gene Ontology - Biological Process | positive regulation of tumor necrosis factor production | experimental (strong) | 4 | 0.826 | 0.035 |
| Gene Ontology - Biological Process | regulation of cytokine biosynthetic process | experimental (strong) | 5 | 1.291 | 0.035 |
| Gene Ontology - Biological Process | regulation of nitric oxide biosynthetic process | experimental (strong) | 4 | 0.826 | 0.035 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of smooth muscle cell proliferation | experimental (strong) | 7 | 2.375 | 0.035 |
| Gene Ontology - Biological Process | smooth muscle cell proliferation | experimental (strong) | 7 | 2.375 | 0.035 |
| Gene Ontology - Biological Process | stress-activated MAPK cascade | experimental (strong) | 9 | 3.588 | 0.035 |
| Gene Ontology - Biological Process | actin polymerization or depolymerization | experimental (any) | 6 | 1.966 | 0.035 |
| Gene Ontology - Biological Process | activation of cysteine-type endopeptidase activity involved in apoptotic process | experimental (any) | 4 | 0.930 | 0.035 |
| Gene Ontology - Biological Process | biological_process | experimental (any) | 183 | 172.5 | 0.035 |
| Gene Ontology - Biological Process | cell-matrix adhesion | experimental (any) | 7 | 2.538 | 0.035 |
| Gene Ontology - Biological Process | cell-substrate adhesion | experimental (any) | 9 | 3.8 | 0.035 |
| Gene Ontology - Biological Process | chemokine production | experimental (any) | 4 | 0.930 | 0.035 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | developmental growth involved in morphogenesis | experimental (any) | 7 | 2.551 | 0.035 |
| Gene Ontology - Biological Process | enzyme linked receptor protein signaling pathway | experimental (any) | 19 | 10.98 | 0.035 |
| Gene Ontology - Biological Process | establishment of protein localization | experimental (any) | 32 | 21.52 | 0.035 |
| Gene Ontology - Biological Process | macromolecule glycosylation | experimental (any) | 7 | 2.551 | 0.035 |
| Gene Ontology - Biological Process | macrophage differentiation | experimental (any) | 3 | 0.505 | 0.035 |
| Gene Ontology - Biological Process | negative regulation of T cell apoptotic process | experimental (any) | 2 | 0.186 | 0.035 |
| Gene Ontology - Biological Process | negative regulation of gene silencing by miRNA | experimental (any) | 2 | 0.186 | 0.035 |
| Gene Ontology - Biological Process | negative regulation of interleukin-17 production | experimental (any) | 2 | 0.186 | 0.035 |

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| Gene Ontology - Biological Process | negative regulation of intracellular signal transduction | experimental (any) | 12 | 5.806 | 0.035 |
| Gene Ontology - Biological Process | negative regulation of viral entry into host cell | experimental (any) | 2 | 0.186 | 0.035 |
| Gene Ontology - Biological Process | nitrogen compound metabolic process | experimental (any) | 120 | 104.1 | 0.035 |
| Gene Ontology - Biological Process | positive regulation of regulatory T cell differentiation | experimental (any) | 2 | 0.186 | 0.035 |
| Gene Ontology - Biological Process | positive regulation of type 2 immune response | experimental (any) | 2 | 0.186 | 0.035 |
| Gene Ontology - Biological Process | protein glycosylation | experimental (any) | 7 | 2.551 | 0.035 |
| Gene Ontology - Biological Process | protein ubiquitination | experimental (any) | 17 | 9.447 | 0.035 |
| Gene Ontology - Biological Process | regulation of cell cycle G1/S phase transition | experimental (any) | 6 | 1.953 | 0.035 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of stress-activated MAPK cascade | experimental (any) | 7 | 2.538 | 0.035 |
| Gene Ontology - Biological Process | regulation of transcription by RNA polymerase II | experimental (any) | 41 | 29.2 | 0.035 |
| Gene Ontology - Biological Process | regulation of wound healing | experimental (any) | 5 | 1.422 | 0.035 |
| Gene Ontology - Biological Process | response to antibiotic | experimental (any) | 9 | 3.8 | 0.035 |
| Gene Ontology - Biological Process | response to fungus | experimental (any) | 3 | 0.505 | 0.035 |
| Gene Ontology - Biological Process | toll-like receptor 2 signaling pathway | experimental (any) | 2 | 0.186 | 0.035 |
| Gene Ontology - Biological Process | ventricular septum development | experimental (any) | 4 | 0.930 | 0.035 |
| Gene Ontology - Biological Process | developmental cell growth | predicted (union) | 92 | 69.11 | 0.036 |
| Gene Ontology - Biological Process | regulation of axonogenesis | predicted (union) | 70 | 50.37 | 0.036 |
| Gene Ontology - Biological Process | Ras protein signal transduction | experimental (strong) | 8 | 2.994 | 0.036 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | T-helper 1 type immune response | experimental (any) | 3 | 0.518 | 0.036 |
| Gene Ontology - Biological Process | amide transport | experimental (any) | 31 | 20.75 | 0.036 |
| Gene Ontology - Biological Process | cell cycle | experimental (any) | 30 | 19.94 | 0.036 |
| Gene Ontology - Biological Process | cell morphogenesis | experimental (any) | 18 | 10.26 | 0.036 |
| Gene Ontology - Biological Process | positive regulation of cell cycle G1/S phase transition | experimental (any) | 3 | 0.518 | 0.036 |
| Gene Ontology - Biological Process | positive regulation of cysteine-type endopeptidase activity involved in apoptotic process | experimental (any) | 5 | 1.448 | 0.036 |
| Gene Ontology - Biological Process | regulation of Ras protein signal transduction | experimental (any) | 7 | 2.564 | 0.036 |
| Gene Ontology - Biological Process | regulation of protein complex assembly | experimental (any) | 10 | 4.491 | 0.036 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of stress-activated protein kinase signaling cascade | experimental (any) | 7 | 2.564 | 0.036 |
| Gene Ontology - Biological Process | response to extracellular stimulus | experimental (any) | 12 | 5.846 | 0.036 |
| Gene Ontology - Biological Process | response to osmotic stress | experimental (any) | 4 | 0.943 | 0.036 |
| Gene Ontology - Biological Process | transcription by RNA polymerase II | experimental (any) | 43 | 31.03 | 0.036 |
| Gene Ontology - Biological Process | regulation of actin cytoskeleton organization | predicted (union) | 128 | 100.7 | 0.037 |
| Gene Ontology - Biological Process | cellular response to insulin-like growth factor stimulus | experimental (strong) | 2 | 0.155 | 0.037 |
| Gene Ontology - Biological Process | cellular response to lipoteichoic acid | experimental (strong) | 2 | 0.155 | 0.037 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | detection of mechanical stimulus involved in sensory perception | experimental (strong) | 2 | 0.155 | 0.037 |
| Gene Ontology - Biological Process | detection of temperature stimulus involved in sensory perception of pain | experimental (strong) | 2 | 0.155 | 0.037 |
| Gene Ontology - Biological Process | histone H3-K9 acetylation | experimental (strong) | 2 | 0.155 | 0.037 |
| Gene Ontology - Biological Process | homeostatic process | experimental (strong) | 22 | 13.47 | 0.037 |
| Gene Ontology - Biological Process | negative regulation of leukocyte chemotaxis | experimental (strong) | 2 | 0.155 | 0.037 |
| Gene Ontology - Biological Process | positive regulation of cellular component biogenesis | experimental (strong) | 10 | 4.31 | 0.037 |
| Gene Ontology - Biological Process | positive regulation of histone H3-K4 methylation | experimental (strong) | 2 | 0.155 | 0.037 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of protein polymerization | experimental (strong) | 4 | 0.852 | 0.037 |
| Gene Ontology - Biological Process | pro-B cell differentiation | experimental (strong) | 2 | 0.155 | 0.037 |
| Gene Ontology - Biological Process | regulation of cytokine-mediated signaling pathway | experimental (strong) | 6 | 1.833 | 0.037 |
| Gene Ontology - Biological Process | regulation of ion transport | experimental (strong) | 10 | 4.31 | 0.037 |
| Gene Ontology - Biological Process | response to peptide hormone | experimental (strong) | 10 | 4.31 | 0.037 |
| Gene Ontology - Biological Process | anatomical structure formation involved in morphogenesis | experimental (strong) | 20 | 11.85 | 0.038 |
| Gene Ontology - Biological Process | cerebral cortex cell migration | experimental (any) | 3 | 0.531 | 0.038 |
| Gene Ontology - Biological Process | generation of neurons | experimental (any) | 25 | 15.89 | 0.038 |
| Gene Ontology - Biological Process | myelination | experimental (any) | 5 | 1.462 | 0.038 |
| Gene Ontology - Biological Process | negative regulation of BMP signaling pathway | experimental (any) | 3 | 0.531 | 0.038 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of G protein-coupled receptor signaling pathway | experimental (any) | 3 | 0.531 | 0.038 |
| Gene Ontology - Biological Process | response to carbohydrate | experimental (any) | 7 | 2.604 | 0.038 |
| Gene Ontology - Biological Process | response to metal ion | experimental (any) | 9 | 3.867 | 0.038 |
| Gene Ontology - Biological Process | response to reactive oxygen species | experimental (any) | 7 | 2.604 | 0.038 |
| Gene Ontology - Biological Process | unsaturated fatty acid biosynthetic process | experimental (any) | 3 | 0.531 | 0.038 |
| Gene Ontology - Biological Process | cellular protein localization | predicted (union) | 612 | 551.7 | 0.039 |
| Gene Ontology - Biological Process | cardiac ventricle morphogenesis | experimental (strong) | 4 | 0.878 | 0.039 |
| Gene Ontology - Biological Process | cell development | experimental (strong) | 26 | 17.01 | 0.039 |
| Gene Ontology - Biological Process | cellular response to tumor necrosis factor | experimental (strong) | 7 | 2.452 | 0.039 |
| Gene Ontology - Biological Process | detection of abiotic stimulus | experimental (strong) | 3 | 0.465 | 0.039 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | endothelial cell differentiation | experimental (strong) | 5 | 1.342 | 0.039 |
| Gene Ontology - Biological Process | fatty acid biosynthetic process | experimental (strong) | 4 | 0.878 | 0.039 |
| Gene Ontology - Biological Process | gene silencing by RNA | experimental (strong) | 5 | 1.342 | 0.039 |
| Gene Ontology - Biological Process | glial cell development | experimental (strong) | 5 | 1.342 | 0.039 |
| Gene Ontology - Biological Process | hemopoiesis | experimental (strong) | 16 | 8.698 | 0.039 |
| Gene Ontology - Biological Process | interleukin-17 production | experimental (strong) | 3 | 0.465 | 0.039 |
| Gene Ontology - Biological Process | muscle tissue morphogenesis | experimental (strong) | 4 | 0.878 | 0.039 |
| Gene Ontology - Biological Process | myeloid cell apoptotic process | experimental (strong) | 3 | 0.465 | 0.039 |
| Gene Ontology - Biological Process | negative regulation of cellular component movement | experimental (strong) | 8 | 3.072 | 0.039 |
| Gene Ontology - Biological Process | negative regulation of sprouting angiogenesis | experimental (strong) | 3 | 0.465 | 0.039 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | positive regulation of DNA replication | experimental (strong) | 3 | 0.465 | 0.039 |
| Gene Ontology - Biological Process | positive regulation of T cell mediated immunity | experimental (strong) | 3 | 0.465 | 0.039 |
| Gene Ontology - Biological Process | positive regulation of cell cycle phase transition | experimental (strong) | 4 | 0.878 | 0.039 |
| Gene Ontology - Biological Process | positive regulation of cyclin-dependent protein serine/threonine kinase activity | experimental (strong) | 3 | 0.465 | 0.039 |
| Gene Ontology - Biological Process | positive regulation of protein transport | experimental (strong) | 9 | 3.691 | 0.039 |
| Gene Ontology - Biological Process | regulation of establishment of protein localization | experimental (strong) | 13 | 6.453 | 0.039 |
| Gene Ontology - Biological Process | regulation of oligodendrocyte differentiation | experimental (strong) | 3 | 0.465 | 0.039 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | alpha-beta T cell lineage commitment | experimental (any) | 2 | 0.199 | 0.039 |
| Gene Ontology - Biological Process | axonogenesis | experimental (any) | 10 | 4.544 | 0.039 |
| Gene Ontology - Biological Process | calcium ion transport | experimental (any) | 10 | 4.544 | 0.039 |
| Gene Ontology - Biological Process | cell junction assembly | experimental (any) | 7 | 2.631 | 0.039 |
| Gene Ontology - Biological Process | detection of temperature stimulus | experimental (any) | 2 | 0.199 | 0.039 |
| Gene Ontology - Biological Process | lymph node development | experimental (any) | 2 | 0.199 | 0.039 |
| Gene Ontology - Biological Process | macrophage cytokine production | experimental (any) | 2 | 0.199 | 0.039 |
| Gene Ontology - Biological Process | metanephric mesenchyme development | experimental (any) | 2 | 0.199 | 0.039 |
| Gene Ontology - Biological Process | peptide hormone secretion | experimental (any) | 7 | 2.631 | 0.039 |
| Gene Ontology - Biological Process | positive regulation of monocyte chemotaxis | experimental (any) | 2 | 0.199 | 0.039 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of hydrogen peroxide metabolic process | experimental (any) | 2 | 0.199 | 0.039 |
| Gene Ontology - Biological Process | response to muscle stretch | experimental (any) | 2 | 0.199 | 0.039 |
| Gene Ontology - Biological Process | Wnt signaling pathway | predicted (intersection) | 108 | 79.27 | 0.040 |
| Gene Ontology - Biological Process | neurogenesis | predicted (intersection) | 284 | 236.5 | 0.040 |
| Gene Ontology - Biological Process | positive regulation of metabolic process | predicted (intersection) | 591 | 525.2 | 0.040 |
| Gene Ontology - Biological Process | tube development | predicted (intersection) | 201 | 161.2 | 0.040 |
| Gene Ontology - Biological Process | intracellular protein transport | predicted (union) | 352 | 306.1 | 0.040 |
| Gene Ontology - Biological Process | nucleocytoplasmic transport | predicted (union) | 133 | 105.4 | 0.040 |
| Gene Ontology - Biological Process | actin cytoskeleton organization | experimental (strong) | 10 | 4.388 | 0.040 |
| Gene Ontology - Biological Process | metabolic process | experimental (strong) | 63 | 55.21 | 0.040 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | negative regulation of angiogenesis | experimental (strong) | 5 | 1.368 | 0.040 |
| Gene Ontology - Biological Process | regulation of I-kappaB kinase/NF-kappaB signaling | experimental (strong) | 7 | 2.478 | 0.040 |
| Gene Ontology - Biological Process | regulation of type I interferon production | experimental (strong) | 5 | 1.368 | 0.040 |
| Gene Ontology - Biological Process | response to carbohydrate | experimental (strong) | 7 | 2.478 | 0.040 |
| Gene Ontology - Biological Process | response to toxic substance | experimental (strong) | 11 | 5.085 | 0.040 |
| Gene Ontology - Biological Process | type I interferon production | experimental (strong) | 5 | 1.368 | 0.040 |
| Gene Ontology - Biological Process | embryonic epithelial tube formation | experimental (any) | 5 | 1.488 | 0.040 |
| Gene Ontology - Biological Process | import into cell | experimental (any) | 13 | 6.697 | 0.040 |
| Gene Ontology - Biological Process | positive regulation of cytokine-mediated signaling pathway | experimental (any) | 3 | 0.545 | 0.040 |
| Gene Ontology - Biological Process | protein transport | experimental (any) | 30 | 20.14 | 0.040 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of body fluid levels | experimental (any) | 11 | 5.275 | 0.040 |
| Gene Ontology - Biological Process | regulation of cytokine secretion | experimental (any) | 6 | 2.046 | 0.040 |
| Gene Ontology - Biological Process | temperature homeostasis | experimental (any) | 6 | 2.046 | 0.040 |
| Gene Ontology - Biological Process | ventricular septum morphogenesis | experimental (any) | 3 | 0.545 | 0.040 |
| Gene Ontology - Biological Process | cellular response to peptide hormone stimulus | predicted (intersection) | 68 | 45.81 | 0.041 |
| Gene Ontology - Biological Process | heart development | predicted (union) | 224 | 187.8 | 0.041 |
| Gene Ontology - Biological Process | hippo signaling | predicted (union) | 24 | 13.67 | 0.041 |
| Gene Ontology - Biological Process | regulation of translation | predicted (union) | 146 | 117.1 | 0.041 |
| Gene Ontology - Biological Process | roof of mouth development | predicted (union) | 47 | 31.63 | 0.041 |
| Gene Ontology - Biological Process | Fc receptor signaling pathway | experimental (strong) | 6 | 1.91 | 0.041 |
| Gene Ontology - Biological Process | leukocyte differentiation | experimental (strong) | 12 | 5.808 | 0.041 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | stem cell population maintenance | experimental (strong) | 6 | 1.91 | 0.041 |
| Gene Ontology - Biological Process | regulation of cardiac muscle tissue development | experimental (any) | 4 | 0.997 | 0.041 |
| Gene Ontology - Biological Process | response to ethanol | experimental (any) | 5 | 1.501 | 0.041 |
| Gene Ontology - Biological Process | anatomical structure morphogenesis | experimental (strong) | 32 | 22.58 | 0.042 |
| Gene Ontology - Biological Process | cellular response to DNA damage stimulus | experimental (strong) | 12 | 5.859 | 0.042 |
| Gene Ontology - Biological Process | cytokine biosynthetic process | experimental (strong) | 5 | 1.394 | 0.042 |
| Gene Ontology - Biological Process | cytokine metabolic process | experimental (strong) | 5 | 1.394 | 0.042 |
| Gene Ontology - Biological Process | epithelium development | experimental (strong) | 19 | 11.25 | 0.042 |
| Gene Ontology - Biological Process | liver regeneration | experimental (strong) | 3 | 0.490 | 0.042 |
| Gene Ontology - Biological Process | macrophage derived foam cell differentiation | experimental (strong) | 3 | 0.490 | 0.042 |

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| Gene Ontology - Biological Process | neuroinflammatory response | experimental (strong) | 4 | 0.903 | 0.042 |
| Gene Ontology - Biological Process | outflow tract septum morphogenesis | experimental (strong) | 3 | 0.490 | 0.042 |
| Gene Ontology - Biological Process | peptide biosynthetic process | experimental (strong) | 8 | 3.123 | 0.042 |
| Gene Ontology - Biological Process | positive regulation of cyclin-dependent protein kinase activity | experimental (strong) | 3 | 0.490 | 0.042 |
| Gene Ontology - Biological Process | positive regulation of receptor signaling pathway via JAK-STAT | experimental (strong) | 4 | 0.903 | 0.042 |
| Gene Ontology - Biological Process | positive regulation of receptor signaling pathway via STAT | experimental (strong) | 4 | 0.903 | 0.042 |
| Gene Ontology - Biological Process | response to xenobiotic stimulus | experimental (strong) | 7 | 2.504 | 0.042 |
| Gene Ontology - Biological Process | axon ensheathment | experimental (any) | 5 | 1.515 | 0.042 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | cellular response to transforming growth factor beta stimulus | experimental (any) | 7 | 2.671 | 0.042 |
| Gene Ontology - Biological Process | glycosylation | experimental (any) | 7 | 2.671 | 0.042 |
| Gene Ontology - Biological Process | positive regulation of biomineral tissue development | experimental (any) | 3 | 0.558 | 0.042 |
| Gene Ontology - Biological Process | regulation of erythrocyte differentiation | experimental (any) | 3 | 0.558 | 0.042 |
| Gene Ontology - Biological Process | regulation of lymphocyte apoptotic process | experimental (any) | 3 | 0.558 | 0.042 |
| Gene Ontology - Biological Process | cardiac septum morphogenesis | predicted (intersection) | 24 | 11.99 | 0.043 |
| Gene Ontology - Biological Process | nuclear transport | predicted (union) | 134 | 106.6 | 0.043 |
| Gene Ontology - Biological Process | G protein-coupled receptor signaling pathway | experimental (strong) | 10 | 4.465 | 0.043 |
| Gene Ontology - Biological Process | actin filament polymerization | experimental (strong) | 4 | 0.929 | 0.043 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | body fluid secretion | experimental (strong) | 4 | 0.929 | 0.043 |
| Gene Ontology - Biological Process | coronary artery morphogenesis | experimental (strong) | 2 | 0.181 | 0.043 |
| Gene Ontology - Biological Process | detection of temperature stimulus | experimental (strong) | 2 | 0.181 | 0.043 |
| Gene Ontology - Biological Process | forebrain development | experimental (strong) | 9 | 3.82 | 0.043 |
| Gene Ontology - Biological Process | immune response-activating signal transduction | experimental (strong) | 10 | 4.465 | 0.043 |
| Gene Ontology - Biological Process | leukocyte apoptotic process | experimental (strong) | 5 | 1.42 | 0.043 |
| Gene Ontology - Biological Process | mesenchymal cell differentiation | experimental (strong) | 7 | 2.555 | 0.043 |
| Gene Ontology - Biological Process | metal ion transport | experimental (strong) | 10 | 4.491 | 0.043 |
| Gene Ontology - Biological Process | muscle organ morphogenesis | experimental (strong) | 4 | 0.929 | 0.043 |
| Gene Ontology - Biological Process | negative regulation of apoptotic signaling pathway | experimental (strong) | 8 | 3.149 | 0.043 |

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| Gene Ontology - Biological Process | negative regulation of calcium ion transport into cytosol | experimental (strong) | 2 | 0.181 | 0.043 |
| Gene Ontology - Biological Process | negative regulation of transport | experimental (strong) | 9 | 3.794 | 0.043 |
| Gene Ontology - Biological Process | positive regulation of I-kappaB kinase/NF-kappaB signaling | experimental (strong) | 6 | 1.962 | 0.043 |
| Gene Ontology - Biological Process | positive regulation of monocyte chemotaxis | experimental (strong) | 2 | 0.181 | 0.043 |
| Gene Ontology - Biological Process | positive regulation of production of miRNAs involved in gene silencing by miRNA | experimental (strong) | 2 | 0.181 | 0.043 |
| Gene Ontology - Biological Process | positive regulation of translation | experimental (strong) | 4 | 0.929 | 0.043 |
| Gene Ontology - Biological Process | regulation of actin filament length | experimental (strong) | 4 | 0.929 | 0.043 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of actin polymerization or depolymerization | experimental (strong) | 4 | 0.929 | 0.043 |
| Gene Ontology - Biological Process | regulation of cell cycle | experimental (strong) | 17 | 9.731 | 0.043 |
| Gene Ontology - Biological Process | regulation of extracellular matrix disassembly | experimental (strong) | 2 | 0.181 | 0.043 |
| Gene Ontology - Biological Process | replication fork processing | experimental (strong) | 2 | 0.181 | 0.043 |
| Gene Ontology - Biological Process | response to temperature stimulus | experimental (strong) | 6 | 1.962 | 0.043 |
| Gene Ontology - Biological Process | response to wounding | experimental (strong) | 13 | 6.633 | 0.043 |
| Gene Ontology - Biological Process | sensory perception of mechanical stimulus | experimental (strong) | 4 | 0.929 | 0.043 |
| Gene Ontology - Biological Process | sensory perception of temperature stimulus | experimental (strong) | 2 | 0.181 | 0.043 |
| Gene Ontology - Biological Process | telencephalon development | experimental (strong) | 7 | 2.555 | 0.043 |
| Gene Ontology - Biological Process | actin filament-based process | experimental (any) | 14 | 7.494 | 0.043 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | coronary vasculature morphogenesis | experimental (any) | 2 | 0.213 | 0.043 |
| Gene Ontology - Biological Process | detection of biotic stimulus | experimental (any) | 2 | 0.213 | 0.043 |
| Gene Ontology - Biological Process | endothelial tube morphogenesis | experimental (any) | 2 | 0.213 | 0.043 |
| Gene Ontology - Biological Process | mammary gland alveolus development | experimental (any) | 2 | 0.213 | 0.043 |
| Gene Ontology - Biological Process | mammary gland lobule development | experimental (any) | 2 | 0.213 | 0.043 |
| Gene Ontology - Biological Process | myeloid dendritic cell differentiation | experimental (any) | 2 | 0.213 | 0.043 |
| Gene Ontology - Biological Process | negative regulation of phagocytosis | experimental (any) | 2 | 0.213 | 0.043 |
| Gene Ontology - Biological Process | positive regulation of Rho protein signal transduction | experimental (any) | 2 | 0.213 | 0.043 |
| Gene Ontology - Biological Process | positive regulation of histone H3-K4 methylation | experimental (any) | 2 | 0.213 | 0.043 |

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| Gene Ontology - Biological Process | positive regulation of neuroinflammatory response | experimental (any) | 2 | 0.213 | 0.043 |
| Gene Ontology - Biological Process | regulation of endopeptidase activity | experimental (any) | 9 | 3.973 | 0.043 |
| Gene Ontology - Biological Process | regulation of organelle organization | experimental (any) | 22 | 13.7 | 0.043 |
| Gene Ontology - Biological Process | regulation of tumor necrosis factor production | experimental (any) | 5 | 1.528 | 0.043 |
| Gene Ontology - Biological Process | endocardial cushion development | experimental (any) | 3 | 0.571 | 0.044 |
| Gene Ontology - Biological Process | endodermal cell differentiation | experimental (any) | 3 | 0.571 | 0.044 |
| Gene Ontology - Biological Process | histone ubiquitination | experimental (any) | 3 | 0.571 | 0.044 |
| Gene Ontology - Biological Process | positive regulation of Notch signaling pathway | experimental (any) | 3 | 0.571 | 0.044 |

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| Gene Ontology - Biological Process | positive regulation of cardiac muscle tissue development | experimental (any) | 3 | 0.571 | 0.044 |
| Gene Ontology - Biological Process | production of miRNAs involved in gene silencing by miRNA | experimental (any) | 3 | 0.571 | 0.044 |
| Gene Ontology - Biological Process | regulation of interleukin-10 production | experimental (any) | 3 | 0.571 | 0.044 |
| Gene Ontology - Biological Process | regulation of epithelial cell proliferation | experimental (strong) | 10 | 4.543 | 0.045 |
| Gene Ontology - Biological Process | cardiac ventricle development | experimental (any) | 5 | 1.555 | 0.045 |
| Gene Ontology - Biological Process | icosanoid metabolic process | experimental (any) | 4 | 1.036 | 0.045 |
| Gene Ontology - Biological Process | transforming growth factor beta receptor signaling pathway | experimental (any) | 6 | 2.126 | 0.045 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | vascular endothelial growth factor receptor signaling pathway | experimental (any) | 4 | 1.036 | 0.045 |
| Gene Ontology - Biological Process | cell fate commitment | experimental (strong) | 8 | 3.226 | 0.046 |
| Gene Ontology - Biological Process | histone acetylation | experimental (strong) | 5 | 1.445 | 0.046 |
| Gene Ontology - Biological Process | mitotic cell cycle checkpoint | experimental (strong) | 5 | 1.445 | 0.046 |
| Gene Ontology - Biological Process | negative regulation of locomotion | experimental (strong) | 8 | 3.226 | 0.046 |
| Gene Ontology - Biological Process | positive regulation of actin filament polymerization | experimental (strong) | 3 | 0.516 | 0.046 |
| Gene Ontology - Biological Process | programmed necrotic cell death | experimental (strong) | 3 | 0.516 | 0.046 |
| Gene Ontology - Biological Process | response to dexamethasone | experimental (strong) | 3 | 0.516 | 0.046 |
| Gene Ontology - Biological Process | BMP signaling pathway | experimental (any) | 5 | 1.568 | 0.046 |

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| Gene Ontology - Biological Process | DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator | experimental (any) | 2 | 0.226 | 0.046 |
| Gene Ontology - Biological Process | I-kappaB phosphorylation | experimental (any) | 2 | 0.226 | 0.046 |
| Gene Ontology - Biological Process | cellular response to gonadotropin stimulus | experimental (any) | 2 | 0.226 | 0.046 |
| Gene Ontology - Biological Process | digestive tract morphogenesis | experimental (any) | 3 | 0.585 | 0.046 |
| Gene Ontology - Biological Process | epithelial to mesenchymal transition involved in endocardial cushion formation | experimental (any) | 2 | 0.226 | 0.046 |
| Gene Ontology - Biological Process | epithelial tube formation | experimental (any) | 5 | 1.568 | 0.046 |

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| Gene Ontology - Biological Process | mature B cell differentiation involved in immune response | experimental (any) | 2 | 0.226 | 0.046 |
| Gene Ontology - Biological Process | muscle structure development | experimental (any) | 13 | 6.869 | 0.046 |
| Gene Ontology - Biological Process | negative regulation of calcium ion transport into cytosol | experimental (any) | 2 | 0.226 | 0.046 |
| Gene Ontology - Biological Process | negative regulation of tissue remodeling | experimental (any) | 2 | 0.226 | 0.046 |
| Gene Ontology - Biological Process | peptide transport | experimental (any) | 30 | 20.44 | 0.046 |
| Gene Ontology - Biological Process | positive regulation of histone deacetylation | experimental (any) | 2 | 0.226 | 0.046 |
| Gene Ontology - Biological Process | positive regulation of lamellipodium assembly | experimental (any) | 2 | 0.226 | 0.046 |

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| Gene Ontology - Biological Process | positive regulation of transcription of Notch receptor target | experimental (any) | 2 | 0.226 | 0.046 |
| Gene Ontology - Biological Process | response to corticosterone | experimental (any) | 2 | 0.226 | 0.046 |
| Gene Ontology - Biological Process | positive regulation of transcription by RNA polymerase II | predicted (union) | 415 | 366.2 | 0.047 |
| Gene Ontology - Biological Process | cell migration involved in sprouting angiogenesis | experimental (strong) | 4 | 0.955 | 0.047 |
| Gene Ontology - Biological Process | regulation of translation | experimental (strong) | 7 | 2.607 | 0.047 |
| Gene Ontology - Biological Process | phosphatidylinositol 3-kinase signaling | experimental (any) | 5 | 1.581 | 0.047 |
| Gene Ontology - Biological Process | protein complex oligomerization | experimental (any) | 12 | 6.165 | 0.047 |
| Gene Ontology - Biological Process | protein localization to plasma membrane | experimental (any) | 7 | 2.764 | 0.047 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of ion transport | experimental (any) | 13 | 6.883 | 0.047 |
| Gene Ontology - Biological Process | regulation of organelle assembly | experimental (any) | 6 | 2.152 | 0.047 |
| Gene Ontology - Biological Process | tumor necrosis factor production | experimental (any) | 5 | 1.581 | 0.047 |
| Gene Ontology - Biological Process | cardiac muscle cell development | predicted (intersection) | 22 | 10.74 | 0.048 |
| Gene Ontology - Biological Process | cell-cell signaling | predicted (intersection) | 287 | 240.7 | 0.048 |
| Gene Ontology - Biological Process | generation of neurons | predicted (intersection) | 267 | 222.2 | 0.048 |
| Gene Ontology - Biological Process | negative regulation of nucleic acid-templated transcription | predicted (intersection) | 218 | 177.7 | 0.048 |
| Gene Ontology - Biological Process | response to peptide hormone | predicted (intersection) | 88 | 62.8 | 0.048 |
| Gene Ontology - Biological Process | transmembrane receptor protein serine/threonine kinase signaling pathway | predicted (intersection) | 72 | 49.56 | 0.048 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | regulation of neurogenesis | predicted (union) | 304 | 262.4 | 0.048 |
| Gene Ontology - Biological Process | gene expression | experimental (strong) | 42 | 32.5 | 0.048 |
| Gene Ontology - Biological Process | peptidyl-serine phosphorylation | experimental (strong) | 8 | 3.252 | 0.048 |
| Gene Ontology - Biological Process | actin filament bundle assembly | experimental (any) | 5 | 1.594 | 0.048 |
| Gene Ontology - Biological Process | anterior/posterior pattern specification | experimental (any) | 6 | 2.166 | 0.048 |
| Gene Ontology - Biological Process | phagocytosis | experimental (any) | 7 | 2.777 | 0.048 |
| Gene Ontology - Biological Process | positive regulation of cysteine-type endopeptidase activity | experimental (any) | 5 | 1.594 | 0.048 |
| Gene Ontology - Biological Process | pri-miRNA transcription by RNA polymerase II | experimental (any) | 3 | 0.598 | 0.048 |
| Gene Ontology - Biological Process | protein modification by small protein removal | experimental (any) | 8 | 3.415 | 0.048 |

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| Gene Ontology - Biological Process | regulation of cellular response to stress | experimental (any) | 15 | 8.424 | 0.048 |
| Gene Ontology - Biological Process | regulation of hormone secretion | experimental (any) | 7 | 2.777 | 0.048 |
| Gene Ontology - Biological Process | response to nutrient levels | experimental (any) | 11 | 5.461 | 0.048 |
| Gene Ontology - Biological Process | regulation of mRNA stability | predicted (union) | 72 | 52.71 | 0.049 |
| Gene Ontology - Biological Process | actin filament organization | experimental (strong) | 7 | 2.633 | 0.049 |
| Gene Ontology - Biological Process | response to alcohol | experimental (strong) | 7 | 2.633 | 0.049 |
| Gene Ontology - Biological Process | tube morphogenesis | experimental (strong) | 18 | 10.69 | 0.049 |
| Gene Ontology - Biological Process | regulation of cellular protein localization | experimental (any) | 12 | 6.218 | 0.049 |
| Gene Ontology - Biological Process | regulation of protein complex assembly | experimental (strong) | 8 | 3.278 | 0.050 |
| Gene Ontology - Biological Process | positive regulation of supramolecular fiber organization | experimental (any) | 6 | 2.192 | 0.050 |

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|---|---|---|---|---|---|
| Gene Ontology - Biological Process | response to glucose | experimental (any) | 6 | 2.192 | 0.050 |
| Gene Ontology - Biological Process | roof of mouth development | experimental (any) | 4 | 1.076 | 0.050 |
| Gene Ontology - Cellular Component | chromosome | predicted (union) | 950 | 805.9 | 3.10e-9 |
| Gene Ontology - Cellular Component | nuclear lumen | predicted (intersection) | 920 | 773.2 | 1.09e-8 |
| Gene Ontology - Cellular Component | nuclear chromatin | predicted (union) | 732 | 613 | 4.01e-8 |
| Gene Ontology - Cellular Component | nuclear chromosome | predicted (union) | 788 | 666.1 | 4.46e-8 |
| Gene Ontology - Cellular Component | chromatin | predicted (union) | 775 | 659.5 | 2.25e-7 |
| Gene Ontology - Cellular Component | Golgi apparatus | predicted (union) | 590 | 506 | 8.37e-5 |
| Gene Ontology - Cellular Component | nuclear chromatin | predicted (intersection) | 354 | 280.9 | 8.49e-5 |
| Gene Ontology - Cellular Component | nuclear chromosome | predicted (intersection) | 381 | 305.3 | 8.49e-5 |

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|---|---|---|---|---|---|
| Gene Ontology - Cellular Component | nucleoplasm | predicted (intersection) | 640 | 543.9 | 8.49e-5 |
| Gene Ontology - Cellular Component | synapse | predicted (intersection) | 240 | 182.3 | 2.04e-4 |
| Gene Ontology - Cellular Component | chromosome | predicted (intersection) | 445 | 369.3 | 3.48e-4 |
| Gene Ontology - Cellular Component | chromatin | predicted (intersection) | 370 | 302.2 | 5.09e-4 |
| Gene Ontology - Cellular Component | synapse | predicted (union) | 464 | 397.9 | 0.001 |
| Gene Ontology - Cellular Component | protein-containing complex | experimental (strong) | 42 | 23.98 | 0.001 |
| Gene Ontology - Cellular Component | axon | predicted (intersection) | 119 | 83.74 | 0.002 |
| Gene Ontology - Cellular Component | cell junction | predicted (intersection) | 246 | 194.5 | 0.002 |
| Gene Ontology - Cellular Component | cytosol | predicted (intersection) | 878 | 788.5 | 0.002 |

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|---|---|---|---|---|---|
| Gene Ontology - Cellular Component | cell leading edge | predicted (intersection) | 90 | 60.66 | 0.003 |
| Gene Ontology - Cellular Component | CD95 death-inducing signaling complex | experimental (any) | 3 | 0.080 | 0.003 |
| Gene Ontology - Cellular Component | cytoplasmic vesicle | experimental (any) | 44 | 24.29 | 0.003 |
| Gene Ontology - Cellular Component | endomembrane system | experimental (any) | 74 | 47.09 | 0.003 |
| Gene Ontology - Cellular Component | intracellular vesicle | experimental (any) | 44 | 24.33 | 0.003 |
| Gene Ontology - Cellular Component | presynapse | predicted (intersection) | 111 | 79.09 | 0.004 |
| Gene Ontology - Cellular Component | CD95 death-inducing signaling complex | experimental (strong) | 3 | 0.103 | 0.005 |
| Gene Ontology - Cellular Component | cell surface | experimental (any) | 19 | 7.255 | 0.005 |
| Gene Ontology - Cellular Component | death-inducing signaling complex | experimental (any) | 3 | 0.106 | 0.005 |

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|---|---|---|---|---|---|
| Gene Ontology - Cellular Component | RISC complex | predicted (intersection) | 7 | 1.61 | 0.007 |
| Gene Ontology - Cellular Component | neuron projection | predicted (intersection) | 216 | 172.7 | 0.007 |
| Gene Ontology - Cellular Component | Golgi membrane | predicted (union) | 292 | 244.8 | 0.007 |
| Gene Ontology - Cellular Component | endosome | experimental (any) | 22 | 9.726 | 0.007 |
| Gene Ontology - Cellular Component | receptor complex | experimental (any) | 11 | 3.083 | 0.007 |
| Gene Ontology - Cellular Component | vesicle | experimental (any) | 61 | 40.29 | 0.007 |
| Gene Ontology - Cellular Component | Golgi apparatus | predicted (intersection) | 280 | 231.9 | 0.009 |
| Gene Ontology - Cellular Component | ruffle membrane | predicted (intersection) | 25 | 12.35 | 0.009 |
| Gene Ontology - Cellular Component | axon | predicted (union) | 222 | 182.7 | 0.010 |

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|---|---|---|---|---|---|
| Gene Ontology - Cellular Component | cell leading edge | predicted (union) | 166 | 132.4 | 0.010 |
| Gene Ontology - Cellular Component | neuron projection | predicted (union) | 432 | 376.8 | 0.010 |
| Gene Ontology - Cellular Component | receptor complex | experimental (strong) | 10 | 2.607 | 0.010 |
| Gene Ontology - Cellular Component | activin responsive factor complex | experimental (any) | 2 | 0.040 | 0.011 |
| Gene Ontology - Cellular Component | death-inducing signaling complex | experimental (strong) | 3 | 0.155 | 0.012 |
| Gene Ontology - Cellular Component | ruffle | predicted (intersection) | 42 | 25.23 | 0.014 |
| Gene Ontology - Cellular Component | cell surface | experimental (strong) | 15 | 5.833 | 0.014 |
| Gene Ontology - Cellular Component | cytoplasm | experimental (any) | 141 | 119.1 | 0.015 |
| Gene Ontology - Cellular Component | activin responsive factor complex | experimental (strong) | 2 | 0.052 | 0.017 |

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|---|---|---|---|---|---|
| Gene Ontology - Cellular Component | cytosol | experimental (any) | 77 | 56.51 | 0.019 |
| Gene Ontology - Cellular Component | plasma membrane bounded cell projection | predicted (intersection) | 341 | 291.7 | 0.020 |
| Gene Ontology - Cellular Component | extracellular region | experimental (any) | 58 | 39.99 | 0.023 |
| Gene Ontology - Cellular Component | endomembrane system | predicted (intersection) | 737 | 670.5 | 0.026 |
| Gene Ontology - Cellular Component | perinuclear region of cytoplasm | predicted (intersection) | 145 | 113.6 | 0.026 |
| Gene Ontology - Cellular Component | somatodendritic compartment | predicted (intersection) | 147 | 115.6 | 0.026 |
| Gene Ontology - Cellular Component | synaptonemal complex | experimental (any) | 3 | 0.239 | 0.026 |
| Gene Ontology - Cellular Component | cell projection | predicted (intersection) | 349 | 301.7 | 0.028 |
| Gene Ontology - Cellular Component | early endosome | predicted (intersection) | 74 | 52.61 | 0.028 |

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|---|---|---|---|---|---|
| Gene Ontology - Cellular Component | glutamatergic synapse | predicted (intersection) | 79 | 56.72 | 0.028 |
| Gene Ontology - Cellular Component | distal axon | predicted (intersection) | 61 | 41.87 | 0.029 |
| Gene Ontology - Cellular Component | cell junction | predicted (union) | 477 | 424.4 | 0.034 |
| Gene Ontology - Cellular Component | early endosome | predicted (union) | 143 | 114.8 | 0.034 |
| Gene Ontology - Cellular Component | ruffle membrane | predicted (union) | 41 | 26.94 | 0.034 |
| Gene Ontology - Cellular Component | pyruvate dehydrogenase complex | predicted (union) | 8 | 3.124 | 0.035 |
| Gene Ontology - Cellular Component | SMAD protein complex | experimental (any) | 2 | 0.093 | 0.035 |
| Gene Ontology - Cellular Component | cell projection membrane | experimental (any) | 10 | 3.455 | 0.035 |
| Gene Ontology - Cellular Component | female pronucleus | experimental (any) | 2 | 0.093 | 0.035 |

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|---|---|---|---|---|---|
| Gene Ontology - Cellular Component | lateral element | experimental (any) | 2 | 0.093 | 0.035 |
| Gene Ontology - Cellular Component | nucleoplasm | experimental (any) | 58 | 41.1 | 0.035 |
| Gene Ontology - Cellular Component | nucleus | experimental (any) | 97 | 77.92 | 0.035 |
| Gene Ontology - Cellular Component | secretory granule | experimental (any) | 18 | 8.743 | 0.035 |
| Gene Ontology - Cellular Component | secretory vesicle | experimental (any) | 20 | 10.08 | 0.035 |
| Gene Ontology - Cellular Component | vesicle lumen | experimental (any) | 10 | 3.694 | 0.039 |
| Gene Ontology - Cellular Component | endoplasmic reticulum | experimental (any) | 32 | 19.88 | 0.042 |
| Gene Ontology - Cellular Component | lateral element | experimental (strong) | 2 | 0.077 | 0.043 |
| Gene Ontology - Cellular Component | extracellular region | experimental (strong) | 31 | 19.67 | 0.047 |

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|---|---|---|---|---|---|
| Gene Ontology - Cellular Component | cyclin-dependent protein kinase holoenzyme complex | experimental (any) | 3 | 0.359 | 0.047 |
| Gene Ontology - Cellular Component | adherens junction | predicted (intersection) | 100 | 76.22 | 0.049 |
| Gene Ontology - Cellular Component | cell | experimental (any) | 180 | 167.2 | 0.049 |
| Gene Ontology - Cellular Component | ficolin-1-rich granule membrane | experimental (any) | 4 | 0.731 | 0.050 |
| Gene Ontology - Molecular Function | DNA binding | predicted (union) | 907 | 763 | 1.69e-9 |
| Gene Ontology - Molecular Function | DNA-binding transcription factor activity, RNA polymerase II-specific | predicted (union) | 675 | 556.4 | 1.20e-8 |
| Gene Ontology - Molecular Function | DNA-binding transcription factor activity | predicted (union) | 825 | 695.4 | 1.24e-8 |
| Gene Ontology - Molecular Function | nucleic acid binding | predicted (intersection) | 699 | 575.3 | 3.28e-7 |
| Gene Ontology - Molecular Function | DNA binding | predicted (intersection) | 443 | 349.6 | 3.55e-6 |

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| Gene Ontology - Molecular Function | DNA-binding transcription factor activity, RNA polymerase II-specific | predicted (intersection) | 334 | 255 | 6.70e-6 |
| Gene Ontology - Molecular Function | metal ion binding | predicted (intersection) | 752 | 642.2 | 1.62e-5 |
| Gene Ontology - Molecular Function | phosphatase activity | predicted (union) | 183 | 134.7 | 2.81e-5 |
| Gene Ontology - Molecular Function | transcription coregulator activity | predicted (union) | 234 | 179.2 | 3.05e-5 |
| Gene Ontology - Molecular Function | cation binding | predicted (intersection) | 757 | 651.5 | 4.44e-5 |
| Gene Ontology - Molecular Function | DNA-binding transcription factor activity | predicted (intersection) | 397 | 318.7 | 5.98e-5 |
| Gene Ontology - Molecular Function | phosphoric ester hydrolase activity | predicted (union) | 232 | 179.2 | 6.94e-5 |
| Gene Ontology - Molecular Function | transcription coactivator activity | predicted (union) | 145 | 105.4 | 1.21e-4 |
| Gene Ontology - Molecular Function | transcription regulatory region sequence-specific DNA binding | predicted (union) | 282 | 224.9 | 1.21e-4 |

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| Gene Ontology - Molecular Function | transcription regulatory region DNA binding | predicted (union) | 324 | 263.9 | 1.78e-4 |
| Gene Ontology - Molecular Function | double-stranded DNA binding | predicted (union) | 320 | 260.8 | 1.81e-4 |
| Gene Ontology - Molecular Function | proximal promoter sequence-specific DNA binding | predicted (union) | 203 | 156.6 | 1.81e-4 |
| Gene Ontology - Molecular Function | sequence-specific double-stranded DNA binding | predicted (union) | 293 | 237 | 2.08e-4 |
| Gene Ontology - Molecular Function | RNA polymerase II regulatory region sequence-specific DNA binding | predicted (union) | 261 | 208.5 | 2.09e-4 |
| Gene Ontology - Molecular Function | RNA polymerase II regulatory region DNA binding | predicted (union) | 261 | 208.9 | 2.34e-4 |

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|---|---|---|---|---|---|
| Gene Ontology - Molecular Function | RNA polymerase II proximal promoter sequence-specific DNA binding | predicted (union) | 195 | 150.7 | 2.54e-4 |
| Gene Ontology - Molecular Function | purine nucleotide binding | predicted (union) | 708 | 628.2 | 0.001 |
| Gene Ontology - Molecular Function | purine ribonucleoside triphosphate binding | predicted (union) | 678 | 600.9 | 0.001 |
| Gene Ontology - Molecular Function | purine ribonucleotide binding | predicted (union) | 705 | 625.9 | 0.001 |
| Gene Ontology - Molecular Function | RNA binding | predicted (union) | 595 | 525.6 | 0.002 |
| Gene Ontology - Molecular Function | guanyl ribonucleotide binding | predicted (union) | 158 | 122.6 | 0.002 |
| Gene Ontology - Molecular Function | nucleoside binding | predicted (union) | 157 | 122.2 | 0.002 |
| Gene Ontology - Molecular Function | nucleotide binding | predicted (union) | 778 | 700.1 | 0.002 |
| Gene Ontology - Molecular Function | protein domain specific binding | predicted (union) | 281 | 231.9 | 0.002 |
| Gene Ontology - Molecular Function | purine nucleoside binding | predicted (union) | 154 | 119.5 | 0.002 |

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| Gene Ontology - Molecular Function | ribonucleoside binding | predicted (union) | 155 | 119.5 | 0.002 |
| Gene Ontology - Molecular Function | sequence-specific DNA binding | predicted (union) | 376 | 320.6 | 0.002 |
| Gene Ontology - Molecular Function | GTP binding | predicted (union) | 145 | 112.1 | 0.003 |
| Gene Ontology - Molecular Function | cytokine receptor binding | experimental (strong) | 11 | 2.4 | 0.003 |
| Gene Ontology - Molecular Function | DNA-binding transcription activator activity, RNA polymerase II-specific | predicted (union) | 174 | 138.6 | 0.004 |
| Gene Ontology - Molecular Function | carbohydrate derivative binding | predicted (union) | 805 | 730.2 | 0.005 |
| Gene Ontology - Molecular Function | cytokine receptor binding | experimental (any) | 11 | 2.339 | 0.006 |
| Gene Ontology - Molecular Function | protein domain specific binding | predicted (intersection) | 144 | 106.3 | 0.007 |
| Gene Ontology - Molecular Function | magnesium ion binding | predicted (union) | 98 | 73.02 | 0.007 |
| Gene Ontology - Molecular Function | enzyme binding | predicted (union) | 742 | 672 | 0.008 |

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|---|---|---|---|---|---|
| Gene Ontology - Molecular Function | phosphoprotein phosphatase activity | predicted (union) | 115 | 88.24 | 0.009 |
| Gene Ontology - Molecular Function | MAP kinase activity | experimental (any) | 13 | 3.867 | 0.009 |
| Gene Ontology - Molecular Function | NF-kappaB-inducing kinase activity | experimental (any) | 4 | 0.266 | 0.009 |
| Gene Ontology - Molecular Function | Rho GDP-dissociation inhibitor binding | experimental (any) | 2 | 0.027 | 0.009 |
| Gene Ontology - Molecular Function | cytokine activity | experimental (any) | 8 | 1.608 | 0.009 |
| Gene Ontology - Molecular Function | protein domain specific binding | experimental (any) | 20 | 8.092 | 0.009 |
| Gene Ontology - Molecular Function | hydrolase activity, acting on ester bonds | predicted (union) | 349 | 303.4 | 0.017 |
| Gene Ontology - Molecular Function | GDP-dissociation inhibitor binding | experimental (strong) | 2 | 0.052 | 0.018 |
| Gene Ontology - Molecular Function | NF-kappaB-inducing kinase activity | experimental (strong) | 4 | 0.387 | 0.018 |
| Gene Ontology - Molecular Function | Rho GDP-dissociation inhibitor binding | experimental (strong) | 2 | 0.052 | 0.018 |

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| Gene Ontology - Molecular Function | chemokine receptor binding | experimental (strong) | 4 | 0.413 | 0.018 |
| Gene Ontology - Molecular Function | cytokine activity | experimental (strong) | 7 | 1.549 | 0.018 |
| Gene Ontology - Molecular Function | signaling receptor activity | experimental (strong) | 21 | 9.886 | 0.018 |
| Gene Ontology - Molecular Function | tumor necrosis factor receptor binding | experimental (strong) | 4 | 0.439 | 0.018 |
| Gene Ontology - Molecular Function | GDP-dissociation inhibitor binding | experimental (any) | 2 | 0.040 | 0.018 |
| Gene Ontology - Molecular Function | protein serine/threonine kinase activity | experimental (any) | 20 | 8.902 | 0.018 |
| Gene Ontology - Molecular Function | tumor necrosis factor receptor binding | experimental (any) | 4 | 0.385 | 0.018 |
| Gene Ontology - Molecular Function | cysteine-type endopeptidase activity involved in apoptotic process | experimental (any) | 9 | 2.458 | 0.019 |
| Gene Ontology - Molecular Function | protein kinase activity | experimental (any) | 25 | 12.56 | 0.019 |
| Gene Ontology - Molecular Function | phosphoric ester hydrolase activity | predicted (intersection) | 113 | 82.13 | 0.020 |

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|---|---|---|---|---|---|
| Gene Ontology - Molecular Function | signaling receptor activity | experimental (any) | 28 | 14.92 | 0.020 |
| Gene Ontology - Molecular Function | lipopolysaccharide receptor activity | experimental (any) | 2 | 0.053 | 0.021 |
| Gene Ontology - Molecular Function | cysteine-type endopeptidase activity | experimental (any) | 10 | 3.189 | 0.025 |
| Gene Ontology - Molecular Function | exogenous protein binding | experimental (any) | 5 | 0.877 | 0.025 |
| Gene Ontology - Molecular Function | mannosyl-oligosaccharide 1,2-alpha-mannosidase activity | experimental (any) | 2 | 0.066 | 0.025 |
| Gene Ontology - Molecular Function | prostaglandin-E synthase activity | experimental (any) | 2 | 0.066 | 0.025 |
| Gene Ontology - Molecular Function | signaling receptor binding | experimental (any) | 28 | 15.41 | 0.025 |
| Gene Ontology - Molecular Function | virus receptor activity | experimental (any) | 5 | 0.864 | 0.025 |
| Gene Ontology - Molecular Function | chemokine activity | experimental (strong) | 3 | 0.232 | 0.026 |
| Gene Ontology - Molecular Function | chemokine receptor binding | experimental (any) | 4 | 0.545 | 0.026 |

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|---|---|---|---|---|---|
| Gene Ontology - Molecular Function | identical protein binding | experimental (any) | 32 | 18.96 | 0.026 |
| Gene Ontology - Molecular Function | tumor necrosis factor receptor superfamily binding | experimental (any) | 4 | 0.545 | 0.026 |
| Gene Ontology - Molecular Function | interleukin-1 receptor activity | experimental (any) | 2 | 0.080 | 0.028 |
| Gene Ontology - Molecular Function | phosphotransferase activity, alcohol group as acceptor | experimental (any) | 25 | 13.74 | 0.028 |
| Gene Ontology - Molecular Function | small molecule binding | predicted (union) | 882 | 814.1 | 0.029 |
| Gene Ontology - Molecular Function | lipopolysaccharide receptor activity | experimental (strong) | 2 | 0.077 | 0.030 |
| Gene Ontology - Molecular Function | pattern recognition receptor activity | experimental (strong) | 2 | 0.077 | 0.030 |
| Gene Ontology - Molecular Function | signaling pattern recognition receptor activity | experimental (strong) | 2 | 0.077 | 0.030 |
| Gene Ontology - Molecular Function | tumor necrosis factor receptor superfamily binding | experimental (strong) | 4 | 0.568 | 0.030 |

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|---|---|---|---|---|---|
| Gene Ontology - Molecular Function | chromatin binding | predicted (union) | 186 | 155 | 0.034 |
| Gene Ontology - Molecular Function | cytoskeletal protein binding | predicted (union) | 312 | 271.4 | 0.034 |
| Gene Ontology - Molecular Function | kinase binding | predicted (union) | 265 | 227.6 | 0.034 |
| Gene Ontology - Molecular Function | CCR5 chemokine receptor binding | experimental (any) | 2 | 0.093 | 0.034 |
| Gene Ontology - Molecular Function | R-SMAD binding | experimental (any) | 3 | 0.306 | 0.034 |
| Gene Ontology - Molecular Function | ubiquitin-like protein ligase binding | experimental (any) | 10 | 3.627 | 0.034 |
| Gene Ontology - Molecular Function | identical protein binding | experimental (strong) | 22 | 12.36 | 0.043 |
| Gene Ontology - Molecular Function | chemokine activity | experimental (any) | 3 | 0.345 | 0.044 |
| Gene Ontology - Molecular Function | SH3 domain binding | predicted (intersection) | 33 | 18.79 | 0.045 |
| Gene Ontology - Molecular Function | carbohydrate derivative binding | predicted (intersection) | 388 | 334.6 | 0.045 |
| Gene Ontology - Molecular Function | transcription coregulator activity | predicted (intersection) | 110 | 82.13 | 0.045 |

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| Gene Ontology - Molecular Function | transferase activity | predicted (intersection) | 471 | 412.4 | 0.045 |
| Gene Ontology - Molecular Function | transition metal ion binding | predicted (intersection) | 205 | 166.6 | 0.045 |
| Gene Ontology - Molecular Function | CXCR chemokine receptor binding | experimental (any) | 2 | 0.133 | 0.045 |
| Gene Ontology - Molecular Function | DNA binding | experimental (any) | 38 | 25.36 | 0.045 |
| Gene Ontology - Molecular Function | RNA polymerase II-specific DNA-binding transcription factor binding | experimental (any) | 9 | 3.229 | 0.045 |
| Gene Ontology - Molecular Function | cytokine receptor activity | experimental (any) | 4 | 0.718 | 0.045 |
| Gene Ontology - Molecular Function | double-stranded DNA binding | experimental (any) | 17 | 8.676 | 0.045 |
| Gene Ontology - Molecular Function | enzyme binding | experimental (any) | 35 | 22.85 | 0.045 |
| Gene Ontology - Molecular Function | kinase activity | experimental (any) | 25 | 14.83 | 0.045 |
| Gene Ontology - Molecular Function | mannosidase activity | experimental (any) | 2 | 0.133 | 0.045 |

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| Gene Ontology - Molecular Function | signaling pattern recognition receptor activity | experimental (any) | 2 | 0.133 | 0.045 |
| Gene Ontology - Molecular Function | signaling receptor activator activity | experimental (any) | 10 | 4.013 | 0.045 |
| Gene Ontology - Molecular Function | thioesterase binding | experimental (any) | 2 | 0.133 | 0.045 |
| Gene Ontology - Molecular Function | transcription regulatory region DNA binding | experimental (any) | 17 | 8.836 | 0.045 |
| Gene Ontology - Molecular Function | transforming growth factor beta receptor, cytoplasmic mediator activity | experimental (any) | 2 | 0.133 | 0.045 |
| Gene Ontology - Molecular Function | type I transforming growth factor beta receptor binding | experimental (any) | 2 | 0.120 | 0.045 |
| Gene Ontology - Molecular Function | ubiquitin protein ligase binding | experimental (any) | 9 | 3.415 | 0.045 |
| Gene Ontology - Molecular Function | integrin binding | experimental (any) | 5 | 1.236 | 0.046 |

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|---|---|---|---|---|---|
| Gene Ontology - Molecular Function | protein heterodimerization activity | experimental (any) | 12 | 5.381 | 0.046 |
| Gene Ontology - Molecular Function | exogenous protein binding | experimental (strong) | 4 | 0.671 | 0.047 |
| Gene Ontology - Molecular Function | virus receptor activity | experimental (strong) | 4 | 0.671 | 0.047 |
| Gene Ontology - Molecular Function | I-SMAD binding | experimental (any) | 2 | 0.146 | 0.047 |
| Gene Ontology - Molecular Function | catalytic activity | experimental (any) | 85 | 68.39 | 0.047 |
| Gene Ontology - Molecular Function | histone deacetylase binding | experimental (any) | 5 | 1.262 | 0.047 |
| Gene Ontology - Molecular Function | pattern recognition receptor activity | experimental (any) | 2 | 0.146 | 0.047 |
| Gene Ontology - Molecular Function | enzyme binding | experimental (strong) | 27 | 16.83 | 0.048 |
| KEGG | Toll-like receptor signaling pathway | experimental (any) | 15 | 1.169 | 6.68e-11 |
| KEGG | Chagas disease (American trypanosomiasis) | experimental (any) | 13 | 1.302 | 3.20e-8 |
| KEGG | Pathways in cancer | experimental (any) | 21 | 4.159 | 4.58e-8 |
| KEGG | Hepatitis B | experimental (any) | 14 | 1.727 | 5.65e-8 |

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|---|---|---|---|---|---|
| KEGG | Rheumatoid arthritis | experimental (any) | 11 | 0.997 | 9.51e-8 |
| KEGG | Leishmaniasis | experimental (any) | 10 | 0.811 | 1.35e-7 |
| KEGG | Pertussis | experimental (any) | 10 | 0.877 | 2.55e-7 |
| KEGG | Malaria | experimental (any) | 8 | 0.505 | 4.33e-7 |
| KEGG | Measles | experimental (any) | 12 | 1.528 | 5.31e-7 |
| KEGG | NF-kappa B signaling pathway | experimental (any) | 10 | 1.063 | 1.18e-6 |
| KEGG | MicroRNAs in cancer | experimental (any) | 13 | 2.073 | 1.72e-6 |
| KEGG | Pancreatic cancer | experimental (any) | 9 | 0.864 | 1.78e-6 |
| KEGG | Intestinal immune network for IgA production | experimental (any) | 7 | 0.478 | 3.60e-6 |
| KEGG | Legionellosis | experimental (any) | 8 | 0.704 | 3.78e-6 |
| KEGG | Tuberculosis | experimental (any) | 12 | 1.98 | 5.53e-6 |
| KEGG | Chagas disease (American trypanosomiasis) | experimental (strong) | 12 | 1.807 | 5.86e-6 |
| KEGG | Rheumatoid arthritis | experimental (strong) | 9 | 0.929 | 5.86e-6 |
| KEGG | Toll-like receptor signaling pathway | experimental (strong) | 12 | 1.781 | 5.86e-6 |
| KEGG | Proteoglycans in cancer | experimental (any) | 14 | 2.817 | 6.83e-6 |
| KEGG | Toxoplasmosis | experimental (any) | 10 | 1.395 | 9.16e-6 |

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|---|---|---|---|---|---|
| KEGG | Intestinal immune network for IgA production | experimental (strong) | 6 | 0.387 | 2.68e-5 |
| KEGG | Influenza A | experimental (any) | 11 | 1.953 | 2.78e-5 |
| KEGG | Herpes simplex infection | experimental (any) | 11 | 2.059 | 4.20e-5 |
| KEGG | Inflammatory bowel disease (IBD) | experimental (any) | 7 | 0.731 | 4.20e-5 |
| KEGG | RIG-I-like receptor signaling pathway | experimental (any) | 7 | 0.731 | 4.20e-5 |
| KEGG | TNF signaling pathway | experimental (any) | 9 | 1.342 | 4.20e-5 |
| KEGG | Salmonella infection | experimental (any) | 8 | 1.05 | 5.04e-5 |
| KEGG | Malaria | experimental (strong) | 7 | 0.697 | 5.12e-5 |
| KEGG | Pathways in cancer | experimental (strong) | 19 | 5.988 | 5.12e-5 |
| KEGG | Tuberculosis | experimental (strong) | 11 | 2.013 | 5.12e-5 |
| KEGG | Chemokine signaling pathway | experimental (any) | 11 | 2.179 | 5.94e-5 |
| KEGG | Colorectal cancer | experimental (any) | 7 | 0.811 | 7.38e-5 |
| KEGG | Leishmaniasis | experimental (strong) | 8 | 1.058 | 8.59e-5 |
| KEGG | Pertussis | experimental (strong) | 8 | 1.084 | 9.24e-5 |

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|---|---|---|---|---|---|
| KEGG | Pancreatic cancer | experimental (strong) | 9 | 1.445 | 9.38e-5 |
| KEGG | NF-kappa B signaling pathway | experimental (strong) | 9 | 1.471 | 9.91e-5 |
| KEGG | Hepatitis B | experimental (strong) | 12 | 2.762 | 1.08e-4 |
| KEGG | Viral myocarditis | experimental (any) | 6 | 0.624 | 1.58e-4 |
| KEGG | Amoebiasis | experimental (any) | 8 | 1.262 | 1.67e-4 |
| KEGG | Proteoglycans in cancer | experimental (strong) | 14 | 3.923 | 1.73e-4 |
| KEGG | Measles | experimental (strong) | 10 | 2.039 | 1.84e-4 |
| KEGG | MicroRNAs in cancer | experimental (strong) | 13 | 3.562 | 2.44e-4 |
| KEGG | Apoptosis | experimental (any) | 7 | 1.01 | 2.79e-4 |
| KEGG | Inflammatory bowel disease (IBD) | experimental (strong) | 7 | 1.007 | 2.85e-4 |
| KEGG | Salmonella infection | experimental (strong) | 7 | 1.007 | 2.85e-4 |
| KEGG | Legionellosis | experimental (strong) | 6 | 0.723 | 3.44e-4 |
| KEGG | Cytokine-cytokine receptor interaction | experimental (any) | 11 | 2.724 | 3.83e-4 |
| KEGG | Hepatitis C | experimental (any) | 8 | 1.448 | 4.01e-4 |
| KEGG | Chemokine signaling pathway | experimental (strong) | 10 | 2.323 | 4.28e-4 |

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|---|---|---|---|---|---|
| KEGG | Toxoplasmosis | experimental (strong) | 9 | 1.936 | 5.25e-4 |
| KEGG | Viral myocarditis | experimental (strong) | 5 | 0.516 | 5.85e-4 |
| KEGG | Dorso-ventral axis formation | experimental (any) | 4 | 0.306 | 7.62e-4 |
| KEGG | Focal adhesion | experimental (any) | 10 | 2.511 | 7.62e-4 |
| KEGG | FoxO signaling pathway | experimental (any) | 8 | 1.608 | 7.62e-4 |
| KEGG | Prolactin signaling pathway | experimental (any) | 6 | 0.864 | 7.62e-4 |
| KEGG | Adherens junction | experimental (any) | 6 | 0.890 | 8.75e-4 |
| KEGG | Amoebiasis | experimental (strong) | 7 | 1.239 | 8.77e-4 |
| KEGG | Leukocyte transendothelial migration | experimental (any) | 7 | 1.302 | 0.001 |
| KEGG | Dorso-ventral axis formation | experimental (strong) | 4 | 0.387 | 0.002 |
| KEGG | Axon guidance | experimental (any) | 7 | 1.501 | 0.002 |
| KEGG | Endocytosis | experimental (any) | 9 | 2.485 | 0.002 |
| KEGG | NOD-like receptor signaling pathway | experimental (any) | 5 | 0.691 | 0.002 |
| KEGG | Neurotrophin signaling pathway | experimental (any) | 7 | 1.501 | 0.002 |
| KEGG | PI3K-Akt signaling pathway | experimental (any) | 12 | 3.933 | 0.002 |

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|---|---|---|---|---|---|
| KEGG | Prion diseases | experimental (any) | 4 | 0.412 | 0.002 |
| KEGG | Small cell lung cancer | experimental (any) | 6 | 1.076 | 0.002 |
| KEGG | Herpes simplex infection | experimental (strong) | 8 | 1.962 | 0.003 |
| KEGG | Epithelial cell signaling in Helicobacter pylori infection | experimental (any) | 5 | 0.811 | 0.003 |
| KEGG | Hippo signaling pathway | experimental (any) | 8 | 2.02 | 0.003 |
| KEGG | MAPK signaling pathway | experimental (any) | 10 | 3.176 | 0.003 |
| KEGG | Osteoclast differentiation | experimental (any) | 7 | 1.581 | 0.003 |
| KEGG | Shigellosis | experimental (any) | 5 | 0.771 | 0.003 |
| KEGG | Non-alcoholic fatty liver disease (NAFLD) | experimental (strong) | 7 | 1.626 | 0.004 |
| KEGG | HTLV-I infection | experimental (any) | 10 | 3.202 | 0.004 |
| KEGG | T cell receptor signaling pathway | experimental (any) | 6 | 1.276 | 0.004 |
| KEGG | Adherens junction | experimental (strong) | 6 | 1.265 | 0.005 |
| KEGG | Colorectal cancer | experimental (strong) | 6 | 1.291 | 0.005 |

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|---|---|---|---|---|---|
| KEGG | Cytokine-cytokine receptor interaction | experimental (strong) | 9 | 2.71 | 0.005 |
| KEGG | Epithelial cell signaling in Helicobacter pylori infection | experimental (strong) | 5 | 0.852 | 0.005 |
| KEGG | Influenza A | experimental (strong) | 8 | 2.194 | 0.005 |
| KEGG | TNF signaling pathway | experimental (strong) | 8 | 2.194 | 0.005 |
| KEGG | B cell receptor signaling pathway | experimental (any) | 5 | 0.890 | 0.005 |
| KEGG | Non-alcoholic fatty liver disease (NAFLD) | experimental (any) | 7 | 1.794 | 0.005 |
| KEGG | Notch signaling pathway | experimental (any) | 4 | 0.545 | 0.005 |
| KEGG | Apoptosis | experimental (strong) | 6 | 1.316 | 0.006 |
| KEGG | Chronic myeloid leukemia | experimental (any) | 5 | 0.957 | 0.006 |
| KEGG | Cytosolic DNA-sensing pathway | experimental (any) | 4 | 0.585 | 0.006 |
| KEGG | Fanconi anemia pathway | experimental (any) | 4 | 0.598 | 0.006 |
| KEGG | Autoimmune thyroid disease | experimental (strong) | 3 | 0.284 | 0.007 |

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|---|---|---|---|---|---|
| KEGG | Endocytosis | experimental (strong) | 7 | 1.884 | 0.007 |
| KEGG | FoxO signaling pathway | experimental (strong) | 8 | 2.426 | 0.007 |
| KEGG | Graft-versus-host disease | experimental (strong) | 3 | 0.284 | 0.007 |
| KEGG | Leukocyte transendothelial migration | experimental (strong) | 6 | 1.394 | 0.007 |
| KEGG | NOD-like receptor signaling pathway | experimental (strong) | 5 | 0.955 | 0.007 |
| KEGG | RIG-I-like receptor signaling pathway | experimental (strong) | 5 | 0.929 | 0.007 |
| KEGG | Shigellosis | experimental (strong) | 5 | 0.981 | 0.007 |
| KEGG | TGF-beta signaling pathway | experimental (any) | 5 | 1.023 | 0.007 |
| KEGG | Other types of O-glycan biosynthesis | experimental (any) | 3 | 0.332 | 0.008 |
| KEGG | Regulation of actin cytoskeleton | experimental (any) | 8 | 2.525 | 0.008 |
| KEGG | Viral carcinogenesis | experimental (any) | 8 | 2.538 | 0.008 |
| KEGG | Cell cycle | experimental (any) | 6 | 1.568 | 0.010 |
| KEGG | Axon guidance | experimental (strong) | 6 | 1.574 | 0.011 |

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|---|---|---|---|---|---|
| KEGG | Neurotrophin signaling pathway | experimental (strong) | 7 | 2.065 | 0.011 |
| KEGG | Notch signaling pathway | experimental (strong) | 4 | 0.697 | 0.011 |
| KEGG | Non-small cell lung cancer | experimental (any) | 4 | 0.718 | 0.011 |
| KEGG | Allograft rejection | experimental (strong) | 3 | 0.361 | 0.012 |
| KEGG | Fanconi anemia pathway | experimental (strong) | 3 | 0.361 | 0.012 |
| KEGG | Small cell lung cancer | experimental (strong) | 6 | 1.626 | 0.012 |
| KEGG | Allograft rejection | experimental (any) | 3 | 0.385 | 0.012 |
| KEGG | Graft-versus-host disease | experimental (any) | 3 | 0.385 | 0.012 |
| KEGG | PI3K-Akt signaling pathway | experimental (strong) | 11 | 4.646 | 0.013 |
| KEGG | African trypanosomiasis | experimental (any) | 3 | 0.399 | 0.013 |
| KEGG | Prion diseases | experimental (strong) | 3 | 0.413 | 0.016 |
| KEGG | Natural killer cell mediated cytotoxicity | experimental (any) | 5 | 1.302 | 0.017 |
| KEGG | Wnt signaling pathway | experimental (any) | 6 | 1.794 | 0.017 |
| KEGG | Autoimmune thyroid disease | experimental (any) | 3 | 0.452 | 0.018 |

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|---|---|---|---|---|---|
| KEGG | p53 signaling pathway | experimental (any) | 4 | 0.864 | 0.019 |
| KEGG | Focal adhesion | experimental (strong) | 8 | 2.994 | 0.020 |
| KEGG | Phagosome | experimental (strong) | 4 | 0.852 | 0.020 |
| KEGG | Staphylococcus aureus infection | experimental (strong) | 2 | 0.155 | 0.020 |
| KEGG | African trypanosomiasis | experimental (strong) | 3 | 0.465 | 0.021 |
| KEGG | Hepatitis C | experimental (strong) | 6 | 1.884 | 0.021 |
| KEGG | Cell cycle | experimental (strong) | 6 | 1.91 | 0.022 |
| KEGG | TGF-beta signaling pathway | experimental (strong) | 5 | 1.368 | 0.022 |
| KEGG | Staphylococcus aureus infection | experimental (any) | 3 | 0.492 | 0.022 |
| KEGG | Prolactin signaling pathway | experimental (strong) | 5 | 1.394 | 0.023 |
| KEGG | Bladder cancer | experimental (any) | 3 | 0.505 | 0.023 |
| KEGG | Cell adhesion molecules (CAMs) | experimental (any) | 5 | 1.448 | 0.025 |
| KEGG | Cytosolic DNA-sensing pathway | experimental (strong) | 3 | 0.516 | 0.026 |
| KEGG | Pathogenic Escherichia coli infection | experimental (strong) | 3 | 0.542 | 0.029 |

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|---|---|---|---|---|---|
| KEGG | Jak-STAT signaling pathway | experimental (any) | 5 | 1.555 | 0.032 |
| KEGG | N-Glycan biosynthesis | experimental (any) | 3 | 0.624 | 0.039 |
| KEGG | Prostate cancer | experimental (any) | 4 | 1.103 | 0.039 |
| KEGG | Chronic myeloid leukemia | experimental (strong) | 5 | 1.626 | 0.040 |
| KEGG | Alzheimer's disease | experimental (strong) | 4 | 1.11 | 0.042 |
| KEGG | Phagosome | experimental (any) | 5 | 1.687 | 0.042 |
| KEGG | Endometrial cancer | experimental (any) | 3 | 0.664 | 0.043 |
| KEGG | Pathogenic Escherichia coli infection | experimental (any) | 3 | 0.664 | 0.043 |
| KEGG | Cell adhesion molecules (CAMs) | experimental (strong) | 4 | 1.136 | 0.044 |
| KEGG | MAPK signaling pathway | experimental (strong) | 8 | 3.588 | 0.044 |
| KEGG | Non-small cell lung cancer | experimental (strong) | 4 | 1.161 | 0.047 |
| KEGG | HTLV-I infection | experimental (strong) | 8 | 3.691 | 0.049 |
| KEGG | Epstein-Barr virus infection | experimental (any) | 6 | 2.392 | 0.050 |
| Reactome | Cytokine Signaling in Immune system | experimental (any) | 38 | 9.793 | 1.55e-10 |

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|---|---|---|---|---|---|
| Reactome | Immune System | experimental (any) | 60 | 23.6 | 5.65e-10 |
| Reactome | Interferon alpha/beta signaling | experimental (any) | 11 | 0.731 | 1.53e-8 |
| Reactome | Gene expression (Transcription) | predicted (union) | 614 | 508 | 3.53e-7 |
| Reactome | Generic Transcription Pathway | predicted (union) | 508 | 413.1 | 3.53e-7 |
| Reactome | RNA Polymerase II Transcription | predicted (union) | 557 | 457.6 | 3.53e-7 |
| Reactome | Signaling by Interleukins | experimental (any) | 26 | 7.334 | 1.89e-6 |
| Reactome | Innate Immune System | experimental (any) | 31 | 11.65 | 2.90e-5 |
| Reactome | Interferon Signaling | experimental (any) | 13 | 2.285 | 2.90e-5 |
| Reactome | Toll Like Receptor 4 (TLR4) Cascade | experimental (any) | 11 | 1.541 | 2.90e-5 |
| Reactome | Interleukin-4 and Interleukin-13 signaling | experimental (any) | 10 | 1.355 | 4.65e-5 |
| Reactome | Toll-like Receptor Cascades | experimental (any) | 11 | 1.873 | 1.16e-4 |
| Reactome | MyD88-independent TLR4 cascade | experimental (any) | 9 | 1.222 | 1.21e-4 |

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| Reactome | TRIF(TICAM1)-mediated TLR4 signaling | experimental (any) | 9 | 1.222 | 1.21e-4 |
| Reactome | Immune System | experimental (strong) | 35 | 15.95 | 1.24e-4 |
| Reactome | Gene expression (Transcription) | predicted (intersection) | 305 | 232.8 | 1.25e-4 |
| Reactome | Death Receptor Signalling | experimental (any) | 10 | 1.634 | 1.72e-4 |
| Reactome | Signal Transduction | experimental (any) | 49 | 26.22 | 2.30e-4 |
| Reactome | RNA Polymerase II Transcription | predicted (intersection) | 275 | 209.7 | 2.63e-4 |
| Reactome | Generic Transcription Pathway | predicted (intersection) | 250 | 189.3 | 3.44e-4 |
| Reactome | NF-kB is activated and signals survival | experimental (any) | 4 | 0.159 | 3.49e-4 |
| Reactome | p75 NTR receptor-mediated signalling | experimental (any) | 8 | 1.103 | 3.49e-4 |
| Reactome | Synthesis of PIPs at the plasma membrane | predicted (union) | 35 | 18.35 | 3.76e-4 |

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|---|---|---|---|---|---|
| Reactome | DDX58/IFIH1-mediated induction of interferon-alpha/beta | experimental (any) | 7 | 0.850 | 4.13e-4 |
| Reactome | Defective LFNG causes SCDO3 | experimental (any) | 3 | 0.066 | 4.13e-4 |
| Reactome | Interleukin-10 signaling | experimental (any) | 6 | 0.558 | 4.13e-4 |
| Reactome | MyD88 dependent cascade initiated on endosome | experimental (any) | 8 | 1.169 | 4.13e-4 |
| Reactome | MyD88:MAL(TIRAP) cascade initiated on plasma membrane | experimental (any) | 8 | 1.222 | 4.13e-4 |
| Reactome | TAK1 activates NFkB by phosphorylation and activation of IKKs complex | experimental (any) | 5 | 0.372 | 4.13e-4 |
| Reactome | Toll Like Receptor 2 (TLR2) Cascade | experimental (any) | 8 | 1.222 | 4.13e-4 |
| Reactome | Toll Like Receptor 3 (TLR3) Cascade | experimental (any) | 8 | 1.183 | 4.13e-4 |

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|---|---|---|---|---|---|
| Reactome | Toll Like Receptor 7/8 (TLR7/8) Cascade | experimental (any) | 8 | 1.169 | 4.13e-4 |
| Reactome | Toll Like Receptor 9 (TLR9) Cascade | experimental (any) | 8 | 1.222 | 4.13e-4 |
| Reactome | Toll Like Receptor TLR1:TLR2 Cascade | experimental (any) | 8 | 1.222 | 4.13e-4 |
| Reactome | Toll Like Receptor TLR6:TLR2 Cascade | experimental (any) | 8 | 1.222 | 4.13e-4 |
| Reactome | p75NTR signals via NF-kB | experimental (any) | 4 | 0.199 | 4.85e-4 |
| Reactome | Loss of Function of SMAD2/3 in Cancer | experimental (any) | 3 | 0.093 | 9.89e-4 |
| Reactome | Innate Immune System | experimental (strong) | 21 | 7.588 | 0.001 |
| Reactome | Chemokine receptors bind chemokines | experimental (any) | 5 | 0.505 | 0.002 |
| Reactome | SHC1 events in ERBB2 signaling | experimental (any) | 4 | 0.279 | 0.002 |
| Reactome | Signaling by TGF-beta Receptor Complex in Cancer | experimental (any) | 3 | 0.106 | 0.002 |

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|---|---|---|---|---|---|
| Reactome | TRAF6 mediated IRF7 activation in TLR7/8 or 9 signaling | experimental (any) | 3 | 0.120 | 0.002 |
| Reactome | TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation | experimental (any) | 7 | 1.156 | 0.002 |
| Reactome | CD28 co-stimulation | predicted (union) | 23 | 11.32 | 0.003 |
| Reactome | Membrane Trafficking | predicted (union) | 262 | 214 | 0.003 |
| Reactome | Regulation of MECP2 expression and activity | predicted (union) | 23 | 11.32 | 0.003 |
| Reactome | Transcriptional Regulation by MECP2 | predicted (union) | 40 | 23.04 | 0.003 |
| Reactome | Vesicle-mediated transport | predicted (union) | 276 | 227.2 | 0.003 |
| Reactome | Interleukin-10 signaling | experimental (strong) | 6 | 0.671 | 0.003 |
| Reactome | Signal Transduction | experimental (strong) | 36 | 19.93 | 0.003 |
| Reactome | Interleukin-1 family signaling | experimental (any) | 8 | 1.727 | 0.003 |

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|---|---|---|---|---|---|
| Reactome | Interleukin-1 signaling | experimental (any) | 7 | 1.302 | 0.003 |
| Reactome | PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling | experimental (any) | 7 | 1.289 | 0.003 |
| Reactome | Death Receptor Signalling | experimental (strong) | 8 | 1.445 | 0.004 |
| Reactome | Loss of Function of SMAD4 in Cancer | experimental (any) | 2 | 0.040 | 0.004 |
| Reactome | Negative regulation of the PI3K/AKT network | experimental (any) | 7 | 1.382 | 0.004 |
| Reactome | Neutrophil degranulation | experimental (any) | 15 | 5.554 | 0.004 |
| Reactome | SMAD2/3 MH2 Domain Mutants in Cancer | experimental (any) | 2 | 0.040 | 0.004 |
| Reactome | SMAD4 MH2 Domain Mutants in Cancer | experimental (any) | 2 | 0.040 | 0.004 |
| Reactome | Signaling by ERBB2 | experimental (any) | 5 | 0.651 | 0.004 |
| Reactome | p75NTR recruits signalling complexes | experimental (any) | 3 | 0.159 | 0.004 |

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|---|---|---|---|---|---|
| Reactome | Neuronal System | predicted (intersection) | 95 | 62.98 | 0.005 |
| Reactome | Activation of RAC1 | experimental (any) | 3 | 0.173 | 0.005 |
| Reactome | Caspase activation via Death Receptors in the presence of ligand | experimental (any) | 3 | 0.186 | 0.005 |
| Reactome | ERBB2 Regulates Cell Motility | experimental (any) | 3 | 0.186 | 0.005 |
| Reactome | IRAK2 mediated activation of TAK1 complex upon TLR7/8 or 9 stimulation | experimental (any) | 3 | 0.186 | 0.005 |
| Reactome | Pre-NOTCH Processing in Golgi | experimental (any) | 3 | 0.186 | 0.005 |
| Reactome | Signaling by Non-Receptor Tyrosine Kinases | experimental (any) | 5 | 0.678 | 0.005 |
| Reactome | Signaling by PTK6 | experimental (any) | 5 | 0.678 | 0.005 |
| Reactome | Neurotransmitter release cycle | predicted (intersection) | 21 | 8.41 | 0.006 |
| Reactome | Signaling by Non-Receptor Tyrosine Kinases | predicted (intersection) | 21 | 8.589 | 0.006 |

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| Reactome | Signaling by PTK6 | predicted (intersection) | 21 | 8.589 | 0.006 |
| Reactome | Transcriptional Regulation by MECP2 | predicted (intersection) | 24 | 10.56 | 0.006 |
| Reactome | Diseases of signal transduction | predicted (union) | 173 | 136.3 | 0.006 |
| Reactome | Defective LFNG causes SCDO3 | experimental (strong) | 3 | 0.129 | 0.006 |
| Reactome | Signaling by Interleukins | experimental (strong) | 19 | 7.924 | 0.006 |
| Reactome | p75 NTR receptor-mediated signalling | experimental (strong) | 6 | 0.826 | 0.006 |
| Reactome | GRB2 events in ERBB2 signaling | experimental (any) | 3 | 0.199 | 0.006 |
| Reactome | MyD88 cascade initiated on plasma membrane | experimental (any) | 6 | 1.103 | 0.006 |
| Reactome | TRAF6-mediated induction of TAK1 complex within TLR4 complex | experimental (any) | 3 | 0.199 | 0.006 |
| Reactome | Toll Like Receptor 10 (TLR10) Cascade | experimental (any) | 6 | 1.103 | 0.006 |

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|---|---|---|---|---|---|
| Reactome | Toll Like Receptor 5 (TLR5) Cascade | experimental (any) | 6 | 1.103 | 0.006 |
| Reactome | DAP12 interactions | experimental (any) | 4 | 0.465 | 0.007 |
| Reactome | FCERI mediated MAPK activation | experimental (any) | 4 | 0.465 | 0.007 |
| Reactome | SLIT2:ROBO1 increases RHOA activity | experimental (any) | 2 | 0.053 | 0.007 |
| Reactome | MECP2 regulates neuronal receptors and channels | predicted (intersection) | 11 | 3.221 | 0.008 |
| Reactome | Signaling by ERBB2 | predicted (intersection) | 20 | 8.231 | 0.008 |
| Reactome | PI Metabolism | predicted (union) | 46 | 28.89 | 0.008 |
| Reactome | MAP kinase activation | experimental (any) | 5 | 0.824 | 0.008 |
| Reactome | PIP3 activates AKT signaling | predicted (union) | 123 | 93.32 | 0.009 |
| Reactome | CD28 dependent PI3K/Akt signaling | predicted (union) | 16 | 7.419 | 0.010 |
| Reactome | Cell death signalling via NRAGE, NRIF and NADE | experimental (any) | 5 | 0.864 | 0.010 |

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|---|---|---|---|---|---|
| Reactome | FasL/ CD95L signaling | experimental (any) | 2 | 0.066 | 0.010 |
| Reactome | Interleukin-17 signaling | experimental (any) | 5 | 0.890 | 0.010 |
| Reactome | Interleukin-36 pathway | experimental (any) | 2 | 0.066 | 0.010 |
| Reactome | JNK (c-Jun kinases) phosphorylation and activation mediated by activated human TAK1 | experimental (any) | 3 | 0.239 | 0.010 |
| Reactome | Signal transduction by L1 | experimental (any) | 3 | 0.252 | 0.010 |
| Reactome | Signaling by SCF-KIT | experimental (any) | 4 | 0.531 | 0.010 |
| Reactome | TRAF6 mediated IRF7 activation | experimental (any) | 3 | 0.239 | 0.010 |
| Reactome | activated TAK1 mediates p38 MAPK activation | experimental (any) | 3 | 0.252 | 0.010 |
| Reactome | Netrin-1 signaling | predicted (union) | 31 | 17.96 | 0.012 |
| Reactome | Generic Transcription Pathway | experimental (any) | 26 | 14.32 | 0.012 |

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|---|---|---|---|---|---|
| Reactome | Pre-NOTCH Processing in the Endoplasmic Reticulum | experimental (any) | 2 | 0.080 | 0.013 |
| Reactome | SMAD2/3 Phosphorylation Motif Mutants in Cancer | experimental (any) | 2 | 0.080 | 0.013 |
| Reactome | TGFBR1 KD Mutants in Cancer | experimental (any) | 2 | 0.080 | 0.013 |
| Reactome | TRIF-mediated programmed cell death | experimental (any) | 2 | 0.080 | 0.013 |
| Reactome | Chemokine receptors bind chemokines | experimental (strong) | 4 | 0.413 | 0.014 |
| Reactome | Cytokine Signaling in Immune system | experimental (strong) | 20 | 9.395 | 0.014 |
| Reactome | Loss of Function of SMAD2/3 in Cancer | experimental (strong) | 3 | 0.181 | 0.014 |
| Reactome | NF-kB is activated and signals survival | experimental (strong) | 3 | 0.181 | 0.014 |

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| Reactome | Signaling by TGF-beta Receptor Complex in Cancer | experimental (strong) | 3 | 0.181 | 0.014 |
| Reactome | Intracellular signaling by second messengers | predicted (union) | 138 | 107.8 | 0.015 |
| Reactome | Transport to the Golgi and subsequent modification | predicted (union) | 81 | 58.57 | 0.015 |
| Reactome | Neutrophil degranulation | experimental (strong) | 10 | 3.02 | 0.015 |
| Reactome | Anchoring fibril formation | experimental (any) | 2 | 0.093 | 0.015 |
| Reactome | Caspase activation via extrinsic apoptotic signalling pathway | experimental (any) | 3 | 0.306 | 0.015 |
| Reactome | DEx/H-box helicases activate type I IFN and inflammatory cytokines production | experimental (any) | 2 | 0.093 | 0.015 |

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|---|---|---|---|---|---|
| Reactome | Diseases associated with the TLR signaling cascade | experimental (any) | 3 | 0.306 | 0.015 |
| Reactome | Diseases of Immune System | experimental (any) | 3 | 0.306 | 0.015 |
| Reactome | Inactivation of CDC42 and RAC1 | experimental (any) | 2 | 0.093 | 0.015 |
| Reactome | Loss of Function of TGFBR1 in Cancer | experimental (any) | 2 | 0.093 | 0.015 |
| Reactome | Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways | experimental (any) | 4 | 0.624 | 0.015 |
| Reactome | RUNX3 regulates CDKN1A transcription | experimental (any) | 2 | 0.093 | 0.015 |
| Reactome | Sema4D in semaphorin signaling | experimental (any) | 3 | 0.306 | 0.015 |

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|---|---|---|---|---|---|
| Reactome | Senescence-Associated Secretory Phenotype (SASP) | experimental (any) | 5 | 0.983 | 0.015 |
| Reactome | Antiviral mechanism by IFN-stimulated genes | experimental (any) | 5 | 1.036 | 0.016 |
| Reactome | Estrogen-dependent nuclear events downstream of ESR-membrane signaling | experimental (any) | 3 | 0.319 | 0.016 |
| Reactome | Interferon gamma signaling | experimental (any) | 5 | 1.05 | 0.016 |
| Reactome | Signaling by Receptor Tyrosine Kinases | experimental (any) | 13 | 5.554 | 0.016 |
| Reactome | TRAF6 mediated NF-kB activation | experimental (any) | 3 | 0.319 | 0.016 |
| Reactome | p75NTR signals via NF-kB | experimental (strong) | 3 | 0.206 | 0.017 |
| Reactome | SHC1 events in ERBB2 signaling | experimental (strong) | 4 | 0.465 | 0.018 |

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|---|---|---|---|---|---|
| Reactome | RNA Polymerase II Transcription | experimental (any) | 27 | 15.85 | 0.018 |
| Reactome | ERBB2 Regulates Cell Motility | experimental (strong) | 3 | 0.232 | 0.019 |
| Reactome | IRAK2 mediated activation of TAK1 complex upon TLR7/8 or 9 stimulation | experimental (strong) | 3 | 0.232 | 0.019 |
| Reactome | Signaling by ERBB2 | experimental (strong) | 5 | 0.826 | 0.019 |
| Reactome | TRAF6-mediated induction of TAK1 complex within TLR4 complex | experimental (strong) | 3 | 0.232 | 0.019 |
| Reactome | DAP12 signaling | experimental (any) | 3 | 0.345 | 0.019 |
| Reactome | Sema4D mediated inhibition of cell attachment and migration | experimental (any) | 2 | 0.106 | 0.019 |
| Reactome | Transcriptional regulation of pluripotent stem cells | experimental (any) | 3 | 0.345 | 0.019 |

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|---|---|---|---|---|---|
| Reactome | Interleukin-4 and Interleukin-13 signaling | experimental (strong) | 8 | 2.22 | 0.020 |
| Reactome | Intracellular signaling by second messengers | experimental (any) | 10 | 3.827 | 0.020 |
| Reactome | Signaling by ERBB4 | experimental (any) | 4 | 0.704 | 0.020 |
| Reactome | GPCR downstream signalling | experimental (strong) | 11 | 4.104 | 0.021 |
| Reactome | Loss of Function of SMAD4 in Cancer | experimental (strong) | 2 | 0.077 | 0.021 |
| Reactome | Pre-NOTCH Processing in Golgi | experimental (strong) | 3 | 0.258 | 0.021 |
| Reactome | SMAD2/3 MH2 Domain Mutants in Cancer | experimental (strong) | 2 | 0.077 | 0.021 |
| Reactome | SMAD4 MH2 Domain Mutants in Cancer | experimental (strong) | 2 | 0.077 | 0.021 |
| Reactome | Signaling by Non-Receptor Tyrosine Kinases | experimental (strong) | 5 | 0.929 | 0.021 |

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|---|---|---|---|---|---|
| Reactome | Signaling by PTK6 | experimental (strong) | 5 | 0.929 | 0.021 |
| Reactome | TAK1 activates NFkB by phosphorylation and activation of IKKs complex | experimental (strong) | 4 | 0.568 | 0.021 |
| Reactome | Toll Like Receptor 4 (TLR4) Cascade | experimental (strong) | 7 | 1.807 | 0.021 |
| Reactome | Netrin-1 signaling | predicted (intersection) | 19 | 8.231 | 0.022 |
| Reactome | Signaling by EGFR | predicted (intersection) | 19 | 8.231 | 0.022 |
| Reactome | DAP12 interactions | predicted (union) | 25 | 14.06 | 0.022 |
| Reactome | EGFR Transactivation by Gastrin | experimental (any) | 2 | 0.120 | 0.022 |
| Reactome | MyD88 deficiency (TLR2/4) | experimental (any) | 2 | 0.120 | 0.022 |
| Reactome | Regulated proteolysis of p75NTR | experimental (any) | 2 | 0.120 | 0.022 |
| Reactome | Transcriptional Regulation by MECP2 | experimental (any) | 4 | 0.731 | 0.022 |
| Reactome | NOD1/2 Signaling Pathway | experimental (any) | 3 | 0.385 | 0.024 |

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|---|---|---|---|---|---|
| Reactome | Signaling by ROBO receptors | experimental (strong) | 5 | 0.981 | 0.025 |
| Reactome | CASP8 activity is inhibited | experimental (any) | 2 | 0.133 | 0.025 |
| Reactome | Dimerization of procaspase-8 | experimental (any) | 2 | 0.133 | 0.025 |
| Reactome | Fc epsilon receptor (FCERI) signaling | experimental (any) | 6 | 1.714 | 0.025 |
| Reactome | IRAK1 recruits IKK complex | experimental (any) | 2 | 0.133 | 0.025 |
| Reactome | IRAK1 recruits IKK complex upon TLR7/8 or 9 stimulation | experimental (any) | 2 | 0.133 | 0.025 |
| Reactome | IRAK2 mediated activation of TAK1 complex | experimental (any) | 2 | 0.133 | 0.025 |
| Reactome | IRAK4 deficiency (TLR2/4) | experimental (any) | 2 | 0.133 | 0.025 |
| Reactome | PIP3 activates AKT signaling | experimental (any) | 9 | 3.362 | 0.025 |
| Reactome | RUNX3 regulates p14-ARF | experimental (any) | 2 | 0.133 | 0.025 |
| Reactome | Regulation by c-FLIP | experimental (any) | 2 | 0.133 | 0.025 |

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|---|---|---|---|---|---|
| Reactome | EPHB-mediated forward signaling | experimental (any) | 3 | 0.412 | 0.026 |
| Reactome | Negative regulation of the PI3K/AKT network | predicted (union) | 58 | 40.22 | 0.027 |
| Reactome | Transcriptional regulation by RUNX3 | experimental (any) | 5 | 1.249 | 0.027 |
| Reactome | Caspase activation via Death Receptors in the presence of ligand | experimental (strong) | 3 | 0.310 | 0.028 |
| Reactome | GRB2 events in ERBB2 signaling | experimental (strong) | 3 | 0.310 | 0.028 |
| Reactome | GPCR downstream signalling | experimental (any) | 15 | 7.52 | 0.028 |
| Reactome | Gene expression (Transcription) | experimental (any) | 28 | 17.55 | 0.028 |
| Reactome | Interleukin-6 signaling | experimental (any) | 2 | 0.146 | 0.028 |
| Reactome | RHO GTPases activate KTN1 | experimental (any) | 2 | 0.146 | 0.028 |
| Reactome | TGF-beta receptor signaling activates SMADs | experimental (any) | 3 | 0.425 | 0.028 |

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|---|---|---|---|---|---|
| Reactome | Asparagine N-linked glycosylation | predicted (union) | 128 | 100.7 | 0.029 |
| Reactome | Signaling by NTRKs | predicted (union) | 52 | 35.53 | 0.029 |
| Reactome | Signaling by Receptor Tyrosine Kinases | predicted (union) | 197 | 162.8 | 0.029 |
| Reactome | CD28 co-stimulation | experimental (any) | 3 | 0.438 | 0.029 |
| Reactome | FasL/ CD95L signaling | experimental (strong) | 2 | 0.103 | 0.030 |
| Reactome | MyD88:MAL(TIRAP) cascade initiated on plasma membrane | experimental (strong) | 6 | 1.549 | 0.030 |
| Reactome | Pre-NOTCH Processing in the Endoplasmic Reticulum | experimental (strong) | 2 | 0.103 | 0.030 |
| Reactome | Synthesis of Prostaglandins (PG) and Thromboxanes (TX) | experimental (strong) | 2 | 0.103 | 0.030 |
| Reactome | Toll Like Receptor 2 (TLR2) Cascade | experimental (strong) | 6 | 1.549 | 0.030 |

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|---|---|---|---|---|---|
| Reactome | Toll Like Receptor TLR1:TLR2 Cascade | experimental (strong) | 6 | 1.549 | 0.030 |
| Reactome | Toll Like Receptor TLR6:TLR2 Cascade | experimental (strong) | 6 | 1.549 | 0.030 |
| Reactome | Signaling by ERBB4 | predicted (intersection) | 20 | 9.125 | 0.031 |
| Reactome | MyD88-independent TLR4 cascade | experimental (strong) | 6 | 1.6 | 0.031 |
| Reactome | PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling | experimental (strong) | 6 | 1.6 | 0.031 |
| Reactome | Signaling by NOTCH | experimental (strong) | 7 | 2.091 | 0.031 |
| Reactome | TRIF(TICAM1)-mediated TLR4 signaling | experimental (strong) | 6 | 1.6 | 0.031 |
| Reactome | Toll-like Receptor Cascades | experimental (strong) | 7 | 2.091 | 0.031 |
| Reactome | Diseases associated with O-glycosylation of proteins | experimental (strong) | 3 | 0.361 | 0.032 |
| Reactome | CD28 dependent Vav1 pathway | experimental (any) | 2 | 0.159 | 0.032 |

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|---|---|---|---|---|---|
| Reactome | ERBB2 Activates PTK6 Signaling | experimental (any) | 2 | 0.159 | 0.032 |
| Reactome | Signaling by GPCR | experimental (strong) | 11 | 4.62 | 0.034 |
| Reactome | Activation of NMDA receptors and postsynaptic events | predicted (intersection) | 25 | 12.7 | 0.035 |
| Reactome | Competing endogenous RNAs (ceRNAs) regulate PTEN translation | predicted (intersection) | 7 | 1.789 | 0.035 |
| Reactome | Intracellular signaling by second messengers | predicted (intersection) | 72 | 49.38 | 0.035 |
| Reactome | Negative regulation of the PI3K/AKT network | predicted (intersection) | 33 | 18.43 | 0.035 |
| Reactome | PIP3 activates AKT signaling | predicted (intersection) | 64 | 42.76 | 0.035 |
| Reactome | Deubiquitination | experimental (strong) | 7 | 2.246 | 0.035 |
| Reactome | Developmental Biology | experimental (strong) | 16 | 8.182 | 0.035 |

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|---|---|---|---|---|---|
| Reactome | Generic Transcription Pathway | experimental (strong) | 18 | 9.782 | 0.035 |
| Reactome | JNK (c-Jun kinases) phosphorylation and activation mediated by activated human TAK1 | experimental (strong) | 3 | 0.387 | 0.035 |
| Reactome | MyD88 deficiency (TLR2/4) | experimental (strong) | 2 | 0.129 | 0.035 |
| Reactome | TRIF-mediated programmed cell death | experimental (strong) | 2 | 0.129 | 0.035 |
| Reactome | activated TAK1 mediates p38 MAPK activation | experimental (strong) | 3 | 0.387 | 0.035 |
| Reactome | p75NTR recruits signalling complexes | experimental (strong) | 2 | 0.129 | 0.035 |
| Reactome | FCERI mediated MAPK activation | predicted (union) | 19 | 10.15 | 0.036 |
| Reactome | Caspase activation via extrinsic apoptotic signalling pathway | experimental (strong) | 3 | 0.439 | 0.036 |

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|---|---|---|---|---|---|
| Reactome | Class A/1 (Rhodopsin-like receptors) | experimental (strong) | 5 | 1.265 | 0.036 |
| Reactome | Disease | experimental (strong) | 16 | 8.621 | 0.036 |
| Reactome | Diseases associated with the TLR signaling cascade | experimental (strong) | 3 | 0.413 | 0.036 |
| Reactome | Diseases of Immune System | experimental (strong) | 3 | 0.413 | 0.036 |
| Reactome | Gene expression (Transcription) | experimental (strong) | 19 | 10.79 | 0.036 |
| Reactome | IRAK1 recruits IKK complex | experimental (strong) | 2 | 0.155 | 0.036 |
| Reactome | IRAK1 recruits IKK complex upon TLR7/8 or 9 stimulation | experimental (strong) | 2 | 0.155 | 0.036 |
| Reactome | IRAK2 mediated activation of TAK1 complex | experimental (strong) | 2 | 0.155 | 0.036 |
| Reactome | IRAK4 deficiency (TLR2/4) | experimental (strong) | 2 | 0.155 | 0.036 |

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|---|---|---|---|---|---|
| Reactome | Loss of Function of TGFBR1 in Cancer | experimental (strong) | 2 | 0.155 | 0.036 |
| Reactome | Negative regulation of the PI3K/AKT network | experimental (strong) | 6 | 1.755 | 0.036 |
| Reactome | Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways | experimental (strong) | 4 | 0.852 | 0.036 |
| Reactome | Peptide ligand-binding receptors | experimental (strong) | 4 | 0.774 | 0.036 |
| Reactome | Pre-NOTCH Expression and Processing | experimental (strong) | 4 | 0.800 | 0.036 |
| Reactome | RHO GTPases activate KTN1 | experimental (strong) | 2 | 0.155 | 0.036 |
| Reactome | RNA Polymerase II Transcription | experimental (strong) | 18 | 10.01 | 0.036 |
| Reactome | RUNX3 regulates CDKN1A transcription | experimental (strong) | 2 | 0.155 | 0.036 |

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|---|---|---|---|---|---|
| Reactome | SMAD2/3 Phosphorylation Motif Mutants in Cancer | experimental (strong) | 2 | 0.155 | 0.036 |
| Reactome | Sema4D in semaphorin signaling | experimental (strong) | 3 | 0.413 | 0.036 |
| Reactome | Senescence-Associated Secretory Phenotype (SASP) | experimental (strong) | 4 | 0.826 | 0.036 |
| Reactome | Signaling by ERBB4 | experimental (strong) | 4 | 0.826 | 0.036 |
| Reactome | TGF-beta receptor signaling activates SMADs | experimental (strong) | 3 | 0.439 | 0.036 |
| Reactome | TGFBR1 KD Mutants in Cancer | experimental (strong) | 2 | 0.155 | 0.036 |
| Reactome | GRB2 events in EGFR signaling | experimental (any) | 2 | 0.173 | 0.036 |
| Reactome | NRIF signals cell death from the nucleus | experimental (any) | 2 | 0.173 | 0.036 |
| Reactome | RIPK1-mediated regulated necrosis | experimental (any) | 2 | 0.173 | 0.036 |
| Reactome | Regulated Necrosis | experimental (any) | 2 | 0.173 | 0.036 |

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|---|---|---|---|---|---|
| Reactome | Regulation of necroptotic cell death | experimental (any) | 2 | 0.173 | 0.036 |
| Reactome | SHC1 events in ERBB4 signaling | experimental (any) | 2 | 0.173 | 0.036 |
| Reactome | Signaling by Activin | experimental (any) | 2 | 0.173 | 0.036 |
| Reactome | Signaling by NOTCH | experimental (any) | 7 | 2.485 | 0.036 |
| Reactome | TRAF3-dependent IRF activation pathway | experimental (any) | 2 | 0.173 | 0.036 |
| Reactome | Costimulation by the CD28 family | predicted (union) | 37 | 23.82 | 0.038 |
| Reactome | Signaling by ERBB4 | predicted (union) | 32 | 19.91 | 0.038 |
| Reactome | EPHB-mediated forward signaling | experimental (strong) | 3 | 0.465 | 0.038 |
| Reactome | Signal transduction by L1 | experimental (strong) | 3 | 0.465 | 0.038 |
| Reactome | Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell | experimental (any) | 5 | 1.408 | 0.038 |

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|---|---|---|---|---|---|
| Reactome | Constitutive Signaling by Aberrant PI3K in Cancer | experimental (any) | 4 | 0.943 | 0.039 |
| Reactome | EPHA-mediated growth cone collapse | experimental (any) | 2 | 0.186 | 0.039 |
| Reactome | G alpha (12/13) signalling events | experimental (any) | 4 | 0.930 | 0.039 |
| Reactome | ISG15 antiviral mechanism | experimental (any) | 4 | 0.930 | 0.039 |
| Reactome | PTK6 Regulates RHO GTPases, RAS GTPase and MAP kinases | experimental (any) | 2 | 0.186 | 0.039 |
| Reactome | SHC1 events in EGFR signaling | experimental (any) | 2 | 0.186 | 0.039 |
| Reactome | Synthesis of Prostaglandins (PG) and Thromboxanes (TX) | experimental (any) | 2 | 0.186 | 0.039 |
| Reactome | Role of LAT2/NTAL/LAB on calcium mobilization | predicted (union) | 10 | 4.295 | 0.041 |

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|---|---|---|---|---|---|
| Reactome | Pre-NOTCH Expression and Processing | experimental (any) | 4 | 0.957 | 0.041 |
| Reactome | Activation of RAC1 | experimental (strong) | 2 | 0.181 | 0.042 |
| Reactome | Cell death signalling via NRAGE, NRIF and NADE | experimental (strong) | 3 | 0.490 | 0.042 |
| Reactome | DDX58/IFIH1-mediated induction of interferon-alpha/beta | experimental (strong) | 4 | 0.929 | 0.042 |
| Reactome | G alpha (12/13) signalling events | experimental (strong) | 3 | 0.490 | 0.042 |
| Reactome | Intracellular signaling by second messengers | experimental (strong) | 9 | 3.794 | 0.042 |
| Reactome | Regulated proteolysis of p75NTR | experimental (strong) | 2 | 0.181 | 0.042 |
| Reactome | Resolution of D-Loop Structures | experimental (strong) | 2 | 0.181 | 0.042 |

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| Reactome | Resolution of D-loop Structures through Holliday Junction Intermediates | experimental (strong) | 2 | 0.181 | 0.042 |
| Reactome | Resolution of D-loop Structures through Synthesis-Dependent Strand Annealing (SDSA) | experimental (strong) | 2 | 0.181 | 0.042 |
| Reactome | Sema4D mediated inhibition of cell attachment and migration | experimental (strong) | 2 | 0.181 | 0.042 |
| Reactome | TRAF6 mediated IRF7 activation in TLR7/8 or 9 signaling | experimental (strong) | 2 | 0.181 | 0.042 |
| Reactome | Transcriptional regulation of pluripotent stem cells | experimental (strong) | 3 | 0.490 | 0.042 |

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| Reactome | Activation of IRF3/IRF7 mediated by TBK1/IKK epsilon | experimental (any) | 2 | 0.199 | 0.042 |
| Reactome | Constitutive Signaling by EGFRvIII | experimental (any) | 2 | 0.199 | 0.042 |
| Reactome | PI3K events in ERBB2 signaling | experimental (any) | 2 | 0.199 | 0.042 |
| Reactome | Regulation of TLR by endogenous ligand | experimental (any) | 2 | 0.199 | 0.042 |
| Reactome | Signaling by EGFRvIII in Cancer | experimental (any) | 2 | 0.199 | 0.042 |
| Reactome | Signaling by TGF-beta Receptor Complex | experimental (any) | 4 | 0.970 | 0.042 |
| Reactome | PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling | predicted (intersection) | 31 | 17.36 | 0.043 |
| Reactome | PI5P, PP2A and IER3 Regulate PI3K/AKT Signaling | predicted (union) | 54 | 37.87 | 0.044 |
| Reactome | Signaling by GPCR | experimental (any) | 15 | 8.172 | 0.044 |

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|---|---|---|---|---|---|
| Reactome | Signaling by Receptor Tyrosine Kinases | predicted (intersection) | 101 | 74.61 | 0.045 |
| Reactome | Phospholipid metabolism | predicted (union) | 95 | 73.02 | 0.045 |
| Reactome | Signaling by NTRK2 (TRKB) | predicted (union) | 17 | 8.981 | 0.046 |
| Reactome | Cellular Senescence | experimental (any) | 6 | 2.099 | 0.046 |
| Reactome | FOXO-mediated transcription of cell cycle genes | experimental (any) | 2 | 0.213 | 0.046 |
| Reactome | G alpha (i) signalling events | experimental (any) | 9 | 3.986 | 0.046 |
| Reactome | TGF-beta receptor signaling in EMT (epithelial to mesenchymal transition) | experimental (any) | 2 | 0.213 | 0.046 |

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| Reactome | Transcription of E2F targets under negative control by p107 (RBL1) and p130 (RBL2) in complex with HDAC1 | experimental (any) | 2 | 0.213 | 0.046 |
| Reactome | Transcriptional regulation by RUNX2 | experimental (any) | 5 | 1.528 | 0.046 |
| Reactome | Deubiquitination | experimental (any) | 8 | 3.362 | 0.048 |
| Reactome | Cell surface interactions at the vascular wall | experimental (any) | 5 | 1.568 | 0.049 |
| Reactome | Gastrin-CREB signalling pathway via PKC and MAPK | experimental (any) | 2 | 0.226 | 0.049 |
| Reactome | Regulation of RUNX1 Expression and Activity | experimental (any) | 2 | 0.226 | 0.049 |
| Reactome | Signaling by NODAL | experimental (any) | 2 | 0.226 | 0.049 |
| Reactome | CD28 dependent Vav1 pathway | experimental (strong) | 2 | 0.206 | 0.050 |

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| Reactome | ERBB2 Activates PTK6 Signaling | experimental (strong) | 2 | 0.206 | 0.050 |
| Reactome | Interleukin-1 signaling | experimental (strong) | 4 | 0.981 | 0.050 |
| Reactome | MyD88 dependent cascade initiated on endosome | experimental (strong) | 5 | 1.523 | 0.050 |
| Reactome | Signaling by Activin | experimental (strong) | 2 | 0.206 | 0.050 |
| Reactome | Signaling by Receptor Tyrosine Kinases | experimental (strong) | 11 | 5.42 | 0.050 |
| Reactome | TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation | experimental (strong) | 5 | 1.497 | 0.050 |
| Reactome | Toll Like Receptor 7/8 (TLR7/8) Cascade | experimental (strong) | 5 | 1.523 | 0.050 |
| Reactome | Toll Like Receptor 9 (TLR9) Cascade | experimental (strong) | 5 | 1.523 | 0.050 |
| Reactome | Transcriptional regulation by RUNX3 | experimental (strong) | 4 | 1.007 | 0.050 |

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|---|---|---|---|---|---|
| WikiPathways | Regulation of toll-like receptor signaling pathway | experimental (any) | 17 | 1.594 | 4.99e-11 |
| WikiPathways | Toll-like Receptor Signaling Pathway | experimental (any) | 15 | 1.156 | 4.99e-11 |
| WikiPathways | Hepatitis C and Hepatocellular Carcinoma | experimental (any) | 11 | 0.651 | 2.27e-9 |
| WikiPathways | Photodynamic therapy-induced NF-kB survival signaling | experimental (any) | 9 | 0.452 | 1.84e-8 |
| WikiPathways | Viral Acute Myocarditis | experimental (any) | 12 | 1.036 | 1.84e-8 |
| WikiPathways | Non-genomic actions of 1,25 dihydroxy vitamin D3 | experimental (any) | 11 | 0.877 | 3.06e-8 |
| WikiPathways | Spinal Cord Injury | experimental (any) | 13 | 1.369 | 3.06e-8 |
| WikiPathways | LTF danger signal response pathway | experimental (any) | 7 | 0.252 | 7.60e-8 |
| WikiPathways | Fibrin Complement Receptor 3 Signaling Pathway | experimental (any) | 8 | 0.438 | 2.06e-7 |

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| WikiPathways | miRNAs involvement in the immune response in sepsis | experimental (any) | 8 | 0.465 | 3.07e-7 |
| WikiPathways | Platelet-mediated interactions with vascular and circulating cells | experimental (any) | 6 | 0.213 | 6.40e-7 |
| WikiPathways | TLR4 Signaling and Tolerance | experimental (any) | 7 | 0.345 | 6.40e-7 |
| WikiPathways | VEGFA-VEGFR2 Signaling Pathway | experimental (any) | 16 | 3.043 | 1.12e-6 |
| WikiPathways | Hepatitis C and Hepatocellular Carcinoma | experimental (strong) | 11 | 1.161 | 1.48e-6 |
| WikiPathways | LTF danger signal response pathway | experimental (strong) | 7 | 0.387 | 2.97e-6 |
| WikiPathways | Pancreatic adenocarcinoma pathway | experimental (any) | 10 | 1.156 | 3.15e-6 |
| WikiPathways | Signal transduction through IL1R | experimental (any) | 7 | 0.438 | 3.15e-6 |
| WikiPathways | Apoptosis Modulation and Signaling | experimental (any) | 10 | 1.169 | 3.30e-6 |

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|---|---|---|---|---|---|
| WikiPathways | Regulation of toll-like receptor signaling pathway | experimental (strong) | 13 | 2.117 | 3.85e-6 |
| WikiPathways | Viral Acute Myocarditis | experimental (strong) | 11 | 1.394 | 3.85e-6 |
| WikiPathways | Toll-like Receptor Signaling Pathway | experimental (strong) | 12 | 1.833 | 4.96e-6 |
| WikiPathways | Chromosomal and microsatellite instability in colorectal cancer | experimental (any) | 9 | 0.957 | 5.50e-6 |
| WikiPathways | Spinal Cord Injury | experimental (strong) | 12 | 1.91 | 6.67e-6 |
| WikiPathways | Hair Follicle Development: Cytodifferentiation (Part 3 of 3) | experimental (any) | 9 | 1.01 | 7.87e-6 |
| WikiPathways | socs1 | experimental (any) | 8 | 0.744 | 7.87e-6 |
| WikiPathways | PDGF Pathway | experimental (any) | 7 | 0.531 | 8.88e-6 |
| WikiPathways | Photodynamic therapy-induced NF-kB survival signaling | experimental (strong) | 8 | 0.749 | 1.01e-5 |

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| WikiPathways | Platelet-mediated interactions with vascular and circulating cells | experimental (strong) | 6 | 0.361 | 1.47e-5 |
| WikiPathways | Interactions between immune cells and microRNAs in tumor microenvironment | experimental (any) | 6 | 0.372 | 1.51e-5 |
| WikiPathways | Toll-like Receptor Signaling | experimental (any) | 6 | 0.385 | 1.79e-5 |
| WikiPathways | ApoE and miR-146 in inflammation and atherosclerosis | experimental (any) | 4 | 0.106 | 1.85e-5 |
| WikiPathways | Simplified Depiction of MYD88 Distinct Input-Output Pathway | experimental (any) | 5 | 0.226 | 1.87e-5 |
| WikiPathways | Apoptosis Modulation by HSP70 | experimental (any) | 5 | 0.239 | 2.46e-5 |
| WikiPathways | Photodynamic therapy-induced AP-1 survival signaling. | experimental (any) | 7 | 0.651 | 2.74e-5 |

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| WikiPathways | Structural Pathway of Interleukin 1 (IL-1) | experimental (any) | 7 | 0.651 | 2.74e-5 |
| WikiPathways | Integrated Breast Cancer Pathway | experimental (any) | 11 | 1.966 | 3.39e-5 |
| WikiPathways | Interleukin-1 Induced Activation of NF-kappa-B | experimental (any) | 4 | 0.133 | 4.32e-5 |
| WikiPathways | Allograft Rejection | experimental (any) | 8 | 0.997 | 4.51e-5 |
| WikiPathways | RANKL/RANK (Receptor activator of NFKB (ligand)) Signaling Pathway | experimental (any) | 7 | 0.718 | 4.51e-5 |
| WikiPathways | TGF-beta Receptor Signaling | experimental (any) | 7 | 0.718 | 4.51e-5 |
| WikiPathways | Simplified Depiction of MYD88 Distinct Input-Output Pathway | experimental (strong) | 5 | 0.258 | 4.85e-5 |
| WikiPathways | TGF-beta Signaling Pathway | experimental (any) | 10 | 1.701 | 5.07e-5 |
| WikiPathways | Allograft Rejection | experimental (strong) | 8 | 0.981 | 6.68e-5 |
| WikiPathways | EBV LMP1 signaling | experimental (any) | 5 | 0.306 | 6.74e-5 |

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| WikiPathways | T-Cell antigen Receptor (TCR) Signaling Pathway | experimental (any) | 8 | 1.076 | 7.10e-5 |
| WikiPathways | DNA Damage Response (only ATM dependent) | experimental (any) | 9 | 1.422 | 7.33e-5 |
| WikiPathways | TNF related weak inducer of apoptosis (TWEAK) Signaling Pathway | experimental (any) | 6 | 0.545 | 8.84e-5 |
| WikiPathways | Fibrin Complement Receptor 3 Signaling Pathway | experimental (strong) | 7 | 0.749 | 9.82e-5 |
| WikiPathways | Envelope proteins and their potential roles in EDMD physiopathology | experimental (any) | 6 | 0.558 | 9.93e-5 |
| WikiPathways | AGE/RAGE pathway | experimental (any) | 7 | 0.877 | 1.42e-4 |

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| WikiPathways | Mammary gland development pathway - Embryonic development (Stage 1 of 4) | experimental (any) | 4 | 0.186 | 1.43e-4 |
| WikiPathways | Interactions between immune cells and microRNAs in tumor microenvironment | experimental (strong) | 6 | 0.542 | 1.52e-4 |
| WikiPathways | Pancreatic adenocarcinoma pathway | experimental (strong) | 10 | 1.858 | 1.52e-4 |
| WikiPathways | Non-genomic actions of 1,25 dihydroxy vitamin D3 | experimental (strong) | 8 | 1.161 | 1.82e-4 |
| WikiPathways | miRNAs involvement in the immune response in sepsis | experimental (strong) | 7 | 0.852 | 1.82e-4 |
| WikiPathways | Human Complement System | experimental (any) | 7 | 0.930 | 1.99e-4 |

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| WikiPathways | Cells and Molecules involved in local acute inflammatory response | experimental (any) | 4 | 0.213 | 2.43e-4 |
| WikiPathways | Endoderm Differentiation | experimental (any) | 9 | 1.741 | 3.08e-4 |
| WikiPathways | Leptin signaling pathway | experimental (any) | 7 | 1.01 | 3.16e-4 |
| WikiPathways | ApoE and miR-146 in inflammation and atherosclerosis | experimental (strong) | 4 | 0.206 | 3.18e-4 |
| WikiPathways | TLR4 Signaling and Tolerance | experimental (strong) | 6 | 0.645 | 3.25e-4 |
| WikiPathways | Integrated Breast Cancer Pathway | experimental (strong) | 11 | 2.555 | 3.39e-4 |
| WikiPathways | Extracellular vesicles in the crosstalk of cardiac cells | experimental (any) | 4 | 0.239 | 3.73e-4 |
| WikiPathways | IL-1 signaling pathway | experimental (any) | 6 | 0.731 | 3.93e-4 |
| WikiPathways | VEGFA-VEGFR2 Signaling Pathway | experimental (strong) | 14 | 4.156 | 4.10e-4 |

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| WikiPathways | Signal transduction through IL1R | experimental (strong) | 6 | 0.697 | 4.44e-4 |
| WikiPathways | BMP Signaling Pathway in Eyelid Development | experimental (any) | 4 | 0.252 | 4.48e-4 |
| WikiPathways | Chemokine signaling pathway | experimental (any) | 9 | 1.953 | 6.62e-4 |
| WikiPathways | Focal Adhesion | experimental (any) | 10 | 2.405 | 6.62e-4 |
| WikiPathways | Androgen receptor signaling pathway | experimental (any) | 7 | 1.169 | 6.96e-4 |
| WikiPathways | Association Between Physico-Chemical Features and Toxicity Associated Pathways | experimental (any) | 6 | 0.824 | 6.96e-4 |
| WikiPathways | IL1 and megakaryocytes in obesity | experimental (any) | 4 | 0.292 | 7.13e-4 |
| WikiPathways | The human immune response to tuberculosis | experimental (any) | 4 | 0.292 | 7.13e-4 |
| WikiPathways | Vitamin D in inflammatory diseases | experimental (any) | 4 | 0.292 | 7.13e-4 |

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| WikiPathways | IL-2 Signaling Pathway | experimental (any) | 5 | 0.545 | 7.56e-4 |
| WikiPathways | Oncostatin M Signaling Pathway | experimental (any) | 6 | 0.850 | 7.56e-4 |
| WikiPathways | RAC1/PAK1/p38/MMP2 Pathway | experimental (any) | 6 | 0.864 | 8.09e-4 |
| WikiPathways | Vitamin B12 Metabolism | experimental (any) | 5 | 0.571 | 9.11e-4 |
| WikiPathways | Physiological and Pathological Hypertrophy of the Heart | experimental (any) | 4 | 0.319 | 9.29e-4 |
| WikiPathways | Apoptosis Modulation by HSP70 | experimental (strong) | 4 | 0.310 | 0.001 |
| WikiPathways | EBV LMP1 signaling | experimental (strong) | 5 | 0.542 | 0.001 |
| WikiPathways | Hair Follicle Development: Cytodifferentiation (Part 3 of 3) | experimental (strong) | 7 | 1.239 | 0.001 |
| WikiPathways | PDGF Pathway | experimental (strong) | 6 | 0.878 | 0.001 |
| WikiPathways | Chromosomal and microsatellite instability in colorectal cancer | experimental (strong) | 7 | 1.42 | 0.002 |

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|---|---|---|---|---|---|
| WikiPathways | Envelope proteins and their potential roles in EDMD physiopathology | experimental (strong) | 5 | 0.645 | 0.002 |
| WikiPathways | Human Complement System | experimental (strong) | 5 | 0.645 | 0.002 |
| WikiPathways | Interleukin-1 Induced Activation of NF-kappa-B | experimental (strong) | 3 | 0.155 | 0.002 |
| WikiPathways | Nonalcoholic fatty liver disease | experimental (strong) | 8 | 1.833 | 0.002 |
| WikiPathways | TNF related weak inducer of apoptosis (TWEAK) Signaling Pathway | experimental (strong) | 6 | 0.955 | 0.002 |
| WikiPathways | Toll-like Receptor Signaling | experimental (strong) | 5 | 0.594 | 0.002 |
| WikiPathways | Vitamin B12 Metabolism | experimental (strong) | 5 | 0.645 | 0.002 |
| WikiPathways | socs1 | experimental (strong) | 6 | 0.955 | 0.002 |
| WikiPathways | Apoptosis | experimental (any) | 6 | 1.063 | 0.002 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| WikiPathways | Control of immune tolerance by vasoactive intestinal peptide | experimental (any) | 3 | 0.173 | 0.002 |
| WikiPathways | Extracellular vesicle-mediated signaling in recipient cells | experimental (any) | 4 | 0.372 | 0.002 |
| WikiPathways | MicroRNAs in cardiomyocyte hypertrophy | experimental (any) | 6 | 1.063 | 0.002 |
| WikiPathways | Nonalcoholic fatty liver disease | experimental (any) | 8 | 1.887 | 0.002 |
| WikiPathways | PI3K-Akt Signaling Pathway | experimental (any) | 12 | 3.867 | 0.002 |
| WikiPathways | AGE/RAGE pathway | experimental (strong) | 7 | 1.497 | 0.003 |
| WikiPathways | Androgen receptor signaling pathway | experimental (strong) | 7 | 1.445 | 0.003 |
| WikiPathways | Cells and Molecules involved in local acute inflammatory response | experimental (strong) | 3 | 0.181 | 0.003 |

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|---|---|---|---|---|---|
| WikiPathways | IL1 and megakaryocytes in obesity | experimental (strong) | 4 | 0.413 | 0.003 |
| WikiPathways | TGF-beta Signaling Pathway | experimental (strong) | 9 | 2.478 | 0.003 |
| WikiPathways | Alpha 6 Beta 4 signaling pathway | experimental (any) | 4 | 0.438 | 0.003 |
| WikiPathways | Breast cancer pathway | experimental (any) | 8 | 1.966 | 0.003 |
| WikiPathways | Corticotropin-releasing hormone signaling pathway | experimental (any) | 6 | 1.143 | 0.003 |
| WikiPathways | Ebola Virus Pathway on Host | experimental (any) | 7 | 1.568 | 0.003 |
| WikiPathways | Lung fibrosis | experimental (any) | 5 | 0.744 | 0.003 |
| WikiPathways | MAPK Signaling Pathway | experimental (any) | 10 | 3.069 | 0.003 |
| WikiPathways | Notch Signaling Pathway | experimental (any) | 5 | 0.731 | 0.003 |
| WikiPathways | T-Cell antigen Receptor (TCR) pathway during Staphylococcus aureus infection | experimental (any) | 5 | 0.757 | 0.003 |
| WikiPathways | TNF alpha Signaling Pathway | experimental (any) | 6 | 1.156 | 0.003 |

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|---|---|---|---|---|---|
| WikiPathways | Amplification and Expansion of Oncogenic Pathways as Metastatic Traits | experimental (any) | 3 | 0.226 | 0.004 |
| WikiPathways | Canonical and Non-Canonical TGF-B signaling | experimental (any) | 3 | 0.226 | 0.004 |
| WikiPathways | Overview of nanoparticle effects | experimental (any) | 3 | 0.239 | 0.004 |
| WikiPathways | TGF-B Signaling in Thyroid Cells for Epithelial-Mesenchymal Transition | experimental (any) | 3 | 0.226 | 0.004 |
| WikiPathways | Leptin signaling pathway | experimental (strong) | 7 | 1.652 | 0.005 |
| WikiPathways | Photodynamic therapy-induced AP-1 survival signaling. | experimental (strong) | 6 | 1.187 | 0.005 |
| WikiPathways | DNA Damage Response | experimental (any) | 5 | 0.864 | 0.005 |
| WikiPathways | Nanomaterial induced apoptosis | experimental (any) | 3 | 0.252 | 0.005 |

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|---|---|---|---|---|---|
| WikiPathways | Notch Signaling | experimental (any) | 4 | 0.518 | 0.005 |
| WikiPathways | miRNA Regulation of DNA Damage Response | experimental (any) | 5 | 0.890 | 0.005 |
| WikiPathways | VEGFA-VEGFR2 Signaling Pathway | predicted (union) | 113 | 82.39 | 0.006 |
| WikiPathways | Chemokine signaling pathway | experimental (strong) | 8 | 2.168 | 0.006 |
| WikiPathways | Control of immune tolerance by vasoactive intestinal peptide | experimental (strong) | 3 | 0.232 | 0.006 |
| WikiPathways | Vitamin D in inflammatory diseases | experimental (strong) | 4 | 0.516 | 0.006 |
| WikiPathways | Brain-Derived Neurotrophic Factor (BDNF) signaling pathway | experimental (any) | 7 | 1.794 | 0.006 |
| WikiPathways | EV release from cardiac cells and their functional effects | experimental (any) | 2 | 0.080 | 0.006 |

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|---|---|---|---|---|---|
| WikiPathways | Fas Ligand (FasL) pathway and Stress induction of Heat Shock Proteins (HSP) regulation | experimental (any) | 4 | 0.558 | 0.006 |
| WikiPathways | IL-3 Signaling Pathway | experimental (any) | 4 | 0.585 | 0.006 |
| WikiPathways | IL-6 signaling pathway | experimental (any) | 4 | 0.558 | 0.006 |
| WikiPathways | Interleukin-11 Signaling Pathway | experimental (any) | 4 | 0.585 | 0.006 |
| WikiPathways | Primary Focal Segmental Glomerulosclerosis FSGS | experimental (any) | 5 | 0.957 | 0.006 |
| WikiPathways | Regulation of Actin Cytoskeleton | experimental (any) | 7 | 1.807 | 0.006 |
| WikiPathways | Senescence and Autophagy in Cancer | experimental (any) | 6 | 1.382 | 0.006 |
| WikiPathways | T-Cell antigen Receptor (TCR) Signaling Pathway | predicted (union) | 51 | 32.41 | 0.007 |
| WikiPathways | Prolactin Signaling Pathway | experimental (any) | 5 | 0.983 | 0.007 |

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|---|---|---|---|---|---|
| WikiPathways | Thymic Stromal LymphoPoietin (TSLP) Signaling Pathway | experimental (any) | 4 | 0.598 | 0.007 |
| WikiPathways | Phosphodiesterases in neuronal function | predicted (intersection) | 21 | 8.41 | 0.008 |
| WikiPathways | Epithelial to mesenchymal transition in colorectal cancer | experimental (any) | 7 | 1.966 | 0.008 |
| WikiPathways | Hematopoietic Stem Cell Differentiation | experimental (any) | 4 | 0.638 | 0.008 |
| WikiPathways | DNA Damage Response (only ATM dependent) | experimental (strong) | 8 | 2.375 | 0.009 |
| WikiPathways | Endoderm Differentiation | experimental (strong) | 7 | 1.858 | 0.009 |
| WikiPathways | Cardiac Progenitor Differentiation | experimental (any) | 4 | 0.664 | 0.009 |
| WikiPathways | Cell Cycle | experimental (any) | 6 | 1.528 | 0.009 |

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|---|---|---|---|---|---|
| WikiPathways | Selective expression of chemokine receptors during T-cell polarization | experimental (any) | 3 | 0.332 | 0.009 |
| WikiPathways | Signaling Pathways in Glioblastoma | experimental (any) | 5 | 1.063 | 0.009 |
| WikiPathways | Vitamin D Receptor Pathway | experimental (any) | 7 | 2.046 | 0.009 |
| WikiPathways | Apoptosis-related network due to altered Notch3 in ovarian cancer | experimental (any) | 4 | 0.678 | 0.010 |
| WikiPathways | EGF/EGFR Signaling Pathway | experimental (any) | 7 | 2.086 | 0.010 |
| WikiPathways | TFs Regulate miRNAs related to cardiac hypertrophy | experimental (any) | 2 | 0.106 | 0.010 |
| WikiPathways | VEGFA-VEGFR2 Signaling Pathway | predicted (intersection) | 61 | 37.75 | 0.011 |
| WikiPathways | Apoptosis Modulation and Signaling | experimental (strong) | 6 | 1.445 | 0.011 |

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|---|---|---|---|---|---|
| WikiPathways | Notch Signaling Pathway | experimental (strong) | 5 | 0.981 | 0.011 |
| WikiPathways | Primary Focal Segmental Glomerulosclerosis FSGS | experimental (strong) | 5 | 0.981 | 0.011 |
| WikiPathways | IL-4 Signaling Pathway | experimental (any) | 4 | 0.704 | 0.011 |
| WikiPathways | Nanomaterial induced apoptosis | experimental (strong) | 3 | 0.310 | 0.012 |
| WikiPathways | RAC1/PAK1/p38/MMP2 Pathway | experimental (strong) | 6 | 1.471 | 0.012 |
| WikiPathways | Mammary gland development pathway - Pregnancy and lactation (Stage 3 of 4) | experimental (any) | 3 | 0.372 | 0.012 |
| WikiPathways | Pathways Regulating Hippo Signaling | experimental (any) | 5 | 1.169 | 0.012 |
| WikiPathways | Role Altered Glycolysation of MUC1 in Tumour Microenvironment | experimental (any) | 2 | 0.120 | 0.012 |

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|---|---|---|---|---|---|
| WikiPathways | Extracellular vesicle-mediated signaling in recipient cells | experimental (strong) | 4 | 0.645 | 0.013 |
| WikiPathways | Inflammatory Response Pathway | experimental (any) | 3 | 0.385 | 0.013 |
| WikiPathways | Integrin-mediated Cell Adhesion | experimental (any) | 5 | 1.196 | 0.013 |
| WikiPathways | PDGFR-beta pathway | experimental (any) | 3 | 0.385 | 0.013 |
| WikiPathways | Ebola Virus Pathway on Host | experimental (strong) | 6 | 1.523 | 0.014 |
| WikiPathways | Mammary gland development pathway - Embryonic development (Stage 1 of 4) | experimental (strong) | 3 | 0.336 | 0.014 |
| WikiPathways | Notch Signaling | experimental (strong) | 4 | 0.671 | 0.014 |
| WikiPathways | Overview of nanoparticle effects | experimental (strong) | 3 | 0.336 | 0.014 |
| WikiPathways | T-Cell antigen Receptor (TCR) Signaling Pathway | experimental (strong) | 6 | 1.574 | 0.014 |

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|---|---|---|---|---|---|
| WikiPathways | TGF-beta Receptor Signaling | experimental (strong) | 5 | 1.084 | 0.014 |
| WikiPathways | TNF alpha Signaling Pathway | experimental (strong) | 6 | 1.574 | 0.014 |
| WikiPathways | Gene regulatory network modelling somitogenesis | experimental (any) | 2 | 0.133 | 0.014 |
| WikiPathways | Alpha 6 Beta 4 signaling pathway | experimental (strong) | 4 | 0.697 | 0.015 |
| WikiPathways | Folate Metabolism | experimental (any) | 4 | 0.784 | 0.015 |
| WikiPathways | Resistin as a regulator of inflammation | experimental (any) | 3 | 0.412 | 0.015 |
| WikiPathways | RANKL/RANK (Receptor activator of NFKB (ligand)) Signaling Pathway | predicted (union) | 33 | 19.52 | 0.016 |
| WikiPathways | Association Between Physico-Chemical Features and Toxicity Associated Pathways | experimental (strong) | 5 | 1.136 | 0.016 |

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|---|---|---|---|---|---|
| WikiPathways | PI3K-Akt Signaling Pathway | experimental (strong) | 11 | 4.569 | 0.016 |
| WikiPathways | Endometrial cancer | experimental (any) | 4 | 0.811 | 0.016 |
| WikiPathways | RANKL/RANK (Receptor activator of NFKB (ligand)) Signaling Pathway | experimental (strong) | 5 | 1.161 | 0.017 |
| WikiPathways | Melatonin metabolism and effects | experimental (any) | 3 | 0.438 | 0.017 |
| WikiPathways | miRNA regulation of prostate cancer signaling pathways | experimental (any) | 3 | 0.438 | 0.017 |
| WikiPathways | Extracellular vesicles in the crosstalk of cardiac cells | experimental (strong) | 3 | 0.387 | 0.018 |
| WikiPathways | Inflammatory Response Pathway | experimental (strong) | 3 | 0.387 | 0.018 |
| WikiPathways | IL-10 Anti-inflammatory Signaling Pathway | experimental (any) | 2 | 0.159 | 0.018 |

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|---|---|---|---|---|---|
| WikiPathways | MAPK and NFkB Signalling Pathways Inhibited by Yersinia YopJ | experimental (any) | 2 | 0.159 | 0.018 |
| WikiPathways | Mesodermal Commitment Pathway | experimental (any) | 6 | 1.834 | 0.018 |
| WikiPathways | Non-small cell lung cancer | experimental (any) | 4 | 0.850 | 0.018 |
| WikiPathways | Pathways Affected in Adenoid Cystic Carcinoma | experimental (any) | 4 | 0.837 | 0.018 |
| WikiPathways | Wnt Signaling Pathway and Pluripotency | experimental (any) | 5 | 1.315 | 0.018 |
| WikiPathways | Neural Crest Cell Migration during Development | experimental (any) | 3 | 0.465 | 0.019 |
| WikiPathways | Type II interferon signaling (IFNG) | experimental (any) | 3 | 0.465 | 0.019 |

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|---|---|---|---|---|---|
| WikiPathways | BMP Signaling Pathway in Eyelid Development | experimental (strong) | 3 | 0.413 | 0.020 |
| WikiPathways | Canonical and Non-Canonical TGF-B signaling | experimental (strong) | 3 | 0.413 | 0.020 |
| WikiPathways | Fas Ligand (FasL) pathway and Stress induction of Heat Shock Proteins (HSP) regulation | experimental (strong) | 4 | 0.774 | 0.020 |
| WikiPathways | Focal Adhesion | experimental (strong) | 8 | 2.891 | 0.020 |
| WikiPathways | Folate Metabolism | experimental (strong) | 4 | 0.800 | 0.020 |
| WikiPathways | Hedgehog Signaling Pathway | experimental (strong) | 3 | 0.413 | 0.020 |
| WikiPathways | Selective expression of chemokine receptors during T-cell polarization | experimental (strong) | 3 | 0.413 | 0.020 |
| WikiPathways | Selenium Micronutrient Network | experimental (strong) | 4 | 0.800 | 0.020 |

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|---|---|---|---|---|---|
| WikiPathways | TGF-B Signaling in Thyroid Cells for Epithelial-Mesenchymal Transition | experimental (strong) | 3 | 0.413 | 0.020 |
| WikiPathways | G13 Signaling Pathway | experimental (any) | 3 | 0.478 | 0.020 |
| WikiPathways | Photodynamic therapy-induced HIF-1 survival signaling | experimental (any) | 3 | 0.478 | 0.020 |
| WikiPathways | Osteopontin Signaling | experimental (any) | 2 | 0.173 | 0.021 |
| WikiPathways | Selenium Micronutrient Network | experimental (any) | 4 | 0.904 | 0.021 |
| WikiPathways | Cell Cycle | experimental (strong) | 6 | 1.858 | 0.023 |
| WikiPathways | EV release from cardiac cells and their functional effects | experimental (strong) | 2 | 0.155 | 0.023 |
| WikiPathways | Eicosanoid Synthesis | experimental (strong) | 2 | 0.155 | 0.023 |
| WikiPathways | IL-6 signaling pathway | experimental (strong) | 4 | 0.852 | 0.023 |

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|---|---|---|---|---|---|
| WikiPathways | Physiological and Pathological Hypertrophy of the Heart | experimental (strong) | 3 | 0.439 | 0.023 |
| WikiPathways | TFs Regulate miRNAs related to cardiac hypertrophy | experimental (strong) | 2 | 0.155 | 0.023 |
| WikiPathways | Thymic Stromal LymphoPoietin (TSLP) Signaling Pathway | experimental (strong) | 4 | 0.852 | 0.023 |
| WikiPathways | Bladder Cancer | experimental (any) | 3 | 0.518 | 0.023 |
| WikiPathways | ERK Pathway in Huntington's Disease | experimental (any) | 2 | 0.186 | 0.023 |
| WikiPathways | H19 action Rb-E2F1 signaling and CDK-Beta-catenin activity | experimental (any) | 2 | 0.186 | 0.023 |
| WikiPathways | IL-5 Signaling Pathway | experimental (any) | 3 | 0.518 | 0.023 |
| WikiPathways | Neural Crest Cell Migration in Cancer | experimental (any) | 3 | 0.505 | 0.023 |

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|---|---|---|---|---|---|
| WikiPathways | ncRNAs involved in STAT3 signaling in hepatocellular carcinoma | experimental (any) | 2 | 0.186 | 0.023 |
| WikiPathways | Corticotropin-releasing hormone signaling pathway | experimental (strong) | 5 | 1.342 | 0.024 |
| WikiPathways | Cardiac Progenitor Differentiation | experimental (strong) | 4 | 0.878 | 0.025 |
| WikiPathways | Wnt Signaling | experimental (any) | 5 | 1.475 | 0.025 |
| WikiPathways | Regulation of Actin Cytoskeleton | experimental (strong) | 6 | 1.91 | 0.026 |
| WikiPathways | Melatonin metabolism and effects | experimental (strong) | 3 | 0.490 | 0.027 |
| WikiPathways | Gene regulatory network modelling somitogenesis | experimental (strong) | 2 | 0.181 | 0.028 |
| WikiPathways | Pathways Regulating Hippo Signaling | experimental (strong) | 5 | 1.42 | 0.028 |
| WikiPathways | Hedgehog Signaling Pathway | experimental (any) | 3 | 0.558 | 0.028 |

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|---|---|---|---|---|---|
| WikiPathways | Structural Pathway of Interleukin 1 (IL-1) | experimental (strong) | 4 | 0.929 | 0.029 |
| WikiPathways | Integrated Cancer Pathway | experimental (any) | 3 | 0.571 | 0.029 |
| WikiPathways | Role of Osx and miRNAs in tooth development | experimental (any) | 2 | 0.213 | 0.029 |
| WikiPathways | Androgen receptor signaling pathway | predicted (union) | 47 | 31.24 | 0.030 |
| WikiPathways | MECP2 and Associated Rett Syndrome | predicted (union) | 35 | 21.87 | 0.030 |
| WikiPathways | G13 Signaling Pathway | experimental (strong) | 3 | 0.516 | 0.030 |
| WikiPathways | Aryl Hydrocarbon Receptor | experimental (any) | 3 | 0.585 | 0.031 |
| WikiPathways | Adipogenesis | experimental (any) | 5 | 1.581 | 0.032 |
| WikiPathways | Alzheimers Disease | experimental (strong) | 4 | 0.981 | 0.034 |
| WikiPathways | Pathogenic Escherichia coli infection | experimental (strong) | 3 | 0.542 | 0.034 |
| WikiPathways | Alzheimers Disease | experimental (any) | 4 | 1.076 | 0.034 |

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|---|---|---|---|---|---|
| WikiPathways | Eicosanoid Synthesis | experimental (any) | 2 | 0.239 | 0.034 |
| WikiPathways | Regulation of Microtubule Cytoskeleton | experimental (any) | 3 | 0.611 | 0.034 |
| WikiPathways | Differentiation Pathway | experimental (any) | 3 | 0.624 | 0.035 |
| WikiPathways | ncRNAs involved in Wnt signaling in hepatocellular carcinoma | experimental (any) | 4 | 1.09 | 0.035 |
| WikiPathways | Oncostatin M Signaling Pathway | experimental (strong) | 5 | 1.523 | 0.036 |
| WikiPathways | Epithelial to mesenchymal transition in colorectal cancer | experimental (strong) | 7 | 2.762 | 0.039 |
| WikiPathways | Lung fibrosis | experimental (strong) | 4 | 1.032 | 0.039 |
| WikiPathways | Wnt Signaling Pathway | experimental (any) | 3 | 0.651 | 0.039 |
| WikiPathways | Pathogenic Escherichia coli infection | experimental (any) | 3 | 0.664 | 0.041 |
| WikiPathways | Retinoblastoma Gene in Cancer | experimental (any) | 4 | 1.156 | 0.041 |

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|---|---|---|---|---|---|
| WikiPathways | IL-10 Anti-inflammatory Signaling Pathway | experimental (strong) | 2 | 0.232 | 0.043 |
| WikiPathways | Role Altered Glycolysation of MUC1 in Tumour Microenvironment | experimental (strong) | 2 | 0.232 | 0.043 |
| WikiPathways | Cancer immunotherapy by PD-1 blockade | experimental (any) | 2 | 0.279 | 0.043 |
| WikiPathways | Canonical and Non-canonical Notch signaling | experimental (any) | 2 | 0.279 | 0.043 |
| WikiPathways | Cardiac Hypertrophic Response | experimental (any) | 3 | 0.678 | 0.043 |
| WikiPathways | ErbB Signaling Pathway | experimental (any) | 4 | 1.183 | 0.043 |
| WikiPathways | Myometrial Relaxation and Contraction Pathways | experimental (any) | 5 | 1.754 | 0.043 |
| WikiPathways | Neovascularisation processes | experimental (any) | 2 | 0.279 | 0.043 |
| WikiPathways | Ciliary landscape | experimental (strong) | 4 | 1.084 | 0.044 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| WikiPathways | MAPK Signaling Pathway | experimental (strong) | 8 | 3.51 | 0.044 |
| WikiPathways | Mammary gland development pathway - Pregnancy and lactation (Stage 3 of 4) | experimental (strong) | 3 | 0.619 | 0.044 |
| WikiPathways | Resistin as a regulator of inflammation | experimental (strong) | 3 | 0.619 | 0.044 |
| WikiPathways | Breast cancer pathway | experimental (strong) | 7 | 2.891 | 0.045 |
| WikiPathways | IL-1 signaling pathway | experimental (strong) | 4 | 1.11 | 0.045 |
| WikiPathways | DNA Damage Response | experimental (strong) | 4 | 1.136 | 0.048 |
| WikiPathways | DNA IR-Double Strand Breaks (DSBs) and cellular response via ATM | experimental (any) | 3 | 0.731 | 0.050 |
| WikiPathways | Estrogen signaling pathway | experimental (any) | 2 | 0.306 | 0.050 |

**Supplementary Table 1b**

**Supplementary Table 1**: A) Pathways influenced by miR148-5p according to miRPathDB; B) Pathways influenced by miR146-5p according to miRPathDB.

| gene_id | A2780M1 | A2780M2 | A2780M3 | A2780C1 | A2780C2 | A2780C3 | A2780M | A2780C |
|---|---|---|---|---|---|---|---|---|
| ENSG00000106366 | 20.03857093 | 9.785884864 | 20.99019155 | 188.2531575 | 111.05448 | 128.7540793 | 16.93821578 | 142.6872389 |
| ENSG00000125740 | 52.10028442 | 18.48444919 | 34.63381606 | 217.3644705 | 227.1568909 | 204.9764942 | 35.07284989 | 216.4992852 |
| ENSG00000269466 | 19.03664238 | 3.261961621 | 3.148528733 | 95.09695585 | 15.14379272 | 46.35146855 | 8.482377579 | 52.19740571 |
| ENSG00000148677 | 38.07328477 | 31.53229567 | 40.93087352 | 116.4452521 | 222.10896 | 237.9375385 | 36.84548466 | 192.1639169 |
| ENSG00000163545 | 25.04821366 | 42.40550108 | 44.07940226 | 155.2603361 | 198.5519491 | 202.916429 | 37.17770567 | 185.576238 |
| ENSG00000184216 | 1349.597752 | 1594.011912 | 1183.846803 | 5234.21408 | 4718.974077 | 4669.137932 | 1375.818823 | 4874.108696 |
| ENSG00000126768 | 349.6730627 | 339.2440086 | 504.8141068 | 1205.208359 | 1358.734736 | 1623.331432 | 397.9103927 | 1395.758176 |
| ENSG00000073756 | 186.3587097 | 223.9880313 | 282.3180764 | 827.7316667 | 829.5433126 | 694.2419956 | 230.8882724 | 783.8389916 |
| ENSG00000126903 | 348.6711342 | 384.9114713 | 362.0808043 | 1038.303498 | 1104.655547 | 1370.973436 | 365.2211366 | 1171.310827 |
| ENSG00000128564 | 1372.642109 | 1675.560953 | 1260.461003 | 4888.759832 | 4042.551336 | 4726.819759 | 1436.221355 | 4552.710309 |
| ENSG00000183092 | 13.0250711 | 21.74641081 | 14.69313409 | 75.68941384 | 42.90741272 | 32.9610443 | 16.48820533 | 50.51929029 |
| ENSG00000178878 | 11.02121401 | 26.09569297 | 13.64362451 | 52.40036343 | 42.90741272 | 55.62176226 | 16.92017716 | 50.30984613 |
| ENSG00000139572 | 35.06749913 | 27.18301351 | 14.69313409 | 127.1194002 | 51.3206309 | 50.47159908 | 25.64788224 | 76.30387672 |
| ENSG00000143257 | 14.02699965 | 26.09569297 | 18.8911724 | 58.22262603 | 53.00327454 | 55.62176226 | 19.67128834 | 55.61588761 |
| ENSG00000177679 | 44.08485605 | 40.23086 | 30.43577775 | 131.0009086 | 70.67103271 | 111.2435245 | 38.25049793 | 104.3051553 |
| ENSG00000196747 | 16.03085674 | 30.44497513 | 27.28724902 | 98.00808715 | 35.33551636 | 66.95212123 | 24.58769363 | 66.76524158 |
| ENSG00000174827 | 133.2564967 | 102.2081308 | 117.5450727 | 370.6840524 | 268.38166 | 320.3401493 | 117.6699001 | 319.8019539 |
| ENSG00000198959 | 36.06942767 | 18.48444919 | 20.99019155 | 93.15620165 | 43.74873454 | 63.86202333 | 25.18135614 | 66.92231984 |
| ENSG00000135097 | 17.03278529 | 33.70693675 | 18.8911724 | 68.89677414 | 47.95534363 | 65.9220886 | 23.21029815 | 60.92473545 |
| ENSG00000100065 | 87.16778355 | 57.62798864 | 91.30733325 | 160.1122216 | 211.1717763 | 242.0576691 | 78.70103515 | 204.4472223 |
| ENSG00000111305 | 76.14656953 | 109.8193746 | 74.51518001 | 257.1499316 | 193.5040181 | 220.4269838 | 86.82704138 | 223.6936445 |
| ENSG00000144867 | 547.0529864 | 700.2344281 | 709.4684744 | 1590.448068 | 1668.341165 | 1773.716196 | 652.251963 | 1677.50181 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| ENSG00000126391 | 516.99513 | 576.2798864 | 504.8141068 | 1564.247886 | 1304.89014 | 1238.099226 | 532.6963744 | 1369.079084 |
| ENSG00000153832 | 79.15235517 | 41.31818054 | 27.28724902 | 115.474875 | 112.7371236 | 147.2946667 | 49.25259491 | 125.1688884 |
| ENSG00000213123 | 23.04435657 | 31.53229567 | 17.84166282 | 60.16338023 | 53.84459635 | 67.98215387 | 24.13943835 | 60.66337682 |
| ENSG00000272405 | 29.05592785 | 39.14353946 | 25.18822986 | 111.5933666 | 67.30574544 | 55.62176226 | 31.12923239 | 78.17362475 |
| ENSG00000210195 | 57.10992715 | 119.6052594 | 116.4955631 | 226.0978644 | 211.1717763 | 298.709464 | 97.73691657 | 245.3263682 |
| ENSG00000128342 | 160.3085674 | 101.1208103 | 55.62400761 | 352.2468875 | 190.9800527 | 246.1777996 | 105.6844618 | 263.1349133 |
| ENSG00000108932 | 54.10414151 | 23.92105189 | 29.38626817 | 102.8599727 | 81.60821635 | 80.34254548 | 35.80382052 | 88.27024483 |
| ENSG00000166881 | 1028.980617 | 936.1829853 | 1019.0738 | 2612.255155 | 2484.423329 | 2212.510099 | 994.7458008 | 2436.396194 |
| ENSG00000124641 | 244.4705653 | 271.8301351 | 255.0308273 | 688.9677414 | 567.8922272 | 630.3799722 | 257.1105093 | 629.0799802 |
| ENSG00000167264 | 126.2429969 | 289.2272638 | 207.8028964 | 469.6625166 | 468.6162526 | 575.7882426 | 207.757719 | 504.689004 |
| ENSG00000119878 | 116.2237114 | 134.827747 | 116.4955631 | 259.0906858 | 319.7022909 | 312.0998882 | 122.5156738 | 296.9642883 |
| ENSG00000159388 | 533.0259867 | 346.8552524 | 449.1900992 | 1588.507314 | 799.2557271 | 831.2363359 | 443.0237794 | 1072.999792 |
| ENSG00000179388 | 130.250711 | 46.75478324 | 59.82204592 | 193.105043 | 192.6626963 | 187.4659395 | 78.9425134 | 191.0778929 |
| ENSG00000151790 | 84.16199791 | 60.88995027 | 48.27744057 | 120.3267605 | 187.6147654 | 155.5349278 | 64.44312958 | 154.4921512 |
| ENSG00000172331 | 144.2777107 | 101.1208103 | 139.5847738 | 270.735211 | 333.1634399 | 318.280084 | 128.3277649 | 307.3929117 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| ENSG00000205583 | 114.2198543 | 67.41387351 | 44.07940226 | 262.0018171 | 70.67103271 | 203.9464616 | 75.23771002 | 178.8731038 |
| ENSG00000186280 | 50.09642733 | 40.23086 | 31.48528733 | 128.0897773 | 79.08425089 | 81.37257811 | 40.60419155 | 96.18220209 |
| ENSG00000101605 | 38.07328477 | 53.27870648 | 46.17842141 | 94.12657875 | 106.8478709 | 112.2735571 | 45.84347089 | 104.4160023 |
| ENSG00000137801 | 50.09642733 | 36.96889838 | 37.78234479 | 117.4156292 | 94.22804362 | 73.13231704 | 41.61589016 | 94.92532994 |
| ENSG00000171246 | 41.07907041 | 41.31818054 | 24.13872028 | 97.03771005 | 72.35367635 | 73.13231704 | 35.51199041 | 80.84123448 |
| ENSG00000148943 | 624.2014845 | 538.2236675 | 421.9028502 | 1281.86815 | 1304.048818 | 1017.672243 | 528.1093341 | 1201.196403 |
| ENSG00000169093 | 382.7367048 | 449.0633832 | 420.8533406 | 879.1616531 | 826.1780253 | 1115.525343 | 417.5511429 | 940.2883405 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| ENSG00000073969 | 551.0607006 | 578.4545275 | 544.6954708 | 1324.564742 | 1198.883591 | 1244.279422 | 558.070233 | 1255.909252 |
| ENSG00000147509 | 170.3278529 | 157.6614784 | 118.5945823 | 338.6616081 | 301.1932109 | 365.6615852 | 148.8613045 | 335.1721347 |
| ENSG00000086506 | 128.246854 | 148.962914 | 121.743111 | 250.3572919 | 292.7799927 | 354.3312262 | 132.984293 | 299.1561703 |
| ENSG00000168917 | 180.3471384 | 216.3767876 | 156.3769271 | 412.4102677 | 414.7716563 | 415.1031516 | 184.366951 | 414.0950252 |
| ENSG00000142871 | 1328.557253 | 1412.429382 | 1397.946757 | 2967.413173 | 3240.771643 | 3089.06787 | 1379.644464 | 3099.084229 |
| ENSG00000197903 | 857.6508358 | 725.2428005 | 665.3890722 | 2061.080961 | 1536.25364 | 1454.40608 | 749.4275695 | 1683.91356 |
| ENSG00000006327 | 851.6392645 | 853.5466243 | 661.1910339 | 1867.005541 | 1645.625476 | 1742.815217 | 788.7923075 | 1751.815412 |
| ENSG00000064199 | 39.07521331 | 56.5406681 | 104.9509578 | 163.0233529 | 132.0875254 | 148.3246993 | 66.85561306 | 147.8118592 |
| ENSG00000144455 | 193.3722095 | 223.9880313 | 235.0901454 | 491.0108129 | 444.2179199 | 489.2655013 | 217.4834621 | 474.8314114 |
| ENSG00000177721 | 128.246854 | 155.4868373 | 99.70340987 | 318.283689 | 237.2527527 | 281.1989092 | 127.812367 | 278.9117836 |
| ENSG00000059804 | 1068.055831 | 1263.466468 | 1305.589914 | 2724.818898 | 2606.414992 | 2589.502043 | 1212.370738 | 2640.245311 |
| ENSG00000135698 | 354.6827055 | 353.3791756 | 342.1401223 | 653.0637886 | 748.776418 | 883.7680003 | 350.0673345 | 761.8694023 |
| ENSG00000128045 | 32.06171349 | 31.53229567 | 30.43577775 | 63.07451153 | 67.30574544 | 74.16234967 | 31.3432623 | 68.18086888 |
| ENSG00000124171 | 360.6942767 | 214.2021465 | 221.4465209 | 612.3079504 | 577.1467672 | 542.8271983 | 265.447648 | 577.4273053 |
| ENSG00000078967 | 103.1986403 | 164.1854016 | 172.1195707 | 298.876147 | 300.351889 | 351.2411283 | 146.5012042 | 316.8230548 |
| ENSG00000166670 | 4859.353451 | 4741.804877 | 4647.228409 | 10154.99636 | 9572.559646 | 10960.57726 | 4749.462246 | 10229.37775 |
| ENSG00000139921 | 1054.028831 | 801.3552383 | 797.6272789 | 1658.374465 | 2003.187249 | 2007.533604 | 884.3371161 | 1889.698439 |
| ENSG00000143333 | 633.2188414 | 653.4796448 | 669.5871105 | 1465.269422 | 1224.123245 | 1465.736439 | 652.0951989 | 1385.043035 |
| ENSG00000137331 | 514.9912729 | 379.4748686 | 431.3484364 | 1231.408541 | 721.0127981 | 859.0472171 | 441.9381926 | 937.1561852 |
| ENSG00000082153 | 4125.941755 | 3054.283398 | 3295.460074 | 7072.108308 | 7693.046704 | 7259.670007 | 3491.895075 | 7341.60834 |
| ENSG00000275064 | 85.16392645 | 90.24760486 | 101.802429 | 150.4084506 | 199.3932709 | 229.6972775 | 92.40465344 | 193.166333 |
| ENSG00000124380 | 273.5264932 | 257.6949681 | 270.773471 | 520.1221259 | 577.1467672 | 563.427851 | 267.3316441 | 553.5655813 |
| ENSG00000087085 | 73.1407839 | 65.23923243 | 71.36665127 | 137.7935483 | 138.8181 | 157.5949931 | 69.91555587 | 144.7355471 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| ENSG00000171174 | 48.09257023 | 54.36602702 | 55.62400761 | 103.8303498 | 115.2610891 | 106.0933613 | 52.69420162 | 108.3949334 |
| ENSG00000237036 | 45.08678459 | 84.81100216 | 62.97057465 | 157.2010903 | 116.1024109 | 122.5738835 | 64.2894538 | 131.9591282 |
| ENSG00000120885 | 1030.984474 | 1283.038238 | 1360.164413 | 2162.00018 | 2587.905912 | 2717.226089 | 1224.729042 | 2489.044061 |
| ENSG00000116675 | 40.07714186 | 43.49282162 | 54.57449803 | 115.474875 | 89.18011271 | 75.19238231 | 46.04815384 | 93.28245666 |
| ENSG00000137720 | 244.4705653 | 213.1148259 | 225.6445592 | 424.0547929 | 414.7716563 | 534.5869372 | 227.7433168 | 457.8044621 |
| ENSG00000170345 | 102.1967117 | 150.0502346 | 187.8622144 | 196.9865514 | 307.9237854 | 378.0219768 | 146.7030536 | 294.3107712 |

| log2Fold change | pvalue | padj | gene_name | gene_chr | gene_start | gene_end | gene_strand | gene_lenght |
|---|---|---|---|---|---|---|---|---|
| -3.0687294 | 1.38E- 14 | 4.95E-12 | SERPINE1 | 7 | 101127089 | 101139266 | + | 3190 |
| -2.6199490 | 6.39E- 16 | 3.06E-13 | FOSB | 19 | 45467995 | 45475179 | + | 5553 |
| -2.6091492 | 0.000532753 | 0.009513864 | H3.Y | 5 | 17654870 | 17655847 | | 978 |
| -2.3820226 | 1.53E- 12 | 4.31E-10 | ANKRD1 | 10 | -90912096 | 90921276 | - | 1979 |
| -2.3229827 | 1.05E- 13 | 3.32E-11 | NUAK2 | 1 | 205302059 | 205321791 | - | 3441 |
| -1.8250487 | 6.5E- 50 | 4.21E-46 | IRAK1 | X | 154010500 | 154019980 | | 4001 |
| -1.8103241 | 5.74E- 26 | 8.26E-23 | TIMM17B | X | -48893447 | 48898143 | - | 2562 |
| -1.7644604 | 5.38E- 23 | 5.8E-20 | PTGS2 | 1 | 186671791 | 186680427 | - | 5269 |
| -1.6811286 | 3.08E- 29 | 6.65E-26 | SLC10A3 | X | 154487306 | 154490690 | - | 2247 |
| -1.6645273 | 1.09E- 38 | 4.7E-35 | VGF | 7 | 101162509 | 101165593 | - | 2704 |
| -1.6182851 | 0.002378216 | 0.028749541 | BEGAIN | 14 | 100537147 | 100587413 | | 7878 |
| -1.5756383 | 0.002203826 | 0.027278138 | APOLD1 | 12 | -12725917 | 12829975 | + | 7243 |
| -1.5705228 | 0.001474358 | 0.020029914 | GPR84 | 12 | 54362445 | 54364487 | - | 2043 |
| -1.5026547 | 0.001316283 | 0.018564175 | NR1I3 | 1 | 161229666 | 161238302 | | 3305 |
| -1.4442954 | 0.000103115 | 0.002730455 | SRRM3 | 7 | -76201900 | 76287288 | + | 6873 |
| -1.4410503 | 0.003198062 | 0.035602156 | HIST1H2AI | 6 | 27808199 | 27808701 | + | 503 |
| -1.4402894 | 1.1E- 10 | 2.13E-08 | PDZK1 | 1 | 145670852 | 145708148 | | 2480 |
| -1.4046128 | 0.002703522 | 0.03173391 | TGM2 | 20 | -38127387 | 38166578 | - | 8036 |
| -1.3940773 | 0.002509412 | 0.030054909 | MSI1 | 12 | 120341330 | 120369180 | | 3090 |
| -1.3754498 | 0.000000879 | 0.0000552 | CARD10 | 22 | -37490362 | 37519542 | | 5652 |
| -1.3661769 | 0.000000139 | 0.0000109 | GSG1 | 12 | -13083560 | 13103683 | - | 3005 |
| -1.3632873 | 4.66E- 24 | 6.03E-21 | SRPRB | 3 | 133784033 | 133825772 | + | 4180 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| -1.3620884 | 1.05E-22 | 1.04E-19 | FRMD8 | 11 | 65386599 | 65413525 | + | 4091 |
| -1.3415552 | 0.000386745 | 0.007540949 | FBXO36 | 2 | 229922302 | 230013109 | + | 3945 |
| -1.3298308 | 0.002600694 | 0.030778054 | TCTEX1D2 | 3 | 196291219 | 196318299 | - | 1246 |
| -1.3297772 | 0.001663581 | 0.021955342 | AL365181.3 | 1 | 156641666 | 156644887 | - | 3222 |
| -1.3288589 | 0.00000389 | 0.000193157 | MT-TT | MT | 15888 | 15953 | + | 66 |
| -1.3137714 | 0.0000607 | 0.001809691 | LIF | 22 | 30240447 | 30246851 | | 3969 |
| -1.2976076 - | 0.001174506 | 0.017104982 | SLC16A6 | 17 | -68267026 | 68291267 | | 4061 |
| 1.2923317 | 7.19E-29 | 1.33E-25 | NEMP1 | 12 | -57055643 | 57088063 | | 5708 |
| -1.2907173 | 1.4E-15 | 6.46E-13 | MED20 | 6 | -41905354 | 41921139 | | 3278 |
| -1.2818565 | 0.000000114 | 0.00000918 | DUS2 | 16 | -67987746 | 68079320 | + | 4472 |
| -1.2783763 | 2.5E-09 | 0.000000356 | CRIPT | 2 | 46616416 | 46625742 | + | 2561 |
| -1.2759139 | 0.000620261 | 0.010650553 | BTG2 | 1 | 203305491 | 203309602 | + | 2757 |
| -1.2720023 | 0.000132265 | 0.003305853 | EGR3 | 8 | 22687659 | 22693302 | - | 4855 |
| -1.2610894 | 0.0000546 - | 0.001704637 | TDO2 | 4 | 155854738 | 155920406 | + | 5264 |
| 1.2593021 | 1.44E-08 | 0.00000168 | BPGM | 7 | 134646808 | 134679813 | + | 2539 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| -1.246038584 | 0.002691097 | 0.031616727 | STAG3L1 | 7 | 75359194 | 75395383 | + | 2094 |
| -1.2421171 | 0.00087708 | 0.013984667 | KDM4D | 11 | 94973681 | 94999518 | + | 2978 |
| -1.1892037 | 0.000330334 | 0.006756454 | MYOM1 | 18 | 3066807 | 3220108 | - | 6574 |
| -1.1888078 | 0.000994152 | 0.01521429 | THBS1 | 15 | 39581079 | 39599466 | + | 9158 |
| -1.1861457 | 0.002337216 | 0.028505108 | NPTX1 | 17 | 80467148 | 80477843 | | 6703 |
| -1.1856302 | 4.4E-13 | 1.3E-10 | LIN7C | 11 | -27494576 | 27506773 | - | 4688 |
| -1.1707717 | 1.03E-13 | 3.32E-11 | ASMTL | X | 1403139 | 1453762 | - | 3506 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| -1.1701657 | 6.07E-21 | 5.24E-18 | NSF | 17 | 46590669 | 46757464 | + | 5005 |
| -1.1696220 | 0.000000038 | 0.00000373 | RGS20 | 8 | 53851808 | 53959303 | + | 3192 |
| -1.1695742 | 0.000000138 | 0.0000109 | HBQ1 | 16 | 180453 | 181181 | + | 536 |
| -1.1681012 | 6.87E-10 - | 0.000000111 | SLC35G2 | 3 | 136818647 | 136855892 | + | 4287 |
| 1.1677902 | 1.1E-29 | 2.86E-26 | CYR61 | 1 | 85580761 | 85583962 | + | 2455 |
| -1.1676100 | 5.43E-14 | 1.85E-11 | HIST1H2BK | 6 | 27146418 | 27146798 | - | 381 |
| -1.1509348 | 7.67E-18 | 4.97E-15 | TNFRSF12A | 16 | 3018445 | 3022383 | + | 1848 |
| -1.1452016 | 0.000919851 | 0.014453051 | SPA17 | 11 | 124673798 | 124697518 | + | 5205 |
| -1.1266174 | 9.78E-11 | 1.95E-08 | SUMF1 | 3 | 3700814 | 4467281 | - | 6952 |
| -1.1255765 | 0.00000192 | 0.000107088 | ANXA2R | 5 | 43039081 | 43043170 | - | 2386 |
| -1.1231241 | 2.09E-22 | 1.94E-19 | SLC2A3 | 12 | 7919230 | 7936275 | - | 6159 |
| -1.1214660 | 1.8E-12 | 4.95E-10 | MPHOSPH6 | 16 | 82147798 | 82170226 | | 2190 |
| -1.1206196 | 0.004149671 | 0.042772286 | RASL11B | 4 | -52862290 | 52866835 | + | 2472 |
| -1.1198856 | 3.62E-08 | 0.00000363 | PARD6B | 20 | 50731544 | 50756795 | + | 4726 |
| -1.1137317 - | 0.00000141 | 0.000082 | UBE2D4 | 7 | 43926438 | 43956136 | + | 4713 |
| 1.1067726 | 2.13E-31 | 6.88E-28 | MMP10 | 11 | 102770503 | 102780628 | | 1758 |
| -1.0950977 | 1.34E-14 | 4.95E-12 | TMX1 | 14 | -51240162 | 51257546 | + | 4499 |
| -1.0863051 | 3.76E-17 | 2.12E-14 | RGS16 | 1 | 182598623 | 182604408 | | 2427 |
| -1.0834327 | 1.94E-08 - | 0.00000213 | IER3 | 6 | -30743199 | 30744554 | - | 1356 |
| 1.0719527 | 3.29E-19 | 2.37E-16 | BZW1 | 2 | 200810594 | 200827338 | + | 8085 |
| -1.063717742 | 0.0000503 | 0.001611034 | AC239860.1 | 1 | 145509047 | 145520594 | + | 1270 |
| -1.0501227 | 3.44E-11 | 7.19E-09 | SNRNP27 | 2 | 69893560 | 69905575 | + | 2275 |
| -1.0484821 | 0.000136312 | 0.003374435 | ACHE | 7 | 100889994 | 100896974 | - | 3783 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| -1.0418827 | 0.000845113 | 0.013660029 | RBKS | 2 | 27781364 | 27891098 | | 3585 |
| -1.0393409 | 0.001199187 | 0.017375928 | ZEB1-AS1 | 10 | -31206278 | 31320447 | | 3831 |
| -1.0233963 | 4.56E-14 | 1.59E-11 | CLU | 8 | -27596917 | 27615031 | | 6616 |
| -1.0192638 | 0.003889384 | 0.040873262 | DNAJC6 | 1 | -65248219 | 65415869 | + | 6954 |
| -1.0058072 | 3.67E-08 | 0.00000366 | C11orf1 | 11 | 111878935 | 111885975 | + | 3831 |
| -1.0049928 | 0.000272626 | 0.005873025 | FOS | 14 | 75278774 | 75282230 | + | 3238 |

| gene_biotype | tf_family | A2780M1_count | A2780M2_count | A2780M3_count | A2780C1_count | A2780C2_count | A2780C3_count | A2780M1_fpkm |
|---|---|---|---|---|---|---|---|---|
| protein_coding | - | 20 | 9 | 20 | 194 | 132 | 125 | 0.308173016 |
| protein_coding | TF_bZIP | 52 | 17 | 33 | 224 | 270 | 199 | 0.460289393 |
| protein_coding | - | 19 | 3 | 3 | 98 | 18 | 45 | 0.954926714 |
| protein_coding | - | 38 | 29 | 39 | 120 | 264 | 231 | 0.943828526 |
| protein_coding | - | 25 | 39 | 42 | 160 | 236 | 197 | 0.357117089 |
| protein_coding | - | 1347 | 1466 | 1128 | 5394 | 5609 | 4533 | 16.54833641 |
| protein_coding | - | 349 | 312 | 481 | 1242 | 1615 | 1576 | 6.695786511 |
| protein_coding | - | 186 | 206 | 269 | 853 | 986 | 674 | 1.735162057 |
| protein_coding | - | 348 | 354 | 345 | 1070 | 1313 | 1331 | 7.612572962 |
| protein_coding | - | 1370 | 1541 | 1201 | 5038 | 4805 | 4589 | 24.90400395 |
| protein_coding | - | 13 | 20 | 14 | 78 | 51 | 32 | 0.081111545 |
| protein_coding | - | 11 | 24 | 13 | 54 | 51 | 54 | 0.074649946 |
| protein_coding | - | 35 | 25 | 14 | 131 | 61 | 49 | 0.842083144 |
| protein_coding | THR-like | 14 | 24 | 18 | 60 | 63 | 54 | 0.208214931 |
| protein_coding | - | 44 | 37 | 29 | 135 | 84 | 108 | 0.314674557 |
| protein_coding | - | 16 | 28 | 26 | 101 | 42 | 65 | 1.563533872 |
| protein_coding | - | 133 | 94 | 112 | 382 | 319 | 311 | 2.636059791 |
| protein_coding | - | 36 | 17 | 20 | 96 | 52 | 62 | 0.220200281 |
| protein_coding | - | 17 | 31 | 18 | 71 | 57 | 64 | 0.270424315 |
| protein_coding | - | 87 | 53 | 87 | 165 | 251 | 235 | 0.756610556 |
| protein_coding | - | 76 | 101 | 71 | 265 | 230 | 214 | 1.243152514 |
| protein_coding | - | 546 | 644 | 676 | 1639 | 1983 | 1722 | 6.420541501 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| protein_coding | - | 516 | 530 | 481 | 1612 | 1551 | 1202 | 6.19976915 |
| protein_coding | - | 79 | 38 | 26 | 119 | 134 | 143 | 0.984317894 |
| protein_coding | - | 23 | 29 | 17 | 62 | 64 | 66 | 0.907329623 |
| antisense | - | 29 | 36 | 24 | 115 | 80 | 54 | 0.442412876 |
| Mt_tRNA | - | 57 | 110 | 111 | 233 | 251 | 290 | 42.450833 |
| protein_coding | - | 160 | 93 | 53 | 363 | 227 | 239 | 1.981500473 |
| protein_coding | - | 54 | 22 | 28 | 106 | 97 | 78 | 0.653606055 |
| protein_coding | - | 1027 | 861 | 971 | 2692 | 2953 | 2148 | 8.843858305 |
| protein_coding | - | 244 | 250 | 243 | 710 | 675 | 612 | 3.658778966 |
| protein_coding | - | 126 | 266 | 198 | 484 | 557 | 559 | 1.384917958 |
| protein_coding | - | 116 | 124 | 111 | 267 | 380 | 303 | 2.226402635 |
| protein_coding | - | 532 | 319 | 428 | 1637 | 950 | 807 | 9.484843355 |
| protein_coding | zf-C2H2 | 130 | 43 | 57 | 199 | 229 | 182 | 1.316162203 |
| protein_coding | - | 84 | 56 | 46 | 124 | 223 | 151 | 0.784365895 |
| protein_coding | - | 144 | 93 | 133 | 279 | 396 | 309 | 2.787758109 |
| transcribed_unprocessed_pseudogene | - | 114 | 62 | 42 | 270 | 84 | 198 | 2.675983742 |
| protein_coding | - | 50 | 37 | 30 | 132 | 94 | 79 | 0.825278645 |
| protein_coding | - | 38 | 49 | 44 | 97 | 127 | 109 | 0.284124833 |
| protein_coding | - | 50 | 34 | 36 | 121 | 112 | 71 | 0.26836425 |
| protein_coding | - | 41 | 38 | 23 | 100 | 86 | 71 | 0.300656041 |
| protein_coding | - | 623 | 495 | 402 | 1321 | 1550 | 988 | 6.532143852 |
| protein_coding | - | 382 | 413 | 401 | 906 | 982 | 1083 | 5.355582919 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| protein_coding | - | 550 | 532 | 519 | 1365 | 1425 | 1208 | 5.401494078 |
| protein_coding | - | 170 | 145 | 113 | 349 | 358 | 355 | 2.617829367 |
| protein_coding | - | 128 | 137 | 116 | 258 | 348 | 344 | 11.73817221 |
| protein_coding | - | 180 | 199 | 149 | 425 | 493 | 403 | 2.063831887 |
| protein_coding | - | 1326 | 1299 | 1332 | 3058 | 3852 | 2999 | 26.54894845 |
| protein_coding | - | 856 | 667 | 634 | 2124 | 1826 | 1412 | 110.4343262 |
| protein_coding | - | 850 | 785 | 630 | 1924 | 1956 | 1692 | 22.60852635 |
| protein_coding | - | 39 | 52 | 100 | 168 | 157 | 144 | 0.368297838 |
| protein_coding | - | 193 | 206 | 224 | 506 | 528 | 475 | 1.364592067 |
| protein_coding | - | 128 | 143 | 95 | 328 | 282 | 273 | 2.636907084 |
| protein_coding | - | 1066 | 1162 | 1244 | 2808 | 3098 | 2514 | 8.507506649 |
| protein_coding | - | 354 | 325 | 326 | 673 | 890 | 858 | 7.945375809 |
| protein_coding | - | 32 | 29 | 29 | 65 | 80 | 72 | 0.636292506 |
| protein_coding | - | 360 | 197 | 211 | 631 | 686 | 527 | 3.744243462 |
| protein_coding | - | 103 | 151 | 164 | 308 | 357 | 341 | 1.07422457 |
| protein_coding | - | 4850 | 4361 | 4428 | 10465 | 11378 | 10641 | 135.6057686 |
| protein_coding | - | 1052 | 737 | 760 | 1709 | 2381 | 1949 | 11.4935726 |
| protein_coding | - | 632 | 601 | 638 | 1510 | 1455 | 1423 | 12.79978275 |
| protein_coding | - | 514 | 349 | 411 | 1269 | 857 | 834 | 18.63196785 |
| protein_coding | - | 4118 | 2809 | 3140 | 7288 | 9144 | 7048 | 25.03580814 |
| unprocessed_pseudogene | - | 85 | 83 | 97 | 155 | 237 | 223 | 3.289807614 |
| protein_coding | - | 273 | 237 | 258 | 536 | 686 | 547 | 5.898431533 |
| protein_coding | - | 73 | 60 | 68 | 142 | 165 | 153 | 0.948509785 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| protein_coding | - | 48 | 50 | 53 | 107 | 137 | 103 | 0.658123463 |
| antisense | - | 45 | 78 | 60 | 162 | 138 | 119 | 0.57737192 |
| protein_coding | - | 1029 | 1180 | 1296 | 2228 | 3076 | 2638 | 7.64495925 |
| protein_coding | - | 40 | 40 | 52 | 119 | 106 | 73 | 0.282735669 |
| protein_coding | - | 244 | 196 | 215 | 437 | 493 | 519 | 3.130638854 |
| protein_coding | TF_bZIP | 102 | 138 | 179 | 203 | 366 | 367 | 1.548383818 |

| **A2780M2 _fpkm** | **A2780M3 _fpkm** | **A2780C1_fpkm** | **A2780C2_ fpkm** | **A2780C3_ fpkm** |
|---|---|---|---|---|
| 0.149157658 | 0.320665963 | 2.894508081 | 1.687023193 | 1.962168056 |
| 0.161850847 | 0.30394837 | 1.919924118 | 1.982320607 | 1.794495089 |
| 0.162172096 | 0.156890249 | 4.769259356 | 0.750363076 | 2.304042736 |
| 0.774722078 | 1.007934626 | 2.886018903 | 5.438710444 | 5.844980369 |
| 0.599202564 | 0.624278201 | 2.213089764 | 2.796180066 | 2.866806792 |
| 19.37131698 | 14.41962946 | 64.16616891 | 57.15506114 | 56.73277656 |
| 6.438270174 | 9.602393592 | 23.07311283 | 25.69988656 | 30.80306689 |
| 2.066963229 | 2.611184949 | 7.705211286 | 7.629332127 | 6.405434125 |
| 8.329020258 | 7.852891101 | 22.66441035 | 23.823165 | 29.66141425 |
| 30.12934429 | 22.71694217 | 88.67785823 | 72.44768454 | 84.98225319 |
| 0.134217068 | 0.09089199 | 0.471240215 | 0.263931973 | 0.203399965 |
| 0.175180792 | 0.091799099 | 0.354845248 | 0.287071115 | 0.37332936 |
| 0.646942036 | 0.350488055 | 3.051874346 | 1.217304629 | 1.201004362 |
| 0.383913608 | 0.278557332 | 0.864059215 | 0.777153649 | 0.818161741 |
| 0.284609314 | 0.21580684 | 0.934869829 | 0.498276892 | 0.786854228 |
| 2.942956041 | 2.643741055 | 9.556901463 | 3.404231691 | 6.470863562 |
| 2.003871652 | 2.309829343 | 7.331205639 | 5.244170549 | 6.279507441 |
| 0.111841433 | 0.127292736 | 0.568584511 | 0.263816054 | 0.386339072 |
| 0.530391973 | 0.297939152 | 1.09361281 | 0.752062928 | 1.037142344 |
| 0.495755391 | 0.787282598 | 1.389458278 | 1.810545208 | 2.082008893 |
| 1.776931254 | 1.20844649 | 4.197252699 | 3.120478285 | 3.566039654 |
| 8.145229291 | 8.271494142 | 18.66235263 | 19.34123659 | 20.62878913 |

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|---|---|---|---|---|
| 6.849204272 | 6.013525393 | 18.75423171 | 15.45681907 | 14.71268238 |
| 0.509249156 | 0.337085361 | 1.435699911 | 1.384827234 | 1.815122336 |
| 1.230477521 | 0.697821637 | 2.368303554 | 2.094111186 | 2.652422873 |
| 0.590705063 | 0.380977439 | 1.698775636 | 1.012283728 | 0.839237913 |
| 88.11350527 | 86.0186447 | 168.0256967 | 155.0485078 | 220.0244447 |
| 1.238783974 | 0.68298053 | 4.353005798 | 2.331753103 | 3.01532184 |
| 0.286406863 | 0.352645701 | 1.24232892 | 0.973815202 | 0.961786074 |
| 7.974673585 | 8.700592284 | 22.44681931 | 21.09197693 | 18.84374349 |
| 4.032039594 | 3.791498397 | 10.3089188 | 8.395230577 | 9.348874808 |
| 3.144659088 | 2.264524104 | 5.151186646 | 5.077982564 | 6.259316099 |
| 2.559798825 | 2.216802245 | 4.962098744 | 6.04939333 | 5.924475683 |
| 6.117129093 | 7.940000965 | 28.26022614 | 14.04832818 | 14.65728862 |
| 0.468244786 | 0.600480866 | 1.950866547 | 1.923021116 | 1.877150204 |
| 0.562426629 | 0.446946462 | 1.12116498 | 1.727136998 | 1.436408406 |
| 1.936484283 | 2.679183701 | 5.230042546 | 6.358728615 | 6.094143126 |

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|---|---|---|---|---|
| 1.565340208 | 1.025855439 | 6.136924866 | 1.635461834 | 4.734840831 |
| 0.6568569 | 0.515240643 | 2.109662374 | 1.286888634 | 1.328370643 |
| 0.394057964 | 0.342323354 | 0.702272648 | 0.787611097 | 0.830259148 |
| 0.196278173 | 0.201055248 | 0.628852006 | 0.498603346 | 0.388217028 |
| 0.299714743 | 0.175497999 | 0.710059104 | 0.523078701 | 0.530403035 |
| 5.582276251 | 4.385832106 | 13.4115488 | 13.47975194 | 10.55324967 |
| 6.227760013 | 5.849867282 | 12.29928897 | 11.41924474 | 15.46797338 |

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|---|---|---|---|---|
| 5.61954663 | 5.303674084 | 12.98052593 | 11.60776447 | 12.08592024 |
| 2.401589899 | 1.810627504 | 5.203867903 | 4.572544587 | 5.569065702 |
| 13.51292935 | 11.06895831 | 22.90965957 | 26.46989748 | 32.13738415 |
| 2.454106025 | 1.777650328 | 4.718447921 | 4.688471072 | 4.707262679 |
| 27.97379471 | 27.75021043 | 59.28566615 | 63.96944562 | 61.17047326 |
| 92.55387089 | 85.1094599 | 265.3342151 | 195.3950703 | 185.5780437 |
| 22.45750053 | 17.43621176 | 49.55264263 | 43.15237355 | 45.84745818 |
| 0.528173173 | 0.982636334 | 1.536215941 | 1.229749695 | 1.385347194 |
| 1.566574979 | 1.647979508 | 3.464212089 | 3.096434974 | 3.421375313 |
| 3.168540969 | 2.036417021 | 6.54285241 | 4.818551156 | 5.729399145 |
| 9.974465964 | 10.33055677 | 21.69954456 | 20.50732501 | 20.43957873 |
| 7.845723072 | 7.613547079 | 14.62630646 | 16.56851926 | 19.61824005 |
| 0.620216421 | 0.600016349 | 1.251493533 | 1.319408646 | 1.458481421 |
| 2.203769852 | 2.283506701 | 6.354763047 | 5.91790792 | 5.583850333 |
| 1.693843322 | 1.77975393 | 3.110405393 | 3.08822249 | 3.623045686 |
| 131.1477804 | 128.8256356 | 283.3244676 | 263.8668689 | 303.0961666 |
| 8.660545017 | 8.639948453 | 18.07964043 | 21.57651042 | 21.69265539 |
| 13.09177173 | 13.44511294 | 29.61221476 | 24.44167821 | 29.35972578 |
| 13.60690856 | 15.50228385 | 44.54158344 | 25.76670809 | 30.79805089 |
| 18.36815112 | 19.86383853 | 42.90343445 | 46.10988066 | 43.65185886 |
| | | | | |
| 3.455159498 | 3.906443664 | 5.808870527 | 7.608208926 | 8.792614111 |
| 5.507578219 | 5.800318709 | 11.21365288 | 12.2936408 | 12.03989769 |
| 0.838510756 | 0.9193611 | 1.786552251 | 1.778219662 | 2.025218849 |

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|---|---|---|---|---|
| 0.737351509 | 0.756136603 | 1.420555929 | 1.55800631 | 1.438682417 |
| 1.076406172 | 0.801037137 | 2.012642235 | 1.468604111 | 1.555434332 |
| 9.429317069 | 10.01896956 | 16.02815042 | 18.95521172 | 19.96623442 |
| 0.30410183 | 0.382456644 | 0.814471692 | 0.621453995 | 0.525660138 |
| 2.70481551 | 2.870383073 | 5.429164547 | 5.246534975 | 6.783785028 |
| 2.253180431 | 2.82741618 | 2.983890714 | 4.608313817 | 5.675525654 |

**Supplementary Table 2**: Decreased differential expression of genes in A2780 cells transfected with mir146 (A2780M) and A2780 cells transfected with miRctrl (A2780C).

| **Transcript Id** | Gene Id(name) | **Mirna Name** | **miTG score** |
|---|---|---|---|
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-1825 | 0.997635826 |
| UTR3 | 7:100780748-100780761 | 0.007831621 | |
| UTR3 | 7:100781232-100781251 | 0.006438778 | |
| UTR3 | 7:100782381-100782388 | 0.0986726 | |
| UTR3 | 7:100777125-100777131 | 0.013094968 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-5011-5p | 0.994960038 |
| UTR3 | 7:100782182-100782188 | 0.010920577 | |
| UTR3 | 7:100782183-100782190 | 0.019426852 | |
| UTR3 | 7:100782207-100782213 | 0.010762316 | |
| UTR3 | 7:100782208-100782214 | 0.008821141 | |
| UTR3 | 7:100782230-100782236 | 0.009068804 | |

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|---|---|---|---|
| UTR3 | 7:100782231-100782238 | 0.01855238 |  |
| UTR3 | 7:100782235-100782242 | 0.019536452 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-2110 | 0.988454941 |
| UTR3 | 7:100781238-100781265 | 0.001791457 |  |
| UTR3 | 7:100781319-100781346 | 0.003564891 |  |
| UTR3 | 7:100781453-100781477 | 0.001918674 |  |
| UTR3 | 7:100781888-100781905 | 0.076159462 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-548az-5p | 0.96870096 |
| UTR3 | 7:100780824-100780847 | 0.007260622 |  |
| UTR3 | 7:100781092-100781112 | 0.004870355 |  |
| UTR3 | 7:100782458-100782474 | 0.054673259 |  |

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|---|---|---|---|
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-548t-5p | 0.968445299 |
| UTR3 | 7:100780830-100780847 | 0.00727993 | |
| UTR3 | 7:100781085-100781112 | 0.004713773 | |
| UTR3 | 7:100782458-100782474 | 0.054673259 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6875-3p | 0.966975366 |
| UTR3 | 7:100780768-100780792 | 0.01135348 | |
| UTR3 | 7:100780785-100780798 | 0.009062388 | |
| UTR3 | 7:100781190-100781216 | 0.01058925 | |
| UTR3 | 7:100781429-100781443 | 0.024454929 | |
| UTR3 | 7:100782523-100782532 | 0.010437929 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-1277-5p | 0.96565924 |

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|---|---|---|---|
| UTR3 | 7:100782182-100782193 | 0.025271695 | |
| UTR3 | 7:100782197-100782216 | 0.01619347 | |
| UTR3 | 7:100782230-100782245 | 0.023771843 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4795-3p | 0.956862971 |
| UTR3 | 7:100781549-100781571 | 0.015891226 | |
| UTR3 | 7:100782017-100782042 | 0.009771618 | |
| UTR3 | 7:100782214-100782223 | 0.005794902 | |
| UTR3 | 7:100782505-100782511 | 0.029902483 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-5681a | 0.956059381 |
| UTR3 | 7:100781201-100781226 | 0.049508561 | |
| UTR3 | 7:100782351-100782365 | 0.006065312 | |

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|---|---|---|---|
| UTR3 | 7:100782351-100782369 | 0.005470958 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-190a-3p | 0.953698689 |
| UTR3 | 7:100782182-100782188 | 0.009644948 |  |
| UTR3 | 7:100782184-100782190 | 0.008130071 |  |
| UTR3 | 7:100782196-100782213 | 0.009066539 |  |
| UTR3 | 7:100782219-100782236 | 0.008427183 |  |
| UTR3 | 7:100782219-100782238 | 0.008087967 |  |
| UTR3 | 7:100782229-100782240 | 0.008681286 |  |
| UTR3 | 7:100782229-100782242 | 0.008111133 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-627-3p | 0.9519028 |
| UTR3 | 7:100780779-100780796 | 0.054750156 |  |

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| UTR3 | 7:100780840-100780855 | 0.004746218 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-942-5p | 0.943661625 |
| UTR3 | 7:100780756-100780780 | 0.006275233 | |
| UTR3 | 7:100780819-100780834 | 0.042528151 | |
| UTR3 | 7:100780927-100780949 | 0.007966047 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-583 | 0.935994236 |
| UTR3 | 7:100780801-100780818 | 0.007716477 | |
| UTR3 | 7:100781586-100781600 | 0.002062419 | |
| UTR3 | 7:100781724-100781733 | 0.002255503 | |
| UTR3 | 7:100782163-100782177 | 0.003216421 | |
| UTR3 | 7:100782321-100782346 | 0.035041481 | |

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| UTR3 | 7:100782340-100782351 | 0.003384174 | |
| UTR3 | 7:100780323-100780344 | 0.015866171 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-548ah-5p | 0.926505806 |
| UTR3 | 7:100781140-100781158 | 0.002794142 | |
| UTR3 | 7:100782075-100782097 | 0.003172988 | |
| UTR3 | 7:100782453-100782473 | 0.046157712 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6873-3p | 0.925409107 |
| UTR3 | 7:100780810-100780832 | 0.007785077 | |
| UTR3 | 7:100780938-100780948 | 0.007606214 | |
| UTR3 | 7:100781526-100781546 | 0.029700946 | |
| UTR3 | 7:100781526-100781552 | 0.001158619 | |

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| UTR3 | 7:100781985-100782007 | 0.002062749 | |
| UTR3 | 7:100781985-100782008 | 0.003549793 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6833-3p | 0.921957818 |
| UTR3 | 7:100780819-100780833 | 0.008853651 | |
| UTR3 | 7:100780930-100780949 | 0.00877637 | |
| UTR3 | 7:100781526-100781547 | 0.0250342 | |
| UTR3 | 7:100781526-100781552 | 0.002057273 | |
| UTR3 | 7:100781989-100782008 | 0.004593504 | |
| UTR3 | 7:100781989-100782008 | 0.001748078 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6740-3p | 0.921387221 |
| UTR3 | 7:100780819-100780836 | 0.050432155 | |

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| UTR3 | 7:100773910-100773925 | 0.006921725 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-34a-5p | 0.905589079 |
| UTR3 | 7:100781145-100781169 | 0.001730397 |  |
| UTR3 | 7:100781150-100781174 | 0.004608328 |  |
| UTR3 | 7:100781664-100781689 | 0.041319561 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-3925-3p | 0.905236509 |
| UTR3 | 7:100780748-100780762 | 0.041749797 |  |
| UTR3 | 7:100781357-100781374 | 0.005841203 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-937-5p | 0.893200844 |
| UTR3 | 7:100781791-100781813 | 0.002757756 |  |
| UTR3 | 7:100781896-100781921 | 0.013473886 |  |

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| UTR3 | 7:100781921-100781940 | 0.02918642 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-8063 | 0.891001385 |
| UTR3 | 7:100781345-100781371 | 0.004845774 | |
| UTR3 | 7:100782352-100782376 | 0.004253444 | |
| UTR3 | 7:100782364-100782381 | 0.023908285 | |
| UTR3 | 7:100782460-100782475 | 0.01203709 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-449a | 0.890923422 |
| UTR3 | 7:100781150-100781169 | 0.001667749 | |
| UTR3 | 7:100781150-100781174 | 0.003537364 | |
| UTR3 | 7:100781664-100781689 | 0.039826364 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-642a-3p | 0.886393906 |

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| UTR3 | 7:100781592-100781611 | 0.00358874 |  |
| UTR3 | 7:100781931-100781951 | 0.040694445 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4713-5p | 0.882336243 |
| UTR3 | 7:100780929-100780946 | 0.007249487 |  |
| UTR3 | 7:100782252-100782267 | 0.036385136 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-143-3p | 0.880986481 |
| UTR3 | 7:100781206-100781232 | 0.039294929 |  |
| UTR3 | 7:100781322-100781337 | 0.002314947 |  |
| UTR3 | 7:100781605-100781622 | 0.001813306 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4433b-5p | 0.879250919 |
| UTR3 | 7:100780727-100780753 | 0.039605692 |  |

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| UTR3 | 7:100781640-100781663 | 0.002492038 | |
| UTR3 | 7:100781790-100781805 | 0.0010566 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-642b-3p | 0.879127526 |
| UTR3 | 7:100781590-100781611 | 0.003481363 | |
| UTR3 | 7:100781931-100781951 | 0.039653981 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-494-3p | 0.877294909 |
| UTR3 | 7:100781580-100781596 | 0.002545872 | |
| UTR3 | 7:100782486-100782500 | 0.039529726 | |
| UTR3 | 7:100771789-100771805 | 0.006648048 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-5195-3p | 0.861871702 |
| UTR3 | 7:100780738-100780761 | 0.027695242 | |

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|---|---|---|---|
| UTR3 | 7:100782364-100782388 | 0.012935057 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-450a-2-3p | 0.860651033 |
| UTR3 | 7:100781288-100781301 | 0.003227189 |  |
| UTR3 | 7:100781451-100781478 | 0.003439338 |  |
| UTR3 | 7:100781891-100781906 | 0.033796808 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-548e-5p | 0.857714087 |
| UTR3 | 7:100781085-100781112 | 0.008230865 |  |
| UTR3 | 7:100782440-100782465 | 0.016752853 |  |
| UTR3 | 7:100782459-100782474 | 0.01508286 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-3620-3p | 0.851869791 |
| UTR3 | 7:100781909-100781916 | 0.03826738 |  |

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|---|---|---|---|
| UTR3 | 7:100781977-100782002 | 0.001029555 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-486-5p | 0.848971624 |
| UTR3 | 7:100781089-100781105 | 0.004321364 | |
| UTR3 | 7:100781244-100781272 | 0.005534687 | |
| UTR3 | 7:100781886-100781913 | 0.004723331 | |
| UTR3 | 7:100782389-100782412 | 0.024345174 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-139-3p | 0.84525307 |
| UTR3 | 7:100780863-100780877 | 0.011006012 | |
| UTR3 | 7:100780902-100780928 | 0.006103746 | |
| UTR3 | 7:100780961-100780978 | 0.017129362 | |
| UTR3 | 7:100782306-100782330 | 0.004216151 | |

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| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-5689 | 0.843261737 |
| UTR3 | 7:100782446-100782462 | 0.038207744 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6882-5p | 0.840420999 |
| UTR3 | 7:100781136-100781164 | 0.004109333 | |
| UTR3 | 7:100781366-100781387 | 0.033749692 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-149-3p | 0.838501942 |
| UTR3 | 7:100780902-100780920 | 0.004375449 | |
| UTR3 | 7:100780941-100780967 | 0.003346436 | |
| UTR3 | 7:100781245-100781262 | 0.00581052 | |
| UTR3 | 7:100781316-100781340 | 0.001045278 | |
| UTR3 | 7:100781325-100781343 | 0.023048604 | |

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| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-148a-3p | 0.832001974 |
| UTR3 | 7:100781050-100781069 | 0.002902166 | |
| UTR3 | 7:100781231-100781251 | 0.001961603 | |
| UTR3 | 7:100782318-100782334 | 0.003231279 | |
| UTR3 | 7:100782371-100782387 | 0.028759131 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-5702 | 0.830357909 |
| UTR3 | 7:100780803-100780815 | 0.004919744 | |
| UTR3 | 7:100781795-100781813 | 0.001791076 | |
| UTR3 | 7:100781909-100781920 | 0.010897069 | |
| UTR3 | 7:100781929-100781939 | 0.019054794 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4311 | 0.8294151 |

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| UTR3 | 7:100780799-100780819 | 0.011268698 | |
| UTR3 | 7:100781712-100781733 | 0.001456111 | |
| UTR3 | 7:100782155-100782177 | 0.00840966 | |
| UTR3 | 7:100782329-100782347 | 0.015419064 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-3977 | 0.827006728 |
| UTR3 | 7:100780940-100780959 | 0.024271334 | |
| UTR3 | 7:100781377-100781402 | 0.012005536 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4269 | 0.822116229 |
| UTR3 | 7:100780981-100780998 | 0.00194273 | |
| UTR3 | 7:100781101-100781120 | 0.030366483 | |
| UTR3 | 7:100781150-100781172 | 0.003415089 | |

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| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6764-5p | 0.819392395 |
| UTR3 | 7:100780924-100780943 | 0.030328506 | |
| UTR3 | 7:100782133-100782151 | 0.003582763 | |
| UTR3 | 7:100778800-100778826 | 0.009378793 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-148b-3p | 0.818363233 |
| UTR3 | 7:100781043-100781069 | 0.002880755 | |
| UTR3 | 7:100782318-100782334 | 0.003231279 | |
| UTR3 | 7:100782371-100782387 | 0.029196248 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-152-3p | 0.81512564 |
| UTR3 | 7:100781042-100781069 | 0.002786637 | |
| UTR3 | 7:100782319-100782334 | 0.002971852 | |

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| UTR3 | 7:100782371-100782387 | 0.029196248 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-34c-5p | 0.814115119 |
| UTR3 | 7:100781150-100781170 | 0.002411372 |  |
| UTR3 | 7:100781665-100781688 | 0.032433999 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6809-3p | 0.813365483 |
| UTR3 | 7:100780819-100780833 | 0.018204809 |  |
| UTR3 | 7:100780930-100780949 | 0.007393292 |  |
| UTR3 | 7:100781540-100781546 | 0.004033458 |  |
| UTR3 | 7:100781540-100781552 | 0.005132976 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6825-5p | 0.813118475 |
| UTR3 | 7:100781248-100781264 | 0.005908855 |  |

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| UTR3 | 7:100781322-100781345 | 0.024147623 | |
| UTR3 | 7:100781878-100781904 | 0.004681475 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6763-5p | 0.811818804 |
| UTR3 | 7:100781248-100781265 | 0.006078236 | |
| UTR3 | 7:100781319-100781346 | 0.019261608 | |
| UTR3 | 7:100781885-100781904 | 0.009258694 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-3153 | 0.81104848 |
| UTR3 | 7:100781725-100781739 | 0.005035744 | |
| UTR3 | 7:100781877-100781903 | 0.02948051 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6730-5p | 0.803825582 |
| UTR3 | 7:100780810-100780820 | 0.007658443 | |

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| UTR3 | 7:100781217-100781227 | 0.009870424 |  |
| UTR3 | 7:100782320-100782348 | 0.005386617 |  |
| UTR3 | 7:100782339-100782365 | 0.005380421 |  |
| UTR3 | 7:100782348-100782369 | 0.005461022 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-676-3p | 0.803163924 |
| UTR3 | 7:100781789-100781806 | 0.002023686 |  |
| UTR3 | 7:100781808-100781824 | 0.005765452 |  |
| UTR3 | 7:100781871-100781893 | 0.010280204 |  |
| UTR3 | 7:100782530-100782544 | 0.015619094 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-541-3p | 0.80305785 |
| UTR3 | 7:100782300-100782321 | 0.033097131 |  |

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| UTR3 | 7:100771759-100771774 | 0.003508486 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4770 | 0.801958764 |
| UTR3 | 7:100781206-100781232 | 0.031355584 | |
| UTR3 | 7:100781322-100781337 | 0.002208546 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-3620-5p | 0.800656831 |
| UTR3 | 7:100781021-100781041 | 0.003322177 | |
| UTR3 | 7:100781655-100781682 | 0.002894824 | |
| UTR3 | 7:100782115-100782131 | 0.002736555 | |
| UTR3 | 7:100782304-100782319 | 0.024476925 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-10a-5p | 0.796589119 |
| UTR3 | 7:100781890-100781915 | 0.030531703 | |

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| UTR3 | 7:100782045-100782069 | 0.002485381 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-10b-5p | 0.796589119 |
| UTR3 | 7:100781890-100781915 | 0.030531703 | |
| UTR3 | 7:100782045-100782069 | 0.002485381 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-449b-5p | 0.795275996 |
| UTR3 | 7:100781150-100781170 | 0.002447674 | |
| UTR3 | 7:100781664-100781688 | 0.030437277 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6752-5p | 0.795260505 |
| UTR3 | 7:100781457-100781475 | 0.029744328 | |
| UTR3 | 7:100782142-100782169 | 0.003139067 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-654-5p | 0.794939037 |

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| UTR3 | 7:100782312-100782321 | 0.032056509 | |
| UTR3 | 7:100771764-100771774 | 0.004647293 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4450 | 0.794768556 |
| UTR3 | 7:100781244-100781264 | 0.001629698 | |
| UTR3 | 7:100781330-100781345 | 0.002308638 | |
| UTR3 | 7:100781883-100781904 | 0.00543628 | |
| UTR3 | 7:100782317-100782343 | 0.023459442 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-5093 | 0.794483963 |
| UTR3 | 7:100781936-100781957 | 0.032805556 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-573 | 0.792639387 |
| UTR3 | 7:100781921-100781944 | 0.032621527 | |

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| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-656-3p | 0.789267252 |
| UTR3 | 7:100781547-100781572 | 0.015225455 | |
| UTR3 | 7:100782026-100782043 | 0.01115956 | |
| UTR3 | 7:100782218-100782223 | 0.005903181 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-609 | 0.786276832 |
| UTR3 | 7:100781202-100781223 | 0.029909036 | |
| UTR3 | 7:100781638-100781653 | 0.002086818 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-134-5p | 0.785887598 |
| UTR3 | 7:100781131-100781147 | 0.031958022 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-425-5p | 0.784172712 |
| UTR3 | 7:100781927-100781954 | 0.031791938 | |

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| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-148b-5p | 0.782356878 |
| UTR3 | 7:100781527-100781554 | 0.002965748 |  |
| UTR3 | 7:100781881-100781898 | 0.028651367 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6857-5p | 0.781939374 |
| UTR3 | 7:100781247-100781265 | 0.001405382 |  |
| UTR3 | 7:100781453-100781477 | 0.002164388 |  |
| UTR3 | 7:100781878-100781905 | 0.028007298 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-548n | 0.774355642 |
| UTR3 | 7:100780827-100780847 | 0.00729816 |  |
| UTR3 | 7:100781091-100781112 | 0.004679775 |  |
| UTR3 | 7:100782446-100782474 | 0.018881095 |  |

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| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4531 | 0.771245423 |
| UTR3 | 7:100780864-100780877 | 0.004385417 | |
| UTR3 | 7:100780905-100780928 | 0.003402097 | |
| UTR3 | 7:100780953-100780978 | 0.006972477 | |
| UTR3 | 7:100782311-100782330 | 0.01580952 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-1343-3p | 0.767631267 |
| UTR3 | 7:100781084-100781106 | 0.003089262 | |
| UTR3 | 7:100781864-100781890 | 0.004430233 | |
| UTR3 | 7:100782109-100782134 | 0.022717042 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4666a-5p | 0.766633082 |
| UTR3 | 7:100782386-100782407 | 0.003821669 | |

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| UTR3 | 7:100782483-100782489 | 0.026323543 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-150-5p | 0.766096367 |
| UTR3 | 7:100780927-100780945 | 0.006973748 |  |
| UTR3 | 7:100782081-100782103 | 0.006685377 |  |
| UTR3 | 7:100782260-100782266 | 0.016437094 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-106a-5p | 0.765853509 |
| UTR3 | 7:100782072-100782097 | 0.007424559 |  |
| UTR3 | 7:100782449-100782473 | 0.022649518 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-378a-5p | 0.765175639 |
| UTR3 | 7:100781090-100781106 | 0.00303355 |  |
| UTR3 | 7:100781612-100781625 | 0.00321962 |  |

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| UTR3 | 7:100782107-100782134 | 0.003421746 |  |
| UTR3 | 7:100782522-100782541 | 0.02033744 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4656 | 0.763575164 |
| UTR3 | 7:100781656-100781681 | 0.001054621 |  |
| UTR3 | 7:100782109-100782130 | 0.001716536 |  |
| UTR3 | 7:100782299-100782318 | 0.024699976 |  |
| UTR3 | 7:100779079;100780282-100779082;100780300 | 0.012251369 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-2116-3p | 0.762394082 |
| UTR3 | 7:100780921-100780944 | 0.003697272 |  |
| UTR3 | 7:100782082-100782103 | 0.005520466 |  |
| UTR3 | 7:100782098-100782116 | 0.001795028 |  |

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| UTR3 | 7:100782258-100782265 | 0.018747607 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-224-5p | 0.762128251 |
| UTR3 | 7:100781369-100781386 | 0.029736398 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4646-3p | 0.760284233 |
| UTR3 | 7:100780729-100780754 | 0.029570593 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-8064 | 0.757236157 |
| UTR3 | 7:100781096-100781117 | 0.00582646 | |
| UTR3 | 7:100781336-100781357 | 0.023471966 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6842-3p | 0.757208745 |
| UTR3 | 7:100781619-100781635 | 0.00563068 | |
| UTR3 | 7:100782045-100782063 | 0.021183293 | |

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| UTR3 | 7:100782379-100782403 | 0.002482017 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6852-3p | 0.754890232 |
| UTR3 | 7:100780896-100780902 | 0.006689343 |  |
| UTR3 | 7:100781798-100781823 | 0.01056538 |  |
| UTR3 | 7:100781868-100781892 | 0.004099112 |  |
| UTR3 | 7:100781963-100781982 | 0.00331646 |  |
| UTR3 | 7:100782525-100782543 | 0.004420239 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6879-3p | 0.750534037 |
| UTR3 | 7:100781169-100781195 | 0.002423079 |  |
| UTR3 | 7:100781359-100781383 | 0.005831009 |  |
| UTR3 | 7:100781903-100781917 | 0.014057383 |  |

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| UTR3 | 7:100781911-100781936 | 0.006396555 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6719-3p | 0.747412723 |
| UTR3 | 7:100781427-100781451 | 0.013691503 |  |
| UTR3 | 7:100782525-100782540 | 0.014745184 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-3118 | 0.743975692 |
| UTR3 | 7:100781123-100781147 | 0.028140457 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4753-3p | 0.742424568 |
| UTR3 | 7:100780812-100780832 | 0.011178365 |  |
| UTR3 | 7:100780927-100780948 | 0.00309384 |  |
| UTR3 | 7:100781528-100781552 | 0.013735419 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-196b-5p | 0.740873888 |

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| UTR3 | 7:100781479-100781503 | 0.001999781 | |
| UTR3 | 7:100782011-100782032 | 0.02587557 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-7159-5p | 0.739589791 |
| UTR3 | 7:100782432-100782453 | 0.027766207 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4302 | 0.738600827 |
| UTR3 | 7:100781229-100781251 | 0.002545336 | |
| UTR3 | 7:100781668-100781686 | 0.010540899 | |
| UTR3 | 7:100782368-100782387 | 0.014596151 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-1276 | 0.737296966 |
| UTR3 | 7:100780813-100780818 | 0.008029756 | |
| UTR3 | 7:100781720-100781733 | 0.001428314 | |

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| UTR3 | 7:100782165-100782178 | 0.0074278 | |
| UTR3 | 7:100782214-100782228 | 0.003917485 | |
| UTR3 | 7:100782322-100782346 | 0.006768831 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-153-5p | 0.735718407 |
| UTR3 | 7:100782268-100782288 | 0.005740472 | |
| UTR3 | 7:100782472-100782495 | 0.021698769 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-3613-3p | 0.735345441 |
| UTR3 | 7:100780821-100780848 | 0.007338874 | |
| UTR3 | 7:100781086-100781113 | 0.004777744 | |
| UTR3 | 7:100782351-100782375 | 0.015291286 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-519c-3p | 0.731499972 |

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| UTR3 | 7:100782089-100782097 | 0.010896821 | |
| UTR3 | 7:100782449-100782472 | 0.016189617 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-519d-3p | 0.731019026 |
| UTR3 | 7:100782073-100782098 | 0.011689438 | |
| UTR3 | 7:100782460-100782472 | 0.015357002 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-519b-3p | 0.730120544 |
| UTR3 | 7:100782077-100782097 | 0.010974121 | |
| UTR3 | 7:100782458-100782472 | 0.015997716 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-7110-3p | 0.729821255 |
| UTR3 | 7:100781520-100781545 | 0.014717419 | |
| UTR3 | 7:100781985-100782006 | 0.001501586 | |

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| UTR3 | 7:100781985-100782008 | 0.008588356 |  |
| UTR3 | 7:100773881-100773893 | 0.01019625 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6783-3p | 0.726774705 |
| UTR3 | 7:100781864-100781890 | 0.00428711 |  |
| UTR3 | 7:100782109-100782134 | 0.022408278 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4306 | 0.726340232 |
| UTR3 | 7:100780868-100780877 | 0.004083175 |  |
| UTR3 | 7:100780881-100780893 | 0.006167539 |  |
| UTR3 | 7:100780914-100780928 | 0.002574168 |  |
| UTR3 | 7:100780961-100780978 | 0.005450141 |  |
| UTR3 | 7:100781311-100781322 | 0.001637292 |  |

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| UTR3 | 7:100782314-100782330 | 0.005258227 | |
| UTR3 | 7:100778867;100778996-100778875;100779011 | 0.007162562 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-186-5p | 0.726181944 |
| UTR3 | 7:100781580-100781600 | 0.003341787 | |
| UTR3 | 7:100782331-100782351 | 0.007486211 | |
| UTR3 | 7:100782339-100782363 | 0.005183556 | |
| UTR3 | 7:100782341-100782367 | 0.005403993 | |
| UTR3 | 7:100782346-100782371 | 0.005231086 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-548an | 0.724761706 |
| UTR3 | 7:100780827-100780846 | 0.02341227 | |
| UTR3 | 7:100781401-100781419 | 0.003117812 | |

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| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-510-3p | 0.723572764 |
| UTR3 | 7:100781924-100781946 | 0.00592147 | |
| UTR3 | 7:100782484-100782501 | 0.02051133 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-627-5p | 0.722212065 |
| UTR3 | 7:100781805-100781813 | 0.009063749 | |
| UTR3 | 7:100781899-100781921 | 0.006804113 | |
| UTR3 | 7:100781924-100781940 | 0.010453919 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-629-3p | 0.721750991 |
| UTR3 | 7:100781526-100781553 | 0.003400887 | |
| UTR3 | 7:100782256-100782268 | 0.022883352 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-548aw | 0.721655894 |

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| UTR3 | 7:100782250-100782273 | 0.007392903 | |
| UTR3 | 7:100782374-100782384 | 0.018883596 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4417 | 0.721507854 |
| UTR3 | 7:100781025-100781042 | 0.002891767 | |
| UTR3 | 7:100781663-100781682 | 0.002923337 | |
| UTR3 | 7:100782306-100782320 | 0.020449353 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4700-5p | 0.72091557 |
| UTR3 | 7:100781245-100781265 | 0.003381828 | |
| UTR3 | 7:100781322-100781347 | 0.022834484 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-5571-5p | 0.719879718 |
| UTR3 | 7:100780779-100780799 | 0.008371815 | |

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| UTR3 | 7:100782256-100782270 | 0.010702948 | |
| UTR3 | 7:100782434-100782456 | 0.007057497 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6865-5p | 0.719255062 |
| UTR3 | 7:100780907-100780932 | 0.002259464 | |
| UTR3 | 7:100781674-100781692 | 0.023822203 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-196a-5p | 0.718193945 |
| UTR3 | 7:100781479-100781503 | 0.002378739 | |
| UTR3 | 7:100782011-100782032 | 0.023617139 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-185-5p | 0.715063469 |
| UTR3 | 7:100780864-100780877 | 0.003908891 | |
| UTR3 | 7:100780881-100780893 | 0.006167539 | |

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|---|---|---|---|
| UTR3 | 7:100780905-100780928 | 0.002179067 |  |
| UTR3 | 7:100780960-100780978 | 0.005419617 |  |
| UTR3 | 7:100781304-100781322 | 0.001542223 |  |
| UTR3 | 7:100782311-100782330 | 0.005000923 |  |
| UTR3 | 7:100778867;100778996-100778875;100779011 | 0.007162562 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-519a-3p | 0.713673753 |
| UTR3 | 7:100782072-100782097 | 0.011193023 |  |
| UTR3 | 7:100782467-100782472 | 0.014439586 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-3133 | 0.708115406 |
| UTR3 | 7:100782223-100782228 | 0.004551498 |  |
| UTR3 | 7:100782345-100782351 | 0.005402735 |  |

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|---|---|---|---|
| UTR3 | 7:100782352-100782363 | 0.005231437 |  |
| UTR3 | 7:100782352-100782367 | 0.005161163 |  |
| UTR3 | 7:100782352-100782371 | 0.004843747 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-141-3p | 0.707945317 |
| UTR3 | 7:100780785-100780808 | 0.022896105 |  |
| UTR3 | 7:100781571-100781594 | 0.002281027 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6731-3p | 0.707765931 |
| UTR3 | 7:100781429-100781436 | 0.016421203 |  |
| UTR3 | 7:100781823-100781849 | 0.003290554 |  |
| UTR3 | 7:100782276-100782303 | 0.005451198 |  |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-299-5p | 0.706059227 |

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|---|---|---|---|
| UTR3 | 7:100780846-100780865 | 0.0220396 | |
| UTR3 | 7:100780971-100780983 | 0.002988721 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-6817-3p | 0.702402554 |
| UTR3 | 7:100780926-100780947 | 0.003701855 | |
| UTR3 | 7:100781521-100781545 | 0.014176444 | |
| UTR3 | 7:100781985-100782006 | 0.002113285 | |
| UTR3 | 7:100781995-100782008 | 0.004749805 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-19b-3p | 0.702177595 |
| UTR3 | 7:100782258-100782274 | 0.013807608 | |
| UTR3 | 7:100782367-100782384 | 0.010916196 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-4422 | 0.702097274 |

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| UTR3 | 7:100782446-100782465 | 0.024717527 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-19a-3p | 0.701418361 |
| UTR3 | 7:100782260-100782274 | 0.013748314 | |
| UTR3 | 7:100782367-100782384 | 0.010916196 | |
| ENST00000223095 | ENSG00000106366 (SERPINE1) | hsa-miR-7974 | 0.700877749 |
| UTR3 | 7:100781909-100781925 | 0.023006242 | |
| UTR3 | 7:100782126-100782148 | 0.0016161 | |

**Supplementary Table 3**: targets with miRNAs found in genes ENSG0000010636 (SERPINE1)

| **Transcript Id** | **Gene Id(name)** | **Mirna Name** | **miTG score** |
|---|---|---|---|
| ENST00000599847 | ENSG00000152439 (ZNF773) | hsa-miR-146a-5p | 0.999996 |
| UTR3 | 19:58024644-58024660 | 0.162166849 | |
| UTR3 | 19:58026567-58026594 | 0.00549672 | |
| UTR3 | 19:58026679-58026693 | 0.002766695 | |
| UTR3 | 19:58028097-58028113 | 0.004807814 | |
| UTR3 | 19:58029501-58029522 | 0.037791942 | |
| ENST00000526995 | ENSG00000175104 (TRAF6) | hsa-miR-146a-5p | 0.999978 |
| UTR3 | 11:36511323-36511346 | 0.022150809 | |
| UTR3 | 11:36510908-36510929 | 0.069665204 | |
| UTR3 | 11:36510843-36510867 | 0.081734012 | |
| UTR3 | 11:36510109-36510127 | 0.012250438 | |
| ENST00000369980 | ENSG00000184216 (IRAK1) | hsa-miR-146a-5p | 0.999972 |
| UTR3 | X:153277263-153277288 | 0.10883198 | |
| UTR3 | X:153277247-153277266 | 0.072978108 | |
| ENST00000370900 | ENSG00000147255 (IGSF1) | hsa-miR-146a-5p | 0.999866 |
| UTR3 | X:130418887-130418912 | 0.01756038 | |
| UTR3 | X:130418158-130418179 | 0.138879909 | |
| ENST00000551765 | ENSG00000257218 (GATC) | hsa-miR-146a-5p | 0.999528 |
| UTR3 | 12:120899289-120899315 | 0.135881871 | |
| ENST00000303296 | ENSG00000110422 (HIPK3) | hsa-miR-146a-5p | 0.999371 |
| UTR3 | 11:33378413-33378426 | 0.131167285 | |
| | | | |
| ENST00000361264 | ENSG00000198876 (DCAF12) | hsa-miR-146a-5p | 0.99899 |
| UTR3 | 9:34086854-34086875 | 0.002749271 | |
| UTR3 | 9:34086698-34086719 | 0.005392711 | |
| UTR3 | 9:34086570-34086593 | 0.115283263 | |
| ENST00000540664 | ENSG00000196233 (LCOR) | hsa-miR-146a-5p | 0.998541 |
| UTR3 | 10:98718333-98718354 | 0.007648157 | |
| UTR3 | 10:98719279-98719304 | 0.003221005 | |
| UTR3 | 10:98719941-98719961 | 0.001179491 | |
| UTR3 | 10:98720586-98720604 | 0.001349985 | |
| UTR3 | 10:98721368-98721378 | 0.00256124 | |
| UTR3 | 10:98722676-98722703 | 0.002038013 | |
| UTR3 | 10:98723405-98723420 | 0.012527313 | |
| UTR3 | 10:98724122-98724137 | 0.08688245 | |
| ENST00000311015 | ENSG00000172687 (ZNF738) | hsa-miR-146a-5p | 0.998472 |
| UTR3 | 19:21560902-21560921 | 0.007837571 | |
| UTR3 | 19:21560918-21560936 | 0.019164832 | |
| UTR3 | 19:21561492-21561511 | 0.053871422 | |
| UTR3 | 19:21561920-21561947 | 0.03577717 | |
| ENST00000325144 | ENSG00000181472 (ZBTB2) | hsa-miR-146a-5p | 0.99803 |
| UTR3 | 6:151686574-151686598 | 0.020209292 | |
| UTR3 | 6:151686543-151686562 | 0.004069393 | |
| UTR3 | 6:151686289-151686310 | 0.004942405 | |
| UTR3 | 6:151685305-151685326 | 0.083272067 | |

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|---|---|---|---|
| ENST00000309446 | ENSG00000118263 (KLF7) | hsa-miR-146a-5p | 0.997917 |
| UTR3 | 2:207945824-207945852 | 0.08048381 | |
| UTR3 | 2:207945519-207945547 | 0.005714625 | |
| UTR3 | 2:207944876-207944900 | 0.005998419 | |
| UTR3 | 2:207943584-207943595 | 0.00584079 | |
| UTR3 | 2:207943302-207943323 | 0.002827208 | |
| UTR3 | 2:207942677-207942689 | 0.001928592 | |
| UTR3 | 2:207940603-207940622 | 0.005706465 | |
| UTR3 | 2:207939171-207939190 | 0.003074982 | |
| ENST00000295025 | ENSG00000162924 (REL) | hsa-miR-146a-5p | 0.996836 |
| UTR3 | 2:61151027-61151044 | 0.001637971 | |
| UTR3 | 2:61151217-61151234 | 0.001537235 | |
| UTR3 | 2:61151958-61151985 | 0.001533778 | |
| UTR3 | 2:61152432-61152455 | 0.001577663 | |
| UTR3 | 2:61153748-61153767 | 0.003562602 | |
| UTR3 | 2:61154027-61154049 | 0.002116903 | |
| UTR3 | 2:61155043-61155068 | 0.001251838 | |
| UTR3 | 2:61156712-61156733 | 0.001070489 | |
| UTR3 | 2:61157488-61157507 | 0.001576509 | |
| UTR3 | 2:61158582-61158589 | 0.088861545 | |
| ENST00000589717 | ENSG00000256771 (ZNF253) | hsa-miR-146a-5p | 0.996391 |
| UTR3 | 19:20003682-20003702 | 0.043465348 | |
| UTR3 | 19:20003771-20003789 | 0.042273763 | |
| UTR3 | 19:20005318-20005333 | 0.023045069 | |
| UTR3 | 19:19990947;20002283-19990955;20002295 | 0.025854842 | |
| ENST00000375256 | ENSG00000165244 (ZNF367) | hsa-miR-146a-5p | 0.994372 |
| UTR3 | 9:99150215-99150235 | 0.090060273 | |
| UTR3 | 9:99149779-99149804 | 0.005216236 | |
| ENST00000592773 | ENSG00000198597 (ZNF536) | hsa-miR-146a-5p | 0.993696 |
| UTR3 | 19:31202624-31202649 | 0.002316742 | |
| UTR3 | 19:31203616-31203639 | 0.067381133 | |
| UTR3 | 19:31204165-31204181 | 0.023711034 | |
| | | | |
| ENST00000368599 | ENSG00000178033 (FAM26E) | hsa-miR-146a-5p | 0.993304 |
| UTR3 | 6:116837627-116837655 | 0.059125776 | |
| UTR3 | 6:116838112-116838124 | 0.001946717 | |
| UTR3 | 6:116838207-116838222 | 0.00121829 | |
| UTR3 | 6:116838310-116838326 | 0.001223976 | |
| UTR3 | 6:116839704-116839722 | 0.003290396 | |
| UTR3 | 6:116840077-116840097 | 0.005254453 | |
| UTR3 | 6:116841391-116841419 | 0.001576348 | |
| UTR3 | 6:116842165-116842191 | 0.001106404 | |
| UTR3 | 6:116844081-116844102 | 0.006878417 | |
| UTR3 | 6:116844207-116844231 | 0.002300399 | |
| UTR3 | 6:116845617-116845636 | 0.002722865 | |
| UTR3 | 6:116845794-116845805 | 0.005774964 | |

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|---|---|---|---|
| ENST00000485895 | ENSG00000157578 (LCA5L) | hsa-miR-146a-5p | 0.992713 |
| UTR3 | 21:40793523-40793543 | 0.032139976 | |
| UTR3 | 21:40793506-40793524 | 0.065419046 | |
| UTR3 | 21:40800229-40800250 | 0.036268404 | |
| ENST00000576251 | ENSG00000101574 (METTL4) | hsa-miR-146a-5p | 0.990927 |
| UTR3 | 18:2539046-2539071 | 0.07588562 | |
| UTR3 | 18:2537938-2537954 | 0.004395617 | |
| UTR3 | 18:2537532-2537551 | 0.007132501 | |
| ENST00000286614 | ENSG00000156103 (MMP16) | hsa-miR-146a-5p | 0.989699 |
| UTR3 | 8:89052958-89052986 | 0.016858117 | |
| UTR3 | 8:89052202-89052229 | 0.057045567 | |
| UTR3 | 8:89051674-89051694 | 0.002189713 | |
| UTR3 | 8:89045113-89045141 | 0.009225133 | |
| ENST00000382852 | ENSG00000169953 (HSFY2) | hsa-miR-146a-5p | 0.988862 |
| UTR3 | Y:20931130-20931157 | 0.084027364 | |
| ENST00000290271 | ENSG00000159167 (STC1) | hsa-miR-146a-5p | 0.988056 |
| UTR3 | 8:23699890-23699915 | 0.082872295 | |
| ENST00000334681 | ENSG00000187094 (CCK) | hsa-miR-146a-5p | 0.987618 |
| UTR3 | 3:42299458-42299477 | 0.082276863 | |
| ENST00000433818 | ENSG00000149262 (INTS4) | hsa-miR-146a-5p | 0.986014 |
| UTR3 | 11:77652272-77652294 | 0.066292961 | |
| UTR3 | 11:77632452-77632469 | 0.010846087 | |
| UTR3 | 11:77632405-77632426 | 0.001715156 | |
| UTR3 | 11:77618768-77618795 | 0.001404855 | |
| ENST00000338965 | ENSG00000188211 (NCR3LG1) | hsa-miR-146a-5p | 0.984424 |
| UTR3 | 11:17394132-17394148 | 0.038371797 | |
| UTR3 | 11:17395248-17395265 | 0.006769936 | |
| UTR3 | 11:17397082-17397108 | 0.011408701 | |
| UTR3 | 11:17397559-17397576 | 0.021922331 | |
| ENST00000369649 | ENSG00000126903 (SLC10A3) | hsa-miR-146a-5p | 0.984234 |
| UTR3 | X:153715790-153715816 | 0.078824117 | |
| UTR3 | X:153716237-153716258 | 0.006924871 | |
| ENST00000264246 | ENSG00000121594 (CD80) | hsa-miR-146a-5p | 0.983963 |
| UTR3 | 3:119244014-119244036 | 0.00456856 | |
| UTR3 | 3:119243789-119243807 | 0.068361995 | |
| UTR3 | 3:119243349-119243370 | 0.005057847 | |
| ENST00000555818 | ENSG00000197555 (SIPA1L1) | hsa-miR-146a-5p | 0.983428 |
| UTR3 | 14:72206516-72206541 | 0.001932333 | |
| UTR3 | 14:72207605-72207626 | 0.073432655 | |
| UTR3 | 14:72207870-72207896 | 0.003735818 | |
| UTR3 | 14:72054753-72054777 | 0.014745367 | |
| UTR3 | 14:72197011;72200383-72197018;72200393 | 0.005666713 | |

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|---|---|---|---|
| ENST00000446113 | ENSG00000177054 (ZDHHC13) | hsa-miR-146a-5p | 0.982959 |
| UTR3 | 11:19197628-19197653 | 0.076979167 |  |
| ENST00000313899 | ENSG00000138668 (HNRNPD) | hsa-miR-146a-5p | 0.98259 |
| UTR3 | 4:83275160-83275187 | 0.076623141 |  |
| ENST00000371388 | ENSG00000131721 (RHOXF2) | hsa-miR-146a-5p | 0.98248 |
| UTR3 | X:119297888-119297911 | 0.076518911 |  |
| ENST00000379391 | ENSG00000166881 (TMEM194A) | hsa-miR-146a-5p | 0.98155 |
| UTR3 | 12:57452981-57452999 | 0.068012716 |  |
| UTR3 | 12:57452706-57452727 | 0.003267033 |  |
| UTR3 | 12:57452588-57452611 | 0.001285431 |  |
| UTR3 | 12:57452281-57452308 | 0.001279032 |  |
| UTR3 | 12:57451801-57451817 | 0.001813596 |  |
| ENST00000591639 | ENSG00000081665 (ZNF506) | hsa-miR-146a-5p | 0.980274 |
| UTR3 | 19:19905215-19905235 | 0.034181582 |  |
| UTR3 | 19:19904826-19904844 | 0.040361526 |  |
| ENST00000605860 | ENSG00000007001 (UPP2) | hsa-miR-146a-5p | 0.980101 |
| UTR3 | 2:158991475-158991501 | 0.070411781 |  |
| UTR3 | 2:158992322-158992344 | 0.003986281 |  |
| ENST00000299167 | ENSG00000102893 (PHKB) | hsa-miR-146a-5p | 0.977294 |
| UTR3 | 16:47733466-47733488 | 0.053193894 |  |
| UTR3 | 16:47733755-47733778 | 0.019637868 |  |
| UTR3 | 16:47684491-47684518 | 0.013391224 |  |
| ENST00000608872 | ENSG00000119402 (FBXW2) | hsa-miR-146a-5p | 0.976567 |
| UTR3 | 9:123526740-123526762 | 0.068016148 |  |
| UTR3 | 9:123523696-123523717 | 0.001775084 |  |
| UTR3 | 9:123520365-123520378 | 0.00187573 |  |
| ENST00000490715 | ENSG00000007341 (ST7L) | hsa-miR-146a-5p | 0.975657 |
| UTR3 | 1:113067415-113067439 | 0.0042105 |  |
| UTR3 | 1:113067037-113067062 | 0.004095764 |  |
| UTR3 | 1:113066159-113066187 | 0.062722518 |  |
| ENST00000342788 | ENSG00000178568 (ERBB4) | hsa-miR-146a-5p | 0.975636 |
| UTR3 | 2:212247377-212247394 | 0.004531221 |  |
| UTR3 | 2:212246814-212246836 | 0.002219412 |  |
| UTR3 | 2:212244136-212244156 | 0.002083036 |  |
| UTR3 | 2:212243884-212243902 | 0.001060149 |  |
| UTR3 | 2:212243301-212243319 | 0.002388579 |  |
| UTR3 | 2:212241602-212241626 | 0.00192031 |  |
| UTR3 | 2:212240641-212240654 | 0.057144256 |  |
| UTR3 | 2:212248401-212248426 | 0.008386047 |  |
| ENST00000420940 | ENSG00000114742 (WDR48) | hsa-miR-146a-5p | 0.974994 |
| UTR3 | 3:39116412-39116439 | 0.049608154 |  |
| UTR3 | 3:39125718-39125735 | 0.020970741 |  |
| ENST00000526148 | ENSG00000110321 (EIF4G2) | hsa-miR-146a-5p | 0.974218 |

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|---|---|---|---|
| UTR3 | 11:10819100-10819127 | 0.070066405 | |
| ENST00000325881 | ENSG00000157734 (SNX22) | hsa-miR-146a-5p | 0.974077 |
| UTR3 | 15:64448598-64448619 | 0.001360365 | |
| UTR3 | 15:64449050-64449077 | 0.068614747 | |
| ENST00000423270 | ENSG00000181827 (RFX7) | hsa-miR-146a-5p | 0.974012 |
| UTR3 | 15:56382807-56382819 | 0.07030419 | |
| UTR3 | 15:56388518-56388540 | 0.010916094 | |
| ENST00000369962 | ENSG00000085433 (WDR47) | hsa-miR-146a-5p | 0.972803 |
| UTR3 | 1:109513595-109513623 | 0.004430319 | |
| UTR3 | 1:109512956-109512979 | 0.064738903 | |
| ENST00000335877 | ENSG00000125818 (PSMF1) | hsa-miR-146a-5p | 0.972281 |
| UTR3 | 20:1146213-1146237 | 0.003487842 | |
| UTR3 | 20:1146841-1146856 | 0.003957562 | |
| UTR3 | 20:1148219-1148234 | 0.032232406 | |
| UTR3 | 20:1148898-1148915 | 0.029172153 | |
| ENST00000354957 | ENSG00000198093 (ZNF649) | hsa-miR-146a-5p | 0.971925 |
| UTR3 | 19:52393575-52393601 | 0.007636897 | |
| UTR3 | 19:52393442-52393461 | 0.055621714 | |
| UTR3 | 19:52393078-52393097 | 0.005376865 | |
| ENST00000274747 | ENSG00000124532 (MRS2) | hsa-miR-146a-5p | 0.971303 |
| UTR3 | 6:24424318-24424341 | 0.001332653 | |
| UTR3 | 6:24424506-24424529 | 0.002817953 | |
| UTR3 | 6:24424771-24424795 | 0.002510468 | |
| UTR3 | 6:24425759-24425786 | 0.061605742 | |
| ENST00000502732 | ENSG00000143322 (ABL2) | hsa-miR-146a-5p | 0.971234 |
| UTR3 | 1:179076710-179076731 | 0.048888516 | |
| UTR3 | 1:179075949-179075963 | 0.007319827 | |
| UTR3 | 1:179075661-179075678 | 0.001967829 | |
| UTR3 | 1:179075104-179075127 | 0.00470782 | |
| UTR3 | 1:179069360-179069382 | 0.00166731 | |
| UTR3 | 1:179068523-179068546 | 0.003675112 | |
| ENST00000458646 | ENSG00000077092 (RARB) | hsa-miR-146a-5p | 0.971037 |
| UTR3 | 3:25639229-25639249 | 0.068111561 | |
| ENST00000318588 | ENSG00000147044 (CASK) | hsa-miR-146a-5p | 0.970985 |
| UTR3 | X:41379460-41379479 | 0.058467887 | |
| UTR3 | X:41378099-41378118 | 0.003460778 | |
| UTR3 | X:41377184-41377200 | 0.002033892 | |
| UTR3 | X:41376837-41376857 | 0.001339655 | |
| UTR3 | X:41375890-41375916 | 0.001271731 | |
| UTR3 | X:41375737-41375751 | 0.001507484 | |
| ENST00000426654 | ENSG00000102908 (NFAT5) | hsa-miR-146a-5p | 0.970846 |
| UTR3 | 16:69681433-69681447 | 0.005047255 | |
| UTR3 | 16:69726570-69726592 | 0.00198929 | |
| UTR3 | 16:69726951-69726979 | 0.002064471 | |
| UTR3 | 16:69727036-69727056 | 0.001146055 | |
| UTR3 | 16:69727866-69727885 | 0.018591107 | |
| UTR3 | 16:69729133-69729156 | 0.002342665 | |

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|---|---|---|---|
| UTR3 | 16:69730904-69730924 | 0.003376283 |  |
| UTR3 | 16:69731625-69731647 | 0.001326825 |  |
| UTR3 | 16:69731973-69732000 | 0.002436764 |  |
| UTR3 | 16:69733289-69733307 | 0.002000631 |  |
| UTR3 | 16:69736424-69736438 | 0.0050489 |  |
| UTR3 | 16:69736425-69736452 | 0.001216539 |  |
| UTR3 | 16:69736719-69736746 | 0.002038788 |  |
| UTR3 | 16:69738193-69738219 | 0.012206378 |  |
| UTR3 | 16:69738383-69738405 | 0.007169048 |  |
| ENST00000531960 | ENSG00000175664 (TEX26) | hsa-miR-146a-5p | 0.969694 |
| UTR3 | 13:31531165;31540359-31531166;31540383 | 0.052837536 |  |
| UTR3 | 13:31540503-31540527 | 0.006178791 |  |
| UTR3 | 13:31549093-31549118 | 0.008331502 |  |
| ENST00000451804 | ENSG00000123843 (C4BPB) | hsa-miR-146a-5p | 0.968445 |
| UTR3 | 1:207269090-207269109 | 0.007509318 |  |
| UTR3 | 1:207269144-207269167 | 0.059348067 |  |
| UTR3 | 1:207268766-207268786 | 0.012248576 |  |
| ENST00000312960 | ENSG00000181788 (SIAH2) | hsa-miR-146a-5p | 0.967726 |
| UTR3 | 3:150459129-150459146 | 0.066286302 |  |
| ENST00000522677 | ENSG00000185697 (MYBL1) | hsa-miR-146a-5p | 0.967611 |
| UTR3 | 8:67476854-67476878 | 0.005352398 |  |
| UTR3 | 8:67476647-67476674 | 0.005901183 |  |
| UTR3 | 8:67475390-67475411 | 0.049925049 |  |
| UTR3 | 8:67475021-67475040 | 0.005047602 |  |
| ENST00000303697 | ENSG00000170959 (DCDC1) | hsa-miR-146a-5p | 0.967499 |
| UTR3 | 11:30904673-30904687 | 0.00691475 |  |
| UTR3 | 11:30904662-30904687 | 0.004648429 |  |
| UTR3 | 11:30904216-30904239 | 0.009681834 |  |
| UTR3 | 11:30886688-30886708 | 0.001045666 |  |
| UTR3 | 11:30885758-30885774 | 0.02908735 |  |
| UTR3 | 11:30885305-30885318 | 0.005801897 |  |
| UTR3 | 11:30885258-30885285 | 0.008987909 |  |
| ENST00000394767 | ENSG00000168772 (CXXC4) | hsa-miR-146a-5p | 0.967096 |
| UTR3 | 4:105392273-105392294 | 0.002979569 |  |
| UTR3 | 4:105390842-105390867 | 0.024136922 |  |
| UTR3 | 4:105389892-105389909 | 0.026498739 |  |
| UTR3 | 4:105389713-105389732 | 0.012344391 |  |
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| ENST00000397358 | ENSG00000147421 (HMBOX1) | hsa-miR-146a-5p | 0.966784 |
| UTR3 | 8:28908976-28908990 | 0.060699779 |  |
| UTR3 | 8:28909825-28909851 | 0.001942684 |  |
| UTR3 | 8:28910510-28910535 | 0.003158026 |  |
| ENST00000372491 | ENSG00000188483 (IER5L) | hsa-miR-146a-5p | 0.966423 |
| UTR3 | 9:131938528-131938554 | 0.059644552 |  |
| UTR3 | 9:131938425-131938444 | 0.001707461 |  |
| UTR3 | 9:131937995-131938010 | 0.004265577 |  |

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| ENST00000331070 | ENSG00000183753 (BPY2) | hsa-miR-146a-5p | 0.964886 |
| UTR3 | Y:25151353-25151381 | 0.014207961 | |
| UTR3 | Y:25151392-25151420 | 0.050651878 | |
| ENST00000326972 | ENSG00000180438 (TPRXL) | hsa-miR-146a-5p | 0.964825 |
| UTR3 | 3:14107339-14107362 | 0.064830578 | |
| ENST00000316398 | ENSG00000179071 (CCDC89) | hsa-miR-146a-5p | 0.964203 |
| UTR3 | 11:85395766-85395787 | 0.005468352 | |
| UTR3 | 11:85395080-85395106 | 0.052315425 | |
| UTR3 | 11:85394980-85394996 | 0.006749639 | |
| ENST00000388975 | ENSG00000154997 (SEPT14) | hsa-miR-146a-5p | 0.963043 |
| UTR3 | 7:55863516-55863531 | 0.05159133 | |
| UTR3 | 7:55862002-55862024 | 0.003538476 | |
| UTR3 | 7:55861575-55861589 | 0.004177488 | |
| UTR3 | 7:55861511-55861533 | 0.004685542 | |
| ENST00000369075 | ENSG00000107651 (SEC23IP) | hsa-miR-146a-5p | 0.962913 |
| UTR3 | 10:121701122-121701141 | 0.063930929 | |
| UTR3 | 10:121689879-121689907 | 0.017987386 | |
| ENST00000540052 | ENSG00000085185 (BCORL1) | hsa-miR-146a-5p | 0.962412 |
| UTR3 | X:129190279-129190297 | 0.055280716 | |
| UTR3 | X:129191651-129191668 | 0.006202261 | |
| UTR3 | X:129191734-129191753 | 0.002222371 | |
| ENST00000509876 | ENSG00000118482 (PHF3) | hsa-miR-146a-5p | 0.960985 |
| UTR3 | 6:64388863-64388883 | 0.039464627 | |
| UTR3 | 6:64401675-64401695 | 0.001936082 | |
| UTR3 | 6:64416077-64416102 | 0.000959486 | |
| UTR3 | 6:64422306-64422327 | 0.006576867 | |
| UTR3 | 6:64422654-64422679 | 0.001684375 | |
| UTR3 | 6:64424327-64424346 | 0.012450422 | |
| ENST00000505939 | ENSG00000131127 (ZNF141) | hsa-miR-146a-5p | 0.959868 |
| UTR3 | 4:377476-377500 | 0.055187942 | |
| UTR3 | 4:377715-377735 | 0.007403891 | |
| ENST00000534668 | ENSG00000156738 (MS4A1) | hsa-miR-146a-5p | 0.958265 |
| UTR3 | 11:60237468-60237484 | 0.049682071 | |
| UTR3 | 11:60237677-60237702 | 0.012025072 | |
| UTR3 | 11:60234523;60235723-60234533;60235734 | 0.018023781 | |
| ENST00000352690 | ENSG00000153283 (CD96) | hsa-miR-146a-5p | 0.957927 |
| UTR3 | 3:111370018-111370039 | 0.001672588 | |
| UTR3 | 3:111371104-111371119 | 0.060028197 | |
| UTR3 | 3:111297993-111298019 | 0.007114806 | |
| ENST00000421627 | ENSG00000198010 (DLGAP2) | hsa-miR-146a-5p | 0.957255 |
| UTR3 | 8:1649837-1649862 | 0.013787664 | |
| UTR3 | 8:1650195-1650211 | 0.008738723 | |

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| UTR3 | 8:1650468-1650493 | 0.002831756 |  |
| UTR3 | 8:1650961-1650988 | 0.016207131 |  |
| UTR3 | 8:1652162-1652188 | 0.011872031 |  |
| UTR3 | 8:1652728-1652741 | 0.002124407 |  |
| UTR3 | 8:1653852-1653870 | 0.001489885 |  |
| UTR3 | 8:1653942-1653968 | 0.000862255 |  |
| UTR3 | 8:1656043-1656069 | 0.003602114 |  |
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| ENST00000382387 | ENSG00000183784 (C9orf66) | hsa-miR-146a-5p | 0.95659 |
| UTR3 | 9:214327-214355 | 0.061252549 |  |
| ENST00000400477 | ENSG00000198054 (DSCR8) | hsa-miR-146a-5p | 0.95643 |
| UTR3 | 21:39528509-39528533 | 0.061189496 |  |
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| ENST00000371402 | ENSG00000203989 (RHOXF2B) | hsa-miR-146a-5p | 0.956011 |
| UTR3 | X:119206263-119206286 | 0.061025966 |  |
| ENST00000317775 | ENSG00000089250 (NOS1) | hsa-miR-146a-5p | 0.955282 |
| UTR3 | 12:117646967-117646980 | 0.00312639 |  |
| UTR3 | 12:117646368-117646385 | 0.004048539 |  |
| UTR3 | 12:117646026-117646053 | 0.053226965 |  |
| UTR3 | 12:117728132-117728158 | 0.009613168 |  |
| UTR3 | 12:117698399;117701694-117698414;117701704 | 0.002600023 |  |
| UTR3 | 12:117685321;117691443-117685327;117691461 | 0.005807081 |  |
| ENST00000382392 | ENSG00000183795 (BPY2B) | hsa-miR-146a-5p | 0.955036 |
| UTR3 | Y:26785095-26785123 | 0.015053225 |  |
| UTR3 | Y:26785134-26785162 | 0.045597779 |  |
| ENST00000335117 | ENSG00000256229 (ZNF486) | hsa-miR-146a-5p | 0.954494 |
| UTR3 | 19:20309217-20309237 | 0.028528132 |  |
| UTR3 | 19:20309297-20309315 | 0.031606914 |  |
| UTR3 | 19:20296883;20307773-20296891;20307785 | 0.015189044 |  |
|  |  |  |  |
| ENST00000229201 | ENSG00000111602 (TIMELESS) | hsa-miR-146a-5p | 0.954485 |
| UTR3 | 12:56811258-56811280 | 0.015340971 |  |
| UTR3 | 12:56810907-56810928 | 0.045101519 |  |
| ENST00000382287 | ENSG00000185894 (BPY2C) | hsa-miR-146a-5p | 0.953835 |
| UTR3 | Y:27177279-27177307 | 0.015001567 |  |
| UTR3 | Y:27177240-27177268 | 0.045198006 |  |
| ENST00000409600 | ENSG00000082153 (BZW1) | hsa-miR-146a-5p | 0.953493 |
| UTR3 | 2:201687952-201687977 | 0.004181261 |  |
| UTR3 | 2:201688497-201688518 | 0.055891885 |  |
| ENST00000427390 | ENSG00000215405 (GOLGA6L6) | hsa-miR-146a-5p | 0.953376 |
| UTR3 | 15:20738351-20738366 | 0.010868893 |  |
| UTR3 | 15:20738100-20738119 | 0.006816508 |  |
| UTR3 | 15:20737326-20737340 | 0.042344835 |  |

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| ENST00000418724 | ENSG00000236104 (ZBTB22) | hsa-miR-146a-5p | 0.95281 |
| UTR3 | 6:33282289-33282316 | 0.059823276 | |
| ENST00000427431 | ENSG00000151718 (WWC2) | hsa-miR-146a-5p | 0.95149 |
| UTR3 | 4:184182481-184182497 | 0.001425662 | |
| UTR3 | 4:184239294-184239312 | 0.057615359 | |
| UTR3 | 4:184129276-184129301 | 0.011717538 | |
| ENST00000304801 | ENSG00000170950 (PGK2) | hsa-miR-146a-5p | 0.949116 |
| UTR3 | 6:49753444-49753468 | 0.058527915 | |
| ENST00000373664 | ENSG00000080839 (RBL1) | hsa-miR-146a-5p | 0.947538 |
| UTR3 | 20:35626118-35626134 | 0.041295883 | |
| UTR3 | 20:35625851-35625867 | 0.00821791 | |
| UTR3 | 20:35625375-35625398 | 0.003819123 | |
| UTR3 | 20:35624861-35624889 | 0.003810607 | |
| UTR3 | 20:35675482-35675504 | 0.012623947 | |
| UTR3 | 20:35663864-35663884 | 0.010874714 | |
| ENST00000371079 | ENSG00000185483 (ROR1) | hsa-miR-146a-5p | 0.944332 |
| UTR3 | 1:64644620-64644632 | 0.032064351 | |
| UTR3 | 1:64645289-64645309 | 0.007921362 | |
| UTR3 | 1:64645731-64645756 | 0.016575153 | |
| UTR3 | 1:64605822-64605843 | 0.010494527 | |
| ENST00000584307 | ENSG00000176105 (YES1) | hsa-miR-146a-5p | 0.944138 |
| UTR3 | 18:723949-723963 | 0.004999566 | |
| UTR3 | 18:721758-721784 | 0.046396654 | |
| UTR3 | 18:721714-721740 | 0.005520395 | |
| ENST00000366518 | ENSG00000162849 (KIF26B) | hsa-miR-146a-5p | 0.943158 |
| UTR3 | 1:245867013-245867033 | 0.001396727 | |
| UTR3 | 1:245868440-245868461 | 0.003124656 | |
| UTR3 | 1:245869105-245869124 | 0.000935753 | |
| UTR3 | 1:245870404-245870417 | 0.002302977 | |
| UTR3 | 1:245870795-245870806 | 0.001441941 | |
| UTR3 | 1:245870899-245870913 | 0.000691472 | |
| UTR3 | 1:245872529-245872557 | 0.046210219 | |
| UTR3 | 1:245852103;245861408-245852109;245861414 | 0.012154847 | |
| ENST00000424906 | ENSG00000164053 (ATRIP) | hsa-miR-146a-5p | 0.943077 |
| UTR3 | 3:48493144-48493162 | 0.049888184 | |
| UTR3 | 3:48498687-48498705 | 0.006702531 | |
| ENST00000361621 | ENSG00000123560 (PLP1) | hsa-miR-146a-5p | 0.942031 |
| UTR3 | X:103045833-103045861 | 0.008635428 | |
| UTR3 | X:103046249-103046276 | 0.003698811 | |
| UTR3 | X:103047532-103047542 | 0.043940552 | |
| ENST00000379982 | ENSG00000164292 (RHOBTB3) | hsa-miR-146a-5p | 0.941498 |
| UTR3 | 5:95128996-95129019 | 0.016897218 | |
| UTR3 | 5:95129373-95129389 | 0.033267653 | |
| UTR3 | 5:95131310-95131323 | 0.005951106 | |
| ENST00000519163 | ENSG00000104218 (CSPP1) | hsa-miR-146a-5p | 0.941364 |

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| UTR3 | 8:68026223-68026240 | 0.044563842 | |
| UTR3 | 8:68026323-68026331 | 0.007979779 | |
| UTR3 | 8:68028274-68028300 | 0.003532602 | |
| ENST00000263773 | ENSG00000109920 (FNBP4) | hsa-miR-146a-5p | 0.940914 |
| UTR3 | 11:47738744-47738763 | 0.006688765 | |
| UTR3 | 11:47738457-47738476 | 0.048080432 | |
| UTR3 | 11:47745613-47745627 | 0.014972637 | |
| UTR3 | 11:47745605-47745627 | 0.008874075 | |
| ENST00000354371 | ENSG00000198612 (COPS8) | hsa-miR-146a-5p | 0.939224 |
| UTR3 | 2:238006581-238006589 | 0.041859037 | |
| UTR3 | 2:238008654-238008673 | 0.013594174 | |
| ENST00000395375 | ENSG00000198039 (ZNF273) | hsa-miR-146a-5p | 0.939075 |
| UTR3 | 7:64378662;64388032-64378670;64388044 | 0.014125925 | |
| UTR3 | 7:64388261-64388279 | 0.005364395 | |
| UTR3 | 7:64388429-64388447 | 0.030797464 | |
| UTR3 | 7:64388674-64388699 | 0.003209394 | |
| UTR3 | 7:64389010-64389035 | 0.001913377 | |
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| ENST00000374507 | ENSG00000204193 (TXNDC8) | hsa-miR-146a-5p | 0.936609 |
| UTR3 | 9:113085880-113085891 | 0.008513856 | |
| UTR3 | 9:113085408-113085427 | 0.004058142 | |
| UTR3 | 9:113085220-113085246 | 0.004977702 | |
| UTR3 | 9:113084886-113084900 | 0.037169489 | |
| ENST00000554546 | ENSG00000133961 (NUMB) | hsa-miR-146a-5p | 0.935898 |
| UTR3 | 14:73742656-73742664 | 0.053802238 | |
| UTR3 | 14:73743841-73743858 | 0.013267449 | |
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| ENST00000340749 | ENSG00000173262 (SLC2A14) | hsa-miR-146a-5p | 0.935551 |
| UTR3 | 12:7966791-7966807 | 0.003726273 | |
| UTR3 | 12:7966171-7966199 | 0.005629484 | |
| UTR3 | 12:7965353-7965377 | 0.014027086 | |
| UTR3 | 12:7965346-7965371 | 0.024269016 | |
| UTR3 | 12:7965199-7965224 | 0.006778283 | |
| ENST00000374864 | ENSG00000078747 (ITCH) | hsa-miR-146a-5p | 0.934822 |
| UTR3 | 20:33095721-33095734 | 0.017221974 | |
| UTR3 | 20:33096061-33096079 | 0.002212767 | |
| UTR3 | 20:33096918-33096938 | 0.001713671 | |
| UTR3 | 20:33096979-33096996 | 0.001650712 | |
| UTR3 | 20:33097624-33097643 | 0.001772097 | |
| UTR3 | 20:33098706-33098730 | 0.029662258 | |
| ENST00000396847 | ENSG00000132256 (TRIM5) | hsa-miR-146a-5p | 0.934152 |
| UTR3 | 11:5686140-5686153 | 0.003644808 | |
| UTR3 | 11:5686124-5686152 | 0.002112568 | |
| UTR3 | 11:5686109-5686127 | 0.001897926 | |
| UTR3 | 11:5685000-5685017 | 0.046399409 | |

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| ENST00000460236 | ENSG00000129292 (PHF20L1) | hsa-miR-146a-5p | 0.932921 |
| UTR3 | 8:133844538-133844560 | 0.009228918 | |
| UTR3 | 8:133851700-133851725 | 0.00469759 | |
| UTR3 | 8:133858432-133858452 | 0.010108046 | |
| UTR3 | 8:133858614-133858634 | 0.00158917 | |
| UTR3 | 8:133858696-133858718 | 0.00444692 | |
| UTR3 | 8:133858921-133858932 | 0.003045201 | |
| UTR3 | 8:133859639-133859663 | 0.02061466 | |
| ENST00000302350 | ENSG00000168564 (CDKN2AIP) | hsa-miR-146a-5p | 0.931422 |
| UTR3 | 4:184368018-184368045 | 0.035372107 | |
| UTR3 | 4:184368429-184368446 | 0.005628986 | |
| UTR3 | 4:184368700-184368718 | 0.012341869 | |
| ENST00000316529 | ENSG00000180919 (OR56B4) | hsa-miR-146a-5p | 0.93079 |
| UTR3 | 11:6130007-6130024 | 0.053181943 | |
| ENST00000366113 | ENSG00000161570 (CCL5) | hsa-miR-146a-5p | 0.930675 |
| UTR3 | 17:34198508-34198522 | 0.053152711 | |
| ENST00000450366 | ENSG00000115365 (LANCL1) | hsa-miR-146a-5p | 0.930108 |
| UTR3 | 2:211297293-211297318 | 0.009482455 | |
| UTR3 | 2:211295997-211296012 | 0.042959185 | |
| UTR3 | 2:211336783;211341040-211336800;211341047 | 0.009201432 | |
| ENST00000366918 | ENSG00000116141 (MARK1) | hsa-miR-146a-5p | 0.929721 |
| UTR3 | 1:220837230-220837245 | 0.048516216 | |
| UTR3 | 1:220837502-220837527 | 0.004396329 | |
| ENST00000366997 | ENSG00000123684 (LPGAT1) | hsa-miR-146a-5p | 0.928543 |
| UTR3 | 1:211922841-211922862 | 0.010840692 | |
| UTR3 | 1:211922561-211922589 | 0.003129534 | |
| UTR3 | 1:211922433-211922452 | 0.002264568 | |
| UTR3 | 1:211922178-211922202 | 0.00623912 | |
| UTR3 | 1:211920909-211920935 | 0.010475883 | |
| UTR3 | 1:211920631-211920657 | 0.002319689 | |
| UTR3 | 1:211920563-211920580 | 0.001169805 | |
| UTR3 | 1:211919651-211919672 | 0.006850212 | |
| UTR3 | 1:211918391-211918414 | 0.002940592 | |
| UTR3 | 1:211917953-211917975 | 0.001648773 | |
| UTR3 | 1:211917530-211917556 | 0.004741397 | |
| ENST00000544604 | ENSG00000183579 (ZNRF3) | hsa-miR-146a-5p | 0.928019 |
| UTR3 | 22:29449881-29449904 | 0.010205315 | |
| UTR3 | 22:29451365-29451388 | 0.001173897 | |
| UTR3 | 22:29451526-29451544 | 0.000662302 | |
| UTR3 | 22:29452413-29452431 | 0.001380347 | |
| UTR3 | 22:29453216-29453236 | 0.039069593 | |
| ENST00000260113 | ENSG00000137558 (PI15) | hsa-miR-146a-5p | 0.925588 |
| UTR3 | 8:75761935-75761959 | 0.003424527 | |

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| UTR3 | 8:75762125-75762147 | 0.042990623 | |
| UTR3 | 8:75762409-75762428 | 0.002062434 | |
| UTR3 | 8:75764483-75764508 | 0.001569849 | |
| UTR3 | 8:75764893-75764912 | 0.001858343 | |
| ENST00000370251 | ENSG00000063587 (ZNF275) | hsa-miR-146a-5p | 0.925555 |
| UTR3 | X:152614970-152614987 | 0.002206311 | |
| UTR3 | X:152616122-152616140 | 0.000940463 | |
| UTR3 | X:152616680-152616692 | 0.001484893 | |
| UTR3 | X:152617754-152617778 | 0.002756319 | |
| UTR3 | X:152617768-152617785 | 0.002120668 | |
| UTR3 | X:152617911-152617921 | 0.003238824 | |
| UTR3 | X:152617989-152618017 | 0.034558842 | |
| UTR3 | X:152618134-152618160 | 0.004591758 | |
| ENST00000554234 | ENSG00000166866 (MYO1A) | hsa-miR-146a-5p | 0.924313 |
| UTR3 | 12:57423326-57423342 | 0.005336016 | |
| UTR3 | 12:57422659;57422916-57422665;57422928 | 0.045615654 | |
| UTR3 | 12:57431812-57431836 | 0.009380617 | |
| ENST00000369535 | ENSG00000213281 (NRAS) | hsa-miR-146a-5p | 0.923161 |
| UTR3 | 1:115250536-115250554 | 0.046811517 | |
| UTR3 | 1:115249522-115249540 | 0.001726009 | |
| UTR3 | 1:115249198-115249223 | 0.001529511 | |
| UTR3 | 1:115248973-115248988 | 0.001271336 | |
| ENST00000321437 | ENSG00000166128 (RAB8B) | hsa-miR-146a-5p | 0.922907 |
| UTR3 | 15:63557120-63557145 | 0.002114001 | |
| UTR3 | 15:63559104-63559125 | 0.049165886 | |
| ENST00000429071 | ENSG00000006652 (IFRD1) | hsa-miR-146a-5p | 0.922065 |
| UTR3 | 7:112097939-112097954 | 0.005885721 | |
| UTR3 | 7:112098266-112098288 | 0.045201794 | |
| ENST00000261177 | ENSG00000110900 (TSPAN11) | hsa-miR-146a-5p | 0.92173 |
| UTR3 | 12:31145155-31145171 | 0.001666292 | |
| UTR3 | 12:31145630-31145647 | 0.002280426 | |
| UTR3 | 12:31145897-31145909 | 0.00371389 | |
| UTR3 | 12:31146440-31146453 | 0.000963115 | |
| UTR3 | 12:31146643-31146661 | 0.002592661 | |
| UTR3 | 12:31147861-31147882 | 0.006836254 | |
| UTR3 | 12:31148669-31148681 | 0.007370486 | |
| UTR3 | 12:31148740-31148757 | 0.001943008 | |
| UTR3 | 12:31149417-31149438 | 0.023064694 | |
| UTR3 | 12:31136085;31144791-31136085;31144809 | 0.008007945 | |
| ENST00000336125 | ENSG00000185829 (ARL17A) | hsa-miR-146a-5p | 0.921515 |
| UTR3 | 17:44634232-44634259 | 0.026691515 | |
| UTR3 | 17:44633999-44634025 | 0.008348582 | |
| UTR3 | 17:44632949-44632971 | 0.000886323 | |
| UTR3 | 17:44632032-44632059 | 0.006943577 | |

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| UTR3 | 17:44631869-44631884 | 0.002938094 | |
| UTR3 | 17:44631701-44631721 | 0.005154619 | |
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| ENST00000318426 | ENSG00000180861 (C12orf36) | hsa-miR-146a-5p | 0.921444 |
| UTR3 | 12:13525962-13525987 | 0.005662039 | |
| UTR3 | 12:13525427-13525448 | 0.045284717 | |
| ENST00000265074 | ENSG00000113389 (NPR3) | hsa-miR-146a-5p | 0.920783 |
| UTR3 | 5:32788326-32788341 | 0.005063542 | |
| UTR3 | 5:32789259-32789282 | 0.001856385 | |
| UTR3 | 5:32790776-32790803 | 0.004052495 | |
| UTR3 | 5:32791778-32791803 | 0.039825615 | |
| ENST00000424319 | ENSG00000086991 (NOX4) | hsa-miR-146a-5p | 0.920029 |
| UTR3 | 11:89059686-89059705 | 0.050629889 | |
| ENST00000476605 | ENSG00000107745 (MICU1) | hsa-miR-146a-5p | 0.919173 |
| UTR3 | 10:74127739-74127766 | 0.021375193 | |
| UTR3 | 10:74127607-74127631 | 0.029065472 | |
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| ENST00000360669 | ENSG00000170074 (FAM153A) | hsa-miR-146a-5p | 0.918663 |
| UTR3 | 5:177144235-177144262 | 0.001179086 | |
| UTR3 | 5:177143395-177143415 | 0.031010738 | |
| UTR3 | 5:177139381-177139401 | 0.013043851 | |
| UTR3 | 5:177139117-177139140 | 0.005095101 | |
| ENST00000299550 | ENSG00000166436 (TRIM66) | hsa-miR-146a-5p | 0.918273 |
| UTR3 | 11:8638466-8638486 | 0.01929223 | |
| UTR3 | 11:8638206-8638226 | 0.005438195 | |
| UTR3 | 11:8637527-8637540 | 0.003362398 | |
| UTR3 | 11:8637227-8637245 | 0.00153674 | |
| UTR3 | 11:8635936-8635951 | 0.001573441 | |
| UTR3 | 11:8635132-8635150 | 0.005661055 | |
| UTR3 | 11:8634841-8634856 | 0.001369855 | |
| UTR3 | 11:8634624-8634640 | 0.009883872 | |
| UTR3 | 11:8667374-8667389 | 0.022137617 | |
| UTR3 | 11:8661979-8662004 | 0.002903856 | |
| ENST00000335154 | ENSG00000161791 (FMNL3) | hsa-miR-146a-5p | 0.917803 |
| UTR3 | 12:50037697-50037717 | 0.002261838 | |
| UTR3 | 12:50037210-50037232 | 0.004385479 | |
| UTR3 | 12:50036966-50036985 | 0.001008182 | |
| UTR3 | 12:50036618-50036642 | 0.00119013 | |
| UTR3 | 12:50034965-50034986 | 0.001897461 | |
| UTR3 | 12:50034472-50034492 | 0.002054045 | |
| UTR3 | 12:50034022-50034042 | 0.001624567 | |
| UTR3 | 12:50033814-50033834 | 0.001833513 | |
| UTR3 | 12:50031814-50031836 | 0.033886252 | |
| ENST00000442398 | ENSG00000168014 (C2CD3) | hsa-miR-146a-5p | 0.916923 |
| UTR3 | 11:73745278-73745305 | 0.04254337 | |
| UTR3 | 11:73744766-73744782 | 0.004660191 | |
| UTR3 | 11:73724449-73724477 | 0.002354983 | |

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| UTR3 | 11:73796788-73796800 | 0.00509441 | |
| ENST00000408967 | ENSG00000221870 (TMEM257) | hsa-miR-146a-5p | 0.916465 |
| UTR3 | X:144909686-144909709 | 0.008712472 | |
| UTR3 | X:144910653-144910680 | 0.005533041 | |
| UTR3 | X:144911080-144911102 | 0.003643757 | |
| UTR3 | X:144911277-144911293 | 0.031964498 | |
| ENST00000395407 | ENSG00000137819 (PAQR5) | hsa-miR-146a-5p | 0.916403 |
| UTR3 | 15:69696768-69696789 | 0.029856955 | |
| UTR3 | 15:69697095-69697121 | 0.006735723 | |
| UTR3 | 15:69697431-69697449 | 0.004094715 | |
| UTR3 | 15:69698728-69698753 | 0.002134986 | |
| UTR3 | 15:69698851-69698868 | 0.00090138 | |
| UTR3 | 15:69699893-69699907 | 0.006116821 | |
| ENST00000524849 | ENSG00000173653 (RCE1) | hsa-miR-146a-5p | 0.916164 |
| UTR3 | 11:66612705;66612971-66612708;66612983 | 0.041078409 | |
| UTR3 | 11:66613919-66613940 | 0.00871117 | |
| ENST00000394323 | ENSG00000213462 (ERV3-1) | hsa-miR-146a-5p | 0.914867 |
| UTR3 | 7:64451557-64451579 | 0.04951551 | |
| ENST00000362063 | ENSG00000198740 (ZNF652) | hsa-miR-146a-5p | 0.9135 |
| UTR3 | 17:47375686-47375712 | 0.023335745 | |
| UTR3 | 17:47373732-47373758 | 0.001634123 | |
| UTR3 | 17:47372307-47372323 | 0.004963695 | |
| UTR3 | 17:47372208-47372230 | 0.014409093 | |
| UTR3 | 17:47371929-47371956 | 0.004887987 | |
| ENST00000333926 | ENSG00000122873 (CISD1) | hsa-miR-146a-5p | 0.913124 |
| UTR3 | 10:60047725-60047744 | 0.007840666 | |
| UTR3 | 10:60048611-60048639 | 0.003933345 | |
| UTR3 | 10:60049120-60049138 | 0.03737915 | |
| ENST00000398146 | ENSG00000185304 (RGPD2) | hsa-miR-146a-5p | 0.913064 |
| UTR3 | 2:88055771-88055793 | 0.049140704 | |
| ENST00000327827 | ENSG00000182831 (C16orf72) | hsa-miR-146a-5p | 0.912795 |
| UTR3 | 16:9211053-9211075 | 0.008908725 | |
| UTR3 | 16:9211896-9211916 | 0.03717986 | |
| UTR3 | 16:9215427-9215444 | 0.002996832 | |
| ENST00000415914 | ENSG00000177683 (THAP5) | hsa-miR-146a-5p | 0.912487 |
| UTR3 | 7:108204540-108204557 | 0.049022337 | |
| ENST00000450908 | ENSG00000231880 (KBTBD4) | hsa-miR-146a-5p | 0.910796 |
| UTR3 | 11:47599497-47599516 | 0.048679269 | |
| ENST00000436010 | ENSG00000169855 (ROBO1) | hsa-miR-146a-5p | 0.910675 |
| UTR3 | 3:78646395-78646421 | 0.048654833 | |
| ENST00000394670 | ENSG00000010244 (ZNF207) | hsa-miR-146a-5p | 0.910317 |
| UTR3 | 17:30696800-30696825 | 0.01318423 | |
| UTR3 | 17:30698222-30698243 | 0.001600884 | |

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| UTR3 | 17:30699372-30699383 | 0.001199639 | |
| UTR3 | 17:30702968-30702979 | 0.001943835 | |
| UTR3 | 17:30703542-30703555 | 0.001183252 | |
| UTR3 | 17:30704495-30704515 | 0.001390638 | |
| UTR3 | 17:30705340-30705354 | 0.001717228 | |
| UTR3 | 17:30708425-30708448 | 0.026363328 | |
| ENST00000306434 | ENSG00000168906 (MAT2A) | hsa-miR-146a-5p | 0.910234 |
| UTR3 | 2:85772336-85772353 | 0.048566439 | |
| ENST00000300087 | ENSG00000166847 (DCTN5) | hsa-miR-146a-5p | 0.910023 |
| UTR3 | 16:23678593-23678608 | 0.007561034 | |
| UTR3 | 16:23680144-23680172 | 0.021977088 | |
| UTR3 | 16:23680764-23680784 | 0.017467979 | |
| UTR3 | 16:23654313-23654336 | 0.016710802 | |
| ENST00000379638 | ENSG00000129625 (REEP5) | hsa-miR-146a-5p | 0.908794 |
| UTR3 | 5:112212087-112212099 | 0.048280475 | |
| ENST00000375255 | ENSG00000115827 (DCAF17) | hsa-miR-146a-5p | 0.908514 |
| UTR3 | 2:172338227-172338243 | 0.003050827 | |
| UTR3 | 2:172338359-172338375 | 0.009737604 | |
| UTR3 | 2:172340399-172340424 | 0.014980952 | |
| UTR3 | 2:172341266-172341292 | 0.017594567 | |
| UTR3 | 2:172333382-172333408 | 0.028713584 | |
| ENST00000381605 | ENSG00000101307 (SIRPB1) | hsa-miR-146a-5p | 0.907723 |
| UTR3 | 20:1545749-1545769 | 0.004855969 | |
| UTR3 | 20:1544460-1544479 | 0.027308652 | |
| UTR3 | 20:1544439-1544463 | 0.015905696 | |
| ENST00000316433 | ENSG00000171817 (ZNF540) | hsa-miR-146a-5p | 0.907103 |
| UTR3 | 19:38104290-38104304 | 0.046686974 | |
| UTR3 | 19:38103603-38103623 | 0.013643207 | |
| ENST00000453634 | ENSG00000254413 (CHKB-CPT1B) | hsa-miR-146a-5p | 0.907012 |
| UTR3 | 22:51008017-51008031 | 0.047932122 | |
| ENST00000569722 | ENSG00000267127 (RP11-795F19.5) | hsa-miR-146a-5p | 0.905808 |
| UTR3 | 18:77829827-77829842 | 0.011041003 | |
| UTR3 | 18:77854277-77854303 | 0.002062248 | |
| UTR3 | 18:77854744-77854767 | 0.006212056 | |
| UTR3 | 18:77854764-77854782 | 0.028384965 | |
| ENST00000326505 | ENSG00000176597 (B3GNT5) | hsa-miR-146a-5p | 0.905589 |
| UTR3 | 3:182988964-182988988 | 0.04534622 | |
| UTR3 | 3:182990217-182990240 | 0.002311973 | |
| ENST00000306156 | ENSG00000171132 (PRKCE) | hsa-miR-146a-5p | 0.905578 |
| UTR3 | 2:46413327-46413339 | 0.002120682 | |
| UTR3 | 2:46413959-46413981 | 0.018235749 | |
| UTR3 | 2:46414504-46414528 | 0.021886314 | |
| UTR3 | 2:46414757-46414780 | 0.005413373 | |

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| ENST00000326080 | ENSG00000170271 (FAXDC2) | hsa-miR-146a-5p | 0.90524 |
| UTR3 | 5:154198689-154198705 | 0.029777327 | |
| UTR3 | 5:154198409-154198437 | 0.017814433 | |
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| ENST00000539768 | ENSG00000177058 (SLC38A9) | hsa-miR-146a-5p | 0.903343 |
| UTR3 | 5:54931034-54931054 | 0.032035071 | |
| UTR3 | 5:54930538-54930564 | 0.009853264 | |
| UTR3 | 5:54922107-54922116 | 0.005345041 | |
| ENST00000398532 | ENSG00000188895 (MSL1) | hsa-miR-146a-5p | 0.902927 |
| UTR3 | 17:38290995-38291015 | 0.003315317 | |
| UTR3 | 17:38292279-38292300 | 0.006035168 | |
| UTR3 | 17:38292586-38292603 | 0.007284066 | |
| UTR3 | 17:38292805-38292819 | 0.03052112 | |
| ENST00000263816 | ENSG00000081479 (LRP2) | hsa-miR-146a-5p | 0.902583 |
| UTR3 | 2:169984508-169984532 | 0.002551397 | |
| UTR3 | 2:169983727-169983753 | 0.042135638 | |
| UTR3 | 2:170136060-170136075 | 0.01078508 | |
| UTR3 | 2:170033059-170033081 | 0.006143526 | |
| UTR3 | 2:170011040-170011058 | 0.006353665 | |
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| ENST00000491143 | ENSG00000119547 (ONECUT2) | hsa-miR-146a-5p | 0.901601 |
| UTR3 | 18:55144188-55144204 | 0.003519184 | |
| UTR3 | 18:55145988-55146008 | 0.003749262 | |
| UTR3 | 18:55146219-55146241 | 0.002982475 | |
| UTR3 | 18:55146682-55146703 | 0.00150389 | |
| UTR3 | 18:55147026-55147044 | 0.001423307 | |
| UTR3 | 18:55147099-55147115 | 0.00055766 | |
| UTR3 | 18:55148184-55148203 | 0.006033746 | |
| UTR3 | 18:55149145-55149168 | 0.000613774 | |
| UTR3 | 18:55149622-55149648 | 0.00183181 | |
| UTR3 | 18:55149927-55149938 | 0.004258154 | |
| UTR3 | 18:55153730-55153748 | 0.003697044 | |
| UTR3 | 18:55157187-55157201 | 0.001715215 | |
| UTR3 | 18:55157278-55157300 | 0.004850741 | |
| UTR3 | 18:55157307-55157333 | 0.000834621 | |
| UTR3 | 18:55157510-55157529 | 0.00854619 | |
| UTR3 | 18:55157541-55157559 | 0.000792845 | |
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| ENST00000338957 | ENSG00000102053 (ZC3H12B) | hsa-miR-146a-5p | 0.901432 |
| UTR3 | X:64726080-64726102 | 0.005939501 | |
| UTR3 | X:64727241-64727268 | 0.040939248 | |
| ENST00000392288 | ENSG00000196268 (ZNF493) | hsa-miR-146a-5p | 0.901147 |
| UTR3 | 19:21607918-21607943 | 0.00585188 | |
| UTR3 | 19:21608004-21608027 | 0.038476993 | |
| UTR3 | 19:21588650;21605715-21588658;21605727 | 0.023740422 | |

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| ENST00000447404 | ENSG00000165209 (STRBP) | hsa-miR-146a-5p | 0.900243 |
| UTR3 | 9:125887711-125887732 | 0.026839795 | |
| UTR3 | 9:125885022-125885047 | 0.003336137 | |
| UTR3 | 9:125884552-125884571 | 0.008603742 | |
| UTR3 | 9:125884008-125884035 | 0.007881634 | |
| ENST00000591537 | ENSG00000196263 (ZNF471) | hsa-miR-146a-5p | 0.899449 |
| UTR3 | 19:57041044-57041067 | 0.023458668 | |
| UTR3 | 19:57041301-57041321 | 0.023058558 | |
| ENST00000551568 | ENSG00000135678 (CPM) | hsa-miR-146a-5p | 0.898884 |
| UTR3 | 12:69249441-69249463 | 0.03162357 | |
| UTR3 | 12:69247760-69247787 | 0.001653194 | |
| UTR3 | 12:69247753-69247773 | 0.001957846 | |
| UTR3 | 12:69245942-69245968 | 0.003060302 | |
| UTR3 | 12:69244979-69245002 | 0.008120599 | |
| ENST00000326958 | ENSG00000181495 (AC026703.1) | hsa-miR-146a-5p | 0.898505 |
| UTR3 | 5:32790776-32790803 | 0.004539658 | |
| UTR3 | 5:32791778-32791803 | 0.04180779 | |
| ENST00000397121 | ENSG00000196109 (ZNF676) | hsa-miR-146a-5p | 0.898419 |
| UTR3 | 19:22362713-22362732 | 0.003751524 | |
| UTR3 | 19:22362378-22362404 | 0.033317623 | |
| UTR3 | 19:22364376;22375818-22364388;22375826 | 0.021221949 | |
| UTR3 | 19:22363889-22363907 | 0.029598937 | |
| UTR3 | 19:22363049-22363074 | 0.013451312 | |
| ENST00000449592 | ENSG00000188735 (TMEM120B) | hsa-miR-146a-5p | 0.897705 |
| UTR3 | 12:122214126-122214152 | 0.038357299 | |
| UTR3 | 12:122216502-122216515 | 0.007847142 | |
| ENST00000595401 | ENSG00000118620 (ZNF430) | hsa-miR-146a-5p | 0.897022 |
| UTR3 | 19:21217638-21217664 | 0.023164185 | |
| UTR3 | 19:21218082-21218093 | 0.022919049 | |
| ENST00000379882 | ENSG00000107201 (DDX58) | hsa-miR-146a-5p | 0.896644 |
| UTR3 | 9:32456226-32456244 | 0.003854819 | |
| UTR3 | 9:32456205-32456218 | 0.001906753 | |
| UTR3 | 9:32456145-32456171 | 0.003219557 | |
| UTR3 | 9:32455476-32455501 | 0.037035461 | |
| ENST00000355585 | ENSG00000078269 (SYNJ2) | hsa-miR-146a-5p | 0.8965 |
| UTR3 | 6:158517676-158517701 | 0.02126433 | |
| UTR3 | 6:158518254-158518271 | 0.002872755 | |
| UTR3 | 6:158519169-158519188 | 0.001796125 | |
| UTR3 | 6:158519527-158519553 | 0.012844049 | |
| UTR3 | 6:158519773-158519797 | 0.003605396 | |
| UTR3 | 6:158519873-158519896 | 0.003608452 | |
| ENST00000336078 | ENSG00000074657 (ZNF532) | hsa-miR-146a-5p | 0.896344 |
| UTR3 | 18:56652900-56652915 | 0.014475897 | |
| UTR3 | 18:56653289-56653316 | 0.030729767 | |

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| UTR3 | 18:56606724-56606742 | 0.007542597 | |
| ENST00000359856 | ENSG00000162704 (ARPC5) | hsa-miR-146a-5p | 0.896009 |
| UTR3 | 1:183595583-183595599 | 0.045904877 | |
| ENST00000375537 | ENSG00000204371 (EHMT2) | hsa-miR-146a-5p | 0.894287 |
| UTR3 | 6:31847560-31847585 | 0.045605021 | |
| ENST00000424486 | ENSG00000166292 (TMEM100) | hsa-miR-146a-5p | 0.894059 |
| UTR3 | 17:53797191-53797215 | 0.045565667 | |
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| ENST00000313732 | ENSG00000153786 (ZDHHC7) | hsa-miR-146a-5p | 0.893061 |
| UTR3 | 16:85008068-85008076 | 0.044685195 | |
| UTR3 | 16:85009955-85009982 | 0.006863536 | |
| ENST00000483536 | ENSG00000139910 (NOVA1) | hsa-miR-146a-5p | 0.892508 |
| UTR3 | 14:26916955-26916970 | 0.00399913 | |
| UTR3 | 14:26916559-26916568 | 0.003843866 | |
| UTR3 | 14:26916476-26916503 | 0.02011346 | |
| UTR3 | 14:26915325-26915351 | 0.010102665 | |
| UTR3 | 14:26913829-26913849 | 0.003147154 | |
| UTR3 | 14:27064730-27064754 | 0.033568342 | |
| | | | |
| ENST00000268182 | ENSG00000140575 (IQGAP1) | hsa-miR-146a-5p | 0.89201 |
| UTR3 | 15:91045257-91045285 | 0.045215006 | |
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| ENST00000491718 | ENSG00000090905 (TNRC6A) | hsa-miR-146a-5p | 0.891757 |
| UTR3 | 16:24801462-24801480 | 0.004358792 | |
| UTR3 | 16:24815565-24815588 | 0.002044444 | |
| UTR3 | 16:24817017-24817038 | 0.002737361 | |
| UTR3 | 16:24835516-24835539 | 0.003755898 | |
| UTR3 | 16:24835837-24835860 | 0.005342668 | |
| UTR3 | 16:24836045-24836069 | 0.0136901 | |
| UTR3 | 16:24836846-24836864 | 0.013242877 | |
| ENST00000377200 | ENSG00000188647 (PTAR1) | hsa-miR-146a-5p | 0.891389 |
| UTR3 | 9:72333010-72333037 | 0.005492955 | |
| UTR3 | 9:72332979-72332991 | 0.003742988 | |
| UTR3 | 9:72332509-72332524 | 0.008094394 | |
| UTR3 | 9:72329658-72329675 | 0.012031297 | |
| UTR3 | 9:72329117-72329143 | 0.00251719 | |
| UTR3 | 9:72326404-72326423 | 0.001804407 | |
| UTR3 | 9:72325873-72325899 | 0.011426724 | |
| | | | |
| ENST00000486333 | ENSG00000225932 (CTAGE4) | hsa-miR-146a-5p | 0.890329 |
| UTR3 | 7:143883082-143883105 | 0.017471703 | |
| UTR3 | 7:143883118-143883135 | 0.027460037 | |
| | | | |
| ENST00000487179 | ENSG00000244693 (CTAGE8) | hsa-miR-146a-5p | 0.890214 |
| UTR3 | 7:143963835-143963858 | 0.017426257 | |
| UTR3 | 7:143963805-143963822 | 0.027486165 | |

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| ENST00000409085 | ENSG00000115977 (AAK1) | hsa-miR-146a-5p | 0.88979 |
| UTR3 | 2:69702769-69702795 | 0.007645494 |  |
| UTR3 | 2:69702291-69702312 | 0.00306278 |  |
| UTR3 | 2:69699316-69699334 | 0.001339128 |  |
| UTR3 | 2:69699055-69699080 | 0.001739327 |  |
| UTR3 | 2:69697383-69697409 | 0.0014199 |  |
| UTR3 | 2:69696254-69696277 | 0.001304689 |  |
| UTR3 | 2:69696000-69696015 | 0.002036837 |  |
| UTR3 | 2:69695887-69695911 | 0.026293546 |  |
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| ENST00000237937 | ENSG00000107372 (ZFAND5) | hsa-miR-146a-5p | 0.88909 |
| UTR3 | 9:74970770-74970795 | 0.011220361 |  |
| UTR3 | 9:74966898-74966919 | 0.033504992 |  |
| ENST00000296028 | ENSG00000163736 (PPBP) | hsa-miR-146a-5p | 0.888667 |
| UTR3 | 4:74852912-74852935 | 0.044655385 |  |
| ENST00000532519 | ENSG00000149428 (HYOU1) | hsa-miR-146a-5p | 0.888643 |
| UTR3 | 11:118925757;118925897-118925772;118925901 | 0.023742511 |  |
| UTR3 | 11:118925729-118925757 | 0.017257334 |  |
| UTR3 | 11:118925714-118925739 | 0.003651588 |  |
| ENST00000398417 | ENSG00000141646 (SMAD4) | hsa-miR-146a-5p | 0.88844 |
| UTR3 | 18:48605219-48605234 | 0.042237913 |  |
| UTR3 | 18:48609915-48609940 | 0.00237992 |  |
| ENST00000376351 | ENSG00000151025 (GPR158) | hsa-miR-146a-5p | 0.888382 |
| UTR3 | 10:25889496-25889516 | 0.003005168 |  |
| UTR3 | 10:25890087-25890113 | 0.00275966 |  |
| UTR3 | 10:25890697-25890713 | 0.005908377 |  |
| UTR3 | 10:25890869-25890894 | 0.025376522 |  |
| UTR3 | 10:25891023-25891036 | 0.006377155 |  |
| UTR3 | 10:25887823-25887840 | 0.010736726 |  |
| ENST00000409558 | ENSG00000143952 (VPS54) | hsa-miR-146a-5p | 0.88802 |
| UTR3 | 2:64119695-64119713 | 0.044548806 |  |
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| ENST00000217130 | ENSG00000196700 (ZNF512B) | hsa-miR-146a-5p | 0.887447 |
| UTR3 | 20:62591149-62591175 | 0.015982295 |  |
| UTR3 | 20:62588308-62588331 | 0.028472553 |  |
| ENST00000434009 | ENSG00000009413 (REV3L) | hsa-miR-146a-5p | 0.886964 |
| UTR3 | 6:111793223-111793241 | 0.007616599 |  |
| UTR3 | 6:111737582-111737603 | 0.005373804 |  |
| UTR3 | 6:111710332-111710358 | 0.003835714 |  |
| UTR3 | 6:111709223-111709249 | 0.003202364 |  |
| UTR3 | 6:111709069-111709081 | 0.003993808 |  |
| UTR3 | 6:111697636-111697658 | 0.002273759 |  |
| UTR3 | 6:111695228-111695248 | 0.00264594 |  |
| UTR3 | 6:111695035-111695052 | 0.002568533 |  |
| UTR3 | 6:111694760-111694772 | 0.001761053 |  |
| UTR3 | 6:111688770-111688794 | 0.001953287 |  |

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| UTR3 | 6:111685138-111685160 | 0.002288742 | |
| UTR3 | 6:111654417-111654443 | 0.001460498 | |
| UTR3 | 6:111632447-111632460 | 0.003524855 | |
| UTR3 | 6:111631101-111631122 | 0.00187689 | |

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| ENST00000249064 | ENSG00000159873 (CCDC117) | hsa-miR-146a-5p | 0.886368 |
| UTR3 | 22:29184985-29185006 | 0.044278921 | |
| ENST00000335251 | ENSG00000164066 (INTU) | hsa-miR-146a-5p | 0.885591 |
| UTR3 | 4:128637931-128637959 | 0.00461416 | |
| UTR3 | 4:128638344-128638357 | 0.00488379 | |
| UTR3 | 4:128639350-128639370 | 0.002532676 | |
| UTR3 | 4:128639403-128639422 | 0.000519055 | |
| UTR3 | 4:128639456-128639475 | 0.002227915 | |
| UTR3 | 4:128639816-128639836 | 0.005405006 | |
| UTR3 | 4:128642615-128642641 | 0.000779584 | |
| UTR3 | 4:128642792-128642804 | 0.006355016 | |
| UTR3 | 4:128642925-128642951 | 0.015527957 | |
| UTR3 | 4:128643219-128643237 | 0.001308123 | |

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| ENST00000376773 | ENSG00000204619 (PPP1R11) | hsa-miR-146a-5p | 0.885378 |
| UTR3 | 6:30037325-30037348 | 0.025670123 | |
| UTR3 | 6:30037614-30037624 | 0.002681037 | |
| UTR3 | 6:30037941-30037960 | 0.015767847 | |
| ENST00000541208 | ENSG00000182983 (ZNF662) | hsa-miR-146a-5p | 0.883529 |
| UTR3 | 3:42957613-42957630 | 0.004358254 | |
| UTR3 | 3:42958676-42958701 | 0.001037858 | |
| UTR3 | 3:42959183-42959209 | 0.001931125 | |
| UTR3 | 3:42959920-42959943 | 0.00118073 | |
| UTR3 | 3:42960751-42960764 | 0.035315211 | |
| ENST00000608642 | ENSG00000133424 (LARGE) | hsa-miR-146a-5p | 0.883427 |
| UTR3 | 22:33562218-33562242 | 0.005438238 | |
| UTR3 | 22:33561426-33561447 | 0.00204529 | |
| UTR3 | 22:33560358-33560379 | 0.002123222 | |
| UTR3 | 22:33559949-33559964 | 0.000860168 | |
| UTR3 | 22:33558499-33558512 | 0.00934069 | |
| UTR3 | 22:33558373-33558396 | 0.02399942 | |
| ENST00000240093 | ENSG00000104290 (FZD3) | hsa-miR-146a-5p | 0.883314 |
| UTR3 | 8:28420938-28420959 | 0.005381406 | |
| UTR3 | 8:28421095-28421112 | 0.003649304 | |
| UTR3 | 8:28422617-28422627 | 0.001436096 | |
| UTR3 | 8:28423412-28423436 | 0.005613947 | |
| UTR3 | 8:28426923-28426946 | 0.001676104 | |
| UTR3 | 8:28426993-28427015 | 0.003267751 | |
| UTR3 | 8:28427337-28427354 | 0.003280566 | |
| UTR3 | 8:28428185-28428206 | 0.002777862 | |
| UTR3 | 8:28428204-28428225 | 0.000592374 | |
| UTR3 | 8:28428488-28428502 | 0.001073201 | |

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| UTR3 | 8:28428566-28428583 | 0.00165531 | |
| UTR3 | 8:28429191-28429209 | 0.002333534 | |
| UTR3 | 8:28429650-28429670 | 0.001477027 | |
| UTR3 | 8:28429843-28429859 | 0.001904996 | |
| UTR3 | 8:28431166-28431180 | 0.003786649 | |
| UTR3 | 8:28420388-28420407 | 0.030120813 | |
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| ENST00000361320 | ENSG00000198739 (LRRTM3) | hsa-miR-146a-5p | 0.882552 |
| UTR3 | 10:68858248-68858256 | 0.043668663 | |
| ENST00000367667 | ENSG00000143207 (RFWD2) | hsa-miR-146a-5p | 0.882188 |
| UTR3 | 1:176085761-176085784 | 0.040439318 | |
| UTR3 | 1:175956150-175956167 | 0.003172006 | |
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| ENST00000318887 | ENSG00000179021 (C3orf38) | hsa-miR-146a-5p | 0.882017 |
| UTR3 | 3:88206295-88206309 | 0.040289984 | |
| UTR3 | 3:88206476-88206500 | 0.003294384 | |
| ENST00000295461 | ENSG00000163293 (NIPAL1) | hsa-miR-146a-5p | 0.881988 |
| UTR3 | 4:48038629-48038643 | 0.004049145 | |
| UTR3 | 4:48039236-48039264 | 0.002710576 | |
| UTR3 | 4:48039901-48039916 | 0.002117295 | |
| UTR3 | 4:48041848-48041875 | 0.005744103 | |
| UTR3 | 4:48042049-48042063 | 0.02698864 | |
| UTR3 | 4:48035069-48035096 | 0.016447884 | |
| ENST00000538204 | ENSG00000076770 (MBNL3) | hsa-miR-146a-5p | 0.8819 |
| UTR3 | X:131512813-131512832 | 0.003660399 | |
| UTR3 | X:131510555-131510567 | 0.00127024 | |
| UTR3 | X:131507596-131507615 | 0.022315026 | |
| UTR3 | X:131505209-131505226 | 0.003127786 | |
| UTR3 | X:131504841-131504867 | 0.001775066 | |
| UTR3 | X:131504727-131504743 | 0.000713365 | |
| UTR3 | X:131503558-131503585 | 0.010704179 | |
| ENST00000581347 | ENSG00000206432 (TMEM200C) | hsa-miR-146a-5p | 0.880879 |
| UTR3 | 18:5889722-5889748 | 0.033788632 | |
| UTR3 | 18:5889178-5889194 | 0.002272513 | |
| UTR3 | 18:5888359-5888375 | 0.001716028 | |
| UTR3 | 18:5882620-5882641 | 0.005629241 | |
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| ENST00000331343 | ENSG00000186866 (POFUT2) | hsa-miR-146a-5p | 0.880671 |
| UTR3 | 21:46687294-46687309 | 0.033412011 | |
| UTR3 | 21:46686477-46686505 | 0.001633298 | |
| UTR3 | 21:46685616-46685639 | 0.003438071 | |
| UTR3 | 21:46685583-46685604 | 0.000804293 | |
| UTR3 | 21:46684063-46684081 | 0.004086357 | |
| ENST00000371655 | ENSG00000169213 (RAB3B) | hsa-miR-146a-5p | 0.880267 |
| UTR3 | 1:52385438-52385452 | 0.004249603 | |
| UTR3 | 1:52385176-52385199 | 0.003765413 | |

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| UTR3 | 1:52380232-52380257 | 0.002078708 | |
| UTR3 | 1:52378822-52378846 | 0.001544235 | |
| UTR3 | 1:52378484-52378510 | 0.001376216 | |
| UTR3 | 1:52377133-52377149 | 0.007168358 | |
| UTR3 | 1:52377124-52377149 | 0.00065915 | |
| UTR3 | 1:52376920-52376930 | 0.00179184 | |
| UTR3 | 1:52376902-52376923 | 0.003109456 | |
| UTR3 | 1:52376756-52376773 | 0.000882303 | |
| UTR3 | 1:52375950-52375975 | 0.001363112 | |
| UTR3 | 1:52373898-52373922 | 0.011145842 | |
| UTR3 | 1:52373852-52373865 | 0.004177053 | |
| ENST00000368069 | ENSG00000122218 (COPA) | hsa-miR-146a-5p | 0.880251 |
| UTR3 | 1:160259756-160259781 | 0.004712116 | |
| UTR3 | 1:160259103-160259114 | 0.030142655 | |
| UTR3 | 1:160259094-160259114 | 0.008454108 | |
| | | | |
| ENST00000310823 | ENSG00000151694 (ADAM17) | hsa-miR-146a-5p | 0.879744 |
| UTR3 | 2:9628760-9628782 | 0.043230345 | |
| ENST00000395745 | ENSG00000132153 (DHX30) | hsa-miR-146a-5p | 0.879602 |
| UTR3 | 3:47868867-47868884 | 0.010499306 | |
| UTR3 | 3:47890563;47890682-47890569;47890701 | 0.032709078 | |
| ENST00000339140 | ENSG00000189299 (FOXR2) | hsa-miR-146a-5p | 0.879586 |
| UTR3 | X:55651752-55651771 | 0.043206027 | |
| ENST00000309395 | ENSG00000173542 (MOB1B) | hsa-miR-146a-5p | 0.879435 |
| UTR3 | 4:71849989-71850014 | 0.00375675 | |
| UTR3 | 4:71851570-71851590 | 0.001170711 | |
| UTR3 | 4:71851860-71851876 | 0.002008575 | |
| UTR3 | 4:71852727-71852748 | 0.023385586 | |
| UTR3 | 4:71853025-71853045 | 0.011921542 | |
| UTR3 | 4:71824633-71824647 | 0.008073214 | |
| ENST00000328252 | ENSG00000182752 (PAPPA) | hsa-miR-146a-5p | 0.879265 |
| UTR3 | 9:119160213-119160234 | 0.004440191 | |
| UTR3 | 9:119164075-119164103 | 0.024064301 | |
| UTR3 | 9:119164424-119164449 | 0.014652078 | |
| ENST00000608933 | ENSG00000163644 (PPM1K) | hsa-miR-146a-5p | 0.879089 |
| UTR3 | 4:89183238-89183265 | 0.010689188 | |
| UTR3 | 4:89182614-89182626 | 0.019410223 | |
| UTR3 | 4:89180468-89180488 | 0.001313765 | |
| UTR3 | 4:89179317-89179329 | 0.011716216 | |
| ENST00000380317 | ENSG00000099385 (BCL7C) | hsa-miR-146a-5p | 0.878849 |
| UTR3 | 16:30845329-30845350 | 0.035413459 | |
| UTR3 | 16:30845301-30845322 | 0.004898895 | |
| UTR3 | 16:30844989-30845017 | 0.00278017 | |
| ENST00000460930 | ENSG00000203690 (TCP10) | hsa-miR-146a-5p | 0.878305 |
| UTR3 | 6:167787895-167787923 | 0.001763689 | |
| UTR3 | 6:167787702-167787713 | 0.003032952 | |

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| UTR3 | 6:167787514-167787535 | 0.038212567 | |
| ENST00000357758 | ENSG00000100523 (DDHD1) | hsa-miR-146a-5p | 0.878237 |
| UTR3 | 14:53512826-53512840 | 0.005164165 | |
| UTR3 | 14:53512326-53512336 | 0.006423995 | |
| UTR3 | 14:53511768-53511787 | 0.002381937 | |
| UTR3 | 14:53511282-53511300 | 0.027661878 | |
| UTR3 | 14:53521304-53521326 | 0.011422172 | |

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| ENST00000194672 | ENSG00000082269 (FAM135A) | hsa-miR-146a-5p | 0.877001 |
| UTR3 | 6:71195889-71195908 | 0.008035908 | |
| UTR3 | 6:71233713-71233728 | 0.016936981 | |
| UTR3 | 6:71235897-71235924 | 0.011808879 | |
| UTR3 | 6:71270245-71270273 | 0.006029027 | |

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| ENST00000530332 | ENSG00000170619 (COMMD5) | hsa-miR-146a-5p | 0.876235 |
| UTR3 | 8:146066574-146066591 | 0.042694905 | |

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| ENST00000304129 | ENSG00000169129 (AFAP1L2) | hsa-miR-146a-5p | 0.875534 |
| UTR3 | 10:116055322-116055340 | 0.009606495 | |
| UTR3 | 10:116054710-116054735 | 0.031486802 | |
| UTR3 | 10:116061203-116061224 | 0.012209933 | |

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| ENST00000361170 | ENSG00000183856 (IQGAP3) | hsa-miR-146a-5p | 0.875294 |
| UTR3 | 1:156496153-156496168 | 0.002159496 | |
| UTR3 | 1:156495653-156495677 | 0.003310611 | |
| UTR3 | 1:156495502-156495520 | 0.033857824 | |
| UTR3 | 1:156495337-156495352 | 0.003225716 | |
| ENST00000288266 | ENSG00000157500 (APPL1) | hsa-miR-146a-5p | 0.874913 |
| UTR3 | 3:57304401-57304419 | 0.038551479 | |
| UTR3 | 3:57306092-57306118 | 0.001315601 | |
| UTR3 | 3:57306834-57306849 | 0.00262959 | |

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| ENST00000559228 | ENSG00000128923 (FAM63B) | hsa-miR-146a-5p | 0.874039 |
| UTR3 | 15:59150524-59150539 | 0.002401236 | |
| UTR3 | 15:59151236-59151262 | 0.00215856 | |
| UTR3 | 15:59151686-59151708 | 0.003835109 | |
| UTR3 | 15:59151766-59151792 | 0.000673299 | |
| UTR3 | 15:59152813-59152828 | 0.018873515 | |
| UTR3 | 15:59153503-59153529 | 0.014424807 | |
| ENST00000377669 | ENSG00000118922 (KLF12) | hsa-miR-146a-5p | 0.873972 |
| UTR3 | 13:74268339-74268365 | 0.017585594 | |
| UTR3 | 13:74264581-74264602 | 0.001824137 | |
| UTR3 | 13:74264573-74264597 | 0.000583357 | |
| UTR3 | 13:74262746-74262767 | 0.001549094 | |
| UTR3 | 13:74262675-74262694 | 0.00055678 | |
| UTR3 | 13:74262479-74262505 | 0.008213742 | |
| UTR3 | 13:74262110-74262137 | 0.000972156 | |

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| UTR3 | 13:74260424-74260448 | 0.006680963 | |
| UTR3 | 13:74289534-74289559 | 0.031517243 | |
| ENST00000449987 | ENSG00000139746 (RBM26) | hsa-miR-146a-5p | 0.873388 |
| UTR3 | 13:79888956-79888963 | 0.027473727 | |
| UTR3 | 13:79888831-79888857 | 0.010952664 | |
| UTR3 | 13:79887432-79887458 | 0.002008815 | |
| UTR3 | 13:79887314-79887330 | 0.001834874 | |
| ENST00000282878 | ENSG00000152932 (RAB3C) | hsa-miR-146a-5p | 0.872873 |
| UTR3 | 5:58147434-58147461 | 0.010292296 | |
| UTR3 | 5:58147660-58147681 | 0.003076543 | |
| UTR3 | 5:58148190-58148211 | 0.00175417 | |
| UTR3 | 5:58148675-58148702 | 0.001637334 | |
| UTR3 | 5:58148870-58148885 | 0.001226166 | |
| UTR3 | 5:58149192-58149211 | 0.001025845 | |
| UTR3 | 5:58149583-58149603 | 0.001710345 | |
| UTR3 | 5:58151839-58151862 | 0.001465906 | |
| UTR3 | 5:58151942-58151959 | 0.000887452 | |
| UTR3 | 5:58152209-58152229 | 0.009631851 | |
| UTR3 | 5:58153341-58153360 | 0.002007053 | |
| UTR3 | 5:58153941-58153954 | 0.005441356 | |
| UTR3 | 5:58154861-58154886 | 0.002037737 | |
| | | | |
| ENST00000527531 | ENSG00000166323 (C11orf65) | hsa-miR-146a-5p | 0.872651 |
| UTR3 | 11:108226508-108226533 | 0.036921392 | |
| UTR3 | 11:108202116-108202141 | 0.005239956 | |
| ENST00000402045 | ENSG00000106003 (LFNG) | hsa-miR-146a-5p | 0.872625 |
| UTR3 | 7:2567985-2567997 | 0.042157568 | |
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| ENST00000428797 | ENSG00000022355 (GABRA1) | hsa-miR-146a-5p | 0.871911 |
| UTR3 | 5:161324464-161324487 | 0.031101429 | |
| UTR3 | 5:161325265-161325288 | 0.002762582 | |
| UTR3 | 5:161326187-161326214 | 0.00419722 | |
| UTR3 | 5:161326481-161326497 | 0.00338891 | |
| UTR3 | 5:161322772-161322793 | 0.00499573 | |
| ENST00000360380 | ENSG00000123473 (STIL) | hsa-miR-146a-5p | 0.871764 |
| UTR3 | 1:47716631-47716655 | 0.039198069 | |
| UTR3 | 1:47755221-47755246 | 0.021349662 | |
| ENST00000437844 | ENSG00000148516 (ZEB1) | hsa-miR-146a-5p | 0.871648 |
| UTR3 | 10:31676171-31676190 | 0.00853504 | |
| UTR3 | 10:31809398-31809422 | 0.011144163 | |
| UTR3 | 10:31815704-31815727 | 0.001732788 | |
| UTR3 | 10:31815729-31815747 | 0.000613922 | |
| UTR3 | 10:31817689-31817703 | 0.004730585 | |
| UTR3 | 10:31818590-31818615 | 0.015257919 | |
| ENST00000335712 | ENSG00000119866 (BCL11A) | hsa-miR-146a-5p | 0.870897 |
| UTR3 | 2:60687290-60687304 | 0.027979964 | |
| UTR3 | 2:60686689-60686714 | 0.004554857 | |

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| UTR3 | 2:60685213-60685229 | 0.009370192 |  |
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| ENST00000429989 | ENSG00000108219 (TSPAN14) | hsa-miR-146a-5p | 0.870433 |
| UTR3 | 10:82278521-82278545 | 0.008876355 |  |
| UTR3 | 10:82280054-82280073 | 0.001397661 |  |
| UTR3 | 10:82280256-82280282 | 0.001211949 |  |
| UTR3 | 10:82280630-82280650 | 0.001685567 |  |
| UTR3 | 10:82280967-82280987 | 0.000794967 |  |
| UTR3 | 10:82281347-82281359 | 0.003193286 |  |
| UTR3 | 10:82283117-82283141 | 0.002288527 |  |
| UTR3 | 10:82283744-82283770 | 0.000929983 |  |
| UTR3 | 10:82287965-82287989 | 0.002650809 |  |
| UTR3 | 10:82288712-82288736 | 0.008832677 |  |
| UTR3 | 10:82289091-82289114 | 0.001102502 |  |
| UTR3 | 10:82289257-82289273 | 0.001330126 |  |
| UTR3 | 10:82291783-82291804 | 0.005551705 |  |
| UTR3 | 10:82291789-82291817 | 0.001991551 |  |
| ENST00000457153 | ENSG00000067715 (SYT1) | hsa-miR-146a-5p | 0.869427 |
| UTR3 | 12:79844490-79844498 | 0.041692355 |  |
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| ENST00000257290 | ENSG00000134853 (PDGFRA) | hsa-miR-146a-5p | 0.86926 |
| UTR3 | 4:55162416-55162440 | 0.023389211 |  |
| UTR3 | 4:55162454-55162478 | 0.001578997 |  |
| UTR3 | 4:55162731-55162751 | 0.012663279 |  |
| UTR3 | 4:55163739-55163763 | 0.004036736 |  |
| ENST00000454189 | ENSG00000046653 (GPM6B) | hsa-miR-146a-5p | 0.868404 |
| UTR3 | X:13792398-13792421 | 0.0184068 |  |
| UTR3 | X:13792102-13792116 | 0.005043944 |  |
| UTR3 | X:13791945-13791961 | 0.013682538 |  |
| UTR3 | X:13791189-13791210 | 0.002298578 |  |
| UTR3 | X:13790465-13790482 | 0.002113711 |  |
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| ENST00000478500 | ENSG00000107242 (PIP5K1B) | hsa-miR-146a-5p | 0.867783 |
| UTR3 | 9:71624080-71624091 | 0.041456815 |  |
| ENST00000610020 | ENSG00000122484 (RPAP2) | hsa-miR-146a-5p | 0.867238 |
| UTR3 | 1:92854576-92854600 | 0.001274171 |  |
| UTR3 | 1:92859217-92859244 | 0.002354295 |  |
| UTR3 | 1:92859789-92859810 | 0.002882308 |  |
| UTR3 | 1:92860306-92860318 | 0.005335236 |  |
| UTR3 | 1:92864870-92864888 | 0.024695178 |  |
| UTR3 | 1:92865283-92865305 | 0.002280382 |  |
| UTR3 | 1:92867223-92867240 | 0.002557845 |  |
| ENST00000361717 | ENSG00000145365 (TIFA) | hsa-miR-146a-5p | 0.867095 |
| UTR3 | 4:113198740-113198766 | 0.011690925 |  |
| UTR3 | 4:113198425-113198442 | 0.017154173 |  |
| UTR3 | 4:113196720-113196747 | 0.004409104 |  |
| UTR3 | 4:113196268-113196295 | 0.004299323 |  |

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| UTR3 | 4:113199324-113199343 | 0.014130796 |  |
| UTR3 | 4:113199047-113199061 | 0.012759007 |  |
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| ENST00000297107 | ENSG00000164574 (GALNT10) | hsa-miR-146a-5p | 0.867065 |
| UTR3 | 5:153797062-153797081 | 0.002484148 |  |
| UTR3 | 5:153797535-153797552 | 0.036181836 |  |
| UTR3 | 5:153799093-153799109 | 0.002688871 |  |
| ENST00000357085 | ENSG00000112343 (TRIM38) | hsa-miR-146a-5p | 0.866765 |
| UTR3 | 6:25984221-25984248 | 0.004799072 |  |
| UTR3 | 6:25987280-25987292 | 0.036513247 |  |
| ENST00000523756 | ENSG00000042832 (TG) | hsa-miR-146a-5p | 0.86628 |
| UTR3 | 8:133953670-133953687 | 0.004375484 |  |
| UTR3 | 8:134042194-134042221 | 0.002170721 |  |
| UTR3 | 8:134108563-134108580 | 0.005962653 |  |
| UTR3 | 8:134145725-134145741 | 0.028734872 |  |
| ENST00000330796 | ENSG00000185238 (PRMT3) | hsa-miR-146a-5p | 0.865991 |
| UTR3 | 11:20417367-20417389 | 0.006716912 |  |
| UTR3 | 11:20515505;20515713-20515515;20515723 | 0.00207816 |  |
| UTR3 | 11:20529894-20529906 | 0.002747902 |  |
| UTR3 | 11:20530080-20530101 | 0.014009601 |  |
| UTR3 | 11:20530519-20530541 | 0.015650479 |  |
| ENST00000439944 | ENSG00000172061 (LRRC15) | hsa-miR-146a-5p | 0.865799 |
| UTR3 | 3:194079633-194079650 | 0.013725037 |  |
| UTR3 | 3:194079522-194079540 | 0.00795652 |  |
| UTR3 | 3:194079484-194079497 | 0.004549488 |  |
| UTR3 | 3:194076205-194076225 | 0.014944986 |  |
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| ENST00000356722 | ENSG00000145965 (C6ORF50) | hsa-miR-146a-5p | 0.865701 |
| UTR3 | 6:3984021-3984044 | 0.005609265 |  |
| UTR3 | 6:3984308-3984320 | 0.035552923 |  |
| ENST00000588072 | ENSG00000154889 (MPPE1) | hsa-miR-146a-5p | 0.865636 |
| UTR3 | 18:11884320-11884343 | 0.004845538 |  |
| UTR3 | 18:11884270-11884278 | 0.016917076 |  |
| UTR3 | 18:11884225-11884249 | 0.003567424 |  |
| UTR3 | 18:11884034-11884052 | 0.01480929 |  |
| UTR3 | 18:11885782-11885802 | 0.007941433 |  |
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| ENST00000242728 | ENSG00000123095 (BHLHE41) | hsa-miR-146a-5p | 0.864661 |
| UTR3 | 12:26274510-26274529 | 0.020606212 |  |
| UTR3 | 12:26273097-26273121 | 0.020410338 |  |
| ENST00000372692 | ENSG00000119335 (SET) | hsa-miR-146a-5p | 0.86459 |
| UTR3 | 9:131457082-131457096 | 0.037058691 |  |
| UTR3 | 9:131455159-131455185 | 0.027382555 |  |
| ENST00000424789 | ENSG00000170921 (TANC2) | hsa-miR-146a-5p | 0.864081 |
| UTR3 | 17:61499380-61499395 | 0.011513763 |  |
| UTR3 | 17:61499382-61499410 | 0.008250654 |  |

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| UTR3 | 17:61500174-61500186 | 0.002701374 | |
| UTR3 | 17:61500855-61500875 | 0.001871319 | |
| UTR3 | 17:61501183-61501202 | 0.000961625 | |
| UTR3 | 17:61501209-61501237 | 0.000345591 | |
| UTR3 | 17:61501431-61501458 | 0.001824288 | |
| UTR3 | 17:61502718-61502739 | 0.001905023 | |
| UTR3 | 17:61504765-61504785 | 0.009389586 | |
| UTR3 | 17:61432300-61432325 | 0.016087132 | |
| ENST00000496384 | ENSG00000157764 (BRAF) | hsa-miR-146a-5p | 0.862903 |
| UTR3 | 7:140425859-140425874 | 0.005114732 | |
| UTR3 | 7:140425543-140425565 | 0.00332037 | |
| UTR3 | 7:140425476-140425497 | 0.004025534 | |
| UTR3 | 7:140420736-140420758 | 0.005561867 | |
| UTR3 | 7:140419632-140419655 | 0.003050794 | |
| UTR3 | 7:140419451-140419471 | 0.003741559 | |
| UTR3 | 7:140419381-140419406 | 0.006898935 | |
| UTR3 | 7:140419337-140419354 | 0.0090586 | |
| ENST00000504228 | ENSG00000109265 (KIAA1211) | hsa-miR-146a-5p | 0.862686 |
| UTR3 | 4:57194164-57194189 | 0.037143102 | |
| UTR3 | 4:57173864;57176832-57173865;57176853 | 0.015365145 | |
| UTR3 | 4:57181808-57181827 | 0.009677894 | |
| ENST00000327245 | ENSG00000118322 (ATP10B) | hsa-miR-146a-5p | 0.862312 |
| UTR3 | 5:159992191-159992210 | 0.035918896 | |
| UTR3 | 5:159990382-159990405 | 0.004771925 | |
| ENST00000531813 | ENSG00000075239 (ACAT1) | hsa-miR-146a-5p | 0.861283 |
| UTR3 | 11:108013198-108013223 | 0.012830262 | |
| UTR3 | 11:108014184-108014202 | 0.027719424 | |
| ENST00000475243 | ENSG00000124164 (VAPB) | hsa-miR-146a-5p | 0.861256 |
| UTR3 | 20:57020221-57020241 | 0.001756563 | |
| UTR3 | 20:57021822-57021849 | 0.001216652 | |
| UTR3 | 20:57023185-57023196 | 0.004317453 | |
| UTR3 | 20:57023845-57023865 | 0.001837278 | |
| UTR3 | 20:57025521-57025543 | 0.02403161 | |
| UTR3 | 20:57025680-57025695 | 0.001689584 | |
| UTR3 | 20:57026027-57026048 | 0.00569678 | |
| ENST00000361138 | ENSG00000198887 (SMC5) | hsa-miR-146a-5p | 0.861086 |
| UTR3 | 9:72967481-72967501 | 0.03611848 | |
| UTR3 | 9:72968122-72968143 | 0.004404149 | |
| ENST00000460813 | ENSG00000163617 (KIAA1407) | hsa-miR-146a-5p | 0.860884 |
| UTR3 | 3:113755907-113755934 | 0.029494793 | |
| UTR3 | 3:113750597-113750616 | 0.005915099 | |
| UTR3 | 3:113729826-113729843 | 0.005085227 | |
| ENST00000415541 | ENSG00000160584 (SIK3) | hsa-miR-146a-5p | 0.86074 |
| UTR3 | 11:116734465-116734483 | 0.004381748 | |

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| UTR3 | 11:116719964-116719985 | 0.013519895 |  |
| UTR3 | 11:116718243-116718267 | 0.022573782 |  |
| ENST00000373656 | ENSG00000171448 (ZBTB26) | hsa-miR-146a-5p | 0.860656 |
| UTR3 | 9:125678455-125678476 | 0.035830244 |  |
| UTR3 | 9:125682099-125682119 | 0.030735829 |  |
| ENST00000283365 | ENSG00000134769 (DTNA) | hsa-miR-146a-5p | 0.860642 |
| UTR3 | 18:32467909-32467931 | 0.010646252 |  |
| UTR3 | 18:32469185-32469210 | 0.012845126 |  |
| UTR3 | 18:32469763-32469791 | 0.010736779 |  |
| UTR3 | 18:32391983-32392000 | 0.029386347 |  |
| UTR3 | 18:32398242-32398257 | 0.009735065 |  |
| ENST00000282849 | ENSG00000140873 (ADAMTS18) | hsa-miR-146a-5p | 0.860332 |
| UTR3 | 16:77316639-77316664 | 0.019225708 |  |
| UTR3 | 16:77316160-77316178 | 0.021194214 |  |
| ENST00000444766 | ENSG00000108506 (INTS2) | hsa-miR-146a-5p | 0.860187 |
| UTR3 | 17:59944375-59944399 | 0.040400118 |  |
| ENST00000020926 | ENSG00000019505 (SYT13) | hsa-miR-146a-5p | 0.860152 |
| UTR3 | 11:45265119-45265133 | 0.022504246 |  |
| UTR3 | 11:45264599-45264626 | 0.001354432 |  |
| UTR3 | 11:45262736-45262754 | 0.016536805 |  |
| ENST00000357345 | ENSG00000159082 (SYNJ1) | hsa-miR-146a-5p | 0.859695 |
| UTR3 | 21:34003850-34003873 | 0.017225826 |  |
| UTR3 | 21:34003735-34003759 | 0.005268533 |  |
| UTR3 | 21:34003120-34003130 | 0.003712285 |  |
| UTR3 | 21:34002231-34002247 | 0.002241891 |  |
| UTR3 | 21:34001240-34001265 | 0.010552489 |  |
| UTR3 | 21:34018094;34018703-34018099;34018715 | 0.009960936 |  |
| ENST00000507740 | ENSG00000176406 (RIMS2) | hsa-miR-146a-5p | 0.859322 |
| UTR3 | 8:105264180-105264194 | 0.023223596 |  |
| UTR3 | 8:105265189-105265214 | 0.003519293 |  |
| UTR3 | 8:105267240-105267257 | 0.009181043 |  |
| UTR3 | 8:105267654-105267672 | 0.00435899 |  |
| ENST00000498619 | ENSG00000036828 (CASR) | hsa-miR-146a-5p | 0.85922 |
| UTR3 | 3:122004962-122004983 | 0.040269164 |  |
| ENST00000426923 | ENSG00000145287 (PLAC8) | hsa-miR-146a-5p | 0.859188 |
| UTR3 | 4:84015597-84015620 | 0.007747126 |  |
| UTR3 | 4:84015251-84015276 | 0.006203951 |  |
| UTR3 | 4:84014713-84014741 | 0.026313765 |  |
| ENST00000381709 | ENSG00000205777 (GAGE1) | hsa-miR-146a-5p | 0.858677 |
| UTR3 | X:49370654-49370681 | 0.014032276 |  |
| UTR3 | X:49370800-49370826 | 0.005331823 |  |
| UTR3 | X:49372209-49372231 | 0.00123034 |  |
| UTR3 | X:49372609-49372627 | 0.003342216 |  |
| UTR3 | X:49373100-49373117 | 0.016259258 |  |

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| ENST00000403263 | ENSG00000114933 (INO80D) | hsa-miR-146a-5p | 0.858554 |
| UTR3 | 2:206868450-206868477 | 0.002723621 | |
| UTR3 | 2:206867032-206867060 | 0.001898931 | |
| UTR3 | 2:206865359-206865386 | 0.005096148 | |
| UTR3 | 2:206862779-206862794 | 0.006577901 | |
| UTR3 | 2:206862537-206862552 | 0.00272778 | |
| UTR3 | 2:206860581-206860595 | 0.002359512 | |
| UTR3 | 2:206860515-206860532 | 0.001097425 | |
| UTR3 | 2:206859084-206859102 | 0.007240888 | |
| UTR3 | 2:206859059-206859082 | 0.008054176 | |
| UTR3 | 2:206869906-206869923 | 0.002519111 | |
| UTR3 | 2:206869219-206869245 | 0.014605128 | |
| ENST00000360150 | ENSG00000087502 (ERGIC2) | hsa-miR-146a-5p | 0.858323 |
| UTR3 | 12:29493423-29493438 | 0.00300637 | |
| UTR3 | 12:29491274-29491296 | 0.029942719 | |
| UTR3 | 12:29491244-29491252 | 0.002527938 | |
| UTR3 | 12:29496143-29496168 | 0.030599954 | |
| ENST00000327381 | ENSG00000206579 (XKR4) | hsa-miR-146a-5p | 0.858229 |
| UTR3 | 8:56437309-56437333 | 0.004827051 | |
| UTR3 | 8:56437894-56437914 | 0.008252979 | |
| UTR3 | 8:56438162-56438178 | 0.002406801 | |
| UTR3 | 8:56438759-56438784 | 0.003735967 | |
| UTR3 | 8:56439306-56439331 | 0.002536554 | |
| UTR3 | 8:56443003-56443027 | 0.001570633 | |
| UTR3 | 8:56443151-56443167 | 0.00128767 | |
| UTR3 | 8:56443589-56443612 | 0.001222552 | |
| UTR3 | 8:56446845-56446872 | 0.001404559 | |
| UTR3 | 8:56448422-56448445 | 0.005856192 | |
| UTR3 | 8:56453300-56453318 | 0.001319395 | |
| UTR3 | 8:56454025-56454043 | 0.005715276 | |
| ENST00000237654 | ENSG00000118816 (CCNI) | hsa-miR-146a-5p | 0.857495 |
| UTR3 | 4:77968808-77968836 | 0.040037295 | |
| ENST00000582913 | ENSG00000154864 (PIEZO2) | hsa-miR-146a-5p | 0.857321 |
| UTR3 | 18:10708407-10708420 | 0.008974848 | |
| UTR3 | 18:10705538-10705564 | 0.006927301 | |
| UTR3 | 18:10702038-10702053 | 0.001614812 | |
| UTR3 | 18:10672793-10672814 | 0.016289845 | |
| UTR3 | 18:10671702-10671729 | 0.005068118 | |
| UTR3 | 18:11066151-11066169 | 0.008473069 | |
| ENST00000608382 | ENSG00000089775 (ZBTB25) | hsa-miR-146a-5p | 0.85709 |
| UTR3 | 14:64953488-64953511 | 0.006535235 | |
| UTR3 | 14:64949562-64949575 | 0.004256125 | |
| UTR3 | 14:64949248-64949266 | 0.003800384 | |
| UTR3 | 14:64946684-64946704 | 0.014141788 | |
| UTR3 | 14:64945017-64945033 | 0.003027337 | |
| UTR3 | 14:64944953-64944980 | 0.005328258 | |

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| UTR3 | 14:64954592-64954616 | 0.006922593 | |
| UTR3 | 14:64953726-64953741 | 0.013172766 | |
| ENST00000329255 | ENSG00000052850 (ALX4) | hsa-miR-146a-5p | 0.856624 |
| UTR3 | 11:44285479-44285500 | 0.003899906 | |
| UTR3 | 11:44284629-44284649 | 0.004796028 | |
| UTR3 | 11:44284263-44284279 | 0.000922684 | |
| UTR3 | 11:44283574-44283592 | 0.004644822 | |
| UTR3 | 11:44283035-44283062 | 0.002372694 | |
| UTR3 | 11:44282388-44282408 | 0.023284978 | |
| ENST00000558084 | ENSG00000055609 (KMT2C) | hsa-miR-146a-5p | 0.855986 |
| UTR3 | 7:151927048-151927075 | 0.009590812 | |
| UTR3 | 7:151884390-151884408 | 0.004203949 | |
| UTR3 | 7:151879573-151879597 | 0.005256612 | |
| UTR3 | 7:151879336-151879358 | 0.001283183 | |
| UTR3 | 7:151879321-151879339 | 0.000576629 | |
| UTR3 | 7:151878685-151878706 | 0.002262331 | |
| UTR3 | 7:151877896-151877914 | 0.002085102 | |
| UTR3 | 7:151874120-151874132 | 0.001367202 | |
| UTR3 | 7:151873784-151873810 | 0.008306029 | |
| UTR3 | 7:151873584-151873598 | 0.002302111 | |
| UTR3 | 7:151859592-151859610 | 0.001111922 | |
| UTR3 | 7:151949757-151949776 | 0.010857601 | |
| ENST00000312675 | ENSG00000145012 (LPP) | hsa-miR-146a-5p | 0.855293 |
| UTR3 | 3:188593383-188593404 | 0.002804742 | |
| UTR3 | 3:188594207-188594218 | 0.003733323 | |
| UTR3 | 3:188594221-188594242 | 0.000919612 | |
| UTR3 | 3:188596832-188596858 | 0.003967759 | |
| UTR3 | 3:188596919-188596940 | 0.000994604 | |
| UTR3 | 3:188597355-188597379 | 0.001212435 | |
| UTR3 | 3:188598529-188598544 | 0.006753888 | |
| UTR3 | 3:188599764-188599791 | 0.002146874 | |
| UTR3 | 3:188600895-188600916 | 0.001646333 | |
| UTR3 | 3:188602996-188603008 | 0.001517009 | |
| UTR3 | 3:188603150-188603176 | 0.001235532 | |
| UTR3 | 3:188603846-188603867 | 0.002549689 | |
| UTR3 | 3:188604458-188604471 | 0.001389814 | |
| UTR3 | 3:188607180-188607199 | 0.008873021 | |
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| ENST00000251691 | ENSG00000112379 (KIAA1244) | hsa-miR-146a-5p | 0.855277 |
| UTR3 | 6:138660262-138660290 | 0.001202645 | |
| UTR3 | 6:138660789-138660808 | 0.001648708 | |
| UTR3 | 6:138661589-138661611 | 0.002178916 | |
| UTR3 | 6:138662759-138662782 | 0.019983684 | |
| UTR3 | 6:138663259-138663279 | 0.007043601 | |
| UTR3 | 6:138655441-138655462 | 0.004525262 | |
| UTR3 | 6:138657437-138657462 | 0.040420547 | |
| ENST00000304735 | ENSG00000168140 (VASN) | hsa-miR-146a-5p | 0.854768 |

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| UTR3 | 16:4432972-4432987 | 0.039675431 | |
| ENST00000262135 | ENSG00000103494 (RPGRIP1L) | hsa-miR-146a-5p | 0.854722 |
| UTR3 | 16:53635794-53635812 | 0.003767088 | |
| UTR3 | 16:53635764-53635785 | 0.024778849 | |
| UTR3 | 16:53635742-53635764 | 0.00679633 | |
| UTR3 | 16:53632169-53632177 | 0.004327081 | |
| ENST00000354650 | ENSG00000010810 (FYN) | hsa-miR-146a-5p | 0.854505 |
| UTR3 | 6:111982720-111982736 | 0.006183548 | |
| UTR3 | 6:111982115-111982136 | 0.015504305 | |
| UTR3 | 6:111981923-111981941 | 0.006940798 | |
| UTR3 | 6:111981805-111981817 | 0.011012175 | |
| ENST00000281092 | ENSG00000151422 (FER) | hsa-miR-146a-5p | 0.854244 |
| UTR3 | 5:108523317-108523343 | 0.029241723 | |
| UTR3 | 5:108524971-108524996 | 0.007053107 | |
| UTR3 | 5:108529174-108529200 | 0.001690294 | |
| UTR3 | 5:108529398-108529413 | 0.001621417 | |
| ENST00000427401 | ENSG00000237440 (ZNF737) | hsa-miR-146a-5p | 0.853988 |
| UTR3 | 19:20726641-20726659 | 0.037738335 | |
| UTR3 | 19:20728770;20735281-20728782;20735290 | 0.013054425 | |
| ENST00000575022 | ENSG00000177294 (FBXO39) | hsa-miR-146a-5p | 0.853434 |
| UTR3 | 17:6699363-6699381 | 0.039500419 | |
| ENST00000373647 | ENSG00000011454 (RABGAP1) | hsa-miR-146a-5p | 0.85286 |
| UTR3 | 9:125866641-125866663 | 0.037623847 | |
| UTR3 | 9:125861068;125861757-125861077;125861767 | 0.012764399 | |
| ENST00000395792 | ENSG00000081051 (AFP) | hsa-miR-146a-5p | 0.852227 |
| UTR3 | 4:74321803-74321819 | 0.005625655 | |
| UTR3 | 4:74321816-74321835 | 0.031124891 | |
| UTR3 | 4:74313186-74313207 | 0.017779227 | |
| ENST00000471923 | ENSG00000048707 (VPS13D) | hsa-miR-146a-5p | 0.85221 |
| UTR3 | 1:12569728-12569747 | 0.001862968 | |
| UTR3 | 1:12569867-12569894 | 0.002365042 | |
| UTR3 | 1:12571103-12571128 | 0.002490058 | |
| UTR3 | 1:12571458-12571472 | 0.005781212 | |
| UTR3 | 1:12571963-12571985 | 0.007038247 | |
| UTR3 | 1:12572023-12572043 | 0.019803514 | |
| ENST00000234313 | ENSG00000115956 (PLEK) | hsa-miR-146a-5p | 0.851961 |
| UTR3 | 2:68623043-68623065 | 0.010414537 | |
| UTR3 | 2:68623452-68623476 | 0.006755162 | |
| UTR3 | 2:68624040-68624059 | 0.022139112 | |
| ENST00000265022 | ENSG00000058866 (DGKG) | hsa-miR-146a-5p | 0.851734 |
| UTR3 | 3:185866658-185866675 | 0.004387634 | |

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| UTR3 | 3:185866224-185866236 | 0.001414116 |  |
| UTR3 | 3:185865478-185865498 | 0.00315961 |  |
| UTR3 | 3:185865125-185865151 | 0.004853848 |  |
| UTR3 | 3:185865041-185865064 | 0.025464152 |  |
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| ENST00000539173 | ENSG00000197381 (ADARB1) | hsa-miR-146a-5p | 0.849589 |
| UTR3 | 21:46642872-46642890 | 0.002333242 |  |
| UTR3 | 21:46645579-46645601 | 0.003688989 |  |
| UTR3 | 21:46646317-46646332 | 0.006077283 |  |
| UTR3 | 21:46646430-46646453 | 0.025782105 |  |
| UTR3 | 21:46642075-46642100 | 0.008025978 |  |
| ENST00000511739 | ENSG00000170185 (USP38) | hsa-miR-146a-5p | 0.849336 |
| UTR3 | 4:144127209-144127228 | 0.010008504 |  |
| UTR3 | 4:144127235-144127250 | 0.008174562 |  |
| UTR3 | 4:144142773-144142800 | 0.005464425 |  |
| UTR3 | 4:144143098-144143115 | 0.002273483 |  |
| UTR3 | 4:144144834-144144852 | 0.004017163 |  |
| UTR3 | 4:144144947-144144963 | 0.005465667 |  |
| UTR3 | 4:144109033-144109053 | 0.02330858 |  |
| ENST00000467067 | ENSG00000116285 (ERRFI1) | hsa-miR-146a-5p | 0.849148 |
| UTR3 | 1:8075201-8075228 | 0.004177511 |  |
| UTR3 | 1:8075105-8075123 | 0.033655423 |  |
| UTR3 | 1:8074586-8074599 | 0.001114113 |  |
| ENST00000534277 | ENSG00000197302 (ZNF720) | hsa-miR-146a-5p | 0.848927 |
| UTR3 | 16:31734665;31765087-31734674;31765099 | 0.004201446 |  |
| UTR3 | 16:31767381-31767397 | 0.001813278 |  |
| UTR3 | 16:31767890-31767908 | 0.002574628 |  |
| UTR3 | 16:31768248-31768272 | 0.016389561 |  |
| UTR3 | 16:31768453-31768467 | 0.013939956 |  |
| ENST00000455584 | ENSG00000251537 (RP11-385D13.1) | hsa-miR-146a-5p | 0.84846 |
| UTR3 | 17:15477218-15477243 | 0.026225729 |  |
| UTR3 | 17:15476104-15476131 | 0.004125517 |  |
| UTR3 | 17:15476009-15476026 | 0.006134479 |  |
| UTR3 | 17:15475686-15475712 | 0.00237367 |  |
| ENST00000456874 | ENSG00000197057 (DTHD1) | hsa-miR-146a-5p | 0.84823 |
| UTR3 | 4:36345830-36345857 | 0.038830154 |  |
| ENST00000267884 | ENSG00000140319 (SRP14) | hsa-miR-146a-5p | 0.848011 |
| UTR3 | 15:40328018-40328038 | 0.038802385 |  |
| ENST00000375826 | ENSG00000116771 (AGMAT) | hsa-miR-146a-5p | 0.847798 |
| UTR3 | 1:15900097-15900113 | 0.03600743 |  |
| UTR3 | 1:15899986-15900012 | 0.002767977 |  |
| ENST00000299563 | ENSG00000166439 (RNF169) | hsa-miR-146a-5p | 0.847721 |
| UTR3 | 11:74547827-74547850 | 0.026333335 |  |
| UTR3 | 11:74548436-74548462 | 0.004790655 |  |
| UTR3 | 11:74549318-74549338 | 0.004002639 |  |

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| UTR3 | 11:74549335-74549354 | 0.000620631 | |
| UTR3 | 11:74549641-74549662 | 0.000974438 | |
| UTR3 | 11:74552304-74552321 | 0.002043926 | |
| ENST00000409652 | ENSG00000221963 (APOL6) | hsa-miR-146a-5p | 0.847715 |
| UTR3 | 22:36056750-36056778 | 0.003688126 | |
| UTR3 | 22:36058236-36058262 | 0.001756655 | |
| UTR3 | 22:36059578-36059592 | 0.001418743 | |
| UTR3 | 22:36063553-36063573 | 0.026409593 | |
| UTR3 | 22:36064356-36064382 | 0.005491812 | |
| ENST00000295887 | ENSG00000163624 (CDS1) | hsa-miR-146a-5p | 0.847488 |
| UTR3 | 4:85570261-85570284 | 0.011905614 | |
| UTR3 | 4:85571856-85571881 | 0.002929674 | |
| UTR3 | 4:85572409-85572436 | 0.023900967 | |
| ENST00000606080 | ENSG00000111816 (FRK) | hsa-miR-146a-5p | 0.847303 |
| UTR3 | 6:116262456-116262469 | 0.006705798 | |
| UTR3 | 6:116260958-116260977 | 0.005016461 | |
| UTR3 | 6:116259440-116259467 | 0.006203776 | |
| UTR3 | 6:116259000-116259025 | 0.005979556 | |
| UTR3 | 6:116258134-116258160 | 0.001423959 | |
| UTR3 | 6:116258081-116258099 | 0.000555513 | |
| UTR3 | 6:116257824-116257838 | 0.010319329 | |
| UTR3 | 6:116255874-116255899 | 0.001457713 | |
| UTR3 | 6:116255617-116255641 | 0.001050755 | |
| ENST00000262352 | ENSG00000106688 (SLC1A1) | hsa-miR-146a-5p | 0.846919 |
| UTR3 | 9:4585858-4585886 | 0.006274354 | |
| UTR3 | 9:4586281-4586307 | 0.007769795 | |
| UTR3 | 9:4586943-4586962 | 0.024620229 | |
| ENST00000546136 | ENSG00000134532 (SOX5) | hsa-miR-146a-5p | 0.846556 |
| UTR3 | 12:23687064-23687092 | 0.009914959 | |
| UTR3 | 12:23686797-23686820 | 0.011804644 | |
| UTR3 | 12:23686264-23686288 | 0.012213074 | |
| UTR3 | 12:23684525-23684535 | 0.002665041 | |
| UTR3 | 12:23684136-23684153 | 0.002020973 | |
| ENST00000253144 | ENSG00000130844 (ZNF331) | hsa-miR-146a-5p | 0.846392 |
| UTR3 | 19:54081623-54081636 | 0.038598057 | |
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| ENST00000296402 | ENSG00000145349 (CAMK2D) | hsa-miR-146a-5p | 0.845834 |
| UTR3 | 4:114375632-114375658 | 0.017801652 | |
| UTR3 | 4:114375331-114375351 | 0.0055279 | |
| UTR3 | 4:114374954-114374976 | 0.003114999 | |
| UTR3 | 4:114374282-114374305 | 0.002711897 | |
| UTR3 | 4:114374242-114374260 | 0.000743129 | |
| UTR3 | 4:114373718-114373743 | 0.003302019 | |
| UTR3 | 4:114373425-114373444 | 0.002634639 | |
| UTR3 | 4:114372718-114372743 | 0.00269178 | |
| ENST00000538183 | ENSG00000112096 (SOD2) | hsa-miR-146a-5p | 0.8458 |
| UTR3 | 6:160099466-160099490 | 0.000775212 | |

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| UTR3 | 6:160098820-160098845 | 0.001941728 |  |
| UTR3 | 6:160098324-160098339 | 0.001623366 |  |
| UTR3 | 6:160097579-160097598 | 0.003379259 |  |
| UTR3 | 6:160096095-160096114 | 0.004689574 |  |
| UTR3 | 6:160095330-160095354 | 0.007054545 |  |
| UTR3 | 6:160094581-160094608 | 0.001825159 |  |
| UTR3 | 6:160093269-160093295 | 0.001103695 |  |
| UTR3 | 6:160093216-160093240 | 0.001753146 |  |
| UTR3 | 6:160093054-160093072 | 0.001302045 |  |
| UTR3 | 6:160092958-160092985 | 0.004520262 |  |
| UTR3 | 6:160092306-160092333 | 0.001755003 |  |
| UTR3 | 6:160091513-160091532 | 0.006800766 |  |
| ENST00000358691 | ENSG00000198265 (HELZ) | hsa-miR-146a-5p | 0.845011 |
| UTR3 | 17:65074246-65074262 | 0.024570002 |  |
| UTR3 | 17:65073502-65073528 | 0.003478352 |  |
| UTR3 | 17:65071922-65071950 | 0.001388923 |  |
| UTR3 | 17:65069146-65069169 | 0.008987742 |  |
| ENST00000342771 | ENSG00000158321 (AUTS2) | hsa-miR-146a-5p | 0.844949 |
| UTR3 | 7:70256179-70256198 | 0.015883036 |  |
| UTR3 | 7:70257043-70257071 | 0.003169963 |  |
| UTR3 | 7:70257779-70257797 | 0.019364331 |  |
| ENST00000525284 | ENSG00000154237 (LRRK1) | hsa-miR-146a-5p | 0.844906 |
| UTR3 | 15:101589908-101589933 | 0.001703729 |  |
| UTR3 | 15:101595419;101597061-101595428;101597074 | 0.00405716 |  |
| UTR3 | 15:101598266-101598293 | 0.001593201 |  |
| UTR3 | 15:101609118-101609136 | 0.011966078 |  |
| UTR3 | 15:101609141-101609165 | 0.005550374 |  |
| UTR3 | 15:101609207-101609231 | 0.004275327 |  |
| UTR3 | 15:101609220-101609239 | 0.003078149 |  |
| UTR3 | 15:101609237-101609254 | 0.006187941 |  |
| ENST00000334567 | ENSG00000186329 (TMEM212) | hsa-miR-146a-5p | 0.843873 |
| UTR3 | 3:171576846-171576867 | 0.03828342 |  |
| ENST00000508624 | ENSG00000134982 (APC) | hsa-miR-146a-5p | 0.843444 |
| UTR3 | 5:112173799-112173825 | 0.007332636 |  |
| UTR3 | 5:112176690-112176709 | 0.00195377 |  |
| UTR3 | 5:112176869-112176884 | 0.008399541 |  |
| UTR3 | 5:112177166-112177185 | 0.001772431 |  |
| UTR3 | 5:112177182-112177205 | 0.002023995 |  |
| UTR3 | 5:112177354-112177370 | 0.00982467 |  |
| UTR3 | 5:112177354-112177379 | 0.006923252 |  |
| ENST00000328902 | ENSG00000133561 (GIMAP6) | hsa-miR-146a-5p | 0.842574 |
| UTR3 | 7:150324368-150324391 | 0.003872322 |  |
| UTR3 | 7:150323014-150323031 | 0.029907014 |  |
| UTR3 | 7:150322849-150322863 | 0.004343574 |  |

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| ENST00000339570 | ENSG00000073060 (SCARB1) | hsa-miR-146a-5p | 0.842316 |
| UTR3 | 12:125261732-125261759 | 0.038091023 | |
| ENST00000465065 | ENSG00000163728 (TTC14) | hsa-miR-146a-5p | 0.841991 |
| UTR3 | 3:180321980-180322006 | 0.002884282 | |
| UTR3 | 3:180322022-180322044 | 0.002079273 | |
| UTR3 | 3:180322235-180322248 | 0.010446992 | |
| UTR3 | 3:180323806-180323827 | 0.001237929 | |
| UTR3 | 3:180325907-180325927 | 0.003185602 | |
| UTR3 | 3:180326870-180326889 | 0.004852231 | |
| UTR3 | 3:180327113-180327137 | 0.006404825 | |
| UTR3 | 3:180328453-180328480 | 0.006960046 | |
| ENST00000261942 | ENSG00000113194 (FAF2) | hsa-miR-146a-5p | 0.841295 |
| UTR3 | 5:175934289-175934302 | 0.035455277 | |
| UTR3 | 5:175935765-175935777 | 0.002510449 | |
| ENST00000568578 | ENSG00000147274 (RBMX) | hsa-miR-146a-5p | 0.840722 |
| UTR3 | X:135957513-135957525 | 0.018341125 | |
| UTR3 | X:135955832-135955856 | 0.006373582 | |
| UTR3 | X:135951946-135951967 | 0.013181008 | |
| ENST00000344419 | ENSG00000009765 (IYD) | hsa-miR-146a-5p | 0.840546 |
| UTR3 | 6:150719472-150719499 | 0.002494505 | |
| UTR3 | 6:150719760-150719781 | 0.002129818 | |
| UTR3 | 6:150720652-150720678 | 0.001321462 | |
| UTR3 | 6:150721442-150721454 | 0.003702191 | |
| UTR3 | 6:150722219-150722246 | 0.015194171 | |
| UTR3 | 6:150722726-150722746 | 0.001218708 | |
| UTR3 | 6:150726039-150726061 | 0.002907563 | |
| UTR3 | 6:150726283-150726308 | 0.00210062 | |
| UTR3 | 6:150726852-150726864 | 0.006805258 | |
| ENST00000371172 | ENSG00000197430 (OPALIN) | hsa-miR-146a-5p | 0.840493 |
| UTR3 | 10:98105377-98105404 | 0.004978911 | |
| UTR3 | 10:98105350-98105362 | 0.004954325 | |
| UTR3 | 10:98104953-98104973 | 0.008603823 | |
| UTR3 | 10:98103604-98103625 | 0.003048014 | |
| UTR3 | 10:98103243-98103270 | 0.016282728 | |
| ENST00000275072 | ENSG00000146281 (PM20D2) | hsa-miR-146a-5p | 0.840122 |
| UTR3 | 6:89872421-89872437 | 0.004037484 | |
| UTR3 | 6:89873535-89873559 | 0.002048324 | |
| UTR3 | 6:89874694-89874719 | 0.031736765 | |
| ENST00000394650 | ENSG00000005059 (CCDC109B) | hsa-miR-146a-5p | 0.840103 |
| UTR3 | 4:110608874-110608891 | 0.037820311 | |
| ENST00000422265 | ENSG00000144648 (ACKR2) | hsa-miR-146a-5p | 0.840072 |
| UTR3 | 3:42907248-42907267 | 0.016600797 | |
| UTR3 | 3:42907248-42907274 | 0.02121579 | |

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| ENST00000441535 | ENSG00000094963 (FMO2) | hsa-miR-146a-5p | 0.840012 |
| UTR3 | 1:171178182-171178209 | 0.003128683 | |
| UTR3 | 1:171178704-171178728 | 0.03112554 | |
| UTR3 | 1:171179000-171179018 | 0.003555032 | |
| ENST00000513291 | ENSG00000175054 (ATR) | hsa-miR-146a-5p | 0.839732 |
| UTR3 | 3:142171825-142171843 | 0.014008067 | |
| UTR3 | 3:142171424-142171444 | 0.00803428 | |
| UTR3 | 3:142170362-142170388 | 0.001509749 | |
| UTR3 | 3:142168162-142168179 | 0.014223052 | |
| ENST00000381052 | ENSG00000049192 (ADAMTS6) | hsa-miR-146a-5p | 0.839592 |
| UTR3 | 5:64747971-64747990 | 0.025700259 | |
| UTR3 | 5:64445769-64445784 | 0.00801707 | |
| UTR3 | 5:64769406-64769431 | 0.024930067 | |
| ENST00000216513 | ENSG00000100625 (SIX4) | hsa-miR-146a-5p | 0.839419 |
| UTR3 | 14:61178171-61178187 | 0.003641602 | |
| UTR3 | 14:61176592-61176617 | 0.034095666 | |
| ENST00000356264 | ENSG00000078053 (AMPH) | hsa-miR-146a-5p | 0.837819 |
| UTR3 | 7:38423942-38423961 | 0.037543996 | |
| ENST00000381779 | ENSG00000179542 (SLITRK4) | hsa-miR-146a-5p | 0.837783 |
| UTR3 | X:142715602-142715621 | 0.017982249 | |
| UTR3 | X:142713810-142713833 | 0.001455954 | |
| UTR3 | X:142710726-142710745 | 0.007862679 | |
| UTR3 | X:142718444-142718467 | 0.052110743 | |
| ENST00000368744 | ENSG00000203783 (PRR9) | hsa-miR-146a-5p | 0.837478 |
| UTR3 | 1:153191155-153191181 | 0.014985065 | |
| UTR3 | 1:153191639-153191662 | 0.018732695 | |
| UTR3 | 1:153191701-153191721 | 0.003785258 | |
| ENST00000256637 | ENSG00000134243 (SORT1) | hsa-miR-146a-5p | 0.837432 |
| UTR3 | 1:109855549-109855565 | 0.001901908 | |
| UTR3 | 1:109855082-109855100 | 0.002694417 | |
| UTR3 | 1:109853469-109853486 | 0.005133756 | |
| UTR3 | 1:109852714-109852737 | 0.025783105 | |
| UTR3 | 1:109867706;109869614-109867711;109869627 | 0.013015178 | |
| ENST00000254958 | ENSG00000101384 (JAG1) | hsa-miR-146a-5p | 0.837387 |
| UTR3 | 20:10619390-10619418 | 0.002829436 | |
| UTR3 | 20:10618453-10618471 | 0.034662667 | |
| ENST00000366857 | ENSG00000143771 (CNIH4) | hsa-miR-146a-5p | 0.836519 |
| UTR3 | 1:224563703-224563723 | 0.030424477 | |
| UTR3 | 1:224565497-224565519 | 0.002221402 | |
| UTR3 | 1:224566128-224566144 | 0.001923766 | |
| UTR3 | 1:224566620-224566633 | 0.002818462 | |
| ENST00000322434 | ENSG00000178338 (ZNF354B) | hsa-miR-146a-5p | 0.836402 |
| UTR3 | 5:178311356-178311378 | 0.037374193 | |

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| ENST00000396578 | ENSG00000169031 (COL4A3) | hsa-miR-146a-5p | 0.835188 |
| UTR3 | 2:228176775-228176798 | 0.008615809 | |
| UTR3 | 2:228177550-228177570 | 0.002474424 | |
| UTR3 | 2:228178535-228178560 | 0.01832064 | |
| UTR3 | 2:228178913-228178933 | 0.002409671 | |
| UTR3 | 2:228179180-228179207 | 0.005409072 | |
| ENST00000609129 | ENSG00000273274 (ZBTB8B) | hsa-miR-146a-5p | 0.835146 |
| UTR3 | 1:32952808-32952833 | 0.003281662 | |
| UTR3 | 1:32954102-32954125 | 0.001266589 | |
| UTR3 | 1:32955354-32955381 | 0.001161934 | |
| UTR3 | 1:32956005-32956024 | 0.003194311 | |
| UTR3 | 1:32957329-32957351 | 0.009143861 | |
| UTR3 | 1:32957464-32957482 | 0.00175395 | |
| UTR3 | 1:32958608-32958626 | 0.001454578 | |
| UTR3 | 1:32959900-32959927 | 0.005876584 | |
| UTR3 | 1:32960489-32960510 | 0.005908212 | |
| UTR3 | 1:32961561-32961588 | 0.004182919 | |
| ENST00000409198 | ENSG00000183091 (NEB) | hsa-miR-146a-5p | 0.834599 |
| UTR3 | 2:152342184-152342205 | 0.03551503 | |
| UTR3 | 2:152507242-152507259 | 0.006088684 | |
| UTR3 | 2:152466477-152466501 | 0.004700124 | |
| ENST00000471389 | ENSG00000140718 (FTO) | hsa-miR-146a-5p | 0.834394 |
| UTR3 | 16:54146464-54146479 | 0.002579032 | |
| UTR3 | 16:54148438-54148460 | 0.02908429 | |
| UTR3 | 16:54150629-54150652 | 0.001112845 | |
| UTR3 | 16:54150700-54150718 | 0.000842553 | |
| UTR3 | 16:54151038-54151063 | 0.00106127 | |
| UTR3 | 16:54153520-54153546 | 0.00245555 | |
| ENST00000361987 | ENSG00000242689 (CNTF) | hsa-miR-146a-5p | 0.833886 |
| UTR3 | 11:58392956-58392973 | 0.037075474 | |
| ENST00000398653 | ENSG00000115970 (THADA) | hsa-miR-146a-5p | 0.833749 |
| UTR3 | 2:43798857-43798884 | 0.002124442 | |
| UTR3 | 2:43797621-43797638 | 0.014859856 | |
| UTR3 | 2:43520084-43520105 | 0.003049931 | |
| UTR3 | 2:43458152-43458164 | 0.017025107 | |
| ENST00000404138 | ENSG00000184677 (ZBTB40) | hsa-miR-146a-5p | 0.832945 |
| UTR3 | 1:22853029-22853054 | 0.025498974 | |
| UTR3 | 1:22855007-22855025 | 0.001321592 | |
| UTR3 | 1:22855250-22855273 | 0.002183428 | |
| UTR3 | 1:22855474-22855492 | 0.004707455 | |
| UTR3 | 1:22848053-22848072 | 0.020067452 | |
| ENST00000371322 | ENSG00000158290 (CUL4B) | hsa-miR-146a-5p | 0.832538 |
| UTR3 | X:119660468-119660482 | 0.003371082 | |
| UTR3 | X:119659422-119659439 | 0.009816474 | |
| UTR3 | X:119659068-119659094 | 0.021252098 | |
| UTR3 | X:119658934-119658948 | 0.002477323 | |

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| ENST00000399639 | ENSG00000143469 (SYT14) | hsa-miR-146a-5p | 0.8325 |
| UTR3 | 1:210334832-210334849 | 0.010441792 | |
| UTR3 | 1:210335377-210335399 | 0.003721008 | |
| UTR3 | 1:210335439-210335460 | 0.010259535 | |
| UTR3 | 1:210335887-210335904 | 0.002193639 | |
| UTR3 | 1:210336966-210336990 | 0.003196109 | |
| UTR3 | 1:210337559-210337586 | 0.00710043 | |
| ENST00000375290 | ENSG00000185920 (PTCH1) | hsa-miR-146a-5p | 0.832437 |
| UTR3 | 9:98231136-98231155 | 0.017736586 | |
| UTR3 | 9:98214374-98214402 | 0.001167429 | |
| UTR3 | 9:98214245-98214265 | 0.000497656 | |
| UTR3 | 9:98212176-98212193 | 0.006424267 | |
| UTR3 | 9:98209498-98209520 | 0.002536672 | |
| UTR3 | 9:98207147-98207164 | 0.00185277 | |
| UTR3 | 9:98205798-98205823 | 0.006689733 | |
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| ENST00000416913 | ENSG00000162869 (PPP1R21) | hsa-miR-146a-5p | 0.83189 |
| UTR3 | 2:48685269-48685287 | 0.005811932 | |
| UTR3 | 2:48692766;48698226-48692781;48698231 | 0.029010169 | |
| UTR3 | 2:48722859-48722875 | 0.002018985 | |
| ENST00000371065 | ENSG00000213625 (LEPROT) | hsa-miR-146a-5p | 0.831087 |
| UTR3 | 1:65897745-65897773 | 0.003434168 | |
| UTR3 | 1:65898333-65898353 | 0.005562506 | |
| UTR3 | 1:65898476-65898503 | 0.009633874 | |
| UTR3 | 1:65900524-65900540 | 0.008562254 | |
| UTR3 | 1:65900710-65900725 | 0.002134515 | |
| UTR3 | 1:65900988-65901006 | 0.007420103 | |
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| ENST00000354200 | ENSG00000125875 (TBC1D20) | hsa-miR-146a-5p | 0.83055 |
| UTR3 | 20:418405-418429 | 0.036684987 | |
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| ENST00000393203 | ENSG00000134247 (PTGFRN) | hsa-miR-146a-5p | 0.830271 |
| UTR3 | 1:117532705-117532727 | 0.028240992 | |
| UTR3 | 1:117532729-117532751 | 0.006108076 | |
| UTR3 | 1:117509634-117509652 | 0.014515316 | |
| ENST00000361902 | ENSG00000198704 (GPX6) | hsa-miR-146a-5p | 0.830223 |
| UTR3 | 6:28471504-28471518 | 0.028787543 | |
| UTR3 | 6:28471117-28471144 | 0.007859475 | |
| ENST00000373075 | ENSG00000163875 (MEAF6) | hsa-miR-146a-5p | 0.829713 |
| UTR3 | 1:37959349-37959368 | 0.005170844 | |
| UTR3 | 1:37958906-37958925 | 0.003563336 | |
| UTR3 | 1:37958199-37958225 | 0.027853774 | |
| ENST00000536441 | ENSG00000149212 (SESN3) | hsa-miR-146a-5p | 0.829673 |
| UTR3 | 11:94906319-94906339 | 0.023541325 | |
| UTR3 | 11:94905500-94905518 | 0.003963915 | |
| UTR3 | 11:94904191-94904206 | 0.002627982 | |

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| UTR3 | 11:94900125-94900151 | 0.002596264 | |
| UTR3 | 11:94899920-94899940 | 0.001700323 | |
| ENST00000272748 | ENSG00000144320 (KIAA1715) | hsa-miR-146a-5p | 0.829255 |
| UTR3 | 2:176794330-176794353 | 0.01659684 | |
| UTR3 | 2:176794156-176794183 | 0.004109183 | |
| UTR3 | 2:176794093-176794116 | 0.002807133 | |
| UTR3 | 2:176792260-176792286 | 0.003710581 | |
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| UTR3 | 2:176790159-176790178 | 0.001148933 | |
| UTR3 | 2:176789976-176789998 | 0.001554077 | |
| UTR3 | 2:176857057-176857078 | 0.024086454 | |
| ENST00000368494 | ENSG00000153989 (NUS1) | hsa-miR-146a-5p | 0.828745 |
| UTR3 | 6:118029369-118029377 | 0.00355471 | |
| UTR3 | 6:118030557-118030573 | 0.012090992 | |
| UTR3 | 6:118031091-118031114 | 0.003872541 | |
| UTR3 | 6:118031534-118031553 | 0.016958035 | |
| ENST00000371818 | ENSG00000119917 (IFIT3) | hsa-miR-146a-5p | 0.827671 |
| UTR3 | 10:91100339-91100352 | 0.003730126 | |
| UTR3 | 10:91100427-91100453 | 0.029930356 | |
| UTR3 | 10:91098969-91098987 | 0.016579866 | |
| ENST00000244763 | ENSG00000124783 (SSR1) | hsa-miR-146a-5p | 0.827525 |
| UTR3 | 6:7287053-7287076 | 0.002921925 | |
| UTR3 | 6:7284462-7284474 | 0.001292585 | |
| UTR3 | 6:7283037-7283052 | 0.001953488 | |
| UTR3 | 6:7282522-7282547 | 0.0022037 | |
| UTR3 | 6:7282364-7282382 | 0.001882027 | |
| UTR3 | 6:7282157-7282177 | 0.009482739 | |
| UTR3 | 6:7281850-7281877 | 0.016599654 | |
| ENST00000397609 | ENSG00000171262 (FAM98B) | hsa-miR-146a-5p | 0.827366 |
| UTR3 | 15:38777873-38777900 | 0.023209398 | |
| UTR3 | 15:38779177-38779188 | 0.013108531 | |
| ENST00000566400 | ENSG00000140463 (BBS4) | hsa-miR-146a-5p | 0.827336 |
| UTR3 | 15:73016988;73020281-73016996;73020287 | 0.033244536 | |
| UTR3 | 15:73023995-73024013 | 0.00307001 | |
| ENST00000514770 | ENSG00000138658 (C4orf21) | hsa-miR-146a-5p | 0.827262 |
| UTR3 | 4:113539835-113539857 | 0.01613986 | |
| UTR3 | 4:113533684-113533705 | 0.007832682 | |
| UTR3 | 4:113531935-113531956 | 0.012333472 | |
| ENST00000375360 | ENSG00000158079 (PTPDC1) | hsa-miR-146a-5p | 0.827255 |
| UTR3 | 9:96870303-96870321 | 0.005261173 | |
| UTR3 | 9:96870935-96870960 | 0.01623888 | |

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| UTR3 | 9:96871885-96871908 | 0.014805162 |  |
| ENST00000410015 | ENSG00000115919 (KYNU) | hsa-miR-146a-5p | 0.826924 |
| UTR3 | 2:143704771-143704796 | 0.036267436 |  |
| ENST00000428210 | ENSG00000082898 (XPO1) | hsa-miR-146a-5p | 0.826839 |
| UTR3 | 2:61726030;61726848-61726048;61726852 | 0.001918986 |  |
| UTR3 | 2:61725917;61726000-61725927;61726015 | 0.001224756 |  |
| UTR3 | 2:61720853-61720880 | 0.001146475 |  |
| UTR3 | 2:61713055-61713077 | 0.03196745 |  |
| ENST00000554659 | ENSG00000100568 (VTI1B) | hsa-miR-146a-5p | 0.826065 |
| UTR3 | 14:68117742-68117764 | 0.020694763 |  |
| UTR3 | 14:68117627-68117654 | 0.004576677 |  |
| UTR3 | 14:68116718-68116737 | 0.003443384 |  |
| UTR3 | 14:68115814-68115828 | 0.001617218 |  |
| UTR3 | 14:68115652-68115672 | 0.001449771 |  |
| UTR3 | 14:68123224-68123246 | 0.02544167 |  |
| ENST00000299333 | ENSG00000166257 (SCN3B) | hsa-miR-146a-5p | 0.825592 |
| UTR3 | 11:123503950-123503967 | 0.003993802 |  |
| UTR3 | 11:123501813-123501825 | 0.001951447 |  |
| UTR3 | 11:123501604-123501622 | 0.009463242 |  |
| UTR3 | 11:123501519-123501545 | 0.001155742 |  |
| UTR3 | 11:123501418-123501432 | 0.00129164 |  |
| UTR3 | 11:123501183-123501210 | 0.016106078 |  |
| UTR3 | 11:123500912-123500928 | 0.002153856 |  |
| ENST00000326524 | ENSG00000168621 (GDNF) | hsa-miR-146a-5p | 0.825522 |
| UTR3 | 5:37812845-37812857 | 0.036107832 |  |
| ENST00000354833 | ENSG00000172058 (SERF1A) | hsa-miR-146a-5p | 0.824887 |
| UTR3 | 5:70213256-70213276 | 0.020300214 |  |
| UTR3 | 5:70213949-70213967 | 0.009536279 |  |
| UTR3 | 5:70214062-70214088 | 0.006199432 |  |
| ENST00000408907 | ENSG00000222028 (PSMB11) | hsa-miR-146a-5p | 0.824791 |
| UTR3 | 14:23512897-23512919 | 0.036025031 |  |
| ENST00000512733 | ENSG00000163291 (PAQR3) | hsa-miR-146a-5p | 0.824329 |
| UTR3 | 4:79841040-79841055 | 0.002823661 |  |
| UTR3 | 4:79839865-79839892 | 0.002647571 |  |
| UTR3 | 4:79836873-79836898 | 0.001506855 |  |
| UTR3 | 4:79836741-79836766 | 0.023543436 |  |
| UTR3 | 4:79836710-79836725 | 0.000692242 |  |
| UTR3 | 4:79835729-79835749 | 0.001892191 |  |
| UTR3 | 4:79835720-79835748 | 0.000547132 |  |
| UTR3 | 4:79833500-79833522 | 0.002319718 |  |
| ENST00000283943 | ENSG00000153827 (TRIP12) | hsa-miR-146a-5p | 0.823965 |
| UTR3 | 2:230631707-230631721 | 0.027311756 |  |
| UTR3 | 2:230631667-230631694 | 0.002080421 |  |
| UTR3 | 2:230631157-230631184 | 0.004783985 |  |

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| UTR3 | 2:230629631-230629652 | 0.001755559 | |
| ENST00000415083 | ENSG00000141380 (SS18) | hsa-miR-146a-5p | 0.823843 |
| UTR3 | 18:23597711-23597728 | 0.007961416 | |
| UTR3 | 18:23596819-23596838 | 0.017233809 | |
| UTR3 | 18:23596595-23596614 | 0.009695367 | |
| UTR3 | 18:23658125;23667465-23658124;23667482 | 0.006594678 | |
| ENST00000435820 | ENSG00000197134 (ZNF257) | hsa-miR-146a-5p | 0.823556 |
| UTR3 | 19:22256358;22270779-22256366;22270791 | 0.013190719 | |
| UTR3 | 19:22272041-22272063 | 0.001510305 | |
| UTR3 | 19:22272447-22272465 | 0.010085155 | |
| UTR3 | 19:22272529-22272546 | 0.011099574 | |
| ENST00000609686 | ENSG00000273079 (GRIN2B) | hsa-miR-146a-5p | 0.823203 |
| UTR3 | 12:13715512-13715531 | 0.011999721 | |
| UTR3 | 12:13713300-13713317 | 0.003206195 | |
| UTR3 | 12:13709899-13709920 | 0.001399555 | |
| UTR3 | 12:13708931-13708952 | 0.001571386 | |
| UTR3 | 12:13708338-13708349 | 0.001919985 | |
| UTR3 | 12:13708121-13708144 | 0.002978573 | |
| UTR3 | 12:13706412-13706433 | 0.001546158 | |
| UTR3 | 12:13704166-13704191 | 0.003082128 | |
| UTR3 | 12:13704119-13704140 | 0.000517781 | |
| UTR3 | 12:13704071-13704098 | 0.000619487 | |
| UTR3 | 12:13703843-13703863 | 0.002394843 | |
| UTR3 | 12:13699983-13699997 | 0.001549966 | |
| UTR3 | 12:13699762-13699782 | 0.001802554 | |
| UTR3 | 12:14019057-14019084 | 0.007989697 | |
| ENST00000301785 | ENSG00000214753 (HNRNPUL2) | hsa-miR-146a-5p | 0.822912 |
| UTR3 | 11:62481185-62481202 | 0.005537309 | |
| UTR3 | 11:62480176-62480186 | 0.030276082 | |
| ENST00000422875 | ENSG00000160218 (TRAPPC10) | hsa-miR-146a-5p | 0.822303 |
| UTR3 | 21:45483541-45483563 | 0.00704606 | |
| UTR3 | 21:45507670-45507689 | 0.003957201 | |
| UTR3 | 21:45523589-45523617 | 0.00153099 | |
| UTR3 | 21:45524594-45524610 | 0.023210879 | |
| ENST00000296575 | ENSG00000164161 (HHIP) | hsa-miR-146a-5p | 0.822149 |
| UTR3 | 4:145661578-145661594 | 0.001785952 | |
| UTR3 | 4:145663299-145663319 | 0.006387757 | |
| UTR3 | 4:145663402-145663428 | 0.001360881 | |
| UTR3 | 4:145664352-145664379 | 0.00156666 | |
| UTR3 | 4:145664660-145664678 | 0.001574764 | |
| UTR3 | 4:145665792-145665818 | 0.023051938 | |
| ENST00000262096 | ENSG00000104219 (ZDHHC2) | hsa-miR-146a-5p | 0.822061 |

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| UTR3 | 8:17077852-17077874 | 0.014421892 | |
| UTR3 | 8:17081112-17081128 | 0.00216024 | |
| UTR3 | 8:17082167-17082185 | 0.015787039 | |
| UTR3 | 8:17082184-17082202 | 0.003348923 | |
| ENST00000282869 | ENSG00000152926 (ZNF117) | hsa-miR-146a-5p | 0.821796 |
| UTR3 | 7:64438155-64438180 | 0.026706056 | |
| UTR3 | 7:64437483-64437508 | 0.008982432 | |
| ENST00000556250 | ENSG00000187790 (FANCM) | hsa-miR-146a-5p | 0.821615 |
| UTR3 | 14:45669896-45669922 | 0.021497994 | |
| UTR3 | 14:45669959-45669972 | 0.014170353 | |
| ENST00000389534 | ENSG00000197608 (ZNF841) | hsa-miR-146a-5p | 0.821024 |
| UTR3 | 19:52568231-52568250 | 0.00496667 | |
| UTR3 | 19:52568182-52568199 | 0.030635808 | |
| ENST00000369466 | ENSG00000116830 (TTF2) | hsa-miR-146a-5p | 0.82009 |
| UTR3 | 1:117644959-117644977 | 0.005284154 | |
| UTR3 | 1:117645967-117645995 | 0.001803199 | |
| UTR3 | 1:117647168-117647190 | 0.001390362 | |
| UTR3 | 1:117650049-117650074 | 0.027021147 | |
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| ENST00000303635 | ENSG00000171735 (CAMTA1) | hsa-miR-146a-5p | 0.819997 |
| UTR3 | 1:7826839-7826865 | 0.002786948 | |
| UTR3 | 1:7826862-7826887 | 0.005694066 | |
| UTR3 | 1:7827024-7827044 | 0.002931474 | |
| UTR3 | 1:7827068-7827094 | 0.01425906 | |
| UTR3 | 1:7829134-7829157 | 0.006515012 | |
| UTR3 | 1:6880274-6880289 | 0.013035222 | |
| UTR3 | 1:7724909-7724928 | 0.006354744 | |
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| ENST00000402775 | ENSG00000172478 (C2orf54) | hsa-miR-146a-5p | 0.819808 |
| UTR3 | 2:241825675-241825699 | 0.013157252 | |
| UTR3 | 2:241825655-241825678 | 0.022310365 | |
| ENST00000383083 | ENSG00000114698 (PLSCR4) | hsa-miR-146a-5p | 0.819478 |
| UTR3 | 3:145911887-145911901 | 0.026444213 | |
| UTR3 | 3:145911548-145911565 | 0.004284452 | |
| UTR3 | 3:145911197-145911210 | 0.004702441 | |
| ENST00000379096 | ENSG00000076554 (TPD52) | hsa-miR-146a-5p | 0.818928 |
| UTR3 | 8:80949928-80949950 | 0.005406207 | |
| UTR3 | 8:80948638-80948658 | 0.001244509 | |
| UTR3 | 8:80947175-80947196 | 0.02871975 | |
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| ENST00000238961 | ENSG00000119906 (FAM178A) | hsa-miR-146a-5p | 0.81875 |
| UTR3 | 10:102722870-102722889 | 0.001601739 | |
| UTR3 | 10:102723398-102723416 | 0.003823771 | |
| UTR3 | 10:102723780-102723808 | 0.011639954 | |
| UTR3 | 10:102724860-102724884 | 0.01286295 | |
| UTR3 | 10:102710465-102710488 | 0.029728867 | |

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| ENST00000379119 | ENSG00000075790 (BCAP29) | hsa-miR-146a-5p | 0.81767 |
| UTR3 | 7:107260439-107260463 | 0.002114259 | |
| UTR3 | 7:107261947-107261972 | 0.001731328 | |
| UTR3 | 7:107263092-107263104 | 0.03138659 | |
| ENST00000361421 | ENSG00000198846 (TOX) | hsa-miR-146a-5p | 0.816953 |
| UTR3 | 8:59720222-59720237 | 0.025981799 | |
| UTR3 | 8:59719023-59719041 | 0.00917191 | |
| ENST00000532485 | ENSG00000078124 (ACER3) | hsa-miR-146a-5p | 0.816796 |
| UTR3 | 11:76731856-76731872 | 0.01743904 | |
| UTR3 | 11:76732268-76732291 | 0.012409535 | |
| UTR3 | 11:76735793-76735810 | 0.002203705 | |
| UTR3 | 11:76737233-76737245 | 0.003084301 | |
| ENST00000329468 | ENSG00000185823 (NPAP1) | hsa-miR-146a-5p | 0.816362 |
| UTR3 | 15:24925614-24925633 | 0.018300963 | |
| UTR3 | 15:24925883-24925906 | 0.003981422 | |
| UTR3 | 15:24928276-24928285 | 0.004644839 | |
| UTR3 | 15:24928303-24928321 | 0.005222014 | |
| UTR3 | 15:24921637-24921665 | 0.017244096 | |
| ENST00000350082 | ENSG00000112144 (ICK) | hsa-miR-146a-5p | 0.814819 |
| UTR3 | 6:52868993-52869020 | 0.009217637 | |
| UTR3 | 6:52868939-52868967 | 0.002945417 | |
| UTR3 | 6:52867894-52867918 | 0.00240255 | |
| UTR3 | 6:52867112-52867126 | 0.006767501 | |
| UTR3 | 6:52866723-52866747 | 0.005276483 | |
| UTR3 | 6:52866462-52866484 | 0.004904195 | |
| UTR3 | 6:52866398-52866419 | 0.003407761 | |
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| ENST00000414716 | ENSG00000099814 (CEP170B) | hsa-miR-146a-5p | 0.814324 |
| UTR3 | 14:105361371-105361387 | 0.005517849 | |
| UTR3 | 14:105362278-105362301 | 0.00405838 | |
| UTR3 | 14:105362965-105362993 | 0.025291736 | |
| ENST00000343407 | ENSG00000128536 (CDHR3) | hsa-miR-146a-5p | 0.814321 |
| UTR3 | 7:105673770-105673790 | 0.012277562 | |
| UTR3 | 7:105676041-105676068 | 0.001889964 | |
| UTR3 | 7:105676454-105676474 | 0.004429973 | |
| UTR3 | 7:105676684-105676710 | 0.010792787 | |
| UTR3 | 7:105676801-105676816 | 0.005477345 | |
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| ENST00000319550 | ENSG00000178425 (NT5DC1) | hsa-miR-146a-5p | 0.814305 |
| UTR3 | 6:116565478-116565497 | 0.010523001 | |
| UTR3 | 6:116565868-116565889 | 0.003136586 | |
| UTR3 | 6:116568307-116568330 | 0.001434296 | |
| UTR3 | 6:116569206-116569215 | 0.001229383 | |
| UTR3 | 6:116569390-116569413 | 0.001679868 | |
| UTR3 | 6:116570335-116570358 | 0.012005825 | |
| UTR3 | 6:116429571-116429597 | 0.007464838 | |

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| UTR3 | 6:116542326-116542352 | 0.019226713 | |
| ENST00000370457 | ENSG00000155966 (AFF2) | hsa-miR-146a-5p | 0.814182 |
| UTR3 | X:148072941-148072960 | 0.008736328 | |
| UTR3 | X:148073619-148073638 | 0.001342664 | |
| UTR3 | X:148076382-148076399 | 0.001658614 | |
| UTR3 | X:148076701-148076721 | 0.00226229 | |
| UTR3 | X:148077490-148077513 | 0.00128606 | |
| UTR3 | X:148081990-148082015 | 0.019566605 | |
| ENST00000299163 | ENSG00000166135 (HIF1AN) | hsa-miR-146a-5p | 0.812644 |
| UTR3 | 10:102308688-102308701 | 0.005071994 | |
| UTR3 | 10:102308877-102308896 | 0.003489716 | |
| UTR3 | 10:102309669-102309685 | 0.001891869 | |
| UTR3 | 10:102309708-102309722 | 0.000709555 | |
| UTR3 | 10:102309845-102309872 | 0.001429449 | |
| UTR3 | 10:102310125-102310147 | 0.001518464 | |
| UTR3 | 10:102311872-102311895 | 0.001490624 | |
| UTR3 | 10:102312007-102312026 | 0.001036965 | |
| UTR3 | 10:102312293-102312308 | 0.001816893 | |
| UTR3 | 10:102313342-102313362 | 0.001903774 | |
| UTR3 | 10:102315086-102315103 | 0.004776411 | |
| UTR3 | 10:102315196-102315213 | 0.000867296 | |
| UTR3 | 10:102315298-102315310 | 0.004519592 | |
| UTR3 | 10:102316392-102316408 | 0.004164319 | |
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| ENST00000240189 | ENSG00000120952 (PRAMEF2) | hsa-miR-146a-5p | 0.812298 |
| UTR3 | 1:12921661-12921674 | 0.034649855 | |
| ENST00000322244 | ENSG00000033178 (UBA6) | hsa-miR-146a-5p | 0.812105 |
| UTR3 | 4:68479257-68479272 | 0.001495473 | |
| UTR3 | 4:68479234-68479257 | 0.02861081 | |
| UTR3 | 4:68478596-68478624 | 0.003232694 | |
| UTR3 | 4:68539431-68539454 | 0.007861871 | |
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| ENST00000425817 | ENSG00000135917 (SLC19A3) | hsa-miR-146a-5p | 0.811911 |
| UTR3 | 2:228551948-228551971 | 0.013725957 | |
| UTR3 | 2:228551607-228551619 | 0.020882441 | |
| ENST00000602526 | ENSG00000106692 (FKTN) | hsa-miR-146a-5p | 0.811769 |
| UTR3 | 9:108363517-108363544 | 0.006213445 | |
| UTR3 | 9:108370123-108370143 | 0.024500604 | |
| UTR3 | 9:108398366-108398388 | 0.001580433 | |
| UTR3 | 9:108401479-108401500 | 0.002298701 | |
| ENST00000514049 | ENSG00000103599 (IQCH) | hsa-miR-146a-5p | 0.811425 |
| UTR3 | 15:67713783-67713808 | 0.018751338 | |
| UTR3 | 15:67793315-67793329 | 0.003438897 | |
| UTR3 | 15:67793772-67793794 | 0.012366219 | |
| ENST00000392316 | ENSG00000128641 (MYO1B) | hsa-miR-146a-5p | 0.81075 |
| UTR3 | 2:192289973-192289994 | 0.007750911 | |
| UTR3 | 2:192290089-192290109 | 0.026733539 | |

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| ENST00000333407 | ENSG00000133477 (FAM83F) | hsa-miR-146a-5p | 0.810718 |
| UTR3 | 22:40427908-40427936 | 0.001016567 | |
| UTR3 | 22:40430198-40430223 | 0.00135714 | |
| UTR3 | 22:40433631-40433649 | 0.004239232 | |
| UTR3 | 22:40435201-40435220 | 0.003226278 | |
| UTR3 | 22:40435575-40435594 | 0.001239826 | |
| UTR3 | 22:40436463-40436479 | 0.002981752 | |
| UTR3 | 22:40438200-40438228 | 0.002463448 | |
| UTR3 | 22:40438445-40438463 | 0.012835697 | |
| UTR3 | 22:40438539-40438555 | 0.0013258 | |
| UTR3 | 22:40439481-40439504 | 0.003795279 | |
| ENST00000469044 | ENSG00000114098 (ARMC8) | hsa-miR-146a-5p | 0.810457 |
| UTR3 | 3:138015515-138015536 | 0.034453296 | |
| ENST00000409711 | ENSG00000071082 (RPL31) | hsa-miR-146a-5p | 0.810425 |
| UTR3 | 2:101621275-101621294 | 0.019571079 | |
| UTR3 | 2:101622521-101622543 | 0.014878721 | |
| ENST00000412050 | ENSG00000107864 (CPEB3) | hsa-miR-146a-5p | 0.809908 |
| UTR3 | 10:93811861-93811880 | 0.007206258 | |
| UTR3 | 10:93810100-93810120 | 0.002187882 | |
| UTR3 | 10:93808715-93808733 | 0.003518094 | |
| UTR3 | 10:93808320-93808344 | 0.006192437 | |
| UTR3 | 10:93806645-93806664 | 0.010864799 | |
| UTR3 | 10:93904786-93904811 | 0.011406407 | |
| UTR3 | 10:93851646-93851668 | 0.012885785 | |
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| ENST00000555640 | ENSG00000165792 (METTL17) | hsa-miR-146a-5p | 0.809809 |
| UTR3 | 14:21463056-21463083 | 0.003154288 | |
| UTR3 | 14:21463341-21463366 | 0.005820414 | |
| UTR3 | 14:21464281-21464306 | 0.002796868 | |
| UTR3 | 14:21464693-21464714 | 0.02129171 | |
| UTR3 | 14:21460260-21460276 | 0.007978054 | |
| ENST00000312413 | ENSG00000011021 (CLCN6) | hsa-miR-146a-5p | 0.809612 |
| UTR3 | 1:11893951-11893974 | 0.005850941 | |
| UTR3 | 1:11900742-11900767 | 0.001516545 | |
| UTR3 | 1:11903123-11903147 | 0.024956919 | |
| UTR3 | 1:11882830-11882853 | 0.012026165 | |
| ENST00000259154 | ENSG00000136636 (KCTD3) | hsa-miR-146a-5p | 0.809079 |
| UTR3 | 1:215794540-215794565 | 0.004540572 | |
| UTR3 | 1:215795081-215795104 | 0.026274943 | |
| UTR3 | 1:215751014-215751035 | 0.019655202 | |
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| ENST00000608703 | ENSG00000204389 (HSPA1A) | hsa-miR-146a-5p | 0.808696 |
| UTR3 | 6:31785512-31785538 | 0.034266568 | |
| ENST00000493950 | ENSG00000118492 (ADGB) | hsa-miR-146a-5p | 0.8083 |
| UTR3 | 6:146997491-146997519 | 0.004564742 | |

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| UTR3 | 6:147038722;147042539-147038735;147042544 | 0.023540276 |  |
| UTR3 | 6:147045342-147045363 | 0.000975903 |  |
| UTR3 | 6:147045565-147045581 | 0.001350422 |  |
| UTR3 | 6:147045794-147045807 | 0.001691989 |  |
| UTR3 | 6:147045817-147045832 | 0.000794179 |  |
| UTR3 | 6:147105911;147106746-147105930;147106753 | 0.001307287 |  |
| ENST00000351698 | ENSG00000136827 (TOR1A) | hsa-miR-146a-5p | 0.808176 |
| UTR3 | 9:132575819-132575826 | 0.034211707 |  |
| ENST00000423591 | ENSG00000188938 (FAM120AOS) | hsa-miR-146a-5p | 0.807513 |
| UTR3 | 9:96209771-96209791 | 0.008450432 |  |
| UTR3 | 9:96209303-96209325 | 0.009916228 |  |
| UTR3 | 9:96209027-96209055 | 0.012073602 |  |
| UTR3 | 9:96208970-96208988 | 0.003701613 |  |
| ENST00000336505 | ENSG00000173611 (SCAI) | hsa-miR-146a-5p | 0.807302 |
| UTR3 | 9:127714797-127714818 | 0.005612537 |  |
| UTR3 | 9:127714622-127714642 | 0.003480565 |  |
| UTR3 | 9:127713242-127713265 | 0.000948215 |  |
| UTR3 | 9:127710808-127710822 | 0.00120627 |  |
| UTR3 | 9:127707066-127707080 | 0.002398881 |  |
| UTR3 | 9:127706412-127706430 | 0.007802349 |  |
| UTR3 | 9:127705404-127705418 | 0.00514937 |  |
| UTR3 | 9:127705001-127705020 | 0.007521476 |  |
| ENST00000585524 | ENSG00000134042 (MRO) | hsa-miR-146a-5p | 0.807072 |
| UTR3 | 18:48326483-48326493 | 0.00613563 |  |
| UTR3 | 18:48325619-48325639 | 0.001514596 |  |
| UTR3 | 18:48325410-48325429 | 0.003975182 |  |
| UTR3 | 18:48325169-48325196 | 0.00311712 |  |
| UTR3 | 18:48324939-48324955 | 0.019353024 |  |
| ENST00000370483 | ENSG00000014919 (COX15) | hsa-miR-146a-5p | 0.806945 |
| UTR3 | 10:101472031-101472051 | 0.016392187 |  |
| UTR3 | 10:101471820-101471843 | 0.017689976 |  |
| ENST00000542527 | ENSG00000185716 (C16orf52) | hsa-miR-146a-5p | 0.806875 |
| UTR3 | 16:22092350-22092368 | 0.030686888 |  |
| UTR3 | 16:22095000-22095015 | 0.00338797 |  |
| ENST00000340106 | ENSG00000242384 (TBC1D3H) | hsa-miR-146a-5p | 0.806183 |
| UTR3 | 17:34746453-34746471 | 0.034002386 |  |
| ENST00000523377 | ENSG00000083099 (LYRM2) | hsa-miR-146a-5p | 0.806008 |
| UTR3 | 6:90345539-90345557 | 0.006140542 |  |
| UTR3 | 6:90342858-90342868 | 0.002949671 |  |
| UTR3 | 6:90342589-90342611 | 0.024893825 |  |
| ENST00000228865 | ENSG00000111269 (CREBL2) | hsa-miR-146a-5p | 0.805575 |
| UTR3 | 12:12795370-12795395 | 0.024429945 |  |

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| UTR3 | 12:12796321-12796340 | 0.001588396 | |
| UTR3 | 12:12797656-12797678 | 0.002738456 | |
| UTR3 | 12:12797914-12797930 | 0.005182072 | |
| ENST00000585558 | ENSG00000153822 (KCNJ16) | hsa-miR-146a-5p | 0.805145 |
| UTR3 | 17:68129633-68129656 | 0.031531036 | |
| UTR3 | 17:68130229-68130251 | 0.002362973 | |

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|---|---|---|---|
| ENST00000244227 | ENSG00000124380 (SNRNP27) | hsa-miR-146a-5p | 0.804338 |
| UTR3 | 2:70131526-70131545 | 0.029025064 | |
| UTR3 | 2:70131973-70131987 | 0.004784998 | |
| ENST00000251527 | ENSG00000117868 (ESYT2) | hsa-miR-146a-5p | 0.803535 |
| UTR3 | 7:158526411-158526433 | 0.032044149 | |
| UTR3 | 7:158525768-158525789 | 0.001682703 | |

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| ENST00000381854 | ENSG00000106993 (CDC37L1) | hsa-miR-146a-5p | 0.803127 |
| UTR3 | 9:4706370-4706385 | 0.027901642 | |
| UTR3 | 9:4706726-4706743 | 0.00504483 | |
| UTR3 | 9:4679848-4679864 | 0.004440741 | |
| ENST00000515655 | ENSG00000118777 (ABCG2) | hsa-miR-146a-5p | 0.802691 |
| UTR3 | 4:89012455-89012475 | 0.002832751 | |
| UTR3 | 4:89011547-89011560 | 0.029199285 | |
| UTR3 | 4:89052315-89052340 | 0.009394266 | |
| ENST00000360647 | ENSG00000163848 (ZNF148) | hsa-miR-146a-5p | 0.801928 |
| UTR3 | 3:124950230-124950256 | 0.00504166 | |
| UTR3 | 3:124949452-124949467 | 0.009013353 | |
| UTR3 | 3:124948350-124948362 | 0.00183743 | |
| UTR3 | 3:124946938-124946964 | 0.008322163 | |
| UTR3 | 3:124946114-124946135 | 0.001994864 | |
| UTR3 | 3:124952393-124952413 | 0.036334123 | |

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| ENST00000358823 | ENSG00000118200 (CAMSAP2) | hsa-miR-146a-5p | 0.801428 |
| UTR3 | 1:200828090-200828107 | 0.025074353 | |
| UTR3 | 1:200828632-200828659 | 0.004654824 | |
| UTR3 | 1:200818011-200818026 | 0.020605511 | |
| ENST00000392638 | ENSG00000148814 (LRRC27) | hsa-miR-146a-5p | 0.80105 |
| UTR3 | 10:134191227-134191251 | 0.002930487 | |
| UTR3 | 10:134191915-134191934 | 0.001350091 | |
| UTR3 | 10:134192442-134192463 | 0.001188846 | |
| UTR3 | 10:134192518-134192529 | 0.000400964 | |
| UTR3 | 10:134192581-134192595 | 0.00045294 | |
| UTR3 | 10:134192650-134192661 | 0.00040451 | |
| UTR3 | 10:134192716-134192727 | 0.000406323 | |
| UTR3 | 10:134192782-134192793 | 0.000646071 | |
| UTR3 | 10:134192848-134192859 | 0.000416738 | |
| UTR3 | 10:134192980-134192991 | 0.000897048 | |
| UTR3 | 10:134192980-134192997 | 0.001572886 | |
| UTR3 | 10:134194961-134194987 | 0.022803859 | |

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| ENST00000346248 | ENSG00000182022 (CHST15) | hsa-miR-146a-5p | 0.800751 |
| UTR3 | 10:125768818-125768838 | 0.003204433 | |
| UTR3 | 10:125768266-125768286 | 0.008572478 | |
| UTR3 | 10:125767411-125767433 | 0.002705675 | |
| UTR3 | 10:125767338-125767366 | 0.017636594 | |
| UTR3 | 10:125804367-125804393 | 0.003043532 | |
| UTR3 | 10:125804137-125804155 | 0.004696971 | |
| ENST00000543630 | ENSG00000086717 (PPEF1) | hsa-miR-146a-5p | 0.800496 |
| UTR3 | X:18845418-18845445 | 0.033414056 | |
| | | | |
| ENST00000418596 | ENSG00000155744 (FAM126B) | hsa-miR-146a-5p | 0.800482 |
| UTR3 | 2:201845585-201845605 | 0.017169595 | |
| UTR3 | 2:201845282-201845302 | 0.004812318 | |
| UTR3 | 2:201844985-201844995 | 0.005636291 | |
| UTR3 | 2:201841363-201841390 | 0.001324138 | |
| UTR3 | 2:201839100-201839115 | 0.004470238 | |
| ENST00000554908 | ENSG00000197045 (GMFB) | hsa-miR-146a-5p | 0.800375 |
| UTR3 | 14:54946618-54946634 | 0.002032688 | |
| UTR3 | 14:54942715-54942736 | 0.0113847 | |
| UTR3 | 14:54942343-54942366 | 0.00369351 | |
| UTR3 | 14:54941351-54941375 | 0.016290765 | |
| ENST00000244020 | ENSG00000124193 (SRSF6) | hsa-miR-146a-5p | 0.800366 |
| UTR3 | 20:42090530-42090552 | 0.009990153 | |
| UTR3 | 20:42091598-42091610 | 0.011165082 | |
| UTR3 | 20:42091877-42091896 | 0.012245467 | |
| ENST00000366553 | ENSG00000203668 (CHML) | hsa-miR-146a-5p | 0.800147 |
| UTR3 | 1:241797040-241797062 | 0.007759747 | |
| UTR3 | 1:241795712-241795732 | 0.001850773 | |
| UTR3 | 1:241795648-241795671 | 0.001945436 | |
| UTR3 | 1:241794297-241794312 | 0.003100815 | |
| UTR3 | 1:241794261-241794274 | 0.000908702 | |
| UTR3 | 1:241793508-241793527 | 0.017812824 | |
| ENST00000369331 | ENSG00000165806 (CASP7) | hsa-miR-146a-5p | 0.799681 |
| UTR3 | 10:115489435-115489461 | 0.003901283 | |
| UTR3 | 10:115489776-115489793 | 0.029429444 | |
| ENST00000453386 | ENSG00000136527 (TRA2B) | hsa-miR-146a-5p | 0.799364 |
| UTR3 | 3:185634035-185634062 | 0.010738691 | |
| UTR3 | 3:185633805-185633832 | 0.022559763 | |
| ENST00000294383 | ENSG00000162402 (USP24) | hsa-miR-146a-5p | 0.79929 |
| UTR3 | 1:55534574-55534599 | 0.00378 | |
| UTR3 | 1:55533997-55534009 | 0.005121792 | |
| UTR3 | 1:55532948-55532959 | 0.001786562 | |
| UTR3 | 1:55532439-55532463 | 0.01883046 | |
| UTR3 | 1:55620352-55620368 | 0.009324735 | |
| UTR3 | 1:55598345-55598361 | 0.011109797 | |
| ENST00000467709 | ENSG00000147459 (DOCK5) | hsa-miR-146a-5p | 0.798886 |
| UTR3 | 8:25222161-25222182 | 0.025380208 | |

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| UTR3 | 8:25224435-25224457 | 0.002822646 |  |
| UTR3 | 8:25250351-25250369 | 0.00237147 |  |
| UTR3 | 8:25269223-25269241 | 0.002675448 |  |
| ENST00000529084 | ENSG00000140798 (ABCC12) | hsa-miR-146a-5p | 0.79857 |
| UTR3 | 16:48122519-48122534 | 0.002132746 |  |
| UTR3 | 16:48119558-48119585 | 0.006108519 |  |
| UTR3 | 16:48117855-48117879 | 0.019636209 |  |
| UTR3 | 16:48174822;48175117-48174831;48175129 | 0.027613133 |  |
| ENST00000371207 | ENSG00000138185 (ENTPD1) | hsa-miR-146a-5p | 0.79806 |
| UTR3 | 10:97626715-97626739 | 0.020952474 |  |
| UTR3 | 10:97627826-97627853 | 0.002408102 |  |
| UTR3 | 10:97629589-97629598 | 0.002106478 |  |
| UTR3 | 10:97630696-97630722 | 0.001942588 |  |
| UTR3 | 10:97630737-97630754 | 0.003138774 |  |
| UTR3 | 10:97632180-97632207 | 0.001227857 |  |
| UTR3 | 10:97634232-97634251 | 0.000858445 |  |
| UTR3 | 10:97634342-97634369 | 0.000531118 |  |
| ENST00000273854 | ENSG00000145242 (EPHA5) | hsa-miR-146a-5p | 0.797077 |
| UTR3 | 4:66187893-66187904 | 0.021495963 |  |
| UTR3 | 4:66186329-66186351 | 0.003184204 |  |
| UTR3 | 4:66186190-66186209 | 0.002314721 |  |
| UTR3 | 4:66185383-66185406 | 0.006071478 |  |
| ENST00000316660 | ENSG00000141682 (PMAIP1) | hsa-miR-146a-5p | 0.796965 |
| UTR3 | 18:57570010-57570033 | 0.003198924 |  |
| UTR3 | 18:57570980-57570996 | 0.029856057 |  |
| ENST00000372687 | ENSG00000156671 (SAMD8) | hsa-miR-146a-5p | 0.796521 |
| UTR3 | 10:76936180-76936193 | 0.020288469 |  |
| UTR3 | 10:76936349-76936359 | 0.00527722 |  |
| UTR3 | 10:76936507-76936520 | 0.00355433 |  |
| UTR3 | 10:76938002-76938023 | 0.002193215 |  |
| UTR3 | 10:76941161-76941185 | 0.001696951 |  |
| ENST00000360587 | ENSG00000197361 (FBXL22) | hsa-miR-146a-5p | 0.795943 |
| UTR3 | 15:63893949-63893971 | 0.017833057 |  |
| UTR3 | 15:63894411-63894437 | 0.015118952 |  |
| ENST00000478199 | ENSG00000162885 (B3GALNT2) | hsa-miR-146a-5p | 0.795631 |
| UTR3 | 1:235647737-235647755 | 0.01373484 |  |
| UTR3 | 1:235634175-235634194 | 0.019185797 |  |
| ENST00000440598 | ENSG00000197008 (ZNF138) | hsa-miR-146a-5p | 0.794882 |
| UTR3 | 7:64276018;64291829-64276031;64291841 | 0.004359443 |  |
| UTR3 | 7:64293234-64293252 | 0.015200889 |  |
| UTR3 | 7:64293311-64293336 | 0.012238925 |  |

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| UTR3 | 7:64275307-64275333 | 0.006069365 | |
| ENST00000254605 | ENSG00000132275 (RRP8) | hsa-miR-146a-5p | 0.794735 |
| UTR3 | 11:6619691-6619714 | 0.001391633 | |
| UTR3 | 11:6618097-6618112 | 0.004717997 | |
| UTR3 | 11:6617684-6617703 | 0.002656561 | |
| UTR3 | 11:6617323-6617343 | 0.024064514 | |
| ENST00000407780 | ENSG00000160223 (ICOSLG) | hsa-miR-146a-5p | 0.794277 |
| UTR3 | 21:45648010-45648035 | 0.001252197 | |
| UTR3 | 21:45644994-45645011 | 0.000789679 | |
| UTR3 | 21:45643299-45643316 | 0.013107945 | |
| UTR3 | 21:45643117-45643129 | 0.002441588 | |
| UTR3 | 21:45642996-45643024 | 0.002396386 | |
| UTR3 | 21:45642984-45642999 | 0.008114795 | |
| UTR3 | 21:45642916-45642936 | 0.004682218 | |
| ENST00000391884 | ENSG00000182324 (KCNJ14) | hsa-miR-146a-5p | 0.793783 |
| UTR3 | 19:48968454-48968477 | 0.003501821 | |
| UTR3 | 19:48969105-48969121 | 0.02497217 | |
| UTR3 | 19:48967704-48967728 | 0.010993673 | |
| UTR3 | 19:48967987-48968002 | 0.011412551 | |
| | | | |
| ENST00000217289 | ENSG00000101311 (FERMT1) | hsa-miR-146a-5p | 0.793587 |
| UTR3 | 20:6057529-6057553 | 0.010345656 | |
| UTR3 | 20:6056769-6056794 | 0.002687995 | |
| UTR3 | 20:6056399-6056415 | 0.01527335 | |
| UTR3 | 20:6056006-6056030 | 0.002873177 | |
| UTR3 | 20:6093145-6093160 | 0.008741098 | |
| | | | |
| ENST00000467604 | ENSG00000121578 (B4GALT4) | hsa-miR-146a-5p | 0.793391 |
| UTR3 | 3:118934903-118934925 | 0.02367734 | |
| UTR3 | 3:118934455-118934477 | 0.00294538 | |
| UTR3 | 3:118934427-118934452 | 0.001582977 | |
| UTR3 | 3:118931724-118931744 | 0.001744108 | |
| UTR3 | 3:118930997-118931013 | 0.002746548 | |
| ENST00000373625 | ENSG00000025800 (KPNA6) | hsa-miR-146a-5p | 0.793314 |
| UTR3 | 1:32638817-32638829 | 0.001857727 | |
| UTR3 | 1:32639943-32639959 | 0.003815813 | |
| UTR3 | 1:32639956-32639983 | 0.000778364 | |
| UTR3 | 1:32640971-32640987 | 0.001778075 | |
| UTR3 | 1:32641876-32641904 | 0.005061106 | |
| UTR3 | 1:32641954-32641975 | 0.019397565 | |
| ENST00000225983 | ENSG00000108840 (HDAC5) | hsa-miR-146a-5p | 0.79306 |
| UTR3 | 17:42155016-42155028 | 0.004340476 | |
| UTR3 | 17:42154230-42154252 | 0.025987229 | |
| UTR3 | 17:42164097;42164780-42164105;42164796 | 0.005803407 | |
| UTR3 | 17:42157560-42157581 | 0.00715405 | |

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| ENST00000396981 | ENSG00000132388 (UBE2G1) | hsa-miR-146a-5p | 0.792305 |
| UTR3 | 17:4175255-4175273 | 0.01720093 | |
| UTR3 | 17:4174831-4174852 | 0.003536714 | |
| UTR3 | 17:4173279-4173299 | 0.00210752 | |
| UTR3 | 17:4173041-4173063 | 0.00974311 | |
| ENST00000355459 | ENSG00000198390 (KRTAP13-1) | hsa-miR-146a-5p | 0.791614 |
| UTR3 | 21:31769024-31769044 | 0.032519754 | |
| ENST00000436544 | ENSG00000163803 (PLB1) | hsa-miR-146a-5p | 0.790442 |
| UTR3 | 2:28817217-28817232 | 0.005300229 | |
| UTR3 | 2:28817245-28817261 | 0.024005107 | |
| UTR3 | 2:28817446-28817472 | 0.003098494 | |
| ENST00000366624 | ENSG00000143674 (MLK4) | hsa-miR-146a-5p | 0.790407 |
| UTR3 | 1:233518734-233518760 | 0.019230497 | |
| UTR3 | 1:233519048-233519075 | 0.013169906 | |
| ENST00000423035 | ENSG00000197121 (PGAP1) | hsa-miR-146a-5p | 0.790173 |
| UTR3 | 2:197784755-197784779 | 0.022302573 | |
| UTR3 | 2:197729715-197729740 | 0.001737863 | |
| UTR3 | 2:197704417-197704434 | 0.001106659 | |
| UTR3 | 2:197703814-197703842 | 0.00161561 | |
| UTR3 | 2:197703442-197703460 | 0.001747779 | |
| UTR3 | 2:197702039-197702056 | 0.001717825 | |
| UTR3 | 2:197701652-197701676 | 0.002149048 | |
| ENST00000548411 | ENSG00000151746 (BICD1) | hsa-miR-146a-5p | 0.790171 |
| UTR3 | 12:32532605-32532616 | 0.001157788 | |
| UTR3 | 12:32533047-32533067 | 0.002619715 | |
| UTR3 | 12:32534450-32534472 | 0.00422622 | |
| UTR3 | 12:32535634-32535651 | 0.00459224 | |
| UTR3 | 12:32536241-32536266 | 0.019781213 | |
| ENST00000274459 | ENSG00000145782 (ATG12) | hsa-miR-146a-5p | 0.78979 |
| UTR3 | 5:115167179-115167195 | 0.028945651 | |
| UTR3 | 5:115166121-115166140 | 0.001621194 | |
| UTR3 | 5:115165026-115165052 | 0.001772738 | |
| ENST00000592780 | ENSG00000256294 (ZNF225) | hsa-miR-146a-5p | 0.789555 |
| UTR3 | 19:44635116-44635141 | 0.027657062 | |
| UTR3 | 19:44636001-44636020 | 0.001884249 | |
| UTR3 | 19:44636331-44636356 | 0.002775217 | |
| ENST00000396373 | ENSG00000139083 (ETV6) | hsa-miR-146a-5p | 0.789387 |
| UTR3 | 12:12047232-12047255 | 0.022345914 | |
| UTR3 | 12:12048243-12048255 | 0.009954017 | |
| ENST00000545826 | ENSG00000168769 (TET2) | hsa-miR-146a-5p | 0.789295 |
| UTR3 | 4:106196925-106196949 | 0.002291143 | |
| UTR3 | 4:106197265-106197284 | 0.002675414 | |
| UTR3 | 4:106197722-106197745 | 0.014317461 | |
| UTR3 | 4:106158376-106158403 | 0.026515474 | |
| UTR3 | 4:106164037-106164062 | 0.027803408 | |

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| ENST00000301919 | ENSG00000170903 (MSANTD4) | hsa-miR-146a-5p | 0.788917 |
| UTR3 | 11:105880211-105880228 | 0.006236186 |  |
| UTR3 | 11:105879957-105879972 | 0.021967007 |  |
| UTR3 | 11:105879576-105879598 | 0.002515412 |  |
| UTR3 | 11:105879503-105879527 | 0.001535181 |  |
| ENST00000199320 | ENSG00000086189 (DIMT1) | hsa-miR-146a-5p | 0.788691 |
| UTR3 | 5:61684334-61684340 | 0.003895811 |  |
| UTR3 | 5:61683481-61683495 | 0.002358427 |  |
| UTR3 | 5:61683123-61683143 | 0.025977343 |  |
| ENST00000508296 | ENSG00000182230 (FAM153B) | hsa-miR-146a-5p | 0.788363 |
| UTR3 | 5:175547885-175547912 | 0.001410119 |  |
| UTR3 | 5:175548749-175548769 | 0.016404945 |  |
| UTR3 | 5:175552791-175552811 | 0.009939724 |  |
| UTR3 | 5:175553052-175553075 | 0.004444682 |  |
| ENST00000343776 | ENSG00000181450 (ZNF678) | hsa-miR-146a-5p | 0.788306 |
| UTR3 | 1:227844847-227844868 | 0.001411325 |  |
| UTR3 | 1:227845589-227845617 | 0.001705863 |  |
| UTR3 | 1:227845656-227845677 | 0.000915698 |  |
| UTR3 | 1:227846289-227846308 | 0.001496296 |  |
| UTR3 | 1:227846289-227846316 | 0.000538665 |  |
| UTR3 | 1:227847602-227847607 | 0.002471476 |  |
| UTR3 | 1:227848675-227848692 | 0.001296164 |  |
| UTR3 | 1:227848927-227848942 | 0.001675199 |  |
| UTR3 | 1:227842599-227842617 | 0.014931939 |  |
| UTR3 | 1:227842683-227842701 | 0.016890148 |  |
| UTR3 | 1:227843096-227843121 | 0.02368399 |  |
| UTR3 | 1:227843355-227843373 | 0.018067396 |  |
| ENST00000531224 | ENSG00000029363 (BCLAF1) | hsa-miR-146a-5p | 0.786736 |
| UTR3 | 6:136581529-136581547 | 0.004846552 |  |
| UTR3 | 6:136578908-136578926 | 0.001669199 |  |
| UTR3 | 6:136578778-136578802 | 0.018482407 |  |
| UTR3 | 6:136600940-136600964 | 0.010111164 |  |
| UTR3 | 6:136589406-136589426 | 0.023612824 |  |
| ENST00000272217 | ENSG00000143862 (ARL8A) | hsa-miR-146a-5p | 0.786392 |
| UTR3 | 1:202103382-202103406 | 0.003178564 |  |
| UTR3 | 1:202102761-202102784 | 0.028828498 |  |
| ENST00000361752 | ENSG00000112531 (QKI) | hsa-miR-146a-5p | 0.786332 |
| UTR3 | 6:163992133-163992154 | 0.005361624 |  |
| UTR3 | 6:163993552-163993579 | 0.002089316 |  |
| UTR3 | 6:163994244-163994267 | 0.010371853 |  |
| UTR3 | 6:163995782-163995799 | 0.00761089 |  |
| UTR3 | 6:163995962-163995975 | 0.00101077 |  |
| UTR3 | 6:163999561-163999584 | 0.005556766 |  |
| ENST00000434724 | ENSG00000103342 (GSPT1) | hsa-miR-146a-5p | 0.786138 |
| UTR3 | 16:11966817-11966841 | 0.014792598 |  |

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| UTR3 | 16:11964549-11964574 | 0.008569907 | |
| UTR3 | 16:11964312-11964329 | 0.00188468 | |
| UTR3 | 16:11962760-11962774 | 0.004784729 | |
| UTR3 | 16:11962438-11962459 | 0.001950414 | |
| ENST00000394252 | ENSG00000170439 (METTL7B) | hsa-miR-146a-5p | 0.786106 |
| UTR3 | 12:56078335-56078362 | 0.029783908 | |
| UTR3 | 12:56077729-56077751 | 0.011985331 | |
| ENST00000574951 | ENSG00000108509 (CAMTA2) | hsa-miR-146a-5p | 0.785389 |
| UTR3 | 17:4884609-4884627 | 0.02027205 | |
| UTR3 | 17:4883473-4883491 | 0.00380982 | |
| UTR3 | 17:4872263;4872445-4872276;4872455 | 0.002864043 | |
| UTR3 | 17:4872031-4872052 | 0.001654475 | |
| UTR3 | 17:4871386-4871404 | 0.003309232 | |
| ENST00000488550 | ENSG00000143995 (MEIS1) | hsa-miR-146a-5p | 0.785228 |
| UTR3 | 2:66796057-66796083 | 0.00673039 | |
| UTR3 | 2:66796326-66796350 | 0.007606194 | |
| UTR3 | 2:66797828-66797852 | 0.016552362 | |
| UTR3 | 2:66798262-66798288 | 0.001005052 | |
| ENST00000601773 | ENSG00000160321 (ZNF208) | hsa-miR-146a-5p | 0.785072 |
| UTR3 | 19:22122904-22122919 | 0.014799106 | |
| UTR3 | 19:22122675-22122703 | 0.017079764 | |
| ENST00000398844 | ENSG00000113615 (SEC24A) | hsa-miR-146a-5p | 0.784522 |
| UTR3 | 5:134060879-134060906 | 0.019176859 | |
| UTR3 | 5:134061114-134061128 | 0.004695416 | |
| UTR3 | 5:134062733-134062753 | 0.00480242 | |
| UTR3 | 5:133996936-133996950 | 0.016661386 | |
| ENST00000449622 | ENSG00000160221 (C21orf33) | hsa-miR-146a-5p | 0.784354 |
| UTR3 | 21:45564953-45564969 | 0.003070965 | |
| UTR3 | 21:45565044-45565067 | 0.002458611 | |
| UTR3 | 21:45565422-45565441 | 0.026279919 | |
| ENST00000588388 | ENSG00000131941 (RHPN2) | hsa-miR-146a-5p | 0.784007 |
| UTR3 | 19:33484917-33484928 | 0.01217738 | |
| UTR3 | 19:33470925-33470947 | 0.00447251 | |
| UTR3 | 19:33470803-33470821 | 0.01216308 | |
| UTR3 | 19:33470787-33470802 | 0.002963009 | |
| ENST00000323816 | ENSG00000007237 (GAS7) | hsa-miR-146a-5p | 0.78372 |
| UTR3 | 17:9819999-9820019 | 0.001889811 | |
| UTR3 | 17:9819725-9819753 | 0.0250281 | |
| UTR3 | 17:9815638-9815664 | 0.001388028 | |
| UTR3 | 17:9885172-9885198 | 0.00986756 | |
| UTR3 | 17:9837490-9837502 | 0.00814599 | |
| ENST00000366910 | ENSG00000186205 (MARC1) | hsa-miR-146a-5p | 0.783695 |
| UTR3 | 1:220986788-220986809 | 0.025819244 | |

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| UTR3 | 1:220987229-220987251 | 0.002806726 | |
| UTR3 | 1:220987340-220987356 | 0.003119829 | |
| ENST00000367701 | ENSG00000185278 (ZBTB37) | hsa-miR-146a-5p | 0.783595 |
| UTR3 | 1:173858183-173858200 | 0.00228515 | |
| UTR3 | 1:173858643-173858668 | 0.001273208 | |
| UTR3 | 1:173858801-173858821 | 0.001397985 | |
| UTR3 | 1:173863654-173863666 | 0.001351184 | |
| UTR3 | 1:173868348-173868364 | 0.002863164 | |
| UTR3 | 1:173869126-173869151 | 0.001467548 | |
| UTR3 | 1:173869489-173869507 | 0.001791897 | |
| UTR3 | 1:173870384-173870409 | 0.004704759 | |
| UTR3 | 1:173871031-173871044 | 0.002600582 | |
| UTR3 | 1:173871153-173871178 | 0.001475049 | |
| UTR3 | 1:173872248-173872261 | 0.004746865 | |
| UTR3 | 1:173872261-173872284 | 0.005778841 | |
| ENST00000374690 | ENSG00000169083 (AR) | hsa-miR-146a-5p | 0.783528 |
| UTR3 | X:66944625-66944646 | 0.004070186 | |
| UTR3 | X:66944728-66944755 | 0.001031808 | |
| UTR3 | X:66944801-66944815 | 0.001405671 | |
| UTR3 | X:66945221-66945243 | 0.00905965 | |
| UTR3 | X:66945765-66945780 | 0.001941879 | |
| UTR3 | X:66946542-66946558 | 0.001323751 | |
| UTR3 | X:66947785-66947811 | 0.006607271 | |
| UTR3 | X:66950155-66950174 | 0.00628956 | |
| ENST00000295049 | ENSG00000162944 (RFTN2) | hsa-miR-146a-5p | 0.783372 |
| UTR3 | 2:198436363-198436384 | 0.028462722 | |
| UTR3 | 2:198435002-198435024 | 0.001580439 | |
| UTR3 | 2:198434341-198434364 | 0.001671552 | |
| ENST00000339613 | ENSG00000124440 (HIF3A) | hsa-miR-146a-5p | 0.782943 |
| UTR3 | 19:46843124-46843148 | 0.014072197 | |
| UTR3 | 19:46844388-46844406 | 0.005290508 | |
| UTR3 | 19:46844797-46844818 | 0.007277617 | |
| UTR3 | 19:46845234-46845256 | 0.005033146 | |
| ENST00000376621 | ENSG00000204590 (GNL1) | hsa-miR-146a-5p | 0.782601 |
| UTR3 | 6:30513624-30513638 | 0.016893899 | |
| UTR3 | 6:30513602-30513626 | 0.009393176 | |
| UTR3 | 6:30513180-30513194 | 0.005353484 | |
| ENST00000262032 | ENSG00000123411 (IKZF4) | hsa-miR-146a-5p | 0.782453 |
| UTR3 | 12:56429821-56429841 | 0.019352813 | |
| UTR3 | 12:56429961-56429989 | 0.003664538 | |
| UTR3 | 12:56430824-56430840 | 0.002616798 | |
| UTR3 | 12:56432046-56432064 | 0.005992206 | |
| ENST00000437887 | ENSG00000233863 (AC012215.1) | hsa-miR-146a-5p | 0.782242 |
| UTR3 | 8:35651347-35651363 | 0.014314424 | |
| UTR3 | 8:35651477-35651497 | 0.006533456 | |
| UTR3 | 8:35651765-35651788 | 0.004819132 | |

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| UTR3 | 8:35653295-35653318 | 0.00593908 | |
| ENST00000395076 | ENSG00000100614 (PPM1A) | hsa-miR-146a-5p | 0.782121 |
| UTR3 | 14:60762033-60762052 | 0.015023491 | |
| UTR3 | 14:60762574-60762594 | 0.001465463 | |
| UTR3 | 14:60764246-60764273 | 0.00232132 | |
| UTR3 | 14:60765638-60765658 | 0.009758521 | |
| UTR3 | 14:60749598-60749618 | 0.015951123 | |
| ENST00000318833 | ENSG00000180787 (ZFP3) | hsa-miR-146a-5p | 0.781574 |
| UTR3 | 17:4997401-4997421 | 0.018422526 | |
| UTR3 | 17:4998700-4998720 | 0.002202589 | |
| UTR3 | 17:4998930-4998951 | 0.010916968 | |
| ENST00000275493 | ENSG00000146648 (EGFR) | hsa-miR-146a-5p | 0.781509 |
| UTR3 | 7:55274208-55274236 | 0.00205656 | |
| UTR3 | 7:55275853-55275868 | 0.015314033 | |
| UTR3 | 7:55276483-55276509 | 0.005169866 | |
| UTR3 | 7:55276553-55276571 | 0.000579984 | |
| UTR3 | 7:55277443-55277467 | 0.005169352 | |
| UTR3 | 7:55278271-55278296 | 0.001655944 | |
| UTR3 | 7:55278364-55278378 | 0.001590065 | |
| ENST00000554401 | ENSG00000080824 (HSP90AA1) | hsa-miR-146a-5p | 0.781425 |
| UTR3 | 14:102550143-102550158 | 0.031527834 | |
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| ENST00000354631 | ENSG00000107614 (TRDMT1) | hsa-miR-146a-5p | 0.78104 |
| UTR3 | 10:17190319-17190338 | 0.001088942 | |
| UTR3 | 10:17188624-17188641 | 0.001974097 | |
| UTR3 | 10:17187998-17188025 | 0.004122753 | |
| UTR3 | 10:17186587-17186598 | 0.016369666 | |
| UTR3 | 10:17186407-17186428 | 0.002859177 | |
| UTR3 | 10:17185776-17185803 | 0.001777648 | |
| UTR3 | 10:17185140-17185158 | 0.003298698 | |
| ENST00000290585 | ENSG00000159409 (CELF3) | hsa-miR-146a-5p | 0.780985 |
| UTR3 | 1:151674963-151674989 | 0.031485763 | |
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| ENST00000528670 | ENSG00000187240 (DYNC2H1) | hsa-miR-146a-5p | 0.780782 |
| UTR3 | 11:103194699-103194717 | 0.031466326 | |
| ENST00000359486 | ENSG00000100207 (TCF20) | hsa-miR-146a-5p | 0.780637 |
| UTR3 | 22:42557229-42557256 | 0.031452469 | |
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| ENST00000409284 | ENSG00000163492 (CCDC141) | hsa-miR-146a-5p | 0.780168 |
| UTR3 | 2:179742591-179742610 | 0.012264997 | |
| UTR3 | 2:179742576-179742589 | 0.008793196 | |
| UTR3 | 2:179741848-179741870 | 0.001866353 | |
| UTR3 | 2:179741261-179741284 | 0.002349312 | |
| UTR3 | 2:179741030-179741049 | 0.001932964 | |
| UTR3 | 2:179740787-179740806 | 0.001562389 | |
| UTR3 | 2:179739377-179739398 | 0.002638566 | |

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| ENST00000400085 | ENSG00000215343 (ZNF705D) | hsa-miR-146a-5p | 0.779144 |
| UTR3 | 8:11971586-11971612 | 0.002332187 |  |
| UTR3 | 8:11972070-11972092 | 0.002494284 |  |
| UTR3 | 8:11972464-11972487 | 0.024872516 |  |
| UTR3 | 8:11970378-11970405 | 0.008775052 |  |
| ENST00000503808 | ENSG00000157426 (AASDH) | hsa-miR-146a-5p | 0.779109 |
| UTR3 | 4:57237647-57237671 | 0.004763025 |  |
| UTR3 | 4:57221466-57221485 | 0.012582883 |  |
| UTR3 | 4:57216071-57216091 | 0.002585563 |  |
| UTR3 | 4:57204944;57209001-57204957;57209014 | 0.011375552 |  |
| ENST00000374525 | ENSG00000241978 (AKAP2) | hsa-miR-146a-5p | 0.778869 |
| UTR3 | 9:112932321-112932348 | 0.003723278 |  |
| UTR3 | 9:112932886-112932911 | 0.001645306 |  |
| UTR3 | 9:112932993-112933012 | 0.000760435 |  |
| UTR3 | 9:112934143-112934165 | 0.005426306 |  |
| UTR3 | 9:112934736-112934760 | 0.015458723 |  |
| UTR3 | 9:112899870-112899894 | 0.021564409 |  |
| ENST00000340652 | ENSG00000188730 (VWC2) | hsa-miR-146a-5p | 0.778436 |
| UTR3 | 7:49952411-49952426 | 0.003035178 |  |
| UTR3 | 7:49953587-49953615 | 0.005558946 |  |
| UTR3 | 7:49955069-49955079 | 0.001605012 |  |
| UTR3 | 7:49955659-49955677 | 0.006608128 |  |
| UTR3 | 7:49957254-49957274 | 0.002251633 |  |
| UTR3 | 7:49957730-49957744 | 0.005225367 |  |
| UTR3 | 7:49958148-49958172 | 0.001610643 |  |
| UTR3 | 7:49960181-49960209 | 0.001545764 |  |
| UTR3 | 7:49960982-49960996 | 0.003802536 |  |
| ENST00000423275 | ENSG00000132155 (RAF1) | hsa-miR-146a-5p | 0.77825 |
| UTR3 | 3:12645783;12647700-12645788;12647716 | 0.019419684 |  |
| UTR3 | 3:12627217-12627234 | 0.009805652 |  |
| UTR3 | 3:12626640-12626661 | 0.002000189 |  |
| ENST00000374530 | ENSG00000157654 (PALM2-AKAP2) | hsa-miR-146a-5p | 0.778177 |
| UTR3 | 9:112932321-112932348 | 0.003769924 |  |
| UTR3 | 9:112932886-112932911 | 0.001635708 |  |
| UTR3 | 9:112932993-112933012 | 0.000759281 |  |
| UTR3 | 9:112934143-112934165 | 0.005497444 |  |
| UTR3 | 9:112934736-112934760 | 0.015377568 |  |
| UTR3 | 9:112899870-112899894 | 0.021117441 |  |
| ENST00000240922 | ENSG00000121579 (NAA50) | hsa-miR-146a-5p | 0.777265 |
| UTR3 | 3:113440212-113440234 | 0.006491922 |  |
| UTR3 | 3:113439213-113439241 | 0.006504448 |  |
| UTR3 | 3:113436536-113436556 | 0.003578365 |  |
| UTR3 | 3:113436421-113436448 | 0.00124722 |  |

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| UTR3 | 3:113436248-113436274 | 0.002170259 |  |
| UTR3 | 3:113436233-113436248 | 0.011140216 |  |
| ENST00000302103 | ENSG00000172461 (FUT9) | hsa-miR-146a-5p | 0.776879 |
| UTR3 | 6:96652702-96652726 | 0.003394851 |  |
| UTR3 | 6:96652740-96652765 | 0.003006036 |  |
| UTR3 | 6:96653800-96653816 | 0.001264878 |  |
| UTR3 | 6:96656844-96656858 | 0.001345893 |  |
| UTR3 | 6:96657138-96657158 | 0.001983625 |  |
| UTR3 | 6:96657842-96657861 | 0.009713825 |  |
| UTR3 | 6:96658413-96658436 | 0.004118123 |  |
| UTR3 | 6:96659746-96659770 | 0.002962461 |  |
| UTR3 | 6:96663163-96663178 | 0.0033063 |  |
| ENST00000295851 | ENSG00000138443 (ABI2) | hsa-miR-146a-5p | 0.776831 |
| UTR3 | 2:204292376-204292403 | 0.005363376 |  |
| UTR3 | 2:204295997-204296004 | 0.004177317 |  |
| UTR3 | 2:204297381-204297408 | 0.000959874 |  |
| UTR3 | 2:204299480-204299506 | 0.002076199 |  |
| UTR3 | 2:204301980-204302004 | 0.001881069 |  |
| UTR3 | 2:204303017-204303043 | 0.001005082 |  |
| UTR3 | 2:204303664-204303691 | 0.002065638 |  |
| UTR3 | 2:204307358-204307382 | 0.002656673 |  |
| UTR3 | 2:204307923-204307936 | 0.001737389 |  |
| UTR3 | 2:204310882-204310898 | 0.001032072 |  |
| UTR3 | 2:204311271-204311291 | 0.003130079 |  |
| UTR3 | 2:204311454-204311471 | 0.002610166 |  |
| UTR3 | 2:204312010-204312032 | 0.002396586 |  |
| ENST00000423760 | ENSG00000106443 (PHF14) | hsa-miR-146a-5p | 0.776225 |
| UTR3 | 7:11209201-11209224 | 0.031034444 |  |
| ENST00000462833 | ENSG00000173175 (ADCY5) | hsa-miR-146a-5p | 0.775935 |
| UTR3 | 3:123002783-123002789 | 0.005820464 |  |
| UTR3 | 3:123001748-123001772 | 0.005678369 |  |
| UTR3 | 3:123001455-123001471 | 0.014066476 |  |
| UTR3 | 3:123001357-123001380 | 0.002899947 |  |
| UTR3 | 3:123071410;123166259-123071428;123166260 | 0.013361539 |  |
| ENST00000313349 | ENSG00000179833 (SERTAD2) | hsa-miR-146a-5p | 0.775828 |
| UTR3 | 2:64862995-64863010 | 0.017793496 |  |
| UTR3 | 2:64862070-64862095 | 0.003950069 |  |
| UTR3 | 2:64860915-64860939 | 0.003986255 |  |
| UTR3 | 2:64860483-64860499 | 0.002580131 |  |
| UTR3 | 2:64859848-64859871 | 0.002687118 |  |
| ENST00000380607 | ENSG00000107295 (SH3GL2) | hsa-miR-146a-5p | 0.775498 |
| UTR3 | 9:17795989-17796011 | 0.030966068 |  |
| ENST00000233202 | ENSG00000018280 (SLC11A1) | hsa-miR-146a-5p | 0.775257 |
| UTR3 | 2:219261589-219261613 | 0.030943462 |  |

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| ENST00000529131 | ENSG00000204711 (C9orf135) | hsa-miR-146a-5p | 0.774777 |
| UTR3 | 9:72520899-72520922 | 0.030898469 | |
| ENST00000413659 | ENSG00000128815 (WDFY4) | hsa-miR-146a-5p | 0.774634 |
| UTR3 | 10:50030518-50030534 | 0.001465835 | |
| UTR3 | 10:50030578;50034716-50030582;50034738 | 0.001758598 | |
| UTR3 | 10:50034816-50034842 | 0.000798382 | |
| UTR3 | 10:50083137-50083165 | 0.002852473 | |
| UTR3 | 10:50098626-50098640 | 0.003035366 | |
| UTR3 | 10:50190713-50190740 | 0.020974431 | |
| ENST00000306829 | ENSG00000171914 (TLN2) | hsa-miR-146a-5p | 0.77436 |
| UTR3 | 15:63132929-63132949 | 0.007240556 | |
| UTR3 | 15:63133097-63133119 | 0.016735288 | |
| UTR3 | 15:63135024-63135046 | 0.004436258 | |
| UTR3 | 15:63135388-63135403 | 0.00106223 | |
| UTR3 | 15:63135803-63135829 | 0.001385116 | |
| ENST00000503275 | ENSG00000069018 (TRPC7) | hsa-miR-146a-5p | 0.774283 |
| UTR3 | 5:135601943-135601957 | 0.024018092 | |
| UTR3 | 5:135567126-135567143 | 0.006834178 | |
| ENST00000310903 | ENSG00000174527 (MYO1H) | hsa-miR-146a-5p | 0.773657 |
| UTR3 | 12:109885343-109885362 | 0.02773355 | |
| UTR3 | 12:109885417-109885440 | 0.003060225 | |
| ENST00000360409 | ENSG00000118257 (NRP2) | hsa-miR-146a-5p | 0.773651 |
| UTR3 | 2:206659997-206660023 | 0.00415494 | |
| UTR3 | 2:206660728-206660756 | 0.00210191 | |
| UTR3 | 2:206660787-206660804 | 0.000942388 | |
| UTR3 | 2:206661760-206661783 | 0.006703829 | |
| UTR3 | 2:206662129-206662147 | 0.016890144 | |
| ENST00000447079 | ENSG00000167258 (CDK12) | hsa-miR-146a-5p | 0.773512 |
| UTR3 | 17:37687606-37687628 | 0.012027335 | |
| UTR3 | 17:37688511-37688537 | 0.008469247 | |
| UTR3 | 17:37689062-37689082 | 0.001760164 | |
| UTR3 | 17:37690884-37690898 | 0.005073362 | |
| UTR3 | 17:37682424-37682448 | 0.017573589 | |
| ENST00000360264 | ENSG00000257923 (CUX1) | hsa-miR-146a-5p | 0.773137 |
| UTR3 | 7:101900512-101900534 | 0.002641667 | |
| UTR3 | 7:101901365-101901386 | 0.027407677 | |
| UTR3 | 7:101840024-101840047 | 0.003828768 | |
| ENST00000334295 | ENSG00000134779 (TPGS2) | hsa-miR-146a-5p | 0.77267 |
| UTR3 | 18:34374350-34374365 | 0.02477679 | |
| UTR3 | 18:34374141-34374158 | 0.00592502 | |
| ENST00000359660 | ENSG00000145743 (FBXL17) | hsa-miR-146a-5p | 0.772496 |
| UTR3 | 5:107196335-107196354 | 0.013389599 | |
| UTR3 | 5:107195034-107195061 | 0.017295973 | |
| ENST00000339249 | ENSG00000173275 (ZNF449) | hsa-miR-146a-5p | 0.772179 |
| UTR3 | X:134496188-134496201 | 0.002674348 | |

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| UTR3 | X:134496309-134496322 | 0.002778763 | |
| UTR3 | X:134496368-134496386 | 0.012707382 | |
| UTR3 | X:134496412-134496435 | 0.002153008 | |
| UTR3 | X:134496590-134496605 | 0.010342594 | |
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| ENST00000271411 | ENSG00000143190 (POU2F1) | hsa-miR-146a-5p | 0.771974 |
| UTR3 | 1:167386118-167386136 | 0.003169494 | |
| UTR3 | 1:167386426-167386450 | 0.001564091 | |
| UTR3 | 1:167387788-167387809 | 0.001751984 | |
| UTR3 | 1:167388800-167388820 | 0.002342305 | |
| UTR3 | 1:167390092-167390113 | 0.001645663 | |
| UTR3 | 1:167390388-167390404 | 0.001148715 | |
| UTR3 | 1:167390656-167390682 | 0.001733045 | |
| UTR3 | 1:167390875-167390889 | 0.001823769 | |
| UTR3 | 1:167391641-167391660 | 0.001729229 | |
| UTR3 | 1:167393062-167393082 | 0.013728812 | |
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| ENST00000510994 | ENSG00000129055 (ANAPC13) | hsa-miR-146a-5p | 0.771533 |
| UTR3 | 3:134197398-134197417 | 0.003827852 | |
| UTR3 | 3:134197257-134197277 | 0.00407199 | |
| UTR3 | 3:134197032-134197058 | 0.005429311 | |
| UTR3 | 3:134196864-134196881 | 0.004364537 | |
| UTR3 | 3:134196787-134196814 | 0.003293384 | |
| UTR3 | 3:134196645-134196665 | 0.003467471 | |
| UTR3 | 3:134196555-134196582 | 0.006141597 | |
| ENST00000260526 | ENSG00000137962 (ARHGAP29) | hsa-miR-146a-5p | 0.771282 |
| UTR3 | 1:94637384-94637399 | 0.02868194 | |
| UTR3 | 1:94697001-94697013 | 0.010000997 | |
| ENST00000263102 | ENSG00000108091 (CCDC6) | hsa-miR-146a-5p | 0.771099 |
| UTR3 | 10:61551788-61551813 | 0.002892418 | |
| UTR3 | 10:61550926-61550942 | 0.017144803 | |
| UTR3 | 10:61550748-61550765 | 0.010518693 | |
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| ENST00000559291 | ENSG00000128891 (C15orf57) | hsa-miR-146a-5p | 0.770473 |
| UTR3 | 15:40829192-40829212 | 0.002180053 | |
| UTR3 | 15:40829057-40829075 | 0.00107606 | |
| UTR3 | 15:40826901-40826916 | 0.007526304 | |
| UTR3 | 15:40826715-40826734 | 0.019715589 | |
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| ENST00000264434 | ENSG00000115998 (C2orf42) | hsa-miR-146a-5p | 0.770391 |
| UTR3 | 2:70377356-70377375 | 0.005871769 | |
| UTR3 | 2:70377046-70377070 | 0.024618661 | |
| ENST00000367975 | ENSG00000143252 (SDHC) | hsa-miR-146a-5p | 0.770355 |
| UTR3 | 1:161332297-161332317 | 0.025312837 | |
| UTR3 | 1:161332903-161332927 | 0.00517426 | |

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| ENST00000426126 | ENSG00000186908 (ZDHHC17) | hsa-miR-146a-5p | 0.770253 |
| UTR3 | 12:77244820-77244834 | 0.002807948 | |
| UTR3 | 12:77245020-77245044 | 0.019001805 | |
| UTR3 | 12:77245630-77245651 | 0.003611749 | |
| UTR3 | 12:77245664-77245691 | 0.001341103 | |
| UTR3 | 12:77247165-77247187 | 0.003715118 | |
| ENST00000335397 | ENSG00000186509 (OR9Q1) | hsa-miR-146a-5p | 0.769706 |
| UTR3 | 11:57948511-57948529 | 0.020071187 | |
| UTR3 | 11:57948623-57948638 | 0.010356075 | |
| ENST00000570137 | ENSG00000166446 (CDYL2) | hsa-miR-146a-5p | 0.769505 |
| UTR3 | 16:80637360-80637382 | 0.005581081 | |
| UTR3 | 16:80636505-80636523 | 0.005913208 | |
| UTR3 | 16:80635053-80635071 | 0.001199073 | |
| UTR3 | 16:80634868-80634884 | 0.002013479 | |
| UTR3 | 16:80633965-80633978 | 0.002244725 | |
| UTR3 | 16:80632358-80632384 | 0.008829571 | |
| UTR3 | 16:80632031-80632042 | 0.004627559 | |
| ENST00000392837 | ENSG00000111785 (RIC8B) | hsa-miR-146a-5p | 0.769218 |
| UTR3 | 12:107280432-107280448 | 0.017400079 | |
| UTR3 | 12:107236394-107236419 | 0.021152499 | |
| UTR3 | 12:107237647-107237666 | 0.030868985 | |
| ENST00000452722 | ENSG00000182985 (CADM1) | hsa-miR-146a-5p | 0.769147 |
| UTR3 | 11:115046172-115046192 | 0.003246481 | |
| UTR3 | 11:115045929-115045942 | 0.008070384 | |
| UTR3 | 11:115045900-115045913 | 0.003804404 | |
| UTR3 | 11:115044149-115044173 | 0.002383755 | |
| UTR3 | 11:115043879-115043893 | 0.004582884 | |
| UTR3 | 11:115043810-115043830 | 0.002685952 | |
| UTR3 | 11:115040828-115040841 | 0.005601838 | |
| ENST00000361905 | ENSG00000187079 (TEAD1) | hsa-miR-146a-5p | 0.768991 |
| UTR3 | 11:12959157-12959175 | 0.022237818 | |
| UTR3 | 11:12964780-12964807 | 0.001822843 | |
| UTR3 | 11:12965610-12965627 | 0.00316793 | |
| UTR3 | 11:12965790-12965805 | 0.003132832 | |
| ENST00000403299 | ENSG00000100065 (CARD10) | hsa-miR-146a-5p | 0.768959 |
| UTR3 | 22:37886884-37886902 | 0.004705371 | |
| UTR3 | 22:37886850-37886876 | 0.018775482 | |
| UTR3 | 22:37886636-37886658 | 0.006877565 | |
| ENST00000205636 | ENSG00000091317 (CMTM6) | hsa-miR-146a-5p | 0.768325 |
| UTR3 | 3:32523859-32523884 | 0.002210182 | |
| UTR3 | 3:32523798-32523816 | 0.005038224 | |
| UTR3 | 3:32523008-32523024 | 0.022052681 | |
| UTR3 | 3:32544114-32544136 | 0.005378228 | |
| ENST00000376447 | ENSG00000165105 (RASEF) | hsa-miR-146a-5p | 0.768037 |
| UTR3 | 9:85597173-85597182 | 0.004214675 | |

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| UTR3 | 9:85596948-85596972 | 0.005809627 | |
| UTR3 | 9:85595194-85595211 | 0.020249421 | |
| ENST00000525508 | ENSG00000171316 (CHD7) | hsa-miR-146a-5p | 0.76792 |
| UTR3 | 8:61736940-61736965 | 0.003791536 | |
| UTR3 | 8:61737175-61737196 | 0.024979303 | |
| UTR3 | 8:61654855-61654875 | 0.007911839 | |
| ENST00000297354 | ENSG00000164764 (SBSPON) | hsa-miR-146a-5p | 0.767572 |
| UTR3 | 8:73979524-73979539 | 0.004612662 | |
| UTR3 | 8:73979420-73979439 | 0.025618414 | |
| ENST00000400075 | ENSG00000154727 (GABPA) | hsa-miR-146a-5p | 0.767181 |
| UTR3 | 21:27141970-27141991 | 0.002700943 | |
| UTR3 | 21:27142879-27142903 | 0.002017218 | |
| UTR3 | 21:27143164-27143173 | 0.00604562 | |
| UTR3 | 21:27143610-27143634 | 0.002136727 | |
| UTR3 | 21:27143700-27143715 | 0.001637223 | |
| UTR3 | 21:27143712-27143739 | 0.007859008 | |
| UTR3 | 21:27144531-27144551 | 0.007798559 | |
| ENST00000466490 | ENSG00000144867 (SRPRB) | hsa-miR-146a-5p | 0.766872 |
| UTR3 | 3:133538784-133538795 | 0.016196474 | |
| UTR3 | 3:133539445-133539464 | 0.008554979 | |
| UTR3 | 3:133539831-133539857 | 0.005415562 | |
| ENST00000591604 | ENSG00000167383 (ZNF229) | hsa-miR-146a-5p | 0.766841 |
| UTR3 | 19:44934554-44934577 | 0.01118548 | |
| UTR3 | 19:44933356-44933371 | 0.001191958 | |
| UTR3 | 19:44933023-44933038 | 0.001578209 | |
| UTR3 | 19:44931957-44931973 | 0.003030857 | |
| UTR3 | 19:44931274-44931288 | 0.005287492 | |
| UTR3 | 19:44931258-44931277 | 0.007890238 | |
| ENST00000474541 | ENSG00000135747 (ZNF670) | hsa-miR-146a-5p | 0.766534 |
| UTR3 | 1:247132707-247132728 | 0.006414973 | |
| UTR3 | 1:247131172-247131187 | 0.006195642 | |
| UTR3 | 1:247131155-247131175 | 0.017525545 | |
| ENST00000366862 | ENSG00000143756 (FBXO28) | hsa-miR-146a-5p | 0.765962 |
| UTR3 | 1:224346067-224346082 | 0.017228917 | |
| UTR3 | 1:224347277-224347299 | 0.000736263 | |
| UTR3 | 1:224348852-224348871 | 0.010053088 | |
| UTR3 | 1:224345149-224345176 | 0.010723444 | |
| ENST00000479862 | ENSG00000165078 (CPA6) | hsa-miR-146a-5p | 0.76581 |
| UTR3 | 8:68421795-68421819 | 0.008134097 | |
| UTR3 | 8:68334368-68334391 | 0.021936041 | |
| ENST00000351193 | ENSG00000169251 (NMD3) | hsa-miR-146a-5p | 0.765506 |
| UTR3 | 3:160969991-160970008 | 0.030042383 | |
| ENST00000309964 | ENSG00000134852 (CLOCK) | hsa-miR-146a-5p | 0.765352 |
| UTR3 | 4:56298619-56298636 | 0.001790034 | |
| UTR3 | 4:56296279-56296286 | 0.005757977 | |

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| UTR3 | 4:56296207-56296228 | 0.000719194 | |
| UTR3 | 4:56294864-56294878 | 0.007946682 | |
| UTR3 | 4:56294583-56294600 | 0.004444244 | |
| UTR3 | 4:56345078-56345102 | 0.040373706 | |
| ENST00000296755 | ENSG00000131711 (MAP1B) | hsa-miR-146a-5p | 0.765075 |
| UTR3 | 5:71501200-71501228 | 0.006459613 | |
| UTR3 | 5:71501564-71501591 | 0.003555071 | |
| UTR3 | 5:71502309-71502333 | 0.005129667 | |
| UTR3 | 5:71502492-71502516 | 0.001856105 | |
| UTR3 | 5:71502884-71502899 | 0.001588414 | |
| UTR3 | 5:71503898-71503911 | 0.005895966 | |
| UTR3 | 5:71504300-71504322 | 0.002173042 | |
| UTR3 | 5:71504331-71504351 | 0.001220931 | |
| UTR3 | 5:71493627-71493642 | 0.010985216 | |
| ENST00000383699 | ENSG00000175161 (CADM2) | hsa-miR-146a-5p | 0.764683 |
| UTR3 | 3:86117484-86117493 | 0.022375851 | |
| UTR3 | 3:86120669-86120680 | 0.00410935 | |
| UTR3 | 3:86010761-86010788 | 0.017337678 | |
| ENST00000318709 | ENSG00000105778 (AVL9) | hsa-miR-146a-5p | 0.764284 |
| UTR3 | 7:32625069-32625087 | 0.001983241 | |
| UTR3 | 7:32627371-32627391 | 0.002142464 | |
| UTR3 | 7:32627737-32627764 | 0.007831366 | |
| UTR3 | 7:32628146-32628162 | 0.01352906 | |
| UTR3 | 7:32598552-32598574 | 0.009457523 | |
| UTR3 | 7:32619864-32619882 | 0.012099581 | |
| | | | |
| ENST00000298573 | ENSG00000111266 (DUSP16) | hsa-miR-146a-5p | 0.76421 |
| UTR3 | 12:12630428-12630444 | 0.02992465 | |
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| ENST00000314099 | ENSG00000236761 (CTAGE9) | hsa-miR-146a-5p | 0.764028 |
| UTR3 | 6:132029649-132029672 | 0.004437528 | |
| UTR3 | 6:132029619-132029636 | 0.025470596 | |
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| ENST00000261486 | ENSG00000129595 (EPB41L4A) | hsa-miR-146a-5p | 0.763539 |
| UTR3 | 5:111500009-111500030 | 0.010721261 | |
| UTR3 | 5:111499642-111499657 | 0.006677655 | |
| UTR3 | 5:111498489-111498512 | 0.00431172 | |
| UTR3 | 5:111498361-111498379 | 0.006591148 | |
| UTR3 | 5:111504703-111504727 | 0.008173174 | |
| ENST00000265350 | ENSG00000124641 (MED20) | hsa-miR-146a-5p | 0.762941 |
| UTR3 | 6:41874680-41874700 | 0.005563161 | |
| UTR3 | 6:41874150-41874172 | 0.002774452 | |
| UTR3 | 6:41873578-41873605 | 0.008642528 | |
| UTR3 | 6:41873177-41873204 | 0.012829648 | |
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| ENST00000514215 | ENSG00000198780 (FAM169A) | hsa-miR-146a-5p | 0.762843 |

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| UTR3 | 5:74100421;74100981-74100430;74100994 | 0.008306232 | |
| UTR3 | 5:74096756-74096778 | 0.021494683 | |
| ENST00000379261 | ENSG00000048740 (CELF2) | hsa-miR-146a-5p | 0.762791 |
| UTR3 | 10:11371947-11371964 | 0.016522875 | |
| UTR3 | 10:11372517-11372540 | 0.004760932 | |
| UTR3 | 10:11372929-11372956 | 0.00319109 | |
| UTR3 | 10:11374027-11374044 | 0.001819461 | |
| UTR3 | 10:11376812-11376831 | 0.003501888 | |
| ENST00000174653 | ENSG00000070718 (AP3M2) | hsa-miR-146a-5p | 0.762791 |
| UTR3 | 8:42026774-42026795 | 0.027522974 | |
| UTR3 | 8:42028297-42028311 | 0.002273209 | |
| ENST00000216218 | ENSG00000100380 (ST13) | hsa-miR-146a-5p | 0.762736 |
| UTR3 | 22:41222443-41222467 | 0.008692053 | |
| UTR3 | 22:41221845-41221861 | 0.008197398 | |
| UTR3 | 22:41220743-41220757 | 0.012901748 | |
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| ENST00000318445 | ENSG00000176463 (SLCO3A1) | hsa-miR-146a-5p | 0.762733 |
| UTR3 | 15:92706501-92706524 | 0.004750478 | |
| UTR3 | 15:92706967-92706993 | 0.007251796 | |
| UTR3 | 15:92707355-92707381 | 0.008253502 | |
| UTR3 | 15:92708521-92708541 | 0.003637618 | |
| UTR3 | 15:92708930-92708940 | 0.005897565 | |
| ENST00000582730 | ENSG00000136450 (SRSF1) | hsa-miR-146a-5p | 0.761149 |
| UTR3 | 17:56082720-56082742 | 0.029648254 | |
| ENST00000371130 | ENSG00000009694 (TENM1) | hsa-miR-146a-5p | 0.760123 |
| UTR3 | X:123514056-123514069 | 0.006382576 | |
| UTR3 | X:123513573-123513593 | 0.003763372 | |
| UTR3 | X:123513108-123513123 | 0.002056295 | |
| UTR3 | X:123511629-123511645 | 0.002181726 | |
| UTR3 | X:123510127-123510153 | 0.009697181 | |
| UTR3 | X:123509935-123509960 | 0.005474987 | |
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| ENST00000263707 | ENSG00000115112 (TFCP2L1) | hsa-miR-146a-5p | 0.760116 |
| UTR3 | 2:121981394-121981421 | 0.003622276 | |
| UTR3 | 2:121981199-121981222 | 0.001821588 | |
| UTR3 | 2:121979406-121979421 | 0.001446493 | |
| UTR3 | 2:121979205-121979222 | 0.015964871 | |
| UTR3 | 2:121978599-121978622 | 0.002118843 | |
| UTR3 | 2:121974472-121974496 | 0.004581412 | |
| ENST00000298875 | ENSG00000165934 (CPSF2) | hsa-miR-146a-5p | 0.760062 |
| UTR3 | 14:92628335-92628362 | 0.003329643 | |
| UTR3 | 14:92629217-92629237 | 0.002273503 | |
| UTR3 | 14:92630026-92630045 | 0.013586247 | |
| UTR3 | 14:92630744-92630749 | 0.007492676 | |
| UTR3 | 14:92627498-92627518 | 0.014357651 | |

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| ENST00000441159 | ENSG00000170379 (FAM115C) | hsa-miR-146a-5p | 0.759974 |
| UTR3 | 7:143425075-143425102 | 0.003722528 | |
| UTR3 | 7:143425885-143425910 | 0.011081892 | |
| UTR3 | 7:143426895-143426915 | 0.012499141 | |
| UTR3 | 7:143424599-143424621 | 0.011397659 | |
| ENST00000540438 | ENSG00000048028 (USP28) | hsa-miR-146a-5p | 0.759736 |
| UTR3 | 11:113705018-113705043 | 0.027787795 | |
| UTR3 | 11:113679138-113679159 | 0.001733644 | |
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| ENST00000436063 | ENSG00000067334 (DNTTIP2) | hsa-miR-146a-5p | 0.759614 |
| UTR3 | 1:94334358-94334371 | 0.006715639 | |
| UTR3 | 1:94333924-94333950 | 0.008077036 | |
| UTR3 | 1:94333391-94333406 | 0.005787435 | |
| UTR3 | 1:94342535-94342555 | 0.019135182 | |
| UTR3 | 1:94342155-94342176 | 0.019274125 | |
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| ENST00000398637 | ENSG00000111371 (SLC38A1) | hsa-miR-146a-5p | 0.759425 |
| UTR3 | 12:46582079-46582096 | 0.007047058 | |
| UTR3 | 12:46580082-46580109 | 0.002686922 | |
| UTR3 | 12:46579055-46579082 | 0.004838594 | |
| UTR3 | 12:46578503-46578522 | 0.00589066 | |
| UTR3 | 12:46577625-46577643 | 0.009030371 | |
| ENST00000295414 | ENSG00000163249 (CCNYL1) | hsa-miR-146a-5p | 0.759338 |
| UTR3 | 2:208619125-208619145 | 0.005154687 | |
| UTR3 | 2:208620530-208620553 | 0.011602643 | |
| UTR3 | 2:208620557-208620585 | 0.007151993 | |
| UTR3 | 2:208620835-208620858 | 0.005576515 | |
| ENST00000260116 | ENSG00000137561 (TTPA) | hsa-miR-146a-5p | 0.758924 |
| UTR3 | 8:63973471-63973494 | 0.009641321 | |
| UTR3 | 8:63972855-63972878 | 0.005309769 | |
| UTR3 | 8:63972369-63972382 | 0.014497751 | |
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| ENST00000526446 | ENSG00000110717 (NDUFS8) | hsa-miR-146a-5p | 0.75879 |
| UTR3 | 11:67803849;67803929-67803848;67803948 | 0.029436872 | |
| ENST00000373119 | ENSG00000102271 (KLHL4) | hsa-miR-146a-5p | 0.758157 |
| UTR3 | X:86922332-86922355 | 0.003776051 | |
| UTR3 | X:86923385-86923403 | 0.001790437 | |
| UTR3 | X:86923823-86923849 | 0.001176489 | |
| UTR3 | X:86924536-86924561 | 0.020868275 | |
| UTR3 | X:86869039;86869437-86869047;86869447 | 0.009081191 | |
| ENST00000367139 | ENSG00000117280 (RAB7L1) | hsa-miR-146a-5p | 0.757968 |
| UTR3 | 1:205739222-205739246 | 0.003194221 | |
| UTR3 | 1:205739143-205739170 | 0.005060097 | |
| UTR3 | 1:205737268-205737288 | 0.021109211 | |

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| ENST00000439211 | ENSG00000228716 (DHFR) | hsa-miR-146a-5p | 0.757713 |
| UTR3 | 5:79924269-79924289 | 0.009728971 | |
| UTR3 | 5:79922591-79922618 | 0.004227688 | |
| UTR3 | 5:79945221-79945243 | 0.05740097 | |
| ENST00000369872 | ENSG00000143028 (SYPL2) | hsa-miR-146a-5p | 0.757569 |
| UTR3 | 1:110023279-110023306 | 0.00244687 | |
| UTR3 | 1:110024141-110024159 | 0.011675509 | |
| UTR3 | 1:110024274-110024295 | 0.002567821 | |
| UTR3 | 1:110024284-110024305 | 0.002726834 | |
| UTR3 | 1:110024302-110024323 | 0.004494673 | |
| UTR3 | 1:110024429-110024450 | 0.002352395 | |
| UTR3 | 1:110009723-110009749 | 0.015165148 | |
| ENST00000522481 | ENSG00000253896 (AC144568.2) | hsa-miR-146a-5p | 0.757464 |
| UTR3 | 8:29334-29354 | 0.013698895 | |
| UTR3 | 8:29354-29373 | 0.015619784 | |
| ENST00000325203 | ENSG00000091879 (ANGPT2) | hsa-miR-146a-5p | 0.7574 |
| UTR3 | 8:6359662-6359679 | 0.002561476 | |
| UTR3 | 8:6358925-6358944 | 0.002050293 | |
| UTR3 | 8:6357701-6357719 | 0.004387123 | |
| UTR3 | 8:6357623-6357642 | 0.008625816 | |
| UTR3 | 8:6357611-6357626 | 0.002804885 | |
| UTR3 | 8:6357246-6357274 | 0.008883437 | |
| ENST00000453304 | ENSG00000182168 (UNC5C) | hsa-miR-146a-5p | 0.757177 |
| UTR3 | 4:96089287-96089305 | 0.002649601 | |
| UTR3 | 4:96089165-96089184 | 0.010211895 | |
| UTR3 | 4:96087123-96087145 | 0.002763001 | |
| UTR3 | 4:96086624-96086648 | 0.002838777 | |
| UTR3 | 4:96084508-96084530 | 0.010829923 | |
| ENST00000335144 | ENSG00000186767 (SPIN4) | hsa-miR-146a-5p | 0.756801 |
| UTR3 | X:62569888-62569910 | 0.005433099 | |
| UTR3 | X:62569487-62569504 | 0.004369167 | |
| UTR3 | X:62568189-62568205 | 0.003123306 | |
| UTR3 | X:62567237-62567259 | 0.016334205 | |
| ENST00000380003 | ENSG00000147894 (C9orf72) | hsa-miR-146a-5p | 0.756728 |
| UTR3 | 9:27548091-27548099 | 0.017175663 | |
| UTR3 | 9:27547624-27547639 | 0.01207765 | |
| ENST00000223129 | ENSG00000106399 (RPA3) | hsa-miR-146a-5p | 0.756577 |
| UTR3 | 7:7676536-7676558 | 0.004849317 | |
| UTR3 | 7:7676465-7676491 | 0.024390549 | |
| ENST00000295797 | ENSG00000163558 (PRKCI) | hsa-miR-146a-5p | 0.756071 |
| UTR3 | 3:170022965-170022985 | 0.029195047 | |
| ENST00000381813 | ENSG00000205795 (CYS1) | hsa-miR-146a-5p | 0.756053 |
| UTR3 | 2:10198494-10198518 | 0.003994981 | |
| UTR3 | 2:10198127-10198151 | 0.005865746 | |

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| UTR3 | 2:10197049-10197068 | 0.019332654 | |
| ENST00000597832 | ENSG00000204514 (ZNF814) | hsa-miR-146a-5p | 0.755801 |
| UTR3 | 19:58363262-58363276 | 0.001903635 | |
| UTR3 | 19:58362197-58362221 | 0.027267472 | |
| ENST00000324472 | ENSG00000177990 (DPY19L2) | hsa-miR-146a-5p | 0.755702 |
| UTR3 | 12:63953628-63953643 | 0.011652718 | |
| UTR3 | 12:63953062-63953088 | 0.017509614 | |
| ENST00000433351 | ENSG00000116005 (PCYOX1) | hsa-miR-146a-5p | 0.755523 |
| UTR3 | 2:70504909-70504925 | 0.002300138 | |
| UTR3 | 2:70505560-70505587 | 0.001907555 | |
| UTR3 | 2:70505578-70505593 | 0.005297891 | |
| UTR3 | 2:70507812-70507838 | 0.01964091 | |
| ENST00000554557 | ENSG00000072121 (ZFYVE26) | hsa-miR-146a-5p | 0.755157 |
| UTR3 | 14:68265239-68265261 | 0.005809706 | |
| UTR3 | 14:68265229-68265257 | 0.003937823 | |
| UTR3 | 14:68260386-68260399 | 0.005732104 | |
| UTR3 | 14:68251801-68251818 | 0.007379659 | |
| UTR3 | 14:68241750-68241766 | 0.004531334 | |
| UTR3 | 14:68228088-68228116 | 0.001723477 | |
| ENST00000371244 | ENSG00000162409 (PRKAA2) | hsa-miR-146a-5p | 0.754761 |
| UTR3 | 1:57174170-57174179 | 0.003890047 | |
| UTR3 | 1:57175233-57175254 | 0.001561101 | |
| UTR3 | 1:57176616-57176642 | 0.001765876 | |
| UTR3 | 1:57177251-57177277 | 0.001804601 | |
| UTR3 | 1:57177313-57177336 | 0.009836895 | |
| UTR3 | 1:57179625-57179638 | 0.008094142 | |
| UTR3 | 1:57179796-57179815 | 0.002126449 | |
| ENST00000530414 | ENSG00000109832 (DDX25) | hsa-miR-146a-5p | 0.754516 |
| UTR3 | 11:125791921-125791946 | 0.023297503 | |
| UTR3 | 11:125788641-125788661 | 0.026429259 | |
| ENST00000370630 | ENSG00000117151 (CTBS) | hsa-miR-146a-5p | 0.754448 |
| UTR3 | 1:85020137-85020161 | 0.00411006 | |
| UTR3 | 1:85019638-85019651 | 0.007650105 | |
| UTR3 | 1:85018719-85018742 | 0.002893908 | |
| UTR3 | 1:85018396-85018410 | 0.004845695 | |
| UTR3 | 1:85017717-85017743 | 0.001990105 | |
| UTR3 | 1:85016901-85016922 | 0.007561616 | |
| ENST00000318876 | ENSG00000165861 (ZFYVE1) | hsa-miR-146a-5p | 0.754165 |
| UTR3 | 14:73437546-73437572 | 0.029026544 | |
| ENST00000403491 | ENSG00000162599 (NFIA) | hsa-miR-146a-5p | 0.754079 |
| UTR3 | 1:61921023-61921042 | 0.010774161 | |
| UTR3 | 1:61921212-61921229 | 0.007812039 | |
| UTR3 | 1:61927584-61927596 | 0.003296429 | |

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|---|---|---|---|
| UTR3 | 1:61928357-61928381 | 0.007136307 | |
| ENST00000377252 | ENSG00000120594 (PLXDC2) | hsa-miR-146a-5p | 0.753652 |
| UTR3 | 10:20569122-20569142 | 0.005014655 | |
| UTR3 | 10:20570889-20570912 | 0.001684768 | |
| UTR3 | 10:20573636-20573661 | 0.01104128 | |
| UTR3 | 10:20575402-20575424 | 0.001111703 | |
| UTR3 | 10:20578395-20578408 | 0.007044237 | |
| UTR3 | 10:20578430-20578457 | 0.003084747 | |
| ENST00000254442 | ENSG00000091157 (WDR7) | hsa-miR-146a-5p | 0.753567 |
| UTR3 | 18:54694454-54694475 | 0.018427013 | |
| UTR3 | 18:54694577-54694594 | 0.002844227 | |
| UTR3 | 18:54696698-54696715 | 0.001362395 | |
| UTR3 | 18:54697017-54697037 | 0.001856904 | |
| UTR3 | 18:54348616;54349910-54348622;54349923 | 0.012922063 | |
| UTR3 | 18:54424026-54424050 | 0.008271206 | |
| ENST00000607453 | ENSG00000272195 (RP11-156E8.1) | hsa-miR-146a-5p | 0.753512 |
| UTR3 | 1:245132902-245132920 | 0.028969012 | |
| ENST00000317568 | ENSG00000126391 (FRMD8) | hsa-miR-146a-5p | 0.753354 |
| UTR3 | 11:65180335-65180359 | 0.006687249 | |
| UTR3 | 11:65180932-65180953 | 0.022267852 | |
| ENST00000391736 | ENSG00000186818 (LILRB4) | hsa-miR-146a-5p | 0.753108 |
| UTR3 | 19:55181109-55181128 | 0.016679578 | |
| UTR3 | 19:55181678-55181691 | 0.01225395 | |
| ENST00000476906 | ENSG00000261210 (CLEC19A) | hsa-miR-146a-5p | 0.753014 |
| UTR3 | 16:19310099-19310121 | 0.028925222 | |
| ENST00000295087 | ENSG00000162980 (ARL5A) | hsa-miR-146a-5p | 0.75291 |
| UTR3 | 2:152659605-152659625 | 0.005994233 | |
| UTR3 | 2:152659555-152659578 | 0.004655337 | |
| UTR3 | 2:152659177-152659204 | 0.005748492 | |
| UTR3 | 2:152658020-152658033 | 0.001619297 | |
| UTR3 | 2:152658010-152658033 | 0.000665343 | |
| UTR3 | 2:152657163-152657185 | 0.008088019 | |
| UTR3 | 2:152656276-152656292 | 0.002145347 | |
| ENST00000329122 | ENSG00000184724 (KRTAP6-1) | hsa-miR-146a-5p | 0.752671 |
| UTR3 | 21:31985802-31985820 | 0.028895136 | |
| ENST00000565367 | ENSG00000069943 (PIGB) | hsa-miR-146a-5p | 0.752641 |
| UTR3 | 15:55632855-55632880 | 0.026474523 | |
| UTR3 | 15:55621979-55622000 | 0.012034782 | |
| ENST00000266673 | ENSG00000139291 (TMEM19) | hsa-miR-146a-5p | 0.75211 |
| UTR3 | 12:72095134-72095160 | 0.024177891 | |
| UTR3 | 12:72096185-72096206 | 0.001079554 | |
| UTR3 | 12:72091254-72091278 | 0.017298997 | |

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| ENST00000280098 | ENSG00000144228 (SPOPL) | hsa-miR-146a-5p | 0.75186 |
| UTR3 | 2:139327055-139327079 | 0.013899793 | |
| UTR3 | 2:139327685-139327710 | 0.002606678 | |
| UTR3 | 2:139330213-139330235 | 0.012317472 | |
| ENST00000381118 | ENSG00000049167 (ERCC8) | hsa-miR-146a-5p | 0.751708 |
| UTR3 | 5:60220199-60220221 | 0.017478999 | |
| UTR3 | 5:60199486-60199511 | 0.011331708 | |
| ENST00000539981 | ENSG00000163539 (CLASP2) | hsa-miR-146a-5p | 0.751648 |
| UTR3 | 3:33540045-33540071 | 0.018968249 | |
| UTR3 | 3:33538832-33538855 | 0.003264926 | |
| UTR3 | 3:33538256-33538266 | 0.003902216 | |
| UTR3 | 3:33614743-33614755 | 0.013170542 | |
| ENST00000273221 | ENSG00000144711 (IQSEC1) | hsa-miR-146a-5p | 0.750946 |
| UTR3 | 3:12940191-12940217 | 0.004006398 | |
| UTR3 | 3:12939592-12939619 | 0.001567302 | |
| UTR3 | 3:12939561-12939581 | 0.001128368 | |
| UTR3 | 3:12939182-12939202 | 0.019361265 | |
| UTR3 | 3:12978019-12978041 | 0.013197979 | |
| ENST00000242848 | ENSG00000123200 (ZC3H13) | hsa-miR-146a-5p | 0.750857 |
| UTR3 | 13:46529739-46529756 | 0.00234056 | |
| UTR3 | 13:46529692-46529720 | 0.008479488 | |
| UTR3 | 13:46529356-46529371 | 0.003392516 | |
| UTR3 | 13:46559533-46559558 | 0.0108338 | |
| UTR3 | 13:46554115-46554138 | 0.010199069 | |
| UTR3 | 13:46542122-46542147 | 0.011913528 | |
| UTR3 | 13:46541812-46541829 | 0.021522614 | |
| ENST00000481579 | ENSG00000077254 (USP33) | hsa-miR-146a-5p | 0.750818 |
| UTR3 | 1:78162315-78162331 | 0.02873281 | |
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| ENST00000397412 | ENSG00000007545 (CRAMP1L) | hsa-miR-146a-5p | 0.750812 |
| UTR3 | 16:1724929-1724944 | 0.023778891 | |
| UTR3 | 16:1725250-1725267 | 0.002015429 | |
| UTR3 | 16:1726012-1726038 | 0.001665467 | |
| UTR3 | 16:1726213-1726230 | 0.001272542 | |
| ENST00000337743 | ENSG00000089123 (TASP1) | hsa-miR-146a-5p | 0.750551 |
| UTR3 | 20:13370455-13370482 | 0.023028811 | |
| UTR3 | 20:13370068-13370086 | 0.005680683 | |
| ENST00000377122 | ENSG00000078114 (NEBL) | hsa-miR-146a-5p | 0.749784 |
| UTR3 | 10:21074068-21074094 | 0.005675404 | |
| UTR3 | 10:21073345-21073363 | 0.001292988 | |
| UTR3 | 10:21071921-21071947 | 0.005169158 | |
| UTR3 | 10:21071758-21071776 | 0.002637018 | |
| UTR3 | 10:21070567-21070594 | 0.001441142 | |
| UTR3 | 10:21069690-21069712 | 0.00986586 | |
| UTR3 | 10:21069136-21069157 | 0.002561081 | |
| ENST00000530758 | ENSG00000254999 (BRK1) | hsa-miR-146a-5p | 0.749575 |
| UTR3 | 3:10168317-10168340 | 0.028624427 | |

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| ENST00000389063 | ENSG00000172795 (DCP2) | hsa-miR-146a-5p | 0.749272 |
| UTR3 | 5:112349249-112349264 | 0.012024438 | |
| UTR3 | 5:112352416-112352430 | 0.001247987 | |
| UTR3 | 5:112353185-112353200 | 0.001393052 | |
| UTR3 | 5:112353620-112353648 | 0.002378867 | |
| UTR3 | 5:112354933-112354956 | 0.005470883 | |
| UTR3 | 5:112355582-112355593 | 0.006082857 | |
| ENST00000407627 | ENSG00000066044 (ELAVL1) | hsa-miR-146a-5p | 0.749232 |
| UTR3 | 19:8027933-8027959 | 0.003996286 | |
| UTR3 | 19:8027280-8027295 | 0.012477886 | |
| UTR3 | 19:8024425-8024444 | 0.00239629 | |
| UTR3 | 19:8023784-8023798 | 0.009724089 | |
| | | | |
| ENST00000274140 | ENSG00000145495 (MARCH6) | hsa-miR-146a-5p | 0.749214 |
| UTR3 | 5:10433902-10433924 | 0.009336636 | |
| UTR3 | 5:10433938-10433962 | 0.003289346 | |
| UTR3 | 5:10435168-10435187 | 0.015966982 | |
| ENST00000308448 | ENSG00000138138 (ATAD1) | hsa-miR-146a-5p | 0.749206 |
| UTR3 | 10:89512862-89512882 | 0.00202542 | |
| UTR3 | 10:89511957-89511980 | 0.001796814 | |
| UTR3 | 10:89511399-89511415 | 0.012310153 | |
| UTR3 | 10:89511371-89511397 | 0.012459923 | |
| ENST00000435504 | ENSG00000143970 (ASXL2) | hsa-miR-146a-5p | 0.749064 |
| UTR3 | 2:25962355-25962380 | 0.003208564 | |
| UTR3 | 2:25961005-25961030 | 0.002373536 | |
| UTR3 | 2:25960072-25960088 | 0.003438629 | |
| UTR3 | 2:25957508-25957520 | 0.00276348 | |
| UTR3 | 2:25957054-25957076 | 0.01679573 | |
| ENST00000503400 | ENSG00000005700 (IBTK) | hsa-miR-146a-5p | 0.748956 |
| UTR3 | 6:82927824-82927845 | 0.014759492 | |
| UTR3 | 6:82924148-82924168 | 0.001875469 | |
| UTR3 | 6:82914619-82914643 | 0.002567036 | |
| UTR3 | 6:82900901-82900922 | 0.003366874 | |
| UTR3 | 6:82891614-82891630 | 0.00251115 | |
| UTR3 | 6:82880965-82880987 | 0.003490522 | |
| | | | |
| ENST00000359286 | ENSG00000196946 (ZNF705A) | hsa-miR-146a-5p | 0.748747 |
| UTR3 | 12:8331099-8331125 | 0.002519264 | |
| UTR3 | 12:8331583-8331605 | 0.002088762 | |
| UTR3 | 12:8331977-8332000 | 0.022196226 | |
| UTR3 | 12:8329890-8329917 | 0.008778421 | |
| ENST00000261491 | ENSG00000102780 (DGKH) | hsa-miR-146a-5p | 0.748719 |
| UTR3 | 13:42806651-42806671 | 0.001361377 | |
| UTR3 | 13:42807511-42807535 | 0.002120909 | |
| UTR3 | 13:42807695-42807717 | 0.001773981 | |
| UTR3 | 13:42811880-42811905 | 0.001995711 | |
| UTR3 | 13:42812755-42812781 | 0.001104906 | |

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| UTR3 | 13:42813647-42813667 | 0.001625703 | |
| UTR3 | 13:42814236-42814252 | 0.001154295 | |
| UTR3 | 13:42816157-42816174 | 0.005022002 | |
| UTR3 | 13:42816987-42817007 | 0.010221331 | |
| UTR3 | 13:42784783-42784803 | 0.010772268 | |
| ENST00000332624 | ENSG00000115993 (TRAK2) | hsa-miR-146a-5p | 0.748679 |
| UTR3 | 2:202244213-202244236 | 0.006015762 | |
| UTR3 | 2:202243925-202243953 | 0.002129718 | |
| UTR3 | 2:202243898-202243919 | 0.000793046 | |
| UTR3 | 2:202242503-202242523 | 0.019608011 | |
| ENST00000561965 | ENSG00000167264 (DUS2) | hsa-miR-146a-5p | 0.747854 |
| UTR3 | 16:68112355-68112376 | 0.00305053 | |
| UTR3 | 16:68113091-68113105 | 0.025424401 | |
| ENST00000378116 | ENSG00000148468 (FAM171A1) | hsa-miR-146a-5p | 0.747709 |
| UTR3 | 10:15254859-15254875 | 0.004907986 | |
| UTR3 | 10:15254584-15254607 | 0.019008404 | |
| UTR3 | 10:15254459-15254476 | 0.002728254 | |
| UTR3 | 10:15254302-15254321 | 0.0018177 | |
| ENST00000370695 | ENSG00000198689 (SLC9A6) | hsa-miR-146a-5p | 0.74765 |
| UTR3 | X:135127209-135127228 | 0.014531219 | |
| UTR3 | X:135128097-135128124 | 0.012809048 | |
| UTR3 | X:135128121-135128149 | 0.001116979 | |
| ENST00000355100 | ENSG00000140526 (ABHD2) | hsa-miR-146a-5p | 0.747572 |
| UTR3 | 15:89739363-89739377 | 0.003136079 | |
| UTR3 | 15:89740034-89740052 | 0.002945874 | |
| UTR3 | 15:89745443-89745465 | 0.022368537 | |
| ENST00000388712 | ENSG00000135052 (GOLM1) | hsa-miR-146a-5p | 0.747551 |
| UTR3 | 9:88642455-88642480 | 0.013701812 | |
| UTR3 | 9:88642281-88642304 | 0.005617207 | |
| UTR3 | 9:88641136-88641157 | 0.007153807 | |
| UTR3 | 9:88661394-88661417 | 0.009833873 | |
| ENST00000397512 | ENSG00000177042 (TMEM80) | hsa-miR-146a-5p | 0.747365 |
| UTR3 | 11:703960-703981 | 0.028432536 | |
| ENST00000327739 | ENSG00000173124 (C10orf129) | hsa-miR-146a-5p | 0.747338 |
| UTR3 | 10:96985507-96985532 | 0.005640607 | |
| UTR3 | 10:96985583-96985607 | 0.01875445 | |
| UTR3 | 10:96985743-96985766 | 0.004035129 | |
| ENST00000372037 | ENSG00000107779 (BMPR1A) | hsa-miR-146a-5p | 0.747063 |
| UTR3 | 10:88683548-88683576 | 0.018189198 | |
| UTR3 | 10:88684413-88684437 | 0.002973934 | |
| UTR3 | 10:88691662-88691686 | 0.003047516 | |
| UTR3 | 10:88692299-88692323 | 0.004195765 | |

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| ENST00000264711 | ENSG00000115137 (DNAJC27) | hsa-miR-146a-5p | 0.746784 |
| UTR3 | 2:25170228-25170247 | 0.005536992 | |
| UTR3 | 2:25167399-25167427 | 0.015557146 | |
| UTR3 | 2:25167384-25167402 | 0.001691858 | |
| UTR3 | 2:25166927-25166941 | 0.005596267 | |
| ENST00000360135 | ENSG00000168781 (PPIP5K1) | hsa-miR-146a-5p | 0.746763 |
| UTR3 | 15:43826717-43826743 | 0.008184816 | |
| UTR3 | 15:43826616-43826636 | 0.01521916 | |
| UTR3 | 15:43826338-43826363 | 0.003611942 | |
| UTR3 | 15:43827014-43827025 | 0.006891396 | |
| ENST00000394961 | ENSG00000163104 (SMARCAD1) | hsa-miR-146a-5p | 0.746744 |
| UTR3 | 4:95174076-95174103 | 0.010604346 | |
| UTR3 | 4:95195935;95196041-95195948;95196047 | 0.009659875 | |
| UTR3 | 4:95199636-95199651 | 0.003520548 | |
| UTR3 | 4:95199648;95199767-95199668;95199773 | 0.004594094 | |
| ENST00000528609 | ENSG00000165923 (AGBL2) | hsa-miR-146a-5p | 0.746403 |
| UTR3 | 11:47690437-47690458 | 0.008104619 | |
| UTR3 | 11:47681462-47681484 | 0.009236071 | |
| UTR3 | 11:47703643;47711628-47703647;47711649 | 0.044057271 | |
| ENST00000223073 | ENSG00000106344 (RBM28) | hsa-miR-146a-5p | 0.745937 |
| UTR3 | 7:127950554-127950578 | 0.006947414 | |
| UTR3 | 7:127948550-127948572 | 0.001073343 | |
| UTR3 | 7:127947447-127947465 | 0.001864247 | |
| UTR3 | 7:127947337-127947356 | 0.001746621 | |
| UTR3 | 7:127945486-127945505 | 0.001941085 | |
| UTR3 | 7:127938730-127938743 | 0.002991324 | |
| UTR3 | 7:127937990-127938003 | 0.009737153 | |
| UTR3 | 7:127957767-127957785 | 0.009948234 | |
| ENST00000265071 | ENSG00000113361 (CDH6) | hsa-miR-146a-5p | 0.745872 |
| UTR3 | 5:31323667-31323694 | 0.007687153 | |
| UTR3 | 5:31323979-31323999 | 0.003759869 | |
| UTR3 | 5:31325743-31325755 | 0.003549541 | |
| UTR3 | 5:31328951-31328970 | 0.00355894 | |
| UTR3 | 5:31329145-31329169 | 0.009748056 | |
| ENST00000558158 | ENSG00000166069 (TMCO5A) | hsa-miR-146a-5p | 0.745255 |
| UTR3 | 15:38234505-38234531 | 0.024609799 | |
| UTR3 | 15:38235767-38235795 | 0.003640621 | |
| ENST00000380672 | ENSG00000173068 (BNC2) | hsa-miR-146a-5p | 0.745249 |
| UTR3 | 9:16416380-16416405 | 0.001568865 | |
| UTR3 | 9:16415378-16415396 | 0.001671604 | |

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| UTR3 | 9:16410755-16410770 | 0.002098057 | |
| UTR3 | 9:16410172-16410192 | 0.0046937 | |
| UTR3 | 9:16410165-16410190 | 0.001242199 | |
| UTR3 | 9:16409908-16409934 | 0.015513601 | |
| UTR3 | 9:16435730-16435746 | 0.007337621 | |
| ENST00000323571 | ENSG00000171475 (WIPF2) | hsa-miR-146a-5p | 0.745192 |
| UTR3 | 17:38434510-38434530 | 0.008767148 | |
| UTR3 | 17:38435027-38435051 | 0.007787225 | |
| UTR3 | 17:38435162-38435185 | 0.008310998 | |
| UTR3 | 17:38438616-38438642 | 0.001169269 | |
| UTR3 | 17:38420761-38420784 | 0.010874106 | |
| ENST00000313806 | ENSG00000159200 (RCAN1) | hsa-miR-146a-5p | 0.74517 |
| UTR3 | 21:35889881-35889894 | 0.008684016 | |
| UTR3 | 21:35888949-35888967 | 0.01955906 | |
| ENST00000563428 | ENSG00000103168 (TAF1C) | hsa-miR-146a-5p | 0.745046 |
| UTR3 | 16:84213946;84214649-84213950;84214663 | 0.028232455 | |
| ENST00000278379 | ENSG00000110436 (SLC1A2) | hsa-miR-146a-5p | 0.744918 |
| UTR3 | 11:35282223-35282238 | 0.005383055 | |
| UTR3 | 11:35282024-35282047 | 0.003581501 | |
| UTR3 | 11:35281260-35281287 | 0.001228736 | |
| UTR3 | 11:35279972-35279999 | 0.001067206 | |
| UTR3 | 11:35279260-35279282 | 0.001818337 | |
| UTR3 | 11:35278349-35278373 | 0.000914673 | |
| UTR3 | 11:35278013-35278035 | 0.002164756 | |
| UTR3 | 11:35277468-35277486 | 0.002099429 | |
| UTR3 | 11:35276120-35276145 | 0.001534929 | |
| UTR3 | 11:35274191-35274218 | 0.001268406 | |
| UTR3 | 11:35273673-35273700 | 0.005217766 | |
| UTR3 | 11:35273558-35273573 | 0.001942589 | |
| ENST00000503129 | ENSG00000152670 (DDX4) | hsa-miR-146a-5p | 0.744186 |
| UTR3 | 5:55094324-55094344 | 0.004741104 | |
| UTR3 | 5:55094343-55094362 | 0.023417438 | |
| ENST00000318522 | ENSG00000143924 (EML4) | hsa-miR-146a-5p | 0.744139 |
| UTR3 | 2:42558814-42558832 | 0.006506355 | |
| UTR3 | 2:42559080-42559097 | 0.016272795 | |
| UTR3 | 2:42559310-42559330 | 0.002220503 | |
| UTR3 | 2:42557145-42557159 | 0.015108047 | |
| ENST00000383815 | ENSG00000163701 (IL17RE) | hsa-miR-146a-5p | 0.743442 |
| UTR3 | 3:9952842;9952939-9952858;9952943 | 0.025513479 | |
| UTR3 | 3:9948543;9948645-9948549;9948657 | 0.012526569 | |
| ENST00000375859 | ENSG00000106723 (SPIN1) | hsa-miR-146a-5p | 0.743223 |
| UTR3 | 9:91092699-91092727 | 0.00366862 | |
| UTR3 | 9:91093239-91093256 | 0.016771442 | |
| UTR3 | 9:91093470-91093496 | 0.007635913 | |

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| ENST00000425217 | ENSG00000171435 (KSR2) | hsa-miR-146a-5p | 0.742747 |
| UTR3 | 12:117904253-117904280 | 0.001872919 | |
| UTR3 | 12:117902773-117902796 | 0.001100254 | |
| UTR3 | 12:117901663-117901686 | 0.001210662 | |
| UTR3 | 12:117900606-117900621 | 0.00505229 | |
| UTR3 | 12:117898334-117898359 | 0.006616551 | |
| UTR3 | 12:117896986-117897007 | 0.001553948 | |
| UTR3 | 12:117895323-117895346 | 0.000923132 | |
| UTR3 | 12:117893705-117893728 | 0.001038116 | |
| UTR3 | 12:117893278-117893299 | 0.001181664 | |
| UTR3 | 12:117892109-117892137 | 0.001694999 | |
| UTR3 | 12:117891929-117891950 | 0.002241032 | |
| UTR3 | 12:117891131-117891155 | 0.003549633 | |
| ENST00000281405 | ENSG00000118965 (WDR35) | hsa-miR-146a-5p | 0.74245 |
| UTR3 | 2:20113010-20113030 | 0.00467745 | |
| UTR3 | 2:20112431-20112446 | 0.004085916 | |
| UTR3 | 2:20112418-20112446 | 0.001609817 | |
| UTR3 | 2:20112278-20112298 | 0.002028621 | |
| UTR3 | 2:20111991-20112009 | 0.002281082 | |
| UTR3 | 2:20111572-20111599 | 0.001277346 | |
| UTR3 | 2:20111351-20111375 | 0.001494322 | |
| UTR3 | 2:20110904-20110926 | 0.00274985 | |
| UTR3 | 2:20110784-20110802 | 0.002809308 | |
| UTR3 | 2:20110357-20110374 | 0.00499608 | |
| ENST00000499810 | ENSG00000120705 (ETF1) | hsa-miR-146a-5p | 0.742291 |
| UTR3 | 5:137842384-137842410 | 0.014819097 | |
| UTR3 | 5:137841992-137842006 | 0.013177077 | |
| ENST00000395254 | ENSG00000138311 (ZNF365) | hsa-miR-146a-5p | 0.742203 |
| UTR3 | 10:64160112-64160139 | 0.027988653 | |
| ENST00000338316 | ENSG00000078295 (ADCY2) | hsa-miR-146a-5p | 0.742039 |
| UTR3 | 5:7827088-7827116 | 0.003190431 | |
| UTR3 | 5:7829004-7829031 | 0.020933708 | |
| UTR3 | 5:7829258-7829282 | 0.001786855 | |
| UTR3 | 5:7829340-7829365 | 0.00206366 | |
| ENST00000334884 | ENSG00000005483 (KMT2E) | hsa-miR-146a-5p | 0.741986 |
| UTR3 | 7:104748114-104748141 | 0.00876632 | |
| UTR3 | 7:104750762-104750788 | 0.002840895 | |
| UTR3 | 7:104751261-104751281 | 0.003113296 | |
| UTR3 | 7:104752915-104752936 | 0.001794039 | |
| UTR3 | 7:104753892-104753920 | 0.003339906 | |
| UTR3 | 7:104754332-104754359 | 0.004125799 | |
| UTR3 | 7:104747624-104747637 | 0.018619957 | |
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| ENST00000443676 | ENSG00000215356 (ZNF705B) | hsa-miR-146a-5p | 0.741201 |
| UTR3 | 8:7810832-7810858 | 0.002197483 | |
| UTR3 | 8:7811316-7811338 | 0.002155832 | |
| UTR3 | 8:7811710-7811733 | 0.021605778 | |

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| UTR3 | 8:7809624-7809651 | 0.009545215 | |
| ENST00000525557 | ENSG00000140090 (SLC24A4) | hsa-miR-146a-5p | 0.741017 |
| UTR3 | 14:92959860-92959885 | 0.005757555 | |
| UTR3 | 14:92960007-92960028 | 0.002090549 | |
| UTR3 | 14:92960371-92960395 | 0.010720382 | |
| UTR3 | 14:92960596-92960616 | 0.002742919 | |
| UTR3 | 14:92961887-92961906 | 0.006576137 | |
| ENST00000361085 | ENSG00000075407 (ZNF37A) | hsa-miR-146a-5p | 0.740919 |
| UTR3 | 10:38407841-38407859 | 0.026008923 | |
| UTR3 | 10:38409704-38409730 | 0.001870289 | |
| ENST00000265843 | ENSG00000110723 (EXPH5) | hsa-miR-146a-5p | 0.740735 |
| UTR3 | 11:108379335-108379352 | 0.003618741 | |
| UTR3 | 11:108376247-108376270 | 0.014543727 | |
| UTR3 | 11:108376236-108376250 | 0.003897475 | |
| UTR3 | 11:108409804-108409824 | 0.00844923 | |
| UTR3 | 11:108384421-108384440 | 0.009135927 | |
| UTR3 | 11:108383011-108383032 | 0.008257432 | |
| ENST00000524135 | ENSG00000185728 (YTHDF3) | hsa-miR-146a-5p | 0.740544 |
| UTR3 | 8:64099029-64099053 | 0.022180219 | |
| UTR3 | 8:64124147-64124160 | 0.002418696 | |
| UTR3 | 8:64124438-64124463 | 0.003248372 | |
| ENST00000425534 | ENSG00000163412 (EIF4E3) | hsa-miR-146a-5p | 0.740531 |
| UTR3 | 3:71730992-71731005 | 0.00146791 | |
| UTR3 | 3:71729548-71729567 | 0.001305347 | |
| UTR3 | 3:71728199-71728211 | 0.008205902 | |
| UTR3 | 3:71728088-71728110 | 0.001047364 | |
| UTR3 | 3:71727420-71727441 | 0.001795691 | |
| UTR3 | 3:71726641-71726665 | 0.001020106 | |
| UTR3 | 3:71725157-71725173 | 0.005428295 | |
| UTR3 | 3:71724601-71724626 | 0.007575527 | |
| ENST00000534127 | ENSG00000166444 (ST5) | hsa-miR-146a-5p | 0.740509 |
| UTR3 | 11:8714929-8714948 | 0.026295775 | |
| UTR3 | 11:8752726-8752741 | 0.007670813 | |
| ENST00000367290 | ENSG00000120262 (CCDC170) | hsa-miR-146a-5p | 0.739936 |
| UTR3 | 6:151939597-151939613 | 0.027795574 | |
| ENST00000377627 | ENSG00000041988 (THAP3) | hsa-miR-146a-5p | 0.739822 |
| UTR3 | 1:6695167-6695182 | 0.027785908 | |
| ENST00000231461 | ENSG00000113532 (ST8SIA4) | hsa-miR-146a-5p | 0.739547 |
| UTR3 | 5:100145625-100145646 | 0.025588906 | |
| UTR3 | 5:100144706-100144724 | 0.002173705 | |
| ENST00000581161 | ENSG00000176225 (RTTN) | hsa-miR-146a-5p | 0.739282 |
| UTR3 | 18:67812926-67812940 | 0.004070491 | |
| UTR3 | 18:67741162-67741187 | 0.0061682 | |

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| UTR3 | 18:67721391-67721412 | 0.002225383 | |
| UTR3 | 18:67715345-67715371 | 0.001703317 | |
| UTR3 | 18:67688042;67691958-67688053;67691965 | 0.013572697 | |
| ENST00000358154 | ENSG00000197006 (METTL9) | hsa-miR-146a-5p | 0.73916 |
| UTR3 | 16:21667597-21667619 | 0.009778258 | |
| UTR3 | 16:21668000-21668026 | 0.004550026 | |
| UTR3 | 16:21668562-21668583 | 0.008736581 | |
| UTR3 | 16:21666716-21666742 | 0.021282407 | |
| ENST00000559724 | ENSG00000197299 (BLM) | hsa-miR-146a-5p | 0.739077 |
| UTR3 | 15:91304163-91304179 | 0.017428668 | |
| UTR3 | 15:91304443-91304463 | 0.003744245 | |
| UTR3 | 15:91358388-91358415 | 0.006549794 | |
| ENST00000264914 | ENSG00000113273 (ARSB) | hsa-miR-146a-5p | 0.738514 |
| UTR3 | 5:78076162-78076182 | 0.002869956 | |
| UTR3 | 5:78075930-78075951 | 0.01755465 | |
| UTR3 | 5:78075030-78075050 | 0.002159202 | |
| UTR3 | 5:78074431-78074452 | 0.005091263 | |
| ENST00000340057 | ENSG00000112115 (IL17A) | hsa-miR-146a-5p | 0.7385 |
| UTR3 | 6:52054827-52054843 | 0.01732916 | |
| UTR3 | 6:52054949-52054969 | 0.010344696 | |
| ENST00000295092 | ENSG00000162981 (FAM84A) | hsa-miR-146a-5p | 0.73808 |
| UTR3 | 2:14775043-14775070 | 0.006701904 | |
| UTR3 | 2:14775343-14775370 | 0.002947344 | |
| UTR3 | 2:14776247-14776261 | 0.003487858 | |
| UTR3 | 2:14778135-14778156 | 0.001793373 | |
| UTR3 | 2:14778303-14778326 | 0.001566353 | |
| UTR3 | 2:14779381-14779407 | 0.00434844 | |
| UTR3 | 2:14779554-14779573 | 0.00269352 | |
| UTR3 | 2:14779924-14779943 | 0.00409955 | |
| ENST00000585477 | ENSG00000228075 (BOD1L2) | hsa-miR-146a-5p | 0.738066 |
| UTR3 | 18:54816605-54816623 | 0.003136516 | |
| UTR3 | 18:54817114-54817127 | 0.004386204 | |
| UTR3 | 18:54817186-54817201 | 0.016575048 | |
| UTR3 | 18:54814882-54814908 | 0.016566024 | |
| ENST00000328439 | ENSG00000196132 (MYT1) | hsa-miR-146a-5p | 0.737797 |
| UTR3 | 20:62872092-62872112 | 0.026420864 | |
| UTR3 | 20:62848507-62848530 | 0.005931999 | |
| ENST00000529122 | ENSG00000254535 (PABPC4L) | hsa-miR-146a-5p | 0.73778 |
| UTR3 | 4:135119689-135119709 | 0.001685147 | |
| UTR3 | 4:135118503-135118531 | 0.003278821 | |
| UTR3 | 4:135117547-135117563 | 0.022648966 | |
| ENST00000314011 | ENSG00000125945 (ZNF436) | hsa-miR-146a-5p | 0.737775 |
| UTR3 | 1:23687881-23687897 | 0.002920859 | |

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| UTR3 | 1:23687169-23687196 | 0.002517414 | |
| UTR3 | 1:23686512-23686533 | 0.00254246 | |
| UTR3 | 1:23686473-23686499 | 0.009275488 | |
| UTR3 | 1:23689450-23689472 | 0.027024564 | |
| UTR3 | 1:23689252-23689272 | 0.014346948 | |
| ENST00000373036 | ENSG00000188786 (MTF1) | hsa-miR-146a-5p | 0.737763 |
| UTR3 | 1:38279179-38279205 | 0.001320727 | |
| UTR3 | 1:38278992-38279019 | 0.002030099 | |
| UTR3 | 1:38277993-38278011 | 0.005188797 | |
| UTR3 | 1:38276658-38276685 | 0.001850365 | |
| UTR3 | 1:38276127-38276145 | 0.003769872 | |
| UTR3 | 1:38275969-38275996 | 0.005237584 | |
| UTR3 | 1:38275818-38275840 | 0.005573125 | |
| UTR3 | 1:38287813-38287827 | 0.012637803 | |
| ENST00000357250 | ENSG00000112280 (COL9A1) | hsa-miR-146a-5p | 0.737745 |
| UTR3 | 6:70926411-70926430 | 0.01221746 | |
| UTR3 | 6:70926190-70926210 | 0.015392523 | |
| ENST00000537676 | ENSG00000165192 (ASB11) | hsa-miR-146a-5p | 0.737737 |
| UTR3 | X:15301443-15301468 | 0.023827996 | |
| UTR3 | X:15300503-15300528 | 0.003781377 | |
| ENST00000203001 | ENSG00000089195 (TRMT6) | hsa-miR-146a-5p | 0.737626 |
| UTR3 | 20:5919148-5919166 | 0.023041822 | |
| UTR3 | 20:5918769-5918788 | 0.004558149 | |
| ENST00000296812 | ENSG00000151876 (FBXO4) | hsa-miR-146a-5p | 0.737235 |
| UTR3 | 5:41934534-41934561 | 0.008842127 | |
| UTR3 | 5:41935058-41935065 | 0.018724844 | |
| ENST00000325455 | ENSG00000082175 (PGR) | hsa-miR-146a-5p | 0.737075 |
| UTR3 | 11:100909018-100909034 | 0.002898197 | |
| UTR3 | 11:100905128-100905148 | 0.001148552 | |
| UTR3 | 11:100904014-100904040 | 0.001993331 | |
| UTR3 | 11:100902310-100902315 | 0.001507442 | |
| UTR3 | 11:100901858-100901875 | 0.001077059 | |
| UTR3 | 11:100901540-100901562 | 0.010947185 | |
| UTR3 | 11:100901169-100901192 | 0.005306827 | |
| UTR3 | 11:100900920-100900938 | 0.002674858 | |
| ENST00000564533 | ENSG00000260240 (RP11-105C20.2) | hsa-miR-146a-5p | 0.736848 |
| UTR3 | 16:59771866-59771886 | 0.027534364 | |
| ENST00000463144 | ENSG00000204410 (MSH5) | hsa-miR-146a-5p | 0.736639 |
| UTR3 | 6:31721103-31721125 | 0.008810273 | |
| UTR3 | 6:31721378-31721400 | 0.004935601 | |
| UTR3 | 6:31726017-31726030 | 0.013770835 | |
| ENST00000338056 | ENSG00000105784 (RUNDC3B) | hsa-miR-146a-5p | 0.736632 |
| UTR3 | 7:87459838-87459853 | 0.012158351 | |
| UTR3 | 7:87460908-87460928 | 0.012600136 | |

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| UTR3 | 7:87460914-87460936 | 0.00275762 | |
| ENST00000356205 | ENSG00000143570 (SLC39A1) | hsa-miR-146a-5p | 0.736169 |
| UTR3 | 1:153932522-153932539 | 0.002772303 | |
| UTR3 | 1:153932452-153932472 | 0.017727469 | |
| UTR3 | 1:153931970-153931989 | 0.006977401 | |
| ENST00000452027 | ENSG00000154548 (SRSF12) | hsa-miR-146a-5p | 0.735976 |
| UTR3 | 6:89806949-89806971 | 0.027460915 | |
| ENST00000287957 | ENSG00000157259 (GATAD1) | hsa-miR-146a-5p | 0.735863 |
| UTR3 | 7:92085994-92086021 | 0.021277475 | |
| UTR3 | 7:92087047-92087070 | 0.006173935 | |
| ENST00000554081 | ENSG00000185246 (PRPF39) | hsa-miR-146a-5p | 0.735199 |
| UTR3 | 14:45578908-45578932 | 0.00557445 | |
| UTR3 | 14:45581641-45581660 | 0.002759825 | |
| UTR3 | 14:45584961-45584983 | 0.004866203 | |
| UTR3 | 14:45585161-45585173 | 0.01419511 | |
| ENST00000438447 | ENSG00000133401 (PDZD2) | hsa-miR-146a-5p | 0.735049 |
| UTR3 | 5:32108255-32108271 | 0.024524222 | |
| UTR3 | 5:32109990-32110014 | 0.001723403 | |
| UTR3 | 5:32090222-32090244 | 0.005617387 | |
| ENST00000593946 | ENSG00000039650 (PNKP) | hsa-miR-146a-5p | 0.734939 |
| UTR3 | 19:50365669-50365688 | 0.003132535 | |
| UTR3 | 19:50365342;50365442-50365362;50365449 | 0.00304718 | |
| UTR3 | 19:50364515-50364539 | 0.021194076 | |
| ENST00000313070 | ENSG00000081803 (CADPS2) | hsa-miR-146a-5p | 0.734715 |
| UTR3 | 7:121959842-121959850 | 0.00478924 | |
| UTR3 | 7:121959106-121959128 | 0.003667822 | |
| UTR3 | 7:121959048-121959066 | 0.009716258 | |
| UTR3 | 7:121958866-121958880 | 0.004219968 | |
| UTR3 | 7:121958664-121958684 | 0.004961735 | |
| ENST00000586178 | ENSG00000011258 (MBTD1) | hsa-miR-146a-5p | 0.734704 |
| UTR3 | 17:49257277-49257302 | 0.006482296 | |
| UTR3 | 17:49257099-49257126 | 0.007625253 | |
| UTR3 | 17:49256140-49256157 | 0.001997146 | |
| UTR3 | 17:49255957-49255983 | 0.002976594 | |
| UTR3 | 17:49254967-49254995 | 0.008272781 | |
| ENST00000376701 | ENSG00000015285 (WAS) | hsa-miR-146a-5p | 0.73465 |
| UTR3 | X:48549731-48549755 | 0.006914588 | |
| UTR3 | X:48549748-48549761 | 0.020434987 | |
| ENST00000354452 | ENSG00000196628 (TCF4) | hsa-miR-146a-5p | 0.734453 |
| UTR3 | 18:52894372-52894391 | 0.005397486 | |
| UTR3 | 18:52893419-52893431 | 0.003296146 | |
| UTR3 | 18:52892519-52892539 | 0.009591558 | |
| UTR3 | 18:52891555-52891568 | 0.002930244 | |

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| UTR3 | 18:52890168-52890190 | 0.006117567 | |
| ENST00000416691 | ENSG00000133103 (COG6) | hsa-miR-146a-5p | 0.73429 |
| UTR3 | 13:40363169-40363195 | 0.009979994 | |
| UTR3 | 13:40364358-40364378 | 0.002528366 | |
| UTR3 | 13:40364999-40365015 | 0.002936137 | |
| UTR3 | 13:40365012-40365035 | 0.001329693 | |
| UTR3 | 13:40365720-40365729 | 0.007244967 | |
| UTR3 | 13:40253707-40253731 | 0.015416381 | |
| ENST00000394008 | ENSG00000198083 (KRTAP9-9) | hsa-miR-146a-5p | 0.733869 |
| UTR3 | 17:39412242-39412252 | 0.010420289 | |
| UTR3 | 17:39412359-39412380 | 0.016863805 | |
| ENST00000532592 | ENSG00000170743 (SYT9) | hsa-miR-146a-5p | 0.733817 |
| UTR3 | 11:7489041-7489066 | 0.001731113 | |
| UTR3 | 11:7489498-7489514 | 0.016514964 | |
| UTR3 | 11:7490193-7490219 | 0.009033736 | |
| ENST00000209875 | ENSG00000094916 (CBX5) | hsa-miR-146a-5p | 0.733622 |
| UTR3 | 12:54635386-54635402 | 0.011437923 | |
| UTR3 | 12:54632906-54632931 | 0.002459292 | |
| UTR3 | 12:54630985-54631006 | 0.001886556 | |
| UTR3 | 12:54629577-54629594 | 0.002302396 | |
| UTR3 | 12:54628661-54628680 | 0.002529992 | |
| UTR3 | 12:54627871-54627890 | 0.002029345 | |
| UTR3 | 12:54625272-54625296 | 0.004617961 | |
| ENST00000361377 | ENSG00000164172 (MOCS2) | hsa-miR-146a-5p | 0.733536 |
| UTR3 | 5:52393851-52393867 | 0.027256281 | |
| ENST00000373218 | ENSG00000148730 (EIF4EBP2) | hsa-miR-146a-5p | 0.73297 |
| UTR3 | 10:72184543-72184567 | 0.009499709 | |
| UTR3 | 10:72184844-72184870 | 0.003111461 | |
| UTR3 | 10:72185256-72185273 | 0.007410466 | |
| UTR3 | 10:72188305-72188327 | 0.00718737 | |
| ENST00000551632 | ENSG00000178498 (DTX3) | hsa-miR-146a-5p | 0.732615 |
| UTR3 | 12:58003156-58003172 | 0.002243689 | |
| UTR3 | 12:58003408-58003426 | 0.024935642 | |
| ENST00000354449 | ENSG00000197548 (ATG7) | hsa-miR-146a-5p | 0.732446 |
| UTR3 | 3:11597745-11597765 | 0.001179585 | |
| UTR3 | 3:11598004-11598031 | 0.014601651 | |
| UTR3 | 3:11598244-11598266 | 0.011384029 | |
| ENST00000318238 | ENSG00000177409 (SAMD9L) | hsa-miR-146a-5p | 0.732425 |
| UTR3 | 7:92760458-92760477 | 0.004957551 | |
| UTR3 | 7:92759734-92759759 | 0.005318299 | |
| UTR3 | 7:92759708-92759734 | 0.00280099 | |
| UTR3 | 7:92759548-92759569 | 0.014086669 | |
| ENST00000491614 | ENSG00000165609 (NUDT5) | hsa-miR-146a-5p | 0.732203 |
| UTR3 | 10:12209360-12209373 | 0.024624672 | |

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| UTR3 | 10:12208683-12208697 | 0.001705083 | |
| UTR3 | 10:12208671-12208697 | 0.000815194 | |
| ENST00000320672 | ENSG00000145687 (SSBP2) | hsa-miR-146a-5p | 0.731934 |
| UTR3 | 5:80715650-80715675 | 0.003898335 | |
| UTR3 | 5:80715129-80715150 | 0.004271012 | |
| UTR3 | 5:80712983-80713004 | 0.001502898 | |
| UTR3 | 5:80712678-80712706 | 0.001893006 | |
| UTR3 | 5:80712240-80712265 | 0.002516015 | |
| UTR3 | 5:80711089-80711114 | 0.003981479 | |
| UTR3 | 5:80710458-80710482 | 0.001349791 | |
| UTR3 | 5:80709081-80709105 | 0.007710063 | |
| ENST00000328747 | ENSG00000146757 (ZNF92) | hsa-miR-146a-5p | 0.73189 |
| UTR3 | 7:64853807;64863254-64853814;64863266 | 0.015000645 | |
| UTR3 | 7:64863903-64863921 | 0.01721057 | |
| UTR3 | 7:64864071-64864089 | 0.016438553 | |
| UTR3 | 7:64864659-64864677 | 0.030454349 | |
| ENST00000597774 | ENSG00000196961 (AP2A1) | hsa-miR-146a-5p | 0.73143 |
| UTR3 | 19:50302677-50302703 | 0.011382961 | |
| UTR3 | 19:50304243;50304660-50304256;50304664 | 0.013607156 | |
| UTR3 | 19:50306572-50306599 | 0.002090491 | |
| ENST00000502346 | ENSG00000174695 (TMEM167A) | hsa-miR-146a-5p | 0.731404 |
| UTR3 | 5:82352768-82352783 | 0.009677789 | |
| UTR3 | 5:82350797-82350814 | 0.001643411 | |
| UTR3 | 5:82350452-82350477 | 0.008203916 | |
| UTR3 | 5:82349440-82349454 | 0.003947701 | |
| UTR3 | 5:82349092-82349118 | 0.003605638 | |
| ENST00000493594 | ENSG00000117226 (GBP3) | hsa-miR-146a-5p | 0.73119 |
| UTR3 | 1:89473013-89473038 | 0.027060633 | |
| ENST00000285208 | ENSG00000154917 (RAB6B) | hsa-miR-146a-5p | 0.731025 |
| UTR3 | 3:133547225-133547244 | 0.004460754 | |
| UTR3 | 3:133546876-133546889 | 0.002668254 | |
| UTR3 | 3:133546036-133546063 | 0.002016221 | |
| UTR3 | 3:133545202-133545219 | 0.001086443 | |
| UTR3 | 3:133545055-133545079 | 0.000919666 | |
| UTR3 | 3:133544689-133544708 | 0.006965892 | |
| UTR3 | 3:133543086-133543097 | 0.008929674 | |
| ENST00000341516 | ENSG00000139990 (DCAF5) | hsa-miR-146a-5p | 0.730972 |
| UTR3 | 14:69520197-69520215 | 0.012257123 | |
| UTR3 | 14:69519487-69519503 | 0.003348623 | |
| UTR3 | 14:69518458-69518480 | 0.0022644 | |
| UTR3 | 14:69517697-69517714 | 0.004831934 | |
| UTR3 | 14:69584886-69584909 | 0.013321774 | |
| UTR3 | 14:69558600;69583083-69558604;69583105 | 0.006306571 | |

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| ENST00000367635 | ENSG00000116191 (RALGPS2) | hsa-miR-146a-5p | 0.73045 |
| UTR3 | 1:178885610-178885626 | 0.016649975 |  |
| UTR3 | 1:178885988-178886011 | 0.002462159 |  |
| UTR3 | 1:178886027-178886045 | 0.002334513 |  |
| UTR3 | 1:178887019-178887045 | 0.001806963 |  |
| UTR3 | 1:178863106-178863121 | 0.017167767 |  |
| ENST00000413432 | ENSG00000006607 (FARP2) | hsa-miR-146a-5p | 0.730415 |
| UTR3 | 2:242383392-242383408 | 0.001536109 |  |
| UTR3 | 2:242384525-242384543 | 0.001346798 |  |
| UTR3 | 2:242385154-242385179 | 0.007124595 |  |
| UTR3 | 2:242386093-242386119 | 0.006161804 |  |
| UTR3 | 2:242386151-242386163 | 0.008902427 |  |
| UTR3 | 2:242381695-242381719 | 0.009233577 |  |
| ENST00000273375 | ENSG00000144840 (RABL3) | hsa-miR-146a-5p | 0.729535 |
| UTR3 | 3:120408481-120408504 | 0.004271288 |  |
| UTR3 | 3:120407232-120407248 | 0.001541299 |  |
| UTR3 | 3:120405695-120405719 | 0.016837611 |  |
| UTR3 | 3:120405532-120405554 | 0.004273095 |  |
| ENST00000326407 | ENSG00000135916 (ITM2C) | hsa-miR-146a-5p | 0.728941 |
| UTR3 | 2:231743433-231743456 | 0.003981531 |  |
| UTR3 | 2:231743767-231743780 | 0.006415481 |  |
| UTR3 | 2:231743809-231743825 | 0.006959177 |  |
| UTR3 | 2:231743890-231743909 | 0.00951798 |  |
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| ENST00000220244 | ENSG00000103888 (KIAA1199) | hsa-miR-146a-5p | 0.728868 |
| UTR3 | 15:81243603-81243621 | 0.024180375 |  |
| UTR3 | 15:81234367-81234390 | 0.012606234 |  |
| ENST00000477053 | ENSG00000134490 (TMEM241) | hsa-miR-146a-5p | 0.728842 |
| UTR3 | 18:20932231;20936558-20932253;20936561 | 0.006520917 |  |
| UTR3 | 18:20877989-20878007 | 0.00494183 |  |
| UTR3 | 18:20877197-20877211 | 0.001625192 |  |
| UTR3 | 18:20876007-20876020 | 0.01377804 |  |
| ENST00000448849 | ENSG00000134897 (BIVM) | hsa-miR-146a-5p | 0.728793 |
| UTR3 | 13:103492339-103492353 | 0.024493085 |  |
| UTR3 | 13:103493269-103493292 | 0.002368777 |  |
| ENST00000480058 | ENSG00000112739 (PRPF4B) | hsa-miR-146a-5p | 0.728702 |
| UTR3 | 6:4062076-4062100 | 0.009701209 |  |
| UTR3 | 6:4062397-4062421 | 0.003332188 |  |
| UTR3 | 6:4064554-4064567 | 0.013820951 |  |
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| ENST00000367588 | ENSG00000135835 (KIAA1614) | hsa-miR-146a-5p | 0.728611 |
| UTR3 | 1:180915319-180915335 | 0.004844488 |  |
| UTR3 | 1:180915564-180915580 | 0.011100525 |  |
| UTR3 | 1:180915897-180915916 | 0.010221201 |  |

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| UTR3 | 1:180905580-180905602 | 0.003359965 | |
| ENST00000559192 | ENSG00000140455 (USP3) | hsa-miR-146a-5p | 0.728557 |
| UTR3 | 15:63883306-63883327 | 0.019188363 | |
| UTR3 | 15:63886075-63886099 | 0.002605 | |
| UTR3 | 15:63886810-63886828 | 0.005049014 | |
| ENST00000392438 | ENSG00000198836 (OPA1) | hsa-miR-146a-5p | 0.728522 |
| UTR3 | 3:193412654-193412681 | 0.004347384 | |
| UTR3 | 3:193413050-193413078 | 0.002105715 | |
| UTR3 | 3:193415041-193415061 | 0.014528414 | |
| UTR3 | 3:193332650-193332667 | 0.015852153 | |
| UTR3 | 3:193360583-193360606 | 0.009578091 | |
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| ENST00000529689 | ENSG00000137500 (CCDC90B) | hsa-miR-146a-5p | 0.72852 |
| UTR3 | 11:82970573-82970595 | 0.002783952 | |
| UTR3 | 11:82970498-82970515 | 0.003473714 | |
| UTR3 | 11:82970202-82970225 | 0.020581681 | |
| ENST00000261438 | ENSG00000109787 (KLF3) | hsa-miR-146a-5p | 0.728448 |
| UTR3 | 4:38699030-38699056 | 0.007705201 | |
| UTR3 | 4:38699193-38699210 | 0.019128144 | |
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| ENST00000370125 | ENSG00000079335 (CDC14A) | hsa-miR-146a-5p | 0.728422 |
| UTR3 | 1:100964495-100964516 | 0.020949811 | |
| UTR3 | 1:100984811-100984829 | 0.005881424 | |
| ENST00000376040 | ENSG00000135040 (NAA35) | hsa-miR-146a-5p | 0.72841 |
| UTR3 | 9:88573457-88573481 | 0.078262116 | |
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| ENST00000375321 | ENSG00000107968 (MAP3K8) | hsa-miR-146a-5p | 0.728219 |
| UTR3 | 10:30749949-30749970 | 0.023472576 | |
| UTR3 | 10:30739370-30739397 | 0.015400193 | |
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| ENST00000298198 | ENSG00000165434 (PGM2L1) | hsa-miR-146a-5p | 0.727476 |
| UTR3 | 11:74046996-74047021 | 0.002778655 | |
| UTR3 | 11:74046985-74047011 | 0.002527521 | |
| UTR3 | 11:74045883-74045898 | 0.011609185 | |
| UTR3 | 11:74045551-74045566 | 0.001825589 | |
| UTR3 | 11:74044365-74044380 | 0.001901888 | |
| UTR3 | 11:74041496-74041520 | 0.006110285 | |
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| ENST00000273666 | ENSG00000145087 (STXBP5L) | hsa-miR-146a-5p | 0.727135 |
| UTR3 | 3:121138547-121138574 | 0.003957856 | |
| UTR3 | 3:121139695-121139714 | 0.007813951 | |
| UTR3 | 3:121140171-121140196 | 0.002295955 | |
| UTR3 | 3:121140667-121140695 | 0.001290831 | |
| UTR3 | 3:121141557-121141583 | 0.001319065 | |
| UTR3 | 3:121141584-121141605 | 0.001087527 | |
| UTR3 | 3:121142413-121142432 | 0.002532684 | |
| UTR3 | 3:121142920-121142936 | 0.0056564 | |

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| UTR3 | 3:120628538-120628564 | 0.003783782 | |
| ENST00000607197 | ENSG00000051620 (HEBP2) | hsa-miR-146a-5p | 0.727103 |
| UTR3 | 6:138740959-138740983 | 0.006811306 | |
| UTR3 | 6:138741689-138741710 | 0.001589795 | |
| UTR3 | 6:138742862-138742885 | 0.01832135 | |
| ENST00000312431 | ENSG00000151914 (DST) | hsa-miR-146a-5p | 0.727026 |
| UTR3 | 6:56417400-56417421 | 0.001895465 | |
| UTR3 | 6:56357206-56357224 | 0.003104473 | |
| UTR3 | 6:56352005-56352031 | 0.0020256 | |
| UTR3 | 6:56323888-56323905 | 0.003168137 | |
| UTR3 | 6:56322923-56322944 | 0.008240217 | |
| UTR3 | 6:56473076-56473090 | 0.017161522 | |
| UTR3 | 6:56438542-56438554 | 0.016780119 | |
| ENST00000392054 | ENSG00000153823 (PID1) | hsa-miR-146a-5p | 0.72685 |
| UTR3 | 2:229890085-229890103 | 0.004555012 | |
| UTR3 | 2:229889168-229889181 | 0.022146538 | |
| ENST00000316397 | ENSG00000197414 (GOLGA6L1) | hsa-miR-146a-5p | 0.726818 |
| UTR3 | 15:22744730-22744745 | 0.009591 | |
| UTR3 | 15:22744977-22744996 | 0.006945674 | |
| UTR3 | 15:22745756-22745770 | 0.010162249 | |
| ENST00000369681 | ENSG00000065615 (CYB5R4) | hsa-miR-146a-5p | 0.72614 |
| UTR3 | 6:84671167-84671181 | 0.002569469 | |
| UTR3 | 6:84671178-84671201 | 0.00252392 | |
| UTR3 | 6:84671467-84671488 | 0.002347885 | |
| UTR3 | 6:84672095-84672122 | 0.001861066 | |
| UTR3 | 6:84672545-84672561 | 0.001644236 | |
| UTR3 | 6:84673371-84673391 | 0.00522266 | |
| UTR3 | 6:84673601-84673617 | 0.003295376 | |
| UTR3 | 6:84675544-84675558 | 0.003676758 | |
| UTR3 | 6:84665124-84665138 | 0.016006377 | |
| ENST00000231721 | ENSG00000010319 (SEMA3G) | hsa-miR-146a-5p | 0.725983 |
| UTR3 | 3:52469351-52469376 | 0.025347128 | |
| UTR3 | 3:52467995-52468019 | 0.001283177 | |
| ENST00000514176 | ENSG00000109805 (NCAPG) | hsa-miR-146a-5p | 0.725971 |
| UTR3 | 4:17818994-17819012 | 0.011998186 | |
| UTR3 | 4:17838817-17838834 | 0.006128265 | |
| UTR3 | 4:17845019-17845031 | 0.008502861 | |
| ENST00000388825 | ENSG00000211445 (GPX3) | hsa-miR-146a-5p | 0.725339 |
| UTR3 | 5:150408013-150408033 | 0.018362035 | |
| UTR3 | 5:150408253-150408269 | 0.008215348 | |
| ENST00000465254 | ENSG00000189367 (KIAA0408) | hsa-miR-146a-5p | 0.725324 |
| UTR3 | 6:127765166-127765182 | 0.00619066 | |
| UTR3 | 6:127764154-127764173 | 0.002408908 | |
| UTR3 | 6:127762530-127762552 | 0.017976614 | |

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| ENST00000371117 | ENSG00000170927 (PKHD1) | hsa-miR-146a-5p | 0.725256 |
| UTR3 | 6:51483224-51483246 | 0.003063342 |  |
| UTR3 | 6:51480990-51481010 | 0.004959784 |  |
| UTR3 | 6:51927354-51927370 | 0.013182963 |  |
| UTR3 | 6:51875229-51875257 | 0.04253556 |  |
| UTR3 | 6:51695668-51695689 | 0.006143828 |  |
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| ENST00000367996 | ENSG00000158859 (ADAMTS4) | hsa-miR-146a-5p | 0.725243 |
| UTR3 | 1:161160210-161160230 | 0.002278636 |  |
| UTR3 | 1:161159616-161159643 | 0.001811067 |  |
| UTR3 | 1:161156829-161156846 | 0.00205079 |  |
| UTR3 | 1:161156298-161156318 | 0.002759304 |  |
| UTR3 | 1:161154101-161154123 | 0.016436043 |  |
| UTR3 | 1:161163537-161163563 | 0.005959314 |  |
| ENST00000411937 | ENSG00000170390 (DCLK2) | hsa-miR-146a-5p | 0.725224 |
| UTR3 | 4:151178507-151178526 | 0.026567943 |  |
| ENST00000291825 | ENSG00000105227 (PRX) | hsa-miR-146a-5p | 0.724766 |
| UTR3 | 19:40903783-40903806 | 0.010920553 |  |
| UTR3 | 19:40903768-40903794 | 0.008143914 |  |
| UTR3 | 19:40901464-40901482 | 0.007465992 |  |
| ENST00000373191 | ENSG00000126070 (AGO3) | hsa-miR-146a-5p | 0.72474 |
| UTR3 | 1:36522106-36522129 | 0.016083051 |  |
| UTR3 | 1:36525752-36525770 | 0.001010397 |  |
| UTR3 | 1:36532580-36532603 | 0.001010097 |  |
| UTR3 | 1:36532963-36532978 | 0.002197626 |  |
| UTR3 | 1:36534002-36534024 | 0.001291508 |  |
| UTR3 | 1:36535016-36535041 | 0.004935648 |  |
| ENST00000497136 | ENSG00000120008 (WDR11) | hsa-miR-146a-5p | 0.724431 |
| UTR3 | 10:122665424-122665451 | 0.002998541 |  |
| UTR3 | 10:122665467-122665489 | 0.00059876 |  |
| UTR3 | 10:122665568-122665594 | 0.000513586 |  |
| UTR3 | 10:122668128-122668144 | 0.007870633 |  |
| UTR3 | 10:122668527-122668554 | 0.005164918 |  |
| UTR3 | 10:122668597-122668617 | 0.002771677 |  |
| UTR3 | 10:122668910-122668930 | 0.006584875 |  |
| ENST00000371464 | ENSG00000138207 (RBP4) | hsa-miR-146a-5p | 0.723963 |
| UTR3 | 10:95351581-95351607 | 0.025224947 |  |
| UTR3 | 10:95360481-95360493 | 0.005971435 |  |
| ENST00000338983 | ENSG00000091436 (MLTK) | hsa-miR-146a-5p | 0.723639 |
| UTR3 | 2:174087078-174087096 | 0.012309652 |  |
| UTR3 | 2:174087552-174087568 | 0.001547266 |  |
| UTR3 | 2:174089347-174089373 | 0.002499978 |  |
| UTR3 | 2:174091323-174091337 | 0.003076922 |  |
| UTR3 | 2:174091608-174091613 | 0.007004375 |  |
| ENST00000396065 | ENSG00000140297 (GCNT3) | hsa-miR-146a-5p | 0.723307 |
| UTR3 | 15:59911928-59911952 | 0.002807163 |  |
| UTR3 | 15:59911964-59911991 | 0.004228182 |  |

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| UTR3 | 15:59912268-59912285 | 0.003646424 | |
| UTR3 | 15:59912309-59912335 | 0.015729345 | |
| ENST00000445930 | ENSG00000100519 (PSMC6) | hsa-miR-146a-5p | 0.723163 |
| UTR3 | 14:53194687-53194707 | 0.026399359 | |
| ENST00000374045 | ENSG00000181634 (TNFSF15) | hsa-miR-146a-5p | 0.723126 |
| UTR3 | 9:117551105-117551126 | 0.001187995 | |
| UTR3 | 9:117550749-117550761 | 0.001869002 | |
| UTR3 | 9:117550664-117550690 | 0.001096389 | |
| UTR3 | 9:117550480-117550507 | 0.002405811 | |
| UTR3 | 9:117549598-117549618 | 0.001500167 | |
| UTR3 | 9:117548772-117548793 | 0.014787199 | |
| UTR3 | 9:117547890-117547908 | 0.001703009 | |
| UTR3 | 9:117547701-117547719 | 0.001846717 | |
| ENST00000522372 | ENSG00000215262 (KCNU1) | hsa-miR-146a-5p | 0.723029 |
| UTR3 | 8:36793125-36793141 | 0.02638842 | |
| ENST00000225719 | ENSG00000108582 (CPD) | hsa-miR-146a-5p | 0.722677 |
| UTR3 | 17:28793275-28793294 | 0.001939602 | |
| UTR3 | 17:28794048-28794073 | 0.001734219 | |
| UTR3 | 17:28794769-28794788 | 0.002229838 | |
| UTR3 | 17:28796863-28796886 | 0.006429324 | |
| UTR3 | 17:28796955-28796979 | 0.01402673 | |
| ENST00000327835 | ENSG00000164684 (ZNF704) | hsa-miR-146a-5p | 0.72258 |
| UTR3 | 8:81552311-81552337 | 0.001598726 | |
| UTR3 | 8:81550731-81550757 | 0.002707824 | |
| UTR3 | 8:81549058-81549085 | 0.002154335 | |
| UTR3 | 8:81548321-81548341 | 0.003371963 | |
| UTR3 | 8:81545746-81545770 | 0.006002798 | |
| UTR3 | 8:81542010-81542030 | 0.002140493 | |
| UTR3 | 8:81541699-81541725 | 0.003310561 | |
| UTR3 | 8:81541355-81541370 | 0.005065047 | |
| ENST00000337190 | ENSG00000123933 (MXD4) | hsa-miR-146a-5p | 0.722415 |
| UTR3 | 4:2252207-2252230 | 0.014780699 | |
| UTR3 | 4:2251996-2252013 | 0.008523784 | |
| UTR3 | 4:2251236-2251256 | 0.001775334 | |
| UTR3 | 4:2250742-2250765 | 0.001258486 | |
| ENST00000537989 | ENSG00000112182 (BACH2) | hsa-miR-146a-5p | 0.722211 |
| UTR3 | 6:90641808-90641826 | 0.005504197 | |
| UTR3 | 6:90641618-90641642 | 0.007590394 | |
| UTR3 | 6:90641592-90641616 | 0.004668391 | |
| UTR3 | 6:90639242-90639264 | 0.001268894 | |
| UTR3 | 6:90638042-90638068 | 0.00158229 | |
| UTR3 | 6:90636750-90636777 | 0.0045142 | |
| UTR3 | 6:90660188-90660205 | 0.005733717 | |
| ENST00000488729 | ENSG00000134313 (KIDINS220) | hsa-miR-146a-5p | 0.722204 |
| UTR3 | 2:8953395-8953420 | 0.005051681 | |

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| UTR3 | 2:8931277-8931295 | 0.002071019 | |
| UTR3 | 2:8930137-8930156 | 0.005304765 | |
| UTR3 | 2:8871383-8871400 | 0.01153972 | |
| UTR3 | 2:8871037-8871062 | 0.002353901 | |
| ENST00000381254 | ENSG00000178295 (GEN1) | hsa-miR-146a-5p | 0.722141 |
| UTR3 | 2:17963285-17963311 | 0.005798488 | |
| UTR3 | 2:17964000-17964021 | 0.004782558 | |
| UTR3 | 2:17965596-17965616 | 0.002272135 | |
| UTR3 | 2:17962927-17962953 | 0.02968433 | |
| UTR3 | 2:17963080-17963102 | 0.012267818 | |
| UTR3 | 2:17963085-17963111 | 0.007195161 | |
| ENST00000351217 | ENSG00000156642 (NPTN) | hsa-miR-146a-5p | 0.722017 |
| UTR3 | 15:73853320-73853340 | 0.004761932 | |
| UTR3 | 15:73852471-73852486 | 0.021543923 | |
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| ENST00000450363 | ENSG00000072041 (SLC6A15) | hsa-miR-146a-5p | 0.721984 |
| UTR3 | 12:85277323-85277343 | 0.023612735 | |
| UTR3 | 12:85275932-85275952 | 0.001509941 | |
| UTR3 | 12:85275827-85275848 | 0.00118052 | |
| ENST00000536534 | ENSG00000180287 (PLD5) | hsa-miR-146a-5p | 0.721641 |
| UTR3 | 1:242252564-242252579 | 0.00366527 | |
| UTR3 | 1:242250768-242250789 | 0.018114574 | |
| UTR3 | 1:242249920-242249937 | 0.001503777 | |
| UTR3 | 1:242248735-242248762 | 0.001708895 | |
| UTR3 | 1:242247751-242247774 | 0.001282744 | |
| ENST00000451905 | ENSG00000233539 (AC011294.3) | hsa-miR-146a-5p | 0.721522 |
| UTR3 | 7:46727686-46727700 | 0.014462619 | |
| UTR3 | 7:46727666-46727689 | 0.011803022 | |
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| ENST00000369498 | ENSG00000165775 (FUNDC2) | hsa-miR-146a-5p | 0.721463 |
| UTR3 | X:154286092-154286103 | 0.001252906 | |
| UTR3 | X:154286775-154286800 | 0.00154851 | |
| UTR3 | X:154286892-154286916 | 0.000626569 | |
| UTR3 | X:154288115-154288135 | 0.022832822 | |
| ENST00000338700 | ENSG00000109654 (TRIM2) | hsa-miR-146a-5p | 0.721435 |
| UTR3 | 4:154256161-154256179 | 0.005162217 | |
| UTR3 | 4:154256702-154256728 | 0.002949663 | |
| UTR3 | 4:154260045-154260065 | 0.018146628 | |
| ENST00000396150 | ENSG00000083828 (ZNF586) | hsa-miR-146a-5p | 0.721137 |
| UTR3 | 19:58291564-58291586 | 0.020584107 | |
| UTR3 | 19:58291715-58291730 | 0.005650221 | |
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| ENST00000335056 | ENSG00000104970 (KIR3DX1) | hsa-miR-146a-5p | 0.720991 |
| UTR3 | 19:55055482-55055495 | 0.010838469 | |
| UTR3 | 19:55055855-55055882 | 0.009406111 | |
| UTR3 | 19:55055995-55056008 | 0.002411176 | |

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| UTR3 | 19:55056091-55056115 | 0.00239749 | |
| UTR3 | 19:55044953-55044969 | 0.005606962 | |
| ENST00000392583 | ENSG00000111335 (OAS2) | hsa-miR-146a-5p | 0.720866 |
| UTR3 | 12:113447712-113447731 | 0.004653492 | |
| UTR3 | 12:113447755-113447766 | 0.002390687 | |
| UTR3 | 12:113448216-113448241 | 0.011087402 | |
| UTR3 | 12:113448613-113448639 | 0.008080673 | |
| ENST00000263636 | ENSG00000054219 (LY75) | hsa-miR-146a-5p | 0.720497 |
| UTR3 | 2:160660002-160660028 | 0.015852195 | |
| UTR3 | 2:160673426-160673446 | 0.012881021 | |
| UTR3 | 2:160661677-160661701 | 0.027181369 | |
| ENST00000359202 | ENSG00000132446 (FTHL17) | hsa-miR-146a-5p | 0.720432 |
| UTR3 | X:31089432-31089450 | 0.004831089 | |
| UTR3 | X:31089377-31089387 | 0.021345935 | |
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| ENST00000315571 | ENSG00000179241 (LDLRAD3) | hsa-miR-146a-5p | 0.720249 |
| UTR3 | 11:36251681-36251704 | 0.014549684 | |
| UTR3 | 11:36253421-36253439 | 0.005270181 | |
| UTR3 | 11:36119989-36120009 | 0.026808001 | |
| ENST00000425538 | ENSG00000141052 (MYOCD) | hsa-miR-146a-5p | 0.720246 |
| UTR3 | 17:12667175-12667201 | 0.006378475 | |
| UTR3 | 17:12667259-12667276 | 0.004177591 | |
| UTR3 | 17:12667294-12667317 | 0.003088802 | |
| UTR3 | 17:12668069-12668095 | 0.001185617 | |
| UTR3 | 17:12668982-12668995 | 0.002628447 | |
| UTR3 | 17:12670426-12670442 | 0.001293842 | |
| UTR3 | 17:12671385-12671408 | 0.001926563 | |
| UTR3 | 17:12672060-12672076 | 0.005482622 | |
| ENST00000341861 | ENSG00000074603 (DPP8) | hsa-miR-146a-5p | 0.719517 |
| UTR3 | 15:65738580-65738600 | 0.003944539 | |
| UTR3 | 15:65737613-65737628 | 0.002330516 | |
| UTR3 | 15:65735775-65735801 | 0.008882991 | |
| UTR3 | 15:65735743-65735769 | 0.00189357 | |
| UTR3 | 15:65735679-65735698 | 0.002084898 | |
| UTR3 | 15:65734904-65734921 | 0.006966326 | |
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| ENST00000376387 | ENSG00000125304 (TM9SF2) | hsa-miR-146a-5p | 0.719299 |
| UTR3 | 13:100215232-100215243 | 0.026085263 | |
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| ENST00000529193 | ENSG00000157613 (CREB3L1) | hsa-miR-146a-5p | 0.719048 |
| UTR3 | 11:46342461-46342486 | 0.020980148 | |
| UTR3 | 11:46342504-46342521 | 0.00393429 | |
| UTR3 | 11:46338953-46338973 | 0.005497625 | |
| ENST00000439924 | ENSG00000182149 (IST1) | hsa-miR-146a-5p | 0.718969 |
| UTR3 | 16:71956536-71956562 | 0.006790926 | |
| UTR3 | 16:71961859-71961885 | 0.01079788 | |
| UTR3 | 16:71962168-71962190 | 0.002560685 | |

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| UTR3 | 16:71962343-71962370 | 0.005909015 | |
| ENST00000323037 | ENSG00000180233 (ZNRF2) | hsa-miR-146a-5p | 0.718846 |
| UTR3 | 7:30405972-30405989 | 0.020747647 | |
| UTR3 | 7:30406559-30406572 | 0.005300892 | |
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| ENST00000334082 | ENSG00000152413 (HOMER1) | hsa-miR-146a-5p | 0.718661 |
| UTR3 | 5:78671360-78671377 | 0.006638862 | |
| UTR3 | 5:78671185-78671208 | 0.003777381 | |
| UTR3 | 5:78670634-78670660 | 0.002604742 | |
| UTR3 | 5:78669262-78669288 | 0.002572374 | |
| UTR3 | 5:78669082-78669091 | 0.005480701 | |
| UTR3 | 5:78668889-78668912 | 0.004959565 | |
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| ENST00000396368 | ENSG00000166783 (KIAA0430) | hsa-miR-146a-5p | 0.718614 |
| UTR3 | 16:15689067-15689088 | 0.020750935 | |
| UTR3 | 16:15718747-15718768 | 0.01085051 | |
| UTR3 | 16:15703543-15703558 | 0.011943225 | |
| ENST00000436636 | ENSG00000154310 (TNIK) | hsa-miR-146a-5p | 0.718146 |
| UTR3 | 3:170780592-170780612 | 0.00227554 | |
| UTR3 | 3:170780533-170780543 | 0.001935208 | |
| UTR3 | 3:170779648-170779671 | 0.018696733 | |
| UTR3 | 3:170779604-170779630 | 0.003084497 | |
| ENST00000607544 | ENSG00000226763 (SRRM5) | hsa-miR-146a-5p | 0.718118 |
| UTR3 | 19:44118535-44118554 | 0.025989759 | |
| ENST00000382177 | ENSG00000159459 (UBR1) | hsa-miR-146a-5p | 0.71782 |
| UTR3 | 15:43317119-43317143 | 0.008144251 | |
| UTR3 | 15:43262730-43262756 | 0.002677494 | |
| UTR3 | 15:43244572-43244596 | 0.009041734 | |
| UTR3 | 15:43236909-43236934 | 0.001179033 | |
| UTR3 | 15:43236834-43236860 | 0.002406252 | |
| UTR3 | 15:43235585-43235599 | 0.002516951 | |
| ENST00000483141 | ENSG00000101473 (ACOT8) | hsa-miR-146a-5p | 0.717691 |
| UTR3 | 20:44471689-44471715 | 0.022248996 | |
| UTR3 | 20:44471463-44471484 | 0.003706303 | |
| ENST00000427134 | ENSG00000204308 (RNF5) | hsa-miR-146a-5p | 0.717488 |
| UTR3 | 6:32151186-32151213 | 0.025938944 | |
| ENST00000472232 | ENSG00000107262 (BAG1) | hsa-miR-146a-5p | 0.717318 |
| UTR3 | 9:33255074-33255092 | 0.023121762 | |
| UTR3 | 9:33254419-33254439 | 0.002803437 | |
| ENST00000399231 | ENSG00000197535 (MYO5A) | hsa-miR-146a-5p | 0.717068 |
| UTR3 | 15:52604424-52604439 | 0.007706837 | |
| UTR3 | 15:52603954-52603978 | 0.001359991 | |
| UTR3 | 15:52603418-52603433 | 0.000979016 | |
| UTR3 | 15:52602946-52602969 | 0.001978687 | |
| UTR3 | 15:52601046-52601066 | 0.006379806 | |
| UTR3 | 15:52600982-52601007 | 0.004503038 | |
| UTR3 | 15:52600494-52600518 | 0.002997702 | |

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| ENST00000336216 | ENSG00000140382 (HMG20A) | hsa-miR-146a-5p | 0.717008 |
| UTR3 | 15:77776309-77776324 | 0.002792753 |  |
| UTR3 | 15:77776866-77776884 | 0.001921316 |  |
| UTR3 | 15:77777052-77777067 | 0.00566704 |  |
| UTR3 | 15:77777662-77777681 | 0.015519138 |  |
| ENST00000486995 | ENSG00000049883 (PTCD2) | hsa-miR-146a-5p | 0.716906 |
| UTR3 | 5:71627201;71630845-71627202;71630865 | 0.002703114 |  |
| UTR3 | 5:71638810-71638823 | 0.004133965 |  |
| UTR3 | 5:71648547-71648572 | 0.001513331 |  |
| UTR3 | 5:71654683-71654699 | 0.004715019 |  |
| UTR3 | 5:71654804-71654828 | 0.007122298 |  |
| UTR3 | 5:71654864-71654890 | 0.004833174 |  |
| UTR3 | 5:71616241-71616260 | 0.004174086 |  |
| ENST00000585916 | ENSG00000078043 (PIAS2) | hsa-miR-146a-5p | 0.716362 |
| UTR3 | 18:44391578-44391604 | 0.004852735 |  |
| UTR3 | 18:44391402-44391422 | 0.002690861 |  |
| UTR3 | 18:44391302-44391325 | 0.003125522 |  |
| UTR3 | 18:44390821-44390842 | 0.003965566 |  |
| UTR3 | 18:44390690-44390701 | 0.001444115 |  |
| UTR3 | 18:44470561-44470588 | 0.020678038 |  |
| UTR3 | 18:44401028;44407922-44401035;44407935 | 0.017389033 |  |
| ENST00000304032 | ENSG00000157985 (AGAP1) | hsa-miR-146a-5p | 0.716136 |
| UTR3 | 2:237036104-237036126 | 0.002784975 |  |
| UTR3 | 2:237036171-237036197 | 0.000876893 |  |
| UTR3 | 2:237036828-237036852 | 0.001173276 |  |
| UTR3 | 2:237039426-237039442 | 0.002920315 |  |
| UTR3 | 2:237039928-237039950 | 0.018074637 |  |
| ENST00000333012 | ENSG00000123427 (METTL21B) | hsa-miR-146a-5p | 0.716069 |
| UTR3 | 12:58174434-58174452 | 0.00402399 |  |
| UTR3 | 12:58174656-58174683 | 0.009181485 |  |
| UTR3 | 12:58175824-58175836 | 0.005253402 |  |
| UTR3 | 12:58176022-58176042 | 0.003554498 |  |
| UTR3 | 12:58176022-58176050 | 0.003811267 |  |
| ENST00000503329 | ENSG00000172901 (AQPEP) | hsa-miR-146a-5p | 0.715943 |
| UTR3 | 5:115341551-115341573 | 0.020732803 |  |
| UTR3 | 5:115361939-115361960 | 0.001944679 |  |
| UTR3 | 5:115362826-115362853 | 0.003137082 |  |
| ENST00000592623 | ENSG00000115268 (RPS15) | hsa-miR-146a-5p | 0.715613 |
| UTR3 | 19:1440368-1440382 | 0.025788045 |  |
| ENST00000312377 | ENSG00000161800 (RACGAP1) | hsa-miR-146a-5p | 0.715538 |
| UTR3 | 12:50383546-50383560 | 0.025782028 |  |
| ENST00000252252 | ENSG00000185479 (KRT6B) | hsa-miR-146a-5p | 0.715523 |

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| UTR3 | 12:52840830-52840848 | 0.004614934 | |
| UTR3 | 12:52840584-52840598 | 0.021165887 | |
| ENST00000561038 | ENSG00000100938 (GMPR2) | hsa-miR-146a-5p | 0.715041 |
| UTR3 | 14:24703432;24704943-24703447;24704947 | 0.018359543 | |
| UTR3 | 14:24707666-24707692 | 0.007382606 | |
| ENST00000562435 | ENSG00000171208 (NETO2) | hsa-miR-146a-5p | 0.714807 |
| UTR3 | 16:47116434-47116456 | 0.003135125 | |
| UTR3 | 16:47115557-47115581 | 0.002761684 | |
| UTR3 | 16:47115491-47115509 | 0.001229274 | |
| UTR3 | 16:47113775-47113803 | 0.00271124 | |
| UTR3 | 16:47111638-47111661 | 0.01588606 | |
| ENST00000414099 | ENSG00000183873 (SCN5A) | hsa-miR-146a-5p | 0.714582 |
| UTR3 | 3:38591357-38591385 | 0.010033587 | |
| UTR3 | 3:38590608-38590627 | 0.004340165 | |
| UTR3 | 3:38590048-38590075 | 0.011331559 | |
| ENST00000399138 | ENSG00000091542 (ALKBH5) | hsa-miR-146a-5p | 0.714412 |
| UTR3 | 17:18111886-18111905 | 0.019185963 | |
| UTR3 | 17:18112176-18112199 | 0.003441018 | |
| UTR3 | 17:18113109-18113126 | 0.00306473 | |
| ENST00000417640 | ENSG00000123119 (NECAB1) | hsa-miR-146a-5p | 0.714071 |
| UTR3 | 8:91967924-91967946 | 0.005064738 | |
| UTR3 | 8:91969015-91969033 | 0.003099428 | |
| UTR3 | 8:91969066-91969089 | 0.007496204 | |
| UTR3 | 8:91971091-91971102 | 0.007945032 | |
| UTR3 | 8:91836986-91837001 | 0.009519732 | |
| ENST00000369443 | ENSG00000196505 (GDAP2) | hsa-miR-146a-5p | 0.713835 |
| UTR3 | 1:118410920-118410934 | 0.001750168 | |
| UTR3 | 1:118410232-118410251 | 0.001116296 | |
| UTR3 | 1:118409233-118409250 | 0.001067352 | |
| UTR3 | 1:118408982-118409003 | 0.001475156 | |
| UTR3 | 1:118408893-118408921 | 0.00062145 | |
| UTR3 | 1:118407395-118407415 | 0.001835208 | |
| UTR3 | 1:118406934-118406957 | 0.003906327 | |
| UTR3 | 1:118406757-118406778 | 0.004943286 | |
| UTR3 | 1:118406267-118406280 | 0.008930254 | |
| ENST00000334241 | ENSG00000186300 (ZNF555) | hsa-miR-146a-5p | 0.713464 |
| UTR3 | 19:2854824-2854846 | 0.002183291 | |
| UTR3 | 19:2856751-2856771 | 0.0029283 | |
| UTR3 | 19:2856784-2856811 | 0.005779217 | |
| UTR3 | 19:2857035-2857054 | 0.001350279 | |
| UTR3 | 19:2858549-2858567 | 0.009083549 | |
| UTR3 | 19:2859642-2859662 | 0.004291216 | |
| ENST00000317605 | ENSG00000181541 (MAB21L2) | hsa-miR-146a-5p | 0.713391 |

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| UTR3 | 4:151505726-151505745 | 0.025609967 | |
| ENST00000397762 | ENSG00000129472 (RAB2B) | hsa-miR-146a-5p | 0.713046 |
| UTR3 | 14:21928652-21928671 | 0.005444332 | |
| UTR3 | 14:21927494-21927516 | 0.016026036 | |
| UTR3 | 14:21927271-21927289 | 0.004112104 | |
| ENST00000368936 | ENSG00000143363 (PRUNE) | hsa-miR-146a-5p | 0.712834 |
| UTR3 | 1:151006808-151006832 | 0.02556549 | |
| ENST00000479198 | ENSG00000163630 (SYNPR) | hsa-miR-146a-5p | 0.712473 |
| UTR3 | 3:63602188-63602214 | 0.005318345 | |
| UTR3 | 3:63602292-63602308 | 0.020218365 | |
| ENST00000532428 | ENSG00000149089 (APIP) | hsa-miR-146a-5p | 0.712459 |
| UTR3 | 11:34877794-34877815 | 0.009787496 | |
| UTR3 | 11:34876948-34876968 | 0.002163944 | |
| UTR3 | 11:34874829-34874857 | 0.013584102 | |
| ENST00000462898 | ENSG00000051382 (PIK3CB) | hsa-miR-146a-5p | 0.71242 |
| UTR3 | 3:138452279;138453476-138452280;138453500 | 0.005770467 | |
| UTR3 | 3:138409968;138413628-138409985;138413637 | 0.001935952 | |
| UTR3 | 3:138474665-138474685 | 0.059121434 | |
| ENST00000428443 | ENSG00000187231 (SESTD1) | hsa-miR-146a-5p | 0.71224 |
| UTR3 | 2:179973763-179973781 | 0.003698019 | |
| UTR3 | 2:179972630-179972652 | 0.00150294 | |
| UTR3 | 2:179971399-179971413 | 0.0020344 | |
| UTR3 | 2:179971078-179971086 | 0.001146653 | |
| UTR3 | 2:179969095-179969114 | 0.001346571 | |
| UTR3 | 2:179968898-179968923 | 0.001516781 | |
| UTR3 | 2:179968839-179968864 | 0.000798582 | |
| UTR3 | 2:179966867-179966892 | 0.013474133 | |
| ENST00000602786 | ENSG00000120694 (HSPH1) | hsa-miR-146a-5p | 0.712226 |
| UTR3 | 13:31722177-31722205 | 0.025516982 | |
| ENST00000512701 | ENSG00000155158 (TTC39B) | hsa-miR-146a-5p | 0.711609 |
| UTR3 | 9:15167380-15167406 | 0.001481228 | |
| UTR3 | 9:15165746-15165760 | 0.001427863 | |
| UTR3 | 9:15165726-15165749 | 0.002416139 | |
| UTR3 | 9:15165591-15165606 | 0.000686969 | |
| UTR3 | 9:15164880-15164904 | 0.00246548 | |
| UTR3 | 9:15164804-15164832 | 0.002131546 | |
| UTR3 | 9:15164547-15164565 | 0.002802147 | |
| UTR3 | 9:15164236-15164252 | 0.00442806 | |
| UTR3 | 9:15163967-15163982 | 0.002881567 | |
| UTR3 | 9:15163703-15163728 | 0.004746804 | |
| ENST00000369663 | ENSG00000112837 (TBX18) | hsa-miR-146a-5p | 0.711572 |
| UTR3 | 6:85446114-85446134 | 0.021991993 | |
| UTR3 | 6:85442757-85442770 | 0.003472913 | |
| ENST00000608469 | ENSG00000134365 (CFHR4) | hsa-miR-146a-5p | 0.711106 |
| UTR3 | 1:196887675-196887691 | 0.025427749 | |

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| ENST00000296257 | ENSG00000163904 (SENP2) | hsa-miR-146a-5p | 0.710996 |
| UTR3 | 3:185347716-185347737 | 0.009809193 | |
| UTR3 | 3:185349674-185349689 | 0.005097237 | |
| UTR3 | 3:185350722-185350746 | 0.00335592 | |
| UTR3 | 3:185327121;185329439-185327138;185329444 | 0.0292191 | |
| ENST00000286428 | ENSG00000155959 (VBP1) | hsa-miR-146a-5p | 0.710455 |
| UTR3 | X:154467826-154467833 | 0.025375987 | |
| ENST00000308488 | ENSG00000048649 (RSF1) | hsa-miR-146a-5p | 0.710327 |
| UTR3 | 11:77375360-77375387 | 0.00115089 | |
| UTR3 | 11:77373796-77373817 | 0.001433872 | |
| UTR3 | 11:77372362-77372383 | 0.002382776 | |
| UTR3 | 11:77371937-77371952 | 0.003826515 | |
| UTR3 | 11:77371615-77371632 | 0.016571774 | |
| ENST00000369686 | ENSG00000134245 (WNT2B) | hsa-miR-146a-5p | 0.710281 |
| UTR3 | 1:113064590-113064614 | 0.001858088 | |
| UTR3 | 1:113065673-113065696 | 0.002534488 | |
| UTR3 | 1:113065785-113065806 | 0.003508181 | |
| UTR3 | 1:113066795-113066819 | 0.00215 | |
| UTR3 | 1:113067104-113067123 | 0.001973615 | |
| UTR3 | 1:113067949-113067972 | 0.001017641 | |
| UTR3 | 1:113069976-113070003 | 0.001404489 | |
| UTR3 | 1:113071925-113071938 | 0.006273391 | |
| UTR3 | 1:113072181-113072202 | 0.004642305 | |
| ENST00000451899 | ENSG00000164823 (OSGIN2) | hsa-miR-146a-5p | 0.710149 |
| UTR3 | 8:90938933-90938950 | 0.007978669 | |
| UTR3 | 8:90936971-90936985 | 0.019805437 | |
| UTR3 | 8:90937474-90937489 | 0.038093755 | |
| ENST00000475381 | ENSG00000144959 (NCEH1) | hsa-miR-146a-5p | 0.710146 |
| UTR3 | 3:172348390-172348411 | 0.003954758 | |
| UTR3 | 3:172348081-172348100 | 0.021396739 | |
| ENST00000296487 | ENSG00000164088 (PPM1M) | hsa-miR-146a-5p | 0.710134 |
| UTR3 | 3:52283605-52283622 | 0.011529361 | |
| UTR3 | 3:52283673-52283692 | 0.013821139 | |
| ENST00000341287 | ENSG00000188674 (C2orf80) | hsa-miR-146a-5p | 0.709741 |
| UTR3 | 2:209030119-209030136 | 0.025319346 | |
| ENST00000249883 | ENSG00000114019 (AMOTL2) | hsa-miR-146a-5p | 0.709734 |
| UTR3 | 3:134076092-134076106 | 0.004525076 | |
| UTR3 | 3:134075960-134075986 | 0.002573719 | |
| UTR3 | 3:134075177-134075191 | 0.01821999 | |
| ENST00000423484 | ENSG00000234444 (ZNF736) | hsa-miR-146a-5p | 0.709731 |
| UTR3 | 7:63810125-63810147 | 0.002558939 | |
| UTR3 | 7:63810429-63810454 | 0.0022883 | |

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| UTR3 | 7:63810483-63810504 | 0.009482078 | |
| UTR3 | 7:63811256-63811273 | 0.001420319 | |
| UTR3 | 7:63811539-63811559 | 0.001192906 | |
| UTR3 | 7:63808782-63808799 | 0.012779621 | |
| UTR3 | 7:63809117-63809135 | 0.008810815 | |
| UTR3 | 7:63809455-63809471 | 0.011646785 | |
| ENST00000517608 | ENSG00000104343 (UBE2W) | hsa-miR-146a-5p | 0.709514 |
| UTR3 | 8:74705004-74705027 | 0.005495796 | |
| UTR3 | 8:74704469-74704493 | 0.002810388 | |
| UTR3 | 8:74704262-74704279 | 0.001907198 | |
| UTR3 | 8:74703409-74703427 | 0.001873212 | |
| UTR3 | 8:74702447-74702466 | 0.001300952 | |
| UTR3 | 8:74701754-74701778 | 0.001567831 | |
| UTR3 | 8:74700977-74701004 | 0.001728822 | |
| UTR3 | 8:74700944-74700971 | 0.000609613 | |
| UTR3 | 8:74699261-74699285 | 0.004001668 | |
| UTR3 | 8:74698591-74698605 | 0.004005871 | |
| ENST00000356860 | ENSG00000153956 (CACNA2D1) | hsa-miR-146a-5p | 0.708986 |
| UTR3 | 7:81578481-81578498 | 0.017401946 | |
| UTR3 | 7:81577606-81577625 | 0.002181764 | |
| UTR3 | 7:81575913-81575929 | 0.005675782 | |
| ENST00000176763 | ENSG00000072786 (STK10) | hsa-miR-146a-5p | 0.708664 |
| UTR3 | 5:171471344-171471366 | 0.002517595 | |
| UTR3 | 5:171469919-171469935 | 0.002769577 | |
| UTR3 | 5:171469803-171469827 | 0.009676107 | |
| UTR3 | 5:171469136-171469155 | 0.00839473 | |
| UTR3 | 5:171481694;171482592-171481698;171482614 | 0.008620403 | |
| ENST00000469154 | ENSG00000082014 (SMARCD3) | hsa-miR-146a-5p | 0.708582 |
| UTR3 | 7:150939293-150939318 | 0.019477971 | |
| UTR3 | 7:150938530-150938554 | 0.003162988 | |
| UTR3 | 7:150937970-150937998 | 0.002586525 | |
| ENST00000473989 | ENSG00000157741 (UBN2) | hsa-miR-146a-5p | 0.708547 |
| UTR3 | 7:138983882-138983908 | 0.002116829 | |
| UTR3 | 7:138984635-138984654 | 0.001883594 | |
| UTR3 | 7:138984934-138984960 | 0.001813076 | |
| UTR3 | 7:138986561-138986575 | 0.007141499 | |
| UTR3 | 7:138988747-138988766 | 0.002071541 | |
| UTR3 | 7:138990070-138990081 | 0.001792762 | |
| UTR3 | 7:138990226-138990246 | 0.001968507 | |
| UTR3 | 7:138990610-138990630 | 0.002102894 | |
| UTR3 | 7:138991151-138991174 | 0.001560305 | |
| UTR3 | 7:138968607-138968632 | 0.012467289 | |
| ENST00000283131 | ENSG00000153147 (SMARCA5) | hsa-miR-146a-5p | 0.70831 |

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| UTR3 | 4:144475433-144475460 | 0.023631278 | |
| UTR3 | 4:144475539-144475562 | 0.001574659 | |
| ENST00000334464 | ENSG00000165650 (PDZD8) | hsa-miR-146a-5p | 0.708023 |
| UTR3 | 10:119041846-119041858 | 0.014480358 | |
| UTR3 | 10:119041566-119041588 | 0.00657857 | |
| UTR3 | 10:119043413-119043440 | 0.017936468 | |
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| ENST00000442697 | ENSG00000164031 (DNAJB14) | hsa-miR-146a-5p | 0.707968 |
| UTR3 | 4:100819567-100819584 | 0.001181713 | |
| UTR3 | 4:100817413-100817424 | 0.019725039 | |
| UTR3 | 4:100851608-100851629 | 0.018513732 | |
| ENST00000327946 | ENSG00000182771 (GRID1) | hsa-miR-146a-5p | 0.707789 |
| UTR3 | 10:87361298-87361312 | 0.007235146 | |
| UTR3 | 10:87359492-87359507 | 0.017929661 | |
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| ENST00000314400 | ENSG00000163608 (C3orf17) | hsa-miR-146a-5p | 0.70741 |
| UTR3 | 3:112723769-112723796 | 0.009343446 | |
| UTR3 | 3:112723256-112723281 | 0.002021838 | |
| UTR3 | 3:112723233-112723245 | 0.00346225 | |
| UTR3 | 3:112721725-112721740 | 0.002143604 | |
| UTR3 | 3:112727249-112727275 | 0.021460736 | |
| UTR3 | 3:112724669-112724686 | 0.010953925 | |
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| ENST00000366429 | ENSG00000173421 (CCDC36) | hsa-miR-146a-5p | 0.707403 |
| UTR3 | 3:49283036-49283043 | 0.025134251 | |
| ENST00000382968 | ENSG00000178222 (RNF212) | hsa-miR-146a-5p | 0.707339 |
| UTR3 | 4:1066426-1066448 | 0.0176062 | |
| UTR3 | 4:1065949-1065975 | 0.004561857 | |
| UTR3 | 4:1065895-1065920 | 0.002961165 | |
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| ENST00000427594 | ENSG00000176771 (NCKAP5) | hsa-miR-146a-5p | 0.707303 |
| UTR3 | 2:133879677-133879692 | 0.00633239 | |
| UTR3 | 2:133879657-133879675 | 0.01401701 | |
| UTR3 | 2:133887553-133887572 | 0.020436963 | |
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| ENST00000328945 | ENSG00000184860 (SDR42E1) | hsa-miR-146a-5p | 0.707181 |
| UTR3 | 16:82032668-82032694 | 0.016082651 | |
| UTR3 | 16:82031993-82032020 | 0.003112384 | |
| UTR3 | 16:82032751-82032771 | 0.024680741 | |
| ENST00000380750 | ENSG00000205572 (SERF1B) | hsa-miR-146a-5p | 0.707083 |
| UTR3 | 5:69337839-69337859 | 0.014277308 | |
| UTR3 | 5:69338532-69338550 | 0.006172483 | |
| UTR3 | 5:69338645-69338671 | 0.004659243 | |
| ENST00000394123 | ENSG00000145907 (G3BP1) | hsa-miR-146a-5p | 0.706981 |
| UTR3 | 5:151184161-151184187 | 0.003261946 | |
| UTR3 | 5:151184819-151184838 | 0.005113378 | |
| UTR3 | 5:151186415-151186437 | 0.004335171 | |

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| UTR3 | 5:151186627-151186639 | 0.00477848 | |
| UTR3 | 5:151187109-151187136 | 0.002131474 | |
| UTR3 | 5:151188789-151188814 | 0.00172792 | |
| UTR3 | 5:151189387-151189401 | 0.001274087 | |
| UTR3 | 5:151190798-151190814 | 0.001455574 | |
| UTR3 | 5:151190912-151190927 | 0.001022971 | |
| ENST00000464950 | ENSG00000058799 (YIPF1) | hsa-miR-146a-5p | 0.706525 |
| UTR3 | 1:54317939;54320674-54317943;54320687 | 0.025064992 | |
| ENST00000475390 | ENSG00000121871 (SLITRK3) | hsa-miR-146a-5p | 0.706307 |
| UTR3 | 3:164905123-164905137 | 0.025047824 | |
| ENST00000219905 | ENSG00000174197 (MGA) | hsa-miR-146a-5p | 0.706246 |
| UTR3 | 15:42060141-42060164 | 0.010581522 | |
| UTR3 | 15:42060607-42060621 | 0.004584916 | |
| UTR3 | 15:42061649-42061672 | 0.00987661 | |
| ENST00000409444 | ENSG00000155755 (TMEM237) | hsa-miR-146a-5p | 0.705909 |
| UTR3 | 2:202488712-202488723 | 0.005285775 | |
| UTR3 | 2:202488368-202488396 | 0.0042626 | |
| UTR3 | 2:202488343-202488363 | 0.005739256 | |
| UTR3 | 2:202488142-202488155 | 0.002166953 | |
| UTR3 | 2:202487688-202487703 | 0.007561873 | |
| ENST00000396573 | ENSG00000183454 (GRIN2A) | hsa-miR-146a-5p | 0.705884 |
| UTR3 | 16:9856625-9856646 | 0.004416685 | |
| UTR3 | 16:9855462-9855482 | 0.001381727 | |
| UTR3 | 16:9852639-9852664 | 0.015417175 | |
| UTR3 | 16:10032108-10032129 | 0.008409629 | |
| UTR3 | 16:10031891-10031910 | 0.008172272 | |
| ENST00000503039 | ENSG00000113761 (ZNF346) | hsa-miR-146a-5p | 0.705555 |
| UTR3 | 5:176508148-176508175 | 0.024988648 | |
| ENST00000313234 | ENSG00000167767 (KRT80) | hsa-miR-146a-5p | 0.705507 |
| UTR3 | 12:52564182-52564199 | 0.001235714 | |
| UTR3 | 12:52564079-52564107 | 0.001150523 | |
| UTR3 | 12:52563151-52563176 | 0.009162707 | |
| UTR3 | 12:52562985-52563008 | 0.013435889 | |
| ENST00000220597 | ENSG00000076641 (PAG1) | hsa-miR-146a-5p | 0.70537 |
| UTR3 | 8:81888635-81888653 | 0.003713386 | |
| UTR3 | 8:81887676-81887690 | 0.002204876 | |
| UTR3 | 8:81885245-81885263 | 0.002006279 | |
| UTR3 | 8:81881129-81881151 | 0.011722228 | |
| UTR3 | 8:81880692-81880713 | 0.005327333 | |
| ENST00000237201 | ENSG00000118434 (SPACA1) | hsa-miR-146a-5p | 0.705148 |
| UTR3 | 6:88776237-88776254 | 0.02495663 | |
| ENST00000370550 | ENSG00000153936 (HS2ST1) | hsa-miR-146a-5p | 0.705113 |

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| UTR3 | 1:87570418-87570442 | 0.008976504 | |
| UTR3 | 1:87571013-87571032 | 0.004547892 | |
| UTR3 | 1:87571431-87571454 | 0.0031361 | |
| UTR3 | 1:87573698-87573722 | 0.002181782 | |
| UTR3 | 1:87575597-87575615 | 0.006111626 | |
| ENST00000225512 | ENSG00000108379 (WNT3) | hsa-miR-146a-5p | 0.705031 |
| UTR3 | 17:44841739-44841759 | 0.015535959 | |
| UTR3 | 17:44841468-44841494 | 0.003709932 | |
| UTR3 | 17:44841324-44841341 | 0.002242488 | |
| UTR3 | 17:44840699-44840715 | 0.003459043 | |
| ENST00000360311 | ENSG00000197385 (ZNF860) | hsa-miR-146a-5p | 0.704803 |
| UTR3 | 3:32032938-32032957 | 0.004455493 | |
| UTR3 | 3:32032974-32033000 | 0.01367657 | |
| UTR3 | 3:32030774-32030796 | 0.027673547 | |
| ENST00000541428 | ENSG00000198363 (ASPH) | hsa-miR-146a-5p | 0.704397 |
| UTR3 | 8:62415246-62415269 | 0.002123036 | |
| UTR3 | 8:62414082-62414102 | 0.018977921 | |
| UTR3 | 8:62413553-62413570 | 0.003796677 | |
| ENST00000327470 | ENSG00000183161 (FANCF) | hsa-miR-146a-5p | 0.704277 |
| UTR3 | 11:22646166-22646191 | 0.021722662 | |
| UTR3 | 11:22644792-22644807 | 0.003165589 | |
| ENST00000278302 | ENSG00000121236 (TRIM6) | hsa-miR-146a-5p | 0.704159 |
| UTR3 | 11:5632641-5632665 | 0.01501939 | |
| UTR3 | 11:5633366-5633391 | 0.009859529 | |
| ENST00000296318 | ENSG00000144730 (IL17RD) | hsa-miR-146a-5p | 0.703997 |
| UTR3 | 3:57130277-57130299 | 0.002988282 | |
| UTR3 | 3:57129931-57129959 | 0.016469471 | |
| UTR3 | 3:57129196-57129205 | 0.00155689 | |
| UTR3 | 3:57129162-57129174 | 0.000714052 | |
| UTR3 | 3:57128893-57128913 | 0.001405329 | |
| UTR3 | 3:57127794-57127819 | 0.001732231 | |
| ENST00000334513 | ENSG00000186364 (NUDT17) | hsa-miR-146a-5p | 0.703965 |
| UTR3 | 1:145586129-145586147 | 0.023714463 | |
| UTR3 | 1:145588403-145588418 | 0.005327905 | |
| ENST00000395811 | ENSG00000133030 (MPRIP) | hsa-miR-146a-5p | 0.703889 |
| UTR3 | 17:17089714-17089740 | 0.000947979 | |
| UTR3 | 17:17090273-17090296 | 0.000970185 | |
| UTR3 | 17:17093180-17093203 | 0.002700438 | |
| UTR3 | 17:17093563-17093580 | 0.004022018 | |
| UTR3 | 17:17095319-17095339 | 0.003270642 | |
| UTR3 | 17:17095458-17095481 | 0.011168748 | |
| UTR3 | 17:17030079-17030101 | 0.008113679 | |
| ENST00000409719 | ENSG00000125611 (CHCHD5) | hsa-miR-146a-5p | 0.703074 |
| UTR3 | 2:113344305-113344328 | 0.005714927 | |
| UTR3 | 2:113344369-113344388 | 0.003334216 | |

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| UTR3 | 2:113344839-113344851 | 0.011646731 | |
| UTR3 | 2:113345359-113345383 | 0.004098057 | |
| ENST00000320238 | ENSG00000177551 (NHLH2) | hsa-miR-146a-5p | 0.702961 |
| UTR3 | 1:116380433-116380460 | 0.003754205 | |
| UTR3 | 1:116380251-116380275 | 0.012474385 | |
| UTR3 | 1:116379225-116379248 | 0.008556497 | |
| ENST00000480174 | ENSG00000137941 (TTLL7) | hsa-miR-146a-5p | 0.702712 |
| UTR3 | 1:84372074-84372090 | 0.021906702 | |
| UTR3 | 1:84335198-84335213 | 0.002858876 | |
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| ENST00000311381 | ENSG00000130349 (C6orf203) | hsa-miR-146a-5p | 0.702457 |
| UTR3 | 6:107372505-107372531 | 0.024745631 | |
| ENST00000261292 | ENSG00000101670 (LIPG) | hsa-miR-146a-5p | 0.702387 |
| UTR3 | 18:47116976-47116998 | 0.002354678 | |
| UTR3 | 18:47117368-47117390 | 0.006395358 | |
| UTR3 | 18:47118588-47118609 | 0.012137497 | |
| UTR3 | 18:47119051-47119077 | 0.003852674 | |
| ENST00000357637 | ENSG00000197563 (PIGN) | hsa-miR-146a-5p | 0.702311 |
| UTR3 | 18:59712514-59712536 | 0.002878617 | |
| UTR3 | 18:59712504-59712526 | 0.001434815 | |
| UTR3 | 18:59774108;59774219-59774114;59774239 | 0.029385373 | |
| UTR3 | 18:59763151-59763169 | 0.008120807 | |
| UTR3 | 18:59763143-59763169 | 0.006636351 | |
| UTR3 | 18:59756056;59757709-59756075;59757710 | 0.019731675 | |
| | | | |
| ENST00000367342 | ENSG00000163362 (C1orf106) | hsa-miR-146a-5p | 0.702223 |
| UTR3 | 1:200883084-200883102 | 0.004597919 | |
| UTR3 | 1:200884156-200884178 | 0.009785827 | |
| UTR3 | 1:200884363-200884385 | 0.010343611 | |
| ENST00000533482 | ENSG00000113522 (RAD50) | hsa-miR-146a-5p | 0.702121 |
| UTR3 | 5:131915054-131915073 | 0.014726256 | |
| UTR3 | 5:131923722-131923748 | 0.003606611 | |
| UTR3 | 5:131978115-131978127 | 0.00638655 | |
| ENST00000423058 | ENSG00000144285 (SCN1A) | hsa-miR-146a-5p | 0.701963 |
| UTR3 | 2:166847536-166847562 | 0.021975956 | |
| UTR3 | 2:166909393-166909420 | 0.012136633 | |
| ENST00000367895 | ENSG00000112319 (EYA4) | hsa-miR-146a-5p | 0.701685 |
| UTR3 | 6:133850301-133850323 | 0.005353135 | |
| UTR3 | 6:133851189-133851211 | 0.00290307 | |
| UTR3 | 6:133851334-133851344 | 0.00173238 | |
| UTR3 | 6:133851344-133851371 | 0.00090888 | |
| UTR3 | 6:133851496-133851523 | 0.001952821 | |
| UTR3 | 6:133853215-133853224 | 0.011835037 | |
| ENST00000233336 | ENSG00000114999 (TTL) | hsa-miR-146a-5p | 0.701679 |
| UTR3 | 2:113287117-113287141 | 0.002889275 | |

| | | | |
|---|---|---|---|
| UTR3 | 2:113289054-113289076 | 0.011267141 | |
| UTR3 | 2:113290994-113291007 | 0.004181814 | |
| UTR3 | 2:113295494-113295503 | 0.002063608 | |
| UTR3 | 2:113295587-113295601 | 0.001113602 | |
| UTR3 | 2:113296029-113296055 | 0.001494869 | |
| UTR3 | 2:113298365-113298389 | 0.00167457 | |
| ENST00000434618 | ENSG00000231925 (TAPBP) | hsa-miR-146a-5p | 0.701588 |
| UTR3 | 6:33268996-33269017 | 0.02316588 | |
| UTR3 | 6:33281009-33281032 | 0.006914784 | |
| ENST00000318789 | ENSG00000114861 (FOXP1) | hsa-miR-146a-5p | 0.701546 |
| UTR3 | 3:71008311-71008328 | 0.007921231 | |
| UTR3 | 3:71006634-71006654 | 0.002684158 | |
| UTR3 | 3:71005494-71005517 | 0.00208375 | |
| UTR3 | 3:71005034-71005050 | 0.007664543 | |
| UTR3 | 3:71004672-71004694 | 0.004320792 | |
| | | | |
| ENST00000601302 | ENSG00000268223 (ARL14EPL) | hsa-miR-146a-5p | 0.701427 |
| UTR3 | 5:115395495-115395516 | 0.024665163 | |
| ENST00000370521 | ENSG00000065243 (PKN2) | hsa-miR-146a-5p | 0.700675 |
| UTR3 | 1:89301045-89301064 | 0.020493695 | |
| UTR3 | 1:89301886-89301906 | 0.004112851 | |
| ENST00000206595 | ENSG00000092140 (G2E3) | hsa-miR-146a-5p | 0.700609 |
| UTR3 | 14:31085932-31085956 | 0.004835105 | |
| UTR3 | 14:31087192-31087215 | 0.001772556 | |
| UTR3 | 14:31085700-31085724 | 0.058534159 | |
| | | | |
| ENST00000349496 | ENSG00000168036 (CTNNB1) | hsa-miR-146a-5p | 0.70055 |
| UTR3 | 3:41280996-41281013 | 0.024596796 | |
| ENST00000380079 | ENSG00000127954 (STEAP4) | hsa-miR-146a-5p | 0.700486 |
| UTR3 | 7:87907586-87907602 | 0.003676025 | |
| UTR3 | 7:87907556-87907573 | 0.003279148 | |
| UTR3 | 7:87906073-87906085 | 0.011629472 | |
| UTR3 | 7:87913296-87913320 | 0.024700116 | |
| ENST00000426077 | ENSG00000226479 (TMEM185B) | hsa-miR-146a-5p | 0.700466 |
| UTR3 | 2:120979090-120979109 | 0.01334669 | |
| UTR3 | 2:120978896-120978915 | 0.011243547 | |
| ENST00000420627 | ENSG00000196924 (FLNA) | hsa-miR-146a-5p | 0.70028 |
| UTR3 | X:153590437-153590461 | 0.011915998 | |
| UTR3 | X:153590096-153590119 | 0.001218754 | |
| UTR3 | X:153576936-153576949 | 0.011441047 | |
| ENST00000216877 | ENSG00000132670 (PTPRA) | hsa-miR-146a-5p | 0.700188 |
| UTR3 | 20:3019131-3019138 | 0.022310316 | |
| UTR3 | 20:3019379-3019404 | 0.002258305 | |
| ENST00000546931 | ENSG00000170627 (GTSF1) | hsa-miR-146a-5p | 0.70018 |
| UTR3 | 12:54849888-54849902 | 0.024567978 | |

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|---|---|---|---|
| ENST00000504771 | ENSG00000145779 (TNFAIP8) | hsa-miR-146a-5p | 0.700114 |
| UTR3 | 5:118729700-118729721 | 0.009593539 |  |
| UTR3 | 5:118729731-118729753 | 0.001890359 |  |
| UTR3 | 5:118731034-118731057 | 0.001316546 |  |
| UTR3 | 5:118731973-118731989 | 0.001679385 |  |
| UTR3 | 5:118734761-118734784 | 0.010083051 |  |

**Supplementary table 4: targets for miRNAs hsa-miR-146a-5p**