

| ONTOLOGY | ID | Description | GeneRatio | BgRatio | pvalue | p.adjust | qvalue | geneID | Count |
|----------|-----------|---------------|-----------|-----------|----------|----------|----------|------------|-------|
| BP | GO:001657 | histone mc | 47/782 | 420/17913 | 3.26E-09 | 7.23E-06 | 5.93E-06 | CAMK2D/F | 47 |
| BP | GO:001050 | regulation | 39/782 | 314/17913 | 4.03E-09 | 7.23E-06 | 5.93E-06 | KIAA1324/ | 39 |
| BP | GO:000705 | cell cycle a | 32/782 | 231/17913 | 7.25E-09 | 7.23E-06 | 5.93E-06 | CNOT6/SO | 32 |
| BP | GO:003133 | negative re | 33/782 | 244/17913 | 7.76E-09 | 7.23E-06 | 5.93E-06 | USP25/USF | 33 |
| BP | GO:001820 | peptidyl-ly | 43/782 | 376/17913 | 8.06E-09 | 7.23E-06 | 5.93E-06 | SOX4/PHF2 | 43 |
| BP | GO:001656 | covalent ct | 47/782 | 433/17913 | 8.66E-09 | 7.23E-06 | 5.93E-06 | CAMK2D/F | 47 |
| BP | GO:003424 | regulation | 48/782 | 452/17913 | 1.21E-08 | 7.73E-06 | 6.35E-06 | CNOT6/SO | 48 |
| BP | GO:000985 | negative re | 36/782 | 288/17913 | 1.35E-08 | 7.73E-06 | 6.35E-06 | CRTC3/USF | 36 |
| BP | GO:000691 | autophagy | 49/782 | 471/17913 | 1.65E-08 | 7.73E-06 | 6.35E-06 | KIAA1324/ | 49 |
| BP | GO:006191 | process uti | 49/782 | 471/17913 | 1.65E-08 | 7.73E-06 | 6.35E-06 | KIAA1324/ | 49 |
| BP | GO:190195 | regulation | 46/782 | 428/17913 | 1.7E-08 | 7.73E-06 | 6.35E-06 | CNOT6/CTI | 46 |
| BP | GO:000008 | G1/S transi | 34/782 | 269/17913 | 2.59E-08 | 1.07E-05 | 8.77E-06 | CNOT6/CTI | 34 |
| BP | GO:000641 | regulation | 43/782 | 397/17913 | 4E-08 | 1.43E-05 | 1.17E-05 | CNOT6/SO | 43 |
| BP | GO:007233 | signal tran: | 33/782 | 264/17913 | 5.44E-08 | 1.7E-05 | 1.4E-05 | CNOT6/SO | 33 |
| BP | GO:007243 | signal tran: | 14/782 | 57/17913 | 1.09E-07 | 2.87E-05 | 2.36E-05 | CNOT6/SO | 14 |
| BP | GO:190240 | intracellular | 14/782 | 57/17913 | 1.09E-07 | 2.87E-05 | 2.36E-05 | CNOT6/SO | 14 |
| BP | GO:190015 | positive re | 8/782 | 16/17913 | 1.2E-07 | 3E-05 | 2.47E-05 | ZFP36/TNFR | 8 |
| BP | GO:000985 | positive re | 41/782 | 392/17913 | 2.15E-07 | 3.99E-05 | 3.28E-05 | KIAA1324/ | 41 |
| BP | GO:000930 | rRNA trans | 10/782 | 30/17913 | 3.22E-07 | 5.05E-05 | 4.14E-05 | GTF3C4/SN | 10 |
| BP | GO:004478 | G1 DNA da | 14/782 | 64/17913 | 5.1E-07 | 6.39E-05 | 5.24E-05 | CNOT6/SO | 14 |
| BP | GO:000690 | vesicle buc | 16/782 | 91/17913 | 1.81E-06 | 0.000171 | 0.000141 | SAR1A/WA | 16 |
| BP | GO:004852 | positive re | 17/782 | 103/17913 | 2.16E-06 | 0.000194 | 0.000159 | NUCKS1/C | 17 |
| BP | GO:000184 | protein ins | 9/782 | 29/17913 | 2.51E-06 | 0.00022 | 0.000181 | YWHAE/YV | 9 |
| BP | GO:003157 | DNA integr | 20/782 | 141/17913 | 3.27E-06 | 0.000265 | 0.000217 | CNOT6/SO | 20 |
| BP | GO:190382 | positive re | 33/782 | 318/17913 | 3.88E-06 | 0.000308 | 0.000253 | ERBB2/ITG | 33 |
| BP | GO:200123 | regulation | 38/782 | 397/17913 | 5.11E-06 | 0.000376 | 0.000308 | TGFBR1/FE | 38 |
| BP | GO:001045 | proteasom | 37/782 | 382/17913 | 5.17E-06 | 0.000376 | 0.000308 | DDI2/ENC1 | 37 |
| BP | GO:001982 | stem cell p | 21/782 | 158/17913 | 5.38E-06 | 0.000385 | 0.000316 | FZD7/SOX4 | 21 |
| BP | GO:000688 | ER to Golgi | 22/782 | 172/17913 | 6.1E-06 | 0.000418 | 0.000344 | SAR1A/CD3 | 22 |
| BP | GO:009872 | maintenan | 21/782 | 160/17913 | 6.57E-06 | 0.000439 | 0.00036 | FZD7/SOX4 | 21 |
| BP | GO:000751 | muscle org | 38/782 | 403/17913 | 7.24E-06 | 0.000466 | 0.000382 | FZD7/EFNE | 38 |
| BP | GO:006201 | regulation | 40/782 | 439/17913 | 9.5E-06 | 0.00057 | 0.000468 | ATCAY/NFI | 40 |
| BP | GO:004325 | regulation | 38/782 | 409/17913 | 1.02E-05 | 0.000592 | 0.000486 | PFN1/CNO | 38 |
| BP | GO:190227 | regulation | 21/782 | 165/17913 | 1.07E-05 | 0.000614 | 0.000504 | CAMK2D/F | 21 |
| BP | GO:007136 | cellular res | 10/782 | 43/17913 | 1.23E-05 | 0.000683 | 0.000561 | ERBB2/ZFP | 10 |
| BP | GO:004390 | positive re | 22/782 | 180/17913 | 1.27E-05 | 0.000701 | 0.000576 | NUCKS1/C | 22 |
| BP | GO:007190 | regulation | 42/782 | 479/17913 | 1.46E-05 | 0.00078 | 0.00064 | CCNT2/DA | 42 |
| BP | GO:003238 | regulation | 37/782 | 400/17913 | 1.46E-05 | 0.00078 | 0.00064 | ERBB2/AB | 37 |
| BP | GO:019873 | cell-cell sig | 43/782 | 500/17913 | 1.85E-05 | 0.000945 | 0.000776 | FZD7/PFN1 | 43 |
| BP | GO:003497 | response to | 27/782 | 254/17913 | 1.88E-05 | 0.000952 | 0.000781 | USP25/SIR | 27 |
| BP | GO:004851 | rhythmic p | 29/782 | 287/17913 | 2.44E-05 | 0.00121 | 0.000994 | RAI1/SIRT1 | 29 |
| BP | GO:000691 | nucleocyto | 30/782 | 302/17913 | 2.46E-05 | 0.00121 | 0.000994 | TNPO1/YW | 30 |
| BP | GO:007084 | response to | 10/782 | 47/17913 | 2.83E-05 | 0.001363 | 0.001119 | ERBB2/ZFP | 10 |
| BP | GO:003315 | regulation | 24/782 | 220/17913 | 3.54E-05 | 0.001613 | 0.001324 | ERBB2/USF | 24 |
| BP | GO:001082 | positive re | 16/782 | 115/17913 | 3.93E-05 | 0.001774 | 0.001456 | DDHD1/US | 16 |
| BP | GO:190336 | negative re | 13/782 | 80/17913 | 3.98E-05 | 0.001781 | 0.001463 | USP25/OG | 13 |

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| BP | GO:009011 | COPII-coat | 12/782 | 70/17913 | 4.55E-05 | 0.002 | 0.001642 | SAR1A/CD | 12 |
| BP | GO:006053 | muscle tiss | 35/782 | 392/17913 | 5.15E-05 | 0.002215 | 0.001819 | FZD7/EFNE | 35 |
| BP | GO:000610 | regulation | 22/782 | 198/17913 | 5.62E-05 | 0.002344 | 0.001925 | NFKB1/SIR | 22 |
| BP | GO:190585 | regulation | 13/782 | 83/17913 | 5.93E-05 | 0.002454 | 0.002015 | USP25/SIR | 13 |
| BP | GO:000705 | mitotic spii | 14/782 | 95/17913 | 6.22E-05 | 0.002535 | 0.002081 | CCNB1/TA | 14 |
| BP | GO:001635 | dendrite di | 23/782 | 216/17913 | 7.45E-05 | 0.002894 | 0.002376 | ADAM10/I | 23 |
| BP | GO:003225 | methylatio | 31/782 | 336/17913 | 7.45E-05 | 0.002894 | 0.002376 | PHF19/SIR | 31 |
| BP | GO:003590 | aorta morç | 8/782 | 34/17913 | 8.41E-05 | 0.003166 | 0.0026 | EFNB2/SO | 8 |
| BP | GO:003433 | cell junctio | 27/782 | 277/17913 | 8.55E-05 | 0.003172 | 0.002604 | TGFBR1/Af | 27 |
| BP | GO:007255 | establishm | 38/782 | 452/17913 | 9.06E-05 | 0.003311 | 0.002718 | TNPO1/RP | 38 |
| BP | GO:004854 | response ti | 33/782 | 375/17913 | 0.00011 | 0.003734 | 0.003066 | CDK7/ABC | 33 |
| BP | GO:000322 | ventricular | 10/782 | 55/17913 | 0.000117 | 0.003828 | 0.003143 | TGFBR1/TE | 10 |
| BP | GO:001624 | regulation | 19/782 | 166/17913 | 0.000119 | 0.003878 | 0.003184 | KIAA1324/ | 19 |
| BP | GO:000611 | regulation | 9/782 | 46/17913 | 0.000142 | 0.004432 | 0.003639 | SIRT1/NLN | 9 |
| BP | GO:003286 | cellular res | 21/782 | 197/17913 | 0.000149 | 0.004623 | 0.003795 | EPRS/GRB | 21 |
| BP | GO:007138 | cellular res | 24/782 | 243/17913 | 0.00017 | 0.005067 | 0.00416 | CDK7/SIRT | 24 |
| BP | GO:004348 | regulation | 18/782 | 158/17913 | 0.000189 | 0.005468 | 0.00449 | TNPO1/ZFI | 18 |
| BP | GO:004343 | response ti | 34/782 | 404/17913 | 0.000205 | 0.005837 | 0.004792 | PRLR/EPRS | 34 |
| BP | GO:004255 | response ti | 19/782 | 174/17913 | 0.000221 | 0.006095 | 0.005005 | KIAA1324/ | 19 |
| BP | GO:007110 | DNA confo | 26/782 | 279/17913 | 0.000236 | 0.006464 | 0.005307 | CCNB1/RA | 26 |
| BP | GO:000600 | glucose mç | 21/782 | 204/17913 | 0.000242 | 0.006542 | 0.005371 | SIRT1/NLN | 21 |
| BP | GO:001605 | vesicle org | 26/782 | 280/17913 | 0.00025 | 0.006622 | 0.005437 | SAR1A/WA | 26 |
| BP | GO:001908 | viral gene ç | 20/782 | 191/17913 | 0.000269 | 0.007001 | 0.005748 | CCNT2/RP | 20 |
| BP | GO:003292 | circadian r | 10/782 | 61/17913 | 0.000284 | 0.007144 | 0.005866 | RAI1/SIRT1 | 10 |
| BP | GO:005165 | establishm | 36/782 | 448/17913 | 0.00033 | 0.008107 | 0.006656 | CCNB1/W/ | 36 |
| BP | GO:004331 | neutrophil | 38/782 | 485/17913 | 0.000375 | 0.008864 | 0.007278 | HGSNAT/A | 38 |
| BP | GO:003164 | regulation | 25/782 | 272/17913 | 0.00038 | 0.008864 | 0.007278 | DDI2/PFN1 | 25 |
| BP | GO:005134 | negative rç | 25/782 | 272/17913 | 0.00038 | 0.008864 | 0.007278 | LRP6/WAR | 25 |
| BP | GO:005181 | modificatic | 14/782 | 113/17913 | 0.000405 | 0.009307 | 0.007642 | NUCKS1/C | 14 |
| BP | GO:000228 | neutrophil | 38/782 | 488/17913 | 0.000423 | 0.009519 | 0.007816 | HGSNAT/A | 38 |
| BP | GO:190571 | positive re | 10/782 | 64/17913 | 0.000424 | 0.009519 | 0.007816 | ATF2/YWH | 10 |
| BP | GO:003158 | cell-substr | 28/782 | 322/17913 | 0.000432 | 0.009574 | 0.00786 | FZD7/ITGB | 28 |
| BP | GO:000322 | ventricular | 5/782 | 16/17913 | 0.000457 | 0.009915 | 0.008141 | TGFBR1/CF | 5 |
| BP | GO:001905 | viral life cy | 28/782 | 324/17913 | 0.000477 | 0.010205 | 0.008379 | EFNB2/ITG | 28 |
| BP | GO:003460 | cellular res | 14/782 | 117/17913 | 0.000579 | 0.012112 | 0.009945 | CAMK2D/Y | 14 |
| BP | GO:000323 | cardiac ver | 15/782 | 131/17913 | 0.000599 | 0.012445 | 0.010218 | SOX4/TGFE | 15 |
| BP | GO:003396 | cytoplasmic | 5/782 | 17/17913 | 0.000625 | 0.012719 | 0.010443 | CNOT6/DY | 5 |
| BP | GO:000244 | neutrophil | 38/782 | 499/17913 | 0.000646 | 0.01305 | 0.010715 | HGSNAT/A | 38 |
| BP | GO:004211 | neutrophil | 38/782 | 499/17913 | 0.000646 | 0.01305 | 0.010715 | HGSNAT/A | 38 |
| BP | GO:000007 | mitotic sist | 15/782 | 132/17913 | 0.000649 | 0.013054 | 0.010718 | CCNB1/CH | 15 |
| BP | GO:014001 | mitotic nuc | 22/782 | 237/17913 | 0.00073 | 0.014388 | 0.011813 | CCNB1/CH | 22 |
| BP | GO:190547 | positive re | 14/782 | 120/17913 | 0.000747 | 0.014559 | 0.011954 | ERBB2/ITG | 14 |
| BP | GO:000754 | sex differe | 24/782 | 269/17913 | 0.000754 | 0.014585 | 0.011975 | TGFBR1/CF | 24 |
| BP | GO:005170 | interaction | 11/782 | 81/17913 | 0.000762 | 0.014687 | 0.012059 | NUCKS1/C | 11 |
| BP | GO:000640 | RNA localiz | 20/782 | 208/17913 | 0.000807 | 0.015355 | 0.012607 | ZFP36/CPS | 20 |
| BP | GO:003526 | multicellul | 16/782 | 149/17913 | 0.000812 | 0.015355 | 0.012607 | RAI1/RC3H | 16 |
| BP | GO:001921 | regulation | 32/782 | 402/17913 | 0.000812 | 0.015355 | 0.012607 | CRTC3/RBL | 32 |

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| BP | GO:00650C protein-DN 20/782 | 210/17913 | 0.000909 | 0.0167 | 0.013712 | CDK7/RAD | 20 |
| BP | GO:190547 regulation 18/782 | 181/17913 | 0.000981 | 0.017382 | 0.014272 | ADAM10/E | 18 |
| BP | GO:00905E regulation 11/782 | 84/17913 | 0.001038 | 0.018174 | 0.014922 | ATF2/YWH | 11 |
| BP | GO:00017C in utero en 28/782 | 342/17913 | 0.001102 | 0.018976 | 0.01558 | TGFBR1/AI | 28 |
| BP | GO:00064I translation 18/782 | 183/17913 | 0.001113 | 0.0191 | 0.015682 | RPS23/EIF3 | 18 |
| BP | GO:00712I cellular res 26/782 | 310/17913 | 0.001157 | 0.019466 | 0.015982 | NFKB1/NU | 26 |
| BP | GO:01040C cellular res 26/782 | 310/17913 | 0.001157 | 0.019466 | 0.015982 | NFKB1/NU | 26 |
| BP | GO:00016E ameoboidal 34/782 | 446/17913 | 0.001197 | 0.019983 | 0.016407 | EFNB2/PFN | 34 |
| BP | GO:00086E cellular am 10/782 | 73/17913 | 0.001222 | 0.020137 | 0.016533 | BCAT2/SEF | 10 |
| BP | GO:00447E multi-orga 10/782 | 73/17913 | 0.001222 | 0.020137 | 0.016533 | RAB40B/R | 10 |
| BP | GO:190257 multi-orga 10/782 | 73/17913 | 0.001222 | 0.020137 | 0.016533 | RAB40B/R | 10 |
| BP | GO:19029C positive re 18/782 | 185/17913 | 0.001261 | 0.020708 | 0.017002 | PFN1/TGFE | 18 |
| BP | GO:00301E B cell diffe 13/782 | 113/17913 | 0.001298 | 0.021173 | 0.017384 | ITGB1/TPD | 13 |
| BP | GO:00456E negative re 19/782 | 201/17913 | 0.00132 | 0.021461 | 0.017621 | EFNB2/CTE | 19 |
| BP | GO:00069E nuclear po 4/782 | 12/17913 | 0.001347 | 0.021763 | 0.017868 | NUP98/NU | 4 |
| BP | GO:19042E regulation 6/782 | 29/17913 | 0.001362 | 0.021813 | 0.01791 | USP25/EDI | 6 |
| BP | GO:00427E regulation 13/782 | 114/17913 | 0.001408 | 0.022312 | 0.018319 | ZFH3/MA | 13 |
| BP | GO:00091E ribonucleo 27/782 | 331/17913 | 0.001415 | 0.022354 | 0.018354 | CCNB1/UC | 27 |
| BP | GO:00082C cholesterol 15/782 | 143/17913 | 0.001481 | 0.023179 | 0.019031 | TTC39B/D | 15 |
| BP | GO:19052E positive re 12/782 | 101/17913 | 0.001487 | 0.023201 | 0.019049 | PHF19/CC | 12 |
| BP | GO:005164 vesicle loc 23/782 | 270/17913 | 0.001776 | 0.026634 | 0.021867 | WASL/CD5 | 23 |
| BP | GO:00606I adipose tis 7/782 | 41/17913 | 0.001806 | 0.026692 | 0.021915 | ATF2/SIRT | 7 |
| BP | GO:00107E positive re 4/782 | 13/17913 | 0.001879 | 0.027119 | 0.022266 | THBS1/PR | 4 |
| BP | GO:00431I negative re 4/782 | 13/17913 | 0.001879 | 0.027119 | 0.022266 | PDE3A/PT | 4 |
| BP | GO:00451E developme 20/782 | 223/17913 | 0.001886 | 0.027141 | 0.022284 | TGFBR1/CE | 20 |
| BP | GO:007182 protein-DN 21/782 | 240/17913 | 0.001993 | 0.028356 | 0.023281 | CDK7/RAD | 21 |
| BP | GO:00714E cellular res 19/782 | 210/17913 | 0.00219 | 0.030375 | 0.024939 | CCNB1/SIR | 19 |
| BP | GO:00613E heart trabe 6/782 | 32/17913 | 0.002325 | 0.031647 | 0.025984 | TGFBR1/CF | 6 |
| BP | GO:00224C membrane 15/782 | 150/17913 | 0.002377 | 0.032088 | 0.026346 | ESYT1/YWI | 15 |
| BP | GO:00459E negative re 4/782 | 14/17913 | 0.00254 | 0.033569 | 0.027562 | DOCK5/PT | 4 |
| BP | GO:00094I response tr 14/782 | 137/17913 | 0.00268 | 0.035229 | 0.028925 | SIRT1/REV | 14 |
| BP | GO:00987E bone cell d 6/782 | 33/17913 | 0.002738 | 0.035629 | 0.029253 | ANXA2/ME | 6 |
| BP | GO:190357 negative re 7/782 | 44/17913 | 0.00275 | 0.035684 | 0.029298 | USP25/PA | 7 |
| BP | GO:009732 response tr 11/782 | 96/17913 | 0.003075 | 0.038414 | 0.03154 | DDI2/ADA | 11 |
| BP | GO:004227 ribosomal : 5/782 | 24/17913 | 0.00333 | 0.040084 | 0.032911 | RIOK3/RPL | 5 |
| BP | GO:00439E negative re 5/782 | 24/17913 | 0.00333 | 0.040084 | 0.032911 | CRTC3/PDI | 5 |
| BP | GO:006014 positive re 5/782 | 24/17913 | 0.00333 | 0.040084 | 0.032911 | ZFP36/FMI | 5 |
| BP | GO:00469E pore comp 4/782 | 15/17913 | 0.003345 | 0.040084 | 0.032911 | NUP98/NU | 4 |
| BP | GO:00600C Sertoli cell 4/782 | 15/17913 | 0.003345 | 0.040084 | 0.032911 | ATRX/FLN | 4 |
| BP | GO:00463E ribose pho 23/782 | 284/17913 | 0.003371 | 0.040295 | 0.033084 | UCK2/OGT | 23 |
| BP | GO:00163I dephosphc 33/782 | 458/17913 | 0.003439 | 0.040916 | 0.033594 | CAMTA1/C | 33 |
| BP | GO:01400E organelle l 14/782 | 141/17913 | 0.003489 | 0.041411 | 0.034 | ESYT1/YWI | 14 |
| BP | GO:010602 neuron prc 10/782 | 85/17913 | 0.003856 | 0.044714 | 0.036712 | ADAM10/V | 10 |
| BP | GO:00159E nucleobase 19/782 | 221/17913 | 0.003866 | 0.044717 | 0.036715 | SLC25A25/ | 19 |
| BP | GO:003572 interleukin 7/782 | 47/17913 | 0.004031 | 0.045583 | 0.037426 | CFL1/PAK2 | 7 |
| BP | GO:00002E nuclear div 27/782 | 357/17913 | 0.004073 | 0.045949 | 0.037727 | CCNB1/CH | 27 |
| BP | GO:00102I response tr 14/782 | 144/17913 | 0.004218 | 0.047217 | 0.038767 | NUCKS1/L | 14 |

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| BP | GO:004426 | cellular car | 21/782 | 256/17913 | 0.004276 | 0.047665 | 0.039135 | SIRT1/NLN | 21 |
| BP | GO:190165 | response to | 17/782 | 191/17913 | 0.004307 | 0.047665 | 0.039135 | KIF1B/SIRT | 17 |
| BP | GO:007163 | regulation of | 6/782 | 36/17913 | 0.004311 | 0.047665 | 0.039135 | ATF2/THBS | 6 |
| BP | GO:004581 | negative regulation of | 11/782 | 101/17913 | 0.004557 | 0.049519 | 0.040657 | PHF19/SIRT | 11 |
| BP | GO:004887 | homeostasis | 20/782 | 241/17913 | 0.004595 | 0.049814 | 0.0409 | TSC22D3/F | 20 |
| CC | GO:000591 | adherens junction | 58/800 | 496/18678 | 3.58E-12 | 2.06E-09 | 1.54E-09 | EFNB2/PFN | 58 |
| CC | GO:000592 | focal adhesion | 46/800 | 397/18678 | 8.82E-10 | 1.99E-07 | 1.49E-07 | EFNB2/PFN | 46 |
| CC | GO:000592 | cell-substrate | 46/800 | 399/18678 | 1.04E-09 | 1.99E-07 | 1.49E-07 | EFNB2/PFN | 46 |
| CC | GO:003005 | cell-substrate | 46/800 | 404/18678 | 1.56E-09 | 2.23E-07 | 1.67E-07 | EFNB2/PFN | 46 |
| CC | GO:000078 | chromatin | 51/800 | 500/18678 | 8.86E-09 | 1.02E-06 | 7.63E-07 | MORF4L1/ | 51 |
| CC | GO:003577 | ribonucleosome | 25/800 | 188/18678 | 4.94E-07 | 4.46E-05 | 3.34E-05 | RC3H2/ZFF | 25 |
| CC | GO:000079 | heterochromatin | 15/800 | 75/18678 | 5.43E-07 | 4.46E-05 | 3.34E-05 | CBX2/SIRT | 15 |
| CC | GO:001705 | transcription | 15/800 | 78/18678 | 9.23E-07 | 5.94E-05 | 4.46E-05 | SIRT1/REST | 15 |
| CC | GO:003066 | coated vesicle | 23/800 | 169/18678 | 9.32E-07 | 5.94E-05 | 4.46E-05 | SAR1A/CD | 23 |
| CC | GO:003646 | cytoplasmic | 23/800 | 176/18678 | 1.91E-06 | 0.000109 | 8.2E-05 | RC3H2/ZFF | 23 |
| CC | GO:003013 | coated vesicle | 29/800 | 261/18678 | 2.73E-06 | 0.000135 | 0.000101 | SAR1A/LM | 29 |
| CC | GO:001049 | cytoplasmic | 12/800 | 55/18678 | 2.82E-06 | 0.000135 | 0.000101 | ZFP36/LSM | 12 |
| CC | GO:000579 | Golgi-associated | 20/800 | 145/18678 | 3.83E-06 | 0.000169 | 0.000127 | SAR1A/AD | 20 |
| CC | GO:004445 | nuclear chromatin | 42/800 | 469/18678 | 5.56E-06 | 0.000228 | 0.000171 | MORF4L1/ | 42 |
| CC | GO:003066 | Golgi-associated | 16/800 | 102/18678 | 6.67E-06 | 0.000255 | 0.000191 | SAR1A/CD | 16 |
| CC | GO:000079 | nuclear chromatin | 31/800 | 309/18678 | 1.04E-05 | 0.000372 | 0.000279 | MORF4L1/ | 31 |
| CC | GO:000015 | ubiquitin ligase | 25/800 | 224/18678 | 1.21E-05 | 0.000409 | 0.000307 | ENC1/CBX | 25 |
| CC | GO:000566 | transcription | 28/800 | 270/18678 | 1.49E-05 | 0.000477 | 0.000357 | CDK7/BCL | 28 |
| CC | GO:003012 | vesicle coat | 10/800 | 48/18678 | 2.92E-05 | 0.000884 | 0.000663 | SAR1A/AP | 10 |
| CC | GO:000591 | cell-cell junction | 36/800 | 414/18678 | 4.78E-05 | 0.001371 | 0.001028 | TGFBR1/R | 36 |
| CC | GO:001666 | nuclear speckle | 34/800 | 386/18678 | 5.96E-05 | 0.00163 | 0.001222 | STK17A/EA | 34 |
| CC | GO:003146 | Cul3-RING | 8/800 | 34/18678 | 7.36E-05 | 0.001921 | 0.001441 | ENC1/GAN | 8 |
| CC | GO:000563 | nuclear envelope | 35/800 | 420/18678 | 0.000141 | 0.003514 | 0.002635 | SIRT1/GTF | 35 |
| CC | GO:000586 | cis-Golgi network | 8/800 | 39/18678 | 0.000206 | 0.004937 | 0.003703 | BCL9/HOO | 8 |
| CC | GO:009868 | chromosome | 29/800 | 337/18678 | 0.000301 | 0.006911 | 0.005183 | CCNB1/PPI | 29 |
| CC | GO:004479 | nuclear transcription | 16/800 | 140/18678 | 0.000331 | 0.007313 | 0.005485 | CDK7/BCL | 16 |
| CC | GO:000572 | nuclear heterochromatin | 7/800 | 33/18678 | 0.000415 | 0.008605 | 0.006454 | SIRT1/TCP | 7 |
| CC | GO:190291 | protein kinase | 11/800 | 77/18678 | 0.00042 | 0.008605 | 0.006454 | CCNT2/CD | 11 |
| CC | GO:001256 | ER to Golgi | 9/800 | 55/18678 | 0.000502 | 0.009935 | 0.007452 | SAR1A/CD | 9 |
| CC | GO:000591 | cell-cell adhesion | 11/800 | 79/18678 | 0.000525 | 0.010053 | 0.00754 | FRS2/PARK | 11 |
| CC | GO:000577 | late endosome | 22/800 | 240/18678 | 0.000674 | 0.011762 | 0.008822 | MCOLN2/K | 22 |
| CC | GO:000078 | nuclear chromatin | 14/800 | 121/18678 | 0.000676 | 0.011762 | 0.008822 | MCM6/XR | 14 |
| CC | GO:003013 | COPII-coated | 10/800 | 69/18678 | 0.000676 | 0.011762 | 0.008822 | SAR1A/CD | 10 |
| CC | GO:003146 | cullin-RING | 14/800 | 124/18678 | 0.000863 | 0.013778 | 0.010334 | ENC1/GAN | 14 |
| CC | GO:009057 | RNA polymerase | 14/800 | 124/18678 | 0.000863 | 0.013778 | 0.010334 | CDK7/BCL | 14 |
| CC | GO:001716 | aminoacyl-tRNA | 4/800 | 11/18678 | 0.000866 | 0.013778 | 0.010334 | EPRS/IARS | 4 |
| CC | GO:001006 | endosome | 35/800 | 464/18678 | 0.000888 | 0.013778 | 0.010334 | FZD7/MCC | 35 |
| CC | GO:000828 | protein serine | 7/800 | 38/18678 | 0.001017 | 0.014927 | 0.011196 | PPP2CA/PF | 7 |
| CC | GO:190329 | phosphatase | 7/800 | 38/18678 | 0.001017 | 0.014927 | 0.011196 | PPP2CA/PF | 7 |
| CC | GO:003011 | membrane | 11/800 | 86/18678 | 0.001085 | 0.014927 | 0.011196 | SAR1A/AP | 11 |
| CC | GO:004847 | coated membrane | 11/800 | 86/18678 | 0.001085 | 0.014927 | 0.011196 | SAR1A/AP | 11 |
| CC | GO:000078 | chromosome | 16/800 | 156/18678 | 0.001092 | 0.014927 | 0.011196 | MCM6/XR | 16 |

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|----|--|--------|-----------|----------|----------|----------|-----------|----|
| CC | GO:003125 cell leading edge | 30/800 | 384/18678 | 0.00117 | 0.015615 | 0.011712 | ITGB1/WA | 30 |
| CC | GO:000030 cyclin-dependent kinase activity | 6/800 | 29/18678 | 0.001235 | 0.01575 | 0.011813 | CCNT2/CD | 6 |
| CC | GO:003012 COPII vesicle transport | 4/800 | 12/18678 | 0.001255 | 0.01575 | 0.011813 | SAR1A/SEC | 4 |
| CC | GO:000024 pericentriole organization | 5/800 | 20/18678 | 0.00129 | 0.01575 | 0.011813 | HOOK3/TN | 5 |
| CC | GO:000572 pericentriole organization | 5/800 | 20/18678 | 0.00129 | 0.01575 | 0.011813 | H2AFY/DN | 5 |
| CC | GO:005503 recycling endosome | 10/800 | 76/18678 | 0.001451 | 0.017354 | 0.013016 | FZD7/MCC | 10 |
| CC | GO:190255 serine/threonine phosphorylation | 9/800 | 65/18678 | 0.001725 | 0.020041 | 0.015032 | CCNT2/CD | 9 |
| CC | GO:005503 recycling endosome | 16/800 | 164/18678 | 0.001846 | 0.020041 | 0.015032 | FZD7/MCC | 16 |
| CC | GO:001623 aggresome | 7/800 | 42/18678 | 0.001874 | 0.020041 | 0.015032 | TRIM37/EC | 7 |
| CC | GO:003151 PcG protein complex | 7/800 | 42/18678 | 0.001874 | 0.020041 | 0.015032 | PHF19/CB | 7 |
| CC | GO:000576 lysosomal lumen | 27/800 | 344/18678 | 0.001885 | 0.020041 | 0.015032 | HGSNAT/LI | 27 |
| CC | GO:009885 lytic vacuole | 27/800 | 344/18678 | 0.001885 | 0.020041 | 0.015032 | HGSNAT/LI | 27 |
| CC | GO:190411 axon cytoplasm | 8/800 | 54/18678 | 0.001984 | 0.020704 | 0.015529 | KIF1B/RAB | 8 |
| CC | GO:006165 transferase | 17/800 | 181/18678 | 0.002035 | 0.020863 | 0.015648 | CCNT2/CD | 17 |
| CC | GO:000577 vacuolar membrane | 29/800 | 382/18678 | 0.002152 | 0.021358 | 0.01602 | HGSNAT/LI | 29 |
| CC | GO:003013 clathrin-coated vesicle | 17/800 | 182/18678 | 0.002158 | 0.021358 | 0.01602 | LMBRD1/A | 17 |
| CC | GO:003013 transport vesicle | 27/800 | 349/18678 | 0.002312 | 0.021626 | 0.01622 | SAR1A/AD | 27 |
| CC | GO:000075 condensed nucleosome | 18/800 | 199/18678 | 0.002317 | 0.021626 | 0.01622 | CCNB1/CEI | 18 |
| CC | GO:009956 cytoplasmic vesicle | 30/800 | 402/18678 | 0.002358 | 0.021626 | 0.01622 | PFN1/WAS | 30 |
| CC | GO:000172 ruffle | 16/800 | 168/18678 | 0.002362 | 0.021626 | 0.01622 | ITGB1/CFL | 16 |
| CC | GO:007060 SWI/SNF complex | 9/800 | 68/18678 | 0.002374 | 0.021626 | 0.01622 | SMARCA4/ | 9 |
| CC | GO:190481 ficolin-1 receptor | 13/800 | 124/18678 | 0.002548 | 0.022486 | 0.016866 | XRCC6/CAI | 13 |
| CC | GO:000077 chromosome | 17/800 | 185/18678 | 0.002564 | 0.022486 | 0.016866 | CCNB1/PPI | 17 |
| CC | GO:003197 organelle | 10/800 | 82/18678 | 0.002586 | 0.022486 | 0.016866 | COA4/ARL | 10 |
| CC | GO:003013 endocytic vesicle | 23/800 | 289/18678 | 0.003324 | 0.028475 | 0.021358 | CAMK2D/V | 23 |
| CC | GO:000564 nuclear pore | 8/800 | 59/18678 | 0.003506 | 0.029594 | 0.022197 | XPOT/NUP | 8 |
| CC | GO:003005 desmosome | 5/800 | 25/18678 | 0.003701 | 0.030675 | 0.023007 | PNN/UBA1 | 5 |
| CC | GO:004512 membrane | 24/800 | 309/18678 | 0.003741 | 0.030675 | 0.023007 | TGFBR1/LR | 24 |
| CC | GO:000575 mitochondrion | 9/800 | 73/18678 | 0.00387 | 0.031058 | 0.023295 | COA4/ARL | 9 |
| CC | GO:009885 membrane | 24/800 | 310/18678 | 0.003896 | 0.031058 | 0.023295 | TGFBR1/LR | 24 |
| CC | GO:003001 CCR4-NOT complex | 4/800 | 16/18678 | 0.004024 | 0.03164 | 0.023732 | CNOT6/ZFI | 4 |
| CC | GO:000011 histone dimer | 7/800 | 48/18678 | 0.004099 | 0.031793 | 0.023846 | MORF4L1/ | 7 |
| CC | GO:000581 centrosome | 33/800 | 473/18678 | 0.004229 | 0.032366 | 0.024276 | CCNB1/AR | 33 |
| CC | GO:000593 cell cortex | 19/800 | 229/18678 | 0.004645 | 0.035079 | 0.026311 | PFN1/WAS | 19 |
| CC | GO:004325 apical junction | 13/800 | 134/18678 | 0.004979 | 0.037118 | 0.02784 | TGFBR1/R/ | 13 |
| CC | GO:000093 P-body | 8/800 | 63/18678 | 0.005274 | 0.038809 | 0.029109 | RC3H2/ZFF | 8 |
| CC | GO:190494 ATPase core | 10/800 | 92/18678 | 0.005954 | 0.042943 | 0.032209 | ABCA2/SM | 10 |
| CC | GO:009858 membrane | 24/800 | 321/18678 | 0.005985 | 0.042943 | 0.032209 | TGFBR1/LR | 24 |
| CC | GO:003295 protein-DNA complex | 16/800 | 187/18678 | 0.006717 | 0.046865 | 0.035151 | TCF7L2/XR | 16 |
| CC | GO:000590 clathrin-coated vesicle | 8/800 | 66/18678 | 0.006994 | 0.046865 | 0.035151 | LRP10/AP2 | 8 |
| CC | GO:003065 transport vesicle | 16/800 | 188/18678 | 0.00706 | 0.046865 | 0.035151 | SAR1A/CD | 16 |
| CC | GO:003124 protein acetylation | 9/800 | 80/18678 | 0.007101 | 0.046865 | 0.035151 | MORF4L1/ | 9 |
| CC | GO:012011 neuron process | 9/800 | 80/18678 | 0.007101 | 0.046865 | 0.035151 | KIF1B/RAB | 9 |
| CC | GO:190245 acetyltransferase | 9/800 | 80/18678 | 0.007101 | 0.046865 | 0.035151 | MORF4L1/ | 9 |
| CC | GO:008000 Cul4-RING complex | 5/800 | 29/18678 | 0.007185 | 0.046865 | 0.035151 | CDKN1B/D | 5 |
| CC | GO:199035 DNA repair | 5/800 | 29/18678 | 0.007185 | 0.046865 | 0.035151 | RAD23B/XI | 5 |
| CC | GO:000080 X chromosome | 3/800 | 10/18678 | 0.007493 | 0.047429 | 0.035574 | SIN3B/H2A | 3 |

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|----|------------------------|--------|-----------|----------|----------|----------|------------|----|
| CC | GO:003108 nuclear po | 3/800 | 10/18678 | 0.007493 | 0.047429 | 0.035574 | NUP98/NU | 3 |
| CC | GO:003066 clathrin-co | 11/800 | 110/18678 | 0.007519 | 0.047429 | 0.035574 | AP2B1/CLT | 11 |
| CC | GO:001623 inclusion b | 9/800 | 81/18678 | 0.007693 | 0.047762 | 0.035824 | TRIM37/NI | 9 |
| CC | GO:003194 filamentou | 4/800 | 19/18678 | 0.007738 | 0.047762 | 0.035824 | ARPC3/CD | 4 |
| CC | GO:003002 lamellipod | 16/800 | 191/18678 | 0.008173 | 0.049771 | 0.03733 | ITGB1/WA | 16 |
| CC | GO:007101 catalytic st | 9/800 | 82/18678 | 0.008323 | 0.049771 | 0.03733 | HNRNPF/S | 9 |
| CC | GO:004278 polysomal | 5/800 | 30/18678 | 0.008324 | 0.049771 | 0.03733 | RPS23/RPL | 5 |
| MF | GO:000368 chromatin | 54/781 | 437/16969 | 3.43E-11 | 2.53E-08 | 2.12E-08 | CCNT2/RBI | 54 |
| MF | GO:005083 cell adhesi | 47/781 | 444/16969 | 9.15E-08 | 2.74E-05 | 2.29E-05 | PFN1/ADA | 47 |
| MF | GO:004525 cadherin bi | 36/781 | 297/16969 | 1.11E-07 | 2.74E-05 | 2.29E-05 | PFN1/ITGB | 36 |
| MF | GO:004235 histone bir | 25/781 | 174/16969 | 4.15E-07 | 7.64E-05 | 6.4E-05 | PHF19/BRI | 25 |
| MF | GO:000373 mRNA 3'-U | 14/781 | 67/16969 | 1.72E-06 | 0.000253 | 0.000212 | ZFP36/FMI | 14 |
| MF | GO:000801 beta-caten | 15/781 | 78/16969 | 2.24E-06 | 0.000275 | 0.00023 | BCL9/LZIC/ | 15 |
| MF | GO:003162 ubiquitin p | 31/781 | 270/16969 | 2.7E-06 | 0.000284 | 0.000238 | USP25/YW | 31 |
| MF | GO:004438 ubiquitin-li | 32/781 | 286/16969 | 3.26E-06 | 0.0003 | 0.000251 | CCNB1/US | 32 |
| MF | GO:000108 RNA polyr | 18/781 | 113/16969 | 3.89E-06 | 0.000318 | 0.000266 | ATF2/TCF7 | 18 |
| MF | GO:000371 transcriptic | 45/781 | 494/16969 | 1.02E-05 | 0.000753 | 0.00063 | SOX4/CDK | 45 |
| MF | GO:014003 modificatic | 19/781 | 135/16969 | 1.35E-05 | 0.000905 | 0.000757 | PHF19/RAI | 19 |
| MF | GO:000372 double-str | 12/781 | 62/16969 | 2.15E-05 | 0.001232 | 0.001031 | RC3H2/LSN | 12 |
| MF | GO:000097 RNA polyr | 40/781 | 432/16969 | 2.17E-05 | 0.001232 | 0.001031 | SOX4/ATF2 | 40 |
| MF | GO:000098 proximal p | 40/781 | 452/16969 | 6.02E-05 | 0.003168 | 0.002651 | SOX4/ATF2 | 40 |
| MF | GO:004633 SMAD binc | 12/781 | 72/16969 | 0.0001 | 0.004923 | 0.004121 | TGFBR1/PI | 12 |
| MF | GO:004302 ribonucleo | 15/781 | 107/16969 | 0.000112 | 0.005154 | 0.004314 | SRP54/SBC | 15 |
| MF | GO:005068 androgen r | 9/781 | 44/16969 | 0.000147 | 0.00637 | 0.005331 | CDK7/SMA | 9 |
| MF | GO:003148 chromatin | 12/781 | 77/16969 | 0.000194 | 0.007952 | 0.006656 | ZIC2/SMAF | 12 |
| MF | GO:000122 DNA-bindin | 23/781 | 224/16969 | 0.000277 | 0.009877 | 0.008266 | NFKB1/RES | 23 |
| MF | GO:000552 GTP bindin | 29/781 | 313/16969 | 0.000283 | 0.009877 | 0.008266 | RAB2B/SAI | 29 |
| MF | GO:003022 lipoprotein | 5/781 | 14/16969 | 0.000288 | 0.009877 | 0.008266 | LRP10/LRP | 5 |
| MF | GO:004518 translation | 9/781 | 48/16969 | 0.000295 | 0.009877 | 0.008266 | PAIP1/FMF | 9 |
| MF | GO:000371 transcriptic | 27/781 | 285/16969 | 0.000318 | 0.010199 | 0.008536 | SOX4/CDK | 27 |
| MF | GO:003255 purine ribc | 29/781 | 318/16969 | 0.000368 | 0.0113 | 0.009457 | RAB2B/SAI | 29 |
| MF | GO:000188 purine nuc | 29/781 | 321/16969 | 0.000429 | 0.012659 | 0.010595 | RAB2B/SAI | 29 |
| MF | GO:003254 ribonucleo | 29/781 | 322/16969 | 0.000452 | 0.012808 | 0.01072 | RAB2B/SAI | 29 |
| MF | GO:004802 mRNA 5'-U | 6/781 | 23/16969 | 0.00048 | 0.013099 | 0.010964 | FMR1/IGF2 | 6 |
| MF | GO:001688 ATPase act | 26/781 | 280/16969 | 0.000553 | 0.014564 | 0.01219 | CDK7/LMB | 26 |
| MF | GO:000188 nucleoside | 29/781 | 329/16969 | 0.00064 | 0.016258 | 0.013607 | RAB2B/SAI | 29 |
| MF | GO:001900 guanyl nuc | 29/781 | 331/16969 | 0.000705 | 0.016699 | 0.013976 | RAB2B/SAI | 29 |
| MF | GO:003256 guanyl ribc | 29/781 | 331/16969 | 0.000705 | 0.016699 | 0.013976 | RAB2B/SAI | 29 |
| MF | GO:000203 p53 bindin | 10/781 | 65/16969 | 0.000725 | 0.016699 | 0.013976 | SIRT1/SMA | 10 |
| MF | GO:004282 histone de | 13/781 | 102/16969 | 0.0008 | 0.016786 | 0.014049 | YWHAE/GI | 13 |
| MF | GO:000438 helicase ac | 15/781 | 128/16969 | 0.000803 | 0.016786 | 0.014049 | SMARCA4/ | 15 |
| MF | GO:003506 methylater | 10/781 | 66/16969 | 0.00082 | 0.016786 | 0.014049 | PHF19/CB | 10 |
| MF | GO:014003 methylatio | 10/781 | 66/16969 | 0.00082 | 0.016786 | 0.014049 | PHF19/CB | 10 |
| MF | GO:000109 RNA polyr | 5/781 | 18/16969 | 0.001058 | 0.02108 | 0.017643 | TAF2/ZNHI | 5 |
| MF | GO:000109 TFIIID-class | 4/781 | 11/16969 | 0.001133 | 0.021677 | 0.018143 | TAF2/ZNHI | 4 |
| MF | GO:004262 ATPase act | 21/781 | 218/16969 | 0.001147 | 0.021677 | 0.018143 | CDK7/LMB | 21 |
| MF | GO:009711 scaffold pri | 9/781 | 58/16969 | 0.001242 | 0.02289 | 0.019158 | YWHAE/KII | 9 |

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|----|-------------------------------|-----------|----------|----------|----------|------------|----|
| MF | GO:003532 enhancer t 14/781 | 121/16969 | 0.001342 | 0.024119 | 0.020187 | NFKB1/ATF | 14 |
| MF | GO:00190C GDP bindir 9/781 | 59/16969 | 0.001407 | 0.024119 | 0.020187 | RAP2B/SRF | 9 |
| MF | GO:00704C repressing 9/781 | 59/16969 | 0.001407 | 0.024119 | 0.020187 | TCF7L2/PA | 9 |
| MF | GO:00080C DNA-depe 10/781 | 72/16969 | 0.001627 | 0.026834 | 0.022459 | CDK7/SMA | 10 |
| MF | GO:000504 low-densit 4/781 | 12/16969 | 0.001638 | 0.026834 | 0.022459 | LRP10/LRP | 4 |
| MF | GO:00011C RNA polyr 6/781 | 29/16969 | 0.001784 | 0.028587 | 0.023926 | TCF7L2/M1 | 6 |
| MF | GO:000467 protein ser 30/781 | 371/16969 | 0.002039 | 0.03197 | 0.026758 | CAMK2D/S | 30 |
| MF | GO:00009C RNA polyr 11/781 | 87/16969 | 0.002108 | 0.032258 | 0.026999 | NFKB1/ATF | 11 |
| MF | GO:00718C 14-3-3 prot 6/781 | 30/16969 | 0.002145 | 0.032258 | 0.026999 | ZFP36/FOX | 6 |
| MF | GO:00506C WW doma 5/781 | 21/16969 | 0.002241 | 0.033034 | 0.027648 | DAZAP2/PI | 5 |
| MF | GO:00352C steroid hor 11/781 | 88/16969 | 0.002311 | 0.033395 | 0.02795 | CDK7/SMA | 11 |
| MF | GO:00044C histone ac 8/781 | 52/16969 | 0.002424 | 0.034356 | 0.028755 | ATF2/GTF3 | 8 |
| MF | GO:001921 kinase inhi 9/781 | 64/16969 | 0.002515 | 0.034973 | 0.029271 | LRP6/SH3B | 9 |
| MF | GO:000371 transcriptio 19/781 | 205/16969 | 0.002987 | 0.040693 | 0.034058 | SIRT1/SMA | 19 |
| MF | GO:001641 S-acyltrans 4/781 | 14/16969 | 0.003078 | 0.040693 | 0.034058 | ZDHHC5/ZI | 4 |
| MF | GO:006173 peptide-lys 8/781 | 54/16969 | 0.003092 | 0.040693 | 0.034058 | ATF2/GTF3 | 8 |
| MF | GO:00352C nuclear ho 15/781 | 147/16969 | 0.003215 | 0.041568 | 0.034791 | CDK7/SIRT | 15 |
| MF | GO:00199C phosphata: 17/781 | 177/16969 | 0.003357 | 0.04218 | 0.035303 | ERBB2/SYK | 17 |
| MF | GO:003037 translation 5/781 | 23/16969 | 0.003434 | 0.04218 | 0.035303 | FMR1/CPE | 5 |
| MF | GO:00313C translation 5/781 | 23/16969 | 0.003434 | 0.04218 | 0.035303 | FMR1/EIF5 | 5 |
| MF | GO:000392 GTPase act 20/781 | 224/16969 | 0.003618 | 0.043707 | 0.036581 | RAP2B/ARI | 20 |
| MF | GO:000202 protease b 13/781 | 121/16969 | 0.003785 | 0.044998 | 0.037661 | ITGB1/RIO1 | 13 |
| MF | GO:003107 heat shock 12/781 | 108/16969 | 0.004034 | 0.047187 | 0.039494 | STIP1/ZFP3 | 12 |