

| PathwayName | PathwayID | Patient 1 | Patient 2 | Patient 3 | Parent PathwayID | Parent Pathway in PathwayID | Child PathwayID | Child Pathway in PathwayID | Parent or Child Pathway in PathwayID | Parent or Child Pathway in PathwayID Unique | Path Length | Lowest Level Pathway | Mean Pathway Score | Median Pathway Score | Patient 1 Uniprot List | Patient 1 Gene List | Patient 1 Targetome | Patient 2 Uniprot List | Patient 2 Gene List | Patient 2 Targetome | Patient 2 Uniprot List | Patient 3 Gene List | Patient 3 Targetome | |
|---|---------------|-----------|-----------|-----------|------------------|-----------------------------|-----------------|----------------------------|--------------------------------------|---|-------------|----------------------|--------------------|----------------------|-----------------------------|--|---------------------|------------------------|---|---------------------|------------------------------------|---|---|----|
| Acetylation | R-HSA-156582 | NA | NA | 1 | R-HSA-156580 | FALSE | NA | FALSE | FALSE | FALSE | 2 | TRUE | 1 | 1 | NA | NA | NA | NA | NA | NA | P18440 | NAT1,AAC1 | NA | |
| Butyrophilin (BTN) family interactions | R-HSA-8851680 | 1 | NA | NA | R-HSA-1280218 | FALSE | NA | FALSE | FALSE | FALSE | 12 | TRUE | 1.41666667 | 1 | Q8WVV5 | BTN2A2,BT2.2,BTF2 | NA | NA | NA | NA | NA | NA | NA | |
| Carboxyterminal post-translational modifications of tubulin | R-HSA-8955332 | 2 | 1 | 1 | R-HSA-597592 | FALSE | NA | FALSE | FALSE | FALSE | 38 | TRUE | 2.71052632 | 1 | Q3ZCM7,Q8NHH1 | TUBB8,TTL11,C9orf20 | NA | Q8IUZ0 | LRRRC49 | NA | Q5VU57 | AGBL4,CCP6 | NA | |
| Cellular hexose transport | R-HSA-189200 | NA | 1 | 3 | R-HSA-425407 | FALSE | NA | FALSE | FALSE | FALSE | 22 | TRUE | 1.86363636 | 1 | NA | NA | NA | A0PIK1 | SLC5A10,SGLT5 | NA | P11168,P14672,Q9NY64 | SLC2A2,GLUT2,SLC2A4, GLUT4,SLC2A8, GLUT8, GLUTX1 | NA | |
| Chondroitin sulfate biosynthesis | R-HSA-2022870 | 1 | NA | NA | R-HSA-1793185 | FALSE | NA | FALSE | FALSE | FALSE | 20 | TRUE | 5 | 1 | Q8N6G5 | CSGALNACT2,CHGN2, GALNACT2,PRO0082 | NA | NA | NA | NA | NA | NA | NA | |
| Cytosolic iron-sulfur cluster assembly | R-HSA-2564830 | NA | NA | 2 | R-HSA-1430728 | FALSE | NA | FALSE | FALSE | FALSE | 13 | TRUE | 6.15384615 | 1 | NA | NA | NA | NA | NA | NA | P18074,P53384 | ERCC2,XPDP,XPDC,NUBP1,NBP,NBP1 | NA | |
| Cytosolic sulfonation of small molecules | R-HSA-156584 | NA | NA | 1 | R-HSA-156580 | FALSE | R-HSA-174362 | FALSE | FALSE | FALSE | 24 | TRUE | 1.875 | 1 | NA | NA | NA | NA | NA | NA | O43704 | SULT1B1,ST1B2,SULT1B2 | NA | |
| Estrogen biosynthesis | R-HSA-193144 | 1 | NA | 1 | R-HSA-196071 | FALSE | NA | FALSE | FALSE | FALSE | 6 | TRUE | 1.83333333 | 1 | P11511 | CYP19A1,ARO1,CYAR,CYP19 | NA | NA | NA | NA | C9JRZ8 | AKR1B15 | NA | |
| Gap junction assembly | R-HSA-190861 | 1 | NA | 2 | R-HSA-190828 | FALSE | R-HSA-190827 | FALSE | FALSE | FALSE | 19 | TRUE | 1.78947368 | 1 | Q3ZCM7 | TUBB8 | NA | NA | NA | NA | NA | P36383,Q8N144 | GJC1,GJA7,GJD3,GJA11 | NA |
| Gap junction assembly | R-HSA-190861 | 1 | NA | 2 | R-HSA-190828 | FALSE | R-HSA-190704 | FALSE | FALSE | FALSE | 19 | TRUE | 1.78947368 | 1 | Q3ZCM7 | TUBB8 | NA | NA | NA | NA | NA | P36383,Q8N144 | GJC1,GJA7,GJD3,GJA11 | NA |
| Gap junction assembly | R-HSA-190861 | 1 | NA | 2 | R-HSA-190828 | FALSE | R-HSA-190872 | FALSE | FALSE | FALSE | 19 | TRUE | 1.78947368 | 1 | Q3ZCM7 | TUBB8 | NA | NA | NA | NA | NA | P36383,Q8N144 | GJC1,GJA7,GJD3,GJA11 | NA |
| Glucuronidation | R-HSA-156588 | 1 | NA | NA | R-HSA-156580 | FALSE | R-HSA-173599 | FALSE | FALSE | FALSE | 24 | TRUE | 1.41666667 | 1 | P35504 | UGT1A5,GNT1,UGT1 | NA | NA | NA | NA | NA | NA | NA | NA |
| HCN channels | R-HSA-1296061 | NA | NA | 1 | R-HSA-1296071 | FALSE | NA | FALSE | FALSE | FALSE | 4 | TRUE | 1 | 1 | NA | NA | NA | NA | NA | NA | NA | Q9Y3Q4 | HCN4 | NA |
| IL-6-type cytokine receptor ligand interactions | R-HSA-6788467 | 1 | NA | NA | R-HSA-6783589 | FALSE | NA | FALSE | FALSE | FALSE | 17 | TRUE | 6 | 1 | P42702 | FALSE | LIFR | NA | NA | NA | NA | NA | NA | NA |
| Interaction With The Zona Pellucida | R-HSA-1300644 | 1 | NA | 1 | R-HSA-1187000 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 1.7 | 1 | Q9UKF2 | ADAM30,UNQ2509/PRO5997 | NA | NA | NA | NA | NA | Q9UKJ8 | ADAM21 | NA |
| Intracellular oxygen transport | R-HSA-8981607 | NA | NA | 1 | R-HSA-382551 | FALSE | NA | FALSE | FALSE | FALSE | 3 | TRUE | 1.33333333 | 1 | NA | NA | NA | NA | NA | NA | NA | Q9NPG2 | NGB | NA |
| Keratinization | R-HSA-6805567 | 4 | 1 | 5 | R-HSA-1266738 | FALSE | R-HSA-6809371 | TRUE | TRUE | TRUE | 217 | TRUE | 1.60829493 | 1 | O43790,Q86Y46,Q99456,Q99959 | KRT86,KRTHB6,KRT73,K6IRS3,KB36,KRT6IRS3,KRT12,PKP2 | NA | Q9BYQ5 | KRTAP4-6,KAP4.15,KRTAP4-15,KRTAP4.15,KRTAP4.6 | NA | P19013,P78386,Q02487,Q86Y46,Q99569 | KRT4,CYK4,KRT85,KRTHB5,DS2,CDHF2,DS3,KRT73,K6IRS3,KB36,KRT6RS3,PKP4 | NA | |
| Miscellaneous transport and binding events | R-HSA-5223345 | NA | NA | 1 | R-HSA-382551 | FALSE | NA | FALSE | FALSE | FALSE | 24 | TRUE | 1.375 | 1 | NA | NA | NA | NA | NA | NA | NA | Q7RTP0 | NIPAI1,SPG6 | NA |
| Mitochondrial rRNA aminoacylation | R-HSA-379726 | 2 | 1 | NA | R-HSA-379724 | FALSE | NA | FALSE | FALSE | FALSE | 21 | TRUE | 1.28571429 | 1 | Q5JPH6,Q96GW9 | EARS2,KIAA1970,MARS2 | NA | Q9NP81 | SARS2,SARSM | NA | NA | NA | NA | NA |
| Neurexins and neuroligins | R-HSA-6794361 | 4 | NA | 3 | R-HSA-6794362 | FALSE | NA | FALSE | FALSE | FALSE | 57 | TRUE | 3.66666667 | 1 | Q15700,Q6XYQ8,Q9HD85,Q9Y4CD | DLG2,SYT10,NRXN3,KIAA0743,C14orf60 | NA | NA | NA | NA | NA | O14490,Q12879,Q9N5CS | DLGAP1,DAP1,GKAP,GRIIN2A,NMDAR2A,HOMER3 | NA |
| Phenylalanine and tyrosine catabolism | R-HSA-71182 | NA | NA | 1 | R-HSA-6788656 | FALSE | NA | FALSE | FALSE | FALSE | 11 | TRUE | 1.45454545 | 1 | NA | NA | NA | NA | NA | NA | NA | Q16773 | KYAT1,CCBL1 | NA |
| Post-translational modification: synthesis of GPI-anchored proteins | R-HSA-163125 | NA | NA | 1 | R-HSA-597592 | FALSE | R-HSA-162710 | TRUE | TRUE | TRUE | 94 | TRUE | 1.60638298 | 1 | NA | NA | NA | NA | NA | NA | NA | O95867 | LY6G6C,C6orf24,G6C,NG24,UNQ1947/PRO4430 | NA |
| Post-translational modification: synthesis of GPI-anchored proteins | R-HSA-163125 | NA | NA | 1 | R-HSA-597592 | FALSE | R-HSA-162791 | FALSE | FALSE | TRUE | 94 | TRUE | 1.60638298 | 1 | NA | NA | NA | NA | NA | NA | NA | O95867 | LY6G6C,C6orf24,G6C,NG24,UNQ1947/PRO4430 | NA |
| Post-translational modification: synthesis of GPI-anchored proteins | R-HSA-163125 | NA | NA | 1 | R-HSA-597592 | FALSE | R-HSA-162699 | FALSE | FALSE | TRUE | 94 | TRUE | 1.60638298 | 1 | NA | NA | NA | NA | NA | NA | NA | O95867 | LY6G6C,C6orf24,G6C,NG24,UNQ1947/PRO4430 | NA |
| PTK6 Regulates Proteins Involved in RNA Processing | R-HSA-8849468 | NA | NA | 1 | R-HSA-8848021 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 3.6 | 1 | NA | NA | NA | NA | NA | NA | NA | O75525 | KHDRBS3,SALP,SLM2 | NA |

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|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|-----|--|---|-------|--------|-------------|----|--|--|---|----|
| Purine salvage | R-HSA-74217 | 1 | NA | 1 | R-HSA-8956321 | FALSE | NA | FALSE | FALSE | FALSE | 13 | TRUE | 1.53846154 | 1 | P23109 | AMPD1 | NA | NA | NA | NA | Q6DHV7 | ADAL | NA | |
| SDK interactions | R-HSA-373756 | NA | NA | 1 | R-HSA-421270 | FALSE | NA | FALSE | FALSE | FALSE | 2 | TRUE | 1 | 1 | NA | NA | NA | NA | NA | NA | Q58EX2 | SDK2,KIAA1514 | NA | |
| Sphingolipid de novo biosynthesis | R-HSA-1660661 | 1 | NA | NA | R-HSA-428157 | FALSE | NA | FALSE | FALSE | FALSE | 44 | TRUE | 1.34090909 | 1 | P48448 | ALDH3B2,ALDH8 | NA | NA | NA | NA | NA | NA | NA | |
| Striated Muscle Contraction | R-HSA-390522 | NA | NA | 2 | R-HSA-397014 | FALSE | NA | FALSE | FALSE | FALSE | 34 | TRUE | 1.70588235 | 1 | NA | NA | NA | NA | NA | NA | P35609,Q00872 | ACTN2,MYBPC1,MYBPC5 | NA | |
| Synthesis of pyrophosphates in the cytosol | R-HSA-1855167 | NA | NA | 1 | R-HSA-1483249 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 1.4 | 1 | NA | NA | NA | NA | NA | NA | Q13572 | ITPK1 | NA | |
| TET1,2,3 and TDG demethylate DNA | R-HSA-5221030 | NA | NA | 2 | R-HSA-212165 | FALSE | NA | FALSE | FALSE | FALSE | 4 | TRUE | 2.25 | 1 | NA | NA | NA | NA | NA | NA | Q13569,Q6N021 | TDG,TET2,KIAA1546,Nbl a00191 | NA | |
| tRNA modification in the nucleus and cytosol | R-HSA-6782315 | 2 | NA | NA | R-HSA-72306 | FALSE | R-HSA-6782861 | FALSE | FALSE | FALSE | 43 | TRUE | 1.34883721 | 1 | Q7Z6V5,Q8YL2 | ADAT2,DEADCI,TRMT44,C4orf23,METT119 | NA | NA | NA | NA | NA | NA | NA | |
| Tryptophan catabolism | R-HSA-71240 | NA | NA | 2 | R-HSA-6788656 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 1.92857143 | 1 | NA | NA | NA | NA | NA | NA | P48775,Q16773 | TDO2,TDO,KYAT1,CCBL1 | NA | |
| Vitamin B1 (thiamin) metabolism | R-HSA-196819 | NA | NA | 1 | R-HSA-196849 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 1 | 1 | NA | NA | NA | NA | NA | NA | Q9B2V2 | SLC19A3 | NA | |
| Voltage gated Potassium channels | R-HSA-1296072 | 2 | NA | 5 | R-HSA-1296071 | FALSE | NA | FALSE | FALSE | FALSE | 43 | TRUE | 1.53488372 | 1 | O43525,P22459 | KCNQ3,KCNA4,KCNA4L | NA | NA | NA | NA | NA | O95259,Q8NCM2,Q8TDN1,Q9H3M0,Q9NR82 | KCNH1,EAG,EAG1,KCNH5,EAG2,KCNG4,KCNG3,KCNF1,KCNQ5 | NA |
| Choline catabolism | R-HSA-6798163 | 2 | NA | NA | R-HSA-71291 | FALSE | NA | FALSE | FALSE | FALSE | 6 | TRUE | 1.83333333 | 1.5 | O8NE62,Q8WW15 | CHDH,SLC44A1,CD92,CDW92,CTL1 | NA | NA | NA | NA | NA | NA | NA | |
| LGI-ADAM interactions | R-HSA-5682910 | 1 | NA | 1 | R-HSA-1266738 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 4.28571429 | 1.5 | Q8N145 | LGI3,LGIL4,UNQ8190/PRO23199 | NA | NA | NA | NA | NA | Q9P0K1 | ADAM22,MDC2 | NA |
| Receptor-type tyrosine-protein phosphatases | R-HSA-388844 | 1 | NA | 2 | R-HSA-6794362 | FALSE | NA | FALSE | FALSE | FALSE | 20 | TRUE | 3.15 | 1.5 | P23468 | PTPRD | NA | NA | NA | NA | NA | O94991,P23468 | SLITRKS,KIAA0918,LRRC11,PTPRD | NA |
| Signaling by Hippo | R-HSA-2028269 | NA | NA | 2 | R-HSA-162582 | FALSE | NA | FALSE | FALSE | FALSE | 20 | TRUE | 6 | 1.5 | NA | NA | NA | NA | NA | NA | NA | O14641,Q9Y214 | DVL2,AMOTL2,KIAA0989 | NA |
| ABC transporters in lipid homeostasis | R-HSA-1369062 | 1 | NA | NA | R-HSA-382556 | TRUE | NA | FALSE | TRUE | TRUE | 18 | TRUE | 3.27777778 | 2 | Q8IU47 | ABCA9 | NA | NA | NA | NA | NA | NA | NA | |
| Adherens junctions interactions | R-HSA-418990 | 3 | NA | 2 | R-HSA-421270 | FALSE | R-HSA-420597 | FALSE | FALSE | FALSE | 31 | TRUE | 3.03225806 | 2 | P55285,Q12864,Q86UP0 | CDH6,CDH17,CDH24,CDH11L,UNQ2834/PRO34009 | NA | NA | NA | NA | NA | Q9ULB4,Q9ULB5 | CDH9,CDH7,CDH7L1 | NA |
| Amino acid synthesis and interconversion (transamination) | R-HSA-70614 | NA | NA | 3 | R-HSA-71291 | FALSE | R-HSA-977347 | FALSE | FALSE | FALSE | 34 | TRUE | 2 | 2 | NA | NA | NA | NA | NA | NA | NA | P49448,Q16773,Q9Y3Q0 | GLUD2,GLUDP1,KYAT1,CBLL1,NAALAD2 | NA |
| Antigen processing: Ubiquitination & Proteasome degradation | R-HSA-983168 | 7 | 1 | 9 | R-HSA-983169 | FALSE | NA | FALSE | FALSE | FALSE | 309 | TRUE | 17.4854369 | 2 | A6NK59,Q60291,P25786,P51868,Q5GLZ8,Q8UWE0,Q9Y297 | ASB14,MGRN1,KIAA0544,RNF156,PSMA1,HC2,N U,PROS30,PS2,UBE2D1,SFT,UBCSA,UBCH5,UBC5A,HERC4,KIAA1593,LR SAM1,TAL,UNQ6496/PRO21356,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | Q9UJX4 | ANAPCS,APCS | NA | P61289,Q13200,Q14669,Q7267,Q8JVV7,Q8TB1,Q96PUS,Q9H765,Q9UH77 | PSME3,PSMD2,TRAP2,TRIP12,KIAA0045,ULF,HUWE1,KIAA0312,KIAA1578,UBE1,KIAA0312,KIAA1578,UBR1,LNX1,LNX,PDZRN2,UNQ574/PRO1136,NEDD4L,KIAA0439,NEDL3,ASB8,PP14212,KLHL3,KIAA1129 | PSMD2 | |
| BBSome-mediated cargo-targeting to cilium | R-HSA-5620922 | NA | NA | 1 | R-HSA-5620920 | FALSE | NA | FALSE | FALSE | FALSE | 23 | TRUE | 4.08695652 | 2 | NA | NA | NA | NA | NA | NA | NA | P50991 | CCT4,CCTD,SRB | NA |
| Cation-coupled Chloride cotransporters | R-HSA-426117 | NA | NA | 1 | R-HSA-425393 | TRUE | NA | FALSE | TRUE | TRUE | 7 | TRUE | 2 | 2 | NA | NA | NA | NA | NA | NA | NA | Q13621 | SLC12A1,NKCC2 | NA |
| Cell-extracellular matrix interactions | R-HSA-446353 | 1 | NA | NA | R-HSA-446728 | FALSE | R-HSA-446388 | FALSE | FALSE | FALSE | 16 | TRUE | 4.375 | 2 | Q14315 | FLNC,ABPL,FLN2 | NA | NA | NA | NA | NA | NA | NA | |
| Cell-extracellular matrix interactions | R-HSA-446353 | 1 | NA | NA | R-HSA-446728 | FALSE | R-HSA-446343 | FALSE | FALSE | FALSE | 16 | TRUE | 4.375 | 2 | Q14315 | FLNC,ABPL,FLN2 | NA | NA | NA | NA | NA | NA | NA | |
| Citric acid cycle (TCA cycle) | R-HSA-71403 | 1 | NA | NA | R-HSA-71406 | FALSE | NA | FALSE | FALSE | FALSE | 22 | TRUE | 1.90909091 | 2 | P50213 | IDH3A | NA | NA | NA | NA | NA | NA | NA | |
| Class C/3 (Metabotropic glutamate/phero mone receptors) | R-HSA-420499 | NA | 1 | 1 | R-HSA-500792 | FALSE | NA | FALSE | FALSE | FALSE | 40 | TRUE | 2.325 | 2 | NA | NA | NA | Q9NYW7 | TAS2R1 | NA | Q14831 | GRM7,GPRC1G,MGLUR7 | NA | |
| Coenzyme A biosynthesis | R-HSA-196783 | NA | NA | 1 | R-HSA-199220 | TRUE | NA | FALSE | TRUE | TRUE | 8 | TRUE | 2 | 2 | NA | NA | NA | NA | NA | NA | NA | Q9NVE7 | PANK4 | NA |

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|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|---|------------------------------------|--|----|--------|-----------------------------|---|---|--|----|
| Complex I biogenesis | R-HSA-6799198 | NA | NA | 2 | R-HSA-611105 | TRUE | NA | FALSE | TRUE | TRUE | 55 | TRUE | 2.47272727 | 2 | NA | NA | NA | NA | NA | Q16718,Q9Y6M9 | NDUF5A,NDUF9,LYRM3,UQROR22 | NA | |
| Conjugation of benzoate with glycine | R-HSA-177135 | NA | 1 | NA | R-HSA-159424 | FALSE | NA | FALSE | FALSE | FALSE | 6 | TRUE | 2.16666667 | 2 | NA | NA | NA | Q6IB77 | GLYAT,ACGNAT,CAT,GAT | NA | NA | NA | |
| Conjugation of salicylate with glycine | R-HSA-177128 | NA | 1 | NA | R-HSA-159424 | FALSE | NA | FALSE | FALSE | FALSE | 8 | TRUE | 1.75 | 2 | NA | NA | NA | Q6IB77 | GLYAT,ACGNAT,CAT,GAT | NA | NA | NA | |
| Creatine metabolism | R-HSA-71288 | 1 | NA | NA | R-HSA-351202 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 3.6 | 2 | P50440 | GATM,AGAT | NA | NA | NA | NA | NA | NA | |
| Cristae formation | R-HSA-8949613 | NA | 1 | NA | R-HSA-1592230 | FALSE | NA | FALSE | FALSE | FALSE | 31 | TRUE | 2.16129032 | 2 | NA | NA | NA | P38646 | HSPA9,GRP75,HSPA9B,mt-HSP70 | NA | NA | NA | |
| Digestion | R-HSA-8935690 | NA | NA | 1 | R-HSA-8963743 | FALSE | R-HSA-192456 | FALSE | FALSE | TRUE | 22 | TRUE | 2.22727273 | 2 | NA | NA | NA | NA | NA | NA | O00625 | PIR | NA |
| Digestion | R-HSA-8935690 | NA | NA | 1 | R-HSA-8963743 | FALSE | R-HSA-189085 | TRUE | TRUE | TRUE | 22 | TRUE | 2.22727273 | 2 | NA | NA | NA | NA | NA | NA | O00625 | PIR | NA |
| Digestion of dietary carbohydrate | R-HSA-189085 | NA | NA | 1 | R-HSA-8935690 | TRUE | NA | FALSE | TRUE | TRUE | 10 | TRUE | 2.2 | 2 | NA | NA | NA | NA | NA | NA | P14410 | SI | NA |
| Electric Transmission Across Gap Junctions | R-HSA-112303 | NA | NA | 1 | R-HSA-112307 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 1.8 | 2 | NA | NA | NA | NA | NA | NA | P36383 | GJC1,GJA7 | NA |
| Fatty acyl-CoA biosynthesis | R-HSA-75105 | NA | NA | 1 | R-HSA-8978868 | FALSE | R-HSA-75876 | TRUE | TRUE | TRUE | 37 | TRUE | 2.59459459 | 2 | NA | NA | NA | NA | NA | NA | P49327 | FASN,FAS | NA |
| Formation of the cornified envelope | R-HSA-6809371 | 5 | NA | 6 | R-HSA-6805567 | TRUE | NA | FALSE | TRUE | TRUE | 75 | TRUE | 2.74666667 | 2 | O43790,P22735,Q86Y46,Q99456,Q99959 | KRT86,KRTHB6,TGM1,KTG,KRT73,KGIR53,KB36,KRT6IR53,KRT12,PKP2 | NA | NA | NA | P19013,P78386,Q02487,Q5W064,Q86Y46,Q99569 | KRT4,CYK4,KRT85,KRTHB5,D5C2,CDHF2,D5C3,LIPI,LIPL1,KRT73,KGIR53,KB36,KRT6IR53,PKP4 | NA | |
| Formation of the Edosome | R-HSA-75094 | NA | NA | 1 | R-HSA-72200 | TRUE | NA | FALSE | TRUE | TRUE | 8 | TRUE | 2 | 2 | NA | NA | NA | NA | NA | NA | Q9NQ94 | A1CF,ACF,ASP | NA |
| Fructose catabolism | R-HSA-70350 | NA | NA | 2 | R-HSA-5652084 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 2.4 | 2 | NA | NA | NA | NA | NA | NA | P05062,P5053 | ALDOB,ALDB,KHK | NA |
| G alpha (s) signalling events | R-HSA-418555 | 3 | 1 | 5 | R-HSA-388396 | FALSE | R-HSA-381753 | FALSE | FALSE | FALSE | 575 | TRUE | 3.70086957 | 2 | P12272,P23945,P34947 | PTHLH,PTHRP,FSHR,LGR1,GRK5,GPRK5 | NA | Q08462 | ADCY2,KIAA1060 | NA | P27815,P35626,Q08493,Q96R18,Q9Y233 | PDE4A,DPDE2,GRK3,ADRBK2,BARK2,PDE4C,DPD1,TAAR6,TA4,TAR4,TRAR4,PDE10A | NA |
| Gluconeogenesis | R-HSA-70263 | 2 | NA | 1 | R-HSA-70326 | FALSE | NA | FALSE | FALSE | FALSE | 34 | TRUE | 2.32352941 | 2 | P07205,P35558 | PGK2,PGKB,PKC1,PEPK1 | NA | NA | NA | NA | P05062 | ALDOB,ALDB | NA |
| Glycerophospholipid catabolism | R-HSA-6814848 | 1 | NA | NA | R-HSA-1483255 | TRUE | NA | FALSE | TRUE | TRUE | 7 | TRUE | 2 | 2 | Q6UWR7 | ENPP6,UNQ1889/PRO4334 | NA | NA | NA | NA | NA | NA | NA |
| Glycogen breakdown (glycogenolysis) | R-HSA-70221 | NA | NA | 1 | R-HSA-8982491 | FALSE | NA | FALSE | FALSE | FALSE | 16 | TRUE | 6 | 2 | NA | NA | NA | NA | NA | NA | P06737 | PYGL | NA |
| Glyoxylate metabolism and glycine degradation | R-HSA-389661 | NA | NA | 1 | R-HSA-71291 | FALSE | R-HSA-6783984 | FALSE | FALSE | FALSE | 31 | TRUE | 2.5483871 | 2 | NA | NA | NA | NA | NA | NA | Q9NR77 | PXMP2,PMP22 | NA |
| HDMs demethylate histones | R-HSA-3214842 | 4 | NA | 1 | R-HSA-3247509 | TRUE | NA | FALSE | TRUE | TRUE | 27 | TRUE | 6.7037037 | 2 | O94953,P62805,Q6ZMT4,Q9UGL1 | KDM4B,JHDM3B,JMJD2B,KIAA0876,HIST1H4A,H4A/H4FA,HIST1H4B,H4I/H4FI,HIST1H4C,H4G/H4FG,HIST1H4D,H4B/H4FB,HIST1H4E,H4J/H4FJ,HIST1H4F,H4C/H4FC,HIST1H4H,H4/H4HF,HIST1H4I,H4M/H4FM,HIST1H4J,H4E/H4FE,HIST1H4K,H4D/H4FD,HIST1H4L,H4K/H4FK,HIST2H4A,H4/N,H4F2,H4FN,HIST2H4,HIST2H4B,H4/O,H4FO,HIST4H4,KDM7A,JHDM1D,KDM7,KIAA1718,KDMSB,JARID1B,PLU1,RBBP2H1 | NA | NA | NA | NA | Q6NYC1 | JMID6,KIAA0585,PTDSR | NA |
| Heme degradation | R-HSA-189483 | NA | NA | 1 | R-HSA-189445 | FALSE | NA | FALSE | FALSE | FALSE | 6 | TRUE | 2 | 2 | NA | NA | NA | NA | NA | NA | P53004 | BLVRA,BLVR,BVR | NA |
| Hyaluronan uptake and degradation | R-HSA-2160916 | NA | NA | 1 | R-HSA-2142845 | FALSE | NA | FALSE | FALSE | FALSE | 12 | TRUE | 2.83333333 | 2 | NA | NA | NA | NA | NA | NA | Q12891 | HYAL2,LUCA2 | NA |
| Intraflagellar transport | R-HSA-5620924 | 2 | NA | NA | R-HSA-5617833 | TRUE | NA | FALSE | TRUE | TRUE | 41 | TRUE | 3.65853659 | 2 | Q86WT1,Q96RY7 | TT3C0A,IFT140,KIAA0590,WDT2C2 | NA | NA | NA | NA | NA | NA | NA |
| Metabolism of Angiotensinogen to Angiotensins | R-HSA-2022377 | 1 | NA | 1 | R-HSA-2980736 | FALSE | NA | FALSE | FALSE | FALSE | 17 | TRUE | 3.05882353 | 2 | P15088 | CPA3 | NA | NA | NA | NA | P15088 | CPA3 | NA |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|---|---|---|-------|--------|-----------------------------|--------|--|---|-------|----|
| Mitochondrial calcium ion transport | R-HSA-8949215 | NA | NA | 1 | R-HSA-382551 | FALSE | R-HSA-8949664 | TRUE | TRUE | TRUE | 23 | TRUE | 2.60869565 | 2 | NA | NA | NA | NA | NA | P57103 | SLC8A3,NCX3 | NA | | |
| Mitochondrial protein import | R-HSA-1268020 | NA | 1 | 1 | R-HSA-9609507 | FALSE | NA | FALSE | FALSE | FALSE | 65 | TRUE | 1.92307692 | 2 | NA | NA | NA | P38646 | HSPA9,GRP75,HSPA9B,mt-HSP70 | NA | P62072 | TIMM10,TIM10 | NA | |
| mRNA Editing: C to U Conversion | R-HSA-72200 | NA | NA | 1 | R-HSA-75072 | FALSE | R-HSA-75094 | TRUE | TRUE | TRUE | 8 | TRUE | 2 | 2 | NA | NA | NA | NA | NA | NA | Q9NQ94 | A1CF,ACF,ASP | NA | |
| Neddylation | R-HSA-8951664 | 8 | 1 | 7 | R-HSA-597592 | FALSE | NA | FALSE | FALSE | FALSE | 235 | TRUE | 21.3276596 | 2 | A6NK59,P25786,P51668,Q13619,Q5TAQ9,Q968M1,Q9P000,Q9Y297 | ASB14,PSMA1,HC2,NU,P,ROS30,PS2,U,BE2D1,SFT,UBCSA,UBCH5,UBCH5A,CUL4A,DCAF8,H326,WDR42A,ANKRD9,COMMD9,HSPC166,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | Q8N5D0 | WDTC1,KIAA1037 | NA | Q94888,P61289,Q13200,Q92905,Q9H765,Q9NZ10,Q9UH77 | UBXN7,KIAA0794,UBXD7,PSME3,PSMD2,TRAP2,COP55,CSN5,JAB1,ASB8,PP14212,DTL,CDT2,CDW1,DCAF2,L2DTL,RAMP,KLHL3,KIAA1129 | PSMD2 | |
| Nicotinamide salvaging | R-HSA-197264 | NA | NA | 2 | R-HSA-196807 | FALSE | NA | FALSE | FALSE | FALSE | 19 | TRUE | 4 | 2 | NA | NA | NA | NA | NA | NA | Q460N5,Q6XQN6 | PARP14,BAL2,KIAA1268,NAPRT,FHIP,NAPRT1 | NA | |
| Organic anion transport | R-HSA-561048 | 1 | NA | NA | R-HSA-549132 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 2 | 2 | Q9NSA0 | SLC22A11,OA4 | NA | NA | NA | NA | NA | NA | NA | |
| Passive transport by Aquaporins | R-HSA-432047 | NA | NA | 1 | R-HSA-445717 | FALSE | NA | FALSE | FALSE | FALSE | 13 | TRUE | 1.69230769 | 2 | NA | NA | NA | NA | NA | NA | P55087 | AQP4 | NA | |
| Phase 4 - resting membrane potential | R-HSA-5576886 | NA | NA | 1 | R-HSA-5576891 | FALSE | NA | FALSE | FALSE | FALSE | 19 | TRUE | 2.63157895 | 2 | NA | NA | NA | NA | NA | NA | Q96T54 | KCNK17,TALK2,TASK4,U,NC5816/PRO19634 | NA | |
| PIWI-interacting RNA (piRNA) biogenesis | R-HSA-5601884 | NA | NA | 2 | R-HSA-211000 | FALSE | NA | FALSE | FALSE | FALSE | 29 | TRUE | 23.1034483 | 2 | NA | NA | NA | NA | NA | NA | O60522,Q9BXT6 | TDRD6,MOV10L1 | NA | |
| Processing of SMDT1 | R-HSA-8949664 | NA | NA | 2 | R-HSA-8949215 | TRUE | NA | FALSE | TRUE | TRUE | 16 | TRUE | 2.4375 | 2 | NA | NA | NA | NA | NA | NA | Q9U9Q0,Q9Y4W6 | SPG7,CAR,CMAR,PGN,A,FG3L2 | NA | |
| Protein methylation | R-HSA-8876725 | NA | NA | 1 | R-HSA-597592 | FALSE | NA | FALSE | FALSE | FALSE | 17 | TRUE | 8.17647059 | 2 | NA | NA | NA | NA | NA | NA | P55072 | VCP | NA | |
| RAB geranylgeranylation | R-HSA-8873719 | NA | NA | 2 | R-HSA-597592 | FALSE | NA | FALSE | FALSE | FALSE | 65 | TRUE | 3.09230769 | 2 | NA | NA | NA | NA | NA | NA | P20336,Q14964 | RAB3A,RAB39A,RAB39 | NA | |
| Regulation of gene expression in endocrine-committed (NEUROG3+) progenitor cells | R-HSA-210746 | NA | NA | 1 | R-HSA-186712 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 1.6 | 2 | NA | NA | NA | NA | NA | NA | Q01101 | INSM1,IA1 | NA | |
| Respiratory electron transport | R-HSA-611105 | NA | NA | 4 | R-HSA-163200 | FALSE | R-HSA-6799198 | TRUE | TRUE | TRUE | 101 | TRUE | 2.51485149 | 2 | NA | NA | NA | NA | NA | NA | Q16718,Q8N8Q8,Q9B5H4,Q9Y6M9 | NDUFA5,COX18,OXAL12,TACO1,CCDC4,PROD477,NDUFB9,LYRM3,UQQR22 | NA | |
| Retrograde transport at the Trans-Golgi-Network | R-HSA-6811440 | NA | NA | 4 | R-HSA-6811442 | FALSE | NA | FALSE | FALSE | FALSE | 49 | TRUE | 3.14285714 | 2 | NA | NA | NA | NA | NA | NA | P11717,Q14746,Q8N1B4,Q92738 | IGF2R,MPRI,COG2,LDLC,VPS52,SACM2L,USP6NL,KIAA0019 | NA | |
| rRNA modification in the nucleus and cytosol | R-HSA-6790901 | NA | NA | 5 | R-HSA-8868773 | FALSE | NA | FALSE | FALSE | FALSE | 62 | TRUE | 3.61290323 | 2 | NA | NA | NA | NA | NA | NA | O75691,P46781,Q12788,Q9H0A0,Q9Y2X3 | UTP20,DRIM,RP59,TBL3,SAZD,NAT10,ALP,KIAA1709,NOP58,NOL5,NOPS,HSPC120 | NA | |
| Small interfering RNA (siRNA) biogenesis | R-HSA-426486 | NA | NA | 1 | R-HSA-211000 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 9.22222222 | 2 | NA | NA | NA | NA | NA | NA | Q9UPY3 | DICER1,DICER,HERNA,KIAA0928 | NA | |
| Smooth Muscle Contraction | R-HSA-445355 | 1 | NA | NA | R-HSA-397014 | FALSE | NA | FALSE | FALSE | FALSE | 35 | TRUE | 6.71428571 | 2 | Q15746 | MYLK,MLCK,MLCK1,MYLK1 | MYLK | NA | NA | NA | NA | NA | NA | NA |
| Stimuli-sensing channels | R-HSA-2672351 | 3 | NA | 5 | R-HSA-983712 | FALSE | R-HSA-3295583 | TRUE | TRUE | TRUE | 102 | TRUE | 11.372549 | 2 | P51793,P51798,Q9BYP7 | CLCN4,CLCN7,WNK3,KIAA1566,PRKWNK3 | NA | NA | NA | NA | P51798,Q13061,Q4KMQ2,Q96PU5,Q9Y3S1 | CLCN7,TRDN,ANO6,TMEM16F,NEED4L,KIAA0439,NEDL3,WNK2,KIAA1760,PRKWNK2,SDCCAG43,POKcl.13 | NA | |
| Synthesis of glycosylphosphatidylinositol (GPI) | R-HSA-162710 | NA | NA | 1 | R-HSA-163125 | TRUE | NA | FALSE | TRUE | TRUE | 18 | TRUE | 2.16666667 | 2 | NA | NA | NA | NA | NA | NA | Q9H3S5 | PIGM | NA | |
| Synthesis of very long-chain fatty acyl-CoAs | R-HSA-75876 | NA | NA | 1 | R-HSA-75105 | TRUE | NA | FALSE | TRUE | TRUE | 24 | TRUE | 2.75 | 2 | NA | NA | NA | NA | NA | NA | Q96GR2 | ACSBG1,BGM,KIAA0631,LPD | NA | |
| TBC/RABGAPs | R-HSA-8854214 | 1 | NA | 1 | R-HSA-9007101 | FALSE | NA | FALSE | FALSE | FALSE | 45 | TRUE | 3.06666667 | 2 | P49815 | TSC2,TSC4 | NA | NA | NA | NA | Q8IV04 | TBC1D10C | NA | |
| Terminal pathway of complement | R-HSA-166665 | NA | NA | 1 | R-HSA-166658 | FALSE | NA | FALSE | FALSE | FALSE | 8 | TRUE | 2.875 | 2 | NA | NA | NA | NA | NA | NA | P10643 | C7 | NA | |
| The fatty acid cycling model | R-HSA-167826 | 1 | NA | NA | R-HSA-166187 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 2 | 2 | P55916 | UCP3,SLC25A9 | NA | NA | NA | NA | NA | NA | NA | |
| The proton buffering model | R-HSA-167827 | 1 | NA | NA | R-HSA-166187 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 2 | 2 | P55916 | UCP3,SLC25A9 | NA | NA | NA | NA | NA | NA | NA | |

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|--|---------------|----|----|----|---------------|-------|--------------|-------|-------|-------|-----|------|------------|---|---------------|--|----|----|----|----|--------|--|----|
| TNFs bind their physiological receptors | R-HSA-5669034 | 1 | NA | 1 | R-HSA-5668541 | TRUE | NA | FALSE | TRUE | TRUE | 29 | TRUE | 2.5862069 | 2 | Q07011 | TNFRSF9,CD137,IL1A | NA | NA | NA | NA | Q9Y275 | TNFSF13B,BAFF,BLYS,TALL1,TNFSF20,ZTNF4,UNQ401/PRO738 | NA |
| Transport of fatty acids | R-HSA-804914 | 1 | NA | NA | R-HSA-425397 | FALSE | NA | FALSE | FALSE | FALSE | 8 | TRUE | 2.25 | 2 | Q6P1M0 | SLC27A4,ACSVL4,FATP4 | NA | NA | NA | NA | NA | NA | |
| Transport of inorganic cations/anions and amino acids/oligopeptides | R-HSA-425393 | NA | NA | 1 | R-HSA-425407 | FALSE | R-HSA-427652 | FALSE | FALSE | TRUE | 106 | TRUE | 3.40566038 | 2 | NA | NA | NA | NA | NA | NA | O00341 | SLC1A7,EAAT5 | NA |
| Transport of inorganic cations/anions and amino acids/oligopeptides | R-HSA-425393 | NA | NA | 1 | R-HSA-425407 | FALSE | R-HSA-427975 | FALSE | FALSE | TRUE | 106 | TRUE | 3.40566038 | 2 | NA | NA | NA | NA | NA | NA | O00341 | SLC1A7,EAAT5 | NA |
| Transport of inorganic cations/anions and amino acids/oligopeptides | R-HSA-425393 | NA | NA | 1 | R-HSA-425407 | FALSE | R-HSA-427601 | FALSE | FALSE | TRUE | 106 | TRUE | 3.40566038 | 2 | NA | NA | NA | NA | NA | NA | O00341 | SLC1A7,EAAT5 | NA |
| Transport of inorganic cations/anions and amino acids/oligopeptides | R-HSA-425393 | NA | NA | 1 | R-HSA-425407 | FALSE | R-HSA-425986 | FALSE | FALSE | TRUE | 106 | TRUE | 3.40566038 | 2 | NA | NA | NA | NA | NA | NA | O00341 | SLC1A7,EAAT5 | NA |
| Transport of inorganic cations/anions and amino acids/oligopeptides | R-HSA-425393 | NA | NA | 1 | R-HSA-425407 | FALSE | R-HSA-428643 | FALSE | FALSE | TRUE | 106 | TRUE | 3.40566038 | 2 | NA | NA | NA | NA | NA | NA | O00341 | SLC1A7,EAAT5 | NA |
| Transport of inorganic cations/anions and amino acids/oligopeptides | R-HSA-425393 | NA | NA | 1 | R-HSA-425407 | FALSE | R-HSA-425381 | FALSE | FALSE | TRUE | 106 | TRUE | 3.40566038 | 2 | NA | NA | NA | NA | NA | NA | O00341 | SLC1A7,EAAT5 | NA |
| Transport of inorganic cations/anions and amino acids/oligopeptides | R-HSA-425393 | NA | NA | 1 | R-HSA-425407 | FALSE | R-HSA-352230 | TRUE | TRUE | TRUE | 106 | TRUE | 3.40566038 | 2 | NA | NA | NA | NA | NA | NA | O00341 | SLC1A7,EAAT5 | NA |
| Transport of inorganic cations/anions and amino acids/oligopeptides | R-HSA-425393 | NA | NA | 1 | R-HSA-425407 | FALSE | R-HSA-428559 | FALSE | FALSE | TRUE | 106 | TRUE | 3.40566038 | 2 | NA | NA | NA | NA | NA | NA | O00341 | SLC1A7,EAAT5 | NA |
| Transport of inorganic cations/anions and amino acids/oligopeptides | R-HSA-425393 | NA | NA | 1 | R-HSA-425407 | FALSE | R-HSA-425561 | TRUE | TRUE | TRUE | 106 | TRUE | 3.40566038 | 2 | NA | NA | NA | NA | NA | NA | O00341 | SLC1A7,EAAT5 | NA |
| Transport of inorganic cations/anions and amino acids/oligopeptides | R-HSA-425393 | NA | NA | 1 | R-HSA-425407 | FALSE | R-HSA-426117 | TRUE | TRUE | TRUE | 106 | TRUE | 3.40566038 | 2 | NA | NA | NA | NA | NA | NA | O00341 | SLC1A7,EAAT5 | NA |
| Transport of nucleosides and free purine and pyrimidine bases across the plasma membrane | R-HSA-83936 | NA | NA | 1 | R-HSA-425397 | FALSE | NA | FALSE | FALSE | FALSE | 7 | TRUE | 2 | 2 | NA | NA | NA | NA | NA | NA | Q99808 | SLC29A1,ENT1 | NA |
| Triglyceride biosynthesis | R-HSA-75109 | 2 | NA | NA | R-HSA-8979227 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 3.14285714 | 2 | Q6ZNB7,Q86VF5 | AGMO,TMEM195,MOGAT3,DC7,DGAT2L7,UNQ9383/PRO34208 | NA | NA | NA | NA | NA | NA | NA |
| Triglyceride catabolism | R-HSA-163560 | 2 | NA | NA | R-HSA-8979227 | FALSE | NA | FALSE | FALSE | FALSE | 24 | TRUE | 7.66666667 | 2 | P22612,P41247 | PRKACG,PNPLA4,DXS1283E,GS2 | NA | NA | NA | NA | NA | NA | NA |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|----|------|------------|-----|---------------|---|----|--------|--|----|---|--|--|----|
| tRNA modification in the mitochondrion | R-HSA-6787450 | NA | NA | 1 | R-HSA-72306 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 2 | 2 | NA | NA | NA | NA | NA | NA | Q9Y222 | MT01,CGI-02 | NA | |
| TWIK-related alkaline pH activated K+ channel (TALK) | R-HSA-1299361 | NA | NA | 1 | R-HSA-1296346 | FALSE | NA | FALSE | FALSE | FALSE | 2 | TRUE | 2 | 2 | NA | NA | NA | NA | NA | NA | Q96T54 | KCNK17,TALK2,TASK4,U NQ5816/PRO19634 | NA | |
| Urea cycle | R-HSA-70635 | NA | NA | 1 | R-HSA-351202 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 2.2 | 2 | NA | NA | NA | NA | NA | NA | P31327 | CPS1 | NA | |
| Vitamin B5 (pantothenate) metabolism | R-HSA-199220 | 1 | NA | 1 | R-HSA-196849 | FALSE | R-HSA-196783 | TRUE | TRUE | TRUE | 17 | TRUE | 2.52941176 | 2 | Q13822 | ENPP2,ATX,PDNP2 | NA | NA | NA | NA | P49327 | FASN,FAS | NA | |
| Caspase activation via Dependence Receptors in the absence of ligand | R-HSA-418889 | 1 | NA | NA | R-HSA-5357769 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 4.4 | 2.5 | P43146 | DCC,IGDCC1 | NA | NA | NA | NA | NA | NA | NA | |
| Ethanol oxidation | R-HSA-71384 | 1 | NA | 1 | R-HSA-211945 | TRUE | NA | FALSE | TRUE | TRUE | 12 | TRUE | 3.16666667 | 2.5 | P07327 | ADH1A,ADH1 | NA | NA | NA | NA | P08319 | ADH4 | NA | |
| Interleukin-20 family signaling | R-HSA-8854691 | 1 | NA | NA | R-HSA-449147 | FALSE | NA | FALSE | FALSE | FALSE | 26 | TRUE | 10.8076923 | 2.5 | P42229 | STAT5A,STAT5 | NA | NA | NA | NA | NA | NA | NA | |
| Intestinal hexose absorption | R-HSA-8981373 | NA | NA | 1 | R-HSA-8963676 | FALSE | NA | FALSE | FALSE | FALSE | 4 | TRUE | 3 | 2.5 | NA | NA | NA | NA | NA | NA | P11168 | SLC2A2,GLUT2 | NA | |
| Transport of organic anions | R-HSA-879518 | NA | NA | 2 | R-HSA-425397 | FALSE | NA | FALSE | FALSE | FALSE | 12 | TRUE | 4.08333333 | 2.5 | NA | NA | NA | NA | NA | NA | Q9NYB5,Q9Y616 | SLC01C1,OATP14,OATP1C1,OATPF,SLC21A14,SLC01B1,LST1,OATP1B1,OATP2,OATPC,SLC21A6 | NA | |
| Abacavir metabolism | R-HSA-2161541 | 2 | NA | 1 | R-HSA-2161522 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 3 | 3 | P07327,P35558 | ADH1A,ADH1,PKC1,PEPC K1 | NA | NA | NA | NA | Q6DHV7 | ADAL | NA | |
| Activation of Ca-permeable Kainate Receptor | R-HSA-451308 | NA | NA | 1 | R-HSA-451306 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 11.1 | 3 | NA | NA | NA | NA | NA | NA | P39086 | GRIK1,GLUR5 | NA | |
| Activation of Na-permeable kainate receptors | R-HSA-451307 | NA | NA | 1 | R-HSA-451306 | FALSE | NA | FALSE | FALSE | FALSE | 2 | TRUE | 3 | 3 | NA | NA | NA | NA | NA | NA | P39086 | GRIK1,GLUR5 | NA | |
| Aflatoxin activation and detoxification | R-HSA-5423646 | NA | 1 | NA | R-HSA-211859 | FALSE | NA | FALSE | FALSE | FALSE | 20 | TRUE | 3.5 | 3 | NA | NA | NA | P16444 | DPEP1,MDP,RDP | NA | NA | NA | NA | |
| Amino acid transport across the plasma membrane | R-HSA-352230 | NA | NA | 2 | R-HSA-425393 | TRUE | NA | FALSE | TRUE | TRUE | 33 | TRUE | 3.3030303 | 3 | NA | NA | NA | NA | NA | NA | Q96916,Q99624 | SLC38A4,ATA3,NAT3,SNAT4,SLC38A3,G17,NAT1,SN1,SNAT3 | NA | |
| Antimicrobial peptides | R-HSA-6803157 | 2 | NA | 4 | R-HSA-168249 | FALSE | R-HSA-6803544 | FALSE | FALSE | FALSE | 95 | TRUE | 3.36842105 | 3 | P17213,Q06141 | BPI,REG3A,HIP,PAP,PAP1 | NA | NA | NA | NA | NA | P04279,P17213,Q6UW15,Q8TDL5 | SEMG1,SEMG,BPI,REG3G,PAP1B,UNQ429/PRO162,BPFB1,C2orf114,LP LUNCI,UNQ706/PRO1357 | NA |
| Antimicrobial peptides | R-HSA-6803157 | 2 | NA | 4 | R-HSA-168249 | FALSE | R-HSA-1461973 | FALSE | FALSE | FALSE | 95 | TRUE | 3.36842105 | 3 | P17213,Q06141 | BPI,REG3A,HIP,PAP,PAP1 | NA | NA | NA | NA | NA | P04279,P17213,Q6UW15,Q8TDL5 | SEMG1,SEMG,BPI,REG3G,PAP1B,UNQ429/PRO162,BPFB1,C2orf114,LP LUNCI,UNQ706/PRO1357 | NA |
| Antimicrobial peptides | R-HSA-6803157 | 2 | NA | 4 | R-HSA-168249 | FALSE | R-HSA-6799990 | FALSE | FALSE | FALSE | 95 | TRUE | 3.36842105 | 3 | P17213,Q06141 | BPI,REG3A,HIP,PAP,PAP1 | NA | NA | NA | NA | NA | P04279,P17213,Q6UW15,Q8TDL5 | SEMG1,SEMG,BPI,REG3G,PAP1B,UNQ429/PRO162,BPFB1,C2orf114,LP LUNCI,UNQ706/PRO1357 | NA |
| Association of Tric/CCT with target proteins during biosynthesis | R-HSA-390471 | 1 | 1 | 4 | R-HSA-390466 | FALSE | NA | FALSE | FALSE | FALSE | 39 | TRUE | 6.35897436 | 3 | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | P04637,P50991,Q92526,Q99832 | TP53,P53,CCT4,CCTD,SRB,CCT6B,CCT7,CCTH,NIP7-1 | NA | |
| Biotin transport and metabolism | R-HSA-196780 | NA | NA | 1 | R-HSA-196849 | FALSE | NA | FALSE | FALSE | FALSE | 11 | TRUE | 3.72727273 | 3 | NA | NA | NA | NA | NA | NA | O00763 | ACACB,ACC2,ACCB | NA | |
| CDO in myogenesis | R-HSA-375170 | 1 | NA | 1 | R-HSA-525793 | FALSE | NA | FALSE | FALSE | FALSE | 29 | TRUE | 8.31034483 | 3 | Q4KMG0 | CDON,CDO | NA | NA | NA | NA | P15923 | TCF3,BHLHE21,E2A,ITF1 | NA | |
| Deadenylation of mRNA | R-HSA-429947 | 2 | 1 | 2 | R-HSA-429914 | FALSE | NA | FALSE | FALSE | FALSE | 25 | TRUE | 4.72 | 3 | O75175,P38919 | CNOT3,KIAA0691,LENG2,NOT3,EIF4A3,DDX48,KIAA0111 | NA | Q92600 | CNOT9,RC01,RQCD1 | NA | A5YK6,Q95628 | CNOT1,CDC39,KIAA1007,NOT1,AD005,CNOT4,NOT4 | NA | |
| Defective B3GALT1 causes Peters-plus syndrome (Pp5) | R-HSA-5083635 | 2 | 1 | 6 | R-HSA-3906995 | FALSE | NA | FALSE | FALSE | FALSE | 37 | TRUE | 3.86486486 | 3 | P82987,Q8T60 | ADAMTSL3,KIAA1233,ADAMTSL18,ADAMTSL21 | NA | Q9P2N4 | ADAMTSL3,KIAA1233,ADAMTSL1,ADAMTSL1,C9orf94,UNQ528/PRO1071,THSD7B,KIAA1679,ADAMTSL9,KIAA1312,ADAMTSL7,ADAMTSL6 | NA | P82987,Q8N666,Q9C014,Q9P2N4,Q9UKP4,Q9UKP5 | ADAMTSL3,KIAA1233,ADAMTSL1,ADAMTSL1,C9orf94,UNQ528/PRO1071,THSD7B,KIAA1679,ADAMTSL9,KIAA1312,ADAMTSL7,ADAMTSL6 | NA | |
| Dissolution of Fibrin Clot | R-HSA-75205 | NA | NA | 1 | R-HSA-109582 | FALSE | NA | FALSE | FALSE | FALSE | 13 | TRUE | 3.53846154 | 3 | NA | NA | NA | NA | NA | NA | P07093 | SERPINE2,P17,PN1 | NA | |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|---|---------------|---------------------------------|----|--------|----------|----|-----------------------------|---|-------|
| Effects of PIP2 hydrolysis | R-HSA-114508 | 1 | NA | 4 | R-HSA-416476 | TRUE | R-HSA-426048 | FALSE | TRUE | TRUE | 27 | TRUE | 7.11111111 | 3 | Q14643 | ITPR1,INSP3R1 | NA | NA | NA | NA | Q04759,Q13507,Q9Y210,Q9Y6T7 | PRKCO,PRKCT,TRPC3,TRP3,TRPC6,TRP6,DGKB,DAGK2,KIAA0718 | PRKCO |
| Effects of PIP2 hydrolysis | R-HSA-114508 | 1 | NA | 4 | R-HSA-76002 | FALSE | R-HSA-426048 | FALSE | FALSE | TRUE | 27 | TRUE | 7.11111111 | 3 | Q14643 | ITPR1,INSP3R1 | NA | NA | NA | NA | Q04759,Q13507,Q9Y210,Q9Y6T7 | PRKCO,PRKCT,TRPC3,TRP3,TRPC6,TRP6,DGKB,DAGK2,KIAA0718 | PRKCO |
| Fanconi Anemia Pathway | R-HSA-6783310 | 1 | 1 | 2 | R-HSA-73894 | FALSE | NA | FALSE | FALSE | FALSE | 38 | TRUE | 26.4473684 | 3 | Q8IYD8 | FANCM,KIAA1596 | NA | Q13535 | ATR,FRP1 | NA | Q0VGD6,Q8WXE1 | FAAP100,C17orf70,ATRI P,AGS1 | NA |
| GABA A receptor activation | R-HSA-977441 | 1 | NA | 2 | R-HSA-977443 | TRUE | NA | FALSE | TRUE | TRUE | 13 | TRUE | 3.23076923 | 3 | P47870 | GABRB2 | NA | NA | NA | NA | P14867,P47869 | GABRA1,GABRA2 | NA |
| Gamma carboxylation, hypusine formation and arylsulfatase activation | R-HSA-163841 | 1 | NA | NA | R-HSA-597592 | FALSE | R-HSA-204626 | FALSE | FALSE | TRUE | 39 | TRUE | 4.33333333 | 3 | Q9HA64 | FN3KRP | NA | NA | NA | NA | NA | NA | NA |
| Gamma carboxylation, hypusine formation and arylsulfatase activation | R-HSA-163841 | 1 | NA | NA | R-HSA-597592 | FALSE | R-HSA-5358493 | FALSE | FALSE | TRUE | 39 | TRUE | 4.33333333 | 3 | Q9HA64 | FN3KRP | NA | NA | NA | NA | NA | NA | NA |
| Gamma carboxylation, hypusine formation and arylsulfatase activation | R-HSA-163841 | 1 | NA | NA | R-HSA-597592 | FALSE | R-HSA-159854 | FALSE | FALSE | TRUE | 39 | TRUE | 4.33333333 | 3 | Q9HA64 | FN3KRP | NA | NA | NA | NA | NA | NA | NA |
| Gamma carboxylation, hypusine formation and arylsulfatase activation | R-HSA-163841 | 1 | NA | NA | R-HSA-597592 | FALSE | R-HSA-1663150 | TRUE | TRUE | TRUE | 39 | TRUE | 4.33333333 | 3 | Q9HA64 | FN3KRP | NA | NA | NA | NA | NA | NA | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1483213 | FALSE | FALSE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1482798 | FALSE | FALSE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1483076 | FALSE | FALSE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1483171 | FALSE | FALSE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1483101 | FALSE | FALSE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1483191 | TRUE | TRUE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1482788 | FALSE | FALSE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1482883 | FALSE | FALSE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1483152 | FALSE | FALSE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1482801 | TRUE | TRUE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1482839 | FALSE | FALSE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1483115 | FALSE | FALSE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1483148 | FALSE | FALSE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1483196 | FALSE | FALSE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1482925 | FALSE | FALSE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1483166 | TRUE | TRUE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1483226 | FALSE | FALSE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycerophospholipid biosynthesis | R-HSA-1483206 | NA | NA | 1 | R-HSA-1483257 | FALSE | R-HSA-1482922 | FALSE | FALSE | TRUE | 129 | TRUE | 3.88372093 | 3 | NA | NA | NA | NA | NA | NA | O75131 | CPNE3,CPN3,KIAA0636 | NA |
| Glycosphingolipid metabolism | R-HSA-1660662 | 2 | NA | 2 | R-HSA-428157 | FALSE | NA | FALSE | FALSE | FALSE | 46 | TRUE | 2.67391304 | 3 | P15848,Q9BSJ8 | ARSB,ESYT1,FAM62A,KIAA0747,MBC2 | NA | NA | NA | NA | Q00973,Q96G1 | B4GALNT1,GALGT,SIAT2,ARSG,KIAA1001,UNQ839/PRO1777 | NA |

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|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|----|------|------------|---|--|--|------|---------------|--------------------------------|------|---|---|-------|----|
| Highly calcium permeable nicotinic acetylcholine receptors | R-HSA-629597 | 1 | NA | 1 | R-HSA-622323 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 3.55555556 | 3 | P17787 | CHRN2 | NA | NA | NA | NA | Q05901 | CHRN3 | NA | |
| Highly calcium permeable postsynaptic nicotinic acetylcholine receptors | R-HSA-629594 | 1 | NA | 1 | R-HSA-622327 | FALSE | NA | FALSE | FALSE | FALSE | 11 | TRUE | 3.27272727 | 3 | P17787 | CHRN2 | NA | NA | NA | NA | Q05901 | CHRN3 | NA | |
| Hormone ligand-binding receptors | R-HSA-375281 | 1 | NA | NA | R-HSA-373076 | FALSE | NA | FALSE | FALSE | FALSE | 13 | TRUE | 4.76923077 | 3 | P23945 | F5HR,LGR1 | NA | NA | NA | NA | NA | NA | NA | |
| HuR (ELAVL1) binds and stabilizes mRNA | R-HSA-450520 | NA | NA | 1 | R-HSA-450531 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 11.6 | 3 | NA | NA | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 | NA | |
| Hydroxycarboxylic acid-binding receptors | R-HSA-3296197 | NA | 1 | NA | R-HSA-373076 | FALSE | NA | FALSE | FALSE | FALSE | 3 | TRUE | 3 | 3 | NA | NA | NA | Q98XC0 | HCAR1,GPR104,GPR81,HCA1,FKSG80 | NA | NA | NA | NA | |
| Inactivation, recovery and regulation of the phototransduction cascade | R-HSA-2514859 | 1 | 1 | 3 | R-HSA-2514856 | FALSE | NA | FALSE | FALSE | FALSE | 33 | TRUE | 8.6969697 | 3 | Q15835 | GRK1,RHOK | GRK1 | Q15835 | GRK1,RHOK | GRK1 | P50579,Q02846,Q04759 | METAP2,MNPEP,P67EIF2,GUCY2D,CORD6,GUC1A4,GUC2D,RETGC,RETGC1,PRKCQ,PRKCT | PRKCQ | |
| Interaction between L1 and Ankyrins | R-HSA-445095 | 6 | 2 | 7 | R-HSA-373760 | TRUE | NA | FALSE | TRUE | TRUE | 29 | TRUE | 4.68965517 | 3 | O43525,P32004,P35498,P35499,Q0118,Q15858 | KCNQ3,L1CAM,CAML1,MIC5,SCN1A,NAC1,SCN15,SCN4A,SCN7A,SCN6A,SCN9A,NENA | NA | Q9NY46,Q9YSY9 | SCN3A,KIAA1356,NAC3,SCN10A | NA | O15020,P16157,P35498,P35499,Q0118,Q9UI33,Q9UQD0 | SPTBN2,KIAA0302,SCA5,ANK1,ANK,SCN1A,NAC1,SCN1,SCN4A,SCN7A,SCN6A,SCN11A,SCN12A,SCNS2,SCN8A,MED | NA | NA |
| Interferon alpha/beta signaling | R-HSA-909733 | 1 | NA | 1 | R-HSA-913531 | FALSE | R-HSA-912694 | FALSE | FALSE | FALSE | 69 | TRUE | 7.26086957 | 3 | P09913 | IFIT2,CIG-42,G10P2,IFIS4,ISG54 | NA | NA | NA | NA | P01891,P01892,P04439,P05534,P10314,P13746,P16188,P16189,P16190,P18462,P30443,P30447,P30450,P30453,P30455,P30456,P30457,P30459,P30512,Q09160 | HLA-A,HLAA | NA | |
| Ion transport by P-type ATPases | R-HSA-936837 | 3 | NA | 1 | R-HSA-983712 | FALSE | NA | FALSE | FALSE | FALSE | 55 | TRUE | 5.25454545 | 3 | O14983,P16615,Q8TF62 | ATP2A1,ATP2A2,ATP2B,ATP8B4,KIAA1939 | NA | NA | NA | NA | P54707 | ATP12A,ATP1AL1 | NA | |
| Lectin pathway of complement activation | R-HSA-166662 | NA | NA | 1 | R-HSA-166786 | FALSE | R-HSA-2855086 | FALSE | FALSE | FALSE | 8 | TRUE | 3 | 3 | NA | NA | NA | NA | NA | NA | Q9BWP8 | COLEC11,UNQ596/PRO1182 | NA | |
| Lysophingolipid and LPA receptors | R-HSA-419408 | NA | NA | 1 | R-HSA-373076 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 3 | 3 | NA | NA | NA | NA | NA | NA | Q9H1C0 | LPAR5,GPR92,GPR93 | NA | |
| Metal ion SLC transporters | R-HSA-425410 | NA | NA | 1 | R-HSA-425366 | TRUE | R-HSA-435354 | FALSE | TRUE | TRUE | 26 | TRUE | 3.19230769 | 3 | NA | NA | NA | NA | NA | NA | Q9BQ57 | HEPH,KIAA0698,UNQ2562/PRO6242 | NA | |
| Misspliced LRP5 mutants have enhanced beta-catenin-dependent signaling | R-HSA-5339717 | NA | NA | 1 | R-HSA-4791275 | FALSE | NA | FALSE | FALSE | FALSE | 6 | TRUE | 3.83333333 | 3 | NA | NA | NA | NA | NA | NA | Q8NCW0 | KREMEN2,KRM2 | NA | |
| Mitochondrial translation elongation | R-HSA-5389840 | 3 | NA | 1 | R-HSA-5368287 | FALSE | NA | FALSE | FALSE | FALSE | 91 | TRUE | 3.12087912 | 3 | Q5T653,Q9BZE1,Q9NWT8 | MRPL2,CGI-22,MRPL37,RPML2,HSPC235,AURKAIP1,AIP,AKIP,MRPS38 | NA | NA | NA | NA | P49406 | MRPL19,KIAA0104,MRPL15 | NA | |
| Mitochondrial translation initiation | R-HSA-5368286 | 3 | NA | 1 | R-HSA-5368287 | FALSE | NA | FALSE | FALSE | FALSE | 91 | TRUE | 3.12087912 | 3 | Q5T653,Q9BZE1,Q9NWT8 | MRPL2,CGI-22,MRPL37,RPML2,HSPC235,AURKAIP1,AIP,AKIP,MRPS38 | NA | NA | NA | NA | P49406 | MRPL19,KIAA0104,MRPL15 | NA | |
| Mitochondrial translation termination | R-HSA-5419276 | 3 | NA | 2 | R-HSA-5368287 | FALSE | NA | FALSE | FALSE | FALSE | 91 | TRUE | 3.12087912 | 3 | Q5T653,Q9BZE1,Q9NWT8 | MRPL2,CGI-22,MRPL37,RPML2,HSPC235,AURKAIP1,AIP,AKIP,MRPS38 | NA | NA | NA | NA | P49406,Q9UGC7 | MRPL19,KIAA0104,MRPL15,MTRF1L,MTRF1A | NA | |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|---|--|--|-----|------------------------------|--|----|---|--|--------------|
| mRNA Splicing - Major Pathway | R-HSA-72163 | 5 | 1 | 8 | R-HSA-72172 | FALSE | NA | FALSE | FALSE | FALSE | 180 | TRUE | 7.69444444 | 3 | O75533,P38919,Q00839,Q15366,Q86XP3 | SF3B1,SAP155,EIF4A3,DX48,KIAA0111,HNRNP U,C1orf139,HNRPU,SAFA,U21.1,PCBP2,DDX42 | NA | Q9UNP9 | PPIE,CYP33 | NA | O75643,P52756,Q05519,Q10570,Q8N684,Q99459,Q9UHX1,Q9UKF6 | SNRNP200,ASCC3L1,HELIC2,KIAA0788,RBM5,H37LUCAL5,SRSF11,SFRS11,CPSF1,CPSF160,CPSF7,CDCS1,KIAA0432,PCDC5,RP,PUF60,FIR,ROBPSIAHBP1,CPSF3,CPSF73 | NA |
| Negative regulation of TGF-dependent signaling by WNT ligand antagonists | R-HSA-3772470 | NA | NA | 1 | R-HSA-201681 | TRUE | NA | FALSE | TRUE | TRUE | 15 | TRUE | 4.2 | 3 | NA | NA | NA | NA | NA | NA | Q8NCW0 | KREMEN2,KRM2 | NA |
| Neutrophil degranulation | R-HSA-6798695 | 11 | 4 | 24 | R-HSA-168249 | FALSE | NA | FALSE | FALSE | FALSE | 479 | TRUE | 7.11273486 | 3 | O00391,O94973,P09769,P15848,P17213,P51575,Q6ZNI1,Q8TF62,Q92608,Q9P000,Q9Y336 | QSOX1,QSCN6,UNQ2520/PRO6013,AP2A2,ADT AB,CLAPA2,HIP9,HPY, KIAA0899,FGR,SRC2,ARSB ,BPLP2,RX1,P2X1,NBEAL 2,KIAA0540,UNQ253/PRO 290,ATP884,KIAA1939, DOCK2,KIAA0209,COMM D9,HSPC166,SIGLEC9, JNQ668/PRO1302 | FGR | P41218,Q71576,Q9UNP 9,Q9UQ80 | MNDA,CYFIP1,KIAA0068 ,PPIE,CYP33,PA2G4,EBP 1 | NA | O75131,O94804,P01009,P02766,P06396,P06737,P11717,P17213,P17927,P20336,P30453,P30459,P36222,P48960,P55072,Q12913,Q13200,Q14764,Q4KM02,Q6XN6,Q72627,Q8IV04,Q92932,Q99536,Q9BY15 | CPNE3,CPN3,KIAA0636,STK10,LOK,SERPINA1,AA T,PI,PRO0684,PRO2209, TTR,PALB,GSN,PYGL,IGF 2R,MPRI,BPI,CR1,C3BR, RAB3A,HLA-A,HLAA,CHI3L1,CD97,VC P,PTPRJ,DEP1,PSMD2,TR AP2,MVP,LRP,ANO6,TM EM16F,NAPRT,FHIP,NAP RT1,HUWE1,KIAA0312,K IAA1578,UREB1,HSPC27 2,TBC1D10C,PTPRN2,KIA A0387,VAT1,ADGRE3,EMR3,UNQ683/PRO1562 | STK10,PSM D2 |
| NRAGE signals death through JNK | R-HSA-193648 | 1 | NA | 5 | R-HSA-204998 | FALSE | NA | FALSE | FALSE | FALSE | 59 | TRUE | 7.33898305 | 3 | Q92888 | ARHGEF1 | NA | NA | NA | NA | O14827,O15068,Q8TU6,Q92974,Q9NY61 | RASGRF2,GRF2,MCF2L, KIAA0362,OST,PREX1,KI A1415,ARHGFE2,KIAA0 651,LFP40,AATF,CHE1,D ED,HSPC277 | NA |
| O-glycosylation of TSR domain-containing proteins | R-HSA-5173214 | 2 | 1 | 6 | R-HSA-5173105 | TRUE | NA | FALSE | TRUE | TRUE | 39 | TRUE | 3.76923077 | 3 | P82987,Q8T E60 | ADAMTSL3,KIAA1233,ADAMTSL8,ADAMTSL21 | NA | Q9P2N4 | ADAMT59,KIAA1312 | NA | P82987,Q8N666,Q9C014,Q9P2N4,Q9UKP4,Q9UKP5 | ADAMTSL3,KIAA1233,ADAMTSL1,ADAMTSL1,C 9orf94,UNQ528/PRO10 71,THSD7B,KIAA1679,ADAMT59,KIAA1312,ADAMT57,ADAMT56 | NA |
| O-linked glycosylation | R-HSA-5173105 | 1 | NA | 2 | R-HSA-5173105 | FALSE | R-HSA-913709 | TRUE | TRUE | TRUE | 115 | TRUE | 3.88695652 | 3 | Q9Y6A1 | POMT1 | NA | NA | NA | NA | Q14118,Q8WZA1 | DAG1,POMGNT1,MGAT 1.2,UNQ746/PRO1475 | NA |
| O-linked glycosylation | R-HSA-5173105 | 1 | NA | 2 | R-HSA-5173105 | FALSE | R-HSA-5173214 | TRUE | TRUE | TRUE | 115 | TRUE | 3.88695652 | 3 | Q9Y6A1 | POMT1 | NA | NA | NA | NA | Q14118,Q8WZA1 | DAG1,POMGNT1,MGAT 1.2,UNQ746/PRO1475 | NA |
| O-linked glycosylation of mucins | R-HSA-913709 | 1 | NA | 3 | R-HSA-5173105 | TRUE | R-HSA-977068 | FALSE | TRUE | TRUE | 66 | TRUE | 4.25757576 | 3 | Q9Y2A9 | B3GNT3,B3GALT8,TME M3,UNQ637/PRO1266 | NA | NA | NA | NA | Q49A17,Q61524,Q8IXX2 | GALNT6,GALNT17,WB SCR17,GALNT12 | NA |
| OAS antiviral response | R-HSA-8983711 | NA | NA | 1 | R-HSA-1169410 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 3.4 | 3 | NA | NA | NA | NA | NA | NA | O95786 | DDX58 | NA |
| Peroxisomal protein import | R-HSA-9033241 | 2 | NA | 1 | R-HSA-9609507 | FALSE | R-HSA-9033500 | FALSE | FALSE | FALSE | 63 | TRUE | 16.6190476 | 3 | P51668,Q93008 | UBE2D1,SFT,UBCSA,UB CH5,UBCH5A,USP9X,DFFRX,FAM,USP9 | NA | NA | NA | NA | Q93008 | USP9X,DFFRX,FAM,USP 9 | NA |
| Phase 0 - rapid depolarisation | R-HSA-5576892 | 5 | 2 | 7 | R-HSA-5576891 | FALSE | NA | FALSE | FALSE | FALSE | 44 | TRUE | 5.97727273 | 3 | P35498,P35499,Q01118,Q13936,Q15858 | SCN1A,NAC1,SCN1,SCN 4A,SCN7A,SCN6A,CACN A1C,CACH2,CACN2,CACN L1A1,CCHL1A1,SCN9A, NENA | NA | Q9NY46,Q9YSY9 | SCN3A,KIAA1356,NAC3, SCN10A | NA | P35498,P35499,P61328,Q01118,Q01668,Q9UI3 3,Q9UQD0 | SCN1A,NAC1,SCN1,SCN 4A,FGF12,FGF12B,FHF1 ,SCN7A,SCN6A,CACN11 D,CACH3,CACN4,CACNL1 A2,CCHL1A2,SCN11A,SC N12A,SNS2,SCN8A,MEC | NA |
| Phase 2 - plateau phase | R-HSA-5576893 | 1 | NA | 1 | R-HSA-5576891 | FALSE | NA | FALSE | FALSE | FALSE | 27 | TRUE | 4.25925926 | 3 | Q13936 | CACNA1C,CACH2,CACN2, CACNL1A1,CCHL1A1 | NA | NA | NA | NA | Q01668 | CACNA10,CACH3,CACN4 ,CACNL1A2,CCHL1A2 | NA |
| Pyruvate metabolism | R-HSA-70268 | 1 | NA | NA | R-HSA-71406 | FALSE | R-HSA-204174 | FALSE | FALSE | FALSE | 31 | TRUE | 3.87096774 | 3 | P00338 | LDHA,PIG19 | NA | NA | NA | NA | NA | NA | NA |
| RAB GEFs exchange GTP for GDP on RABs | R-HSA-8876198 | 3 | 1 | 5 | R-HSA-9007101 | FALSE | NA | FALSE | FALSE | FALSE | 90 | TRUE | 4.28888889 | 3 | P48553,Q9H 2M9,Q9Y24 3 | TRAPP10,EHOC1,TME M1,RAB3GAP2,KIAA083 9,AKT3,PKBG | NA | O95248 | SBF1,MTMR5 | NA | P20336,P31751,Q14964,Q8IV53,Q9 6Q42 | RAB3A,AKT2,RAB39A, RAB39, DENND1C, FAM31 C,ALS2,ALS2CR6,KIAA15 63 | AKT2 |
| Recycling of bile acids and salts | R-HSA-159418 | 1 | NA | 1 | R-HSA-194068 | FALSE | NA | FALSE | FALSE | FALSE | 16 | TRUE | 7.375 | 3 | O95342 | ABC11,BSEP | NA | NA | NA | NA | Q9Y6L6 | SLCO1B1,SLT1,OATP1B1 ,OATP2,OATPC,SLC21A6 | NA |
| Reelin signalling pathway | R-HSA-8866376 | NA | NA | 1 | R-HSA-422475 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 11.4 | 3 | NA | NA | NA | NA | NA | NA | P78509 | RELN | NA |

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|--|---------------|----|----|----|---------------|-------|--------------|-------|-------|-------|-----|------|------------|---|---|--|----|---------------|---------------------------|----|--|---|---|----|
| Regulation of gene expression in beta cells | R-HSA-210745 | 1 | NA | 4 | R-HSA-186712 | FALSE | R-HSA-211163 | TRUE | TRUE | TRUE | 21 | TRUE | 8.52380952 | 3 | P20823 | HNF1A,TCF1 | NA | NA | NA | NA | P11168,Q14541,Q8HW53,Q9Y261 | SLC2A2,GLUT2,HNF4G,NR2A2,RFX6,RFKXDC1,FOX2,HNF3B,TCF3B | NA | |
| Rho GTPase cycle | R-HSA-194840 | 6 | 1 | 7 | R-HSA-194315 | FALSE | NA | FALSE | FALSE | FALSE | 141 | TRUE | 4.39716312 | 3 | O14559,O94844,P42331,Q14CB8,Q7Z5H3,Q92888 | ARHGAP33,SNX26,TCGA P,RHOBTB1,KIAA0740,ARHGAP25,KIAA0053,ARHGAP19,ARHGAP22,RHOGAP2,ARHGEF1 | NA | Q7Z6B7 | SRGAP1,ARHGAP13,KIAA1304 | NA | O14827,O15068,O43295,Q7Z6B7,Q8IXI2,Q8TCU6,Q92974 | RASGRF2,GRF2,MCF2L,KIAA0362,OST,SRGAP3,ARHGAP14,KIAA0411,KIAA1156,MEGAP,SRGAP2,SRGAP1,ARHGAP13,KIAA1304,RHOT1,ARHT1,PREX1,KIAA1415,ARHGEF2,KIAA0651,LFP40 | NA | |
| RNA polymerase II transcribes snRNA genes | R-HSA-6807505 | NA | NA | 2 | R-HSA-73857 | FALSE | NA | FALSE | FALSE | FALSE | 81 | TRUE | 14.0493827 | 3 | NA | NA | NA | NA | NA | NA | Q96AH0,Q96HW7 | NABP1,OBFC2A,SSB2,INTS4,M5TP093 | NA | |
| Signaling by BMP | R-HSA-201451 | 1 | NA | NA | R-HSA-9006936 | FALSE | NA | FALSE | FALSE | FALSE | 28 | TRUE | 5.39285714 | 3 | P51668 | UBE2D1,SFT,UBCSA,UBCH5,UBCH5A | NA | NA | NA | NA | NA | NA | NA | |
| Synthesis of active ubiquitin: roles of E1 and E2 enzymes | R-HSA-8866652 | 2 | NA | 1 | R-HSA-8852135 | FALSE | NA | FALSE | FALSE | FALSE | 30 | TRUE | 32.0666667 | 3 | P51668,Q93008 | UBE2D1,SFT,UBCSA,UBCH5,UBCH5A,USP9X,DFFRX,FAM,USP9 | NA | NA | NA | NA | NA | Q93008 | USP9X,DFFRX,FAM,USP9 | NA |
| Synthesis of IP2, IP, and Ins in the cytosol | R-HSA-1855183 | NA | NA | 1 | R-HSA-1483249 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 3 | 3 | NA | NA | NA | NA | NA | NA | NA | Q96PE3 | INPP4A | NA |
| Synthesis of PC | R-HSA-1483191 | 2 | NA | 2 | R-HSA-1483206 | TRUE | NA | FALSE | TRUE | TRUE | 28 | TRUE | 4.64285714 | 3 | Q53GD3,Q8WW15 | SLC44A4,C6orf29,CTL4,NG22,TPPT1,UNQ441/PRO874,SLC44A1,CD92,CDW92,CTL1 | NA | NA | NA | NA | NA | P28329,Q8NCS7 | CHAT,SLC44A5,CTL5 | NA |
| Synthesis of PIPs at the ER membrane | R-HSA-1483248 | NA | 1 | NA | R-HSA-1483255 | TRUE | NA | FALSE | TRUE | TRUE | 5 | TRUE | 3.8 | 3 | NA | NA | NA | O95248 | SBF1,MTMR5 | NA | NA | NA | NA | |
| Synthesis of UDP-N-acetylglucosamine | R-HSA-446210 | NA | NA | 1 | R-HSA-446219 | FALSE | NA | FALSE | FALSE | FALSE | 8 | TRUE | 3.25 | 3 | NA | NA | NA | NA | NA | NA | NA | Q9Y303 | AMDHD2,CGI-14 | NA |
| The activation of arylsulfatases | R-HSA-1663150 | 1 | NA | 1 | R-HSA-163841 | TRUE | NA | FALSE | TRUE | TRUE | 13 | TRUE | 3.23076923 | 3 | P15848 | AR5B | NA | NA | NA | NA | NA | Q96EG1 | ARSG,KIAA1001,UNQ839/PRO1777 | NA |
| TNF receptor superfamily (TNFSF) members mediating non-canonical NF-kB pathway | R-HSA-5676594 | NA | NA | 1 | R-HSA-5668541 | TRUE | NA | FALSE | TRUE | TRUE | 17 | TRUE | 5.64705882 | 3 | NA | NA | NA | NA | NA | NA | NA | Q9Y275 | TNFSF13B,BAFF,BLYS,TNFSF13B,BAFF,BLYS,TNFSF20,2TNF4,UNQ401/PRO738 | NA |
| Toxicity of botulinum toxin type A (BoNT/A) | R-HSA-5250968 | NA | NA | 1 | R-HSA-168799 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 3.88888889 | 3 | NA | NA | NA | NA | NA | NA | NA | Q496J9 | SV2C,KIAA1054 | NA |
| TP53 regulates transcription of additional cell cycle genes whose exact role in the p53 pathway remain uncertain | R-HSA-6804115 | 2 | 2 | 3 | R-HSA-6791312 | FALSE | NA | FALSE | FALSE | FALSE | 21 | TRUE | 5.80952381 | 3 | O75175,P04637 | CNOT3,KIAA0691,LENG2,NOT3,TP53,P53 | NA | P04637,Q92600 | TP53,P53,CNOT9,RCD1,RQCD1 | NA | A5YK6,Q95628,P04637 | CNOT1,CDC39,KIAA1007,NOT1,AD005,CNOT4,NOT4,TP53,P53 | NA | |
| Transport of bile salts and organic acids, metal ions and amine compounds | R-HSA-425366 | 3 | NA | 1 | R-HSA-425407 | FALSE | R-HSA-429593 | FALSE | FALSE | TRUE | 86 | TRUE | 3.41860465 | 3 | Q15849,Q53GD3,Q8W15 | SLC14A2,HUT2,UT2,SLC44A4,C6orf29,CTL4,NG22,TPPT1,UNQ441/PRO874,SLC44A1,CD92,CDW92,CTL1 | NA | NA | NA | NA | Q8NCS7 | SLC44A5,CTL5 | NA | |
| Transport of bile salts and organic acids, metal ions and amine compounds | R-HSA-425366 | 3 | NA | 1 | R-HSA-425407 | FALSE | R-HSA-433692 | FALSE | FALSE | TRUE | 86 | TRUE | 3.41860465 | 3 | Q15849,Q53GD3,Q8W15 | SLC14A2,HUT2,UT2,SLC44A4,C6orf29,CTL4,NG22,TPPT1,UNQ441/PRO874,SLC44A1,CD92,CDW92,CTL1 | NA | NA | NA | NA | Q8NCS7 | SLC44A5,CTL5 | NA | |
| Transport of bile salts and organic acids, metal ions and amine compounds | R-HSA-425366 | 3 | NA | 1 | R-HSA-425407 | FALSE | R-HSA-444411 | FALSE | FALSE | TRUE | 86 | TRUE | 3.41860465 | 3 | Q15849,Q53GD3,Q8W15 | SLC14A2,HUT2,UT2,SLC44A4,C6orf29,CTL4,NG22,TPPT1,UNQ441/PRO874,SLC44A1,CD92,CDW92,CTL1 | NA | NA | NA | NA | Q8NCS7 | SLC44A5,CTL5 | NA | |
| Transport of bile salts and organic acids, metal ions and amine compounds | R-HSA-425366 | 3 | NA | 1 | R-HSA-425407 | FALSE | R-HSA-549132 | FALSE | FALSE | TRUE | 86 | TRUE | 3.41860465 | 3 | Q15849,Q53GD3,Q8W15 | SLC14A2,HUT2,UT2,SLC44A4,C6orf29,CTL4,NG22,TPPT1,UNQ441/PRO874,SLC44A1,CD92,CDW92,CTL1 | NA | NA | NA | NA | Q8NCS7 | SLC44A5,CTL5 | NA | |

| | | | | | | | | | | | | | | | | | | | | | | | |
|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|-----|-----------------------|--|----|--------|--------|----|------------------------------------|--|----|
| Transport of bile salts and organic acids, metal ions and amine compounds | R-HSA-425366 | 3 | NA | 1 | R-HSA-425407 | FALSE | R-HSA-433137 | FALSE | FALSE | TRUE | 86 | TRUE | 3.41860465 | 3 | Q15849,Q53GD3,Q8W W15 | SLC14A2,HUT2,UT2,SLC44A4,C6orf29,CT14,NG22,TPPT1,UNQ441/PRO874,SLC44A1,CD92,CDW92,CT11 | NA | NA | NA | NA | Q8NC57 | SLC44A5,CTL5 | NA |
| Transport of bile salts and organic acids, metal ions and amine compounds | R-HSA-425366 | 3 | NA | 1 | R-HSA-425407 | FALSE | R-HSA-425410 | TRUE | TRUE | TRUE | 86 | TRUE | 3.41860465 | 3 | Q15849,Q53GD3,Q8W W15 | SLC14A2,HUT2,UT2,SLC44A4,C6orf29,CT14,NG22,TPPT1,UNQ441/PRO874,SLC44A1,CD92,CDW92,CT11 | NA | NA | NA | NA | Q8NC57 | SLC44A5,CTL5 | NA |
| Transport of bile salts and organic acids, metal ions and amine compounds | R-HSA-425366 | 3 | NA | 1 | R-HSA-425407 | FALSE | R-HSA-442660 | TRUE | TRUE | TRUE | 86 | TRUE | 3.41860465 | 3 | Q15849,Q53GD3,Q8W W15 | SLC14A2,HUT2,UT2,SLC44A4,C6orf29,CT14,NG22,TPPT1,UNQ441/PRO874,SLC44A1,CD92,CDW92,CT11 | NA | NA | NA | NA | Q8NC57 | SLC44A5,CTL5 | NA |
| TRP channels | R-HSA-3295583 | 2 | NA | 5 | R-HSA-2672351 | TRUE | NA | FALSE | TRUE | TRUE | 25 | TRUE | 4.28 | 3 | O75762,Q9UL62 | TRPA1,ANKTM1,TRPC5,TRP5 | NA | NA | NA | NA | Q13507,Q9H1D0,Q9HCF6,Q9UBN4,Q9Y210 | TRPC3,TRP3,TRPV6,ECA2,TRPM3,KIAA1616,LTRPC3,TRPC4,TRPC6,TRP6 | NA |
| XBP1(S) activates chaperone genes | R-HSA-381038 | 1 | NA | 2 | R-HSA-381070 | FALSE | NA | FALSE | FALSE | FALSE | 59 | TRUE | 5.28813559 | 3 | Q9UBS4 | DNAJB11,EDJ,ER13,HDJ9,PSEC0121,UNQ537/PRO1080 | NA | NA | NA | NA | Q93075,Q9H953 | TATDN2,KIAA0218,SECG1A2 | NA |
| Zinc influx into cells by the SLC39 gene family | R-HSA-442380 | NA | NA | 1 | R-HSA-435354 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 3 | 3 | NA | NA | NA | NA | NA | NA | Q15043 | SLC39A14,KIAA0062,ZIP14 | NA |
| ATP sensitive Potassium channels | R-HSA-1296025 | 1 | NA | NA | R-HSA-1296065 | FALSE | NA | FALSE | FALSE | FALSE | 4 | TRUE | 3.5 | 3.5 | O60706 | ABCC9,SUR2 | NA | NA | NA | NA | NA | NA | NA |
| Molecules associated with elastic fibres | R-HSA-2129379 | 2 | 1 | 3 | R-HSA-1566948 | TRUE | NA | FALSE | TRUE | TRUE | 30 | TRUE | 6.6 | 3.5 | P53708,Q8N251 | ITGA8,LTBP4 | NA | P02751 | FN1,FN | NA | P15502,P3555,Q14766 | ELN,FBN1,FBN,LTBP1 | NA |
| Other interleukin signaling | R-HSA-449836 | 1 | NA | 1 | R-HSA-449147 | FALSE | NA | FALSE | FALSE | FALSE | 26 | TRUE | 7.19230769 | 3.5 | P23471 | PTPRZ1,HTFP2P,PTPRZ,P2TPR2,PTPZ | NA | NA | NA | NA | Q15833 | STXBP2,UNC18B | NA |
| Reactions specific to the complex N-glycan synthesis pathway | R-HSA-975578 | NA | NA | 2 | R-HSA-975576 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 5.1 | 3.5 | NA | NA | NA | NA | NA | NA | Q43529,P49641 | CHST10,MAN2A2,MANA2X | NA |
| Toxicity of botulinum toxin type D (BoNT/D) | R-HSA-5250955 | NA | NA | 1 | R-HSA-168799 | FALSE | NA | FALSE | FALSE | FALSE | 6 | TRUE | 6.16666667 | 3.5 | NA | NA | NA | NA | NA | NA | Q496J9 | SV2C,KIAA1054 | NA |
| Toxicity of botulinum toxin type F (BoNT/F) | R-HSA-5250981 | NA | NA | 1 | R-HSA-168799 | FALSE | NA | FALSE | FALSE | FALSE | 6 | TRUE | 6.16666667 | 3.5 | NA | NA | NA | NA | NA | NA | Q496J9 | SV2C,KIAA1054 | NA |
| Amine ligand-binding receptors | R-HSA-375280 | NA | NA | 1 | R-HSA-373076 | FALSE | R-HSA-390650 | FALSE | FALSE | TRUE | 43 | TRUE | 4.46511628 | 4 | NA | NA | NA | NA | NA | NA | Q96R18 | TAAR6,TA4,TAR4,TRAR4 | NA |
| Amine ligand-binding receptors | R-HSA-375280 | NA | NA | 1 | R-HSA-373076 | FALSE | R-HSA-390696 | TRUE | TRUE | TRUE | 43 | TRUE | 4.46511628 | 4 | NA | NA | NA | NA | NA | NA | Q96R18 | TAAR6,TA4,TAR4,TRAR4 | NA |
| Amine ligand-binding receptors | R-HSA-375280 | NA | NA | 1 | R-HSA-373076 | FALSE | R-HSA-390648 | TRUE | TRUE | TRUE | 43 | TRUE | 4.46511628 | 4 | NA | NA | NA | NA | NA | NA | Q96R18 | TAAR6,TA4,TAR4,TRAR4 | NA |
| Amine ligand-binding receptors | R-HSA-375280 | NA | NA | 1 | R-HSA-373076 | FALSE | R-HSA-390651 | FALSE | FALSE | TRUE | 43 | TRUE | 4.46511628 | 4 | NA | NA | NA | NA | NA | NA | Q96R18 | TAAR6,TA4,TAR4,TRAR4 | NA |
| Amine ligand-binding receptors | R-HSA-375280 | NA | NA | 1 | R-HSA-373076 | FALSE | R-HSA-390666 | TRUE | TRUE | TRUE | 43 | TRUE | 4.46511628 | 4 | NA | NA | NA | NA | NA | NA | Q96R18 | TAAR6,TA4,TAR4,TRAR4 | NA |
| Asparagine N-linked glycosylation | R-HSA-446203 | NA | NA | 2 | R-HSA-597592 | FALSE | R-HSA-948021 | FALSE | FALSE | TRUE | 286 | TRUE | 8.28671329 | 4 | NA | NA | NA | NA | NA | NA | P07911,P46977 | UMOD,STT3A,ITM1,TMC | NA |
| Asparagine N-linked glycosylation | R-HSA-446203 | NA | NA | 2 | R-HSA-597592 | FALSE | R-HSA-532668 | TRUE | TRUE | TRUE | 286 | TRUE | 8.28671329 | 4 | NA | NA | NA | NA | NA | NA | P07911,P46977 | UMOD,STT3A,ITM1,TMC | NA |
| Asparagine N-linked glycosylation | R-HSA-446203 | NA | NA | 2 | R-HSA-597592 | FALSE | R-HSA-446193 | FALSE | FALSE | TRUE | 286 | TRUE | 8.28671329 | 4 | NA | NA | NA | NA | NA | NA | P07911,P46977 | UMOD,STT3A,ITM1,TMC | NA |
| cGMP effects | R-HSA-418457 | 1 | NA | 1 | R-HSA-392154 | TRUE | NA | FALSE | TRUE | TRUE | 18 | TRUE | 6.16666667 | 4 | Q14643 | ITPR1,INSP3R1 | NA | NA | NA | NA | Q9Y233 | PDE10A | NA |
| Cholesterol biosynthesis via desmosterol | R-HSA-6807047 | NA | NA | 1 | R-HSA-191273 | FALSE | NA | FALSE | FALSE | FALSE | 4 | TRUE | 4 | 4 | NA | NA | NA | NA | NA | NA | Q75845 | SC5D,SC5DL | NA |
| Cholesterol biosynthesis via lathosterol | R-HSA-6807062 | NA | NA | 1 | R-HSA-191273 | FALSE | NA | FALSE | FALSE | FALSE | 4 | TRUE | 4 | 4 | NA | NA | NA | NA | NA | NA | Q75845 | SC5D,SC5DL | NA |
| Chromatin modifying enzymes | R-HSA-3247509 | NA | NA | 1 | R-HSA-4839726 | FALSE | R-HSA-3214815 | TRUE | TRUE | TRUE | 241 | TRUE | 9.82572614 | 4 | NA | NA | NA | NA | NA | NA | P51532 | SMARCA4,BAF190A,BRG1,SNF2B,SNF2L4 | NA |
| Chromatin modifying enzymes | R-HSA-3247509 | NA | NA | 1 | R-HSA-4839726 | FALSE | R-HSA-3214842 | TRUE | TRUE | TRUE | 241 | TRUE | 9.82572614 | 4 | NA | NA | NA | NA | NA | NA | P51532 | SMARCA4,BAF190A,BRG1,SNF2B,SNF2L4 | NA |

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|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|---|-----------------------------|--|-------|----------------------|--|----|---|---|-----|----|
| Chromatin modifying enzymes | R-HSA-3247509 | NA | NA | 1 | R-HSA-4839726 | FALSE | R-HSA-3214847 | TRUE | TRUE | TRUE | 241 | TRUE | 9.82572614 | 4 | NA | NA | NA | NA | NA | NA | P51532 | SMARCA4,BAF190A,BR G1,SNF2B,SNF2L4 | NA | |
| Chromatin modifying enzymes | R-HSA-3247509 | NA | NA | 1 | R-HSA-4839726 | FALSE | R-HSA-3214841 | TRUE | TRUE | TRUE | 241 | TRUE | 9.82572614 | 4 | NA | NA | NA | NA | NA | NA | P51532 | SMARCA4,BAF190A,BR G1,SNF2B,SNF2L4 | NA | |
| Chromatin modifying enzymes | R-HSA-3247509 | NA | NA | 1 | R-HSA-4839726 | FALSE | R-HSA-3214858 | TRUE | TRUE | TRUE | 241 | TRUE | 9.82572614 | 4 | NA | NA | NA | NA | NA | NA | P51532 | SMARCA4,BAF190A,BR G1,SNF2B,SNF2L4 | NA | |
| Cilium Assembly | R-HSA-5617833 | 1 | NA | NA | R-HSA-1852241 | FALSE | R-HSA-5620912 | TRUE | TRUE | TRUE | 187 | TRUE | 7.26737968 | 4 | Q3ZCM7 | TUBB8 | NA | NA | NA | NA | NA | NA | NA | NA |
| Cilium Assembly | R-HSA-5617833 | 1 | NA | NA | R-HSA-1852241 | FALSE | R-HSA-5620924 | TRUE | TRUE | TRUE | 187 | TRUE | 7.26737968 | 4 | Q3ZCM7 | TUBB8 | NA | NA | NA | NA | NA | NA | NA | NA |
| Cilium Assembly | R-HSA-5617833 | 1 | NA | NA | R-HSA-1852241 | FALSE | R-HSA-5620920 | FALSE | FALSE | TRUE | 187 | TRUE | 7.26737968 | 4 | Q3ZCM7 | TUBB8 | NA | NA | NA | NA | NA | NA | NA | NA |
| Class B/2 (Secretin family receptors) | R-HSA-373080 | 2 | NA | 3 | R-HSA-500792 | FALSE | R-HSA-419812 | FALSE | FALSE | FALSE | 94 | TRUE | 8.74468085 | 4 | P12272,Q13635 | PTHLH,PTHRP,PTCH1,PTCH | NA | NA | NA | NA | O00144,P48960,Q9BY15 | FZD9,FZD3,CD97,ADGRE3,EMR3,UNC683/PRO1562 | NA | |
| Class B/2 (Secretin family receptors) | R-HSA-373080 | 2 | NA | 3 | R-HSA-500792 | FALSE | R-HSA-420092 | FALSE | FALSE | FALSE | 94 | TRUE | 8.74468085 | 4 | P12272,Q13635 | PTHLH,PTHRP,PTCH1,PTCH | NA | NA | NA | NA | O00144,P48960,Q9BY15 | FZD9,FZD3,CD97,ADGRE3,EMR3,UNC683/PRO1562 | NA | |
| Cobalamin (Cbl, vitamin B12) transport and metabolism | R-HSA-196741 | NA | NA | 1 | R-HSA-196849 | FALSE | NA | FALSE | FALSE | FALSE | 21 | TRUE | 3.23809524 | 4 | NA | NA | NA | NA | NA | NA | P33527 | ABCC1,MRP,MRP1 | NA | |
| COPI-dependent Golgi-to-ER retrograde traffic | R-HSA-6811434 | 1 | NA | 4 | R-HSA-8856688 | FALSE | NA | FALSE | FALSE | FALSE | 83 | TRUE | 4.95180723 | 4 | Q3ZCM7 | TUBB8 | NA | NA | NA | NA | O86Y91,Q8NGH7,Q9GL93,Q9Y678 | KIF18B,ARFGAP2,ZNF289,Nbla10535,KIF16B,C20orf23,KIAA1590,SNX23,COPG1,COPG | NA | |
| CRMPs in Sema3A signaling | R-HSA-399956 | NA | NA | 1 | R-HSA-373755 | FALSE | NA | FALSE | FALSE | FALSE | 16 | TRUE | 7.5 | 4 | NA | NA | NA | NA | NA | NA | P07332 | FES,FP5 | FES | |
| Crosslinking of collagen fibrils | R-HSA-2243919 | 3 | NA | 1 | R-HSA-2022090 | TRUE | NA | FALSE | TRUE | TRUE | 10 | TRUE | 4.6 | 4 | P02462,P53420,Q92626 | COL4A1,COL4A4,PXDN,KIAA0230,MG50,PRG2,VP0,VPO1 | NA | NA | NA | NA | P02462 | COL4A1 | NA | |
| Defective CSF2RA causes pulmonary surfactant metabolism dysfunction 4 (SMDP4) | R-HSA-5688890 | 1 | NA | NA | R-HSA-5687613 | FALSE | NA | FALSE | FALSE | FALSE | 8 | TRUE | 4.625 | 4 | Q8IWL2 | SFTPA1,COLEC4,PSAP,SFTPA1,SFTPA,SFTPA1B | NA | NA | NA | NA | NA | NA | NA | NA |
| Defective CSF2RB causes pulmonary surfactant metabolism dysfunction 5 (SMDP5) | R-HSA-5688849 | 1 | NA | NA | R-HSA-5687613 | FALSE | NA | FALSE | FALSE | FALSE | 8 | TRUE | 4.625 | 4 | Q8IWL2 | SFTPA1,COLEC4,PSAP,SFTPA1,SFTPA,SFTPA1B | NA | NA | NA | NA | NA | NA | NA | NA |
| Displacement of DNA glycosylase by APEX1 | R-HSA-110357 | NA | NA | 2 | R-HSA-73933 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 5.11111111 | 4 | NA | NA | NA | NA | NA | NA | O95243,Q13569 | MBD4,MED1,TDG | NA | |
| Elastic fibre formation | R-HSA-1566948 | NA | NA | 2 | R-HSA-1474244 | TRUE | R-HSA-2129379 | TRUE | TRUE | TRUE | 41 | TRUE | 6.31707317 | 4 | NA | NA | NA | NA | NA | NA | P15502,P35555 | ELN,FBN1,FBN | NA | |
| Elevation of cytosolic Ca2+ levels | R-HSA-139853 | 2 | NA | 3 | R-HSA-418360 | FALSE | NA | FALSE | FALSE | FALSE | 16 | TRUE | 7.6875 | 4 | P51575,Q14643 | P2RX1,P2X1,ITPR1,INSP3R1 | NA | NA | NA | NA | Q13507,Q9571,Q9Y210 | TRPC3,TRP3,P2RX4,TRPC6,TRP6 | NA | |
| Ephrin signaling | R-HSA-3928664 | 1 | NA | NA | R-HSA-2682334 | TRUE | NA | FALSE | TRUE | TRUE | 19 | TRUE | 15 | 4 | P29323 | EPHB2,DRT,EPH3,EPH3_ER,KHEKS,TYRO5 | EPHB2 | NA | NA | NA | NA | NA | NA | NA |
| Factors involved in megakaryocyte development and platelet production | R-HSA-983231 | 4 | 1 | 3 | R-HSA-109582 | FALSE | R-HSA-983189 | TRUE | TRUE | TRUE | 139 | TRUE | 7.35971223 | 4 | P04637,P22612,Q8IZD9,Q92608 | TP53,P53,PRKACG,DOCK3,KIAA0299,MOCA,DOCK2,KIAA0209 | NA | P04637 | TP53,P53 | NA | P04637,Q13572,Q8N110 | TP53,P53,ITPK1,DOCK4,KIAA0716 | NA | |
| Formation of Senescence-Associated Heterochromatin Foci (SAHF) | R-HSA-2559584 | 1 | 1 | 1 | R-HSA-2559586 | TRUE | NA | FALSE | TRUE | TRUE | 17 | TRUE | 7.88235294 | 4 | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | NA |
| G alpha (i) signalling events | R-HSA-418594 | NA | 3 | 6 | R-HSA-388396 | FALSE | R-HSA-2187338 | FALSE | FALSE | FALSE | 395 | TRUE | 8.14683544 | 4 | NA | NA | NA | Q08462,Q9BXC0,Q9NYW7 | ADCY2,KIAA1060,HCAR1,GPR104,GPR81,HCA1,FKSG80,TAS2R1 | NA | ASPLK6,P08172,P08908,Q14831,Q8NE09,Q9H1C0 | RGSL1,RGSL,RGSL2,CHR M2,HTR1A,ADRB2RL1,ADRBR1,GRM7,GPRC1G,MGLUR7,RS22,LPAR5,GPR92,GPR93 | NA | |
| G alpha (i) signalling events | R-HSA-418594 | NA | 3 | 6 | R-HSA-388396 | FALSE | R-HSA-111885 | FALSE | FALSE | FALSE | 395 | TRUE | 8.14683544 | 4 | NA | NA | NA | Q08462,Q9BXC0,Q9NYW7 | ADCY2,KIAA1060,HCAR1,GPR104,GPR81,HCA1,FKSG80,TAS2R1 | NA | ASPLK6,P08172,P08908,Q14831,Q8NE09,Q9H1C0 | RGSL1,RGSL,RGSL2,CHR M2,HTR1A,ADRB2RL1,ADRBR1,GRM7,GPRC1G,MGLUR7,RS22,LPAR5,GPR92,GPR93 | NA | |

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|-------------------------------|--------------|----|----|----|--------------|-------|---------------|-------|-------|------|------|------|------------|---|--|---|----|----------------|--------------------|----|--|---|----|
| G alpha (q) signalling events | R-HSA-416476 | 5 | NA | 6 | R-HSA-388396 | FALSE | R-HSA-114508 | TRUE | TRUE | TRUE | 212 | TRUE | 11.1084906 | 4 | P11229,P21452,P28336,P32238,P34947 | CHRM1,TACR2,NK2R,NK NAR,TAC2R,NMNR,CCKA R,CCKRA,GRK5,GPRK5 | NA | NA | NA | NA | ASPLK6,P25100,P35348,Q8NF16,Q9H1C0,Q9Y5X5 | RGSL1,RGSL,RGSL2,ADR A1D,ADRA1A,ADRA1C,P ROKR2,GPR73L1,PKR2,L PAR5,GPR92,GPR93,NP FFR2,GPR74,NPFF2,NP GPR | NA |
| G alpha (q) signalling events | R-HSA-416476 | 5 | NA | 6 | R-HSA-388396 | FALSE | R-HSA-881907 | FALSE | FALSE | TRUE | 212 | TRUE | 11.1084906 | 4 | P11229,P21452,P28336,P32238,P34947 | CHRM1,TACR2,NK2R,NK NAR,TAC2R,NMNR,CCKA R,CCKRA,GRK5,GPRK5 | NA | NA | NA | NA | ASPLK6,P25100,P35348,Q8NF16,Q9H1C0,Q9Y5X5 | RGSL1,RGSL,RGSL2,ADR A1D,ADRA1A,ADRA1C,P ROKR2,GPR73L1,PKR2,L PAR5,GPR92,GPR93,NP FFR2,GPR74,NPFF2,NP GPR | NA |
| Generic Transcription Pathway | R-HSA-212436 | 15 | 2 | 17 | R-HSA-73857 | FALSE | R-HSA-8878171 | FALSE | FALSE | TRUE | 1169 | TRUE | 11.774166 | 4 | A6NP11,P17017,P52742,Q3ZCX4,Q6ZMY9,Q6ZR52,Q86WZ6,Q8N816,Q8NCK3,Q8NH Y6,Q9B8X82,Q9NZV7,Q9P255,Q9Y2Q1,Q9Y473 | ZNF716,ZNF14,GIOT4,K OX6,ZNF135,ZNF61,ZNF 78L1,ZNF568,ZNF517,Z NF493,ZNF227,ZNF615, ZNF485,ZFP28,KIAA143 1,ZNF471,ERP3,KIAA139 6,ZIM2,ZNF656,ZNF492, KIAA1473,ZNF115,ZNF2 57,BMZF4,ZNF175 | NA | Q8TC21,Q9 UL59 | ZNF596,ZNF214,BAZ1 | NA | O14709,O43345,P17035,P52736,P52742,Q3ZCX4,Q6ZMY9,Q6ZR52,Q86WZ6,Q8N816,Q8NCK3,Q8NH Y6,Q9B8X82,Q9NZV7,Q9P255,Q9Y2Q1,Q9Y473 | ZNF197,ZKSCAN9,ZNF1 66,ZNF208,ZNF91L,ZNF 28,KOX24,ZNF133,ZNF1 50,ZNF135,ZNF61,ZNF7 8L1,ZNF568,ZNF484,ZN F585A,ZNF530,KIAA150 8,ZNF782,ZNF493,ZNF3 4,KOX32,ZNF606,KIAA18 5,ZNF328,ZNF570,ZIM 3,ZNF657,ZNF287,ZKSC AN13,ZNF215,BAZ2,ZKS CAN11 | NA |
| Generic Transcription Pathway | R-HSA-212436 | 15 | 2 | 17 | R-HSA-73857 | FALSE | R-HSA-8953750 | TRUE | TRUE | TRUE | 1169 | TRUE | 11.774166 | 4 | A6NP11,P17017,P52742,Q3ZCX4,Q6ZMY9,Q6ZR52,Q86WZ6,Q8N816,Q8NCK3,Q8NH Y6,Q9B8X82,Q9NZV7,Q9P255,Q9Y2Q1,Q9Y473 | ZNF716,ZNF14,GIOT4,K OX6,ZNF135,ZNF61,ZNF 78L1,ZNF568,ZNF517,Z NF493,ZNF227,ZNF615, ZNF485,ZFP28,KIAA143 1,ZNF471,ERP3,KIAA139 6,ZIM2,ZNF656,ZNF492, KIAA1473,ZNF115,ZNF2 57,BMZF4,ZNF175 | NA | Q8TC21,Q9 UL59 | ZNF596,ZNF214,BAZ1 | NA | O14709,O43345,P17035,P52736,P52742,Q3ZCX4,Q6ZMY9,Q6ZR52,Q86WZ6,Q8N816,Q8NCK3,Q8NH Y6,Q9B8X82,Q9NZV7,Q9P255,Q9Y2Q1,Q9Y473 | ZNF197,ZKSCAN9,ZNF1 66,ZNF208,ZNF91L,ZNF 28,KOX24,ZNF133,ZNF1 50,ZNF135,ZNF61,ZNF7 8L1,ZNF568,ZNF484,ZN F585A,ZNF530,KIAA150 8,ZNF782,ZNF493,ZNF3 4,KOX32,ZNF606,KIAA18 5,ZNF328,ZNF570,ZIM 3,ZNF657,ZNF287,ZKSC AN13,ZNF215,BAZ2,ZKS CAN11 | NA |
| Generic Transcription Pathway | R-HSA-212436 | 15 | 2 | 17 | R-HSA-73857 | FALSE | R-HSA-8864260 | FALSE | FALSE | TRUE | 1169 | TRUE | 11.774166 | 4 | A6NP11,P17017,P52742,Q3ZCX4,Q6ZMY9,Q6ZR52,Q86WZ6,Q8N816,Q8NCK3,Q8NH Y6,Q9B8X82,Q9NZV7,Q9P255,Q9Y2Q1,Q9Y473 | ZNF716,ZNF14,GIOT4,K OX6,ZNF135,ZNF61,ZNF 78L1,ZNF568,ZNF517,Z NF493,ZNF227,ZNF615, ZNF485,ZFP28,KIAA143 1,ZNF471,ERP3,KIAA139 6,ZIM2,ZNF656,ZNF492, KIAA1473,ZNF115,ZNF2 57,BMZF4,ZNF175 | NA | Q8TC21,Q9 UL59 | ZNF596,ZNF214,BAZ1 | NA | O14709,O43345,P17035,P52736,P52742,Q3ZCX4,Q6ZMY9,Q6ZR52,Q86WZ6,Q8N816,Q8NCK3,Q8NH Y6,Q9B8X82,Q9NZV7,Q9P255,Q9Y2Q1,Q9Y473 | ZNF197,ZKSCAN9,ZNF1 66,ZNF208,ZNF91L,ZNF 28,KOX24,ZNF133,ZNF1 50,ZNF135,ZNF61,ZNF7 8L1,ZNF568,ZNF484,ZN F585A,ZNF530,KIAA150 8,ZNF782,ZNF493,ZNF3 4,KOX32,ZNF606,KIAA18 5,ZNF328,ZNF570,ZIM 3,ZNF657,ZNF287,ZKSC AN13,ZNF215,BAZ2,ZKS CAN11 | NA |
| Generic Transcription Pathway | R-HSA-212436 | 15 | 2 | 17 | R-HSA-73857 | FALSE | R-HSA-383280 | TRUE | TRUE | TRUE | 1169 | TRUE | 11.774166 | 4 | A6NP11,P17017,P52742,Q3ZCX4,Q6ZMY9,Q6ZR52,Q86WZ6,Q8N816,Q8NCK3,Q8NH Y6,Q9B8X82,Q9NZV7,Q9P255,Q9Y2Q1,Q9Y473 | ZNF716,ZNF14,GIOT4,K OX6,ZNF135,ZNF61,ZNF 78L1,ZNF568,ZNF517,Z NF493,ZNF227,ZNF615, ZNF485,ZFP28,KIAA143 1,ZNF471,ERP3,KIAA139 6,ZIM2,ZNF656,ZNF492, KIAA1473,ZNF115,ZNF2 57,BMZF4,ZNF175 | NA | Q8TC21,Q9 UL59 | ZNF596,ZNF214,BAZ1 | NA | O14709,O43345,P17035,P52736,P52742,Q3ZCX4,Q6ZMY9,Q6ZR52,Q86WZ6,Q8N816,Q8NCK3,Q8NH Y6,Q9B8X82,Q9NZV7,Q9P255,Q9Y2Q1,Q9Y473 | ZNF197,ZKSCAN9,ZNF1 66,ZNF208,ZNF91L,ZNF 28,KOX24,ZNF133,ZNF1 50,ZNF135,ZNF61,ZNF7 8L1,ZNF568,ZNF484,ZN F585A,ZNF530,KIAA150 8,ZNF782,ZNF493,ZNF3 4,KOX32,ZNF606,KIAA18 5,ZNF328,ZNF570,ZIM 3,ZNF657,ZNF287,ZKSC AN13,ZNF215,BAZ2,ZKS CAN11 | NA |
| Generic Transcription Pathway | R-HSA-212436 | 15 | 2 | 17 | R-HSA-73857 | FALSE | R-HSA-2032785 | FALSE | FALSE | TRUE | 1169 | TRUE | 11.774166 | 4 | A6NP11,P17017,P52742,Q3ZCX4,Q6ZMY9,Q6ZR52,Q86WZ6,Q8N816,Q8NCK3,Q8NH Y6,Q9B8X82,Q9NZV7,Q9P255,Q9Y2Q1,Q9Y473 | ZNF716,ZNF14,GIOT4,K OX6,ZNF135,ZNF61,ZNF 78L1,ZNF568,ZNF517,Z NF493,ZNF227,ZNF615, ZNF485,ZFP28,KIAA143 1,ZNF471,ERP3,KIAA139 6,ZIM2,ZNF656,ZNF492, KIAA1473,ZNF115,ZNF2 57,BMZF4,ZNF175 | NA | Q8TC21,Q9 UL59 | ZNF596,ZNF214,BAZ1 | NA | O14709,O43345,P17035,P52736,P52742,Q3ZCX4,Q6ZMY9,Q6ZR52,Q86WZ6,Q8N816,Q8NCK3,Q8NH Y6,Q9B8X82,Q9NZV7,Q9P255,Q9Y2Q1,Q9Y473 | ZNF197,ZKSCAN9,ZNF1 66,ZNF208,ZNF91L,ZNF 28,KOX24,ZNF133,ZNF1 50,ZNF135,ZNF61,ZNF7 8L1,ZNF568,ZNF484,ZN F585A,ZNF530,KIAA150 8,ZNF782,ZNF493,ZNF3 4,KOX32,ZNF606,KIAA18 5,ZNF328,ZNF570,ZIM 3,ZNF657,ZNF287,ZKSC AN13,ZNF215,BAZ2,ZKS CAN11 | NA |

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|-------------------------------|--------------|----|---|----|-------------|-------|---------------|-------|-------|------|------|------|-----------|---|---|---|----|-------------------|--------------------|----|---|---|----|
| Generic Transcription Pathway | R-HSA-212436 | 15 | 2 | 17 | R-HSA-73857 | FALSE | R-HSA-8878159 | FALSE | FALSE | TRUE | 1169 | TRUE | 11.774166 | 4 | A6NP11,P17 017,P52742, Q3ZCX4,Q6 ZMY9,Q6ZR 52,Q86W26 ,Q8N8I6,Q8 NCK3,Q8NH Y6,Q9B8X82, Q9NZV7,Q9 P255,Q9Y2 Q1,Q9Y473 | ZNF716,ZNF14,GIOT4,K OX6,ZNF135,ZNF61,ZNF 78L1,ZNF568,ZNF517,Z NF493,ZNF227,ZNF615, ZNF485,ZFP28,KIAA143 1,ZNF471,ERP1,KIAA139 6,ZIM2,ZNF656,ZNF492, KIAA1473,ZNF115,ZNF2 57,BMZF4,ZNF175 | NA | Q8TC21,Q9 UL59 | ZNF596,ZNF214,BAZ1 | NA | O14709,O4 3345,P1703 5,P52736,P5 2742,Q3ZCX 4,Q5IVG2,Q 6P3V2,Q6P9 A1,Q6ZMW 2,Q6ZRS52,Q 8I2Z6,Q8W XB4,Q96N18 ,Q96PE6,Q9 HBT7,Q9UL 58 | ZNF197,ZKSCAN9,ZNF1 66,ZNF208,ZNF91L,ZNF 28,KOX24,ZNF133,ZNF1 50,ZNF135,ZNF61,ZNF7 8L1,ZNF568,ZNF484,ZN F585A,ZNF530,KIAA150 8,ZNF782,ZNF493,ZNF3 4,KOX32,ZNF606,KIAA18 52,ZNF328,ZNF570,ZIM 3,ZNF657,ZNF287,ZKSC AN13,ZNF215,BAZ2,ZKS CAN11 | NA |
| Generic Transcription Pathway | R-HSA-212436 | 15 | 2 | 17 | R-HSA-73857 | FALSE | R-HSA-8986944 | TRUE | TRUE | TRUE | 1169 | TRUE | 11.774166 | 4 | A6NP11,P17 017,P52742, Q3ZCX4,Q6 ZMY9,Q6ZR 52,Q86W26 ,Q8N8I6,Q8 NCK3,Q8NH Y6,Q9B8X82, Q9NZV7,Q9 P255,Q9Y2 Q1,Q9Y473 | ZNF716,ZNF14,GIOT4,K OX6,ZNF135,ZNF61,ZNF 78L1,ZNF568,ZNF517,Z NF493,ZNF227,ZNF615, ZNF485,ZFP28,KIAA143 1,ZNF471,ERP1,KIAA139 6,ZIM2,ZNF656,ZNF492, KIAA1473,ZNF115,ZNF2 57,BMZF4,ZNF175 | NA | Q8TC21,Q9 UL59 | ZNF596,ZNF214,BAZ1 | NA | O14709,O4 3345,P1703 5,P52736,P5 2742,Q3ZCX 4,Q5IVG2,Q 6P3V2,Q6P9 A1,Q6ZMW 2,Q6ZRS52,Q 8I2Z6,Q8W XB4,Q96N18 ,Q96PE6,Q9 HBT7,Q9UL 58 | ZNF197,ZKSCAN9,ZNF1 66,ZNF208,ZNF91L,ZNF 28,KOX24,ZNF133,ZNF1 50,ZNF135,ZNF61,ZNF7 8L1,ZNF568,ZNF484,ZN F585A,ZNF530,KIAA150 8,ZNF782,ZNF493,ZNF3 4,KOX32,ZNF606,KIAA18 52,ZNF328,ZNF570,ZIM 3,ZNF657,ZNF287,ZKSC AN13,ZNF215,BAZ2,ZKS CAN11 | NA |
| Generic Transcription Pathway | R-HSA-212436 | 15 | 2 | 17 | R-HSA-73857 | FALSE | R-HSA-350054 | TRUE | TRUE | TRUE | 1169 | TRUE | 11.774166 | 4 | A6NP11,P17 017,P52742, Q3ZCX4,Q6 ZMY9,Q6ZR 52,Q86W26 ,Q8N8I6,Q8 NCK3,Q8NH Y6,Q9B8X82, Q9NZV7,Q9 P255,Q9Y2 Q1,Q9Y473 | ZNF716,ZNF14,GIOT4,K OX6,ZNF135,ZNF61,ZNF 78L1,ZNF568,ZNF517,Z NF493,ZNF227,ZNF615, ZNF485,ZFP28,KIAA143 1,ZNF471,ERP1,KIAA139 6,ZIM2,ZNF656,ZNF492, KIAA1473,ZNF115,ZNF2 57,BMZF4,ZNF175 | NA | Q8TC21,Q9 UL59 | ZNF596,ZNF214,BAZ1 | NA | O14709,O4 3345,P1703 5,P52736,P5 2742,Q3ZCX 4,Q5IVG2,Q 6P3V2,Q6P9 A1,Q6ZMW 2,Q6ZRS52,Q 8I2Z6,Q8W XB4,Q96N18 ,Q96PE6,Q9 HBT7,Q9UL 58 | ZNF197,ZKSCAN9,ZNF1 66,ZNF208,ZNF91L,ZNF 28,KOX24,ZNF133,ZNF1 50,ZNF135,ZNF61,ZNF7 8L1,ZNF568,ZNF484,ZN F585A,ZNF530,KIAA150 8,ZNF782,ZNF493,ZNF3 4,KOX32,ZNF606,KIAA18 52,ZNF328,ZNF570,ZIM 3,ZNF657,ZNF287,ZKSC AN13,ZNF215,BAZ2,ZKS CAN11 | NA |
| Generic Transcription Pathway | R-HSA-212436 | 15 | 2 | 17 | R-HSA-73857 | FALSE | R-HSA-2173793 | FALSE | FALSE | TRUE | 1169 | TRUE | 11.774166 | 4 | A6NP11,P17 017,P52742, Q3ZCX4,Q6 ZMY9,Q6ZR 52,Q86W26 ,Q8N8I6,Q8 NCK3,Q8NH Y6,Q9B8X82, Q9NZV7,Q9 P255,Q9Y2 Q1,Q9Y473 | ZNF716,ZNF14,GIOT4,K OX6,ZNF135,ZNF61,ZNF 78L1,ZNF568,ZNF517,Z NF493,ZNF227,ZNF615, ZNF485,ZFP28,KIAA143 1,ZNF471,ERP1,KIAA139 6,ZIM2,ZNF656,ZNF492, KIAA1473,ZNF115,ZNF2 57,BMZF4,ZNF175 | NA | Q8TC21,Q9 UL59 | ZNF596,ZNF214,BAZ1 | NA | O14709,O4 3345,P1703 5,P52736,P5 2742,Q3ZCX 4,Q5IVG2,Q 6P3V2,Q6P9 A1,Q6ZMW 2,Q6ZRS52,Q 8I2Z6,Q8W XB4,Q96N18 ,Q96PE6,Q9 HBT7,Q9UL 58 | ZNF197,ZKSCAN9,ZNF1 66,ZNF208,ZNF91L,ZNF 28,KOX24,ZNF133,ZNF1 50,ZNF135,ZNF61,ZNF7 8L1,ZNF568,ZNF484,ZN F585A,ZNF530,KIAA150 8,ZNF782,ZNF493,ZNF3 4,KOX32,ZNF606,KIAA18 52,ZNF328,ZNF570,ZIM 3,ZNF657,ZNF287,ZKSC AN13,ZNF215,BAZ2,ZKS CAN11 | NA |
| Generic Transcription Pathway | R-HSA-212436 | 15 | 2 | 17 | R-HSA-73857 | FALSE | R-HSA-8878166 | FALSE | FALSE | TRUE | 1169 | TRUE | 11.774166 | 4 | A6NP11,P17 017,P52742, Q3ZCX4,Q6 ZMY9,Q6ZR 52,Q86W26 ,Q8N8I6,Q8 NCK3,Q8NH Y6,Q9B8X82, Q9NZV7,Q9 P255,Q9Y2 Q1,Q9Y473 | ZNF716,ZNF14,GIOT4,K OX6,ZNF135,ZNF61,ZNF 78L1,ZNF568,ZNF517,Z NF493,ZNF227,ZNF615, ZNF485,ZFP28,KIAA143 1,ZNF471,ERP1,KIAA139 6,ZIM2,ZNF656,ZNF492, KIAA1473,ZNF115,ZNF2 57,BMZF4,ZNF175 | NA | Q8TC21,Q9 UL59 | ZNF596,ZNF214,BAZ1 | NA | O14709,O4 3345,P1703 5,P52736,P5 2742,Q3ZCX 4,Q5IVG2,Q 6P3V2,Q6P9 A1,Q6ZMW 2,Q6ZRS52,Q 8I2Z6,Q8W XB4,Q96N18 ,Q96PE6,Q9 HBT7,Q9UL 58 | ZNF197,ZKSCAN9,ZNF1 66,ZNF208,ZNF91L,ZNF 28,KOX24,ZNF133,ZNF1 50,ZNF135,ZNF61,ZNF7 8L1,ZNF568,ZNF484,ZN F585A,ZNF530,KIAA150 8,ZNF782,ZNF493,ZNF3 4,KOX32,ZNF606,KIAA18 52,ZNF328,ZNF570,ZIM 3,ZNF657,ZNF287,ZKSC AN13,ZNF215,BAZ2,ZKS CAN11 | NA |

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|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|------|------|------------|---|---|--|----|---------------|--------------------|----|--|---|---|----|
| Generic Transcription Pathway | R-HSA-212436 | 15 | 2 | 17 | R-HSA-73857 | FALSE | R-HSA-3700989 | FALSE | FALSE | TRUE | 1169 | TRUE | 11.774166 | 4 | A6NP11,P17017,P52742,Q32C04,Q6ZMY9,Q6ZR52,Q80WZ6,Q8N8I6,Q8NCK3,Q8NH Y6,Q9B8X2,Q9NZV7,Q9P255,Q9Y2Q1,Q9Y473 | ZNF716,ZNF14,GIOT4,KOX6,ZNF135,ZNF61,ZNF78L1,ZNF568,ZNF517,ZNF493,ZNF227,ZNF615,ZNF485,ZFP28,KIAA1431,ZNF471,ERP1,KIAA1396,ZIM2,ZNF656,ZNF492,KIAA1473,ZNF115,ZNF257,BMZFA,ZNF175 | NA | Q8TC21,Q9UL59 | ZNF596,ZNF214,BAZ1 | NA | O14709,Q43345,P17035,P52736,P52742,Q32CX4,Q5IVG2,Q6P3V2,Q6P9A1,Q6ZMW2,Q6ZR52,Q8I2Z6,Q8WXB4,Q96N18,Q96PE6,Q9HB77,Q9UL58 | ZNF197,ZKSCAN9,ZNF166,ZNF208,ZNF91L,ZNF28,KOX24,ZNF133,ZNF150,ZNF135,ZNF61,ZNF78L1,ZNF568,ZNF484,ZNF585A,ZNF530,KIAA1504,ZNF782,ZNF493,ZNF34,KOX32,ZNF606,KIAA1852,ZNF328,ZNF570,ZIM3,ZNF657,ZNF287,ZKSCAN11,ZNF215,BAZ2,ZKSCAN11 | NA | |
| Golgi Associated Vesicle Biogenesis | R-HSA-432722 | NA | NA | 1 | R-HSA-421837 | FALSE | NA | FALSE | FALSE | FALSE | 56 | TRUE | 5.83928571 | 4 | NA | NA | NA | NA | NA | NA | P11717 | IGF2R,MPRI | NA | |
| HATs acetylate histones | R-HSA-3214847 | 2 | NA | 2 | R-HSA-3247509 | TRUE | NA | FALSE | TRUE | TRUE | 108 | TRUE | 12.6851852 | 4 | P62805,Q9H726 | HIST1H4A,H4/A,H4FA;HIST1H4B,H4/J,H4FI;HIST1H4C,H4/G,H4FG;HIST1H4D,H4/B,H4FB;HIST1H4E,H4/J,H4FJ;HIST1H4F,H4/C,H4FC;HIST1H4H,H4/H,H4FH;HIST1H4I,H4/M,H4FM;HIST1H4J,H4/E,H4FE;HIST1H4K,H4/D,H4FD;HIST1H4L,H4/K,H4FK;HIST2H4A,H4/N,H4FN;HIST2H4B,H4/O,H4FO;HIST4H4,KAT8,MOF,MYST1,PP7073 | NA | NA | NA | NA | NA | O75528,Q96E28 | TADA3,ADA3,TADA3L,MCRS1,INO80Q,M5P58 | NA |
| Highly sodium permeable acetylcholine nicotinic receptors | R-HSA-629587 | 1 | NA | NA | R-HSA-622327 | FALSE | NA | FALSE | FALSE | FALSE | 7 | TRUE | 3.28571429 | 4 | P17787 | CHRN2 | NA | NA | NA | NA | NA | NA | NA | |
| Highly sodium permeable acetylcholine nicotinic receptors | R-HSA-629587 | 1 | NA | NA | R-HSA-622323 | FALSE | NA | FALSE | FALSE | FALSE | 7 | TRUE | 3.28571429 | 4 | P17787 | CHRN2 | NA | NA | NA | NA | NA | NA | NA | |
| Interferon gamma signaling | R-HSA-877300 | 1 | NA | 3 | R-HSA-913531 | FALSE | R-HSA-877312 | FALSE | FALSE | FALSE | 93 | TRUE | 7.08602151 | 4 | Q9UDY6 | TRIM10,RFB30,RNF9 | NA | NA | NA | NA | NA | P01891,P01892,P04439,P05534,P10314,P10316,P13746,P16188,P16189,P16190,P18462,P19320,P30443,P30447,P30450,P30453,P30455,P30456,P30457,P30459,P30512,Q09160,Q9C040 | HLA-A,HLAA,VCAM1,TRIM2,KIAA0517,RNF86 | NA |
| Intra-Golgi traffic | R-HSA-6811438 | 1 | 1 | 4 | R-HSA-6811442 | FALSE | NA | FALSE | FALSE | FALSE | 44 | TRUE | 4.06818182 | 4 | Q13948 | CUX1,CUTL1 | NA | O60476 | MAN1A2,MAN1B | NA | P49641,Q13948,Q14746,Q14964 | MAN2A2,MANA2X,CUX1,CUTL1,COG2,LDLC,RAB39A,RAB39 | NA | |
| Intrinsic Pathway of Fibrin Clot Formation | R-HSA-140837 | NA | NA | 2 | R-HSA-140877 | FALSE | NA | FALSE | FALSE | FALSE | 22 | TRUE | 5.45454545 | 4 | NA | NA | NA | NA | NA | NA | NA | P00451,P07093 | F8,F8C,SERPINE2,P17,PN1 | NA |
| Kinesins | R-HSA-983189 | 1 | NA | 2 | R-HSA-983231 | TRUE | NA | FALSE | TRUE | TRUE | 44 | TRUE | 4.81818182 | 4 | Q3ZCM7 | TUBB8 | NA | NA | NA | NA | NA | Q86Y91,Q96L93 | KIF18B,KIF16B,C20orf23,KIAA1590,SNX23 | NA |
| LDL clearance | R-HSA-8964038 | 2 | NA | NA | R-HSA-8964043 | FALSE | NA | FALSE | FALSE | FALSE | 19 | TRUE | 9.47368421 | 4 | O75908,Q94973 | SOAT2,ACACT2,ACAT2,AP2A2,ADTAB,CLAPA2,HIP9,HYPJ,KIAA0899 | NA | NA | NA | NA | NA | NA | NA | |
| Linoleic acid (LA) metabolism | R-HSA-2046105 | NA | NA | 1 | R-HSA-2046104 | FALSE | NA | FALSE | FALSE | FALSE | 8 | TRUE | 4.5 | 4 | NA | NA | NA | NA | NA | NA | NA | O95864 | FADS2 | NA |
| Macroautophagy | R-HSA-1632852 | 1 | NA | 2 | R-HSA-8953897 | FALSE | NA | FALSE | FALSE | FALSE | 68 | TRUE | 5.52941176 | 4 | P49815 | TSC2,TSC4 | NA | NA | NA | NA | NA | P42345,Q8WYNO | MTOR,FRAP,FRAP1,FRAP2,RAFT1,RAPT1,ATG4A,APG4A,AUTL2 | NA |
| mRNA Splicing - Minor Pathway | R-HSA-72165 | 2 | NA | 1 | R-HSA-72172 | FALSE | NA | FALSE | FALSE | FALSE | 55 | TRUE | 16.4727273 | 4 | O75533,Q86XP3 | SF3B1,SAP155,DDX42 | NA | NA | NA | NA | NA | O75643 | SNRNP200,ASCC3L1,HELIC2,KIAA0788 | NA |
| Muscarinic acetylcholine receptors | R-HSA-390648 | 1 | NA | 1 | R-HSA-375280 | TRUE | NA | FALSE | TRUE | TRUE | 5 | TRUE | 5 | 4 | P11229 | CHRM1 | NA | NA | NA | NA | NA | P08172 | CHRM2 | NA |

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|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|---|-----------------------------|--|----|----|----|----|-----------------------------------|--|----|
| Na+/Cl- dependent neurotransmitter transporters | R-HSA-442660 | NA | NA | 2 | R-HSA-425366 | TRUE | NA | FALSE | TRUE | TRUE | 19 | TRUE | 4.52631579 | 4 | NA | NA | NA | NA | NA | NA | P23975,P54219 | SLC6A2,NAT1,NET1,SLC6A5,SLC18A1,VAT1,VMAT1 | NA |
| Neurofascin interactions | R-HSA-447043 | NA | NA | 1 | R-HSA-373760 | TRUE | NA | FALSE | TRUE | TRUE | 7 | TRUE | 4.14285714 | 4 | NA | NA | NA | NA | NA | NA | P16157 | ANK1,ANK | NA |
| Nitric oxide stimulates guanylate cyclase | R-HSA-392154 | NA | NA | 1 | R-HSA-418346 | TRUE | R-HSA-418457 | TRUE | TRUE | TRUE | 25 | TRUE | 5.48 | 4 | NA | NA | NA | NA | NA | NA | P29475 | NOS1 | NA |
| Nuclear Receptor transcription pathway | R-HSA-383280 | NA | NA | 1 | R-HSA-212436 | TRUE | NA | FALSE | TRUE | TRUE | 51 | TRUE | 5.29411765 | 4 | NA | NA | NA | NA | NA | NA | Q14541 | HNF4G,NR2A2 | NA |
| Orexin and neuropeptides FF and QRFP bind to their respective receptors | R-HSA-389397 | NA | NA | 1 | R-HSA-375276 | TRUE | NA | FALSE | TRUE | TRUE | 8 | TRUE | 4 | 4 | NA | NA | NA | NA | NA | NA | Q9Y5X5 | NPFFR2,GPR74,NPFF2,NGGPR | NA |
| Peptide ligand-binding receptors | R-HSA-375276 | 2 | NA | 1 | R-HSA-373076 | FALSE | R-HSA-444473 | FALSE | FALSE | TRUE | 189 | TRUE | 4.55026455 | 4 | P28336,P32238 | NMBR,CCKAR,CCKRA | NA | NA | NA | NA | Q8NFJ6 | PROKR2,GPR73L1,PKR2 | NA |
| Peptide ligand-binding receptors | R-HSA-375276 | 2 | NA | 1 | R-HSA-373076 | FALSE | R-HSA-389397 | TRUE | TRUE | TRUE | 189 | TRUE | 4.55026455 | 4 | P28336,P32238 | NMBR,CCKAR,CCKRA | NA | NA | NA | NA | Q8NFJ6 | PROKR2,GPR73L1,PKR2 | NA |
| Peptide ligand-binding receptors | R-HSA-375276 | 2 | NA | 1 | R-HSA-373076 | FALSE | R-HSA-388479 | FALSE | FALSE | TRUE | 189 | TRUE | 4.55026455 | 4 | P28336,P32238 | NMBR,CCKAR,CCKRA | NA | NA | NA | NA | Q8NFJ6 | PROKR2,GPR73L1,PKR2 | NA |
| Peptide ligand-binding receptors | R-HSA-375276 | 2 | NA | 1 | R-HSA-373076 | FALSE | R-HSA-444821 | FALSE | FALSE | TRUE | 189 | TRUE | 4.55026455 | 4 | P28336,P32238 | NMBR,CCKAR,CCKRA | NA | NA | NA | NA | Q8NFJ6 | PROKR2,GPR73L1,PKR2 | NA |
| Peptide ligand-binding receptors | R-HSA-375276 | 2 | NA | 1 | R-HSA-373076 | FALSE | R-HSA-380108 | FALSE | FALSE | TRUE | 189 | TRUE | 4.55026455 | 4 | P28336,P32238 | NMBR,CCKAR,CCKRA | NA | NA | NA | NA | Q8NFJ6 | PROKR2,GPR73L1,PKR2 | NA |
| Peptide ligand-binding receptors | R-HSA-375276 | 2 | NA | 1 | R-HSA-373076 | FALSE | R-HSA-380095 | TRUE | TRUE | TRUE | 189 | TRUE | 4.55026455 | 4 | P28336,P32238 | NMBR,CCKAR,CCKRA | NA | NA | NA | NA | Q8NFJ6 | PROKR2,GPR73L1,PKR2 | NA |
| PI Metabolism | R-HSA-1483255 | 1 | NA | NA | R-HSA-1483257 | FALSE | R-HSA-8847453 | FALSE | FALSE | TRUE | 84 | TRUE | 6.69047619 | 4 | Q5GJ75 | TNFAIP8L3,TYPE3 | NA | NA | NA | NA | NA | NA | NA |
| PI Metabolism | R-HSA-1483255 | 1 | NA | NA | R-HSA-1483257 | FALSE | R-HSA-6814848 | TRUE | TRUE | TRUE | 84 | TRUE | 6.69047619 | 4 | Q5GJ75 | TNFAIP8L3,TYPE3 | NA | NA | NA | NA | NA | NA | NA |
| PI Metabolism | R-HSA-1483255 | 1 | NA | NA | R-HSA-1483257 | FALSE | R-HSA-1660508 | FALSE | FALSE | TRUE | 84 | TRUE | 6.69047619 | 4 | Q5GJ75 | TNFAIP8L3,TYPE3 | NA | NA | NA | NA | NA | NA | NA |
| PI Metabolism | R-HSA-1483255 | 1 | NA | NA | R-HSA-1483257 | FALSE | R-HSA-1660524 | FALSE | FALSE | TRUE | 84 | TRUE | 6.69047619 | 4 | Q5GJ75 | TNFAIP8L3,TYPE3 | NA | NA | NA | NA | NA | NA | NA |
| PI Metabolism | R-HSA-1483255 | 1 | NA | NA | R-HSA-1483257 | FALSE | R-HSA-1660517 | FALSE | FALSE | TRUE | 84 | TRUE | 6.69047619 | 4 | Q5GJ75 | TNFAIP8L3,TYPE3 | NA | NA | NA | NA | NA | NA | NA |
| PI Metabolism | R-HSA-1483255 | 1 | NA | NA | R-HSA-1483257 | FALSE | R-HSA-1660516 | TRUE | TRUE | TRUE | 84 | TRUE | 6.69047619 | 4 | Q5GJ75 | TNFAIP8L3,TYPE3 | NA | NA | NA | NA | NA | NA | NA |
| PI Metabolism | R-HSA-1483255 | 1 | NA | NA | R-HSA-1483257 | FALSE | R-HSA-1660502 | FALSE | FALSE | TRUE | 84 | TRUE | 6.69047619 | 4 | Q5GJ75 | TNFAIP8L3,TYPE3 | NA | NA | NA | NA | NA | NA | NA |
| PI Metabolism | R-HSA-1483255 | 1 | NA | NA | R-HSA-1483257 | FALSE | R-HSA-1660499 | TRUE | TRUE | TRUE | 84 | TRUE | 6.69047619 | 4 | Q5GJ75 | TNFAIP8L3,TYPE3 | NA | NA | NA | NA | NA | NA | NA |
| PI Metabolism | R-HSA-1483255 | 1 | NA | NA | R-HSA-1483257 | FALSE | R-HSA-1483196 | FALSE | FALSE | TRUE | 84 | TRUE | 6.69047619 | 4 | Q5GJ75 | TNFAIP8L3,TYPE3 | NA | NA | NA | NA | NA | NA | NA |
| PI Metabolism | R-HSA-1483255 | 1 | NA | NA | R-HSA-1483257 | FALSE | R-HSA-1483248 | TRUE | TRUE | TRUE | 84 | TRUE | 6.69047619 | 4 | Q5GJ75 | TNFAIP8L3,TYPE3 | NA | NA | NA | NA | NA | NA | NA |
| PI Metabolism | R-HSA-1483255 | 1 | NA | NA | R-HSA-1483257 | FALSE | R-HSA-1660514 | TRUE | TRUE | TRUE | 84 | TRUE | 6.69047619 | 4 | Q5GJ75 | TNFAIP8L3,TYPE3 | NA | NA | NA | NA | NA | NA | NA |
| PI Metabolism | R-HSA-1483255 | 1 | NA | NA | R-HSA-1483257 | FALSE | R-HSA-1660510 | FALSE | FALSE | TRUE | 84 | TRUE | 6.69047619 | 4 | Q5GJ75 | TNFAIP8L3,TYPE3 | NA | NA | NA | NA | NA | NA | NA |
| PI Metabolism | R-HSA-1483255 | 1 | NA | NA | R-HSA-1483257 | FALSE | R-HSA-1660537 | FALSE | FALSE | TRUE | 84 | TRUE | 6.69047619 | 4 | Q5GJ75 | TNFAIP8L3,TYPE3 | NA | NA | NA | NA | NA | NA | NA |
| PKMTs methylate histone lysines | R-HSA-3214841 | 4 | NA | 1 | R-HSA-3247509 | TRUE | NA | FALSE | TRUE | TRUE | 47 | TRUE | 9.04255319 | 4 | P62805,Q03112,Q9BYW2,Q9UP56 | HIST1H4A,H4/A,H4FA;HIST1H4B,H4/L,H4FI;HIST1H4C,H4/G,H4FG;HIST1H4D,H4/B,H4FB;HIST1H4E,H4/I,H4FI;HIST1H4F,H4/C,H4FC;HIST1H4H,H4/H,H4FH;HIST1H4I,H4/E,H4FE;HIST1H4K,H4/D,H4FD;HIST1H4L,H4/K,H4FK;HIST2H4A,H4/N,H4F2,H4FN,HIST2H4;HIST2H4B,H4/O,H4FO;HIST4H4,MECOM,EVI1,MDS1,SETD2,HIF1,HYPB,KIAA1732,KMT3A,SET2,HSPC069,SETD1B,KIAA1076,KMT2G,SET1B | NA | NA | NA | NA | Q96T68 | SETDB2,C13orf4,CLLD8,KMT1F | NA |
| Post-translational protein phosphorylation | R-HSA-8957275 | 1 | 1 | 5 | R-HSA-597592 | FALSE | NA | FALSE | FALSE | FALSE | 107 | TRUE | 6.28971963 | 4 | O00391 | QSOX1,QSCN6,UNQ2520/PRO6013 | NA | NA | NA | NA | P02751 | FN1,FN | NA |
| | | | | | | | | | | | | | | | | | | | | | P01009,P1047,P35555,Q14766,Q9NRM1 | SERPINA1,AAT,PI,PRO0684,PRO209,LAMC1,LAMB2,FBN1,FBN,LTBP1,ENAM | NA |

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|---|---------------|----|----|----|---------------|-------|-------------|-------|-------|-------|-----|------|------------|---|---------------|--|----|--------|------------------------|----|-----------------------------------|---|-------|
| POU5F1 (OCT4), SOX2, NANOG activate genes related to proliferation | R-HSA-2892247 | 1 | NA | NA | R-HSA-452723 | TRUE | NA | FALSE | TRUE | TRUE | 13 | TRUE | 9.23076923 | 4 | Q9NSC2 | SALL1,SAL1,ZNF794 | NA | NA | NA | NA | NA | NA | NA |
| Processing of Capped Intron-Containing Pre-mRNA | R-HSA-72203 | 2 | NA | NA | R-HSA-8953854 | FALSE | R-HSA-72172 | FALSE | FALSE | TRUE | 243 | TRUE | 9.81069959 | 4 | Q00839,Q15366 | HNRNPU,C1orf199,HNRPU,SAFA,U21.1,PCBP2 | NA | NA | NA | NA | NA | NA | NA |
| Processing of Capped Intron-Containing Pre-mRNA | R-HSA-72203 | 2 | NA | NA | R-HSA-8953854 | FALSE | R-HSA-72202 | FALSE | FALSE | TRUE | 243 | TRUE | 9.81069959 | 4 | Q00839,Q15366 | HNRNPU,C1orf199,HNRPU,SAFA,U21.1,PCBP2 | NA | NA | NA | NA | NA | NA | NA |
| Processing of Capped Intron-Containing Pre-mRNA | R-HSA-72203 | 2 | NA | NA | R-HSA-8953854 | FALSE | R-HSA-72187 | TRUE | TRUE | TRUE | 243 | TRUE | 9.81069959 | 4 | Q00839,Q15366 | HNRNPU,C1orf199,HNRPU,SAFA,U21.1,PCBP2 | NA | NA | NA | NA | NA | NA | NA |
| RA biosynthesis pathway | R-HSA-5365859 | 1 | NA | 1 | R-HSA-5362517 | FALSE | NA | FALSE | FALSE | FALSE | 22 | TRUE | 3.86363636 | 4 | P07327 | ADH1A,ADH1 | NA | NA | NA | NA | P08319 | ADH4 | NA |
| Recognition and association of DNA glycosylase with site containing an affected pyrimidine | R-HSA-110328 | NA | NA | 2 | R-HSA-73928 | FALSE | NA | FALSE | FALSE | FALSE | 8 | TRUE | 4.625 | 4 | NA | NA | NA | NA | NA | NA | O95243,Q13569 | MBD4,MED1,TDG | NA |
| Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | R-HSA-381426 | 2 | 1 | 5 | R-HSA-392499 | FALSE | NA | FALSE | FALSE | FALSE | 124 | TRUE | 6.07258065 | 4 | O00391,P20151 | QSOX1,QSCN6,UNQ2520/PROG013,KLK2 | NA | P02751 | FN1,FN | NA | P01009,P1047,P35555,Q14766,Q9NRM1 | SERPINA1,AAT,PI,PRO0684,PRO2209,LAMC1,LAMB2,FBN1,FBN,LTBP1,ENAM | NA |
| RNA Polymerase III Abortive And Retractive Initiation | R-HSA-749476 | 1 | NA | NA | R-HSA-74158 | FALSE | NA | FALSE | FALSE | FALSE | 41 | TRUE | 11.8536585 | 4 | Q9UKN8 | GTF3C4 | NA | NA | NA | NA | NA | NA | NA |
| SEMA3A-Plexin repulsion signaling by inhibiting Integrin adhesion | R-HSA-399955 | NA | NA | 1 | R-HSA-373755 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 11.3571429 | 4 | NA | NA | NA | NA | NA | NA | P07332 | FES,FPS | FES |
| Sema4D mediated inhibition of cell attachment and migration | R-HSA-416550 | NA | NA | 1 | R-HSA-400685 | FALSE | NA | FALSE | FALSE | FALSE | 8 | TRUE | 14.625 | 4 | NA | NA | NA | NA | NA | NA | O43157 | PLXNB1,KIAA0407,PLXN5,SEP | NA |
| Serotonin receptors | R-HSA-390666 | NA | NA | 1 | R-HSA-375280 | TRUE | NA | FALSE | TRUE | TRUE | 12 | TRUE | 4 | 4 | NA | NA | NA | NA | NA | NA | P08908 | HTR1A,ADRB2,RL1,ADBR1 | NA |
| Signaling by plasma membrane FGFR1 fusions | R-HSA-8853336 | NA | NA | 1 | R-HSA-1839124 | FALSE | NA | FALSE | FALSE | FALSE | 3 | TRUE | 11.6666667 | 4 | NA | NA | NA | NA | NA | NA | P11362 | FGFR1,BFGFR,CEK,FGFBR,FLG,FLT2,HBGFR | FGFR1 |
| Sodium/Calcium exchangers | R-HSA-425561 | NA | NA | 1 | R-HSA-425393 | TRUE | NA | FALSE | TRUE | TRUE | 11 | TRUE | 8.72727273 | 4 | NA | NA | NA | NA | NA | NA | P57103 | SLC8A3,NCX3 | NA |
| Surfactant metabolism | R-HSA-5683826 | 1 | 1 | NA | R-HSA-392499 | FALSE | NA | FALSE | FALSE | FALSE | 30 | TRUE | 3.73333333 | 4 | Q8IWL2 | SFTPA1,COLEC4,PSAP,SFTP1,SFTPA,SFTPA1B | NA | Q8IZF2 | ADGRF5,GPR116,KIAA0758 | NA | NA | NA | NA |
| Synthesis of IP3 and IP4 in the cytosol | R-HSA-1855204 | 1 | NA | 1 | R-HSA-1483249 | FALSE | NA | FALSE | FALSE | FALSE | 26 | TRUE | 8.57692308 | 4 | Q4KWH8 | PLCH1,KIAA1069,PLC3 | NA | NA | NA | NA | Q13572 | ITPK1 | NA |
| Synthesis of PA | R-HSA-1483166 | 1 | NA | NA | R-HSA-1483206 | TRUE | NA | FALSE | TRUE | TRUE | 39 | TRUE | 4.76923077 | 4 | Q9NRZ5 | AGPAT4,UNQ499/PRO1016 | NA | NA | NA | NA | NA | NA | NA |
| Synthesis of PIPs at the early endosome membrane | R-HSA-1660516 | NA | NA | 2 | R-HSA-1483255 | TRUE | NA | FALSE | TRUE | TRUE | 16 | TRUE | 5.1875 | 4 | NA | NA | NA | NA | NA | NA | Q96PE3,Q9BTU6 | INPP4A,PI4K2A | NA |
| Synthesis of PIPs at the Golgi membrane | R-HSA-1660514 | NA | NA | 1 | R-HSA-1483255 | TRUE | NA | FALSE | TRUE | TRUE | 18 | TRUE | 5.77777778 | 4 | NA | NA | NA | NA | NA | NA | Q9BTU6 | PI4K2A | NA |
| Synthesis of PIPs at the plasma membrane | R-HSA-1660499 | NA | NA | 3 | R-HSA-1483255 | TRUE | NA | FALSE | TRUE | TRUE | 53 | TRUE | 8.66037736 | 4 | NA | NA | NA | NA | NA | NA | Q96PE3,Q96T51,Q98TU6 | INPP4A,RUFY1,RABIP4,ZFYVE12,PI4K2A | NA |
| Tachykinin receptors bind tachykinins | R-HSA-380095 | 1 | NA | NA | R-HSA-375276 | TRUE | NA | FALSE | TRUE | TRUE | 5 | TRUE | 4.4 | 4 | P21452 | TACR2,NK2R,NKNAR,TAC2R | NA | NA | NA | NA | NA | NA | NA |

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|--|---------------|---|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|---|--|---|----|---------------|-----------------------------|----|---|---|----|
| Collagen biosynthesis and modifying enzymes | R-HSA-1650814 | 9 | 2 | 14 | R-HSA-1474290 | FALSE | R-HSA-8948216 | TRUE | TRUE | TRUE | 67 | TRUE | 5.2238806 | 5 | A8TX70,000469,P02462,P12107,P20849,P53420,Q05707,Q81V16,Q9UMD9 | COL6A5,COL29A1,VWA4,PLOD2,COL4A1,COL11A1,COL16,COL9A1,COL4A4,COL14A1,UND,P3H3,LEPREL2,COL17A1,BP180,BPAG2 | NA | P13674,Q14993 | P4HA1,P4HA,COL19A1 | NA | A6NMZ7,A8TX70,P02458,P02462,P12107,P20849,P20908,P27658,Q14993,Q17RW2,Q2UY09,Q5TAT6,Q8NFW1,Q9UKZ9 | COL6A6,COL6A5,COL29A1,VWA4,COL2A1,COL4A1,COL11A1,COL16,COL9A1,COL17,COL19A1,COL24A1,COL28A1,COL28,COL13A1,COL22A1,PCOLCE2,PCPE2,UNQ250/PRO287 | NA |
| Competing endogenous RNAs (ceRNAs) regulate PTEN translation | R-HSA-8948700 | 1 | NA | 1 | R-HSA-8943723 | TRUE | NA | FALSE | TRUE | TRUE | 19 | TRUE | 9.84210526 | 5 | Q9UPQ9 | TNRC6B,KIAA1093 | NA | NA | NA | NA | Q9UPQ9 | TNRC6B,KIAA1093 | NA |
| Degradation of the extracellular matrix | R-HSA-1474228 | 3 | 2 | 9 | R-HSA-1474244 | TRUE | R-HSA-1442490 | TRUE | TRUE | TRUE | 111 | TRUE | 6.18018018 | 5 | Q13751,Q8TE60,Q92743 | LAMB3,LAMNB1,ADAMTS18,ADAMTS21,HTRA1,HTRA,PRSS11 | NA | P02751,Q9P2N4 | FN1,FN,ADAMTS9,KIAA1312 | NA | O14815,P11047,P14543,P15502,P3555,P49862,P51511,Q9P2N4,Q9UMQ6 | CAPN9,NCL4,LAMC1,LA MB2,NID1,NID,ELN,FBN1,FBN,CLK7,PRSS6,SCCE,MMP15,ADAMTS9,KIAA1312,CAPN11 | NA |
| Degradation of the extracellular matrix | R-HSA-1474228 | 3 | 2 | 9 | R-HSA-1474244 | TRUE | R-HSA-1592389 | TRUE | TRUE | TRUE | 111 | TRUE | 6.18018018 | 5 | Q13751,Q8TE60,Q92743 | LAMB3,LAMNB1,ADAMTS18,ADAMTS21,HTRA1,HTRA,PRSS11 | NA | P02751,Q9P2N4 | FN1,FN,ADAMTS9,KIAA1312 | NA | O14815,P11047,P14543,P15502,P3555,P49862,P51511,Q9P2N4,Q9UMQ6 | CAPN9,NCL4,LAMC1,LA MB2,NID1,NID,ELN,FBN1,FBN,CLK7,PRSS6,SCCE,MMP15,ADAMTS9,KIAA1312,CAPN11 | NA |
| Extracellular matrix organization | R-HSA-1474244 | 2 | 1 | 3 | NA | FALSE | R-HSA-3000178 | TRUE | TRUE | TRUE | 296 | TRUE | 6.24662162 | 5 | P02462,P53420 | COL4A1,COL4A4 | NA | P02751 | FN1,FN | NA | P02458,P02462,P20908 | COL2A1,COL4A1,COL5A1 | NA |
| Extracellular matrix organization | R-HSA-1474244 | 2 | 1 | 3 | NA | FALSE | R-HSA-1566977 | TRUE | TRUE | TRUE | 296 | TRUE | 6.24662162 | 5 | P02462,P53420 | COL4A1,COL4A4 | NA | P02751 | FN1,FN | NA | P02458,P02462,P20908 | COL2A1,COL4A1,COL5A1 | NA |
| Extracellular matrix organization | R-HSA-1474244 | 2 | 1 | 3 | NA | FALSE | R-HSA-3000157 | TRUE | TRUE | TRUE | 296 | TRUE | 6.24662162 | 5 | P02462,P53420 | COL4A1,COL4A4 | NA | P02751 | FN1,FN | NA | P02458,P02462,P20908 | COL2A1,COL4A1,COL5A1 | NA |
| Extracellular matrix organization | R-HSA-1474244 | 2 | 1 | 3 | NA | FALSE | R-HSA-1566948 | TRUE | TRUE | TRUE | 296 | TRUE | 6.24662162 | 5 | P02462,P53420 | COL4A1,COL4A4 | NA | P02751 | FN1,FN | NA | P02458,P02462,P20908 | COL2A1,COL4A1,COL5A1 | NA |
| Extracellular matrix organization | R-HSA-1474244 | 2 | 1 | 3 | NA | FALSE | R-HSA-1474290 | FALSE | FALSE | TRUE | 296 | TRUE | 6.24662162 | 5 | P02462,P53420 | COL4A1,COL4A4 | NA | P02751 | FN1,FN | NA | P02458,P02462,P20908 | COL2A1,COL4A1,COL5A1 | NA |
| Extracellular matrix organization | R-HSA-1474244 | 2 | 1 | 3 | NA | FALSE | R-HSA-1474228 | TRUE | TRUE | TRUE | 296 | TRUE | 6.24662162 | 5 | P02462,P53420 | COL4A1,COL4A4 | NA | P02751 | FN1,FN | NA | P02458,P02462,P20908 | COL2A1,COL4A1,COL5A1 | NA |
| Extracellular matrix organization | R-HSA-1474244 | 2 | 1 | 3 | NA | FALSE | R-HSA-216083 | TRUE | TRUE | TRUE | 296 | TRUE | 6.24662162 | 5 | P02462,P53420 | COL4A1,COL4A4 | NA | P02751 | FN1,FN | NA | P02458,P02462,P20908 | COL2A1,COL4A1,COL5A1 | NA |
| Extracellular matrix organization | R-HSA-1474244 | 2 | 1 | 3 | NA | FALSE | R-HSA-8941237 | FALSE | FALSE | TRUE | 296 | TRUE | 6.24662162 | 5 | P02462,P53420 | COL4A1,COL4A4 | NA | P02751 | FN1,FN | NA | P02458,P02462,P20908 | COL2A1,COL4A1,COL5A1 | NA |
| Extracellular matrix organization | R-HSA-1474244 | 2 | 1 | 3 | NA | FALSE | R-HSA-3000171 | TRUE | TRUE | TRUE | 296 | TRUE | 6.24662162 | 5 | P02462,P53420 | COL4A1,COL4A4 | NA | P02751 | FN1,FN | NA | P02458,P02462,P20908 | COL2A1,COL4A1,COL5A1 | NA |
| G alpha (12/13) signalling events | R-HSA-416482 | 1 | NA | 7 | R-HSA-388396 | FALSE | NA | FALSE | FALSE | FALSE | 79 | TRUE | 11.556962 | 5 | Q92888 | ARHGEF1 | NA | NA | NA | NA | O14827,O15068,O43157,P25100,P35348,Q8TCU6,Q92974 | RASGRF2,GRF2,MCF2L,KIAA0362,OST,PLXNB1,KIAA0407,PLXN5,SEP,ADR A1D,ADRA1A,ADRA1C,PREX1,KIAA1415,ARHGEF2,KIAA0651,LPF40 | NA |
| Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation | R-HSA-8950505 | 1 | 1 | NA | R-HSA-9020591 | FALSE | NA | FALSE | FALSE | FALSE | 39 | TRUE | 9.1025641 | 5 | O00170 | AIP,XAP2 | NA | P38646 | HSPA9,GRP75,HSPA9B,mt-HSP70 | NA | NA | NA | NA |
| GLI proteins bind promoters of Hh responsive genes to promote transcription | R-HSA-5635851 | 1 | NA | NA | R-HSA-5632684 | TRUE | NA | FALSE | TRUE | TRUE | 7 | TRUE | 5.28571429 | 5 | P10070 | GLI2,THP | NA | NA | NA | NA | NA | NA | NA |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|---|---|--|-----|--------|--------------------------|----|---|---|----|
| Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell | R-HSA-198933 | 6 | NA | 6 | R-HSA-1280218 | FALSE | NA | FALSE | FALSE | FALSE | 217 | TRUE | 7.55760369 | 5 | P32942,P43626,Q6UXN2,Q96LC7,Q9UMD9,Q9Y336 | ICAM3,KIR2DL1,CD158A,NKAT1,TREML4,TLT4,UNQ9425/PRO34675,SIGLEC10,SLG2,UNQ477/PRO940,COL17A1,BP180,BPAG2,SIGLEC9,UNQ668/PRO1302 | NA | NA | NA | NA | P01891,P01892,P02458,P04234,P04439,P05534,P10314,P10316,P13746,P16188,P16189,P16190,P18462,P19320,P30443,P30447,P30450,P30453,P30455,P30456,P30457,P30459,P30512,Q09160,Q8N149,Q8NHL6 | HLA-A,HLAA,CDL2A1,CD3D,T3D,VCAM1,LILRA2,ILT1,LILR7,LILRB1,ILT2,LIR1,MI R7 | NA |
| Interleukin-10 signaling | R-HSA-6783783 | NA | 1 | NA | R-HSA-449147 | FALSE | NA | FALSE | FALSE | FALSE | 47 | TRUE | 6.23404255 | 5 | NA | NA | NA | P33681 | CD80,CD28LG,CD28LG1,LAB7 | NA | NA | NA | NA |
| Keratan sulfate biosynthesis | R-HSA-2022854 | 1 | NA | 1 | R-HSA-1638074 | FALSE | NA | FALSE | FALSE | FALSE | 28 | TRUE | 4.78571429 | 5 | Q9Y2A9 | B3GNT3,B3GALT8,TME M3,UNQ637/PRO1266 | NA | NA | NA | NA | O60512 | B4GALT3 | NA |
| Lysosome Vesicle Biogenesis | R-HSA-432720 | NA | NA | 1 | R-HSA-421837 | FALSE | NA | FALSE | FALSE | FALSE | 35 | TRUE | 8.34285714 | 5 | NA | NA | NA | NA | NA | NA | P09497 | CLTB | NA |
| mitochondrial fatty acid beta-oxidation of unsaturated fatty acids | R-HSA-77288 | NA | NA | 1 | R-HSA-77289 | FALSE | NA | FALSE | FALSE | FALSE | 6 | TRUE | 5.66666667 | 5 | NA | NA | NA | NA | NA | NA | P42126 | EC1,DCI | NA |
| mRNA 3'-end processing | R-HSA-72187 | 1 | NA | 5 | R-HSA-72203 | TRUE | NA | FALSE | TRUE | TRUE | 57 | TRUE | 6.54385965 | 5 | P38919 | EIF4A3,DDX48,KIAA0111 | NA | NA | NA | NA | Q05519,Q10570,Q8N684,Q8NI27,Q9UKF6 | SRSF11,SFRS11,CPSF1,CPSF160,CPSF7,THOC2,CXorf3,CPSF3,CPSF73 | NA |
| N-glycan antennae elongation | R-HSA-975577 | NA | NA | 1 | R-HSA-975576 | FALSE | NA | FALSE | FALSE | FALSE | 15 | TRUE | 5.4 | 5 | NA | NA | NA | NA | NA | NA | O60512 | B4GALT3 | NA |
| N-glycan trimming in the ER and Calnexin/Calreticul in cycle | R-HSA-532668 | 1 | NA | 1 | R-HSA-446203 | TRUE | R-HSA-901042 | FALSE | TRUE | TRUE | 35 | TRUE | 29.6571429 | 5 | Q13724 | MOGS,GCS1 | NA | NA | NA | NA | P55072 | VCP | NA |
| Nef mediated downregulation of MHC Class I complex cell surface expression | R-HSA-164940 | NA | NA | 1 | R-HSA-164938 | FALSE | NA | FALSE | FALSE | FALSE | 11 | TRUE | 6.09090909 | 5 | NA | NA | NA | NA | NA | NA | P01892 | HLA-A,HLAA | NA |
| Netrin mediated repulsion signals | R-HSA-418886 | 2 | NA | 2 | R-HSA-373752 | TRUE | NA | FALSE | TRUE | TRUE | 8 | TRUE | 20.125 | 5 | P12931,P43146 | SRC,SRC1,DCC,IGDC1 | SRC | NA | NA | NA | O95185,Q6UXZ4 | UNC5C,UNC5H3,UNC5D,KIAA1777,UNC5H4,UNQ6012/PRO34692 | NA |
| Phase I - Functionalization of compounds | R-HSA-211945 | 1 | NA | NA | R-HSA-211859 | FALSE | R-HSA-71384 | TRUE | TRUE | TRUE | 106 | TRUE | 5.5754717 | 5 | P27540 | ARNT,BHLHE2 | NA | NA | NA | NA | NA | NA | NA |
| Phase I - Functionalization of compounds | R-HSA-211945 | 1 | NA | NA | R-HSA-211859 | FALSE | R-HSA-211897 | FALSE | FALSE | TRUE | 106 | TRUE | 5.5754717 | 5 | P27540 | ARNT,BHLHE2 | NA | NA | NA | NA | NA | NA | NA |
| Phase I - Functionalization of compounds | R-HSA-211945 | 1 | NA | NA | R-HSA-211859 | FALSE | R-HSA-140179 | FALSE | FALSE | TRUE | 106 | TRUE | 5.5754717 | 5 | P27540 | ARNT,BHLHE2 | NA | NA | NA | NA | NA | NA | NA |
| Phase I - Functionalization of compounds | R-HSA-211945 | 1 | NA | NA | R-HSA-211859 | FALSE | R-HSA-8937144 | TRUE | TRUE | TRUE | 106 | TRUE | 5.5754717 | 5 | P27540 | ARNT,BHLHE2 | NA | NA | NA | NA | NA | NA | NA |
| Phase I - Functionalization of compounds | R-HSA-211945 | 1 | NA | NA | R-HSA-211859 | FALSE | R-HSA-217271 | FALSE | FALSE | TRUE | 106 | TRUE | 5.5754717 | 5 | P27540 | ARNT,BHLHE2 | NA | NA | NA | NA | NA | NA | NA |
| Phase I - Functionalization of compounds | R-HSA-211945 | 1 | NA | NA | R-HSA-211859 | FALSE | R-HSA-140180 | FALSE | FALSE | TRUE | 106 | TRUE | 5.5754717 | 5 | P27540 | ARNT,BHLHE2 | NA | NA | NA | NA | NA | NA | NA |
| PPARA activates gene expression | R-HSA-1989781 | 3 | NA | 2 | R-HSA-400206 | FALSE | NA | FALSE | FALSE | FALSE | 117 | TRUE | 7.45299145 | 5 | A9YTQ3,P27540,Q131333 | AHRR,BHLHE77,KIAA1234,ARNT,BHLHE2,NR1H3,LXRA | NA | NA | NA | NA | P21439,P23786 | ABC4,MDR3,PGY3,CPT2,CPT1 | NA |
| Presynaptic depolarization and calcium channel opening | R-HSA-112308 | 1 | NA | NA | R-HSA-112315 | FALSE | NA | FALSE | FALSE | FALSE | 13 | TRUE | 4.46153846 | 5 | Q15878 | CACNA1E,CACH6,CACNL1A6 | NA | NA | NA | NA | NA | NA | NA |

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|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|----|------|------------|-----|---------------|--|----|--------|-----------------|----|----------------------|---|-------|----|
| Progressive trimming of alpha-1,2-linked mannose residues from Man9/8/7GlcNAc2 to produce Man5GlcNAc2 | R-HSA-964827 | NA | 1 | NA | R-HSA-964739 | FALSE | NA | FALSE | FALSE | FALSE | 3 | TRUE | 5 | 5 | NA | NA | NA | O60476 | MAN1A2,MAN1B | NA | NA | NA | NA | |
| Regulation of PTEN mRNA translation | R-HSA-8943723 | 1 | NA | 1 | R-HSA-6807070 | FALSE | R-HSA-8948700 | TRUE | TRUE | TRUE | 28 | TRUE | 8.07142857 | 5 | Q9UPQ9 | TNRC6B,KIAA1093 | NA | NA | NA | NA | Q9UPQ9 | TNRC6B,KIAA1093 | NA | |
| Retinoid cycle disease events | R-HSA-2453864 | NA | NA | 1 | R-HSA-2474795 | FALSE | R-HSA-2466712 | FALSE | FALSE | FALSE | 9 | TRUE | 4.77777778 | 5 | NA | NA | NA | NA | NA | NA | P02766 | TTR,PALB | NA | |
| RHO GTPases Activate WASPs and WAVES | R-HSA-5663213 | 1 | 1 | NA | R-HSA-195258 | FALSE | NA | FALSE | FALSE | FALSE | 36 | TRUE | 13.5 | 5 | Q96F07 | CYFIP2,KIAA1168,PIR121 | NA | Q7L576 | CYFIP1,KIAA0068 | NA | NA | NA | NA | |
| Scavenging by Class A Receptors | R-HSA-3000480 | 1 | NA | 2 | R-HSA-2173782 | FALSE | NA | FALSE | FALSE | FALSE | 19 | TRUE | 6.84210526 | 5 | P02462 | COL4A1 | NA | NA | NA | NA | P02462,Q9BWP8 | COL4A1,COLEC11,UNQ596/PRO1182 | NA | |
| Serotonin clearance from the synaptic cleft | R-HSA-380615 | 1 | NA | 1 | R-HSA-112311 | FALSE | R-HSA-380612 | FALSE | FALSE | FALSE | 3 | TRUE | 6 | 5 | P31645 | SLC6A4,HTT,SERT | NA | NA | NA | NA | P31645 | SLC6A4,HTT,SERT | NA | |
| Sialic acid metabolism | R-HSA-4085001 | NA | NA | 1 | R-HSA-446219 | FALSE | NA | FALSE | FALSE | FALSE | 33 | TRUE | 4.87878788 | 5 | NA | NA | NA | NA | NA | NA | Q9UNP4 | ST3GAL5,SIAT9,UNQ2510/PRO5998 | NA | |
| Signal regulatory protein family interactions | R-HSA-391160 | 1 | NA | NA | R-HSA-1500931 | FALSE | NA | FALSE | FALSE | FALSE | 13 | TRUE | 23.1538462 | 5 | Q8IWL2 | SFTPA1,COLEC4,PSAP,SFTP1,SFTPA,SFTPA1B | NA | NA | NA | NA | NA | NA | NA | NA |
| The retinoid cycle in cones (daylight vision) | R-HSA-2187335 | 1 | NA | NA | R-HSA-2187338 | FALSE | NA | FALSE | FALSE | FALSE | 7 | TRUE | 4.42857143 | 5 | P10745 | RBP3 | NA | NA | NA | NA | NA | NA | NA | |
| Activation of the TFAP2 (AP-2) family of transcription factors | R-HSA-8866907 | NA | NA | 1 | R-HSA-8864260 | FALSE | NA | FALSE | FALSE | FALSE | 12 | TRUE | 12 | 5.5 | NA | NA | NA | NA | NA | NA | Q9NZC7 | WWOX,FOR,SDR41C1,WOX1 | NA | |
| Activation, myristoylation of BID and translocation to mitochondria | R-HSA-75108 | NA | NA | 1 | R-HSA-109606 | FALSE | NA | FALSE | FALSE | FALSE | 4 | TRUE | 9.5 | 5.5 | NA | NA | NA | NA | NA | NA | Q14790 | CASP8,MCH5 | NA | |
| Apoptotic execution phase | R-HSA-75153 | NA | NA | 1 | R-HSA-109581 | FALSE | R-HSA-140342 | FALSE | FALSE | TRUE | 52 | TRUE | 7.98076923 | 5.5 | NA | NA | NA | NA | NA | NA | Q14790 | CASP8,MCH5 | NA | |
| Apoptotic execution phase | R-HSA-75153 | NA | NA | 1 | R-HSA-109581 | FALSE | R-HSA-111465 | TRUE | TRUE | TRUE | 52 | TRUE | 7.98076923 | 5.5 | NA | NA | NA | NA | NA | NA | Q14790 | CASP8,MCH5 | NA | |
| Apoptotic execution phase | R-HSA-75153 | NA | NA | 1 | R-HSA-109581 | FALSE | R-HSA-211736 | FALSE | FALSE | TRUE | 52 | TRUE | 7.98076923 | 5.5 | NA | NA | NA | NA | NA | NA | Q14790 | CASP8,MCH5 | NA | |
| COP1-mediated vesicle transport | R-HSA-204005 | 1 | NA | 2 | R-HSA-199977 | FALSE | NA | FALSE | FALSE | FALSE | 68 | TRUE | 5.77941176 | 5.5 | P48553 | TRAPP10,EHOC1,TME1 | NA | NA | NA | NA | P00451,P01009 | F8,F8C,SERPINA1,AAT,PI,PRO0684,PRO2209 | NA | |
| Ligand-receptor interactions | R-HSA-5632681 | 2 | NA | NA | R-HSA-5632684 | TRUE | NA | FALSE | TRUE | TRUE | 8 | TRUE | 5.875 | 5.5 | Q13635,Q4KMG0 | PTCH1,PTCH,CDON,CDO | NA | NA | NA | NA | NA | NA | NA | |
| Reduction of cytosolic Ca++ levels | R-HSA-418359 | 2 | NA | 1 | R-HSA-418360 | FALSE | NA | FALSE | FALSE | FALSE | 12 | TRUE | 9.91666667 | 5.5 | O14983,P16615 | ATP2A1,ATP2A2,ATP2B | NA | NA | NA | NA | P57103 | SLC8A3,NXC3 | NA | |
| Activation of gene expression by SREBF (SREBP) | R-HSA-2426168 | NA | NA | 3 | R-HSA-1655829 | TRUE | NA | FALSE | TRUE | TRUE | 43 | TRUE | 8.90697674 | 6 | NA | NA | NA | NA | NA | NA | O00763,O75845,P49327 | ACACB,ACC2,ACCB,SC5D,SC5DL,FASN,FAS | NA | |
| Activation of SMO | R-HSA-5635838 | 2 | NA | 1 | R-HSA-5632684 | TRUE | NA | FALSE | TRUE | TRUE | 18 | TRUE | 7.44444444 | 6 | Q13635,Q4KMG0 | PTCH1,PTCH,CDON,CDO | NA | NA | NA | NA | O95995 | GAS8,DRC4,GAS11 | NA | |
| alpha-linolenic acid (ALA) metabolism | R-HSA-2046106 | NA | NA | 1 | R-HSA-2046104 | FALSE | NA | FALSE | FALSE | FALSE | 13 | TRUE | 5.46153846 | 6 | NA | NA | NA | NA | NA | NA | O95864 | FADS2 | NA | |
| Apoptotic cleavage of cellular proteins | R-HSA-111465 | NA | NA | 3 | R-HSA-75153 | TRUE | R-HSA-351906 | FALSE | TRUE | TRUE | 38 | TRUE | 8.39473684 | 6 | NA | NA | NA | NA | NA | NA | Q01826,Q04759,Q14790 | SATB1,PRKCQ,PRKCT,CA SP8,MCH5 | PRKCQ | |
| Apoptotic cleavage of cellular proteins | R-HSA-111465 | NA | NA | 3 | R-HSA-75153 | TRUE | R-HSA-352238 | FALSE | TRUE | TRUE | 38 | TRUE | 8.39473684 | 6 | NA | NA | NA | NA | NA | NA | Q01826,Q04759,Q14790 | SATB1,PRKCQ,PRKCT,CA SP8,MCH5 | PRKCQ | |
| Apoptotic cleavage of cellular proteins | R-HSA-111465 | NA | NA | 3 | R-HSA-75153 | TRUE | R-HSA-264870 | TRUE | TRUE | TRUE | 38 | TRUE | 8.39473684 | 6 | NA | NA | NA | NA | NA | NA | Q01826,Q04759,Q14790 | SATB1,PRKCQ,PRKCT,CA SP8,MCH5 | PRKCQ | |
| Budding and maturation of HIV virion | R-HSA-162588 | 1 | NA | 2 | R-HSA-162599 | FALSE | NA | FALSE | FALSE | FALSE | 36 | TRUE | 29.0277778 | 6 | Q9NZ09 | UBAP1,NAG20 | NA | NA | NA | NA | Q96PU5,Q9UK41 | NEDD4L,KIAA0439,NEDL3,VP528 | NA | |
| Cargo concentration in the ER | R-HSA-5694530 | 1 | NA | 3 | R-HSA-199977 | FALSE | NA | FALSE | FALSE | FALSE | 33 | TRUE | 6.27272727 | 6 | O15320 | CTAGE5,MEA11,MEA6,MGEA11,MGEA6 | NA | NA | NA | NA | O15320,P00451,P01009 | CTAGE5,MEA11,MEA6,MGEA11,MGEA6,F8,F8C,SERPINA1,AAT,PI,PRO0684,PRO2209 | NA | |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|---|--|--|----|---------------|------------------------------|---|--|--|----|
| Cargo recognition for clathrin-mediated endocytosis | R-HSA-8856825 | 1 | NA | 11 | R-HSA-8856828 | TRUE | NA | FALSE | TRUE | TRUE | 99 | TRUE | 16.5757576 | 6 | O94973 | AP2A2,ADTAB,CLAPA2,HIP9,HYP1,KIAA0899 | NA | NA | NA | NA | O14641,O60641,P01133,P04234,P08172,P09497,P11717,P35626,P53675,Q92905,Q9NY64 | DVL2,SNAP91,KIAA0656,EGF,CD3D,T3D,CHRM2,CLTB,IGF2R,MPRI,GRK3,ADRKBK2,BARK2,CLTCL1,CLH22,CLTCL,CLTD,COP55,CSN5,JAB1,SLC2A8,GLUT8,GLUTX1 | NA |
| Caspase-mediated cleavage of cytoskeletal proteins | R-HSA-264870 | 1 | NA | 2 | R-HSA-111465 | TRUE | NA | FALSE | TRUE | TRUE | 12 | TRUE | 8.08333333 | 6 | O43903 | GAS2 | NA | NA | NA | NA | P06396,Q14790 | GSN,CASP8,MCH5 | NA |
| Clathrin-mediated endocytosis | R-HSA-8856828 | 1 | NA | 9 | R-HSA-199991 | FALSE | R-HSA-8856825 | TRUE | TRUE | TRUE | 137 | TRUE | 13.2992701 | 6 | O94973 | AP2A2,ADTAB,CLAPA2,HIP9,HYP1,KIAA0899 | NA | NA | NA | NA | O14641,O60641,P01133,P04234,P08172,P09497,P11717,P35626,P53675,Q9NY64 | DVL2,SNAP91,KIAA0656,EGF,CD3D,T3D,CHRM2,CLTB,IGF2R,MPRI,CLTCL1,CLH22,CLTCL,CLTD,SLC2A8,GLUT8,GLUTX1 | NA |
| Collagen chain trimerization | R-HSA-8948216 | 7 | 1 | 13 | R-HSA-1650814 | TRUE | NA | FALSE | TRUE | TRUE | 44 | TRUE | 6.09090909 | 6 | A8TX70,P02462,P12107,P20849,P53420,Q05707,Q9UMD9 | COL6A5,COL29A1,VWA4,COL4A1,COL11A1,COLL6,COL9A1,COL4A4,COL14A1,UND,COL17A1,BP180,BPAG2 | NA | Q14993 | COL19A1 | A6NMZ7,A8TX70,P02458,P02462,P12107,P20849,P20908,P27658,Q14993,Q117RW2,Q2UY09,Q5TAT6,Q8NFW1 | COL6A6,COL6A5,COL29A1,VWA4,COL2A1,COL4A1,COL11A1,COL16,COL9A1,COL5A1,COL8A1,C3orf7,COL19A1,COL24A1,COL28A1,COL28,COL13A1,COL22A1 | NA | |
| Collagen degradation | R-HSA-1442490 | 7 | 1 | 11 | R-HSA-1474228 | TRUE | NA | FALSE | TRUE | TRUE | 40 | TRUE | 7.225 | 6 | A8TX70,P02462,P12107,P20849,P53420,Q05707,Q9UMD9 | COL6A5,COL29A1,VWA4,COL4A1,COL11A1,COLL6,COL9A1,COL4A4,COL14A1,UND,COL17A1,BP180,BPAG2 | NA | Q14993 | COL19A1 | A6NMZ7,A8TX70,P02458,P02462,P12107,P20849,P20908,P27658,P51511,Q14993,Q5TAT6 | COL6A6,COL6A5,COL29A1,VWA4,COL2A1,COL4A1,COL11A1,COL16,COL9A1,COL5A1,COL8A1,C3orf7,MMP15,COL19A1,COL13A1 | NA | |
| COPI-mediated anterograde transport | R-HSA-6807878 | 1 | NA | 5 | R-HSA-199977 | FALSE | NA | FALSE | FALSE | FALSE | 83 | TRUE | 7.42168675 | 6 | Q3ZCM7 | TUBB8 | NA | NA | NA | NA | O15020,P16157,Q14746,Q8N6H7,Q9Y678 | SPTBN2,KIAA0302,SCA5,ANK1,ANK,COG2,LDLCA,RF,RFAP2,ZNF289,Nbla10535,COPG1,COPG | NA |
| CYP2E1 reactions | R-HSA-211999 | NA | NA | 1 | R-HSA-211981 | TRUE | NA | FALSE | TRUE | TRUE | 11 | TRUE | 6.63636364 | 6 | NA | NA | NA | NA | NA | NA | P24903 | CYP2F1 | NA |
| DNA Damage Recognition in GGNER | R-HSA-5696394 | 2 | NA | 2 | R-HSA-5696399 | FALSE | NA | FALSE | FALSE | FALSE | 38 | TRUE | 27 | 6 | Q01831,Q13619 | XPC,XPC,CU14A | NA | NA | NA | NA | Q92905,Q96E28 | COP55,CSN5,JAB1,MCRS1,INO80Q,MSF58 | NA |
| E3 ubiquitin ligases ubiquitinate target proteins | R-HSA-8866654 | 1 | NA | 3 | R-HSA-8852135 | FALSE | NA | FALSE | FALSE | FALSE | 57 | TRUE | 26.8421053 | 6 | P51668 | UBE2D1,SFT,UBCSA,UBCH5,UBCH5A | NA | NA | NA | NA | P01892,P04439,P55072,P78527 | HLA-A,HLAA,VCP,PRKDC,HYRCH,HYRC1 | NA |
| Endosomal Sorting Complex Required For Transport (ESCRT) | R-HSA-917729 | 1 | 1 | 1 | R-HSA-199991 | FALSE | NA | FALSE | FALSE | FALSE | 31 | TRUE | 30.0322581 | 6 | Q9NZ09 | UBAP1,NAG20 | NA | Q86VN1 | VPS36,C13orf9,EAP45,CGLI-145 | NA | Q9UK41 | VPS28 | NA |
| ER Quality Control Compartment (ERQC) | R-HSA-901032 | NA | NA | 1 | R-HSA-901042 | FALSE | NA | FALSE | FALSE | FALSE | 21 | TRUE | 42.5238095 | 6 | NA | NA | NA | NA | NA | NA | Q13438 | OS9 | NA |
| HSF1 activation | R-HSA-3371511 | NA | NA | 1 | R-HSA-3371556 | FALSE | NA | FALSE | FALSE | FALSE | 30 | TRUE | 17.2333333 | 6 | NA | NA | NA | NA | NA | NA | P55072 | VCP | NA |
| HSF1-dependent transactivation | R-HSA-3371571 | NA | NA | 1 | R-HSA-3371556 | FALSE | R-HSA-3371568 | FALSE | FALSE | FALSE | 37 | TRUE | 15.8108108 | 6 | NA | NA | NA | NA | NA | NA | P42345 | MTOR,FRAP,FRAP1,FRAP2,RAFT1,RAFT1 | NA |
| Inactivation of CDC42 and RAC1 | R-HSA-428543 | NA | 1 | 3 | R-HSA-376176 | TRUE | NA | FALSE | TRUE | TRUE | 8 | TRUE | 13.375 | 6 | NA | NA | NA | Q7Z6B7 | SRGAP1,ARHGAP13,KIAA1304 | NA | O43295,Q7Z6B7,Q9V6N7 | SRGAP3,ARHGAP14,KIAA0411,KIAA1156,MEGA5,SRGAP2,SRGAP1,ARHGAP13,KIAA1304,ROBO1,DUTT1 | NA |
| Interleukin-4 and Interleukin-13 signaling | R-HSA-6785807 | 2 | 2 | 3 | R-HSA-449147 | FALSE | NA | FALSE | FALSE | FALSE | 112 | TRUE | 10.0178571 | 6 | P00488,P04637 | F13A1,F13A,TP53,P53 | NA | P02751,P04637 | FN1,FN,TP53,P53 | NA | P04637,P18428,P19320 | TP53,P53,LBP,VCAM1 | NA |
| IRAK4 deficiency (TLR5) | R-HSA-5603037 | NA | NA | 1 | R-HSA-5602358 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 11.8 | 6 | NA | NA | NA | NA | NA | NA | Q9BXR5 | TLR10,UNQ315/PRO358 | NA |
| IRF3-mediated induction of type I IFN | R-HSA-3270619 | 1 | NA | 1 | R-HSA-1834941 | FALSE | NA | FALSE | FALSE | FALSE | 13 | TRUE | 8.53846154 | 6 | Q7RTR2 | NLRC3,NOD3 | NA | NA | NA | NA | P78527 | PRKDC,HYRCH,HYRC1 | NA |
| Iron uptake and transport | R-HSA-917937 | NA | NA | 1 | R-HSA-382551 | FALSE | R-HSA-917977 | FALSE | FALSE | FALSE | 59 | TRUE | 19.4745763 | 6 | NA | NA | NA | NA | NA | NA | Q9BQ37 | HEPH,KIAA0698,UNQ2562/PRO6242 | NA |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|----|------|------------|-----|---|---|-----|--------|----------|----|----------------------|--|--|----|
| Membrane binding and targeting of GAG proteins | R-HSA-174490 | 1 | NA | 1 | R-HSA-174495 | FALSE | NA | FALSE | FALSE | FALSE | 15 | TRUE | 58.6 | 6 | Q9NZ09 | UBAP1,NAG20 | NA | NA | NA | NA | Q9UK41 | VPS28 | NA | |
| Negative regulation of activity of TFAP2 (AP-2) family transcription factors | R-HSA-8866904 | NA | NA | 1 | R-HSA-8864260 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 8.8 | 6 | NA | NA | NA | NA | NA | NA | Q9NZC7 | WWOX,FOR,SDR41C1,WOX1 | NA | |
| Netrin-1 signaling | R-HSA-373752 | 2 | NA | 2 | R-HSA-422475 | FALSE | R-HSA-418886 | TRUE | TRUE | TRUE | 50 | TRUE | 12.4 | 6 | O75093,P43146 | SLIT1,KIAA0813,MEGF4,SUL1,DCC,IGDCC1 | NA | NA | NA | NA | Q04759,Q9Y6N7 | PRKCQ,PRKCT,ROBO1,DUTT1 | PRKCQ | |
| Netrin-1 signaling | R-HSA-373752 | 2 | NA | 2 | R-HSA-422475 | FALSE | R-HSA-418890 | TRUE | TRUE | TRUE | 50 | TRUE | 12.4 | 6 | O75093,P43146 | SLIT1,KIAA0813,MEGF4,SUL1,DCC,IGDCC1 | NA | NA | NA | NA | Q04759,Q9Y6N7 | PRKCQ,PRKCT,ROBO1,DUTT1 | PRKCQ | |
| Netrin-1 signaling | R-HSA-373752 | 2 | NA | 2 | R-HSA-422475 | FALSE | R-HSA-418885 | TRUE | TRUE | TRUE | 50 | TRUE | 12.4 | 6 | O75093,P43146 | SLIT1,KIAA0813,MEGF4,SUL1,DCC,IGDCC1 | NA | NA | NA | NA | Q04759,Q9Y6N7 | PRKCQ,PRKCT,ROBO1,DUTT1 | PRKCQ | |
| Netrin-1 signaling | R-HSA-373752 | 2 | NA | 2 | R-HSA-422475 | FALSE | R-HSA-376172 | TRUE | TRUE | TRUE | 50 | TRUE | 12.4 | 6 | O75093,P43146 | SLIT1,KIAA0813,MEGF4,SUL1,DCC,IGDCC1 | NA | NA | NA | NA | Q04759,Q9Y6N7 | PRKCQ,PRKCT,ROBO1,DUTT1 | PRKCQ | |
| Processing of Intronic Pre-mRNAs | R-HSA-77595 | NA | NA | 3 | R-HSA-75067 | FALSE | NA | FALSE | FALSE | FALSE | 19 | TRUE | 8.78947368 | 6 | NA | NA | NA | NA | NA | NA | Q10570,Q8N684,Q9UKF6 | CPSF1,CPSF160,CPSF7,CPSF3,CPSF73 | NA | |
| Regulation of commissural axon pathfinding by SLIT and ROBO | R-HSA-428542 | 4 | NA | 1 | R-HSA-376176 | TRUE | NA | FALSE | TRUE | TRUE | 10 | TRUE | 12.5 | 6 | O75093,P12931,P43146,Q99435 | SLIT1,KIAA0813,MEGF4,SUL1,SRC,SRCC1,DCC,IGDCC1,NELL2,NRP2 | SRC | NA | NA | NA | Q9Y6N7 | ROBO1,DUTT1 | NA | |
| Regulation of FZD by ubiquitination | R-HSA-4641263 | NA | NA | 1 | R-HSA-201681 | TRUE | NA | FALSE | TRUE | TRUE | 21 | TRUE | 41.8571429 | 6 | NA | NA | NA | NA | NA | NA | Q6UXX9 | RSPO2,UNQ9384/PRO34209 | NA | |
| Regulation of gene expression by Hypoxia-inducible Factor | R-HSA-1234158 | 1 | NA | NA | R-HSA-1234174 | FALSE | NA | FALSE | FALSE | FALSE | 11 | TRUE | 12.9090909 | 6 | P27540 | ARNT,BHLHE2 | NA | NA | NA | NA | NA | NA | NA | |
| Retinoid metabolism and transport | R-HSA-975634 | NA | NA | 1 | R-HSA-6806667 | FALSE | NA | FALSE | FALSE | FALSE | 44 | TRUE | 7.70454545 | 6 | NA | NA | NA | NA | NA | NA | P02766 | TTR,PALB | NA | |
| Retinoid metabolism and transport | R-HSA-975634 | NA | NA | 1 | R-HSA-2187338 | FALSE | NA | FALSE | FALSE | FALSE | 44 | TRUE | 7.70454545 | 6 | NA | NA | NA | NA | NA | NA | P02766 | TTR,PALB | NA | |
| ROS, RNS production in phagocytes | R-HSA-1222556 | NA | NA | 1 | R-HSA-168249 | FALSE | NA | FALSE | FALSE | FALSE | 32 | TRUE | 6.15625 | 6 | NA | NA | NA | NA | NA | NA | P29475 | NOS1 | NA | |
| RUNX1 regulates transcription of genes involved in interleukin signaling | R-HSA-8939247 | 1 | NA | NA | R-HSA-8878171 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 12 | 6 | P42702 | LIFR | NA | NA | NA | NA | NA | NA | NA | |
| TP53 Regulates Transcription of Caspase Activators and Caspases | R-HSA-6803207 | 2 | 1 | 1 | R-HSA-5633008 | FALSE | NA | FALSE | FALSE | FALSE | 12 | TRUE | 10 | 6 | P04637,Q13315 | TP53,P53,ATM | NA | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | |
| Translocation of SLC2A4 (GLUT4) to the plasma membrane | R-HSA-1445148 | 1 | NA | 3 | R-HSA-199991 | FALSE | NA | FALSE | FALSE | FALSE | 51 | TRUE | 10.1372549 | 6 | Q3ZCM7 | TUBB8 | NA | NA | NA | NA | P14672,P31751,P31947 | SLC2A4,GLUT4,AKT2,SFN,HME1 | AKT2 | |
| Type I hemidesmosome assembly | R-HSA-446107 | 2 | NA | NA | R-HSA-446728 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 6.44444444 | 6 | Q13751,Q9UMD9 | LAMB3,LAMNB1,COL17A1,BP180,BPAG2 | NA | NA | NA | NA | NA | NA | NA | |
| XAV939 inhibits tankyrase, stabilizing AXIN | R-HSA-5545619 | NA | NA | 1 | R-HSA-4791275 | FALSE | NA | FALSE | FALSE | FALSE | 2 | TRUE | 6 | 6 | NA | NA | NA | NA | NA | NA | O95271 | TNKS,PARP5A,PARPL,TIN1,TINF1,TNKS1 | NA | |
| Xenobiotics | R-HSA-211981 | 1 | NA | 1 | R-HSA-211897 | FALSE | R-HSA-211957 | FALSE | FALSE | TRUE | 23 | TRUE | 6.47826087 | 6 | P27540 | ARNT,BHLHE2 | NA | NA | NA | NA | P24903 | CYP2F1 | NA | |
| Xenobiotics | R-HSA-211981 | 1 | NA | 1 | R-HSA-211897 | FALSE | R-HSA-211999 | TRUE | TRUE | TRUE | 23 | TRUE | 6.47826087 | 6 | P27540 | ARNT,BHLHE2 | NA | NA | NA | NA | P24903 | CYP2F1 | NA | |
| Assembly of collagen fibrils and other multimeric structures | R-HSA-2022090 | 8 | NA | 9 | R-HSA-1474290 | FALSE | R-HSA-2243919 | TRUE | TRUE | TRUE | 58 | TRUE | 6.43103448 | 6.5 | A8TX70,P02462,P12107,P20849,P53420,Q05707,Q13751,Q9UMD9 | COL6A5,COL29A1,VWA4,COL4A1,COL11A1,COLL6,COL9A1,COL4A4,COL14A1,UND,LAMB3,LAMNB1,COL17A1,BP180,BPAG2 | NA | NA | NA | NA | NA | A6NMZ7,A8TX70,P02458,P02462,P12107,P20849,P20908,P290908,P27658,Q17RW2 | COL6A6,COL6A5,COL29A1,VWA4,COL2A1,COL4A1,COL11A1,COLL6,COL9A1,COL5A1,COL8A1,C3orf7,COL24A1 | NA |

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|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|----|------|-------------|-----|---|---|----|--------|----------|--------|---|---|------|
| Assembly of collagen fibrils and other multimeric structures | R-HSA-2022090 | 8 | NA | 9 | R-HSA-1474290 | FALSE | R-HSA-2214320 | TRUE | TRUE | TRUE | 58 | TRUE | 6.43103448 | 6.5 | A8TX70,P02462,P12107,P20849,P53420,Q05707,Q13751,Q9UMD9 | COL6A5,COL29A1,VWA4,COL4A1,COL11A1,COLL6,COL9A1,COL4A4,COL14A1,UND,LAMB3,LAMNB1,COL17A1,BP180,BPAG2 | NA | NA | NA | NA | A6NMZ7,A8TX70,P02458,P02462,P12107,P20849,P53420,Q05707,Q13751,Q9UMD9 | COL6A6,COL6A5,COL29A1,VWA4,COL2A1,COL4A1,COL11A1,COLL6,COL9A1,COL5A1,COL8A1,C3orf77,COL24A1 | NA |
| Regulation of TP53 Activity through Association with Co-factors | R-HSA-6804759 | 3 | 1 | 2 | R-HSA-5633007 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 14.5714286 | 6.5 | P04637,Q8N9N5,Q9Y243 | TP53,P53,BANP,BEND1,SMAR1,AKT3,PKBG | NA | P04637 | TP53,P53 | NA | P04637,P31751 | TP53,P53,AKT2 | AKT2 |
| RUNX1 and FOXP3 control the development of regulatory T lymphocytes (Tregs) | R-HSA-8877330 | NA | NA | 1 | R-HSA-8878171 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 9 | 6.5 | NA | NA | NA | NA | NA | NA | P17927 | CR1,C3BR | NA |
| Acetylcholine Neurotransmitter Release Cycle | R-HSA-264642 | NA | NA | 3 | R-HSA-112310 | FALSE | NA | FALSE | FALSE | FALSE | 17 | TRUE | 8.70588235 | 7 | NA | NA | NA | NA | NA | NA | O14795,P20336,P28329 | UNC13B,UNC13,RAB3A,CHAT | NA |
| Acyl chain remodelling of PS | R-HSA-1482801 | NA | NA | 1 | R-HSA-1483206 | TRUE | NA | FALSE | TRUE | TRUE | 22 | TRUE | 6.27272727 | 7 | NA | NA | NA | NA | NA | NA | Q9BZF1 | OSBP8,KIAA1451,ORP8,OSBP10 | NA |
| Antigen Presentation: Folding, assembly and peptide loading of class I MHC | R-HSA-983170 | 1 | NA | 1 | R-HSA-983169 | FALSE | NA | FALSE | FALSE | FALSE | 25 | TRUE | 6.56 | 7 | Q9NZ08 | ERAP1,APPILS,ARTS1,KIAA0525,UNC584/PRO1154 | NA | NA | NA | NA | P01891,P01892,P04439,P05534,P10314,P13746,P16188,P16189,P16190,P18462,P30443,P30447,P30450,P30453,P30455,P30456,P30457,P30459,P30512,Q09160 | HLA-A,HLAA | NA |
| Aryl hydrocarbon receptor signalling | R-HSA-8937144 | 3 | NA | NA | R-HSA-211945 | TRUE | NA | FALSE | TRUE | TRUE | 7 | TRUE | 7.71428571 | 7 | A9YEQ3,O0170,P27540 | AHRH,BHLHE77,KIAA1234,AIP,XAP2,ARNT,BHLHE2 | NA | NA | NA | NA | NA | NA | NA |
| COPI-independent Golgi-to-ER retrograde traffic | R-HSA-6811436 | 2 | NA | NA | R-HSA-8856688 | FALSE | NA | FALSE | FALSE | FALSE | 34 | TRUE | 8.85294118 | 7 | Q3ZCM7,Q9H2M9 | TUBB8,RAB3GAP2,KIAA0839 | NA | NA | NA | NA | NA | NA | NA |
| Defective GALNT12 causes colorectal cancer 1 (CRC51) | R-HSA-5083636 | NA | NA | 1 | R-HSA-3906995 | FALSE | NA | FALSE | FALSE | FALSE | 18 | TRUE | 7.11111111 | 7 | NA | NA | NA | NA | NA | NA | Q8IXK2 | GALNT12 | NA |
| Dopamine Neurotransmitter Release Cycle | R-HSA-212676 | NA | NA | 2 | R-HSA-112310 | FALSE | NA | FALSE | FALSE | FALSE | 23 | TRUE | 7.47826087 | 7 | NA | NA | NA | NA | NA | NA | O14795,P20336 | UNC13B,UNC13,RAB3A | NA |
| ECM proteoglycans | R-HSA-3000178 | 5 | 1 | 10 | R-HSA-1474244 | TRUE | NA | FALSE | TRUE | TRUE | 56 | TRUE | 8.26785714 | 7 | A8TX70,P02462,P20849,P53420,P53708 | COL6A5,COL29A1,VWA4,COL4A1,COL9A1,COL4A4,ITGA8 | NA | P02751 | FN1,FN | NA | A6NMZ7,A8TX70,O7509,P02458,P02462,P11047,P20849,P20908,Q13797,Q14118 | COL6A6,COL6A5,COL29A1,VWA4,LRP4,KIAA0816,LRP10,MEGF7,COL2A1,COL4A1,LAMC1,LAMB2,COL9A1,COL5A1,ITGA9,DAG1 | NA |
| Eicosanoids | R-HSA-211979 | NA | NA | 1 | R-HSA-211897 | FALSE | NA | FALSE | FALSE | FALSE | 12 | TRUE | 7.83333333 | 7 | NA | NA | NA | NA | NA | NA | Q9HCS2 | CYP4F12,UNQ568/PRO1129 | NA |
| Endogenous sterols | R-HSA-211976 | 2 | NA | NA | R-HSA-211897 | FALSE | R-HSA-211994 | FALSE | FALSE | FALSE | 27 | TRUE | 8.85185185 | 7 | P11511,P27540 | CYP19A1,ARO1,CYAR,CYP19,ARNT,BHLHE2 | NA | NA | NA | NA | NA | NA | NA |
| Fatty acids | R-HSA-211935 | NA | NA | 2 | R-HSA-211897 | FALSE | NA | FALSE | FALSE | FALSE | 15 | TRUE | 6.6 | 7 | NA | NA | NA | NA | NA | NA | P24903,Q9HCS2 | CYP2F1,CYP4F12,UNQ568/PRO1129 | NA |
| Fibronectin matrix formation | R-HSA-1566977 | NA | 1 | NA | R-HSA-1474244 | TRUE | NA | FALSE | TRUE | TRUE | 6 | TRUE | 10.83333333 | 7 | NA | NA | NA | NA | P02751 | FN1,FN | NA | NA | NA |
| Folding of actin by CCT/TriC | R-HSA-390450 | NA | NA | 3 | R-HSA-389958 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 7.4 | 7 | NA | NA | NA | NA | NA | NA | P50991,Q9526,Q99832 | CCT4,CCTD,SRB,CCT6B,CCT7,CCTH,NIP7-1 | NA |
| GABA receptor activation | R-HSA-977443 | 1 | NA | 2 | R-HSA-112314 | TRUE | R-HSA-977442 | FALSE | TRUE | TRUE | 56 | TRUE | 14.125 | 7 | P47870 | GABRB2 | NA | NA | NA | NA | P14867,P47869 | GABRA1,GABRA2 | NA |
| GABA receptor activation | R-HSA-977443 | 1 | NA | 2 | R-HSA-112314 | TRUE | R-HSA-977441 | TRUE | TRUE | TRUE | 56 | TRUE | 14.125 | 7 | P47870 | GABRB2 | NA | NA | NA | NA | P14867,P47869 | GABRA1,GABRA2 | NA |
| GABA receptor activation | R-HSA-977443 | 1 | NA | 2 | R-HSA-112314 | TRUE | R-HSA-977444 | FALSE | TRUE | TRUE | 56 | TRUE | 14.125 | 7 | P47870 | GABRB2 | NA | NA | NA | NA | P14867,P47869 | GABRA1,GABRA2 | NA |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|---|---|---|-------|--------|---------|----|--|--|----|
| GABA synthesis, release, reuptake and degradation | R-HSA-888590 | NA | NA | 1 | R-HSA-112310 | FALSE | R-HSA-888568 | FALSE | FALSE | FALSE | 19 | TRUE | 8.63157895 | 7 | NA | NA | NA | NA | NA | NA | P20336 | RAB3A | NA |
| GABA synthesis, release, reuptake and degradation | R-HSA-888590 | NA | NA | 1 | R-HSA-112310 | FALSE | R-HSA-916853 | FALSE | FALSE | FALSE | 19 | TRUE | 8.63157895 | 7 | NA | NA | NA | NA | NA | NA | P20336 | RAB3A | NA |
| GABA synthesis, release, reuptake and degradation | R-HSA-888590 | NA | NA | 1 | R-HSA-112310 | FALSE | R-HSA-888593 | FALSE | FALSE | FALSE | 19 | TRUE | 8.63157895 | 7 | NA | NA | NA | NA | NA | NA | P20336 | RAB3A | NA |
| Glutamate Neurotransmitter Release Cycle | R-HSA-210500 | NA | NA | 3 | R-HSA-112310 | FALSE | NA | FALSE | FALSE | FALSE | 24 | TRUE | 7.25 | 7 | NA | NA | NA | NA | NA | NA | O00341,O14795,P20336 | SLC1A7,EAAT5,UNC13B,UNC13,RAB3A | NA |
| Integrin cell surface interactions | R-HSA-216083 | 6 | 1 | 11 | R-HSA-1474244 | TRUE | NA | FALSE | TRUE | TRUE | 66 | TRUE | 8.28787879 | 7 | A8TX70,P02462,P20849,P32942,P53420,P53708 | COL6A5,COL29A1,VWA4,COL4A1,COL9A1,ICAM3,COL4A4,ITGA8 | NA | P02751 | FN1, FN | NA | A6NMZ7,A8TX70,P02458,P02462,P19320,P20849,P20908,P27658,P35555,Q13797,Q5TAT6 | COL6A6,COL6A5,COL29A1,VWA4,COL2A1,COL4A1,VCAM1,COL9A1,COL5A1,COL8A1,C3orf77,FBN1,FBN,ITGA9,COL13A1 | NA |
| L1CAM interactions | R-HSA-373760 | 2 | NA | 1 | R-HSA-422475 | FALSE | R-HSA-447038 | TRUE | TRUE | TRUE | 100 | TRUE | 11.73 | 7 | P29323,P32004 | EPHB2,DRT,EPHT3,EPHT3,ERK,HEK5,TYROS5,L1CAM,CAML1,MICS | EPHB2 | NA | NA | NA | P11047 | LAMC1,LAMB2 | NA |
| L1CAM interactions | R-HSA-373760 | 2 | NA | 1 | R-HSA-422475 | FALSE | R-HSA-447043 | TRUE | TRUE | TRUE | 100 | TRUE | 11.73 | 7 | P29323,P32004 | EPHB2,DRT,EPHT3,EPHT3,ERK,HEK5,TYROS5,L1CAM,CAML1,MICS | EPHB2 | NA | NA | NA | P11047 | LAMC1,LAMB2 | NA |
| L1CAM interactions | R-HSA-373760 | 2 | NA | 1 | R-HSA-422475 | FALSE | R-HSA-445144 | TRUE | TRUE | TRUE | 100 | TRUE | 11.73 | 7 | P29323,P32004 | EPHB2,DRT,EPHT3,EPHT3,ERK,HEK5,TYROS5,L1CAM,CAML1,MICS | EPHB2 | NA | NA | NA | P11047 | LAMC1,LAMB2 | NA |
| L1CAM interactions | R-HSA-373760 | 2 | NA | 1 | R-HSA-422475 | FALSE | R-HSA-447041 | TRUE | TRUE | TRUE | 100 | TRUE | 11.73 | 7 | P29323,P32004 | EPHB2,DRT,EPHT3,EPHT3,ERK,HEK5,TYROS5,L1CAM,CAML1,MICS | EPHB2 | NA | NA | NA | P11047 | LAMC1,LAMB2 | NA |
| L1CAM interactions | R-HSA-373760 | 2 | NA | 1 | R-HSA-422475 | FALSE | R-HSA-437239 | TRUE | TRUE | TRUE | 100 | TRUE | 11.73 | 7 | P29323,P32004 | EPHB2,DRT,EPHT3,EPHT3,ERK,HEK5,TYROS5,L1CAM,CAML1,MICS | EPHB2 | NA | NA | NA | P11047 | LAMC1,LAMB2 | NA |
| L1CAM interactions | R-HSA-373760 | 2 | NA | 1 | R-HSA-422475 | FALSE | R-HSA-445095 | TRUE | TRUE | TRUE | 100 | TRUE | 11.73 | 7 | P29323,P32004 | EPHB2,DRT,EPHT3,EPHT3,ERK,HEK5,TYROS5,L1CAM,CAML1,MICS | EPHB2 | NA | NA | NA | P11047 | LAMC1,LAMB2 | NA |
| Major pathway of rRNA processing in the nucleolus and cytosol | R-HSA-6791226 | 1 | 1 | 8 | R-HSA-8868773 | FALSE | NA | FALSE | FALSE | FALSE | 185 | TRUE | 11.372973 | 7 | P23396 | RPS3,OK/SW-cl.26 | NA | O00541 | PES1 | NA | O75691,O95059,P46781,P62277,Q12788,Q96L21,Q99547,Q9Y2X3 | UTP20,DRIM,RPP14,RPS9,RPS13,TBL3,SAZD,RPL10L,MPHOSPH6,MPP6,NOP58,NOLS,NOP5,HSPC120 | NA |
| MHC class II antigen presentation | R-HSA-2132295 | 2 | NA | 1 | R-HSA-1280218 | FALSE | NA | FALSE | FALSE | FALSE | 108 | TRUE | 7.99074074 | 7 | O94973,Q3ZCM7 | AP2A2,ADTAB,CLAPA2,HIP9,HYP1,KIAA0899,TUBB8 | NA | NA | NA | NA | O15020 | SPTBN2,KIAA0302,SCA5 | NA |
| NCAM1 interactions | R-HSA-419037 | 5 | NA | 8 | R-HSA-375165 | TRUE | NA | FALSE | TRUE | TRUE | 37 | TRUE | 6.64864865 | 7 | A8TX70,P02462,P20849,P53420,Q13936 | COL6A5,COL29A1,VWA4,COL4A1,COL9A1,COL4A4,CACNA1C,CACH2,CACN2,CACN11A1,CCHL1A1 | NA | NA | NA | NA | A6NMZ7,A8TX70,O00451,P02458,P02462,P20849,P20908,Q01668 | COL6A6,COL6A5,COL29A1,VWA4,GFRA2,GDNFRB,RET1L,TRNR2,COL2A1,COL4A1,COL9A1,COL5A1,CACNA1D,CACH3,CACN4,CACN11A2,CCHL1A2 | NA |
| Negative regulation of TCF-dependent signaling by DVL-interacting proteins | R-HSA-5368598 | 1 | NA | 1 | R-HSA-201681 | TRUE | NA | FALSE | TRUE | TRUE | 5 | TRUE | 6 | 7 | Q9P219 | CCDC88C,DAPLE,KIAA1509 | NA | NA | NA | NA | O14641 | DVL2 | NA |
| Norepinephrine Neurotransmitter Release Cycle | R-HSA-181430 | NA | NA | 2 | R-HSA-112310 | FALSE | NA | FALSE | FALSE | FALSE | 18 | TRUE | 9.33333333 | 7 | NA | NA | NA | NA | NA | NA | O14795,P20336 | UNC13B,UNC13,RAB3A | NA |
| Regulation of cholesterol biosynthesis by SREBP (SREBF) | R-HSA-1655829 | 1 | NA | NA | R-HSA-8957322 | FALSE | R-HSA-2426168 | TRUE | TRUE | TRUE | 56 | TRUE | 8.16071429 | 7 | P62826 | RAN,ARA24,OK/SW-cl.81 | NA | NA | NA | NA | NA | NA | NA |
| Regulation of cortical dendrite branching | R-HSA-8985801 | 1 | NA | 1 | R-HSA-376176 | TRUE | NA | FALSE | TRUE | TRUE | 4 | TRUE | 7 | 7 | O75093 | SLIT1,KIAA0813,MEGF4,SUL1 | NA | NA | NA | NA | Q9Y6N7 | ROBO1,DUTT1 | NA |
| RHO GTPases Activate Formins | R-HSA-5663220 | 2 | NA | 2 | R-HSA-195258 | FALSE | NA | FALSE | FALSE | FALSE | 121 | TRUE | 13.7768595 | 7 | Q3ZCM7,Q72460 | TUBB8,CLASP1,KIAA0622,MAST1 | MAST1 | NA | NA | NA | O14641,P50748 | DVL2,KNTC1,KIAA0166 | NA |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|----|------|------------|-----|-----------------------------|---|-------------|--------|------------------|-------|--|--|-------------------|----|
| RMTs methylate histone arginines | R-HSA-3214858 | 2 | NA | 2 | R-HSA-3247509 | TRUE | NA | FALSE | TRUE | TRUE | 49 | TRUE | 15.6326531 | 7 | P62805,Q86U86 | HIST1H4A,H4/A,H4FA;,HIST1H4B,H4/J,H4FI;,HIST1H4C,H4/G,H4FG;,HIST1H4D,H4/B,H4FB;,HIST1H4E,H4/J,H4FJ;,HIST1H4F,H4/C,H4FC;,HIST1H4H,H4/H,H4FH;,HIST1H4I,H4/M,H4FM;,HIST1H4J,H4/E,H4FE;,HIST1H4K,H4/D,H4FD;,HIST1H4L,H4/K,H4FK;,HIST2H4A,H4/N,H4F2,H4FN,HIST2H4;,HIST2H4B,H4/O,H4FO;,HIST4H4,PBRM1,BAF180,PB1 | NA | NA | NA | NA | P51532,Q99873 | SMARCA4,BAF190A,BR G1,SNF2B,SNF2L4,PRM1,HMT2,HRMT2L1R1B4 | NA | |
| RNA Polymerase III Transcription Initiation From Type 1 Promoter | R-HSA-76061 | 1 | NA | NA | R-HSA-76046 | FALSE | NA | FALSE | FALSE | FALSE | 28 | TRUE | 16.0714286 | 7 | Q9UKN8 | GTF3C4 | NA | NA | NA | NA | NA | NA | | |
| RNA Polymerase III Transcription Initiation From Type 2 Promoter | R-HSA-76066 | 1 | NA | NA | R-HSA-76046 | FALSE | NA | FALSE | FALSE | FALSE | 27 | TRUE | 16.5925926 | 7 | Q9UKN8 | GTF3C4 | NA | NA | NA | NA | NA | NA | | |
| RUNX1 interacts with co-factors whose precise effect on RUNX1 targets is not known | R-HSA-8939243 | 1 | NA | 1 | R-HSA-8878171 | FALSE | NA | FALSE | FALSE | FALSE | 37 | TRUE | 9.35135135 | 7 | Q86U86 | PBRM1,BAF180,PB1 | NA | NA | NA | NA | P51532 | SMARCA4,BAF190A,BR G1,SNF2B,SNF2L4 | NA | |
| Serotonin Neurotransmitter Release Cycle | R-HSA-181429 | NA | NA | 2 | R-HSA-112310 | FALSE | NA | FALSE | FALSE | FALSE | 18 | TRUE | 8.44444444 | 7 | NA | NA | NA | NA | NA | NA | O14795,P20336 | UNC13B,UNC13,RAB3A | NA | |
| Synaptic adhesion-like molecules | R-HSA-8849932 | 1 | NA | 3 | R-HSA-6794362 | FALSE | NA | FALSE | FALSE | FALSE | 21 | TRUE | 6.47619048 | 7 | P23468 | PTPRD | NA | NA | NA | NA | P23468,P48058,Q12879 | PTPRD,GRIA4,GLUR4,G RIN2A,NMDAR2A | NA | |
| Synthesis of bile acids and bile salts via 7alpha-hydroxycholesterol | R-HSA-193368 | 1 | NA | NA | R-HSA-192105 | FALSE | NA | FALSE | FALSE | FALSE | 24 | TRUE | 8.83333333 | 7 | O95342 | ABCB11,BSEP | NA | NA | NA | NA | NA | NA | NA | |
| Synthesis of Leukotrienes (LT) and Exoins (EX) | R-HSA-2142691 | NA | 1 | 1 | R-HSA-2142753 | FALSE | NA | FALSE | FALSE | FALSE | 21 | TRUE | 7.76190476 | 7 | NA | NA | NA | P16444 | DPEP1,MDP,RDP | NA | P33527 | ABCC1,MRP,MRP1 | NA | |
| TP53 Regulates Metabolic Genes | R-HSA-5628897 | 4 | 1 | 7 | R-HSA-3700989 | FALSE | NA | FALSE | FALSE | FALSE | 89 | TRUE | 9.16853933 | 7 | P04637,P49815,Q9UPQ9,Q9Y243 | TP53,P53,TSC2,TSC4,TNRC6B,KIAA1093,AKT3,PKBG | NA | P04637 | TP53,P53 | NA | P04637,P31751,P31947,P42345,Q8N808,Q985H4,Q9UP09 | TP53,P53,AKT2,SFN,HM E1,MTOR,FRAP,FRAP1,FRAP2,RAFT1,RAP1,COX18,OXAL12,TACO1,CCDC44,PRO0477,TNRC6B,KIAA1093 | AKT2 | |
| TP53 Regulates Transcription of Death Receptors and Ligands | R-HSA-6803211 | 1 | 1 | 1 | R-HSA-5633008 | FALSE | NA | FALSE | FALSE | FALSE | 12 | TRUE | 9.16666667 | 7 | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | |
| TRAF6 mediated IRF7 activation | R-HSA-933541 | NA | NA | 1 | R-HSA-168928 | TRUE | NA | FALSE | TRUE | TRUE | 28 | TRUE | 11.7857143 | 7 | NA | NA | NA | NA | NA | NA | O95786 | DDX58 | NA | |
| Unwinding of DNA | R-HSA-176974 | NA | NA | 1 | R-HSA-69190 | FALSE | NA | FALSE | FALSE | FALSE | 12 | TRUE | 5.08333333 | 7 | NA | NA | NA | NA | NA | NA | Q9BRX5 | GINS3,PSF3 | NA | |
| Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal | R-HSA-141444 | 1 | NA | 1 | R-HSA-141424 | FALSE | NA | FALSE | FALSE | FALSE | 94 | TRUE | 14.606383 | 7.5 | Q7Z460 | CLASP1,KIAA0622,MAST1 | MAST1 | NA | NA | NA | NA | P50748 | KNTC1,KIAA0166 | NA |
| CS/DS degradation | R-HSA-2024101 | 1 | NA | NA | R-HSA-1793185 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 7.78571429 | 7.5 | P15848 | ARSB | NA | NA | NA | NA | NA | NA | NA | |
| EPH-Ephrin signaling | R-HSA-2682334 | 2 | 1 | 3 | R-HSA-422475 | FALSE | R-HSA-3928664 | TRUE | TRUE | TRUE | 92 | TRUE | 11.6413043 | 7.5 | P29323,Q15375 | EPHB2,DRT,EPHT3,EPHT3,ERK,HEKS,TYROS,EPHA7,EHK3,HEK11 | EPHB2,EPHA7 | Q15375 | EPHA7,EHK3,HEK11 | EPHA7 | P29320,P54756,Q15375 | EPHA3,ETK,ETK1,HEK,TYR04,EPHA5,BSK,EHK1,H EK7,EPHA7,EHK3,HEK11 | EPHA3,EPHA5,EPHA7 | |
| EPH-Ephrin signaling | R-HSA-2682334 | 2 | 1 | 3 | R-HSA-422475 | FALSE | R-HSA-3928662 | TRUE | TRUE | TRUE | 92 | TRUE | 11.6413043 | 7.5 | P29323,Q15375 | EPHB2,DRT,EPHT3,EPHT3,ERK,HEKS,TYROS,EPHA7,EHK3,HEK11 | EPHB2,EPHA7 | Q15375 | EPHA7,EHK3,HEK11 | EPHA7 | P29320,P54756,Q15375 | EPHA3,ETK,ETK1,HEK,TYR04,EPHA5,BSK,EHK1,H EK7,EPHA7,EHK3,HEK11 | EPHA3,EPHA5,EPHA7 | |
| EPH-Ephrin signaling | R-HSA-2682334 | 2 | 1 | 3 | R-HSA-422475 | FALSE | R-HSA-3928663 | TRUE | TRUE | TRUE | 92 | TRUE | 11.6413043 | 7.5 | P29323,Q15375 | EPHB2,DRT,EPHT3,EPHT3,ERK,HEKS,TYROS,EPHA7,EHK3,HEK11 | EPHB2,EPHA7 | Q15375 | EPHA7,EHK3,HEK11 | EPHA7 | P29320,P54756,Q15375 | EPHA3,ETK,ETK1,HEK,TYR04,EPHA5,BSK,EHK1,H EK7,EPHA7,EHK3,HEK11 | EPHA3,EPHA5,EPHA7 | |
| EPH-Ephrin signaling | R-HSA-2682334 | 2 | 1 | 3 | R-HSA-422475 | FALSE | R-HSA-3928665 | TRUE | TRUE | TRUE | 92 | TRUE | 11.6413043 | 7.5 | P29323,Q15375 | EPHB2,DRT,EPHT3,EPHT3,ERK,HEKS,TYROS,EPHA7,EHK3,HEK11 | EPHB2,EPHA7 | Q15375 | EPHA7,EHK3,HEK11 | EPHA7 | P29320,P54756,Q15375 | EPHA3,ETK,ETK1,HEK,TYR04,EPHA5,BSK,EHK1,H EK7,EPHA7,EHK3,HEK11 | EPHA3,EPHA5,EPHA7 | |

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|---|---------------|----|----|----|---------------|-------|--------------|-------|-------|-------|-----|------|------------|-----|----------------------|-------------------------------------|-------|--------|------------|----|----------------------|--|------|
| Gamma-carboxylation of protein precursors | R-HSA-159740 | NA | NA | 2 | R-HSA-159854 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 7.5 | 7.5 | NA | NA | NA | NA | NA | NA | P07225,P22891 | PROS1,PROS,PROZ | NA |
| NCAM signaling for neurite out-growth | R-HSA-375165 | NA | 1 | 2 | R-HSA-422475 | FALSE | R-HSA-419037 | TRUE | TRUE | TRUE | 58 | TRUE | 18.1896552 | 7.5 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | O15020,P01112 | SPTBN2,KIAA0302,SCA5,HRAS,HRAS1 | NA |
| Negative regulators of DDX58/FIH1 signaling | R-HSA-936440 | 2 | NA | 1 | R-HSA-168928 | TRUE | NA | FALSE | TRUE | TRUE | 34 | TRUE | 31.1764706 | 7.5 | P51668,Q15366 | UBE2D1,SFT,UBC5A,UBCH5,UBCH5A,PCBP2 | NA | NA | NA | NA | O95786 | DDX58 | NA |
| Neurotransmitter receptors and postsynaptic signal transmission | R-HSA-112314 | NA | NA | 1 | R-HSA-112315 | FALSE | R-HSA-977443 | TRUE | TRUE | TRUE | 154 | TRUE | 13.2337662 | 7.5 | NA | NA | NA | NA | NA | NA | O75311 | GLRA3 | NA |
| Neurotransmitter receptors and postsynaptic signal transmission | R-HSA-112314 | NA | NA | 1 | R-HSA-112315 | FALSE | R-HSA-399721 | FALSE | FALSE | TRUE | 154 | TRUE | 13.2337662 | 7.5 | NA | NA | NA | NA | NA | NA | O75311 | GLRA3 | NA |
| Neurotransmitter receptors and postsynaptic signal transmission | R-HSA-112314 | NA | NA | 1 | R-HSA-112315 | FALSE | R-HSA-181431 | FALSE | FALSE | TRUE | 154 | TRUE | 13.2337662 | 7.5 | NA | NA | NA | NA | NA | NA | O75311 | GLRA3 | NA |
| Neurotransmitter receptors and postsynaptic signal transmission | R-HSA-112314 | NA | NA | 1 | R-HSA-112315 | FALSE | R-HSA-451326 | FALSE | FALSE | TRUE | 154 | TRUE | 13.2337662 | 7.5 | NA | NA | NA | NA | NA | NA | O75311 | GLRA3 | NA |
| Neurotransmitter receptors and postsynaptic signal transmission | R-HSA-112314 | NA | NA | 1 | R-HSA-112315 | FALSE | R-HSA-442755 | FALSE | FALSE | TRUE | 154 | TRUE | 13.2337662 | 7.5 | NA | NA | NA | NA | NA | NA | O75311 | GLRA3 | NA |
| Pre-NOTCH Processing in Golgi | R-HSA-1912420 | 2 | NA | 1 | R-HSA-1912422 | FALSE | NA | FALSE | FALSE | FALSE | 18 | TRUE | 7.83333333 | 7.5 | O14983,P16615 | ATP2A1,ATP2A2,ATP2B | NA | NA | NA | NA | Q04721 | NOTCH2 | NA |
| Regulation of TNFR1 signaling | R-HSA-5357905 | 1 | NA | 1 | R-HSA-75893 | FALSE | NA | FALSE | FALSE | FALSE | 36 | TRUE | 32.0277778 | 7.5 | O75604 | USP2,UBP41 | NA | NA | NA | NA | Q14790 | CASP8,MCH5 | NA |
| Role of ABL in ROBO-SLIT signaling | R-HSA-428890 | 1 | NA | 1 | R-HSA-376176 | TRUE | NA | FALSE | TRUE | TRUE | 8 | TRUE | 7.75 | 7.5 | Q7Z460 | CLASP1,KIAA0622,MAST1 | MAST1 | NA | NA | NA | Q9Y6N7 | ROBO1,DUTT1 | NA |
| Role of second messengers in netrin-1 signaling | R-HSA-418890 | 2 | NA | 3 | R-HSA-373752 | TRUE | NA | FALSE | TRUE | TRUE | 10 | TRUE | 10.6 | 7.5 | P43146,Q9UL62 | DCC,IGDCC1,TRPC5,TRP5 | NA | NA | NA | NA | Q13507,Q9UBN4,Q9Y210 | TRPC3,TRP3,TRPC4,TRPC6,TRP6 | NA |
| Sema4D induced cell migration and growth-cone collapse | R-HSA-416572 | NA | NA | 2 | R-HSA-400685 | FALSE | NA | FALSE | FALSE | FALSE | 20 | TRUE | 8.3 | 7.5 | NA | NA | NA | NA | NA | NA | O43157,Q7Z406 | PLXNB1,KIAA0407,PLXN5,SEP,MYH14,KIAA2034,FP17425 | NA |
| Activation of AMPA receptors | R-HSA-399710 | NA | NA | 2 | R-HSA-399721 | FALSE | NA | FALSE | FALSE | FALSE | 4 | TRUE | 8.5 | 8 | NA | NA | NA | NA | NA | NA | P42262,P48058 | GRIA2,GLUR2,GRIA4,GLUR4 | NA |
| Activation of PUMA and translocation to mitochondria | R-HSA-139915 | 1 | 1 | 1 | R-HSA-114452 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 14 | 8 | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA |
| Anchoring fibril formation | R-HSA-2214320 | 3 | NA | 1 | R-HSA-2022090 | TRUE | NA | FALSE | TRUE | TRUE | 7 | TRUE | 7.57142857 | 8 | P02462,P53420,Q13751 | COL4A1,COL4A4,LAMB3,LAMNB1 | NA | NA | NA | NA | P02462 | COL4A1 | NA |
| CHL1 interactions | R-HSA-447041 | NA | NA | 1 | R-HSA-373760 | TRUE | NA | FALSE | TRUE | TRUE | 9 | TRUE | 9.33333333 | 8 | NA | NA | NA | NA | NA | NA | P16157 | ANK1,ANK | NA |
| Deactivation of the beta-catenin transactivating complex | R-HSA-3769402 | 1 | NA | 3 | R-HSA-201681 | TRUE | NA | FALSE | TRUE | TRUE | 42 | TRUE | 28.452381 | 8 | Q9Y297 | BTRC,BTRCP,FBW1A,FBXW1A | NA | NA | NA | NA | P31751,Q9CK8,Q9HCS4 | AKT2,CHDB,HELNSF1,KIAA1564,TCF7L1,TCF3 | AKT2 |
| DSCAM interactions | R-HSA-376172 | 1 | NA | NA | R-HSA-373752 | TRUE | NA | FALSE | TRUE | TRUE | 11 | TRUE | 18.0909091 | 8 | P43146 | DCC,IGDCC1 | NA | NA | NA | NA | NA | NA | NA |
| EGFR downregulation | R-HSA-182971 | NA | NA | 1 | R-HSA-177929 | TRUE | NA | FALSE | TRUE | TRUE | 25 | TRUE | 44.4 | 8 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|----|------|------------|---|----------------------|----------------------------|-----|--------|-------------------------|-----|--|--|------|
| Endosomal/Vacuolar pathway | R-HSA-1236977 | NA | NA | 1 | R-HSA-1236975 | FALSE | NA | FALSE | FALSE | FALSE | 12 | TRUE | 7.58333333 | 8 | NA | NA | NA | NA | NA | NA | P01891,P01892,P04439,P05534,P10314,P10316,P13746,P16188,P16189,P16190,P18462,P30443,P30447,P30450,P30453,P30455,P30456,P30457,P30459,P30512,Q09160 | HLA-A,HLAA | NA |
| Energy dependent regulation of mTOR by LKB1-AMPK | R-HSA-380972 | 1 | NA | 1 | R-HSA-165159 | TRUE | NA | FALSE | TRUE | TRUE | 29 | TRUE | 8.13793103 | 8 | P49815 | TSC2,TSC4 | NA | NA | NA | NA | P42345 | MTOR_FRAP,FRAP1,FRA P2,RAFT1,RAFT1 | NA |
| Generation of second messenger molecules | R-HSA-202433 | NA | NA | 3 | R-HSA-202403 | FALSE | NA | FALSE | FALSE | FALSE | 40 | TRUE | 9.4 | 8 | NA | NA | NA | NA | NA | NA | P04234,P06239,Q13094 | CD3D,T3D,LCK,LCP2 | LCK |
| HSP90 chaperone cycle for steroid hormone receptors (SHR) | R-HSA-3371497 | 1 | 1 | NA | R-HSA-2262752 | FALSE | NA | FALSE | FALSE | FALSE | 38 | TRUE | 10.0263158 | 8 | Q3ZCM7 | TUBB8 | NA | Q13451 | FKBP5,AIG6,FKBP51 | NA | NA | NA | NA |
| Laminin interactions | R-HSA-3000157 | 3 | NA | 3 | R-HSA-1474244 | TRUE | NA | FALSE | TRUE | TRUE | 23 | TRUE | 8.2173913 | 8 | P02462,P53420,Q13751 | COL4A1,COL4A4,LAMB3,LAMNB1 | NA | NA | NA | NA | P02462,P11047,P14543 | COL4A1,LAMC1,LAMB2,NID1,NID | NA |
| Metalloprotease DUBs | R-HSA-5689901 | NA | NA | 2 | R-HSA-5688426 | FALSE | NA | FALSE | FALSE | FALSE | 31 | TRUE | 41.3870968 | 8 | NA | NA | NA | NA | NA | NA | P38398,Q96RL1 | BRCA1,RNF53,UIMC1,RAP80,RXRIP110 | NA |
| Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane | R-HSA-190840 | 1 | NA | NA | R-HSA-190872 | FALSE | NA | FALSE | FALSE | FALSE | 1 | TRUE | 8 | 8 | Q3ZCM7 | TUBB8 | NA | NA | NA | NA | NA | NA | NA |
| mTOR signalling | R-HSA-165159 | NA | NA | 1 | R-HSA-162582 | FALSE | R-HSA-380972 | TRUE | TRUE | TRUE | 40 | TRUE | 10.4 | 8 | NA | NA | NA | NA | NA | NA | P42345 | MTOR_FRAP,FRAP1,FRA P2,RAFT1,RAFT1 | NA |
| mTOR signalling | R-HSA-165159 | NA | NA | 1 | R-HSA-162582 | FALSE | R-HSA-166208 | TRUE | TRUE | TRUE | 40 | TRUE | 10.4 | 8 | NA | NA | NA | NA | NA | NA | P42345 | MTOR_FRAP,FRAP1,FRA P2,RAFT1,RAFT1 | NA |
| mTOR signalling | R-HSA-165159 | NA | NA | 1 | R-HSA-162582 | FALSE | R-HSA-165181 | TRUE | TRUE | TRUE | 40 | TRUE | 10.4 | 8 | NA | NA | NA | NA | NA | NA | P42345 | MTOR_FRAP,FRAP1,FRA P2,RAFT1,RAFT1 | NA |
| mTORC1-mediated signalling | R-HSA-166208 | NA | NA | 1 | R-HSA-165159 | TRUE | NA | FALSE | TRUE | TRUE | 23 | TRUE | 10.0869565 | 8 | NA | NA | NA | NA | NA | NA | P42345 | MTOR_FRAP,FRAP1,FRA P2,RAFT1,RAFT1 | NA |
| NrCAM interactions | R-HSA-447038 | NA | NA | 1 | R-HSA-373760 | TRUE | NA | FALSE | TRUE | TRUE | 7 | TRUE | 8.28571429 | 8 | NA | NA | NA | NA | NA | NA | P16157 | ANK1,ANK | NA |
| PD-1 signalling | R-HSA-389948 | NA | NA | 2 | R-HSA-388841 | FALSE | NA | FALSE | FALSE | FALSE | 30 | TRUE | 10.7 | 8 | NA | NA | NA | NA | NA | NA | P04234,P06239 | CD3D,T3D,LCK | LCK |
| Phosphorylation of CD3 and TCR zeta chains | R-HSA-202427 | NA | NA | 3 | R-HSA-202403 | FALSE | NA | FALSE | FALSE | FALSE | 29 | TRUE | 8.34482759 | 8 | NA | NA | NA | NA | NA | NA | P04234,P06239,Q12913 | CD3D,T3D,LCK,PTPRJ,DE P1 | LCK |
| Platelet homeostasis | R-HSA-418346 | 1 | NA | 1 | R-HSA-109582 | FALSE | R-HSA-392851 | FALSE | FALSE | TRUE | 89 | TRUE | 16.6179775 | 8 | P51575 | P2RX1,P2X1 | NA | NA | NA | NA | Q99571 | P2RX4 | NA |
| Platelet homeostasis | R-HSA-418346 | 1 | NA | 1 | R-HSA-109582 | FALSE | R-HSA-432142 | TRUE | TRUE | TRUE | 89 | TRUE | 16.6179775 | 8 | P51575 | P2RX1,P2X1 | NA | NA | NA | NA | Q99571 | P2RX4 | NA |
| Platelet homeostasis | R-HSA-418346 | 1 | NA | 1 | R-HSA-109582 | FALSE | R-HSA-418360 | FALSE | FALSE | TRUE | 89 | TRUE | 16.6179775 | 8 | P51575 | P2RX1,P2X1 | NA | NA | NA | NA | Q99571 | P2RX4 | NA |
| Platelet homeostasis | R-HSA-418346 | 1 | NA | 1 | R-HSA-109582 | FALSE | R-HSA-392154 | TRUE | TRUE | TRUE | 89 | TRUE | 16.6179775 | 8 | P51575 | P2RX1,P2X1 | NA | NA | NA | NA | Q99571 | P2RX4 | NA |
| Regulation of RUNX1 Expression and Activity | R-HSA-8934593 | 2 | NA | 1 | R-HSA-8878171 | FALSE | NA | FALSE | FALSE | FALSE | 27 | TRUE | 14.7037037 | 8 | P12931,O9UPQ9 | SRC,SRIC1,TNRC6B,KIAA1093 | SRC | NA | NA | NA | Q9UPQ9 | TNRC6B,KIAA1093 | NA |
| Regulation of TP53 Activity through Acetylation | R-HSA-6804758 | 2 | 1 | 2 | R-HSA-5633007 | FALSE | R-HSA-6811555 | TRUE | TRUE | TRUE | 30 | TRUE | 14.8333333 | 8 | P04637,Q9Y243 | TP53,P53,AKT3,PKBG | NA | P04637 | TP53,P53 | NA | P04637,P31751 | TP53,P53,AKT2 | AKT2 |
| Repression of WNT target genes | R-HSA-4641265 | NA | NA | 1 | R-HSA-195253 | TRUE | NA | FALSE | TRUE | TRUE | 14 | TRUE | 10.0714286 | 8 | NA | NA | NA | NA | NA | NA | Q9HCS4 | TCF7L1,TCF3 | NA |
| RHO GTPases activate CIT | R-HSA-5625900 | NA | 1 | 3 | R-HSA-195258 | FALSE | NA | FALSE | FALSE | FALSE | 19 | TRUE | 10.7894737 | 8 | NA | NA | NA | O14578 | CIT,CRIK,KIAA0949,STK21 | CIT | O14974,Q15058,Q72406 | PPP1R12A,MBS,MYPT1,KIF14,KIAA0042,MYH14,KIAA2034,FP17425 | NA |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|-----|-----------------------------|---|-------|--------|----------|----|---|--|------------------------------------|----|
| RHO GTPases activate PAKs | R-HSA-5627123 | 1 | NA | 2 | R-HSA-195258 | FALSE | NA | FALSE | FALSE | FALSE | 21 | TRUE | 13.952381 | 8 | Q15746 | MYLK,MLCK,MLCK1,MYLK1 | MYLK | NA | NA | NA | O14974,Q7Z406 | PPP1R12A,MBS,MYPT1,MYH14,KIAA2034,FP17425 | NA | |
| RHO GTPases Activate ROCKs | R-HSA-5627117 | NA | NA | 2 | R-HSA-195258 | FALSE | NA | FALSE | FALSE | FALSE | 19 | TRUE | 9.63157895 | 8 | NA | NA | NA | NA | NA | NA | O14974,Q7Z406 | PPP1R12A,MBS,MYPT1,MYH14,KIAA2034,FP17425 | NA | |
| TNFR1-induced proapoptotic signaling | R-HSA-5357786 | 1 | NA | 1 | R-HSA-75893 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 10.7142857 | 8 | O75604 | USP2,UBP41 | NA | NA | NA | NA | Q14790 | CASP8,MCH5 | NA | |
| Translocation of ZAP-70 to Immunological synapse | R-HSA-202430 | NA | NA | 2 | R-HSA-202403 | FALSE | NA | FALSE | FALSE | FALSE | 26 | TRUE | 8.5 | 8 | NA | NA | NA | NA | NA | NA | P04234,P06239 | CD3D,T3D,LCK | LCK | |
| Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus | R-HSA-159763 | NA | NA | 2 | R-HSA-159854 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 8.11111111 | 8 | NA | NA | NA | NA | NA | NA | P07225,P22891 | PROS1,PROS,PROZ | NA | |
| Transport of Mature mRNA derived from an Intron-Containing Transcript | R-HSA-159236 | 2 | NA | 3 | R-HSA-72202 | FALSE | NA | FALSE | FALSE | FALSE | 73 | TRUE | 16.0273973 | 8 | P38919,Q99567 | EIF4A3,DDX48,KIAA0111,NUP88 | NA | NA | NA | NA | P35658,Q05519,Q8N127 | NUP214,CAIN,CAN,KIAA0023,SRSF11,SFRS11,THOC2,Cxorf3 | NA | |
| Circadian Clock | R-HSA-400253 | 1 | NA | NA | NA | FALSE | R-HSA-1368108 | FALSE | FALSE | FALSE | 70 | TRUE | 22.3857143 | 8.5 | Q9Y297 | BTRC,BTRCP,FBW1A,FBXW1A | NA | NA | NA | NA | NA | NA | NA | |
| Circadian Clock | R-HSA-400253 | 1 | NA | NA | NA | FALSE | R-HSA-1368071 | FALSE | FALSE | FALSE | 70 | TRUE | 22.3857143 | 8.5 | Q9Y297 | BTRC,BTRCP,FBW1A,FBXW1A | NA | NA | NA | NA | NA | NA | NA | |
| Circadian Clock | R-HSA-400253 | 1 | NA | NA | NA | FALSE | R-HSA-1368082 | FALSE | FALSE | FALSE | 70 | TRUE | 22.3857143 | 8.5 | Q9Y297 | BTRC,BTRCP,FBW1A,FBXW1A | NA | NA | NA | NA | NA | NA | NA | |
| DCC mediated attractive signaling | R-HSA-418885 | 2 | NA | NA | R-HSA-373752 | TRUE | NA | FALSE | TRUE | TRUE | 14 | TRUE | 19 | 8.5 | P12931,P43146 | SRC,SRC1,DCC,IGDC1 | SRC | NA | NA | NA | NA | NA | NA | |
| MET activates PTK2 signaling | R-HSA-8874081 | 3 | 1 | 5 | R-HSA-8875878 | FALSE | NA | FALSE | FALSE | FALSE | 18 | TRUE | 13.6666667 | 8.5 | P12107,P12931,Q13751 | COL11A1,COLL6,SRC,SRCL,LAMB3,LAMNB1 | SRC | P02751 | FN1,FN | NA | P02458,P11047,P12107,P20908,Q17RW2 | COL2A1,LAMC1,LAMB2,COL11A1,COLL6,COLSA1,COL24A1 | NA | |
| Nephrin family interactions | R-HSA-373753 | 1 | NA | 2 | R-HSA-1500931 | FALSE | NA | FALSE | FALSE | FALSE | 22 | TRUE | 15.5 | 8.5 | Q86U8 | MAGI2,ACVRINP1,AIP1,KIAA0705 | NA | NA | NA | NA | NA | P35609,Q86UL8 | ACTN2,MAGI2,ACVRINP1,AIP1,KIAA0705 | NA |
| Removal of aminoterminal propeptides from gamma-carboxylated proteins | R-HSA-159782 | NA | NA | 2 | R-HSA-159854 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 9.3 | 8.5 | NA | NA | NA | NA | NA | NA | P07225,P22891 | PROS1,PROS,PROZ | NA | |
| Sema3A PAK dependent Axon repulsion | R-HSA-399954 | NA | NA | 1 | R-HSA-373755 | FALSE | NA | FALSE | FALSE | FALSE | 16 | TRUE | 15.8125 | 8.5 | NA | NA | NA | NA | NA | NA | P07332 | FES,FPS | FES | |
| SLIT2:ROBO1 increases RHOA activity | R-HSA-8985586 | NA | NA | 1 | R-HSA-376176 | TRUE | NA | FALSE | TRUE | TRUE | 4 | TRUE | 12.25 | 8.5 | NA | NA | NA | NA | NA | NA | Q9Y6N7 | ROBO1,DUTT1 | NA | |
| SUMOylation of transcription factors | R-HSA-3232118 | 2 | 1 | 1 | R-HSA-3108232 | FALSE | NA | FALSE | FALSE | FALSE | 20 | TRUE | 10.8 | 8.5 | P04637,Q12888 | TP53,P53,TP53BP1 | NA | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | |
| TRAIL signaling | R-HSA-75158 | NA | NA | 1 | R-HSA-73887 | FALSE | NA | FALSE | FALSE | FALSE | 8 | TRUE | 10.75 | 8.5 | NA | NA | NA | NA | NA | NA | Q14790 | CASP8,MCH5 | NA | |
| Transcriptional Regulation by E2F6 | R-HSA-8953750 | NA | NA | 1 | R-HSA-212436 | TRUE | NA | FALSE | TRUE | TRUE | 34 | TRUE | 8.91176471 | 8.5 | NA | NA | NA | NA | NA | NA | P38398 | BRC1,RNF53 | NA | |
| ABC-family proteins mediated transport | R-HSA-382556 | 4 | NA | 6 | R-HSA-382551 | FALSE | R-HSA-1369062 | TRUE | TRUE | TRUE | 103 | TRUE | 42.5436893 | 9 | O60706,P25786,Q96166,Q9NP78 | ABCC9,SUR2,PSMA1,HC2,NU,PROS30,PS2,ABC11,MRP8,ABC9,KIAA1520 | PSMA1 | NA | NA | NA | P21439,P33527,P55072,P61289,Q13200,Q13438 | ABCB4,MDR3,PGY3,ABC11,MRP,MRP1,VCP,PSME3,PSMD2,TRAP2,OS9 | PSMD2 | |
| ABC-family proteins mediated transport | R-HSA-382556 | 4 | NA | 6 | R-HSA-382551 | FALSE | R-HSA-1369007 | FALSE | FALSE | TRUE | 103 | TRUE | 42.5436893 | 9 | O60706,P25786,Q96166,Q9NP78 | ABCC9,SUR2,PSMA1,HC2,NU,PROS30,PS2,ABC11,MRP8,ABC9,KIAA1520 | PSMA1 | NA | NA | NA | P21439,P33527,P55072,P61289,Q13200,Q13438 | ABCB4,MDR3,PGY3,ABC11,MRP,MRP1,VCP,PSME3,PSMD2,TRAP2,OS9 | PSMD2 | |
| Activation of RAC1 | R-HSA-428540 | NA | NA | 1 | R-HSA-376176 | TRUE | NA | FALSE | TRUE | TRUE | 13 | TRUE | 18.3076923 | 9 | NA | NA | NA | NA | NA | NA | Q9Y6N7 | ROBO1,DUTT1 | NA | |
| AKT phosphorylates targets in the nucleus | R-HSA-198693 | 1 | NA | 1 | R-HSA-1257604 | TRUE | NA | FALSE | TRUE | TRUE | 10 | TRUE | 19.1 | 9 | Q9Y243 | AKT3,PKBG | NA | NA | NA | NA | P31751 | AKT2 | AKT2 | |

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|--|---------------|----|----|---|---------------|-------|---------------|-------|-------|-------|-----|------|------------|---|-----------------------------|--|-------------|--------|------------------|-------|--|--|-------------------|
| Anchoring of the basal body to the plasma membrane | R-HSA-5620912 | 2 | NA | 1 | R-HSA-5617833 | TRUE | NA | FALSE | TRUE | TRUE | 97 | TRUE | 10.7731959 | 9 | O95684,Q72460 | FGFR1OP,FOP,CLASP1,KIAA0622,MAST1 | MAST1 | NA | NA | NA | Q965N8 | CDK5RAP2,CEP215,KIAA1633 | NA |
| Calcineurin activates NFAT | R-HSA-2025928 | NA | NA | 1 | R-HSA-1168372 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 14.3333333 | 9 | NA | NA | NA | NA | NA | NA | P16298 | PPP3CB,CALNA2,CALNB,CNA2 | NA |
| Cell surface interactions at the vascular wall | R-HSA-202733 | NA | 1 | 1 | R-HSA-109582 | FALSE | R-HSA-210991 | TRUE | TRUE | TRUE | 231 | TRUE | 12.1558442 | 9 | NA | NA | NA | P02751 | FN1,FN | NA | P07225 | PROS1,PROS | NA |
| Cell surface interactions at the vascular wall | R-HSA-202733 | NA | 1 | 1 | R-HSA-109582 | FALSE | R-HSA-210993 | TRUE | TRUE | TRUE | 231 | TRUE | 12.1558442 | 9 | NA | NA | NA | P02751 | FN1,FN | NA | P07225 | PROS1,PROS | NA |
| Cell surface interactions at the vascular wall | R-HSA-202733 | NA | 1 | 1 | R-HSA-109582 | FALSE | R-HSA-210990 | TRUE | TRUE | TRUE | 231 | TRUE | 12.1558442 | 9 | NA | NA | NA | P02751 | FN1,FN | NA | P07225 | PROS1,PROS | NA |
| Defective LFNG causes SCDO3 | R-HSA-5083630 | NA | NA | 1 | R-HSA-3906995 | FALSE | NA | FALSE | FALSE | FALSE | 4 | TRUE | 11.5 | 9 | NA | NA | NA | NA | NA | NA | Q04721 | NOTCH2 | NA |
| Defective POMGNT1 causes MDDGA3, MDDGB3 and MDDGC3 | R-HSA-5083628 | NA | NA | 2 | R-HSA-3906995 | FALSE | NA | FALSE | FALSE | FALSE | 1 | TRUE | 9 | 9 | NA | NA | NA | NA | NA | NA | Q14118,Q8WZA1 | DAG1,POMGNT1,MGAT1.2,UNQ746/PRO1475 | NA |
| Defective POMT1 causes MDDGA1, MDDGB1 and MDDGC1 | R-HSA-5083633 | 1 | NA | 1 | R-HSA-3906995 | FALSE | NA | FALSE | FALSE | FALSE | 1 | TRUE | 9 | 9 | Q9Y6A1 | POMT1 | NA | NA | NA | NA | Q14118 | DAG1 | NA |
| Defective POMT2 causes MDDGA2, MDDGB2 and MDDGC2 | R-HSA-5083629 | NA | NA | 1 | R-HSA-3906995 | FALSE | NA | FALSE | FALSE | FALSE | 1 | TRUE | 9 | 9 | NA | NA | NA | NA | NA | NA | Q14118 | DAG1 | NA |
| EPH-ephrin mediated repulsion of cells | R-HSA-3928665 | 3 | 1 | 5 | R-HSA-2682334 | TRUE | NA | FALSE | TRUE | TRUE | 49 | TRUE | 12.2244898 | 9 | O94973,P29323,Q15375 | AP2A2,ADTAP,CLAPA2,HIP9,HYPI,KIAA0899,EPHB2,DRT,EPHT3,EPH3,ERK,HEK5,TYROS,EPHA7,EHK3,HEK11 | EPHB2,EPHA7 | Q15375 | EPHA7,EHK3,HEK11 | EPHA7 | P09497,P29320,P53675,P54756,Q15375 | CLTB,EPHA3,ETK,ETK1,HEK,TYRO4,CLTCL1,CLH22,CLTCL,CLTD,EPHA5,BSK,EHK1,HEK7,EPHA7,EHK3,HEK11 | EPHA3,EPHA5,EPHA7 |
| EPHA-mediated growth cone collapse | R-HSA-3928663 | 1 | 1 | 4 | R-HSA-2682334 | TRUE | NA | FALSE | TRUE | TRUE | 15 | TRUE | 18.4 | 9 | Q15375 | EPHA7,EHK3,HEK11 | EPHA7 | Q15375 | EPHA7,EHK3,HEK11 | EPHA7 | P29320,P54756,Q15375,Q72406 | EPHA3,ETK,ETK1,HEK,TYRO4,EPHA5,BSK,EHK1,HEK7,EPHA7,EHK3,HEK11,MYH14,KIAA2034,FP17425 | EPHA3,EPHA5,EPHA7 |
| EPHB-mediated forward signaling | R-HSA-3928662 | 1 | 1 | 1 | R-HSA-2682334 | TRUE | NA | FALSE | TRUE | TRUE | 34 | TRUE | 16.8529412 | 9 | P29323 | EPHB2,DRT,EPHT3,EPHT3,ERK,HEK5,TYROS | EPHB2 | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA |
| Fas/ CD95L signaling | R-HSA-75157 | NA | NA | 1 | R-HSA-73887 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 13.2 | 9 | NA | NA | NA | NA | NA | NA | Q14790 | CASP8,MCH5 | NA |
| Golgi Cisternae Pericentriolar Stack Reorganization | R-HSA-162658 | NA | NA | 1 | R-HSA-68875 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 20.7857143 | 9 | NA | NA | NA | NA | NA | NA | Q9H2G9 | BLZF1,JEM1 | NA |
| Mitotic Prometaphase | R-HSA-68877 | 2 | NA | 1 | R-HSA-68886 | FALSE | R-HSA-380320 | TRUE | TRUE | TRUE | 184 | TRUE | 12.6358696 | 9 | Q3ZCM7,Q72460 | TUBB8,CLASP1,KIAA0622,MAST1 | MAST1 | NA | NA | NA | P50748 | KNTC1,KIAA0166 | NA |
| Mitotic Prometaphase | R-HSA-68877 | 2 | NA | 1 | R-HSA-68886 | FALSE | R-HSA-2514853 | TRUE | TRUE | TRUE | 184 | TRUE | 12.6358696 | 9 | Q3ZCM7,Q72460 | TUBB8,CLASP1,KIAA0622,MAST1 | MAST1 | NA | NA | NA | P50748 | KNTC1,KIAA0166 | NA |
| Mitotic Prometaphase | R-HSA-68877 | 2 | NA | 1 | R-HSA-68886 | FALSE | R-HSA-2500257 | TRUE | TRUE | TRUE | 184 | TRUE | 12.6358696 | 9 | Q3ZCM7,Q72460 | TUBB8,CLASP1,KIAA0622,MAST1 | MAST1 | NA | NA | NA | P50748 | KNTC1,KIAA0166 | NA |
| Non-integrin membrane-ECM interactions | R-HSA-3000171 | 4 | 1 | 7 | R-HSA-1474244 | TRUE | R-HSA-3000170 | TRUE | TRUE | TRUE | 42 | TRUE | 11.547619 | 9 | P02462,P12107,P53420,Q13751 | COL4A1,COL11A1,COL6, COL4A4,LAMB3,LAMNB1 | NA | P02751 | FN1,FN | NA | P02458,P02462,P02766,P11047,P12107,P20908,Q14118 | COL2A1,COL4A1,TRP,PA1B,LAMC1,LAMB2,COL11A1,COL6,COL5A1,DAG1 | NA |
| PISP Regulates TP53 Acetylation | R-HSA-6811555 | 1 | 1 | 1 | R-HSA-6804758 | TRUE | NA | FALSE | TRUE | TRUE | 9 | TRUE | 17.3333333 | 9 | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA |
| Pre-NOTCH Processing in the Endoplasmic Reticulum | R-HSA-1912399 | NA | NA | 1 | R-HSA-1912422 | FALSE | NA | FALSE | FALSE | FALSE | 6 | TRUE | 8 | 9 | NA | NA | NA | NA | NA | NA | Q04721 | NOTCH2 | NA |
| Recruitment of mitotic centrosome proteins and complexes | R-HSA-380270 | 2 | NA | 1 | R-HSA-380287 | FALSE | NA | FALSE | FALSE | FALSE | 81 | TRUE | 12.3333333 | 9 | O95684,Q72460 | FGFR1OP,FOP,CLASP1,KIAA0622,MAST1 | MAST1 | NA | NA | NA | Q965N8 | CDK5RAP2,CEP215,KIAA1633 | NA |
| Recruitment of NuMA to mitotic centrosomes | R-HSA-380320 | 3 | NA | 1 | R-HSA-68877 | TRUE | NA | FALSE | TRUE | TRUE | 80 | TRUE | 12.5 | 9 | O95684,Q3ZCM7,Q72460 | FGFR1OP,FOP,TUBB8,CLASP1,KIAA0622,MAST1 | MAST1 | NA | NA | NA | Q965N8 | CDK5RAP2,CEP215,KIAA1633 | NA |
| Regulation of PTEN gene transcription | R-HSA-8943724 | 2 | 1 | 2 | R-HSA-6807070 | FALSE | NA | FALSE | FALSE | FALSE | 61 | TRUE | 12.4754098 | 9 | P04637,Q03112 | TP53,P53,MECOM,EV11,MDS1 | NA | P04637 | TP53,P53 | NA | P04637,P42345 | TP53,P53,MTOR,FRAP,FRAP1,FRAP2,RAFT1,RAP1 | NA |

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|---|---------------|----|----|----|---------------|-------|--------------|-------|-------|-------|-----|------|------------|-----|-----------------------------|---|-------|--------|----------|----|---|---|--------------------------|------|
| Regulation of TP53 Activity through Methylation | R-HSA-6804760 | 2 | 1 | 1 | R-HSA-5633007 | FALSE | NA | FALSE | FALSE | FALSE | 19 | TRUE | 52.2105263 | 9 | P04637,Q13315 | TP53,P53,ATM | NA | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | |
| Resolution of Sister Chromatid Cohesion | R-HSA-2500257 | 2 | NA | 1 | R-HSA-68877 | TRUE | NA | FALSE | TRUE | TRUE | 107 | TRUE | 14.3551402 | 9 | Q3ZCM7,Q72460 | TUBB8,CLASP1,KIAA0622,MAST1 | MAST1 | NA | NA | NA | NA | P50748 | KNTC1,KIAA0166 | NA |
| Signaling by PDGF | R-HSA-186797 | 4 | NA | 6 | R-HSA-9006934 | FALSE | R-HSA-186763 | TRUE | TRUE | TRUE | 53 | TRUE | 21.5660377 | 9 | A8TX70,P02462,P20849,P53420 | COL6A5,COL29A1,VVAA4,COL4A1,COL9A1,COL4A4 | NA | NA | NA | NA | A6NMZ7,A8TX70,P02458,P02462,P20849,P20908 | COL6A6,COL6A5,COL29A1,VVAA4,COL2A1,COL4A1,COL9A1,COL5A1 | NA | |
| TFAP2 (AP-2) family regulates transcription of cell cycle factors | R-HSA-8866911 | 1 | NA | NA | R-HSA-8864260 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 13.2 | 9 | Q9UGL1 | KDMSB,JARID1B,PLU1,RRBP2H1 | NA | NA | NA | NA | NA | NA | NA | NA |
| AURKA Activation by TPX2 | R-HSA-8854518 | 2 | NA | 1 | R-HSA-69275 | FALSE | NA | FALSE | FALSE | FALSE | 72 | TRUE | 13.625 | 9.5 | O95684,Q72460 | FGFR1OP,FOP,CLASP1,KIAA0622,MAST1 | MAST1 | NA | NA | NA | NA | Q965N8 | CDK5RAP2,CEP215,KIAA1633 | NA |
| Downregulation of TGF-beta receptor signaling | R-HSA-2173788 | NA | NA | 1 | R-HSA-2173789 | FALSE | NA | FALSE | FALSE | FALSE | 26 | TRUE | 38.2307692 | 9.5 | NA | NA | NA | NA | NA | NA | NA | Q96PU5 | NEDD4L,KIAA0439,NEDL3 | NA |
| RUNX2 regulates osteoblast differentiation | R-HSA-8940973 | 1 | NA | NA | R-HSA-8941326 | FALSE | NA | FALSE | FALSE | FALSE | 24 | TRUE | 18 | 9.5 | P12931 | SRC,SRC1 | SRC | NA | NA | NA | NA | NA | NA | NA |
| SUMOylation of transcription cofactors | R-HSA-3899300 | NA | NA | 1 | R-HSA-3108232 | FALSE | NA | FALSE | FALSE | FALSE | 44 | TRUE | 10 | 9.5 | NA | NA | NA | NA | NA | NA | NA | Q9UER7 | DAXX,BING2,DAP6 | NA |
| TNFR1-induced NFkappaB signaling pathway | R-HSA-5357956 | 1 | NA | NA | R-HSA-75893 | FALSE | NA | FALSE | FALSE | FALSE | 26 | TRUE | 16.0384615 | 9.5 | O75604 | USP2,UBP41 | NA | NA | NA | NA | NA | NA | NA | NA |
| Activation of ATR in response to replication stress | R-HSA-176187 | NA | 1 | 1 | R-HSA-69481 | TRUE | NA | FALSE | TRUE | TRUE | 37 | TRUE | 13.6216216 | 10 | NA | NA | NA | Q13535 | ATR,FRP1 | NA | Q8WXE1 | ATRIP,AGS1 | NA | |
| Binding of TCF/LEF-CTNNB1 to target gene promoters | R-HSA-4411364 | NA | NA | 1 | R-HSA-201722 | TRUE | NA | FALSE | TRUE | TRUE | 8 | TRUE | 13.75 | 10 | NA | NA | NA | NA | NA | NA | NA | Q9HCS4 | TCF7L1,TCF3 | NA |
| CASP8 activity is inhibited | R-HSA-5218900 | NA | NA | 1 | R-HSA-5675482 | TRUE | NA | FALSE | TRUE | TRUE | 13 | TRUE | 11.8461538 | 10 | NA | NA | NA | NA | NA | NA | NA | Q14790 | CASP8,MCH5 | NA |
| DDX58/IFIH1-mediated induction of interferon-alpha/beta | R-HSA-168928 | NA | NA | 1 | R-HSA-168249 | FALSE | R-HSA-936440 | TRUE | TRUE | TRUE | 77 | TRUE | 24.1688312 | 10 | NA | NA | NA | NA | NA | NA | NA | O95786 | DDX58 | NA |
| DDX58/IFIH1-mediated induction of interferon-alpha/beta | R-HSA-168928 | NA | NA | 1 | R-HSA-168249 | FALSE | R-HSA-918233 | TRUE | TRUE | TRUE | 77 | TRUE | 24.1688312 | 10 | NA | NA | NA | NA | NA | NA | NA | O95786 | DDX58 | NA |
| DDX58/IFIH1-mediated induction of interferon-alpha/beta | R-HSA-168928 | NA | NA | 1 | R-HSA-168249 | FALSE | R-HSA-933543 | TRUE | TRUE | TRUE | 77 | TRUE | 24.1688312 | 10 | NA | NA | NA | NA | NA | NA | NA | O95786 | DDX58 | NA |
| DDX58/IFIH1-mediated induction of interferon-alpha/beta | R-HSA-168928 | NA | NA | 1 | R-HSA-168249 | FALSE | R-HSA-933541 | TRUE | TRUE | TRUE | 77 | TRUE | 24.1688312 | 10 | NA | NA | NA | NA | NA | NA | NA | O95786 | DDX58 | NA |
| DDX58/IFIH1-mediated induction of interferon-alpha/beta | R-HSA-168928 | NA | NA | 1 | R-HSA-168249 | FALSE | R-HSA-933542 | TRUE | TRUE | TRUE | 77 | TRUE | 24.1688312 | 10 | NA | NA | NA | NA | NA | NA | NA | O95786 | DDX58 | NA |
| Dimerization of procaspase-8 | R-HSA-69416 | NA | NA | 1 | R-HSA-140534 | TRUE | NA | FALSE | TRUE | TRUE | 11 | TRUE | 13.0909091 | 10 | NA | NA | NA | NA | NA | NA | NA | Q14790 | CASP8,MCH5 | NA |
| Inhibition of TSC complex formation by PKB | R-HSA-165181 | 1 | NA | 1 | R-HSA-165159 | TRUE | NA | FALSE | TRUE | TRUE | 3 | TRUE | 19.6666667 | 10 | P49815 | TSC2,TSC4 | NA | NA | NA | NA | NA | P31751 | AKT2 | AKT2 |
| Loss of Nlp from mitotic centrosomes | R-HSA-380259 | 2 | NA | 1 | R-HSA-380284 | TRUE | NA | FALSE | TRUE | TRUE | 69 | TRUE | 14.0144928 | 10 | O95684,Q72460 | FGFR1OP,FOP,CLASP1,KIAA0622,MAST1 | MAST1 | NA | NA | NA | NA | Q965N8 | CDK5RAP2,CEP215,KIAA1633 | NA |

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|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|------|------------------------------------|---|-------|--------|----------|----|--|--|-------|----|
| Loss of proteins required for interphase microtubule organization from the centrosome | R-HSA-380284 | 2 | NA | 1 | R-HSA-380287 | FALSE | R-HSA-380259 | TRUE | TRUE | TRUE | 69 | TRUE | 14.0144928 | 10 | O95684,Q7Z460 | FGFR1OP,FOP,CLASP1,KIAA0622,MAST1 | MAST1 | NA | NA | NA | Q965N8 | CDK5RAP2,CEP215,KIAA1633 | NA | |
| MECP2 regulates transcription factors | R-HSA-9022707 | NA | NA | 1 | R-HSA-8986944 | TRUE | NA | FALSE | TRUE | TRUE | 5 | TRUE | 17.6 | 10 | NA | NA | NA | NA | NA | NA | Q9NWB1 | RBFOX1,A2BP,A2BP1,FOX1,HRNB1 | NA | |
| Negative regulation of MET activity | R-HSA-6807004 | NA | NA | 1 | R-HSA-6806834 | FALSE | NA | FALSE | FALSE | FALSE | 21 | TRUE | 50.1904762 | 10 | NA | NA | NA | NA | NA | NA | Q12913 | PTPRJ,DEP1 | NA | |
| PTK6 promotes HIF1A stabilization | R-HSA-8857538 | 1 | NA | NA | R-HSA-8848021 | FALSE | NA | FALSE | FALSE | FALSE | 7 | TRUE | 11.8571429 | 10 | Q55007 | LRRK2,PARK8 | LRRK2 | NA | NA | NA | NA | NA | NA | |
| Regulation by c-FLIP | R-HSA-3371378 | NA | NA | 1 | R-HSA-140534 | TRUE | NA | FALSE | TRUE | TRUE | 11 | TRUE | 13.0909091 | 10 | NA | NA | NA | NA | NA | NA | Q14790 | CASP8,MCH5 | NA | |
| Regulation of necroptotic cell death | R-HSA-5675482 | NA | NA | 1 | R-HSA-5213460 | TRUE | R-HSA-5218900 | TRUE | TRUE | TRUE | 16 | TRUE | 12.25 | 10 | NA | NA | NA | NA | NA | NA | Q14790 | CASP8,MCH5 | NA | |
| Regulation of PLK1 Activity at G2/M Transition | R-HSA-2565942 | 3 | NA | 2 | R-HSA-69275 | FALSE | NA | FALSE | FALSE | FALSE | 87 | TRUE | 23.2413793 | 10 | O95684,Q7Z460,Q9Y297 | FGFR1OP,FOP,CLASP1,KIAA0622,MAST1,BTRC,BTRCP,FBW1A,FBXW1A | MAST1 | NA | NA | NA | O14974,Q965N8 | PPP1R12A,MBS,MYPT1,CDK5RAP2,CEP215,KIAA1633 | NA | |
| Resolution of D-loop Structures through Holliday Junction Intermediates | R-HSA-5693568 | 1 | NA | 1 | R-HSA-5693537 | FALSE | NA | FALSE | FALSE | FALSE | 32 | TRUE | 10 | 10 | Q13315 | ATM | NA | NA | NA | NA | P38398 | BRCA1,RNF53 | NA | |
| RHO GTPases activate IQGAPs | R-HSA-5626467 | 1 | NA | NA | R-HSA-195258 | FALSE | NA | FALSE | FALSE | FALSE | 11 | TRUE | 18.7272727 | 10 | Q3ZCM7 | TUBB8 | NA | NA | NA | NA | NA | NA | NA | |
| RIPK1-mediated regulated necrosis | R-HSA-5213460 | NA | NA | 1 | R-HSA-5218859 | FALSE | R-HSA-5675482 | TRUE | TRUE | TRUE | 18 | TRUE | 11.5555556 | 10 | NA | NA | NA | NA | NA | NA | Q14790 | CASP8,MCH5 | NA | |
| RUNX2 regulates chondrocyte maturation | R-HSA-8941284 | 1 | NA | NA | R-HSA-8941326 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 13 | 10 | P10070 | GLI2,THP | NA | NA | NA | NA | NA | NA | NA | |
| Signalling to p38 via RIT and RIN | R-HSA-187706 | NA | NA | 1 | R-HSA-187687 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 10.4 | 10 | NA | NA | NA | NA | NA | NA | Q99578 | RIT2,RIN,ROC2 | NA | |
| SUMOylation of DNA methylation proteins | R-HSA-4655427 | 1 | NA | NA | R-HSA-3108232 | FALSE | NA | FALSE | FALSE | FALSE | 16 | TRUE | 10.6875 | 10 | P26358 | DNMT1,AIM,CXXC9,DNMT | NA | NA | NA | NA | NA | NA | NA | NA |
| TRAF3-dependent IRF activation pathway | R-HSA-918233 | NA | NA | 1 | R-HSA-168928 | TRUE | NA | FALSE | TRUE | TRUE | 14 | TRUE | 15.3571429 | 10 | NA | NA | NA | NA | NA | NA | Q95786 | DDX58 | NA | |
| Ub-specific processing proteases | R-HSA-5689880 | 5 | 1 | 10 | R-HSA-5688426 | FALSE | NA | FALSE | FALSE | FALSE | 205 | TRUE | 28.8 | 10 | O75604,P04637,P25786,Q92995,Q93008 | USP2,UBP41,TP53,P53,PSMA1,HC2,NU,PROS30,PSX2,USP13,ISOT3,USP9X,DFFRX,FAM,USP9 | PSMA1 | P04637 | TP53,P53 | NA | O75528,Q95271,Q95786,P04637,P61289,Q1320,Q070CQ1,Q8IX2,Q93008,Q9Y5T5 | TADA3,ADA3,TADA3L,TNKS,PARP5A,PARPL,TIN1,TINF1,TNKS1,DDX58,TP53,P53,PSME3,PSMD2,TRAP2,USP49,RHOT1,ARHT1,USP9X,DFFRX,FAM,USP9,USP16,MSTP039 | PSMD2 | |
| Constitutive Signaling by AKT1 E17K in Cancer | R-HSA-5674400 | 2 | NA | 2 | R-HSA-2219528 | FALSE | NA | FALSE | FALSE | FALSE | 26 | TRUE | 16.8846154 | 10.5 | P49815,Q9Y243 | TSC2,TSC4,AKT3,PKBG | NA | NA | NA | NA | P31751,P42345 | AKT2,MTOR,FRAP,FRAP1,FRAP2,RAFT1,RAPT1 | AKT2 | |
| Gap Junction degradation | R-HSA-190873 | NA | NA | 2 | R-HSA-190828 | FALSE | R-HSA-196025 | TRUE | TRUE | TRUE | 10 | TRUE | 11.5 | 10.5 | NA | NA | NA | NA | NA | NA | P09497,P53675 | CLTB,CLTCL1,CLH22,CLTCL,CLTD | NA | |
| TP53 Regulates Transcription of Genes Involved in G2 Cell Cycle Arrest | R-HSA-6804114 | 1 | 1 | 3 | R-HSA-6791312 | FALSE | NA | FALSE | FALSE | FALSE | 18 | TRUE | 17.7222222 | 10.5 | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | P04637,P31947,Q99873 | TP53,P53,FSN,HME1,PRMT1,HMT2,HRMT1L2,IR1B4 | NA | |
| Cam-PDE 1 activation | R-HSA-111957 | NA | NA | 1 | R-HSA-111933 | FALSE | NA | FALSE | FALSE | FALSE | 4 | TRUE | 21.5 | 11 | NA | NA | NA | NA | NA | NA | Q14123 | PDE1C | NA | |
| CLEC7A (Dectin-1) induces NFAT activation | R-HSA-5607763 | 1 | NA | 1 | R-HSA-5607764 | TRUE | NA | FALSE | TRUE | TRUE | 11 | TRUE | 16.8181818 | 11 | Q14643 | ITPR1,INSP3R1 | NA | NA | NA | NA | P16298 | PPP3CB,CALNA2,CALNB,CNA2 | NA | |
| Defective SLC01B1 causes hyperbilirubinemia, Rotor type (HBLRR) | R-HSA-5619110 | NA | NA | 1 | R-HSA-5619102 | FALSE | NA | FALSE | FALSE | FALSE | 1 | TRUE | 11 | 11 | NA | NA | NA | NA | NA | NA | Q9Y6L6 | SLCO1B1,LIST1,OATP1B1,OATP2,OATPC,SLC21A6 | NA | |
| Defective SLC01B1 causes hyperbilirubinemia, Rotor type (HBLRR) | R-HSA-5661182 | NA | NA | 1 | R-HSA-5619102 | FALSE | NA | FALSE | FALSE | FALSE | 1 | TRUE | 11 | 11 | NA | NA | NA | NA | NA | NA | Q9Y6L6 | SLCO1B1,LIST1,OATP1B1,OATP2,OATPC,SLC21A6 | NA | |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|----|------|------------|------|-----------------------------|--|-----|---------------|--------------------------------------|------------|----------------------------|--|------------|----|
| Formation of annular gap junctions | R-HSA-196025 | NA | NA | 2 | R-HSA-190873 | TRUE | NA | FALSE | TRUE | TRUE | 9 | TRUE | 12.4444444 | 11 | NA | NA | NA | NA | NA | NA | P09497,P53675 | CLTB,CLTCL1,CLH2,CLTCL,CLTD | NA | |
| Nef and signal transduction | R-HSA-164944 | 1 | NA | 1 | R-HSA-164952 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 19.8888889 | 11 | Q92608 | DOCK2,KIAA0209 | NA | NA | NA | NA | P06239 | LCK | LCK | |
| NFG and proNGF binds to p75NTR | R-HSA-205017 | 1 | NA | NA | R-HSA-193704 | FALSE | NA | FALSE | FALSE | FALSE | 3 | TRUE | 10.3333333 | 11 | Q17R88 | SORCS3 | NA | NA | NA | NA | NA | NA | NA | |
| Notch-HH transcription pathway | R-HSA-350054 | NA | NA | 1 | R-HSA-212436 | TRUE | NA | FALSE | TRUE | TRUE | 13 | TRUE | 14.5384615 | 11 | NA | NA | NA | NA | NA | NA | Q04721 | NOTCH2 | NA | |
| NOTCH2 intracellular domain regulates transcription | R-HSA-2197563 | NA | NA | 1 | R-HSA-1980145 | FALSE | NA | FALSE | FALSE | FALSE | 12 | TRUE | 15 | 11 | NA | NA | NA | NA | NA | NA | Q04721 | NOTCH2 | NA | |
| NOTCH4 Intracellular Domain Regulates Transcription | R-HSA-9013695 | NA | NA | 1 | R-HSA-9013694 | FALSE | NA | FALSE | FALSE | FALSE | 20 | TRUE | 14.3 | 11 | NA | NA | NA | NA | NA | NA | Q04721 | NOTCH2 | NA | |
| RNA Polymerase I Transcription Initiation | R-HSA-73762 | NA | NA | 3 | R-HSA-73854 | FALSE | NA | FALSE | FALSE | FALSE | 48 | TRUE | 20.0833333 | 11 | NA | NA | NA | NA | NA | NA | P18074,Q03468,Q9H9Y6 | ERCC2,XPD,XPC,ERCC6,CSB,POLR1B | NA | |
| Signaling by BRAF and RAF fusions | R-HSA-6802952 | 4 | 2 | 3 | R-HSA-6802957 | FALSE | NA | FALSE | FALSE | FALSE | 58 | TRUE | 16.6896552 | 11 | P12931,Q62MT4,Q7Z5R6,Q86XD5 | SRC,SRCL1,KDM7A,JHDM1D,KDM7,KIAA1718,APB B1P,PREL1,RARP1,RIAM,FAM131B,KIAA0773 | SRC | P01112,P02751 | HRAS,HRAS1,FN1,FN | NA | P01112,Q6VAB6,Q8WXI2 | HRAS,HRAS1,KSR2,CNKR2,CNK2,KIAA0902 | NA | |
| Signaling by cytosolic FGFR1 fusion mutants | R-HSA-1839117 | 3 | NA | 2 | R-HSA-1839124 | FALSE | NA | FALSE | FALSE | FALSE | 18 | TRUE | 20.7777778 | 11 | O95684,P39880,P42229 | FGFR1OP,FOP,CUX1,CUTL1,STAT5A,STAT5 | NA | NA | NA | NA | P39880,Q9UBW7 | CUX1,CUTL1,ZMYM2,FI M,RAMP,ZNF198 | NA | |
| Trafficking of AMPA receptors | R-HSA-399719 | NA | NA | 1 | R-HSA-399721 | FALSE | R-HSA-416993 | TRUE | TRUE | TRUE | 31 | TRUE | 11.8064516 | 11 | NA | NA | NA | NA | NA | NA | P48058 | GRIA4,GLUR4 | NA | |
| Trafficking of GluR2-containing AMPA receptors | R-HSA-416993 | NA | NA | 2 | R-HSA-399719 | TRUE | NA | FALSE | TRUE | TRUE | 17 | TRUE | 12.8235294 | 11 | NA | NA | NA | NA | NA | NA | P42262,P48058 | GRIA2,GLUR2,GRIA4,GLUR4 | NA | |
| Unblocking of NMDA receptors, glutamate binding and activation | R-HSA-438066 | 1 | NA | 4 | R-HSA-442755 | FALSE | NA | FALSE | FALSE | FALSE | 20 | TRUE | 11.6 | 11 | Q15700 | DLG2 | NA | NA | NA | NA | P35609,P4262,P48058,Q12879 | ACTN2,GRIA2,GLUR2,GRIA4,GLUR4,GRIN2A,NMDAR2A | NA | |
| MECP2 regulates neuronal receptors and channels | R-HSA-9022699 | NA | 1 | 3 | R-HSA-8986944 | TRUE | NA | FALSE | TRUE | TRUE | 18 | TRUE | 13.8888889 | 11.5 | NA | NA | NA | Q13451 | FKBP5,AIG6,FKBP51 | NA | P42262,Q12879,Q13507 | GRIA2,GLUR2,GRIN2A,NMDAR2A,TRPC3,TRP3 | NA | |
| NOTCH2 Activation and Transmission of Signal to the Nucleus | R-HSA-2979096 | NA | NA | 1 | R-HSA-1980145 | FALSE | NA | FALSE | FALSE | FALSE | 22 | TRUE | 44.6363636 | 11.5 | NA | NA | NA | NA | NA | NA | Q04721 | NOTCH2 | NA | |
| PTK6 Regulates RHO GTPases, RAS GTPase and MAP kinases | R-HSA-8849471 | NA | 1 | 1 | R-HSA-8848021 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 26 | 11.5 | NA | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA |
| Regulation of HSF1-mediated heat shock response | R-HSA-3371453 | 3 | 2 | 1 | R-HSA-3371556 | FALSE | NA | FALSE | FALSE | FALSE | 82 | TRUE | 19.6097561 | 11.5 | Q0VDF9,Q13315,Q99567 | HSPA14,HSP60,HSP70L1,ATM,NUP88 | NA | P38646,Q13535 | HSPA9,GRP75,HSPA9B,mt-HSP70,ATR,FRP1 | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 | NA | |
| A tetrasaccharide linker sequence is required for GAG synthesis | R-HSA-1971475 | NA | NA | 1 | R-HSA-1793185 | FALSE | NA | FALSE | FALSE | FALSE | 26 | TRUE | 9.76923077 | 12 | NA | NA | NA | NA | NA | NA | Q86V38 | XYLT1,XT1 | NA | |
| A tetrasaccharide linker sequence is required for GAG synthesis | R-HSA-1971475 | NA | NA | 1 | R-HSA-1638091 | FALSE | NA | FALSE | FALSE | FALSE | 26 | TRUE | 9.76923077 | 12 | NA | NA | NA | NA | NA | NA | Q86V38 | XYLT1,XT1 | NA | |
| CREB phosphorylation through the activation of CaMKII | R-HSA-442729 | 1 | NA | 2 | R-HSA-438064 | FALSE | NA | FALSE | FALSE | FALSE | 18 | TRUE | 16.6111111 | 12 | Q15700 | DLG2 | NA | NA | NA | NA | P35609,Q12879 | ACTN2,GRIN2A,NMDAR2A | NA | |
| Disassembly of the destruction complex and recruitment of AXIN to the membrane | R-HSA-4641262 | NA | NA | 1 | R-HSA-201681 | TRUE | NA | FALSE | TRUE | TRUE | 31 | TRUE | 20.2580645 | 12 | NA | NA | NA | NA | NA | NA | O14641 | DVL2 | NA | |
| Homologous DNA Pairing and Strand Exchange | R-HSA-5693579 | 1 | NA | 1 | R-HSA-5685942 | TRUE | R-HSA-5693616 | TRUE | TRUE | TRUE | 42 | TRUE | 14.952381 | 12 | Q13315 | ATM | NA | NA | NA | NA | P38398 | BRCA1,RNF53 | NA | |

| | | | | | | | | | | | | | | | | | | | | | | | |
|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|----|------|------------|------|----------------------|--|----|---------------|--------------------------|----|------------------------------------|--|---------|
| NTRK2 activates RAC1 | R-HSA-9032759 | 1 | NA | NA | R-HSA-9032500 | TRUE | NA | FALSE | TRUE | TRUE | 5 | TRUE | 24.4 | 12 | Q8IZD9 | DOCK3,KIAA0299,MOCA | NA | NA | NA | NA | NA | NA | |
| Ras activation upon Ca2+ influx through NMDA receptor | R-HSA-442982 | 1 | 1 | 5 | R-HSA-442742 | TRUE | NA | FALSE | TRUE | TRUE | 20 | TRUE | 17.15 | 12 | Q15700 | DLG2 | NA | P01112 | HRAS,HRAS1 | NA | O14827,P01112,P35609,Q12879,Q13972 | RASGRF2,GRF2,HRAS,HRAS1,ACTN2,GRIN2A,NMDAR2A,RASGRF1,CDC25,GNRP,GRF1 | NA |
| Regulation of TP53 Activity through Phosphorylation | R-HSA-6804756 | 3 | 2 | 5 | R-HSA-5633007 | FALSE | NA | FALSE | FALSE | FALSE | 92 | TRUE | 22.1086957 | 12 | P04637,Q13315,Q8IZX4 | TP53,P53,ATM,TAF1L | NA | P04637,Q13315 | TP53,P53,ATR,FRP1 | NA | P04637,P38398,Q6P1X5,Q8IZX4,Q8WXE1 | TP53,P53,BRCA1,RNF53,TAF2,CIF150,TAF2B,TAF1L,ATRIP,AGS1 | NA |
| Resolution of D-loop Structures through Synthesis-Dependent Strand Annealing (SDSA) | R-HSA-5693554 | 1 | NA | 1 | R-HSA-5693537 | FALSE | NA | FALSE | FALSE | FALSE | 26 | TRUE | 11.6923077 | 12 | Q13315 | ATM | NA | NA | NA | NA | P38398 | BRCA1,RNF53 | NA |
| RUNX3 regulates WNT signaling | R-HSA-8951430 | NA | NA | 1 | R-HSA-8878159 | FALSE | NA | FALSE | FALSE | FALSE | 8 | TRUE | 14.875 | 12 | NA | NA | NA | NA | NA | NA | Q9HCS4 | TCF7L1,TCF3 | NA |
| SUMOylation of DNA damage response and repair proteins | R-HSA-3108214 | 2 | NA | 3 | R-HSA-3108232 | FALSE | NA | FALSE | FALSE | FALSE | 76 | TRUE | 17.4473684 | 12 | Q01831,Q9567 | XPC,XPC,NUP88 | NA | NA | NA | NA | P35658,P38398,Q13569 | NUP214,CAIN,CAN,KIAA0023,BRCA1,RNF53,TDG | NA |
| Transcriptional Regulation by MECP2 | R-HSA-8986944 | 1 | NA | 1 | R-HSA-212436 | TRUE | R-HSA-212436 | FALSE | TRUE | TRUE | 63 | TRUE | 13.7301587 | 12 | Q9UPQ9 | TNRC6B,KIAA1093 | NA | NA | NA | NA | Q9UPQ9 | TNRC6B,KIAA1093 | NA |
| Transcriptional Regulation by MECP2 | R-HSA-8986944 | 1 | NA | 1 | R-HSA-212436 | TRUE | R-HSA-9022702 | FALSE | TRUE | TRUE | 63 | TRUE | 13.7301587 | 12 | Q9UPQ9 | TNRC6B,KIAA1093 | NA | NA | NA | NA | Q9UPQ9 | TNRC6B,KIAA1093 | NA |
| Transcriptional Regulation by MECP2 | R-HSA-8986944 | 1 | NA | 1 | R-HSA-212436 | TRUE | R-HSA-9022699 | TRUE | TRUE | TRUE | 63 | TRUE | 13.7301587 | 12 | Q9UPQ9 | TNRC6B,KIAA1093 | NA | NA | NA | NA | Q9UPQ9 | TNRC6B,KIAA1093 | NA |
| Transcriptional Regulation by MECP2 | R-HSA-8986944 | 1 | NA | 1 | R-HSA-212436 | TRUE | R-HSA-9022707 | TRUE | TRUE | TRUE | 63 | TRUE | 13.7301587 | 12 | Q9UPQ9 | TNRC6B,KIAA1093 | NA | NA | NA | NA | Q9UPQ9 | TNRC6B,KIAA1093 | NA |
| Transcriptional Regulation by MECP2 | R-HSA-8986944 | 1 | NA | 1 | R-HSA-212436 | TRUE | R-HSA-9022692 | TRUE | TRUE | TRUE | 63 | TRUE | 13.7301587 | 12 | Q9UPQ9 | TNRC6B,KIAA1093 | NA | NA | NA | NA | Q9UPQ9 | TNRC6B,KIAA1093 | NA |
| Caspase activation via Death Receptors in the presence of ligand | R-HSA-140534 | NA | NA | 2 | R-HSA-5357769 | FALSE | R-HSA-3371378 | TRUE | TRUE | TRUE | 18 | TRUE | 13.7777778 | 12.5 | NA | NA | NA | NA | NA | NA | O00206,Q14790 | TLR4,CASP8,MCH5 | NA |
| Caspase activation via Death Receptors in the presence of ligand | R-HSA-140534 | NA | NA | 2 | R-HSA-5357769 | FALSE | R-HSA-69416 | TRUE | TRUE | TRUE | 18 | TRUE | 13.7777778 | 12.5 | NA | NA | NA | NA | NA | NA | O00206,Q14790 | TLR4,CASP8,MCH5 | NA |
| Meiotic synapsis | R-HSA-1221632 | 1 | 1 | 1 | R-HSA-1500620 | FALSE | NA | FALSE | FALSE | FALSE | 60 | TRUE | 19.3166667 | 12.5 | P62805 | HIST1H4A,H4/A,H4FA,,HIST1H4B,H4/I,H4FI,,HIST1H4C,H4/G,H4FG,,HIST1H4D,H4/B,H4FB,,HIST1H4E,H4/J,H4FJ,,HIST1H4F,H4/C,H4FC,,HIST1H4H,H4/H,H4FH,,HIST1H4I,H4/I,H4FI,,HIST1H4J,H4/E,H4FE,,HIST1H4K,H4/D,H4FD,,HIST1H4L,H4/K,H4FK,,HIST2H4A,H4/N,H4F2,H4FN,HIST2H4,,HIST2H4B,H4/O,H4FO,,HIST4H4 | NA | Q13535 | ATR,FRP1 | NA | P38398 | BRCA1,RNF53 | NA |
| Ovarian tumor domain proteases | R-HSA-5689896 | 3 | 1 | 4 | R-HSA-5688426 | FALSE | NA | FALSE | FALSE | FALSE | 38 | TRUE | 33.9473684 | 12.5 | P04637,P51668,Q9HC29 | TP53,P53,UBE2D1,SFT,UBC5A,UBCH5,UBCH5A,NOD2,CARD15,IBD1 | NA | P04637 | TP53,P53 | NA | O95786,P04637,P55072,Q9Y239 | DDX58,TP53,P53,VCP,NOD1,CARD4 | NA |
| Rap1 signalling | R-HSA-392517 | 1 | NA | NA | R-HSA-1280218 | FALSE | NA | FALSE | FALSE | FALSE | 16 | TRUE | 15.5 | 12.5 | P22612 | PRKACG | NA | NA | NA | NA | NA | NA | NA |
| Recycling pathway of L1 | R-HSA-437239 | 3 | NA | 1 | R-HSA-373760 | TRUE | NA | FALSE | TRUE | TRUE | 28 | TRUE | 16.5357143 | 12.5 | O94973,P32004,Q3ZCM7 | AP2A2,ADTAB,CLAPA2,HIP9,HYP1,KIAA0899,L1CAM,CAML1,MIC5,TUBB8 | NA | NA | NA | NA | Q9UK32 | RPS6KA6,RSK4 | RPS6KA6 |
| WNT mediated activation of DVL | R-HSA-201688 | NA | NA | 1 | R-HSA-201681 | TRUE | NA | FALSE | TRUE | TRUE | 8 | TRUE | 11.5 | 12.5 | NA | NA | NA | NA | NA | NA | O14641 | DVL2 | NA |
| Activation of NIMA Kinases NEK9, NEK6, NEK7 | R-HSA-2980767 | NA | 1 | NA | R-HSA-2980766 | FALSE | NA | FALSE | FALSE | FALSE | 7 | TRUE | 16.8571429 | 13 | NA | NA | NA | Q8TD19 | NEK9,KIAA1995,NEK8,NERCC | NA | NA | NA | NA |
| Condensation of Prometaphase Chromosomes | R-HSA-2514853 | NA | 1 | NA | R-HSA-68877 | TRUE | NA | FALSE | TRUE | TRUE | 11 | TRUE | 13 | 13 | NA | NA | NA | Q95347 | SMC2,CAPE,SMC2L1,PRO324 | NA | NA | NA | NA |

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|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|----|------|------------|------|-----------------------------|---|-----|---------------|--------------------|----|----------------------|---|--|
| Downregulation of SMAD2/3:SMAD4 transcriptional activity | R-HSA-2173795 | 2 | NA | 2 | R-HSA-2173793 | FALSE | NA | FALSE | FALSE | FALSE | 23 | TRUE | 44.5652174 | 13 | P51668,Q93008 | UBE2D1,SFT,UBCSA,UBCH5,UBCH5A,USP9X,DFFRX,FAM,USP9 | NA | NA | NA | NA | Q93008,Q96PU5 | USP9X,DFFRX,FAM,USP9,NEDD4L,KIAA0439,NE DL3 | NA |
| HDL assembly | R-HSA-8963896 | 1 | NA | NA | R-HSA-8963898 | FALSE | NA | FALSE | FALSE | FALSE | 8 | TRUE | 19.25 | 13 | P22612 | PRKACG | NA | NA | NA | NA | NA | NA | |
| HDR through Homologous Recombination (HRR) | R-HSA-5685942 | 1 | NA | 1 | R-HSA-5693567 | FALSE | R-HSA-5693537 | FALSE | FALSE | TRUE | 66 | TRUE | 25.0454545 | 13 | Q13315 | ATM | NA | NA | NA | NA | P38398 | BRCA1,RNF53 | |
| HDR through Homologous Recombination (HRR) | R-HSA-5685942 | 1 | NA | 1 | R-HSA-5693567 | FALSE | R-HSA-5693579 | TRUE | TRUE | TRUE | 66 | TRUE | 25.0454545 | 13 | Q13315 | ATM | NA | NA | NA | NA | P38398 | BRCA1,RNF53 | |
| HDR through Single Strand Annealing (SSA) | R-HSA-5685938 | 1 | 1 | 2 | R-HSA-5693567 | FALSE | NA | FALSE | FALSE | FALSE | 37 | TRUE | 16.1891892 | 13 | Q13315 | ATM | NA | Q13535 | ATR,FRP1 | NA | P38398,Q8WXE1 | BRCA1,RNF53,ATRIP,AGS1 | |
| NADE modulates death signalling | R-HSA-205025 | NA | NA | 1 | R-HSA-204998 | FALSE | NA | FALSE | FALSE | FALSE | 6 | TRUE | 12.1666667 | 13 | NA | NA | NA | NA | NA | NA | Q00994 | BEX3,DXS6984E,NADE,N GFRAP1 | |
| NOTCH3 Activation and Transmission of Signal to the Nucleus | R-HSA-9013507 | NA | NA | 2 | R-HSA-9012852 | FALSE | R-HSA-9017802 | FALSE | FALSE | FALSE | 25 | TRUE | 42 | 13 | NA | NA | NA | NA | NA | NA | Q00308,P01133 | WWP2,EGF | |
| Presynaptic phase of homologous DNA pairing and strand exchange | R-HSA-5693616 | 1 | 1 | 2 | R-HSA-5693579 | TRUE | NA | FALSE | TRUE | TRUE | 39 | TRUE | 15.7948718 | 13 | Q13315 | ATM | NA | Q13535 | ATR,FRP1 | NA | P38398,Q8WXE1 | BRCA1,RNF53,ATRIP,AGS1 | |
| RNA Polymerase I Transcription Termination | R-HSA-73863 | NA | NA | 2 | R-HSA-73864 | FALSE | NA | FALSE | FALSE | FALSE | 33 | TRUE | 23.1515152 | 13 | NA | NA | NA | NA | NA | NA | P18074,Q9HY6 | ERCC2,XPDP,XPDC,POLR1B | |
| Signaling by RAS mutants | R-HSA-6802949 | 2 | 2 | 3 | R-HSA-6802957 | FALSE | NA | FALSE | FALSE | FALSE | 51 | TRUE | 19 | 13 | P12931,Q75R6 | SRC,SRC1,APBB1IP,PREL1,RARP1,RIAM | SRC | P01112,P02751 | HRAS,HRAS1,FN1,FN1 | NA | P01112,Q6VAB6,Q8WXI2 | HRAS,HRAS1,KSR2,CNKSR2,CNK2,KIAA0902 | |
| Syndecan interactions | R-HSA-3000170 | NA | 1 | 1 | R-HSA-3000171 | TRUE | NA | FALSE | TRUE | TRUE | 20 | TRUE | 16.15 | 13 | NA | NA | NA | P02751 | FN1,FN1 | NA | P20908 | COL5A1 | |
| VEGFA-VEGFR2 Pathway | R-HSA-4420097 | 2 | 1 | NA | R-HSA-194138 | FALSE | R-HSA-5218921 | TRUE | TRUE | TRUE | 95 | TRUE | 19.1263158 | 13 | P22612,Q96F07 | PRKACG,CYFIP2,KIAA1168,PIR121 | NA | Q7L576 | CYFIP1,KIAA0068 | NA | NA | NA | |
| VEGFA-VEGFR2 Pathway | R-HSA-4420097 | 2 | 1 | NA | R-HSA-194138 | FALSE | R-HSA-5218920 | TRUE | TRUE | TRUE | 95 | TRUE | 19.1263158 | 13 | P22612,Q96F07 | PRKACG,CYFIP2,KIAA1168,PIR121 | NA | Q7L576 | CYFIP1,KIAA0068 | NA | NA | NA | |
| NF-kB activation through FADD/RIP-1 pathway mediated by caspase-8 and -10 | R-HSA-933543 | NA | NA | 2 | R-HSA-168928 | TRUE | NA | FALSE | TRUE | TRUE | 12 | TRUE | 20.5 | 13.5 | NA | NA | NA | NA | NA | NA | Q95786,Q14790 | DDX58,CASP8,MCH5 | |
| Nonhomologous End-Joining (NHEJ) | R-HSA-5693571 | 3 | NA | 3 | R-HSA-5693532 | FALSE | NA | FALSE | FALSE | FALSE | 52 | TRUE | 18.6923077 | 13.5 | P62805,Q12888,Q13315 | HIST1H4A,H4/A,H4FA;HIST1H4B,H4/J,H4FI;HIST1H4C,H4/G,H4FG;HIST1H4D,H4/B,H4FB;HIST1H4E,H4/J,H4FJ;HIST1H4F,H4/C,H4FC;HIST1H4H,H4/H,H4FH;HIST1H4I,H4/M,H4FM;HIST1H4J,H4/E,H4FE;HIST1H4K,H4/D,H4FD;HIST1H4L,H4/K,H4FK;HIST2H4A,H4/N,H4F2,H4FN,HIST2H4;HIST2H4B,H4/O,H4FO;HIST4H4,TP53BP1,ATM | NA | NA | NA | NA | NA | P38398,P78527,Q96R11 | BRCA1,RNF53,PRKDC,HYRC,HYR1,UIMC1,RAP80,RXRIP110 |
| Regulation of insulin secretion | R-HSA-422356 | 4 | NA | 2 | R-HSA-163685 | FALSE | R-HSA-381676 | TRUE | TRUE | TRUE | 80 | TRUE | 16.2 | 13.5 | P22612,Q13936,Q14643,Q15878 | PRKACG,CACNA1C,CACH2,CACN2,CACNL1A1,CCHL1A1,ITPR1,INSP3R1,CACNA1E,CACH6,CACNL1A6 | NA | NA | NA | NA | P11168,Q01668 | SLC2A2,GLUT2,CACNA1D,CACH3,CACN4,CACNL1A2,CCHL1A2 | |
| Regulation of insulin secretion | R-HSA-422356 | 4 | NA | 2 | R-HSA-163685 | FALSE | R-HSA-400451 | FALSE | FALSE | TRUE | 80 | TRUE | 16.2 | 13.5 | P22612,Q13936,Q14643,Q15878 | PRKACG,CACNA1C,CACH2,CACN2,CACNL1A1,CCHL1A1,ITPR1,INSP3R1,CACNA1E,CACH6,CACNL1A6 | NA | NA | NA | NA | P11168,Q01668 | SLC2A2,GLUT2,CACNA1D,CACH3,CACN4,CACNL1A2,CCHL1A2 | |
| Regulation of insulin secretion | R-HSA-422356 | 4 | NA | 2 | R-HSA-163685 | FALSE | R-HSA-399997 | FALSE | FALSE | TRUE | 80 | TRUE | 16.2 | 13.5 | P22612,Q13936,Q14643,Q15878 | PRKACG,CACNA1C,CACH2,CACN2,CACNL1A1,CCHL1A1,ITPR1,INSP3R1,CACNA1E,CACH6,CACNL1A6 | NA | NA | NA | NA | P11168,Q01668 | SLC2A2,GLUT2,CACNA1D,CACH3,CACN4,CACNL1A2,CCHL1A2 | |

| | | | | | | | | | | | | | | | | | | | | | | | | |
|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|------|-----------------------------|--|-----|--------|----------|----|---------------|---|---|---------|
| Regulation of insulin secretion | R-HSA-422356 | 4 | NA | 2 | R-HSA-163685 | FALSE | R-HSA-400042 | TRUE | TRUE | TRUE | 80 | TRUE | 16.2 | 13.5 | P22612,Q13936,Q14643,Q15878 | PRKACG,CACNA1C,CACH2,CACN2,CACNL1A1,CCHL1A1,ITPR1,INSP3R1,CACNA1E,CACG6,CACNL1A6 | NA | NA | NA | NA | P11168,Q01668 | SLC2A2,GLUT2,CACNA1D,CACH3,CACN4,CACNL1A2,CCHL1A2 | NA | |
| Transfer of LPS from LBP carrier to CD14 | R-HSA-166020 | NA | NA | 1 | R-HSA-166016 | TRUE | NA | FALSE | TRUE | TRUE | 2 | TRUE | 13.5 | 13.5 | NA | NA | NA | NA | NA | NA | P18428 | LBP | NA | |
| Chk1/Chk2(Cds1) mediated inactivation of Cyclin B:Cdk1 complex | R-HSA-75035 | NA | NA | 1 | R-HSA-69473 | TRUE | NA | FALSE | TRUE | TRUE | 13 | TRUE | 17 | 14 | NA | NA | NA | NA | NA | NA | P31947 | SFN,HME1 | NA | |
| Formation of Incision Complex in GG-NER | R-HSA-5696395 | 2 | NA | 1 | R-HSA-5696399 | FALSE | NA | FALSE | FALSE | FALSE | 43 | TRUE | 35.3023256 | 14 | Q01831,Q13619 | XPC,XPC,CUL4A | NA | NA | NA | NA | P18074 | ERCC2,XPD,XPDC | NA | |
| Interleukin-7 signaling | R-HSA-1266695 | 1 | NA | 3 | R-HSA-449147 | FALSE | NA | FALSE | FALSE | FALSE | 25 | TRUE | 16.16 | 14 | P42229 | STAT5A,STAT5 | NA | NA | NA | NA | NA | P51532,P55895,Q9Y4H2 | SMARCA4,BAF190A,BR G1,SNF2B,SNF2L4,RAG2,IRS2 | NA |
| MyD88 deficiency (TLR2/4) | R-HSA-5602498 | NA | NA | 1 | R-HSA-5602358 | FALSE | NA | FALSE | FALSE | FALSE | 11 | TRUE | 15.2727273 | 14 | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA | |
| Regulation of Complement cascade | R-HSA-977606 | 3 | NA | 3 | R-HSA-166658 | FALSE | NA | FALSE | FALSE | FALSE | 127 | TRUE | 11.0551181 | 14 | P08603,P20023,Q03591 | CFH,HF,HF1,HF2,CR2,C3DR,CFHR1,CFHL,CFHL1,CFHL1P,CFHR1P,FHR1,HF L1,HFL2 | NA | NA | NA | NA | NA | P07225,P10643,P17927 | PROS1,PROS,C7,CR1,C3BR | NA |
| RET signaling | R-HSA-8853659 | 1 | NA | 2 | R-HSA-422475 | FALSE | NA | FALSE | FALSE | FALSE | 41 | TRUE | 23.4878049 | 14 | P22612 | PRKACG | NA | NA | NA | NA | NA | O00451,Q9Y4H2 | GFRA2,GDNFRB,RET,L2,TRNR2,IRS2 | NA |
| TP53 Regulates Transcription of Genes Involved in G1 Cell Cycle Arrest | R-HSA-6804116 | 1 | 1 | 1 | R-HSA-6791312 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 14.7857143 | 14 | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | |
| Interleukin-2 signaling | R-HSA-9020558 | 1 | NA | 1 | R-HSA-451927 | FALSE | NA | FALSE | FALSE | FALSE | 12 | TRUE | 16.4166667 | 14.5 | P42229 | STAT5A,STAT5 | NA | NA | NA | NA | NA | P06239 | LCK | LCK |
| Interleukin-21 signaling | R-HSA-9020958 | 1 | NA | NA | R-HSA-451927 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 14.8 | 14.5 | P42229 | STAT5A,STAT5 | NA | NA | NA | NA | NA | NA | NA | NA |
| RNA Polymerase II Pre-transcription Events | R-HSA-674695 | 1 | NA | 4 | R-HSA-73857 | FALSE | NA | FALSE | FALSE | FALSE | 84 | TRUE | 21.2261905 | 14.5 | Q8IZX4 | TAF1L | NA | NA | NA | NA | NA | P18074,P18615,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPC,NELFE, RD,RDBP,TAF2,CIF150,TA F2B,TAF1L | NA |
| Activated NTRK2 signals through FYN | R-HSA-9032500 | 1 | NA | NA | R-HSA-9006115 | FALSE | R-HSA-9032759 | TRUE | TRUE | TRUE | 7 | TRUE | 30.1428571 | 15 | P12931 | SRC,SRC1 | SRC | NA | NA | NA | NA | NA | NA | NA |
| Cooperation of PDC1 (PhLP1) and TRIC/CCT in G-protein beta folding | R-HSA-6814122 | NA | NA | 3 | R-HSA-390466 | FALSE | NA | FALSE | FALSE | FALSE | 42 | TRUE | 17.0238095 | 15 | NA | NA | NA | NA | NA | NA | NA | P50991,Q92526,Q99832 | CCT4,CCTD,SRB,CCT6B,CCT7,CCTH,NIP7-1 | NA |
| CREB phosphorylation through the activation of Ras | R-HSA-442742 | NA | NA | 1 | R-HSA-438064 | FALSE | R-HSA-442982 | TRUE | TRUE | TRUE | 30 | TRUE | 20.5333333 | 15 | NA | NA | NA | NA | NA | NA | NA | Q9UK32 | RPS6KA6,RSK4 | RPS6KA6 |
| CREB phosphorylation through the activation of Ras | R-HSA-442742 | NA | NA | 1 | R-HSA-438064 | FALSE | R-HSA-444257 | TRUE | TRUE | TRUE | 30 | TRUE | 20.5333333 | 15 | NA | NA | NA | NA | NA | NA | NA | Q9UK32 | RPS6KA6,RSK4 | RPS6KA6 |
| Eukaryotic Translation Termination | R-HSA-72764 | 1 | NA | 3 | R-HSA-72766 | FALSE | NA | FALSE | FALSE | FALSE | 94 | TRUE | 20 | 15 | P23396 | RPS3,OK/SW-cl.26 | NA | NA | NA | NA | NA | P46781,P6277,Q96L21 | RPS9,RPS13,RPL10L | NA |
| Formation of a pool of free 40S subunits | R-HSA-72689 | 1 | NA | 3 | R-HSA-72737 | FALSE | NA | FALSE | FALSE | FALSE | 102 | TRUE | 19.1666667 | 15 | P23396 | RPS3,OK/SW-cl.26 | NA | NA | NA | NA | NA | P46781,P6277,Q96L21 | RPS9,RPS13,RPL10L | NA |
| Growth hormone receptor signaling | R-HSA-982772 | 1 | NA | 1 | R-HSA-1280215 | FALSE | NA | FALSE | FALSE | FALSE | 24 | TRUE | 18.3333333 | 15 | P42229 | STAT5A,STAT5 | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA |
| GTP hydrolysis and joining of the 60S ribosomal subunit | R-HSA-72706 | 1 | NA | 3 | R-HSA-72737 | FALSE | NA | FALSE | FALSE | FALSE | 113 | TRUE | 18.0265487 | 15 | P23396 | RPS3,OK/SW-cl.26 | NA | NA | NA | NA | NA | P46781,P6277,Q96L21 | RPS9,RPS13,RPL10L | NA |
| L13a-mediated translational silencing of Ceruloplasmin expression | R-HSA-156827 | 1 | NA | 3 | R-HSA-72613 | FALSE | NA | FALSE | FALSE | FALSE | 112 | TRUE | 18.2410714 | 15 | P23396 | RPS3,OK/SW-cl.26 | NA | NA | NA | NA | NA | P46781,P6277,Q96L21 | RPS9,RPS13,RPL10L | NA |

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|--|---------------|----|----|---|---------------|-------|---------------|-------|-------|-------|-----|------|------------|------|-----------------------------|---|----|---------------|-------------------|----|-----------------------------|--|------|
| Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC) | R-HSA-975957 | 2 | NA | 3 | R-HSA-927802 | FALSE | NA | FALSE | FALSE | FALSE | 116 | TRUE | 18.7586207 | 15 | P23396,P38919 | RP53,OK/SW-cl.26,EIF4A3,DDX48,KIAA0111 | NA | NA | NA | NA | P46781,P62277,Q96L21 | RP59,RP513,RPL10L | NA |
| Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC) | R-HSA-975956 | 1 | NA | 3 | R-HSA-927802 | FALSE | NA | FALSE | FALSE | FALSE | 96 | TRUE | 20.4479167 | 15 | P23396 | RP53,OK/SW-cl.26 | NA | NA | NA | NA | P46781,P62277,Q96L21 | RP59,RP513,RPL10L | NA |
| Peptide chain elongation | R-HSA-156902 | 1 | NA | 3 | R-HSA-156842 | FALSE | NA | FALSE | FALSE | FALSE | 90 | TRUE | 20.7666667 | 15 | P23396 | RP53,OK/SW-cl.26 | NA | NA | NA | NA | P46781,P62277,Q96L21 | RP59,RP513,RPL10L | NA |
| Processing of DNA double-strand break ends | R-HSA-5693607 | 3 | 1 | 3 | R-HSA-5693567 | FALSE | NA | FALSE | FALSE | FALSE | 81 | TRUE | 28.3333333 | 15 | P62805,Q12888,Q13315 | HIST1H4A,H4/A,H4FA,HIST1H4B,H4/I,H4FI,HIST1H4C,H4/G,H4FG,HIST1H4D,H4/B,H4FB,HIST1H4E,H4/J,H4FJ,HIST1H4F,H4/C,H4FC,HIST1H4H,H4/H,H4FH,HIST1H4I,H4/M,H4FM,HIST1H4J,H4/E,H4FE,HIST1H4K,H4/D,H4FD,HIST1H4L,H4/K,H4FK,HIST2H4A,H4/N,H4F2,H4FN,HIST2H4,H4/O,H4FO,HIST4H4,TP53BP1,ATM | NA | Q13535 | ATR,FRP1 | NA | P38398,Q8WXE1,Q96RL1 | BRCA1,RNF53,ATRIP,AGS1,UIMC1,RAP80,RXRIP110 | NA |
| Selenocysteine synthesis | R-HSA-2408557 | 1 | NA | 3 | R-HSA-2408522 | FALSE | NA | FALSE | FALSE | FALSE | 94 | TRUE | 19.8297872 | 15 | P23396 | RP53,OK/SW-cl.26 | NA | NA | NA | NA | P46781,P62277,Q96L21 | RP59,RP513,RPL10L | NA |
| Signaling by ROBO receptors | R-HSA-376176 | 1 | NA | 1 | R-HSA-422475 | FALSE | R-HSA-9010553 | TRUE | TRUE | TRUE | 219 | TRUE | 30.2420091 | 15 | O75093 | SLIT1,KIAA0813,MEGF4,SLIL1 | NA | NA | NA | NA | Q9Y6N7 | ROBO1,DUTT1 | NA |
| Signaling by ROBO receptors | R-HSA-376176 | 1 | NA | 1 | R-HSA-422475 | FALSE | R-HSA-428543 | TRUE | TRUE | TRUE | 219 | TRUE | 30.2420091 | 15 | O75093 | SLIT1,KIAA0813,MEGF4,SLIL1 | NA | NA | NA | NA | Q9Y6N7 | ROBO1,DUTT1 | NA |
| Signaling by ROBO receptors | R-HSA-376176 | 1 | NA | 1 | R-HSA-422475 | FALSE | R-HSA-8985801 | TRUE | TRUE | TRUE | 219 | TRUE | 30.2420091 | 15 | O75093 | SLIT1,KIAA0813,MEGF4,SLIL1 | NA | NA | NA | NA | Q9Y6N7 | ROBO1,DUTT1 | NA |
| Signaling by ROBO receptors | R-HSA-376176 | 1 | NA | 1 | R-HSA-422475 | FALSE | R-HSA-8985586 | TRUE | TRUE | TRUE | 219 | TRUE | 30.2420091 | 15 | O75093 | SLIT1,KIAA0813,MEGF4,SLIL1 | NA | NA | NA | NA | Q9Y6N7 | ROBO1,DUTT1 | NA |
| Signaling by ROBO receptors | R-HSA-376176 | 1 | NA | 1 | R-HSA-422475 | FALSE | R-HSA-428542 | TRUE | TRUE | TRUE | 219 | TRUE | 30.2420091 | 15 | O75093 | SLIT1,KIAA0813,MEGF4,SLIL1 | NA | NA | NA | NA | Q9Y6N7 | ROBO1,DUTT1 | NA |
| Signaling by ROBO receptors | R-HSA-376176 | 1 | NA | 1 | R-HSA-422475 | FALSE | R-HSA-428890 | TRUE | TRUE | TRUE | 219 | TRUE | 30.2420091 | 15 | O75093 | SLIT1,KIAA0813,MEGF4,SLIL1 | NA | NA | NA | NA | Q9Y6N7 | ROBO1,DUTT1 | NA |
| Signaling by ROBO receptors | R-HSA-376176 | 1 | NA | 1 | R-HSA-422475 | FALSE | R-HSA-428540 | TRUE | TRUE | TRUE | 219 | TRUE | 30.2420091 | 15 | O75093 | SLIT1,KIAA0813,MEGF4,SLIL1 | NA | NA | NA | NA | Q9Y6N7 | ROBO1,DUTT1 | NA |
| Signaling by ROBO receptors | R-HSA-376176 | 1 | NA | 1 | R-HSA-422475 | FALSE | R-HSA-9010642 | TRUE | TRUE | TRUE | 219 | TRUE | 30.2420091 | 15 | O75093 | SLIT1,KIAA0813,MEGF4,SLIL1 | NA | NA | NA | NA | Q9Y6N7 | ROBO1,DUTT1 | NA |
| SRP-dependent cotranslational protein targeting to membrane | R-HSA-1799339 | 1 | NA | 4 | R-HSA-72766 | FALSE | NA | FALSE | FALSE | FALSE | 115 | TRUE | 16.7217391 | 15 | P23396 | RP53,OK/SW-cl.26 | NA | NA | NA | NA | P46781,P62277,Q96L21,Q9H953 | RP59,RP513,RPL10L,SEC61A2 | NA |
| Viral mRNA Translation | R-HSA-192823 | 1 | NA | 3 | R-HSA-166273 | FALSE | NA | FALSE | FALSE | FALSE | 98 | TRUE | 20.2244898 | 15 | P23396 | RP53,OK/SW-cl.26 | NA | NA | NA | NA | P46781,P62277,Q96L21 | RP59,RP513,RPL10L | NA |
| AKT phosphorylates targets in the cytosol | R-HSA-198323 | 2 | NA | 1 | R-HSA-1257604 | TRUE | NA | FALSE | TRUE | TRUE | 14 | TRUE | 19.7142857 | 15.5 | P49815,Q9Y243 | TSC2,TSC4,AKT3,PKBG | NA | NA | NA | NA | P31751 | AKT2 | AKT2 |
| CLEC7A/inflammasome pathway | R-HSA-5660668 | NA | NA | 1 | R-HSA-5607764 | TRUE | NA | FALSE | TRUE | TRUE | 6 | TRUE | 20.1666667 | 15.5 | NA | NA | NA | NA | NA | NA | Q14790 | CASP8,MCH5 | NA |
| G2/M DNA damage checkpoint | R-HSA-69473 | 4 | 2 | 4 | R-HSA-69481 | TRUE | R-HSA-75035 | TRUE | TRUE | TRUE | 78 | TRUE | 20.7948718 | 15.5 | P04637,P62805,Q12888,Q13315 | TP53,P53,HIST1H4A,H4/A,H4FA,HIST1H4B,H4/I,H4FI,HIST1H4C,H4/G,H4FG,HIST1H4D,H4/B,H4FB,HIST1H4E,H4/J,H4FJ,HIST1H4F,H4/C,H4FC,HIST1H4H,H4/H,H4FH,HIST1H4I,H4/M,H4FM,HIST1H4J,H4/E,H4FE,HIST1H4K,H4/D,H4FD,HIST1H4L,H4/K,H4FK,HIST2H4A,H4/N,H4F2,H4FN,HIST2H4,H4/O,H4FO,HIST4H4,TP53BP1,ATM | NA | P04637,Q13535 | TP53,P53,ATR,FRP1 | NA | P04637,P38398,Q8WXE1,Q96RL1 | TP53,P53,BRCA1,RNF53,ATRIP,AGS1,UIMC1,RAP80,RXRIP110 | NA |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|------|----------------------|--|-------|--------|--------------------------|----|------------------------------------|---|-------------------------------|-------------|
| HDACs deacetylate histones | R-HSA-3214815 | 1 | NA | NA | R-HSA-3247509 | TRUE | NA | FALSE | TRUE | TRUE | 60 | TRUE | 19.9833333 | 15.5 | P62805 | HIST1H4A,H4/A,H4FA;,HIST1H4B,H4/J,H4FI;,HIST1H4C,H4/G,H4FG;,HIST1H4D,H4/B,H4FB;,HIST1H4E,H4/J,H4FJ;,HIST1H4F,H4/C,H4FC;,HIST1H4H,H4/H,H4FH;,HIST1H4I,H4/E,M,H4FM;,HIST1H4J,H4/E,H4FE;,HIST1H4K,H4/D,H4FD;,HIST1H4L,H4/K,H4FK;,HIST2H4A,H4/N,H4F2,H4FN,HIST2H4;,HIST2H4B,H4/O,H4FO;,HIST4H4 | NA | NA | NA | NA | NA | NA | NA | NA |
| IRAK4 deficiency (TLR2/4) | R-HSA-5603041 | NA | NA | 1 | R-HSA-5602358 | FALSE | NA | FALSE | FALSE | FALSE | 12 | TRUE | 15.5 | 15.5 | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA | |
| Antigen activates B Cell Receptor (BCR) leading to generation of second messengers | R-HSA-983695 | 1 | NA | NA | R-HSA-983705 | FALSE | NA | FALSE | FALSE | FALSE | 95 | TRUE | 17.1894737 | 16 | Q14643 | ITPR1,INSP3R1 | NA | NA | NA | NA | NA | NA | NA | NA |
| FCERI mediated Ca2 mobilization | R-HSA-2871809 | 1 | NA | 2 | R-HSA-2454202 | FALSE | NA | FALSE | FALSE | FALSE | 107 | TRUE | 17.0934579 | 16 | Q14643 | ITPR1,INSP3R1 | NA | NA | NA | NA | NA | P16298,Q13094 | PPP3CB,CALNA2,CALNB,CNA2,LCP2 | NA |
| FCERI mediated MAPK activation | R-HSA-2871796 | NA | 1 | 2 | R-HSA-2454202 | FALSE | NA | FALSE | FALSE | FALSE | 108 | TRUE | 20.8333333 | 16 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112,Q13094 | HRAS,HRAS1,LCP2 | NA | |
| FCERI mediated NF-kB activation | R-HSA-2871837 | 3 | NA | 3 | R-HSA-2454202 | FALSE | NA | FALSE | FALSE | FALSE | 157 | TRUE | 39.5987261 | 16 | P25786,P51668,Q9V297 | PSMA1,HC2,NU,PROS30,PS2,UBE2D1,SFT,UBC5A,UBCH5,UBCH5A,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | NA | NA | NA | NA | P61289,Q04759,Q13200 | PSME3,PRKCO,PRKCT,PSMD2,TRAP2 | PRKCO,PSMD2 |
| FCGR activation | R-HSA-2029481 | 1 | NA | NA | R-HSA-2029480 | FALSE | NA | FALSE | FALSE | FALSE | 94 | TRUE | 15.712766 | 16 | P09769 | FGR,SR2 | FGR | NA | NA | NA | NA | NA | NA | NA |
| GPVI-mediated activation cascade | R-HSA-114604 | NA | NA | 3 | R-HSA-76002 | FALSE | NA | FALSE | FALSE | FALSE | 33 | TRUE | 21.030303 | 16 | NA | NA | NA | NA | NA | NA | O95866,P06239,Q13094 | MPIG6B,C6orf25,G6B,G6B-B,LCK,LCP2 | LCK | |
| Initial triggering of complement | R-HSA-166663 | NA | NA | 1 | R-HSA-166658 | FALSE | R-HSA-173736 | FALSE | FALSE | FALSE | 103 | TRUE | 12.7961165 | 16 | NA | NA | NA | NA | NA | NA | NA | Q9BWP8 | COLEC11,UNQ596/PRO1182 | NA |
| Initial triggering of complement | R-HSA-166663 | NA | NA | 1 | R-HSA-166658 | FALSE | R-HSA-166786 | FALSE | FALSE | FALSE | 103 | TRUE | 12.7961165 | 16 | NA | NA | NA | NA | NA | NA | NA | Q9BWP8 | COLEC11,UNQ596/PRO1182 | NA |
| Interleukin-3, Interleukin-5 and GM-CSF signaling | R-HSA-512988 | 1 | NA | NA | R-HSA-449147 | FALSE | R-HSA-912526 | FALSE | FALSE | FALSE | 44 | TRUE | 22.75 | 16 | P42229 | STAT5A,STAT5 | NA | NA | NA | NA | NA | NA | NA | NA |
| Interleukin-3, Interleukin-5 and GM-CSF signaling | R-HSA-512988 | 1 | NA | NA | R-HSA-449147 | FALSE | R-HSA-912631 | FALSE | FALSE | FALSE | 44 | TRUE | 22.75 | 16 | P42229 | STAT5A,STAT5 | NA | NA | NA | NA | NA | NA | NA | NA |
| Nuclear signaling by ERBB4 | R-HSA-1251985 | 2 | NA | 1 | R-HSA-1236394 | TRUE | NA | FALSE | TRUE | TRUE | 27 | TRUE | 17.1481481 | 16 | P12931,P42229 | SRC,SR1,STAT5A,STAT5 | SRC | NA | NA | NA | NA | Q9NZC7 | WWOX,FOR,SDR41C1,WOX1 | NA |
| Oncogene Induced Senescence | R-HSA-2559585 | 2 | 1 | 2 | R-HSA-2559583 | FALSE | NA | FALSE | FALSE | FALSE | 35 | TRUE | 36.4857143 | 16 | P04637,Q9UPQ9 | TP53,P53,TNRC6B,KIAA1093 | NA | P04637 | TP53,P53 | NA | P04637,Q9UPQ9 | TP53,P53,TNRC6B,KIAA1093 | NA | |
| PIP3 activates AKT signaling | R-HSA-1257604 | 2 | 1 | 5 | R-HSA-9006925 | FALSE | R-HSA-198323 | TRUE | TRUE | TRUE | 279 | TRUE | 29.5412186 | 16 | P12931,Q9Y243 | SRC,SR1,AKT3,PKBG | SRC | P33681 | CD80,CD28LG,CD28LG1,LAB7 | NA | P01133,P06239,P31751,P42345,Q9Y4H2 | EGF,LCK,AKT2,MTOR,FRAP,FRAP1,FRAP2,RAFT1,RAFT1,IRS2 | LCK,AKT2 | |
| PIP3 activates AKT signaling | R-HSA-1257604 | 2 | 1 | 5 | R-HSA-9006925 | FALSE | R-HSA-6807070 | FALSE | FALSE | TRUE | 279 | TRUE | 29.5412186 | 16 | P12931,Q9Y243 | SRC,SR1,AKT3,PKBG | SRC | P33681 | CD80,CD28LG,CD28LG1,LAB7 | NA | P01133,P06239,P31751,P42345,Q9Y4H2 | EGF,LCK,AKT2,MTOR,FRAP,FRAP1,FRAP2,RAFT1,RAFT1,IRS2 | LCK,AKT2 | |
| PIP3 activates AKT signaling | R-HSA-1257604 | 2 | 1 | 5 | R-HSA-9006925 | FALSE | R-HSA-199418 | TRUE | TRUE | TRUE | 279 | TRUE | 29.5412186 | 16 | P12931,Q9Y243 | SRC,SR1,AKT3,PKBG | SRC | P33681 | CD80,CD28LG,CD28LG1,LAB7 | NA | P01133,P06239,P31751,P42345,Q9Y4H2 | EGF,LCK,AKT2,MTOR,FRAP,FRAP1,FRAP2,RAFT1,RAFT1,IRS2 | LCK,AKT2 | |
| PIP3 activates AKT signaling | R-HSA-1257604 | 2 | 1 | 5 | R-HSA-9006925 | FALSE | R-HSA-198693 | TRUE | TRUE | TRUE | 279 | TRUE | 29.5412186 | 16 | P12931,Q9Y243 | SRC,SR1,AKT3,PKBG | SRC | P33681 | CD80,CD28LG,CD28LG1,LAB7 | NA | P01133,P06239,P31751,P42345,Q9Y4H2 | EGF,LCK,AKT2,MTOR,FRAP,FRAP1,FRAP2,RAFT1,RAFT1,IRS2 | LCK,AKT2 | |
| Regulation of actin dynamics for phagocytic cup formation | R-HSA-2029482 | 1 | 1 | NA | R-HSA-2029480 | FALSE | NA | FALSE | FALSE | FALSE | 143 | TRUE | 13.8251748 | 16 | Q96F07 | CYFIP2,KIAA1168,PIR121 | NA | Q7L576 | CYFIP1,KIAA0068 | NA | NA | NA | NA | NA |
| Role of phospholipids in phagocytosis | R-HSA-2029485 | 1 | NA | NA | R-HSA-2029480 | FALSE | NA | FALSE | FALSE | FALSE | 107 | TRUE | 15.7196262 | 16 | Q14643 | ITPR1,INSP3R1 | NA | NA | NA | NA | NA | NA | NA | NA |
| RUNX3 regulates CDKN1A transcription | R-HSA-8941855 | 1 | 1 | 1 | R-HSA-8878159 | FALSE | NA | FALSE | FALSE | FALSE | 7 | TRUE | 19 | 16 | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|----|----------------|---|----|--------|-------------|----|-----------------------------|---|------|
| Scavenging of heme from plasma | R-HSA-2168880 | NA | NA | 1 | R-HSA-2173782 | FALSE | NA | FALSE | FALSE | FALSE | 92 | TRUE | 13.8478261 | 16 | NA | NA | NA | NA | NA | NA | Q86VB7 | CD163,M130 | NA |
| Signal transduction by L1 | R-HSA-445144 | 1 | NA | 1 | R-HSA-373760 | TRUE | NA | FALSE | TRUE | TRUE | 21 | TRUE | 24.047619 | 16 | P32004 | L1CAM,CAML1,MIC5 | NA | NA | NA | NA | Q13797 | ITGA9 | NA |
| Signaling by EGFR | R-HSA-177929 | NA | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-182971 | TRUE | TRUE | TRUE | 43 | TRUE | 42.8139535 | 16 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |
| Signaling by EGFR | R-HSA-177929 | NA | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-212718 | TRUE | TRUE | TRUE | 43 | TRUE | 42.8139535 | 16 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |
| Signaling by EGFR | R-HSA-177929 | NA | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-179812 | TRUE | TRUE | TRUE | 43 | TRUE | 42.8139535 | 16 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |
| Signaling by EGFR | R-HSA-177929 | NA | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-180292 | TRUE | TRUE | TRUE | 43 | TRUE | 42.8139535 | 16 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |
| Signaling by EGFR | R-HSA-177929 | NA | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-180336 | TRUE | TRUE | TRUE | 43 | TRUE | 42.8139535 | 16 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |
| TCF dependent signaling in response to WNT | R-HSA-201681 | NA | NA | 3 | R-HSA-195721 | FALSE | R-HSA-3772470 | TRUE | TRUE | TRUE | 203 | TRUE | 32.9655172 | 16 | NA | NA | NA | NA | NA | NA | O14641,095271,Q8NCW0 | DVL2,TNKS,PARPSA,PARPL,TIN1,TINF1,TNKS1,KR EMEN2,KRM2 | NA |
| TCF dependent signaling in response to WNT | R-HSA-201681 | NA | NA | 3 | R-HSA-195721 | FALSE | R-HSA-4641257 | TRUE | TRUE | TRUE | 203 | TRUE | 32.9655172 | 16 | NA | NA | NA | NA | NA | NA | O14641,095271,Q8NCW0 | DVL2,TNKS,PARPSA,PARPL,TIN1,TINF1,TNKS1,KR EMEN2,KRM2 | NA |
| TCF dependent signaling in response to WNT | R-HSA-201681 | NA | NA | 3 | R-HSA-195721 | FALSE | R-HSA-4641258 | TRUE | TRUE | TRUE | 203 | TRUE | 32.9655172 | 16 | NA | NA | NA | NA | NA | NA | O14641,095271,Q8NCW0 | DVL2,TNKS,PARPSA,PARPL,TIN1,TINF1,TNKS1,KR EMEN2,KRM2 | NA |
| TCF dependent signaling in response to WNT | R-HSA-201681 | NA | NA | 3 | R-HSA-195721 | FALSE | R-HSA-4641263 | TRUE | TRUE | TRUE | 203 | TRUE | 32.9655172 | 16 | NA | NA | NA | NA | NA | NA | O14641,095271,Q8NCW0 | DVL2,TNKS,PARPSA,PARPL,TIN1,TINF1,TNKS1,KR EMEN2,KRM2 | NA |
| TCF dependent signaling in response to WNT | R-HSA-201681 | NA | NA | 3 | R-HSA-195721 | FALSE | R-HSA-201722 | TRUE | TRUE | TRUE | 203 | TRUE | 32.9655172 | 16 | NA | NA | NA | NA | NA | NA | O14641,095271,Q8NCW0 | DVL2,TNKS,PARPSA,PARPL,TIN1,TINF1,TNKS1,KR EMEN2,KRM2 | NA |
| TCF dependent signaling in response to WNT | R-HSA-201681 | NA | NA | 3 | R-HSA-195721 | FALSE | R-HSA-4641262 | TRUE | TRUE | TRUE | 203 | TRUE | 32.9655172 | 16 | NA | NA | NA | NA | NA | NA | O14641,095271,Q8NCW0 | DVL2,TNKS,PARPSA,PARPL,TIN1,TINF1,TNKS1,KR EMEN2,KRM2 | NA |
| TCF dependent signaling in response to WNT | R-HSA-201681 | NA | NA | 3 | R-HSA-195721 | FALSE | R-HSA-201688 | TRUE | TRUE | TRUE | 203 | TRUE | 32.9655172 | 16 | NA | NA | NA | NA | NA | NA | O14641,095271,Q8NCW0 | DVL2,TNKS,PARPSA,PARPL,TIN1,TINF1,TNKS1,KR EMEN2,KRM2 | NA |
| TCF dependent signaling in response to WNT | R-HSA-201681 | NA | NA | 3 | R-HSA-195721 | FALSE | R-HSA-5368598 | TRUE | TRUE | TRUE | 203 | TRUE | 32.9655172 | 16 | NA | NA | NA | NA | NA | NA | O14641,095271,Q8NCW0 | DVL2,TNKS,PARPSA,PARPL,TIN1,TINF1,TNKS1,KR EMEN2,KRM2 | NA |
| TCF dependent signaling in response to WNT | R-HSA-201681 | NA | NA | 3 | R-HSA-195721 | FALSE | R-HSA-3769402 | TRUE | TRUE | TRUE | 203 | TRUE | 32.9655172 | 16 | NA | NA | NA | NA | NA | NA | O14641,095271,Q8NCW0 | DVL2,TNKS,PARPSA,PARPL,TIN1,TINF1,TNKS1,KR EMEN2,KRM2 | NA |
| VEGFR2 mediated vascular permeability | R-HSA-5218920 | 1 | NA | 2 | R-HSA-4420097 | TRUE | NA | FALSE | TRUE | TRUE | 27 | TRUE | 20.6296296 | 16 | Q9Y243 | AKT3,PKBG | NA | NA | NA | NA | P31751,P42345 | AKT2,MTOR,FRAP,FRAP1,FRAP2,RAFT1,RAPT1 | AKT2 |
| Activation of NOXA and translocation to mitochondria | R-HSA-111448 | 1 | 1 | 1 | R-HSA-114452 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 19.6 | 17 | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA |
| Amyloid fiber formation | R-HSA-977225 | 2 | NA | 4 | R-HSA-392499 | FALSE | NA | FALSE | FALSE | FALSE | 79 | TRUE | 27.2278481 | 17 | P62805,Q93008 | HIST1H4A,H4/A,H4FA;HIST1H4B,H4/L,H4FI;HIST1H4C,H4/G,H4FG;HIST1H4D,H4/B,H4FB;HIST1H4E,H4/J,H4FJ;HIST1H4F,H4/C,H4FC;HIST1H4H,H4/H,H4FH;HIST1H4I,H4/M,H4FM;HIST1H4J,H4/E,H4FE;HIST1H4K,H4/D,H4FD;HIST1H4L,H4/K,H4FK;HIST2H4A,H4/N,H4F2,H4FN;HIST2H4;HIST2H4B,H4/O,H4FO;HIST4H4,USP9X,DFRX,FAM,USP9 | NA | NA | NA | NA | P02766,P04279,P06396,Q93008 | TTR,PALB,SEMG1,SEMG,GSN,USP9X,DFRX,FAM,USP9 | NA |
| APC-Cdc20 mediated degradation of Nek2A | R-HSA-179409 | 1 | 1 | NA | R-HSA-179419 | FALSE | NA | FALSE | FALSE | FALSE | 25 | TRUE | 46.36 | 17 | P51668 | UBE2D1,SFT,UBCSA,UBCH5,UBCH5A | NA | Q9UJX4 | ANAPCS,APCS | NA | NA | NA | NA |
| APC/Cdc20 mediated degradation of Cyclin B | R-HSA-174048 | 1 | 1 | NA | R-HSA-176409 | TRUE | NA | FALSE | TRUE | TRUE | 23 | TRUE | 51.5217391 | 17 | P51668 | UBE2D1,SFT,UBCSA,UBCH5,UBCH5A | NA | Q9UJX4 | ANAPCS,APCS | NA | NA | NA | NA |
| Ca2+ pathway | R-HSA-4086398 | 2 | NA | 3 | R-HSA-3850494 | FALSE | NA | FALSE | FALSE | FALSE | 62 | TRUE | 18.1935484 | 17 | Q14643,Q9LUP09 | ITPR1,INSP3R1,TNRC6B,KIAA1093 | NA | NA | NA | NA | P16298,Q9HCS4,Q9UJX4 | PPP3CB,CALNA2,CALNB,CNA2,TCF7L1,TCF3,TNRC6B,KIAA1093 | NA |

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|---|---------------|----|----|----|---------------|-------|--------------|-------|-------|-------|-----|------|------------|----|------------------------------------|---|-------------|---------------|--------------------------|----|----------------------|--|----------|
| CD28 dependent PI3K/Akt signaling | R-HSA-389357 | 1 | 1 | 3 | R-HSA-389356 | TRUE | NA | FALSE | TRUE | TRUE | 22 | TRUE | 24.6363636 | 17 | Q9Y243 | AKT3,PKBG | NA | P33681 | CD80,CD28LG,CD28LG1,LAB7 | NA | P06239,P31751,P42345 | LCK,AKT2,MTOR,FRAP,FRAP1,FRAP2,RAFT1,RAP1 | LCK,AKT2 |
| Conversion from APC/Cc20 to APC/Ccdh1 in late anaphase | R-HSA-176407 | 1 | 1 | NA | R-HSA-174143 | FALSE | NA | FALSE | FALSE | FALSE | 19 | TRUE | 17.1578947 | 17 | P51668 | UBE2D1,SFT,UBCSA,UBCH5,UBCH5A | NA | Q9UJX4 | ANAPCS,APCS | NA | NA | NA | NA |
| DARPP-32 events | R-HSA-180024 | 1 | NA | 3 | R-HSA-111885 | FALSE | NA | FALSE | FALSE | FALSE | 24 | TRUE | 25.9166667 | 17 | P22612 | PRKACG | NA | NA | NA | NA | P16298,P27815,Q08493 | PPP3CB,CALNA2,CALNB,CNA2,PDE4A,DPDE2,PDE4C,DPDE1 | NA |
| Inactivation of APC/C via direct inhibition of the APC/C complex | R-HSA-141430 | 1 | 1 | NA | R-HSA-141405 | FALSE | NA | FALSE | FALSE | FALSE | 20 | TRUE | 17.3 | 17 | P51668 | UBE2D1,SFT,UBCSA,UBCH5,UBCH5A | NA | Q9UJX4 | ANAPCS,APCS | NA | NA | NA | NA |
| Integrin alpha3 beta3 signaling | R-HSA-354192 | 2 | 1 | NA | R-HSA-9006921 | FALSE | R-HSA-372708 | TRUE | TRUE | TRUE | 27 | TRUE | 24.9259259 | 17 | P12931,Q75R6 | SRC,SRCL,APBB1IP,PREL1,RARP1,RIAM | SRC | P02751 | FN1,FN | NA | NA | NA | NA |
| Integrin alpha3 beta3 signaling | R-HSA-354192 | 2 | 1 | NA | R-HSA-76009 | FALSE | R-HSA-372708 | TRUE | TRUE | TRUE | 27 | TRUE | 24.9259259 | 17 | P12931,Q75R6 | SRC,SRCL,APBB1IP,PREL1,RARP1,RIAM | SRC | P02751 | FN1,FN | NA | NA | NA | NA |
| Integrin alpha3 beta3 signaling | R-HSA-354192 | 2 | 1 | NA | R-HSA-9006921 | FALSE | R-HSA-354194 | TRUE | TRUE | TRUE | 27 | TRUE | 24.9259259 | 17 | P12931,Q75R6 | SRC,SRCL,APBB1IP,PREL1,RARP1,RIAM | SRC | P02751 | FN1,FN | NA | NA | NA | NA |
| Integrin alpha3 beta3 signaling | R-HSA-354192 | 2 | 1 | NA | R-HSA-76009 | FALSE | R-HSA-354194 | TRUE | TRUE | TRUE | 27 | TRUE | 24.9259259 | 17 | P12931,Q75R6 | SRC,SRCL,APBB1IP,PREL1,RARP1,RIAM | SRC | P02751 | FN1,FN | NA | NA | NA | NA |
| Interleukin-15 signaling | R-HSA-8983432 | 1 | NA | NA | R-HSA-451927 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 25.7857143 | 17 | P42229 | STAT5A,STAT5 | NA | NA | NA | NA | NA | NA | NA |
| IRS activation | R-HSA-74713 | NA | NA | 1 | R-HSA-74751 | TRUE | NA | FALSE | TRUE | TRUE | 5 | TRUE | 15 | 17 | NA | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA |
| MAP2K and MAPK activation | R-HSA-5674135 | 2 | 2 | 3 | R-HSA-5673001 | TRUE | NA | FALSE | TRUE | TRUE | 38 | TRUE | 23.5 | 17 | P12931,Q75R6 | SRC,SRCL,APBB1IP,PREL1,RARP1,RIAM | SRC | P01112,P02751 | HRAS,HRAS1,FN1,FN | NA | P01112,Q6VAB6,Q8WXI2 | HRAS,HRAS1,KSR2,CNKSR2,CNK2,KIAA0902 | NA |
| p130Cas linkage to MAPK signaling for integrins | R-HSA-372708 | 2 | 1 | NA | R-HSA-354192 | TRUE | NA | FALSE | TRUE | TRUE | 15 | TRUE | 20.7333333 | 17 | P12931,Q75R6 | SRC,SRCL,APBB1IP,PREL1,RARP1,RIAM | SRC | P02751 | FN1,FN | NA | NA | NA | NA |
| Paradoxical activation of RAF signaling by kinase inactive BRAF | R-HSA-6802955 | 2 | 2 | 3 | R-HSA-6802957 | FALSE | NA | FALSE | FALSE | FALSE | 38 | TRUE | 24.2105263 | 17 | P12931,Q75R6 | SRC,SRCL,APBB1IP,PREL1,RARP1,RIAM | SRC | P01112,P02751 | HRAS,HRAS1,FN1,FN | NA | P01112,Q6VAB6,Q8WXI2 | HRAS,HRAS1,KSR2,CNKSR2,CNK2,KIAA0902 | NA |
| Phosphorylation of the APC/C | R-HSA-176412 | 1 | 1 | NA | R-HSA-176814 | FALSE | NA | FALSE | FALSE | FALSE | 19 | TRUE | 20.5263158 | 17 | P51668 | UBE2D1,SFT,UBCSA,UBCH5,UBCH5A | NA | Q9UJX4 | ANAPCS,APCS | NA | NA | NA | NA |
| Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks | R-HSA-5693565 | 5 | 1 | 3 | R-HSA-5693606 | FALSE | NA | FALSE | FALSE | FALSE | 59 | TRUE | 31.7457627 | 17 | O94953,P04637,P62805,Q12888,Q13315 | KDM4B,JHDM3B,JMJD2B,KIAA0876,TP53,P53,HIST1H4A,H4/A,H4FA,HIST1H4B,H4/J,H4FI,HIST1H4C,H4/G,H4FG,HIST1H4D,H4/B,H4FB,HIST1H4E,H4/J,H4FI,HIST1H4F,H4/C,H4FC,HIST1H4H,H4/H,H4FM,HIST1H4I,H4/M,H4FN,HIST1H4J,H4/E,H4FE,HIST1H4K,H4/D,H4FD,HIST1H4L,H4/K,H4FK,HIST2H4A,H4/N,H4F2,H4FN,HIST2H4,HIST2H4B,H4/O,H4FO,HIST4H4,TP53BP1,ATM | NA | P04637 | TP53,P53 | NA | P04637,P38398,Q96R11 | TP53,P53,BRCA1,RNF53,UIMC1,RAP80,RXRIIP110 | NA |
| Regulation of MECP2 expression and activity | R-HSA-9022692 | 2 | NA | 2 | R-HSA-8986944 | TRUE | NA | FALSE | TRUE | TRUE | 32 | TRUE | 18.21875 | 17 | P42858,Q9UPQ9 | HTT,HD,IT15,TNRC6B,KIAA1093 | NA | NA | NA | NA | P42858,Q9UPQ9 | HTT,HD,IT15,TNRC6B,KIAA1093 | NA |
| Regulation of TLR by endogenous ligand | R-HSA-5686938 | 1 | NA | 2 | R-HSA-168898 | FALSE | NA | FALSE | FALSE | FALSE | 16 | TRUE | 14.0625 | 17 | Q8IWL2 | SFTPA1,COLEC4,PSAP,SFTPT1,SFTPA,SFTPA1B | NA | NA | NA | NA | O00206,P18428 | TLR4,LBP | NA |
| Separation of Sister Chromatids | R-HSA-2467813 | 4 | 1 | 3 | R-HSA-68882 | FALSE | NA | FALSE | FALSE | FALSE | 171 | TRUE | 34.6900585 | 17 | P25786,P51668,Q3ZCM7,Q72460 | PSMA1,HC2,NU,PROS30,PSC2,UBE2D1,SFT,UBC5A,UBCH5,UBCH5A,TUBB8,CLASP1,KIAA0622,MAST1 | PSMA1,MAST1 | Q9UJX4 | ANAPCS,APCS | NA | P50748,P61289,Q13200 | KNTC1,KIAA0166,PSME3,PSMD2,TRAP2 | PSMD2 |
| Signaling by moderate kinase activity BRAF mutants | R-HSA-6802946 | 2 | 2 | 3 | R-HSA-6802957 | FALSE | NA | FALSE | FALSE | FALSE | 38 | TRUE | 24.2105263 | 17 | P12931,Q75R6 | SRC,SRCL,APBB1IP,PREL1,RARP1,RIAM | SRC | P01112,P02751 | HRAS,HRAS1,FN1,FN | NA | P01112,Q6VAB6,Q8WXI2 | HRAS,HRAS1,KSR2,CNKSR2,CNK2,KIAA0902 | NA |
| Transcription of the HIV genome | R-HSA-167172 | 1 | NA | 3 | R-HSA-162599 | FALSE | R-HSA-167152 | TRUE | TRUE | TRUE | 74 | TRUE | 23.6351351 | 17 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPC,TAF2,CIF150,TAF2B,TAF1L | NA |
| Transcription of the HIV genome | R-HSA-167172 | 1 | NA | 3 | R-HSA-162599 | FALSE | R-HSA-167160 | TRUE | TRUE | TRUE | 74 | TRUE | 23.6351351 | 17 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPC,TAF2,CIF150,TAF2B,TAF1L | NA |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|------|---------------|---------------------------------------|-----|---------------|-------------------|----|---|---|-----|
| Transcription of the HIV genome | R-HSA-167172 | 1 | NA | 3 | R-HSA-162599 | FALSE | R-HSA-167287 | TRUE | TRUE | TRUE | 74 | TRUE | 23.6351351 | 17 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPDC,TA2,CIF150,TA2B,TA1L | NA |
| Transcription of the HIV genome | R-HSA-167172 | 1 | NA | 3 | R-HSA-162599 | FALSE | R-HSA-167238 | TRUE | TRUE | TRUE | 74 | TRUE | 23.6351351 | 17 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPDC,TA2,CIF150,TA2B,TA1L | NA |
| Transcription of the HIV genome | R-HSA-167172 | 1 | NA | 3 | R-HSA-162599 | FALSE | R-HSA-167169 | FALSE | FALSE | TRUE | 74 | TRUE | 23.6351351 | 17 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPDC,TA2,CIF150,TA2B,TA1L | NA |
| Transcription of the HIV genome | R-HSA-167172 | 1 | NA | 3 | R-HSA-162599 | FALSE | R-HSA-167290 | TRUE | TRUE | TRUE | 74 | TRUE | 23.6351351 | 17 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPDC,TA2,CIF150,TA2B,TA1L | NA |
| Transcription of the HIV genome | R-HSA-167172 | 1 | NA | 3 | R-HSA-162599 | FALSE | R-HSA-167161 | TRUE | TRUE | TRUE | 74 | TRUE | 23.6351351 | 17 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPDC,TA2,CIF150,TA2B,TA1L | NA |
| Transcription of the HIV genome | R-HSA-167172 | 1 | NA | 3 | R-HSA-162599 | FALSE | R-HSA-167162 | TRUE | TRUE | TRUE | 74 | TRUE | 23.6351351 | 17 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPDC,TA2,CIF150,TA2B,TA1L | NA |
| Transcription of the HIV genome | R-HSA-167172 | 1 | NA | 3 | R-HSA-162599 | FALSE | R-HSA-167243 | TRUE | TRUE | TRUE | 74 | TRUE | 23.6351351 | 17 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPDC,TA2,CIF150,TA2B,TA1L | NA |
| RAF/MAP kinase cascade | R-HSA-5673001 | 1 | 1 | 9 | R-HSA-5684996 | FALSE | R-HSA-5673000 | TRUE | TRUE | TRUE | 244 | TRUE | 31.5327869 | 17.5 | Q15700 | DLG2 | NA | P01112 | HRAS,HRAS1 | NA | O00451,O14827,O15020,P01112,PO1133,P3560,9,Q12879,Q13972,Q9Y4H2 | GFRA2,GDNFRB,RET,L2,TRNR2,RASGRF2,GRF2,SPTBN2,KIAA0302,SCAS,HRAS,HRAS1,EGF,ACTN2,GRIN2A,NMDAR2A,RA SGRF1,CDC25,GNRP,GRF1,IRS2 | NA |
| RAF/MAP kinase cascade | R-HSA-5673001 | 1 | 1 | 9 | R-HSA-5684996 | FALSE | R-HSA-5658442 | TRUE | TRUE | TRUE | 244 | TRUE | 31.5327869 | 17.5 | Q15700 | DLG2 | NA | P01112 | HRAS,HRAS1 | NA | O00451,O14827,O15020,P01112,PO1133,P3560,9,Q12879,Q13972,Q9Y4H2 | GFRA2,GDNFRB,RET,L2,TRNR2,RASGRF2,GRF2,SPTBN2,KIAA0302,SCAS,HRAS,HRAS1,EGF,ACTN2,GRIN2A,NMDAR2A,RA SGRF1,CDC25,GNRP,GRF1,IRS2 | NA |
| RAF/MAP kinase cascade | R-HSA-5673001 | 1 | 1 | 9 | R-HSA-5684996 | FALSE | R-HSA-5674135 | TRUE | TRUE | TRUE | 244 | TRUE | 31.5327869 | 17.5 | Q15700 | DLG2 | NA | P01112 | HRAS,HRAS1 | NA | O00451,O14827,O15020,P01112,PO1133,P3560,9,Q12879,Q13972,Q9Y4H2 | GFRA2,GDNFRB,RET,L2,TRNR2,RASGRF2,GRF2,SPTBN2,KIAA0302,SCAS,HRAS,HRAS1,EGF,ACTN2,GRIN2A,NMDAR2A,RA SGRF1,CDC25,GNRP,GRF1,IRS2 | NA |
| RAF/MAP kinase cascade | R-HSA-5673001 | 1 | 1 | 9 | R-HSA-5684996 | FALSE | R-HSA-5675221 | TRUE | TRUE | TRUE | 244 | TRUE | 31.5327869 | 17.5 | Q15700 | DLG2 | NA | P01112 | HRAS,HRAS1 | NA | O00451,O14827,O15020,P01112,PO1133,P3560,9,Q12879,Q13972,Q9Y4H2 | GFRA2,GDNFRB,RET,L2,TRNR2,RASGRF2,GRF2,SPTBN2,KIAA0302,SCAS,HRAS,HRAS1,EGF,ACTN2,GRIN2A,NMDAR2A,RA SGRF1,CDC25,GNRP,GRF1,IRS2 | NA |
| Signaling by high-kinase activity BRAF mutants | R-HSA-6802948 | 2 | 2 | 3 | R-HSA-6802957 | FALSE | NA | FALSE | FALSE | FALSE | 34 | TRUE | 25.5 | 17.5 | P12931,Q75R6 | SRC,SRCL,APBB1P,PREL1,RARP1,RIAM | SRC | P01112,PO2751 | HRAS,HRAS1,FN1,FN | NA | P01112,Q6VAB6,Q8WXI2 | HRAS,HRAS1,KSR2,CNKS R2,CNK2,KIAA0902 | NA |
| Downregulation of ERBB2 signaling | R-HSA-8863795 | NA | NA | 1 | R-HSA-1227986 | TRUE | R-HSA-1358803 | TRUE | TRUE | TRUE | 29 | TRUE | 42.3793103 | 18 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |
| ERBB2 Activates PTK6 Signaling | R-HSA-8847993 | NA | NA | 1 | R-HSA-1227986 | TRUE | NA | FALSE | TRUE | TRUE | 13 | TRUE | 19.2307692 | 18 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |
| ERBB2 Activates PTK6 Signaling | R-HSA-8847993 | NA | NA | 1 | R-HSA-8848021 | FALSE | NA | FALSE | FALSE | TRUE | 13 | TRUE | 19.2307692 | 18 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |
| ERBB2 Regulates Cell Motility | R-HSA-6785631 | NA | NA | 1 | R-HSA-1227986 | TRUE | NA | FALSE | TRUE | TRUE | 15 | TRUE | 18 | 18 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |
| Interleukin-9 signaling | R-HSA-8985947 | 1 | NA | NA | R-HSA-451927 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 15.5555556 | 18 | P42229 | STAT5A,STAT5 | NA | NA | NA | NA | NA | NA | NA |
| Nef Mediated CD4 Down-regulation | R-HSA-167590 | 1 | NA | 1 | R-HSA-164938 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 16.9 | 18 | O94973 | AP2A2,ADTAB,CLAPA2,HIP9,HYP1,KIAA0899 | NA | NA | NA | NA | P06239 | LCK | LCK |
| Nef Mediated CD8 Down-regulation | R-HSA-182218 | 1 | NA | NA | R-HSA-164938 | FALSE | NA | FALSE | FALSE | FALSE | 8 | TRUE | 14.375 | 18 | O94973 | AP2A2,ADTAB,CLAPA2,HIP9,HYP1,KIAA0899 | NA | NA | NA | NA | NA | NA | NA |
| PLC beta mediated events | R-HSA-112043 | 1 | NA | NA | R-HSA-112040 | FALSE | R-HSA-111996 | FALSE | FALSE | FALSE | 45 | TRUE | 20.5555556 | 18 | Q14643 | ITPR1,INSP3R1 | NA | NA | NA | NA | NA | NA | NA |
| Post-transcriptional silencing by small RNAs | R-HSA-426496 | 1 | NA | 1 | R-HSA-211000 | FALSE | NA | FALSE | FALSE | FALSE | 7 | TRUE | 18.1428571 | 18 | Q9UPQ9 | TNRC6B,KIAA1093 | NA | NA | NA | NA | Q9UPQ9 | TNRC6B,KIAA1093 | NA |
| Prolactin receptor signaling | R-HSA-1170546 | 2 | NA | NA | R-HSA-1280215 | FALSE | NA | FALSE | FALSE | FALSE | 15 | TRUE | 22.2666667 | 18 | P42229,Q9Y297 | STAT5A,STAT5,BTRC,BTRCP,FBW1A,FBXW1A | NA | NA | NA | NA | NA | NA | NA |

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|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|------|------------------------------------|---|----|--------|-------------------|----|----------------------|--|------|
| Retrograde neurotrophin signalling | R-HSA-177504 | 1 | NA | NA | R-HSA-187037 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 14.6428571 | 18 | O94973 | AP2A2,ADTAB,CLAPA2,HIP9,HYPJ,KIAA0899 | NA | NA | NA | NA | NA | NA | NA |
| RUNX2 regulates genes involved in cell migration | R-HSA-8941332 | 1 | NA | 1 | R-HSA-8878166 | FALSE | NA | FALSE | FALSE | FALSE | 8 | TRUE | 21.375 | 18 | Q9Y243 | AKT3,PKBG | NA | NA | NA | NA | P31751 | AKT2 | AKT2 |
| Signaling by ERBB4 | R-HSA-1236394 | NA | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-1250347 | TRUE | TRUE | TRUE | 45 | TRUE | 42.8 | 18 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |
| Signaling by ERBB4 | R-HSA-1236394 | NA | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-1251985 | TRUE | TRUE | TRUE | 45 | TRUE | 42.8 | 18 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |
| Signaling by ERBB4 | R-HSA-1236394 | NA | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-1250342 | FALSE | FALSE | TRUE | 45 | TRUE | 42.8 | 18 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |
| Signaling by ERBB4 | R-HSA-1236394 | NA | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-1253288 | FALSE | FALSE | TRUE | 45 | TRUE | 42.8 | 18 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |
| VLDL internalisation and degradation | R-HSA-8866427 | 2 | NA | NA | R-HSA-8964043 | FALSE | NA | FALSE | FALSE | FALSE | 12 | TRUE | 12.9166667 | 18 | O94973,Q13133 | AP2A2,ADTAB,CLAPA2,HIP9,HYPJ,KIAA0899,NR1H3,LXRA | NA | NA | NA | NA | NA | NA | NA |
| WNT5A-dependent internalization of FZD2, FZD5 and ROR2 | R-HSA-5140745 | 1 | NA | 1 | R-HSA-4086400 | TRUE | NA | FALSE | TRUE | TRUE | 13 | TRUE | 13.5384615 | 18 | O94973 | AP2A2,ADTAB,CLAPA2,HIP9,HYPJ,KIAA0899 | NA | NA | NA | NA | P09497 | CLTB | NA |
| WNT5A-dependent internalization of FZD4 | R-HSA-5099900 | 1 | NA | 2 | R-HSA-4086400 | TRUE | NA | FALSE | TRUE | TRUE | 15 | TRUE | 17.4 | 18 | O94973 | AP2A2,ADTAB,CLAPA2,HIP9,HYPJ,KIAA0899 | NA | NA | NA | NA | O14641,P09497 | DVL2,CLTB | NA |
| p75NTR negatively regulates cell cycle via SC1 | R-HSA-193670 | NA | NA | 1 | R-HSA-193704 | FALSE | NA | FALSE | FALSE | FALSE | 6 | TRUE | 17.6666667 | 18.5 | NA | NA | NA | NA | NA | NA | Q9UKN5 | PRDM4,PFM1 | NA |
| Sensing of DNA Double Strand Breaks | R-HSA-5693548 | 1 | NA | NA | R-HSA-5693606 | FALSE | NA | FALSE | FALSE | FALSE | 6 | TRUE | 17.6666667 | 18.5 | Q13315 | ATM | NA | NA | NA | NA | NA | NA | NA |
| ARMS-mediated activation | R-HSA-170984 | 1 | NA | NA | R-HSA-169893 | FALSE | NA | FALSE | FALSE | FALSE | 7 | TRUE | 15.4285714 | 19 | Q9ULH0 | KIDINS220,ARMS,KIAA1250 | NA | NA | NA | NA | NA | NA | NA |
| DAP12 signaling | R-HSA-2424491 | NA | 1 | 3 | R-HSA-2172127 | FALSE | NA | FALSE | FALSE | FALSE | 29 | TRUE | 31.9310345 | 19 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112,P06239,Q13094 | HRAS,HRAS1,LCK,LCP2 | LCK |
| Deposition of new CENPA-containing nucleosomes at the centromere | R-HSA-606279 | 1 | NA | NA | R-HSA-774815 | FALSE | NA | FALSE | FALSE | FALSE | 54 | TRUE | 21.1851852 | 19 | P62805 | HIST1H4A,H4/A,H4FA;HIST1H4B,H4/I,H4FI;HIST1H4C,H4/G,H4FG;HIST1H4D,H4/B,H4FB;HIST1H4E,H4/J,H4FJ;HIST1H4F,H4/C,H4FC;HIST1H4H,H4/H,H4FH;HIST1H4I,H4/M,H4FM;HIST1H4J,H4/E,H4FE;HIST1H4K,H4/D,H4FD;HIST1H4L,H4/K,H4FK;HIST2H4A,H4/N,H4FN;HIST2H4B,H4/O,H4FO;HIST4H4 | NA | NA | NA | NA | NA | NA | NA |
| ESR-mediated signaling | R-HSA-8939211 | NA | 1 | NA | R-HSA-9006931 | FALSE | R-HSA-9018519 | TRUE | TRUE | TRUE | 128 | TRUE | 22.7890625 | 19 | NA | NA | NA | Q13451 | FKBP5,AIG6,FKBP51 | NA | NA | NA | NA |
| Estrogen-dependent gene expression | R-HSA-9018519 | 5 | NA | 2 | R-HSA-8939211 | TRUE | NA | FALSE | TRUE | TRUE | 122 | TRUE | 22.6393443 | 19 | O00482,O94953,P62805,Q4ZG55,Q9UPQ9 | NR5A2,B1F,CPF,FTF,KDM4B,JHDM3B,JMJD2B,KIAA0876,HIST1H4A,H4/A,H4FA;HIST1H4B,H4/I,H4FI;HIST1H4C,H4/G,H4FG;HIST1H4D,H4/B,H4FB;HIST1H4E,H4/J,H4FJ;HIST1H4F,H4/C,H4FC;HIST1H4H,H4/H,H4FH;HIST1H4I,H4/M,H4FM;HIST1H4J,H4/E,H4FE;HIST1H4K,H4/D,H4FD;HIST1H4L,H4/K,H4FK;HIST2H4A,H4/N,H4FN;HIST2H4B,H4/O,H4FO;HIST4H4,GRB1,KIAA0575,TNRC6B,KIAA1093 | NA | NA | NA | NA | Q99873,Q9UPQ9 | PRMT1,HMT2,HRMT1L2,IR1B4,TNRC6B,KIAA1093 | NA |
| Formation of the ternary complex, and subsequently, the 43S complex | R-HSA-72695 | 1 | NA | 2 | R-HSA-72737 | FALSE | NA | FALSE | FALSE | FALSE | 52 | TRUE | 19.0961538 | 19 | P23396 | RPS3,OK/SW-cl.26 | NA | NA | NA | NA | P46781,P62277 | RPS9,RPS13 | NA |

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|---|---------------|----|----|---|---------------|-------|--------------|-------|-------|-------|-----|------|------------|------|--------------------------------|---|-------|----------------|----------------------|----|--------------------------------|---|--|-------|
| HIV elongation arrest and recovery | R-HSA-167287 | NA | NA | 1 | R-HSA-167172 | TRUE | NA | FALSE | TRUE | TRUE | 36 | TRUE | 29.25 | 19 | NA | NA | NA | NA | NA | NA | P18615 | NELFE, RD, RDBP | NA | |
| MET interacts with TNS proteins | R-HSA-8875513 | NA | NA | 1 | R-HSA-8875878 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 12.8 | 19 | NA | NA | NA | NA | NA | NA | Q68C22 | TNS3, TEM6, TENS1, TPP | NA | |
| Oxidative Stress Induced Senescence | R-HSA-2559580 | 3 | 1 | 2 | R-HSA-2559583 | FALSE | NA | FALSE | FALSE | FALSE | 95 | TRUE | 29.7789474 | 19 | P04637, P62805, Q9UPQ9 | TP53, P53, HIST1H4A, H4/A, H4FA; HIST1H4B, H4/I, H4FI; HIST1H4C, H4/G, H4FG; HIST1H4D, H4/B, H4FB; HIST1H4E, H4/J, H4FJ; HIST1H4F, H4/C, H4FC; HIST1H4H, H4/H, H4FH; HIST1H4I, H4/M, H4FM; HIST1H4J, H4/E, H4FE; HIST1H4K, H4/D, H4FD; HIST1H4L, H4/K, H4FK; HIST2H4A, H4/N, H4F2, H4FN, HIST2H4; HIST2H4B, H4/O, H4FO; HIST4H4, TNRC6B, KIAA1093 | NA | P04637 | TP53, P53 | NA | P04637, Q9UPQ9 | TP53, P53, TNRC6B, KIAA1093 | NA | |
| Pausing and recovery of HIV elongation | R-HSA-167290 | NA | NA | 1 | R-HSA-167172 | TRUE | NA | FALSE | TRUE | TRUE | 36 | TRUE | 29.25 | 19 | NA | NA | NA | NA | NA | NA | P18615 | NELFE, RD, RDBP | NA | |
| Pausing and recovery of Tat-mediated HIV elongation | R-HSA-167238 | NA | NA | 1 | R-HSA-167172 | TRUE | NA | FALSE | TRUE | TRUE | 35 | TRUE | 29.6 | 19 | NA | NA | NA | NA | NA | NA | P18615 | NELFE, RD, RDBP | NA | |
| PI3K events in ERBB2 signaling | R-HSA-1963642 | NA | NA | 1 | R-HSA-1227986 | TRUE | NA | FALSE | TRUE | TRUE | 16 | TRUE | 31 | 19 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA | |
| Pre-NOTCH Transcription and Translation | R-HSA-1912408 | 3 | 1 | 3 | R-HSA-1912422 | FALSE | NA | FALSE | FALSE | FALSE | 74 | TRUE | 22.2297297 | 19 | P04637, P62805, Q9UPQ9 | TP53, P53, HIST1H4A, H4/A, H4FA; HIST1H4B, H4/I, H4FI; HIST1H4C, H4/G, H4FG; HIST1H4D, H4/B, H4FB; HIST1H4E, H4/J, H4FJ; HIST1H4F, H4/C, H4FC; HIST1H4H, H4/H, H4FH; HIST1H4I, H4/M, H4FM; HIST1H4J, H4/E, H4FE; HIST1H4K, H4/D, H4FD; HIST1H4L, H4/K, H4FK; HIST2H4A, H4/N, H4F2, H4FN, HIST2H4; HIST2H4B, H4/O, H4FO; HIST4H4, TNRC6B, KIAA1093 | NA | P04637 | TP53, P53 | NA | P04637, Q04721, Q9UPQ9 | TP53, P53, NOTCH2, TNRC6B, KIAA1093 | NA | |
| Regulation of expression of SLITs and ROBOs | R-HSA-9010553 | 4 | NA | 7 | R-HSA-376176 | TRUE | NA | FALSE | TRUE | TRUE | 173 | TRUE | 34.3872832 | 19 | O75093, P23396, P25786, P38919 | SLIT1, KIAA0813, MEGF4, SLIL1, RPS3, OK/SW-cl.26, PSMA1, H2C, NU, PR0530, PSC2, EIF4A3, DDX48, KIAA0111 | PSMA1 | NA | NA | NA | NA | P46781, P61289, P62277, Q13200, Q14118, Q96L21, Q9Y6N7 | RPS9, PSME3, RPS13, PSMD2, TRAP2, DAG1, RPL10L, ROBO1, DUTT1 | PSMD2 |
| Ribosomal scanning and start codon recognition | R-HSA-72702 | 1 | NA | 2 | R-HSA-72737 | FALSE | NA | FALSE | FALSE | FALSE | 59 | TRUE | 17.779661 | 19 | P23396 | RPS3, OK/SW-cl.26 | NA | NA | NA | NA | NA | P46781, P62277 | RPS9, RPS13 | NA |
| RNA Polymerase II Transcription Elongation | R-HSA-75955 | NA | NA | 2 | R-HSA-73857 | FALSE | R-HSA-113418 | TRUE | TRUE | TRUE | 61 | TRUE | 24.6557377 | 19 | NA | NA | NA | NA | NA | NA | P18074, P18615 | ERCC2, XPD, XPC, NELFE, RD, RDBP | NA | |
| RNA Polymerase II Transcription Elongation | R-HSA-75955 | NA | NA | 2 | R-HSA-73857 | FALSE | R-HSA-112382 | TRUE | TRUE | TRUE | 61 | TRUE | 24.6557377 | 19 | NA | NA | NA | NA | NA | NA | P18074, P18615 | ERCC2, XPD, XPC, NELFE, RD, RDBP | NA | |
| ROBO receptors bind AKAP5 | R-HSA-9010642 | 1 | NA | 1 | R-HSA-376176 | TRUE | NA | FALSE | TRUE | TRUE | 9 | TRUE | 22.2222222 | 19 | P22612 | PRKACG | NA | NA | NA | NA | P16298 | PPP3CB, CALNA2, CALNB, CNA2 | NA | |
| Tat-mediated HIV elongation arrest and recovery | R-HSA-167243 | NA | NA | 1 | R-HSA-167172 | TRUE | NA | FALSE | TRUE | TRUE | 35 | TRUE | 29.6 | 19 | NA | NA | NA | NA | NA | NA | P18615 | NELFE, RD, RDBP | NA | |
| TP53 Regulates Transcription of DNA Repair Genes | R-HSA-6796648 | 2 | 2 | 4 | R-HSA-3700989 | FALSE | NA | FALSE | FALSE | FALSE | 65 | TRUE | 25.1538462 | 19 | P04637, Q13315 | TP53, P53, ATM | NA | P04637, Q13535 | TP53, P53, ATR, FRP1 | NA | P04637, P18074, P18615, P38398 | TP53, P53, ERCC2, XPD, XPC, NELFE, RD, RDBP, BRC1, RNF53 | NA | |
| Translation initiation complex formation | R-HSA-72649 | 1 | NA | 2 | R-HSA-72662 | FALSE | NA | FALSE | FALSE | FALSE | 59 | TRUE | 17.8983051 | 19 | P23396 | RPS3, OK/SW-cl.26 | NA | NA | NA | NA | NA | P46781, P62277 | RPS9, RPS13 | NA |
| tRNA processing in the nucleus | R-HSA-6784531 | 3 | NA | 4 | R-HSA-72306 | FALSE | NA | FALSE | FALSE | FALSE | 58 | TRUE | 16.5 | 19 | P62826, Q52L10, Q9Y567 | RAN, ARA24, OK/SW-cl.81, FAM988, NUP88 | NA | NA | NA | NA | O95059, P35658, Q10570, Q52L10 | RPP14, NUP214, CAIN, CAIN, KIAA0023, CPSF1, CPSF160, FAM988 | NA | |
| MicroRNA (miRNA) biogenesis | R-HSA-203927 | 2 | NA | 1 | R-HSA-211000 | FALSE | NA | FALSE | FALSE | FALSE | 26 | TRUE | 27.5 | 19.5 | P62826, Q9NRR4 | RAN, ARA24, OK/SW-cl.81, DROSHA, RN3, RNA5E3L, RNA5EN | NA | NA | NA | NA | Q9UPY3 | DICER1, DICER, HERN, KIAA0928 | NA | |

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|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|------|----------------------|---|-----|--------|--------------------------|--------|-----------------------------|---|---------|----|
| RUNX3 regulates p14-ARF | R-HSA-8951936 | NA | NA | 1 | R-HSA-8878159 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 24.8 | 19.5 | NA | NA | NA | NA | NA | P25440 | BRD2,KIAA9001,RING3 | NA | | |
| SHC1 events in ERBB2 signaling | R-HSA-1250196 | NA | 1 | 2 | R-HSA-1227986 | TRUE | NA | FALSE | TRUE | TRUE | 22 | TRUE | 33.5454545 | 19.5 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112,P01133 | HRAS,HRAS1,EGF | NA | |
| Adenylate cyclase inhibitory pathway | R-HSA-170670 | NA | 1 | NA | R-HSA-112040 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 18.4285714 | 20 | NA | NA | NA | Q08462 | ADCY2,KIAA1060 | NA | NA | NA | NA | |
| Adenylate cyclase inhibitory pathway | R-HSA-170670 | NA | 1 | NA | R-HSA-997269 | FALSE | NA | FALSE | FALSE | FALSE | 14 | TRUE | 18.4285714 | 20 | NA | NA | NA | Q08462 | ADCY2,KIAA1060 | NA | NA | NA | NA | |
| Constitutive Signaling by Aberrant PI3K in Cancer | R-HSA-2219530 | 1 | 1 | 3 | R-HSA-2219528 | FALSE | NA | FALSE | FALSE | FALSE | 71 | TRUE | 26.7323944 | 20 | P12931 | SRC,SRC1 | SRC | P33681 | CD80,CD28LG,CD28LG1,LAB7 | NA | P01133,P06239,Q9Y4H2 | EGF,LCK,IRS2 | LCK | |
| DAG and IP3 signaling | R-HSA-1489509 | 1 | NA | NA | R-HSA-9006925 | FALSE | R-HSA-111997 | FALSE | FALSE | FALSE | 33 | TRUE | 22.9090909 | 20 | Q14643 | ITPR1,INSP3R1 | NA | NA | NA | NA | NA | NA | NA | NA |
| Downstream signal transduction | R-HSA-186763 | 2 | 1 | 1 | R-HSA-186797 | TRUE | NA | FALSE | TRUE | TRUE | 29 | TRUE | 33.3448276 | 20 | P12931,P42229 | SRC,SRC1,STAT5A,STAT5 | SRC | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | |
| Erythropoietin activates STAT5 | R-HSA-9027283 | 1 | NA | 1 | R-HSA-9006335 | TRUE | NA | FALSE | TRUE | TRUE | 7 | TRUE | 20 | 20 | P42229 | STAT5A,STAT5 | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA | |
| G alpha (z) signalling events | R-HSA-418597 | NA | 1 | 2 | R-HSA-388396 | FALSE | NA | FALSE | FALSE | FALSE | 47 | TRUE | 19.9148936 | 20 | NA | NA | NA | Q08462 | ADCY2,KIAA1060 | NA | A5PLK6,Q04759 | RGSL1,RGSL,RGSL2,PRKCO,PRKCT | PRKCO | |
| GRB2 events in ERBB2 signaling | R-HSA-1963640 | NA | 1 | 2 | R-HSA-1227986 | TRUE | NA | FALSE | TRUE | TRUE | 16 | TRUE | 38.0625 | 20 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112,P01133 | HRAS,HRAS1,EGF | NA | |
| Negative regulation of the PI3K/AKT network | R-HSA-199418 | 1 | NA | 1 | R-HSA-1257604 | TRUE | R-HSA-6811558 | TRUE | TRUE | TRUE | 106 | TRUE | 26.5943396 | 20 | Q9Y243 | AKT3,PKBG | NA | NA | NA | NA | P31751 | AKT2 | AKT2 | |
| Recognition of DNA damage by PCNA-containing replication complex | R-HSA-110314 | 1 | NA | 1 | R-HSA-73893 | FALSE | NA | FALSE | FALSE | FALSE | 31 | TRUE | 41.6129032 | 20 | Q13619 | CUL4A | NA | NA | NA | NA | Q9NZJ0 | DTL,CDT2,CDW1,DCAF2,L2DTL,RAMP | NA | |
| RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function | R-HSA-8936459 | 3 | NA | 3 | R-HSA-8878171 | FALSE | NA | FALSE | FALSE | FALSE | 67 | TRUE | 22.8059701 | 20 | P62805,Q9UP09,Q9UP56 | HIST1H4A,H4/A,H4FA,HIST1H4B,H4/L,H4FI,HIST1H4C,H4/G,H4FG,HIST1H4D,H4/B,H4FB,HIST1H4E,H4/J,H4FJ,HIST1H4F,H4/C,H4FC,HIST1H4H,H4/H,H4FH,HIST1H4I,H4/M,H4FM,HIST1H4J,H4/E,H4FE,HIST1H4K,H4/D,H4FD,HIST1H4L,H4/K,H4FK,HIST2H4A,H4/N,H4F2,H4FN,HIST2H4,HIST2H4B,H4/O,H4FO,HIST4H4,TNRC6B,KIAA1093,SETD1B,KIAA1076,KMT2G,SET1B | NA | NA | NA | NA | Q04759,Q99873,Q9UP09 | PRKCO,PRKCT,PRMT1,HRMT2,HRMT1L2,IR1B4,TNRC6B,KIAA1093 | PRKCO | |
| SHC1 events in ERBB4 signaling | R-HSA-1250347 | NA | 1 | 1 | R-HSA-1236394 | TRUE | NA | FALSE | TRUE | TRUE | 14 | TRUE | 40.7857143 | 20 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | |
| Signaling by Leptin | R-HSA-2586552 | 1 | NA | 1 | R-HSA-162582 | FALSE | NA | FALSE | FALSE | FALSE | 11 | TRUE | 20.9090909 | 20 | P42229 | STAT5A,STAT5 | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA | |
| Signaling by SCF-KIT | R-HSA-1433557 | 1 | 1 | 4 | R-HSA-9006934 | FALSE | R-HSA-1433559 | TRUE | TRUE | TRUE | 43 | TRUE | 28.4186047 | 20 | P42229 | STAT5A,STAT5 | NA | P01112 | HRAS,HRAS1 | NA | P01112,P06239,P07332,Q92729 | HRAS,HRAS1,LCK,FES,FP5,PTPRU,FMI,PCP2,PTPRO | LCK,FES | |
| Toll Like Receptor 4 (TLR4) Cascade | R-HSA-166016 | 2 | NA | 3 | R-HSA-168898 | FALSE | R-HSA-166020 | TRUE | TRUE | TRUE | 126 | TRUE | 29.1111111 | 20 | P17213,Q81WL2 | BPI,SFTPA1,COLEC4,PSAP,SFTP1,SFTPA,SFTPA1B | NA | NA | NA | NA | Q00206,P17213,P18428 | TLR4,BPI,LBP | NA | |
| Toll Like Receptor 4 (TLR4) Cascade | R-HSA-166016 | 2 | NA | 3 | R-HSA-168898 | FALSE | R-HSA-166058 | TRUE | TRUE | TRUE | 126 | TRUE | 29.1111111 | 20 | P17213,Q81WL2 | BPI,SFTPA1,COLEC4,PSAP,SFTP1,SFTPA,SFTPA1B | NA | NA | NA | NA | Q00206,P17213,P18428 | TLR4,BPI,LBP | NA | |
| Toll Like Receptor 4 (TLR4) Cascade | R-HSA-166016 | 2 | NA | 3 | R-HSA-168898 | FALSE | R-HSA-166166 | TRUE | TRUE | TRUE | 126 | TRUE | 29.1111111 | 20 | P17213,Q81WL2 | BPI,SFTPA1,COLEC4,PSAP,SFTP1,SFTPA,SFTPA1B | NA | NA | NA | NA | Q00206,P17213,P18428 | TLR4,BPI,LBP | NA | |
| Transcription-Coupled Nucleotide Excision Repair (TCNER) | R-HSA-6781827 | 1 | 1 | 2 | R-HSA-5696398 | FALSE | R-HSA-6781823 | TRUE | TRUE | TRUE | 78 | TRUE | 31.8589744 | 20 | Q13619 | CUL4A | NA | Q9UNP9 | PPIE,CYP33 | NA | P18074,Q03468 | ERCC2,XPD,XPC,ERCC6,CSB | NA | |
| Transcription-Coupled Nucleotide Excision Repair (TCNER) | R-HSA-6781827 | 1 | 1 | 2 | R-HSA-5696398 | FALSE | R-HSA-6782135 | TRUE | TRUE | TRUE | 78 | TRUE | 31.8589744 | 20 | Q13619 | CUL4A | NA | Q9UNP9 | PPIE,CYP33 | NA | P18074,Q03468 | ERCC2,XPD,XPC,ERCC6,CSB | NA | |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|----|------|------------|------|--------|---|-----|--------|--------------------------|----|----------------------|--------------------------|-----|----|
| Transcription-Coupled Nucleotide Excision Repair (TCNER) | R-HSA-6781827 | 1 | 1 | 2 | R-HSA-5696398 | FALSE | R-HSA-6782210 | TRUE | TRUE | TRUE | 78 | TRUE | 31.8589744 | 20 | Q13619 | CUL4A | NA | Q9UNP9 | PP1E,CYP33 | NA | P18074,Q03468 | ERCC2,XPB,XPDC,ERCC6,CSB | NA | |
| Signaling by ERBB2 | R-HSA-1227986 | 1 | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-1963642 | TRUE | TRUE | TRUE | 50 | TRUE | 42.34 | 20.5 | P12931 | SRC,SRC1 | SRC | NA | NA | NA | P01133 | EGF | NA | |
| Signaling by ERBB2 | R-HSA-1227986 | 1 | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-8863795 | TRUE | TRUE | TRUE | 50 | TRUE | 42.34 | 20.5 | P12931 | SRC,SRC1 | SRC | NA | NA | NA | P01133 | EGF | NA | |
| Signaling by ERBB2 | R-HSA-1227986 | 1 | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-1251932 | TRUE | TRUE | TRUE | 50 | TRUE | 42.34 | 20.5 | P12931 | SRC,SRC1 | SRC | NA | NA | NA | P01133 | EGF | NA | |
| Signaling by ERBB2 | R-HSA-1227986 | 1 | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-1963640 | TRUE | TRUE | TRUE | 50 | TRUE | 42.34 | 20.5 | P12931 | SRC,SRC1 | SRC | NA | NA | NA | P01133 | EGF | NA | |
| Signaling by ERBB2 | R-HSA-1227986 | 1 | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-1306955 | FALSE | FALSE | TRUE | 50 | TRUE | 42.34 | 20.5 | P12931 | SRC,SRC1 | SRC | NA | NA | NA | P01133 | EGF | NA | |
| Signaling by ERBB2 | R-HSA-1227986 | 1 | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-6785631 | TRUE | TRUE | TRUE | 50 | TRUE | 42.34 | 20.5 | P12931 | SRC,SRC1 | SRC | NA | NA | NA | P01133 | EGF | NA | |
| Signaling by ERBB2 | R-HSA-1227986 | 1 | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-1250196 | TRUE | TRUE | TRUE | 50 | TRUE | 42.34 | 20.5 | P12931 | SRC,SRC1 | SRC | NA | NA | NA | P01133 | EGF | NA | |
| Signaling by ERBB2 | R-HSA-1227986 | 1 | NA | 1 | R-HSA-9006934 | FALSE | R-HSA-8847993 | TRUE | TRUE | TRUE | 50 | TRUE | 42.34 | 20.5 | P12931 | SRC,SRC1 | SRC | NA | NA | NA | P01133 | EGF | NA | |
| TRAF6 mediated NF-kB activation | R-HSA-933542 | NA | NA | 1 | R-HSA-168928 | TRUE | NA | FALSE | TRUE | TRUE | 24 | TRUE | 24.4166667 | 20.5 | NA | NA | NA | NA | NA | NA | O95786 | DDX58 | NA | |
| Activation of IRF3/IRF7 mediated by TBK1/IKK epsilon | R-HSA-936964 | NA | NA | 1 | R-HSA-937061 | FALSE | NA | FALSE | FALSE | FALSE | 17 | TRUE | 61.9411765 | 21 | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA | |
| Adenylate cyclase activating pathway | R-HSA-170660 | NA | 1 | NA | R-HSA-112040 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 20.3 | 21 | NA | NA | NA | Q08462 | ADCY2,KIAA1060 | NA | NA | NA | NA | |
| Dual Incision in GGNER | R-HSA-5696400 | 1 | NA | 1 | R-HSA-5696399 | FALSE | NA | FALSE | FALSE | FALSE | 41 | TRUE | 37.9512195 | 21 | Q13619 | CUL4A | NA | NA | NA | NA | P18074 | ERCC2,XPB,XPDC | NA | |
| PISP, PP2A and IER3 Regulate PI3K/AKT Signaling | R-HSA-6811558 | 1 | 1 | 3 | R-HSA-199418 | TRUE | NA | FALSE | TRUE | TRUE | 99 | TRUE | 27.2525253 | 21 | P12931 | SRC,SRC1 | SRC | P33681 | CD80,CD28LG,CD28LG1,LAB7 | NA | P01133,P06239,Q9Y4H2 | EGF,LCK,IRS2 | LCK | |
| Regulation of KIT signaling | R-HSA-1433559 | NA | NA | 1 | R-HSA-1433557 | TRUE | NA | FALSE | TRUE | TRUE | 16 | TRUE | 30.25 | 21 | NA | NA | NA | NA | NA | NA | P06239 | LCK | LCK | |
| TRIF-mediated programmed cell death | R-HSA-2562578 | NA | NA | 2 | R-HSA-937061 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 19.8888889 | 21 | NA | NA | NA | NA | NA | NA | O00206,Q14790 | TLR4,CASP8,MCH5 | NA | |
| VEGFR2 mediated cell proliferation | R-HSA-5218921 | 1 | 1 | 1 | R-HSA-4420097 | TRUE | NA | FALSE | TRUE | TRUE | 19 | TRUE | 31.8947368 | 21 | Q14643 | ITPR1,INSP3R1 | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | |
| Regulation of TP53 Expression | R-HSA-6804754 | 1 | 1 | 1 | R-HSA-6806003 | FALSE | NA | FALSE | FALSE | FALSE | 2 | TRUE | 21.5 | 21.5 | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | |
| TLR3-mediated TICAM1-dependent programmed cell death | R-HSA-9013957 | NA | NA | 1 | R-HSA-168164 | FALSE | NA | FALSE | FALSE | FALSE | 6 | TRUE | 20 | 21.5 | NA | NA | NA | NA | NA | NA | Q14790 | CASP8,MCH5 | NA | |
| PKA activation | R-HSA-163615 | 1 | 1 | NA | R-HSA-111931 | TRUE | NA | FALSE | TRUE | TRUE | 17 | TRUE | 26.2941176 | 22 | P22612 | PRKACG | NA | Q08462 | ADCY2,KIAA1060 | NA | NA | NA | NA | |
| PKA activation in glucagon signalling | R-HSA-164378 | 1 | 1 | NA | R-HSA-163359 | TRUE | NA | FALSE | TRUE | TRUE | 17 | TRUE | 23.7647059 | 22 | P22612 | PRKACG | NA | Q08462 | ADCY2,KIAA1060 | NA | NA | NA | NA | |
| PKA-mediated phosphorylation of CREB | R-HSA-111931 | 1 | NA | NA | R-HSA-111933 | FALSE | R-HSA-163615 | TRUE | TRUE | TRUE | 19 | TRUE | 26.3684211 | 22 | P22612 | PRKACG | NA | NA | NA | NA | NA | NA | NA | |
| Signalling to RAS | R-HSA-167044 | NA | 1 | 1 | R-HSA-187687 | FALSE | R-HSA-171007 | TRUE | TRUE | TRUE | 20 | TRUE | 33.45 | 22 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | |
| Activation of anterior HOX genes in hindbrain development during early embryogenesis | R-HSA-5617472 | 1 | 1 | NA | R-HSA-5619507 | FALSE | NA | FALSE | FALSE | FALSE | 91 | TRUE | 22.8351648 | 23 | P62805 | HIST1H4A,H4/A,H4FA,HIST1H4B,H4/J,H4FI,HIST1H4C,H4/G,H4FG,HIST1H4D,H4/B,H4FB,HIST1H4E,H4/J,H4FJ,HIST1H4F,H4/C,H4FC,HIST1H4H,H4/H,H4FH,HIST1H4I,H4/E,M,H4FM,HIST1H4J,H4/E,H4FE,HIST1H4K,H4/D,H4FD,HIST1H4L,H4/K,H4FK,HIST2H4A,H4/N,H4F2,H4FN,HIST2H4,HIST2H4B,H4/O,H4FO,HIST4H4 | NA | Q92600 | CNOT9,RCD1,RQCD1 | NA | NA | NA | NA | NA |
| CD28 co-stimulation | R-HSA-389356 | NA | 1 | 1 | R-HSA-388841 | FALSE | R-HSA-389359 | TRUE | TRUE | TRUE | 33 | TRUE | 28.4848485 | 23 | NA | NA | NA | P33681 | CD80,CD28LG,CD28LG1,LAB7 | NA | P06239 | LCK | LCK | |

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|---|---------------|----|----|---|---------------|-------|---------------|-------|-------|-------|----|------|------------|----|-----------------------------|---|----|--------|--------------------------|----|---------------|--------------------------------|-----|
| CD28 co-stimulation | R-HSA-389356 | NA | 1 | 1 | R-HSA-388841 | FALSE | R-HSA-389357 | TRUE | TRUE | TRUE | 33 | TRUE | 28.4848485 | 23 | NA | NA | NA | P33681 | CD80,CD28LG,CD28LG1,LAB7 | NA | P06239 | LCK | LCK |
| DNA Damage/Telomere Stress Induced Senescence | R-HSA-2559586 | 3 | 1 | 1 | R-HSA-2559583 | FALSE | R-HSA-2559584 | TRUE | TRUE | TRUE | 61 | TRUE | 22.2459016 | 23 | P04637,P62805,Q13315 | TP53,P53,HIST1H4A,H4/A,H4FA,HIST1H4B,H4/I,H4FI,HIST1H4C,H4/G,H4FG,HIST1H4D,H4/B,H4FB,HIST1H4E,H4/J,H4FI,;HIST1H4F,H4/C,H4FC,HIST1H4H,H4/H,H4FH,HIST1H4I,H4/M,H4FM,HIST1H4J,H4/E,H4FE,HIST1H4K,H4/D,H4FD,HIST1H4L,H4/K,H4FK,HIST2H4A,H4/N,H4F2,H4FN,HIST2H4,H,HIST2H4B,H4/O,H4FO,HIST4H4,ATM | NA | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA |
| ISG15 antiviral mechanism | R-HSA-1169408 | 4 | NA | 2 | R-HSA-1169410 | FALSE | NA | FALSE | FALSE | FALSE | 75 | TRUE | 28.1866667 | 23 | A9QM74,075369,P38919,Q99567 | KPNA7,FLNB,FLN1L,FLN3,TABP,TAP,EIF4A3,DDX48,KIAA0111,NUP88 | NA | NA | NA | NA | O95786,P35658 | DDX58,NUP214,CAIN,CAN,KIAA0023 | NA |
| MyD88:MAL(TIRAP) cascade initiated on plasma membrane | R-HSA-166058 | NA | NA | 1 | R-HSA-166016 | TRUE | R-HSA-937039 | FALSE | TRUE | TRUE | 95 | TRUE | 33.8526316 | 23 | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA |
| MyD88:MAL(TIRAP) cascade initiated on plasma membrane | R-HSA-166058 | NA | NA | 1 | R-HSA-168188 | FALSE | R-HSA-445989 | TRUE | TRUE | TRUE | 95 | TRUE | 33.8526316 | 23 | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA |
| MyD88:MAL(TIRAP) cascade initiated on plasma membrane | R-HSA-166058 | NA | NA | 1 | R-HSA-168179 | TRUE | R-HSA-445989 | TRUE | TRUE | TRUE | 95 | TRUE | 33.8526316 | 23 | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA |
| MyD88:MAL(TIRAP) cascade initiated on plasma membrane | R-HSA-166058 | NA | NA | 1 | R-HSA-168188 | FALSE | R-HSA-937042 | FALSE | FALSE | TRUE | 95 | TRUE | 33.8526316 | 23 | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA |
| MyD88:MAL(TIRAP) cascade initiated on plasma membrane | R-HSA-166058 | NA | NA | 1 | R-HSA-166016 | TRUE | R-HSA-445989 | TRUE | TRUE | TRUE | 95 | TRUE | 33.8526316 | 23 | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA |
| MyD88:MAL(TIRAP) cascade initiated on plasma membrane | R-HSA-166058 | NA | NA | 1 | R-HSA-168179 | TRUE | R-HSA-937042 | FALSE | TRUE | TRUE | 95 | TRUE | 33.8526316 | 23 | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA |
| MyD88:MAL(TIRAP) cascade initiated on plasma membrane | R-HSA-166058 | NA | NA | 1 | R-HSA-168179 | TRUE | R-HSA-450294 | FALSE | TRUE | TRUE | 95 | TRUE | 33.8526316 | 23 | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA |
| MyD88:MAL(TIRAP) cascade initiated on plasma membrane | R-HSA-166058 | NA | NA | 1 | R-HSA-166016 | TRUE | R-HSA-937042 | FALSE | TRUE | TRUE | 95 | TRUE | 33.8526316 | 23 | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA |
| MyD88:MAL(TIRAP) cascade initiated on plasma membrane | R-HSA-166058 | NA | NA | 1 | R-HSA-168188 | FALSE | R-HSA-937039 | FALSE | FALSE | TRUE | 95 | TRUE | 33.8526316 | 23 | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA |
| MyD88:MAL(TIRAP) cascade initiated on plasma membrane | R-HSA-166058 | NA | NA | 1 | R-HSA-168179 | TRUE | R-HSA-937039 | FALSE | TRUE | TRUE | 95 | TRUE | 33.8526316 | 23 | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA |
| MyD88:MAL(TIRAP) cascade initiated on plasma membrane | R-HSA-166058 | NA | NA | 1 | R-HSA-166016 | TRUE | R-HSA-450294 | FALSE | TRUE | TRUE | 95 | TRUE | 33.8526316 | 23 | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|----|------|------------|------|-----------------------------|--|----|--------|--------------------------|----|-----------------------------|---|---------|----|
| MyD88:MAL(TIRAP) cascade initiated on plasma membrane | R-HSA-166058 | NA | NA | 1 | R-HSA-168188 | FALSE | R-HSA-450294 | FALSE | FALSE | TRUE | 95 | TRUE | 33.8526316 | 23 | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA | |
| Negative regulation of MAPK pathway | R-HSA-5675221 | NA | 1 | 1 | R-HSA-5673001 | TRUE | R-HSA-5674499 | FALSE | TRUE | TRUE | 40 | TRUE | 45.075 | 23 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | |
| NOD1/2 Signaling Pathway | R-HSA-168638 | 1 | NA | 2 | R-HSA-168643 | FALSE | NA | FALSE | FALSE | FALSE | 31 | TRUE | 22 | 23 | Q9HC29 | NOD2,CARD15,IBD1 | NA | NA | NA | NA | Q14790,Q9Y239 | CASP8,MCH5,NOD1,CARD4 | NA | |
| Regulation of TP53 Degradation | R-HSA-6804757 | 4 | 1 | 4 | R-HSA-6806003 | FALSE | NA | FALSE | FALSE | FALSE | 36 | TRUE | 43.1944444 | 23 | O75604,P04637,Q13315,Q9Y243 | USP2,UBP41,TP53,P53,ATM,AKT3,PKBG | NA | P04637 | TP53,P53 | NA | P04637,P31751,P42345,Q9UER7 | TP53,P53,AKT2,MTOR,FRAP,FRAP1,FRAP2,RAFT1,RAPT1,DAXX,BING2,DAP6 | AKT2 | |
| Toll Like Receptor TLR1:TLR2 Cascade | R-HSA-168179 | 1 | NA | NA | R-HSA-181438 | FALSE | R-HSA-166058 | TRUE | TRUE | TRUE | 95 | TRUE | 33.8526316 | 23 | Q8IWL2 | SFTPA1,COLEC4,PSAP,SFTP1,SFTPA,SFTPA1B | NA | NA | NA | NA | NA | NA | NA | NA |
| Activation of AKT2 | R-HSA-165158 | NA | NA | 1 | R-HSA-109704 | TRUE | NA | FALSE | TRUE | TRUE | 4 | TRUE | 26 | 23.5 | NA | NA | NA | NA | NA | NA | P31751 | AKT2 | AKT2 | |
| Erythropoietin activates Phospholipase C gamma (PLCG) | R-HSA-9027277 | NA | NA | 1 | R-HSA-9006335 | TRUE | NA | FALSE | TRUE | TRUE | 7 | TRUE | 22.2857143 | 24 | NA | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA | |
| IKK complex recruitment mediated by RIP1 | R-HSA-937041 | 1 | NA | 1 | R-HSA-937061 | FALSE | NA | FALSE | FALSE | FALSE | 23 | TRUE | 55.9130435 | 24 | P51668 | UBE2D1,SFT,UBCSA,UBCH5,UBCH5A | NA | NA | NA | NA | O00206 | TLR4 | NA | |
| Vasopressin regulates renal water homeostasis via Aquaporins | R-HSA-432040 | 1 | 1 | 1 | R-HSA-445717 | FALSE | NA | FALSE | FALSE | FALSE | 43 | TRUE | 22.372093 | 24 | P22612 | PRKACG | NA | Q08462 | ADCY2,KIAA1060 | NA | P55087 | AQP4 | NA | |
| CD28 dependent Vav1 pathway | R-HSA-389359 | NA | 1 | 1 | R-HSA-389356 | TRUE | NA | FALSE | TRUE | TRUE | 12 | TRUE | 30.1666667 | 25 | NA | NA | NA | P33681 | CD80,CD28LG,CD28LG1,LAB7 | NA | P06239 | LCK | LCK | |
| Glucagon-like Peptide-1 (GLP1) regulates insulin secretion | R-HSA-381676 | 2 | NA | NA | R-HSA-422356 | TRUE | NA | FALSE | TRUE | TRUE | 42 | TRUE | 22.5 | 25 | P22612,Q14643 | PRKACG,ITPR1,INSP3R1 | NA | NA | NA | NA | NA | NA | NA | NA |
| MyD88 cascade initiated on plasma membrane | R-HSA-975871 | NA | NA | 1 | R-HSA-168142 | TRUE | R-HSA-937039 | FALSE | TRUE | TRUE | 85 | TRUE | 36.0588235 | 25 | NA | NA | NA | NA | NA | NA | Q9BXR5 | TLR10,UNQ315/PRO358 | NA | |
| MyD88 cascade initiated on plasma membrane | R-HSA-975871 | NA | NA | 1 | R-HSA-168142 | TRUE | R-HSA-445989 | TRUE | TRUE | TRUE | 85 | TRUE | 36.0588235 | 25 | NA | NA | NA | NA | NA | NA | Q9BXR5 | TLR10,UNQ315/PRO358 | NA | |
| MyD88 cascade initiated on plasma membrane | R-HSA-975871 | NA | NA | 1 | R-HSA-168176 | FALSE | R-HSA-445989 | TRUE | TRUE | TRUE | 85 | TRUE | 36.0588235 | 25 | NA | NA | NA | NA | NA | NA | Q9BXR5 | TLR10,UNQ315/PRO358 | NA | |
| MyD88 cascade initiated on plasma membrane | R-HSA-975871 | NA | NA | 1 | R-HSA-168142 | TRUE | R-HSA-937042 | FALSE | TRUE | TRUE | 85 | TRUE | 36.0588235 | 25 | NA | NA | NA | NA | NA | NA | Q9BXR5 | TLR10,UNQ315/PRO358 | NA | |
| MyD88 cascade initiated on plasma membrane | R-HSA-975871 | NA | NA | 1 | R-HSA-168142 | TRUE | R-HSA-450294 | FALSE | TRUE | TRUE | 85 | TRUE | 36.0588235 | 25 | NA | NA | NA | NA | NA | NA | Q9BXR5 | TLR10,UNQ315/PRO358 | NA | |
| MyD88 cascade initiated on plasma membrane | R-HSA-975871 | NA | NA | 1 | R-HSA-168176 | FALSE | R-HSA-450294 | FALSE | FALSE | TRUE | 85 | TRUE | 36.0588235 | 25 | NA | NA | NA | NA | NA | NA | Q9BXR5 | TLR10,UNQ315/PRO358 | NA | |
| MyD88 cascade initiated on plasma membrane | R-HSA-975871 | NA | NA | 1 | R-HSA-168176 | FALSE | R-HSA-937039 | FALSE | FALSE | TRUE | 85 | TRUE | 36.0588235 | 25 | NA | NA | NA | NA | NA | NA | Q9BXR5 | TLR10,UNQ315/PRO358 | NA | |
| MyD88 cascade initiated on plasma membrane | R-HSA-975871 | NA | NA | 1 | R-HSA-168176 | FALSE | R-HSA-937042 | FALSE | FALSE | TRUE | 85 | TRUE | 36.0588235 | 25 | NA | NA | NA | NA | NA | NA | Q9BXR5 | TLR10,UNQ315/PRO358 | NA | |
| p38MAPK events | R-HSA-171007 | NA | 1 | 1 | R-HSA-167044 | TRUE | NA | FALSE | TRUE | TRUE | 13 | TRUE | 32.2307692 | 25 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | |
| PECAM1 interactions | R-HSA-210990 | NA | NA | 1 | R-HSA-202733 | TRUE | NA | FALSE | TRUE | TRUE | 12 | TRUE | 31.3333333 | 25 | NA | NA | NA | NA | NA | NA | P06239 | LCK | LCK | |
| RSK activation | R-HSA-444257 | NA | NA | 1 | R-HSA-442742 | TRUE | NA | FALSE | TRUE | TRUE | 6 | TRUE | 30.8333333 | 25 | NA | NA | NA | NA | NA | NA | Q9UK32 | RPS6KA6,RSK4 | RPS6KA6 | |

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|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|------|---------------|---|-------|--------|----------------|----|----------------------|----------------------------|--|----|
| Toll Like Receptor 10 (TLR10) Cascade | R-HSA-168142 | NA | NA | 1 | R-HSA-168898 | FALSE | R-HSA-975871 | TRUE | TRUE | TRUE | 85 | TRUE | 36.0588235 | 25 | NA | NA | NA | NA | NA | NA | Q9BXR5 | TLR10,UNQ315/PRO358 | NA | |
| Senescence-Associated Secretory Phenotype (SASP) | R-HSA-2559582 | 2 | 1 | NA | R-HSA-2559583 | FALSE | NA | FALSE | FALSE | FALSE | 80 | TRUE | 34.6875 | 26 | P51668,P62805 | UBE2D1,SFT,UBCSA,UBCH5,UBCH5A,HIST1H4A,H4/A,H4FA,HIST1H4B,H4/I,H4FI,HIST1H4C,H4/G,H4FG,HIST1H4D,H4/B,H4FB,HIST1H4E,H4/J,H4FJ,HIST1H4F,H4/C,H4FC,HIST1H4H,H4/H,H4FH,HIST1H4I,H4/M,H4FM,HIST1H4J,H4/E,H4FE,HIST1H4K,H4/D,H4FD,HIST1H4L,H4/K,H4FK,HIST2H4A,H4/N,H4F2,H4FN,HIST2H4,HIST2H4B,H4/O,H4FO,HIST4H4 | NA | Q9UJX4 | ANAPCS,APCS | NA | NA | NA | NA | |
| PDE3B signalling | R-HSA-165160 | NA | NA | 1 | R-HSA-109703 | FALSE | NA | FALSE | FALSE | FALSE | 2 | TRUE | 26.5 | 26.5 | NA | NA | NA | NA | NA | NA | P31751 | AKT2 | AKT2 | |
| Dual incision in TC-NER | R-HSA-6782135 | 1 | 1 | 2 | R-HSA-6781827 | TRUE | NA | FALSE | TRUE | TRUE | 65 | TRUE | 36.7384615 | 27 | Q13619 | CUL4A | NA | Q9UNP9 | PPIE,CYP33 | NA | P18074,Q03468 | ERCC2,XPD,XPDC,ERCC6,CSB | NA | |
| G2/M Checkpoints | R-HSA-69481 | 2 | 1 | 3 | R-HSA-69620 | FALSE | R-HSA-69473 | TRUE | TRUE | TRUE | 151 | TRUE | 39.7682119 | 27 | P04637,P25786 | TP53,P53,PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | P04637 | TP53,P53 | NA | P04637,P61289,Q13200 | TP53,P53,PSME3,PSMD2,TRAP2 | PSMD2 | |
| G2/M Checkpoints | R-HSA-69481 | 2 | 1 | 3 | R-HSA-69620 | FALSE | R-HSA-176187 | TRUE | TRUE | TRUE | 151 | TRUE | 39.7682119 | 27 | P04637,P25786 | TP53,P53,PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | P04637 | TP53,P53 | NA | P04637,P61289,Q13200 | TP53,P53,PSME3,PSMD2,TRAP2 | PSMD2 | |
| G2/M Checkpoints | R-HSA-69481 | 2 | 1 | 3 | R-HSA-69620 | FALSE | R-HSA-69478 | FALSE | FALSE | TRUE | 151 | TRUE | 39.7682119 | 27 | P04637,P25786 | TP53,P53,PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | P04637 | TP53,P53 | NA | P04637,P61289,Q13200 | TP53,P53,PSME3,PSMD2,TRAP2 | PSMD2 | |
| Glucagon signaling in metabolic regulation | R-HSA-163359 | NA | 1 | NA | R-HSA-163685 | FALSE | R-HSA-164378 | TRUE | TRUE | TRUE | 33 | TRUE | 25.6666667 | 27 | NA | NA | NA | Q08462 | ADCY2,KIAA1060 | NA | NA | NA | NA | |
| RHO GTPases activate PKNs | R-HSA-5625740 | 1 | NA | 3 | R-HSA-195258 | FALSE | R-HSA-5625886 | TRUE | TRUE | TRUE | 63 | TRUE | 23.5238095 | 27 | Q16513 | PKN2,PRK2,PRKCL2 | PKN2 | NA | NA | NA | NA | Q14974,P31947,Q72406 | PPP1R12A,MBS,MYPT1,SFN,HME1,MYH14,KIAA2034,FP17425 | NA |
| Translesion Synthesis by POLH | R-HSA-110320 | NA | NA | 1 | R-HSA-110313 | FALSE | NA | FALSE | FALSE | FALSE | 19 | TRUE | 57.5263158 | 27 | NA | NA | NA | NA | NA | NA | P55072 | VCP | NA | |
| Adrenaline, noradrenaline inhibits insulin secretion | R-HSA-400042 | 1 | NA | 1 | R-HSA-422356 | TRUE | NA | FALSE | TRUE | TRUE | 28 | TRUE | 23.25 | 27.5 | Q13936 | CACNA1C,CACH2,CACN2,CACNL1A1,CCHL1A1 | NA | NA | NA | NA | NA | Q01668 | CACNA1D,CACH3,CACN4,CACNL1A2,CCHL1A2 | NA |
| JNK (c-Jun kinases) phosphorylation and activation mediated by activated human TAK1 | R-HSA-450321 | 1 | NA | 1 | R-HSA-450294 | FALSE | NA | FALSE | FALSE | FALSE | 18 | TRUE | 27.4444444 | 27.5 | Q9HC29 | NOD2,CARD15,IBD1 | NA | NA | NA | NA | NA | Q9Y239 | NOD1,CARD4 | NA |
| Erythropoietin activates Phosphoinositide-3 kinase (PI3K) | R-HSA-9027276 | NA | NA | 1 | R-HSA-9006335 | TRUE | NA | FALSE | TRUE | TRUE | 12 | TRUE | 26.75 | 28 | NA | NA | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA |
| PI3K/AKT activation | R-HSA-198203 | NA | NA | 1 | R-HSA-187037 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 33.1111111 | 28 | NA | NA | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA |
| TRAF6-mediated induction of TAK1 complex within TLR4 complex | R-HSA-937072 | NA | NA | 1 | R-HSA-937061 | FALSE | NA | FALSE | FALSE | FALSE | 17 | TRUE | 65.7647059 | 28 | NA | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA |
| IRAK2 mediated activation of TAK1 complex upon TLR7/8 or 9 stimulation | R-HSA-975163 | NA | NA | 1 | R-HSA-975138 | FALSE | NA | FALSE | FALSE | FALSE | 16 | TRUE | 69.5 | 28.5 | NA | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA |
| RNA Polymerase I Promoter Escape | R-HSA-73772 | NA | NA | 2 | R-HSA-73854 | FALSE | NA | FALSE | FALSE | FALSE | 30 | TRUE | 25.0666667 | 28.5 | NA | NA | NA | NA | NA | NA | NA | P18074,Q9H9Y6 | ERCC2,XPD,XPDC,POLR1B | NA |
| TICAM1, TRAF6-dependent induction of TAK1 complex | R-HSA-9014325 | NA | NA | 1 | R-HSA-168164 | FALSE | NA | FALSE | FALSE | FALSE | 16 | TRUE | 69.5 | 28.5 | NA | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA |
| activated TAK1 mediates p38 MAPK activation | R-HSA-450302 | 1 | NA | 1 | R-HSA-450294 | FALSE | NA | FALSE | FALSE | FALSE | 19 | TRUE | 28.1578947 | 29 | Q9HC29 | NOD2,CARD15,IBD1 | NA | NA | NA | NA | NA | Q9Y239 | NOD1,CARD4 | NA |

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|--|---------------|----|----|----|---------------|-------|--------------|-------|-------|-------|----|------|------------|----|---------------|---|-----|--------|--------------------------|----|---------------|--|
| CREB phosphorylation through the activation of Adenylate Cyclase | R-HSA-442720 | 1 | NA | NA | R-HSA-438064 | FALSE | NA | FALSE | FALSE | FALSE | 8 | TRUE | 29.875 | 29 | P22612 | PRKACG | NA | NA | NA | NA | NA | NA |
| Downregulation of ERBB2/ERBB3 signaling | R-HSA-1358803 | 1 | NA | 1 | R-HSA-8863795 | TRUE | NA | FALSE | TRUE | TRUE | 13 | TRUE | 76.6153846 | 29 | Q9Y243 | AKT3,PKBG | NA | NA | NA | NA | P31751 | AKT2 |
| Gap-filling DNA repair synthesis and ligation in TC-NER | R-HSA-6782210 | 1 | 1 | 2 | R-HSA-6781827 | TRUE | NA | FALSE | TRUE | TRUE | 64 | TRUE | 37.40625 | 29 | Q13619 | CUL4A | NA | Q9UNP9 | PIIE,CYP33 | NA | P18074,Q03468 | ERCC2,XPD,XPC,ERCC6,CSB |
| Glycolysis | R-HSA-70171 | 2 | NA | 2 | R-HSA-70326 | FALSE | R-HSA-170822 | TRUE | TRUE | TRUE | 71 | TRUE | 19.4225352 | 29 | P07205,P22612 | PGK2,PGKB,PRKACG | NA | NA | NA | NA | P05062,Q9BRR6 | ALDOB,ALDB,ADPGK,PS ECO260 |
| NEP/NS2 Interacts with the Cellular Export Machinery | R-HSA-168333 | 2 | NA | 1 | R-HSA-168274 | FALSE | NA | FALSE | FALSE | FALSE | 37 | TRUE | 27.1891892 | 29 | P62826,Q99567 | RAN,ARA24,OK/SW-cl.81,NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 |
| NS1 Mediated Effects on Host Pathways | R-HSA-168276 | 2 | NA | 1 | R-HSA-168253 | FALSE | R-HSA-168305 | FALSE | FALSE | FALSE | 41 | TRUE | 23.4878049 | 29 | A9QM74,Q99567 | KPNA7,NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 |
| NS1 Mediated Effects on Host Pathways | R-HSA-168276 | 2 | NA | 1 | R-HSA-168253 | FALSE | R-HSA-168315 | FALSE | FALSE | FALSE | 41 | TRUE | 23.4878049 | 29 | A9QM74,Q99567 | KPNA7,NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 |
| NS1 Mediated Effects on Host Pathways | R-HSA-168276 | 2 | NA | 1 | R-HSA-168253 | FALSE | R-HSA-169131 | FALSE | FALSE | FALSE | 41 | TRUE | 23.4878049 | 29 | A9QM74,Q99567 | KPNA7,NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 |
| Nuclear import of Rev protein | R-HSA-180746 | 2 | NA | 1 | R-HSA-177243 | FALSE | NA | FALSE | FALSE | FALSE | 33 | TRUE | 27.7272727 | 29 | P62826,Q99567 | RAN,ARA24,OK/SW-cl.81,NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 |
| Nuclear Pore Complex (NPC) Disassembly | R-HSA-3301854 | 1 | 1 | 1 | R-HSA-2980766 | FALSE | NA | FALSE | FALSE | FALSE | 35 | TRUE | 27.9714286 | 29 | Q99567 | NUP88 | NA | Q8TD19 | NEK9,KIAA1995,NEK8,NERCC | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 |
| Platelet sensitization by LDL | R-HSA-432142 | 1 | NA | NA | R-HSA-418346 | TRUE | NA | FALSE | TRUE | TRUE | 17 | TRUE | 34.4117647 | 29 | P09769 | FGR, SRC2 | FGR | NA | NA | NA | NA | NA |
| RAF activation | R-HSA-5673000 | NA | 1 | 1 | R-HSA-5673001 | TRUE | NA | FALSE | TRUE | TRUE | 25 | TRUE | 35.68 | 29 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 |
| Regulation of Glucokinase by Glucokinase Regulatory Protein | R-HSA-170822 | 1 | NA | 1 | R-HSA-70171 | TRUE | NA | FALSE | TRUE | TRUE | 31 | TRUE | 28.8387097 | 29 | Q99567 | NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 |
| Rev-mediated nuclear export of HIV RNA | R-HSA-165054 | 2 | NA | 1 | R-HSA-177243 | FALSE | NA | FALSE | FALSE | FALSE | 35 | TRUE | 26.8571429 | 29 | P62826,Q99567 | RAN,ARA24,OK/SW-cl.81,NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 |
| Rev-mediated nuclear export of HIV RNA | R-HSA-165054 | 2 | NA | 1 | R-HSA-162599 | FALSE | NA | FALSE | FALSE | FALSE | 35 | TRUE | 26.8571429 | 29 | P62826,Q99567 | RAN,ARA24,OK/SW-cl.81,NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 |
| snRNP Assembly | R-HSA-191859 | 1 | NA | 1 | R-HSA-194441 | FALSE | NA | FALSE | FALSE | FALSE | 52 | TRUE | 19.7307692 | 29 | Q99567 | NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 |
| SUMOylation of chromatin organization proteins | R-HSA-4551638 | 2 | NA | 2 | R-HSA-3108232 | FALSE | NA | FALSE | FALSE | FALSE | 57 | TRUE | 21.4912281 | 29 | P62805,Q99567 | HIST1H4A,H4/A,H4FA,HIST1H4B,H4/L,H4FI,HIST1H4C,H4/G,H4FG,HIST1H4D,H4/B,H4FB,HIST1H4E,H4/J,H4FJ,HIST1H4F,H4/C,H4FC,HIST1H4H,H4/H,H4FH,HIST1H4I,H4/M,H4FM,HIST1H4J,H4/E,H4FE,HIST1H4K,H4/D,H4FD,HIST1H4L,H4/K,H4FK,HIST2H4A,H4/N,H4F2,H4FN,HIST2H4,HIST2H4B,H4/O,H4FO,HIST4H4,NUP88 | NA | NA | NA | NA | P35658,Q01826 | NUP214,CAIN,CAN,KIAA0023,SATB1 |
| SUMOylation of DNA replication proteins | R-HSA-4615885 | 1 | NA | 1 | R-HSA-3108232 | FALSE | NA | FALSE | FALSE | FALSE | 45 | TRUE | 23.6222222 | 29 | Q99567 | NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 |
| SUMOylation of RNA binding proteins | R-HSA-4570464 | 1 | NA | 2 | R-HSA-3108232 | FALSE | NA | FALSE | FALSE | FALSE | 46 | TRUE | 23.2173913 | 29 | Q99567 | NUP88 | NA | NA | NA | NA | P35658,Q9Y2X3 | NUP214,CAIN,CAN,KIAA0023,NOP58,NOL5,NOP5,HSPCL20 |
| SUMOylation of SUMOylation proteins | R-HSA-4085377 | 1 | NA | 1 | R-HSA-3108232 | FALSE | NA | FALSE | FALSE | FALSE | 34 | TRUE | 28.3235294 | 29 | Q99567 | NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 |
| SUMOylation of ubiquitinylation proteins | R-HSA-3232142 | 1 | NA | 1 | R-HSA-3108232 | FALSE | NA | FALSE | FALSE | FALSE | 38 | TRUE | 26.1578947 | 29 | Q99567 | NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 |

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|---|---------------|----|----|---|---------------|-------|---------------|-------|-------|-------|----|------|------------|------|--------|---------------------|----|----|----|----|----------------------|---|-------|
| TAK1 activates NFkB by phosphorylation and activation of IKKs complex | R-HSA-445989 | 1 | NA | 1 | R-HSA-166058 | TRUE | NA | FALSE | TRUE | TRUE | 28 | TRUE | 29.0357143 | 29 | Q9HC29 | NOD2,CARD15,IBD1 | NA | NA | NA | NA | Q9Y239 | NOD1,CARD4 | NA |
| TAK1 activates NFkB by phosphorylation and activation of IKKs complex | R-HSA-445989 | 1 | NA | 1 | R-HSA-168164 | FALSE | NA | FALSE | FALSE | TRUE | 28 | TRUE | 29.0357143 | 29 | Q9HC29 | NOD2,CARD15,IBD1 | NA | NA | NA | NA | Q9Y239 | NOD1,CARD4 | NA |
| TAK1 activates NFkB by phosphorylation and activation of IKKs complex | R-HSA-445989 | 1 | NA | 1 | R-HSA-975138 | FALSE | NA | FALSE | FALSE | TRUE | 28 | TRUE | 29.0357143 | 29 | Q9HC29 | NOD2,CARD15,IBD1 | NA | NA | NA | NA | Q9Y239 | NOD1,CARD4 | NA |
| TAK1 activates NFkB by phosphorylation and activation of IKKs complex | R-HSA-445989 | 1 | NA | 1 | R-HSA-975871 | TRUE | NA | FALSE | TRUE | TRUE | 28 | TRUE | 29.0357143 | 29 | Q9HC29 | NOD2,CARD15,IBD1 | NA | NA | NA | NA | Q9Y239 | NOD1,CARD4 | NA |
| TAK1 activates NFkB by phosphorylation and activation of IKKs complex | R-HSA-445989 | 1 | NA | 1 | R-HSA-937061 | FALSE | NA | FALSE | FALSE | TRUE | 28 | TRUE | 29.0357143 | 29 | Q9HC29 | NOD2,CARD15,IBD1 | NA | NA | NA | NA | Q9Y239 | NOD1,CARD4 | NA |
| TAK1 activates NFkB by phosphorylation and activation of IKKs complex | R-HSA-445989 | 1 | NA | 1 | R-HSA-9020702 | TRUE | NA | FALSE | TRUE | TRUE | 28 | TRUE | 29.0357143 | 29 | Q9HC29 | NOD2,CARD15,IBD1 | NA | NA | NA | NA | Q9Y239 | NOD1,CARD4 | NA |
| Transport of Mature mRNA Derived from an Intronless Transcript | R-HSA-159231 | 1 | NA | 3 | R-HSA-159234 | FALSE | NA | FALSE | FALSE | FALSE | 41 | TRUE | 25 | 29 | Q99567 | NUP88 | NA | NA | NA | NA | P35658,Q10570,Q9UKF6 | NUP214,CAIN,CAN,KIAA0023,CPSF1,CP5F160,CP5F3,CP5F73 | NA |
| Transport of Ribonucleoproteins into the Host Nucleus | R-HSA-168271 | 1 | NA | 1 | R-HSA-168255 | FALSE | NA | FALSE | FALSE | FALSE | 36 | TRUE | 27.4166667 | 29 | Q99567 | NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 | NA |
| Transport of the SLBP Dependant Mature mRNA | R-HSA-159230 | 1 | NA | 1 | R-HSA-159234 | FALSE | NA | FALSE | FALSE | FALSE | 35 | TRUE | 28.0857143 | 29 | Q99567 | NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 | NA |
| Transport of the SLBP independent Mature mRNA | R-HSA-159227 | 1 | NA | 1 | R-HSA-159234 | FALSE | NA | FALSE | FALSE | FALSE | 34 | TRUE | 28.7941176 | 29 | Q99567 | NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 | NA |
| Vpr-mediated nuclear import of PICs | R-HSA-180910 | 1 | NA | 1 | R-HSA-176033 | FALSE | NA | FALSE | FALSE | FALSE | 39 | TRUE | 26 | 29 | Q99567 | NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 | NA |
| IRS-related events triggered by IGF1R | R-HSA-2428928 | NA | NA | 2 | R-HSA-2428924 | FALSE | R-HSA-112399 | TRUE | TRUE | TRUE | 52 | TRUE | 33.0576923 | 29.5 | NA | NA | NA | NA | NA | NA | P08069,Q9Y4H2 | IGF1R,IRS2 | IGF1R |
| PI3K Cascade | R-HSA-109704 | NA | NA | 1 | R-HSA-112399 | TRUE | R-HSA-109703 | FALSE | TRUE | TRUE | 44 | TRUE | 32.1136364 | 29.5 | NA | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA |
| PI3K Cascade | R-HSA-109704 | NA | NA | 1 | R-HSA-112399 | TRUE | R-HSA-165158 | TRUE | TRUE | TRUE | 44 | TRUE | 32.1136364 | 29.5 | NA | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA |
| Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R) | R-HSA-2404192 | 1 | NA | 2 | R-HSA-9006934 | FALSE | R-HSA-2428924 | FALSE | FALSE | FALSE | 54 | TRUE | 32.6666667 | 29.5 | O75339 | CILP,UNQ602/PRO1188 | NA | NA | NA | NA | O75339,P08069 | CILP,UNQ602/PRO1188,IGF1R | IGF1R |
| Viral Messenger RNA Synthesis | R-HSA-168325 | 1 | NA | 1 | R-HSA-168273 | FALSE | NA | FALSE | FALSE | FALSE | 48 | TRUE | 34.5833333 | 29.5 | Q99567 | NUP88 | NA | NA | NA | NA | P35658 | NUP214,CAIN,CAN,KIAA0023 | NA |
| Activation of G protein gated Potassium channels | R-HSA-1296041 | NA | NA | 1 | R-HSA-1296059 | FALSE | NA | FALSE | FALSE | FALSE | 25 | TRUE | 19.2 | 30 | NA | NA | NA | NA | NA | NA | P48544 | KCNJ5,GIRK4 | NA |
| Inhibition of voltage gated Ca2+ channels via Gbeta/gamma subunits | R-HSA-997272 | NA | NA | 1 | R-HSA-991365 | FALSE | NA | FALSE | FALSE | FALSE | 25 | TRUE | 19.2 | 30 | NA | NA | NA | NA | NA | NA | P48544 | KCNJ5,GIRK4 | NA |

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|---|---------------|----|----|---|---------------|-------|---------------|-------|-------|-------|----|------|------------|------|---------------|--|----|--------|--------------------------|----|----------------------|---|----------|
| Formation of the beta-catenin:TCF transactivating complex | R-HSA-201722 | 1 | NA | 2 | R-HSA-201681 | TRUE | R-HSA-4411364 | TRUE | TRUE | TRUE | 61 | TRUE | 23.8196721 | 31 | P62805 | HIST1H4A,H4/A,H4FA;HIST1H4B,H4/I,H4FI;HIST1H4C,H4/G,H4FG;HIST1H4D,H4/B,H4FB;HIST1H4E,H4/J,H4FJ;HIST1H4F,H4/C,H4FC;HIST1H4H,H4/H,H4FH;HIST1H4I,H4/M,H4FM;HIST1H4J,H4/E,H4FE;HIST1H4K,H4/D,H4FD;HIST1H4L,H4/K,H4FK;HIST2H4A,H4/N,H4F2,H4FN,HIST2H4;HIST2H4B,H4/O,H4FO;HIST4H4 | NA | NA | NA | NA | P51532,Q9HCS4 | SMARCA4,BAF190A,BRG1,SNF2B,SNF2L4,TCF7L1,TCF3 | NA |
| G beta gamma signalling through PI3Kgamma | R-HSA-392451 | 1 | NA | 1 | R-HSA-397795 | FALSE | NA | FALSE | FALSE | FALSE | 25 | TRUE | 28.24 | 31 | Q9Y243 | AKT3,PKBG | NA | NA | NA | NA | P31751 | AKT2 | AKT2 |
| Inhibition of Signaling by Overexpressed EGFR | R-HSA-5638303 | NA | NA | 1 | R-HSA-5638302 | FALSE | NA | FALSE | FALSE | FALSE | 2 | TRUE | 31.5 | 31.5 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |
| PLC1 events in ERBB2 signaling | R-HSA-1251932 | NA | NA | 1 | R-HSA-1227986 | TRUE | NA | FALSE | TRUE | TRUE | 4 | TRUE | 30.5 | 31.5 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA |
| CTLA4 inhibitory signaling | R-HSA-389513 | 1 | 1 | 2 | R-HSA-388841 | FALSE | NA | FALSE | FALSE | FALSE | 21 | TRUE | 38.3809524 | 32 | Q9Y243 | AKT3,PKBG | NA | P33681 | CD80,CD28LG,CD28LG1,LAB7 | NA | P06239,P31751 | LCK,AKT2 | LCK,AKT2 |
| Formation of HIV elongation complex in the absence of HIV Tat | R-HSA-167152 | NA | NA | 2 | R-HSA-167172 | TRUE | NA | FALSE | TRUE | TRUE | 48 | TRUE | 30.2708333 | 32 | NA | NA | NA | NA | NA | NA | P18074,P18615 | ERCC2,XPD,XPDC,NELFE, RD,RDBP | NA |
| Formation of HIV-1 elongation complex containing HIV-1 Tat | R-HSA-167200 | NA | NA | 2 | R-HSA-167246 | TRUE | NA | FALSE | TRUE | TRUE | 47 | TRUE | 30.5531915 | 32 | NA | NA | NA | NA | NA | NA | P18074,P18615 | ERCC2,XPD,XPDC,NELFE, RD,RDBP | NA |
| Formation of TC-NER Pre-Incision Complex | R-HSA-6781823 | 1 | 1 | 3 | R-HSA-6781827 | TRUE | NA | FALSE | TRUE | TRUE | 53 | TRUE | 37.8867925 | 32 | Q13619 | CUL4A | NA | Q9UNP9 | PPIE,CYP33 | NA | P18074,Q03468,Q92905 | ERCC2,XPD,XPDC,ERCC5,CSB,COP55,CSN5,JAB1 | NA |
| HIV Transcription Initiation | R-HSA-167161 | 1 | NA | 3 | R-HSA-167172 | TRUE | NA | FALSE | TRUE | TRUE | 47 | TRUE | 27.7446809 | 32 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPDC,TAF2,CIF150,TAF2B,TAF1L | NA |
| Meiotic recombination | R-HSA-912446 | 2 | NA | 2 | R-HSA-1500620 | FALSE | NA | FALSE | FALSE | FALSE | 56 | TRUE | 25.3214286 | 32 | P62805,Q13315 | HIST1H4A,H4/A,H4FA;HIST1H4B,H4/I,H4FI;HIST1H4C,H4/G,H4FG;HIST1H4D,H4/B,H4FB;HIST1H4E,H4/J,H4FJ;HIST1H4F,H4/C,H4FC;HIST1H4H,H4/H,H4FH;HIST1H4I,H4/M,H4FM;HIST1H4J,H4/E,H4FE;HIST1H4K,H4/D,H4FD;HIST1H4L,H4/K,H4FK;HIST2H4A,H4/N,H4F2,H4FN,HIST2H4;HIST2H4B,H4/O,H4FO;HIST4H4,ATM | NA | NA | NA | NA | P38398,Q9BXT5 | BRCA1,RNF53,TEX15 | NA |
| NoRC negatively regulates rRNA expression | R-HSA-427413 | 2 | NA | 2 | R-HSA-5250941 | FALSE | NA | FALSE | FALSE | FALSE | 77 | TRUE | 25.1688312 | 32 | P26358,P62805 | DNMT1,AIM,CXXC9,DNMT,HIST1H4A,H4/A,H4FA;HIST1H4B,H4/I,H4FI;HIST1H4C,H4/G,H4FG;HIST1H4D,H4/B,H4FB;HIST1H4E,H4/J,H4FJ;HIST1H4F,H4/C,H4FC;HIST1H4H,H4/H,H4FH;HIST1H4I,H4/M,H4FM;HIST1H4J,H4/E,H4FE;HIST1H4K,H4/D,H4FD;HIST1H4L,H4/K,H4FK;HIST2H4A,H4/N,H4F2,H4FN,HIST2H4;HIST2H4B,H4/O,H4FO;HIST4H4 | NA | NA | NA | NA | P18074,Q9H9Y6 | ERCC2,XPD,XPDC,POLR1B | NA |
| RNA Polymerase II HIV Promoter Escape | R-HSA-167162 | 1 | NA | 3 | R-HSA-167172 | TRUE | NA | FALSE | TRUE | TRUE | 47 | TRUE | 27.7446809 | 32 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPDC,TAF2,CIF150,TAF2B,TAF1L | NA |
| RNA Polymerase II Promoter Escape | R-HSA-73776 | 1 | NA | 3 | R-HSA-76042 | TRUE | NA | FALSE | TRUE | TRUE | 47 | TRUE | 27.7446809 | 32 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPDC,TAF2,CIF150,TAF2B,TAF1L | NA |

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|---|---------------|----|----|---|---------------|-------|---------------|-------|-------|-------|----|------|------------|------|---------------|--|----|--------|------------|------------|-----------------------------|--|------------------|----|
| RNA Polymerase II Transcription Initiation | R-HSA-75953 | 1 | NA | 3 | R-HSA-76042 | TRUE | NA | FALSE | TRUE | TRUE | 47 | TRUE | 27.7446809 | 32 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPDC,TA2,CIF150,TA2B,TA1L | NA | |
| RNA Polymerase II Transcription Initiation And Promoter Clearance | R-HSA-76042 | 1 | NA | 3 | R-HSA-73857 | FALSE | R-HSA-73776 | TRUE | TRUE | TRUE | 47 | TRUE | 27.7446809 | 32 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPDC,TA2,CIF150,TA2B,TA1L | NA | |
| RNA Polymerase II Transcription Initiation And Promoter Clearance | R-HSA-76042 | 1 | NA | 3 | R-HSA-73857 | FALSE | R-HSA-75953 | TRUE | TRUE | TRUE | 47 | TRUE | 27.7446809 | 32 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPDC,TA2,CIF150,TA2B,TA1L | NA | |
| RNA Polymerase II Transcription Pre-Initiation And Promoter Opening | R-HSA-73779 | 1 | NA | 3 | R-HSA-73857 | FALSE | NA | FALSE | FALSE | FALSE | 47 | TRUE | 27.7446809 | 32 | Q8IZX4 | TAF1L | NA | NA | NA | NA | P18074,Q6P1X5,Q8IZX4 | ERCC2,XPD,XPDC,TA2,CIF150,TA2B,TA1L | NA | |
| Signaling by Erythropoietin | R-HSA-9006335 | NA | NA | 1 | R-HSA-162582 | FALSE | R-HSA-9027283 | TRUE | TRUE | TRUE | 25 | TRUE | 35.36 | 32 | NA | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA | |
| Signaling by Erythropoietin | R-HSA-9006335 | NA | NA | 1 | R-HSA-162582 | FALSE | R-HSA-9027277 | TRUE | TRUE | TRUE | 25 | TRUE | 35.36 | 32 | NA | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA | |
| Signaling by Erythropoietin | R-HSA-9006335 | NA | NA | 1 | R-HSA-162582 | FALSE | R-HSA-9027284 | TRUE | TRUE | TRUE | 25 | TRUE | 35.36 | 32 | NA | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA | |
| Signaling by Erythropoietin | R-HSA-9006335 | NA | NA | 1 | R-HSA-162582 | FALSE | R-HSA-9027276 | TRUE | TRUE | TRUE | 25 | TRUE | 35.36 | 32 | NA | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA | |
| Tat-mediated elongation of the HIV-1 transcript | R-HSA-167246 | NA | NA | 2 | R-HSA-167169 | FALSE | R-HSA-167200 | TRUE | TRUE | TRUE | 47 | TRUE | 30.5531915 | 32 | NA | NA | NA | NA | NA | NA | P18074,P18615 | ERCC2,XPD,XPDC,NELFE, RD,RDBP | NA | |
| Insulin receptor signalling cascade | R-HSA-74751 | NA | 1 | 1 | R-HSA-74752 | FALSE | R-HSA-74713 | TRUE | TRUE | TRUE | 54 | TRUE | 35.4259259 | 32.5 | NA | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA |
| Insulin receptor signalling cascade | R-HSA-74751 | NA | 1 | 1 | R-HSA-74752 | FALSE | R-HSA-112399 | TRUE | TRUE | TRUE | 54 | TRUE | 35.4259259 | 32.5 | NA | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA |
| Insulin receptor signalling cascade | R-HSA-74751 | NA | 1 | 1 | R-HSA-74752 | FALSE | R-HSA-74749 | TRUE | TRUE | TRUE | 54 | TRUE | 35.4259259 | 32.5 | NA | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA |
| IRS-mediated signalling | R-HSA-112399 | NA | NA | 1 | R-HSA-74751 | TRUE | R-HSA-112412 | TRUE | TRUE | TRUE | 48 | TRUE | 35.4166667 | 32.5 | NA | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA | |
| IRS-mediated signalling | R-HSA-112399 | NA | NA | 1 | R-HSA-2428928 | TRUE | R-HSA-109704 | TRUE | TRUE | TRUE | 48 | TRUE | 35.4166667 | 32.5 | NA | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA | |
| IRS-mediated signalling | R-HSA-112399 | NA | NA | 1 | R-HSA-74751 | TRUE | R-HSA-109704 | TRUE | TRUE | TRUE | 48 | TRUE | 35.4166667 | 32.5 | NA | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA | |
| IRS-mediated signalling | R-HSA-112399 | NA | NA | 1 | R-HSA-2428928 | TRUE | R-HSA-112412 | TRUE | TRUE | TRUE | 48 | TRUE | 35.4166667 | 32.5 | NA | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA | |
| B-WICH complex positively regulates rRNA expression | R-HSA-5250924 | 2 | NA | 2 | R-HSA-5250913 | FALSE | NA | FALSE | FALSE | FALSE | 60 | TRUE | 27.2166667 | 33 | O75533,P62805 | SF3B1,SAP155,HIST1H4A,H4/A,H4FA,HIST1H4B,H4/I,H4FI,HIST1H4C,H4/G,H4FG,HIST1H4D,H4/J,H4FB,HIST1H4E,H4/J,H4FJ,HIST1H4F,H4/C,H4FC,HIST1H4H,H4/H,H4FH,HIST1H4I,H4/M,H4FM,HIST1H4J,H4/E,H4FE,HIST1H4K,H4/D,H4FD,HIST1H4L,H4/K,H4FK,HIST1H4A,H4/N,H4F2,H4FN,HIST2H4,HIST2H4B,H4/O,H4FO,HIST4H4 | NA | NA | NA | NA | NA | Q03468,Q9H9Y6 | ERCC6,CSB,POLR1B | NA |
| Signaling by FGFR1 in disease | R-HSA-5655302 | 2 | 1 | 4 | R-HSA-1226099 | FALSE | R-HSA-1839124 | FALSE | FALSE | FALSE | 38 | TRUE | 32.7105263 | 33 | O95684,P39880 | FGFR1OP,FOP,CUX1,CUTL1 | NA | P01112 | HRAS,HRAS1 | NA | P01112,P11362,P39880,Q9UBW7 | HRAS,HRAS1,FGFR1,BFGFR,CEK,FGFR,FLG,FLT2,HGFR,CUX1,CUTL1,ZMYM2,FIM,RAMP,ZNF198 | FGFR1 | |
| Erythropoietin activates RAS | R-HSA-9027284 | NA | 1 | 2 | R-HSA-9006335 | TRUE | NA | FALSE | TRUE | TRUE | 14 | TRUE | 40.9285714 | 33.5 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112,Q9Y4H2 | HRAS,HRAS1,IRS2 | NA | |
| CD209 (DC-SIGN) signalling | R-HSA-5621575 | 2 | 1 | 2 | R-HSA-5621481 | FALSE | NA | FALSE | FALSE | FALSE | 21 | TRUE | 33.047619 | 34 | P22612,P32942 | PRKACG,ICAM3 | NA | P01112 | HRAS,HRAS1 | NA | P01112,Q01201 | HRAS,HRAS1,RELB | NA | |

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|---|---------------|----|----|----|---------------|-------|----|-------|-------|-------|----|------|------------|------|----------------------|---|-----|----|----|----|---------------|-------------------------------|------|----|
| ERCC6 (CSB) and EHMT2 (G9a) positively regulate rRNA expression | R-HSA-427389 | 1 | NA | 1 | R-HSA-5250913 | FALSE | NA | FALSE | FALSE | FALSE | 46 | TRUE | 27.3043478 | 34 | P62805 | HIST1H4A,H4/A,H4FA;HIST1H4B,H4/I,H4FI;HIST1H4C,H4/G,H4FG;HIST1H4D,H4/B,H4FB;HIST1H4E,H4/J,H4FJ;HIST1H4F,H4/C,H4FC;HIST1H4H,H4/H,H4FH;HIST1H4I,H4/M,H4FM;HIST1H4J,H4/E,H4FE;HIST1H4K,H4/D,H4FD;HIST1H4L,H4/K,H4FK;HIST2H4A,H4/N,H4F2,H4FN,HIST2H4;HIST2H4B,H4/O,H4FO;HIST4H4 | NA | NA | NA | NA | Q03468 | ERCC6_CSB | NA | |
| PKA-mediated phosphorylation of key metabolic factors | R-HSA-163358 | 1 | NA | NA | R-HSA-163685 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 25.2 | 34 | P22612 | PRKACG | NA | NA | NA | NA | NA | NA | | |
| Signal attenuation | R-HSA-74749 | NA | NA | 1 | R-HSA-74751 | TRUE | NA | FALSE | TRUE | TRUE | 10 | TRUE | 42.8 | 34 | NA | NA | NA | NA | NA | NA | Q9Y4H2 | IRS2 | NA | |
| Transcriptional regulation by small RNAs | R-HSA-5578749 | 3 | NA | 1 | R-HSA-211000 | FALSE | NA | FALSE | FALSE | FALSE | 75 | TRUE | 35.2533333 | 34 | P62805,P62826,Q99567 | HIST1H4A,H4/A,H4FA;HIST1H4B,H4/I,H4FI;HIST1H4C,H4/G,H4FG;HIST1H4D,H4/B,H4FB;HIST1H4E,H4/J,H4FJ;HIST1H4F,H4/C,H4FC;HIST1H4H,H4/H,H4FH;HIST1H4I,H4/M,H4FM;HIST1H4J,H4/E,H4FE;HIST1H4K,H4/D,H4FD;HIST1H4L,H4/K,H4FK;HIST2H4A,H4/N,H4F2,H4FN,HIST2H4;HIST2H4B,H4/O,H4FO;HIST4H4,RAN,ARA24,OK/SW-cl.B1,NUP88 | NA | NA | NA | NA | P35658 | NUUP214,CAIN,CAN,KAAA0023 | NA | |
| EGFR interacts with phospholipase C-gamma | R-HSA-212718 | NA | NA | 1 | R-HSA-177929 | TRUE | NA | FALSE | TRUE | TRUE | 3 | TRUE | 34.3333333 | 35 | NA | NA | NA | NA | NA | NA | P01133 | EGF | NA | |
| GAB1 signalosome | R-HSA-180292 | 1 | NA | 1 | R-HSA-177929 | TRUE | NA | FALSE | TRUE | TRUE | 11 | TRUE | 44 | 35 | P12931 | SRC,SRC1 | SRC | NA | NA | NA | NA | P01133 | EGF | NA |
| RNA Polymerase I Chain Elongation | R-HSA-73777 | 1 | NA | 2 | R-HSA-73864 | FALSE | NA | FALSE | FALSE | FALSE | 59 | TRUE | 31 | 35 | P62805 | HIST1H4A,H4/A,H4FA;HIST1H4B,H4/I,H4FI;HIST1H4C,H4/G,H4FG;HIST1H4D,H4/B,H4FB;HIST1H4E,H4/J,H4FJ;HIST1H4F,H4/C,H4FC;HIST1H4H,H4/H,H4FH;HIST1H4I,H4/M,H4FM;HIST1H4J,H4/E,H4FE;HIST1H4K,H4/D,H4FD;HIST1H4L,H4/K,H4FK;HIST2H4A,H4/N,H4F2,H4FN,HIST2H4;HIST2H4B,H4/O,H4FO;HIST4H4 | NA | NA | NA | NA | P18074,Q9H9Y6 | ERCC2,XPD,XPDC,POLR1B | NA | |
| AKT-mediated inactivation of FOXO1A | R-HSA-211163 | 1 | NA | 1 | R-HSA-210745 | TRUE | NA | FALSE | TRUE | TRUE | 4 | TRUE | 30.25 | 35.5 | Q9Y243 | AKT3,PKBG | NA | NA | NA | NA | P31751 | AKT2 | AKT2 | |
| Formation of the Early Elongation Complex | R-HSA-113418 | NA | NA | 2 | R-HSA-75955 | TRUE | NA | FALSE | TRUE | TRUE | 33 | TRUE | 36.8787879 | 36 | NA | NA | NA | NA | NA | NA | P18074,P18615 | ERCC2,XPD,XPDC,NELFE, RD,RDBP | NA | |
| Formation of the HIV-1 Early Elongation Complex | R-HSA-167158 | NA | NA | 2 | R-HSA-167169 | FALSE | NA | FALSE | FALSE | FALSE | 33 | TRUE | 36.8787879 | 36 | NA | NA | NA | NA | NA | NA | P18074,P18615 | ERCC2,XPD,XPDC,NELFE, RD,RDBP | NA | |

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|---|---------------|----|----|----|---------------|-------|----|-------|-------|-------|----|------|-------------|------|---------------|---|-------|--------|------------|----|----------------------|---|----------------|----|----|
| RNA Pol II CTD phosphorylation and interaction with CE | R-HSA-77075 | NA | NA | 1 | R-HSA-73857 | FALSE | NA | FALSE | FALSE | FALSE | 27 | TRUE | 39.11111111 | 37 | NA | NA | NA | NA | NA | NA | P18074 | ERCC2,XPB,XPDC | NA | | |
| RNA Pol II CTD phosphorylation and interaction with CE during HIV infection | R-HSA-167160 | NA | NA | 1 | R-HSA-167172 | TRUE | NA | FALSE | TRUE | TRUE | 27 | TRUE | 39.11111111 | 37 | NA | NA | NA | NA | NA | NA | NA | P18074 | ERCC2,XPB,XPDC | NA | |
| RNA Polymerase I Promoter Opening | R-HSA-73728 | 1 | NA | NA | R-HSA-73854 | FALSE | NA | FALSE | FALSE | FALSE | 32 | TRUE | 35.875 | 37 | P62805 | HIST1H4A,H4/A,H4FA,HIST1H4B,H4/I,H4FI,HIST1H4C,H4/G,H4FG,HIST1H4D,H4/B,H4FB,HIST1H4E,H4/J,H4FJ,HIST1H4F,H4/C,H4FC,HIST1H4H,H4/H,H4FH,HIST1H4I,H4/M,H4FM,HIST1H4J,H4/E,H4FE,HIST1H4K,H4/D,H4FD,HIST1H4L,H4/K,H4FK,HIST2H4A,H4/N,H4F2,H4FN,HIST2H4,HIST2H4B,H4/O,H4FO,HIST4H4 | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| SIRT1 negatively regulates rRNA expression | R-HSA-427359 | 1 | NA | NA | R-HSA-5250941 | FALSE | NA | FALSE | FALSE | FALSE | 37 | TRUE | 30.6756757 | 37 | P62805 | HIST1H4A,H4/A,H4FA,HIST1H4B,H4/I,H4FI,HIST1H4C,H4/G,H4FG,HIST1H4D,H4/B,H4FB,HIST1H4E,H4/J,H4FJ,HIST1H4F,H4/C,H4FC,HIST1H4H,H4/H,H4FH,HIST1H4I,H4/M,H4FM,HIST1H4J,H4/E,H4FE,HIST1H4K,H4/D,H4FD,HIST1H4L,H4/K,H4FK,HIST2H4A,H4/N,H4F2,H4FN,HIST2H4,HIST2H4B,H4/O,H4FO,HIST4H4 | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| Activated NTRK3 signals through PI3K | R-HSA-9603381 | 1 | NA | NA | R-HSA-9034015 | TRUE | NA | FALSE | TRUE | TRUE | 6 | TRUE | 38.83333333 | 40.5 | P12931 | SRC,SRC1 | SRC | NA | NA | NA | NA | NA | NA | NA | |
| Tie2 Signaling | R-HSA-210993 | NA | 1 | 1 | R-HSA-202733 | TRUE | NA | FALSE | TRUE | TRUE | 18 | TRUE | 39.61111111 | 41 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | | |
| RUNX1 regulates transcription of genes involved in differentiation of HSCs | R-HSA-8939236 | 2 | NA | 3 | R-HSA-8878171 | FALSE | NA | FALSE | FALSE | FALSE | 99 | TRUE | 55.5353535 | 42 | P25786,P62805 | PSMA1,HC2,NU,PROS30,PS2,HIST1H4A,H4/A,H4FA,HIST1H4B,H4/I,H4FI,HIST1H4C,H4/G,H4FG,HIST1H4D,H4/B,H4FB,HIST1H4E,H4/J,H4FJ,HIST1H4F,H4/C,H4FC,HIST1H4H,H4/H,H4FH,HIST1H4I,H4/M,H4FM,HIST1H4J,H4/E,H4FE,HIST1H4K,H4/D,H4FD,HIST1H4L,H4/K,H4FK,HIST2H4A,H4/N,H4F2,H4FN,HIST2H4,HIST2H4B,H4/O,H4FO,HIST4H4 | PSMA1 | NA | NA | NA | P15923,P61289,Q13200 | TCF3,BHLHB21,E2A,ITF1,PSME3,PSMD2,TRAP2 | PSMD2 | | |
| MAP3K8 (TPL2)-dependent MAPK1/3 activation | R-HSA-5684264 | 1 | NA | NA | R-HSA-450294 | FALSE | NA | FALSE | FALSE | TRUE | 16 | TRUE | 77.0625 | 43 | Q9Y297 | BTRC,BTRCP,FBW1A,FBXW1A | NA | NA | NA | NA | NA | NA | NA | NA | |
| MAP3K8 (TPL2)-dependent MAPK1/3 activation | R-HSA-5684264 | 1 | NA | NA | R-HSA-9020702 | TRUE | NA | FALSE | TRUE | TRUE | 16 | TRUE | 77.0625 | 43 | Q9Y297 | BTRC,BTRCP,FBW1A,FBXW1A | NA | NA | NA | NA | NA | NA | NA | NA | |
| Constitutive Signaling by EGFRVIII | R-HSA-5637810 | NA | 1 | 2 | R-HSA-5637812 | FALSE | NA | FALSE | FALSE | FALSE | 15 | TRUE | 50.06666667 | 44 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112,P01133 | HRAS,HRAS1,EGF | NA | | |
| FRS-mediated FGFR1 signaling | R-HSA-5654693 | NA | 1 | 1 | R-HSA-5654687 | FALSE | NA | FALSE | FALSE | FALSE | 23 | TRUE | 45.9130435 | 44 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | | |
| FRS-mediated FGFR2 signaling | R-HSA-5654700 | NA | 1 | 1 | R-HSA-5654696 | FALSE | NA | FALSE | FALSE | FALSE | 25 | TRUE | 44.92 | 44 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | | |
| MET activates RAS signaling | R-HSA-8851805 | NA | 1 | 1 | R-HSA-6806834 | FALSE | NA | FALSE | FALSE | FALSE | 11 | TRUE | 43.8181818 | 44 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | | |
| SHC-mediated cascade:FGFR1 | R-HSA-5654688 | NA | 1 | 1 | R-HSA-5654687 | FALSE | NA | FALSE | FALSE | FALSE | 21 | TRUE | 47.5714286 | 44 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | | |

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|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|------|---------------------------------------|--|-------|--------|----------------|------------|----|---------------------------------------|--|--|-------|
| SHC-mediated cascade:FGFR2 | R-HSA-5654699 | NA | 1 | 1 | R-HSA-5654696 | FALSE | NA | FALSE | FALSE | FALSE | 23 | TRUE | 46.3478261 | 44 | NA | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | |
| Signaling by activated point mutants of FGFR1 | R-HSA-1839122 | NA | NA | 1 | R-HSA-1839124 | FALSE | NA | FALSE | FALSE | FALSE | 11 | TRUE | 42.5454545 | 44 | NA | NA | NA | NA | NA | NA | NA | P11362 | FGFR1,BGFR,CEK,FGFBR,FLG,FLT2,HGFR | FGFR1 | |
| Signaling by NTRK3 (TRKC) | R-HSA-9034015 | NA | NA | 1 | R-HSA-166520 | FALSE | R-HSA-9603505 | FALSE | FALSE | TRUE | 17 | TRUE | 43.3529412 | 44 | NA | NA | NA | NA | NA | NA | NA | Q16827 | PTPRO,GLEPP1,PTPU2 | NA | |
| Signaling by NTRK3 (TRKC) | R-HSA-9034015 | NA | NA | 1 | R-HSA-166520 | FALSE | R-HSA-9603381 | TRUE | TRUE | TRUE | 17 | TRUE | 43.3529412 | 44 | NA | NA | NA | NA | NA | NA | NA | Q16827 | PTPRO,GLEPP1,PTPU2 | NA | |
| Signaling by NTRK3 (TRKC) | R-HSA-9034015 | NA | NA | 1 | R-HSA-166520 | FALSE | R-HSA-9034864 | TRUE | TRUE | TRUE | 17 | TRUE | 43.3529412 | 44 | NA | NA | NA | NA | NA | NA | NA | Q16827 | PTPRO,GLEPP1,PTPU2 | NA | |
| Signaling by NTRK3 (TRKC) | R-HSA-9034015 | NA | NA | 1 | R-HSA-166520 | FALSE | R-HSA-9034013 | FALSE | FALSE | TRUE | 17 | TRUE | 43.3529412 | 44 | NA | NA | NA | NA | NA | NA | NA | Q16827 | PTPRO,GLEPP1,PTPU2 | NA | |
| Signaling by NTRK3 (TRKC) | R-HSA-9034015 | NA | NA | 1 | R-HSA-166520 | FALSE | R-HSA-9034793 | FALSE | FALSE | TRUE | 17 | TRUE | 43.3529412 | 44 | NA | NA | NA | NA | NA | NA | NA | Q16827 | PTPRO,GLEPP1,PTPU2 | NA | |
| FRS-mediated FGFR4 signaling | R-HSA-5654712 | NA | 1 | 1 | R-HSA-5654716 | FALSE | NA | FALSE | FALSE | FALSE | 22 | TRUE | 46.2272727 | 44.5 | NA | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | |
| SHC-mediated cascade:FGFR4 | R-HSA-5654719 | NA | 1 | 1 | R-HSA-5654716 | FALSE | NA | FALSE | FALSE | FALSE | 20 | TRUE | 48 | 44.5 | NA | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | |
| FRS-mediated FGFR3 signaling | R-HSA-5654706 | NA | 1 | 1 | R-HSA-5654708 | FALSE | NA | FALSE | FALSE | FALSE | 20 | TRUE | 49.4 | 45 | NA | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | |
| SHC-mediated cascade:FGFR3 | R-HSA-5654704 | NA | 1 | 1 | R-HSA-5654708 | FALSE | NA | FALSE | FALSE | FALSE | 18 | TRUE | 51.7222222 | 45 | NA | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | |
| Signaling by FGFR3 point mutants in cancer | R-HSA-8853338 | NA | 1 | 1 | R-HSA-5655332 | FALSE | R-HSA-2033514 | FALSE | FALSE | FALSE | 22 | TRUE | 50.8636364 | 45 | NA | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | |
| Abortive elongation of HIV-1 transcript in the absence of Tat | R-HSA-167242 | NA | NA | 1 | R-HSA-167169 | FALSE | NA | FALSE | FALSE | FALSE | 23 | TRUE | 38.3913043 | 46 | NA | NA | NA | NA | NA | NA | NA | P18615 | NELFE,RD,RDBP | NA | |
| Signaling by FGFR2 in disease | R-HSA-5655253 | NA | 1 | 1 | R-HSA-1226099 | FALSE | R-HSA-1839126 | FALSE | FALSE | FALSE | 43 | TRUE | 46.7674419 | 46 | NA | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | |
| Interleukin-1 signaling | R-HSA-9020702 | 3 | NA | 3 | R-HSA-446652 | FALSE | R-HSA-5684264 | TRUE | TRUE | TRUE | 102 | TRUE | 53.2843137 | 49 | P25786,Q9H C29,Q9Y297 | PSMA1,HC2,NU,PROS30 ,PSC2,NOD2,CARD15,IB D1,BTRC,BTRCP,FBW1A, FBXW1A | PSMA1 | NA | NA | NA | NA | P61289,Q13 200,Q9Y239 | PSME3,PSMD2,TRAP2,N OD1,CARD4 | PSMD2 | |
| Interleukin-1 signaling | R-HSA-9020702 | 3 | NA | 3 | R-HSA-446652 | FALSE | R-HSA-445989 | TRUE | TRUE | TRUE | 102 | TRUE | 53.2843137 | 49 | P25786,Q9H C29,Q9Y297 | PSMA1,HC2,NU,PROS30 ,PSC2,NOD2,CARD15,IB D1,BTRC,BTRCP,FBW1A, FBXW1A | PSMA1 | NA | NA | NA | NA | P61289,Q13 200,Q9Y239 | PSME3,PSMD2,TRAP2,N OD1,CARD4 | PSMD2 | |
| InIA-mediated entry of Listeria monocytogenes into host cells | R-HSA-8876493 | 1 | NA | NA | R-HSA-8876384 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 91.9 | 50.5 | P12931 | SRC,SRC1 | SRC | NA | NA | NA | NA | NA | NA | NA | |
| TNFR2 non-canonical NF-kB pathway | R-HSA-5668541 | 1 | NA | 3 | R-HSA-1280215 | FALSE | R-HSA-5676590 | TRUE | TRUE | TRUE | 101 | TRUE | 45.6831683 | 52 | P25786 | PSMA1,HC2,NU,PROS30 ,PSC2 | PSMA1 | NA | NA | NA | NA | NA | P61289,Q13 200,Q9Y275 | PSME3,PSMD2,TRAP2,T NFSF13B,BAFF,BLYS,TA LLL1,TNFSF20,ZTNF4,UN Q401/PRO738 | PSMD2 |
| TNFR2 non-canonical NF-kB pathway | R-HSA-5668541 | 1 | NA | 3 | R-HSA-1280215 | FALSE | R-HSA-5676594 | TRUE | TRUE | TRUE | 101 | TRUE | 45.6831683 | 52 | P25786 | PSMA1,HC2,NU,PROS30 ,PSC2 | PSMA1 | NA | NA | NA | NA | NA | P61289,Q13 200,Q9Y275 | PSME3,PSMD2,TRAP2,T NFSF13B,BAFF,BLYS,TA LLL1,TNFSF20,ZTNF4,UN Q401/PRO738 | PSMD2 |
| TNFR2 non-canonical NF-kB pathway | R-HSA-5668541 | 1 | NA | 3 | R-HSA-1280215 | FALSE | R-HSA-5669034 | TRUE | TRUE | TRUE | 101 | TRUE | 45.6831683 | 52 | P25786 | PSMA1,HC2,NU,PROS30 ,PSC2 | PSMA1 | NA | NA | NA | NA | NA | P61289,Q13 200,Q9Y275 | PSME3,PSMD2,TRAP2,T NFSF13B,BAFF,BLYS,TA LLL1,TNFSF20,ZTNF4,UN Q401/PRO738 | PSMD2 |
| Downstream TCR signaling | R-HSA-202424 | 3 | NA | 5 | R-HSA-202403 | FALSE | NA | FALSE | FALSE | FALSE | 104 | TRUE | 51.4423077 | 52.5 | P25786,P51 668,Q9Y297 | PSMA1,HC2,NU,PROS30 ,PSC2,UBE2D1,SFT,UBC 5A,UBCH5,UBCH5A,BTR C,BTRCP,FBW1A,FBXW1 A | PSMA1 | NA | NA | NA | NA | P04234,P06 239,P61289, Q04759,Q1 3200 | CD3D,T3D,LCK,PSME3,P RKCK,PRKCT,PSMD2,TR AP2 | LCK,PRKCK, PSMD2 | |
| Hedgehog 'off' state | R-HSA-5610787 | 5 | 1 | NA | R-HSA-5358351 | FALSE | R-HSA-5610783 | TRUE | TRUE | TRUE | 100 | TRUE | 49.26 | 52.5 | P10070,P22 612,Q13635 ,Q2M1P5,Q 96RY7 | GLI2,THP,PRKACG,PTCH 1,PTCH,KIF7,UNQ340/P RO539,IFT140,KIAA0590 ,_WDTC2 | NA | Q08462 | ADCY2,KIAA1060 | NA | NA | NA | NA | NA | |
| Hedgehog 'off' state | R-HSA-5610787 | 5 | 1 | NA | R-HSA-5358351 | FALSE | R-HSA-5610785 | TRUE | TRUE | TRUE | 100 | TRUE | 49.26 | 52.5 | P10070,P22 612,Q13635 ,Q2M1P5,Q 96RY7 | GLI2,THP,PRKACG,PTCH 1,PTCH,KIF7,UNQ340/P RO539,IFT140,KIAA0590 ,_WDTC2 | NA | Q08462 | ADCY2,KIAA1060 | NA | NA | NA | NA | NA | |
| Hedgehog 'off' state | R-HSA-5610787 | 5 | 1 | NA | R-HSA-5358351 | FALSE | R-HSA-5610780 | TRUE | TRUE | TRUE | 100 | TRUE | 49.26 | 52.5 | P10070,P22 612,Q13635 ,Q2M1P5,Q 96RY7 | GLI2,THP,PRKACG,PTCH 1,PTCH,KIF7,UNQ340/P RO539,IFT140,KIAA0590 ,_WDTC2 | NA | Q08462 | ADCY2,KIAA1060 | NA | NA | NA | NA | NA | |
| Activated NTRK2 signals through FRS2 and FRS3 | R-HSA-9028731 | NA | 1 | 1 | R-HSA-9006115 | FALSE | NA | FALSE | FALSE | FALSE | 11 | TRUE | 46.9090909 | 62 | NA | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA | |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|-----|------|------------|------|----------------------|--|-------|--------|-------------|----|-----------------------------|--|-------|
| CLE7A (Dectin-1) signaling | R-HSA-5607764 | 3 | NA | 2 | R-HSA-5621481 | FALSE | R-HSA-5660668 | TRUE | TRUE | TRUE | 100 | TRUE | 53.43 | 63 | P25786,P51668,Q9Y297 | PSMA1,HC2,NU,PROS30,PSC2,UBE2D1,SFT,UBC5A,UBCH5,UBCH5A,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| CLE7A (Dectin-1) signaling | R-HSA-5607764 | 3 | NA | 2 | R-HSA-5621481 | FALSE | R-HSA-5607763 | TRUE | TRUE | TRUE | 100 | TRUE | 53.43 | 63 | P25786,P51668,Q9Y297 | PSMA1,HC2,NU,PROS30,PSC2,UBE2D1,SFT,UBC5A,UBCH5,UBCH5A,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| CLE7A (Dectin-1) signaling | R-HSA-5607764 | 3 | NA | 2 | R-HSA-5621481 | FALSE | R-HSA-5607761 | TRUE | TRUE | TRUE | 100 | TRUE | 53.43 | 63 | P25786,P51668,Q9Y297 | PSMA1,HC2,NU,PROS30,PSC2,UBE2D1,SFT,UBC5A,UBCH5,UBCH5A,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Constitutive Signaling by Ligand-Responsive EGFR Cancer Variants | R-HSA-1236382 | NA | 1 | 2 | R-HSA-5637815 | FALSE | NA | FALSE | FALSE | FALSE | 19 | TRUE | 81.7368421 | 65 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112,P01133 | HRAS,HRAS1,EGF | NA |
| Signaling by FGFR4 in disease | R-HSA-5655291 | NA | 1 | 1 | R-HSA-1226099 | FALSE | R-HSA-1839128 | FALSE | FALSE | FALSE | 11 | TRUE | 58.0909091 | 65 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA |
| Signaling by FGFR3 fusions in cancer | R-HSA-8853334 | NA | 1 | 1 | R-HSA-5655332 | FALSE | NA | FALSE | FALSE | FALSE | 10 | TRUE | 60.2 | 67.5 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA |
| MAPK6/MAPK4 signaling | R-HSA-5687128 | 3 | NA | 4 | R-HSA-5683057 | FALSE | NA | FALSE | FALSE | FALSE | 94 | TRUE | 50.8297872 | 69 | P22612,P25786,Q9UPQ9 | PRKACG,PSMA1,HC2,NU,PROS30,PSC2,TNRC6B,KIAA1093 | PSMA1 | NA | NA | NA | P55895,P61289,Q13200,Q9UPQ9 | RAG2,PSME3,PSMD2,TRAP2,TNRC6B,KIAA1093 | PSMD2 |
| UCH proteinases | R-HSA-5689603 | 3 | NA | 3 | R-HSA-5688426 | FALSE | NA | FALSE | FALSE | FALSE | 96 | TRUE | 47.9479167 | 69 | P25786,P85037,Q01167 | PSMA1,HC2,NU,PROS30,PSC2,FOXK1,MNF,FOXK2,ILF,ILF1 | PSMA1 | NA | NA | NA | P61289,Q13200,Q96E28 | PSME3,PSMD2,TRAP2,MCRS1,INO80Q,MSP58 | PSMD2 |
| Activated NTRK2 signals through RAS | R-HSA-9026519 | NA | 1 | 1 | R-HSA-9006115 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 51 | 70 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA |
| Activation of RAS in B cells | R-HSA-1169092 | NA | 1 | 1 | R-HSA-1168372 | FALSE | NA | FALSE | FALSE | FALSE | 5 | TRUE | 45.4 | 70 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA |
| EGFR Transactivation by Gastrin | R-HSA-2179392 | NA | 1 | 1 | R-HSA-881907 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 54.3333333 | 70 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA |
| SHC-related events triggered by IGF1R | R-HSA-2428933 | NA | 1 | 2 | R-HSA-2428924 | FALSE | NA | FALSE | FALSE | FALSE | 9 | TRUE | 49.7777778 | 70 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112,P08069 | HRAS,HRAS1,IGF1R | IGF1R |
| Activated NTRK3 signals through RAS | R-HSA-9034864 | NA | 1 | 1 | R-HSA-9034015 | TRUE | NA | FALSE | TRUE | TRUE | 8 | TRUE | 55.5 | 70.5 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA |
| RAS signaling downstream of NF1 loss-of-function variants | R-HSA-6802953 | NA | 1 | 1 | R-HSA-6802957 | FALSE | NA | FALSE | FALSE | FALSE | 4 | TRUE | 55 | 70.5 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112 | HRAS,HRAS1 | NA |
| SHC1 events in EGFR signaling | R-HSA-180336 | NA | 1 | 2 | R-HSA-177929 | TRUE | NA | FALSE | TRUE | TRUE | 8 | TRUE | 61.75 | 70.5 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112,P01133 | HRAS,HRAS1,EGF | NA |
| GRB2 events in EGFR signaling | R-HSA-179812 | NA | 1 | 2 | R-HSA-177929 | TRUE | NA | FALSE | TRUE | TRUE | 7 | TRUE | 64.2857143 | 71 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112,P01133 | HRAS,HRAS1,EGF | NA |
| SOS-mediated signalling | R-HSA-112412 | NA | 1 | 2 | R-HSA-112399 | TRUE | NA | FALSE | TRUE | TRUE | 7 | TRUE | 61.5714286 | 71 | NA | NA | NA | P01112 | HRAS,HRAS1 | NA | P01112,Q9Y4H2 | HRAS,HRAS1,IRS2 | NA |
| PCP/CE pathway | R-HSA-4086400 | NA | NA | 1 | R-HSA-3858494 | FALSE | R-HSA-5140745 | TRUE | TRUE | TRUE | 92 | TRUE | 50.5434783 | 72 | NA | NA | NA | NA | NA | NA | O14641 | DVL2 | NA |
| PCP/CE pathway | R-HSA-4086400 | NA | NA | 1 | R-HSA-3858494 | FALSE | R-HSA-4608870 | TRUE | TRUE | TRUE | 92 | TRUE | 50.5434783 | 72 | NA | NA | NA | NA | NA | NA | O14641 | DVL2 | NA |
| PCP/CE pathway | R-HSA-4086400 | NA | NA | 1 | R-HSA-3858494 | FALSE | R-HSA-5099900 | TRUE | TRUE | TRUE | 92 | TRUE | 50.5434783 | 72 | NA | NA | NA | NA | NA | NA | O14641 | DVL2 | NA |
| Activation of NF-kappaB in B cells | R-HSA-1169091 | 2 | NA | 2 | R-HSA-1168372 | FALSE | NA | FALSE | FALSE | FALSE | 67 | TRUE | 69.8208955 | 75 | P25786,Q9Y297 | PSMA1,HC2,NU,PROS30,PSC2,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| APC/C.Cdc20 mediated degradation of mitotic proteins | R-HSA-176409 | 1 | 1 | NA | R-HSA-176814 | FALSE | R-HSA-179419 | FALSE | FALSE | TRUE | 75 | TRUE | 62.0933333 | 75 | P51668 | UBE2D1,SFT,UBC5A,UBCH5,UBCH5A | NA | Q9UJX4 | ANAPCS,APCS | NA | NA | NA | NA |
| APC/C.Cdc20 mediated degradation of mitotic proteins | R-HSA-176409 | 1 | 1 | NA | R-HSA-176814 | FALSE | R-HSA-174154 | TRUE | TRUE | TRUE | 75 | TRUE | 62.0933333 | 75 | P51668 | UBE2D1,SFT,UBC5A,UBCH5,UBCH5A | NA | Q9UJX4 | ANAPCS,APCS | NA | NA | NA | NA |
| APC/C.Cdc20 mediated degradation of mitotic proteins | R-HSA-176409 | 1 | 1 | NA | R-HSA-176814 | FALSE | R-HSA-174048 | TRUE | TRUE | TRUE | 75 | TRUE | 62.0933333 | 75 | P51668 | UBE2D1,SFT,UBC5A,UBCH5,UBCH5A | NA | Q9UJX4 | ANAPCS,APCS | NA | NA | NA | NA |

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|--|---------------|---|----|---|---------------|-------|---------------|-------|-------|-------|----|------|------------|----|-----------------------------|--|-------|--------|-------------|----|-----------------------------|---|-------|
| APC/Cdc20 mediated degradation of Securin | R-HSA-174154 | 2 | 1 | 2 | R-HSA-174409 | TRUE | NA | FALSE | TRUE | TRUE | 67 | TRUE | 67.119403 | 75 | P25786,P51668 | PSMA1,HC2,NU,PROS30,PSC2,UBE2D1,SFT,UBC5A,UBCH5,UBCH5A | PSMA1 | Q9UJX4 | ANAPCS,APCS | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| APC/Cdh1 mediated degradation of Cdc20 and other APC/Cdh1 targeted proteins in late mitosis/early G1 | R-HSA-174178 | 2 | 1 | 2 | R-HSA-174143 | FALSE | NA | FALSE | FALSE | FALSE | 72 | TRUE | 63.4305556 | 75 | P25786,P51668 | PSMA1,HC2,NU,PROS30,PSC2,UBE2D1,SFT,UBC5A,UBCH5,UBCH5A | PSMA1 | Q9UJX4 | ANAPCS,APCS | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Asymmetric localization of PCP proteins | R-HSA-4608870 | 1 | NA | 4 | R-HSA-4086400 | TRUE | NA | FALSE | TRUE | TRUE | 64 | TRUE | 66.90625 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | NA | NA | NA | O14641,P61289,Q13200,Q96MT3 | DVL2,PSME3,PSMD2,TRAP2,PRICKLE1,RILP | PSMD2 |
| AUF1 (hnRNP D0) binds and destabilizes mRNA | R-HSA-450408 | 1 | NA | 2 | R-HSA-450531 | FALSE | NA | FALSE | FALSE | FALSE | 55 | TRUE | 77.0181818 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Autodegradation of Cdh1 by Cdh1/APC/C | R-HSA-174084 | 2 | 1 | 2 | R-HSA-174143 | FALSE | NA | FALSE | FALSE | FALSE | 63 | TRUE | 67.9047619 | 75 | P25786,P51668 | PSMA1,HC2,NU,PROS30,PSC2,UBE2D1,SFT,UBC5A,UBCH5,UBCH5A | PSMA1 | Q9UJX4 | ANAPCS,APCS | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Autodegradation of the E3 ubiquitin ligase COP1 | R-HSA-349425 | 3 | 1 | 3 | R-HSA-69541 | TRUE | NA | FALSE | TRUE | TRUE | 52 | TRUE | 81.75 | 75 | P04637,P25786,Q13315 | TP53,P53,PSMA1,HC2,NU,PROS30,PSC2,ATM | PSMA1 | P04637 | TP53,P53 | NA | P04637,P61289,Q13200 | TP53,P53,PSME3,PSMD2,TRAP2 | PSMD2 |
| Cdc20:Phospho-APC/C mediated degradation of Cyclin A | R-HSA-174184 | 2 | 1 | 2 | R-HSA-179419 | FALSE | NA | FALSE | FALSE | FALSE | 72 | TRUE | 64.0972222 | 75 | P25786,P51668 | PSMA1,HC2,NU,PROS30,PSC2,UBE2D1,SFT,UBC5A,UBCH5,UBCH5A | PSMA1 | Q9UJX4 | ANAPCS,APCS | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| CDK-mediated phosphorylation and removal of Cdc6 | R-HSA-69017 | 2 | 1 | 2 | R-HSA-69052 | FALSE | NA | FALSE | FALSE | FALSE | 72 | TRUE | 63.8055556 | 75 | P25786,P51668 | PSMA1,HC2,NU,PROS30,PSC2,UBE2D1,SFT,UBC5A,UBCH5,UBCH5A | PSMA1 | Q9UJX4 | ANAPCS,APCS | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| CDT1 association with the CDC6:ORC:origin complex | R-HSA-68827 | 1 | NA | 2 | R-HSA-68867 | FALSE | NA | FALSE | FALSE | FALSE | 59 | TRUE | 72.4067797 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Cross-presentation of soluble exogenous antigens (endosomes) | R-HSA-1236978 | 1 | NA | 2 | R-HSA-1236975 | FALSE | NA | FALSE | FALSE | FALSE | 50 | TRUE | 67.78 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Cyclin A:Cdk2-associated events at S phase entry | R-HSA-69656 | 1 | NA | 1 | R-HSA-69242 | FALSE | R-HSA-187577 | TRUE | TRUE | TRUE | 85 | TRUE | 55.3764706 | 75 | Q9Y243 | AKT3,PKBG | NA | NA | NA | NA | P31751 | AKT2 | AKT2 |
| Dectin-1 mediated noncanonical NF-kB signaling | R-HSA-5607761 | 2 | NA | 3 | R-HSA-5607764 | TRUE | NA | FALSE | TRUE | TRUE | 62 | TRUE | 72.5645161 | 75 | P25786,Q9Y297 | PSMA1,HC2,NU,PROS30,PSC2,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | NA | NA | NA | P61289,Q13200,Q13200 | PSME3,RELB,PSMD2,TRAP2 | PSMD2 |
| Defective CFTR causes cystic fibrosis | R-HSA-5678895 | 1 | NA | 4 | R-HSA-5619084 | FALSE | NA | FALSE | FALSE | FALSE | 61 | TRUE | 69.7213115 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | NA | NA | NA | P55072,P61289,Q13200,Q13438 | VCP,PSME3,PSMD2,TRAP2,OS9 | PSMD2 |
| Degradation of AXIN | R-HSA-4641257 | 1 | NA | 3 | R-HSA-201681 | TRUE | NA | FALSE | TRUE | TRUE | 55 | TRUE | 77.0363636 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | NA | NA | NA | O95271,P61289,Q13200 | TNKS,PARP5A,PARPL1,TIN1,TINF1,TNKS1,PSME3,PSMD2,TRAP2 | PSMD2 |
| Degradation of beta-catenin by the destruction complex | R-HSA-195253 | 2 | NA | 2 | R-HSA-195721 | FALSE | R-HSA-196299 | FALSE | FALSE | TRUE | 84 | TRUE | 59.9880952 | 75 | P25786,Q9Y297 | PSMA1,HC2,NU,PROS30,PSC2,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Degradation of beta-catenin by the destruction complex | R-HSA-195253 | 2 | NA | 2 | R-HSA-195721 | FALSE | R-HSA-4641265 | TRUE | TRUE | TRUE | 84 | TRUE | 59.9880952 | 75 | P25786,Q9Y297 | PSMA1,HC2,NU,PROS30,PSC2,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Degradation of DVL | R-HSA-4641258 | 1 | NA | 3 | R-HSA-201681 | TRUE | NA | FALSE | TRUE | TRUE | 57 | TRUE | 74.6666667 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | NA | NA | NA | O14641,P61289,Q13200 | DVL2,PSME3,PSMD2,TRAP2 | PSMD2 |
| Degradation of GLI1 by the proteasome | R-HSA-5610780 | 3 | NA | 2 | R-HSA-5610787 | TRUE | NA | FALSE | TRUE | TRUE | 60 | TRUE | 75.0833333 | 75 | P22612,P25786,Q9Y297 | PRKACG,PSMA1,HC2,NU,PROS30,PSC2,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Degradation of GLI2 by the proteasome | R-HSA-5610783 | 4 | NA | 2 | R-HSA-5610787 | TRUE | NA | FALSE | TRUE | TRUE | 60 | TRUE | 75.55 | 75 | P10070,P22612,P25786,Q9Y297 | GLI2,THP,PRKACG,PSMA1,HC2,NU,PROS30,PSC2,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |

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|---|---------------|---|----|----|---------------|-------|---------------|-------|-------|-------|----|------|------------|----|-----------------------------|---|-------|--------|-------------|----|--|---|-------|
| ER-Phagosome pathway | R-HSA-1236974 | 1 | NA | 5 | R-HSA-1236975 | FALSE | NA | FALSE | FALSE | FALSE | 85 | TRUE | 54.2117647 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | NA | NA | NA | O00206,P01891,P01892,P04439,P05534,P10314,P10316,P13746,P16188,P16189,P16190,P18462,P30443,P30447,P30450,P30453,P30455,P30456,P30457,P30459,P30512,P61289,Q09160,Q13200,Q9H953 | TLR4,HLA-A,HLAA,PSME3,PSMD2,TRAP2,SEC61A2 | PSMD2 |
| FBXL7 down-regulates AURKA during mitotic entry and in early mitosis | R-HSA-8854050 | 1 | NA | 2 | R-HSA-69275 | FALSE | NA | FALSE | FALSE | FALSE | 55 | TRUE | 78.8545455 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| GLI3 is processed to GLI3R by the proteasome | R-HSA-5610785 | 3 | NA | 2 | R-HSA-5610787 | TRUE | NA | FALSE | TRUE | TRUE | 60 | TRUE | 75.55 | 75 | P22612,P25786,Q9Y297 | PRKACG,PSMA1,HC2,NU,PROS30,PSC2,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Hedgehog 'on' state | R-HSA-5632684 | 4 | NA | 2 | R-HSA-5358351 | FALSE | R-HSA-5635851 | TRUE | TRUE | TRUE | 86 | TRUE | 51.7093023 | 75 | P10070,P25786,Q13635,Q2M1P5 | GLI2,THP,PSMA1,HC2,NU,PROS30,PSC2,PTCH1,PTCH,KIF7,UNQ340/PROS39 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Hedgehog 'on' state | R-HSA-5632684 | 4 | NA | 2 | R-HSA-5358351 | FALSE | R-HSA-5632681 | TRUE | TRUE | TRUE | 86 | TRUE | 51.7093023 | 75 | P10070,P25786,Q13635,Q2M1P5 | GLI2,THP,PSMA1,HC2,NU,PROS30,PSC2,PTCH1,PTCH,KIF7,UNQ340/PROS39 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Hedgehog 'on' state | R-HSA-5632684 | 4 | NA | 2 | R-HSA-5358351 | FALSE | R-HSA-5635838 | TRUE | TRUE | TRUE | 86 | TRUE | 51.7093023 | 75 | P10070,P25786,Q13635,Q2M1P5 | GLI2,THP,PSMA1,HC2,NU,PROS30,PSC2,PTCH1,PTCH,KIF7,UNQ340/PROS39 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Hedgehog ligand biogenesis | R-HSA-5358346 | 1 | NA | 4 | R-HSA-5358351 | FALSE | R-HSA-5362798 | FALSE | FALSE | FALSE | 65 | TRUE | 66.2 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | NA | NA | NA | P55072,P61289,Q13200,Q13438 | VCP,PSME3,PSMD2,TRAP2,OS9 | PSMD2 |
| Hh mutants that don't undergo autocatalytic processing are degraded by ERAD | R-HSA-5362768 | 1 | NA | 4 | R-HSA-5387390 | FALSE | NA | FALSE | FALSE | FALSE | 56 | TRUE | 75.6785714 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | NA | NA | NA | P55072,P61289,Q13200,Q13438 | VCP,PSME3,PSMD2,TRAP2,OS9 | PSMD2 |
| Negative regulation of NOTCH4 signaling | R-HSA-9604323 | 1 | NA | 2 | R-HSA-9013694 | FALSE | NA | FALSE | FALSE | FALSE | 54 | TRUE | 77.7037037 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| NIK-->noncanonical NF-kB signaling | R-HSA-5676590 | 2 | NA | 3 | R-HSA-5668541 | TRUE | NA | FALSE | TRUE | TRUE | 59 | TRUE | 75.4915254 | 75 | P25786,Q9Y297 | PSMA1,HC2,NU,PROS30,PSC2,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | NA | NA | NA | P61289,Q01201,Q13200 | PSME3,RELB,PSMD2,TRAP2 | PSMD2 |
| Orcl removal from chromatin | R-HSA-68949 | 1 | NA | 2 | R-HSA-69052 | FALSE | NA | FALSE | FALSE | FALSE | 71 | TRUE | 63.9014085 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha | R-HSA-1234176 | 2 | NA | 2 | R-HSA-1234174 | FALSE | NA | FALSE | FALSE | FALSE | 66 | TRUE | 66.1060606 | 75 | P25786,P51668 | PSMA1,HC2,NU,PROS30,PSC2,UBE2D1,SFT,UBC5A,UBCH5,UBCH5A | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Regulation of activated PAK-2p34 by proteasome mediated degradation | R-HSA-211733 | 1 | NA | 2 | R-HSA-169911 | FALSE | NA | FALSE | FALSE | FALSE | 50 | TRUE | 84.1 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PSC2 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Regulation of APC/C activators between G1/S and early anaphase | R-HSA-176408 | 1 | 1 | NA | R-HSA-174143 | FALSE | R-HSA-141405 | FALSE | FALSE | TRUE | 80 | TRUE | 60.6625 | 75 | P51668 | UBE2D1,SFT,UBC5A,UBCH5,UBCH5A | NA | Q9UJX4 | ANAPCS,APCS | NA | NA | NA | NA |
| Regulation of APC/C activators between G1/S and early anaphase | R-HSA-176408 | 1 | 1 | NA | R-HSA-174143 | FALSE | R-HSA-176417 | FALSE | FALSE | TRUE | 80 | TRUE | 60.6625 | 75 | P51668 | UBE2D1,SFT,UBC5A,UBCH5,UBCH5A | NA | Q9UJX4 | ANAPCS,APCS | NA | NA | NA | NA |

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|--|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|----|-------|------------|----|----------------------|---|-----------|--------|-------------|----|------------------------------------|--|------------|
| Regulation of APC/C activators between G1/S and early anaphase | R-HSA-176408 | 1 | 1 | NA | R-HSA-174143 | FALSE | R-HSA-174113 | TRUE | TRUE | TRUE | 80 | TRUE | 60.6625 | 75 | P51668 | UBE2D1,SFT,UBCSA,UBCH5,UBCH5A | NA | Q9UJX4 | ANAPCS,APCS | NA | NA | NA | NA |
| Regulation of ornithine decarboxylase (ODC) | R-HSA-350562 | 1 | NA | 2 | R-HSA-351202 | FALSE | NA | FALSE | FALSE | FALSE | 51 | TRUE | 66.4705882 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PC2 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Regulation of PTEN stability and activity | R-HSA-8948751 | 3 | NA | 5 | R-HSA-6807070 | FALSE | NA | FALSE | FALSE | FALSE | 69 | TRUE | 64.0869565 | 75 | P25786,Q92995,Q9Y243 | PSMA1,HC2,NU,PROS30,PC2,USP13,ISOT3,AKT3,PKBG | PSMA1 | NA | NA | NA | O00308,O95271,P31751,P61289,Q13200 | WWP2,TKNS,PARP5A,PARPL,TIN1,TINF1,TKNS1,AKT2,PSME3,PSMD2,TRAP2 | AKT2,PSMD2 |
| Regulation of RAS by GAPs | R-HSA-5658442 | 1 | 1 | 3 | R-HSA-5673001 | TRUE | NA | FALSE | TRUE | TRUE | 68 | TRUE | 66.0735294 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PC2 | PSMA1 | P01112 | HRAS,HRAS1 | NA | P01112,P61289,Q13200 | HRAS,HRAS1,PSME3,PSMD2,TRAP2 | PSMD2 |
| Regulation of RUNX2 expression and activity | R-HSA-8939902 | 1 | NA | 2 | R-HSA-8878166 | FALSE | NA | FALSE | FALSE | FALSE | 73 | TRUE | 62.1232877 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PC2 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Regulation of RUNX3 expression and activity | R-HSA-8941858 | 2 | NA | 2 | R-HSA-8878159 | FALSE | NA | FALSE | FALSE | FALSE | 55 | TRUE | 76.6363636 | 75 | P12931,P25786 | SRC,SRC1,PSMA1,HC2,NU,PROS30,PC2 | SRC,PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| SCF-beta-TrCP mediated degradation of Emi1 | R-HSA-174113 | 2 | NA | 2 | R-HSA-176408 | TRUE | NA | FALSE | TRUE | TRUE | 55 | TRUE | 79.2545455 | 75 | P25786,Q9Y297 | PSMA1,HC2,NU,PROS30,PC2,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| SCF(Skp2)-mediated degradation of p27/p21 | R-HSA-187577 | 1 | NA | 2 | R-HSA-69656 | TRUE | NA | FALSE | TRUE | TRUE | 60 | TRUE | 71.2 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PC2 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| SCF(Skp2)-mediated degradation of p27/p21 | R-HSA-187577 | 1 | NA | 2 | R-HSA-69202 | TRUE | NA | FALSE | TRUE | TRUE | 60 | TRUE | 71.2 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PC2 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Stabilization of p53 | R-HSA-69541 | 2 | 1 | 1 | R-HSA-69563 | FALSE | R-HSA-349425 | TRUE | TRUE | TRUE | 57 | TRUE | 75.5614035 | 75 | P04637,Q13315 | TP53,PS3,ATM | NA | P04637 | TP53,PS3 | NA | P04637 | TP53,PS3 | NA |
| The role of GTSE1 in G2/M progression after G2 checkpoint | R-HSA-8852276 | 3 | 1 | 3 | R-HSA-69275 | FALSE | NA | FALSE | FALSE | FALSE | 60 | TRUE | 73.5666667 | 75 | P04637,P25786,Q3ZCM7 | TP53,PS3,PSMA1,HC2,NU,PROS30,PC2,TUBB8 | PSMA1 | P04637 | TP53,PS3 | NA | P04637,P61289,Q13200 | TP53,PS3,PSME3,PSMD2,TRAP2 | PSMD2 |
| Ubiquitin Mediated Degradation of Phosphorylated Cdc25A | R-HSA-69601 | 2 | NA | 2 | R-HSA-69610 | FALSE | NA | FALSE | FALSE | FALSE | 53 | TRUE | 80.0566038 | 75 | P25786,Q13315 | PSMA1,HC2,NU,PROS30,PC2,ATM | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Ubiquitin-dependent degradation of Cyclin D1 | R-HSA-69229 | 1 | NA | 2 | R-HSA-75815 | FALSE | NA | FALSE | FALSE | FALSE | 52 | TRUE | 81.4807692 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PC2 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Vif-mediated degradation of APOBEC3G | R-HSA-180585 | 1 | NA | 2 | R-HSA-162909 | FALSE | NA | FALSE | FALSE | FALSE | 55 | TRUE | 77.8 | 75 | P25786 | PSMA1,HC2,NU,PROS30,PC2 | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Vpu mediated degradation of CD4 | R-HSA-180534 | 2 | NA | 2 | R-HSA-162909 | FALSE | NA | FALSE | FALSE | FALSE | 53 | TRUE | 81.2075472 | 75 | P25786,Q9Y297 | PSMA1,HC2,NU,PROS30,PC2,BTRC,BTRCP,FBW1A,FBXW1A | PSMA1 | NA | NA | NA | P61289,Q13200 | PSME3,PSMD2,TRAP2 | PSMD2 |
| Activation of BAD and translocation to mitochondria | R-HSA-111447 | 1 | NA | 2 | R-HSA-114452 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | Q9Y243 | AKT3,PKBG | NA | NA | NA | NA | P31751,P31947 | AKT2,SFN,HME1 | AKT2 |
| Cleavage of Growing Transcript in the Termination Region | R-HSA-109688 | 1 | NA | 5 | R-HSA-73856 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | P38919 | EIF4A3,DDX48,KIAA0111 | NA | NA | NA | NA | Q05519,Q10570,Q8N684,Q8NI27,Q9UKF6 | SRSF11,SFRS11,CPSF1,CPSF160,CPSF7,THOC2,CXorf3,CPSF3,CPSF73 | NA |
| Cleavage of the damaged pyrimidine | R-HSA-110329 | NA | NA | 2 | R-HSA-73928 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | NA | NA | NA | NA | NA | NA | O95243,Q13569 | MBD4,MED1,TDG | NA |
| Cyclin E associated events during G1/S transition | R-HSA-69202 | 1 | NA | 1 | R-HSA-69206 | FALSE | R-HSA-69200 | FALSE | FALSE | TRUE | NA | FALSE | NA | NA | Q9Y243 | AKT3,PKBG | NA | NA | NA | NA | P31751 | AKT2 | AKT2 |
| Cyclin E associated events during G1/S transition | R-HSA-69202 | 1 | NA | 1 | R-HSA-69206 | FALSE | R-HSA-187577 | TRUE | TRUE | TRUE | NA | FALSE | NA | NA | Q9Y243 | AKT3,PKBG | NA | NA | NA | NA | P31751 | AKT2 | AKT2 |
| Cytosolic sensors of pathogen-associated DNA | R-HSA-1834949 | NA | NA | 1 | R-HSA-168249 | FALSE | R-HSA-3134963 | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | NA | NA | NA | NA | NA | NA | P78527 | PRKDC,HYRC,HYRC1 | NA |

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|---|---------------|----|----|----|---------------|-------|---------------|-------|-------|-------|----|-------|----|----|--------------|----------------------------------|-----|--------|--------|---------------|------------------------------|----|
| Cytosolic sensors of pathogen-associated DNA | R-HSA-1834949 | NA | NA | 1 | R-HSA-168249 | FALSE | R-HSA-1606322 | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | NA | NA | NA | NA | NA | P78527 | PRKDC,HYRC,HYRC1 | NA |
| Cytosolic sensors of pathogen-associated DNA | R-HSA-1834949 | NA | NA | 1 | R-HSA-168249 | FALSE | R-HSA-3134975 | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | NA | NA | NA | NA | NA | P78527 | PRKDC,HYRC,HYRC1 | NA |
| Cytosolic sensors of pathogen-associated DNA | R-HSA-1834949 | NA | NA | 1 | R-HSA-168249 | FALSE | R-HSA-1834941 | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | NA | NA | NA | NA | NA | P78527 | PRKDC,HYRC,HYRC1 | NA |
| Cytosolic sensors of pathogen-associated DNA | R-HSA-1834949 | NA | NA | 1 | R-HSA-168249 | FALSE | R-HSA-3134973 | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | NA | NA | NA | NA | NA | P78527 | PRKDC,HYRC,HYRC1 | NA |
| Defective ABCB11 causes progressive familial intrahepatic cholestasis 2 and benign recurrent intrahepatic cholestasis 2 | R-HSA-5678520 | 1 | NA | NA | R-HSA-5619084 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | O95342 | ABCB11,BSEP | NA | NA | NA | NA | NA | NA |
| Defective ABCB4 causes progressive familial intrahepatic cholestasis 3, intrahepatic cholestasis of pregnancy 3 and gallbladder disease 1 | R-HSA-5678771 | NA | NA | 1 | R-HSA-5619084 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | NA | NA | NA | NA | NA | P21439 | ABCB4,MDR3,PGY3 | NA |
| Defective ABCC9 causes dilated cardiomyopathy 10, familial atrial fibrillation 12 and hypertrichotic osteochondrodysplasia | R-HSA-5678420 | 1 | NA | NA | R-HSA-5619084 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | O60706 | ABCC9,SUR2 | NA | NA | NA | NA | NA | NA |
| Defective CYP19A1 causes Aromatase excess syndrome (AEXS) | R-HSA-5579030 | 1 | NA | NA | R-HSA-5579029 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | P11511 | CYP19A1,ARO1,CYAR,CYP19 | NA | NA | NA | NA | NA | NA |
| Defective MOGS causes MOGS-CDG (CDG-2b) | R-HSA-4793954 | 1 | NA | NA | R-HSA-3781860 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | Q13724 | MOGS,GCS1 | NA | NA | NA | NA | NA | NA |
| Defective SLC12A1 causes Bartter syndrome 1 (BS1) | R-HSA-5619104 | NA | NA | 1 | R-HSA-5619102 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | NA | NA | NA | NA | NA | Q13621 | SLC12A1,NKCC2 | NA |
| Defective SLC27A4 causes ichthyosis prematurity syndrome (IPS) | R-HSA-5619108 | 1 | NA | NA | R-HSA-5619102 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | Q6P1M0 | SLC27A4,ACSVL4,FATP4 | NA | NA | NA | NA | NA | NA |
| Defective SLC2A2 causes Fanconi-Bickel syndrome (FBS) | R-HSA-5619098 | NA | NA | 1 | R-HSA-5619102 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | NA | NA | NA | NA | NA | P11168 | SLC2A2,GLUT2 | NA |
| Defective SLC6A2 causes orthostatic intolerance (OI) | R-HSA-5619109 | NA | NA | 1 | R-HSA-5619102 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | NA | NA | NA | NA | NA | P23975 | SLC6A2,NAT1,NET1,SLC6A5 | NA |
| Essential fructosuria | R-HSA-5657562 | NA | NA | 1 | R-HSA-5663084 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | NA | NA | NA | NA | NA | P50053 | KHK | NA |
| Formation of RNA Pol II elongation complex | R-HSA-112382 | NA | NA | 2 | R-HSA-75955 | TRUE | NA | FALSE | TRUE | TRUE | NA | FALSE | NA | NA | NA | NA | NA | NA | NA | P18074,P18615 | ERCC2,XPD,XPC,NELFE, RD,RDBP | NA |
| GRB2-SOS provides linkage to MAPK signaling for Integrins | R-HSA-354194 | 2 | 1 | NA | R-HSA-354192 | TRUE | NA | FALSE | TRUE | TRUE | NA | FALSE | NA | NA | P12931,Q75R6 | SRC,SRCl,APBB1P,PREL1,RARP1,RIAM | SRC | P02751 | FN1,FN | NA | NA | NA |
| Hereditary fructose intolerance | R-HSA-5657560 | NA | NA | 1 | R-HSA-5663084 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | NA | NA | NA | NA | NA | P05062 | ALDOB,ALDB | NA |

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|--|---------------|----|----|----|---------------|-------|--------------|-------|-------|-------|----|-------|----|----|---------------|--|----|--------|----------|----|---|---|----|
| Intestinal saccharidase deficiencies | R-HSA-5659898 | NA | NA | 1 | R-HSA-5663084 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | NA | NA | NA | NA | NA | NA | P14410 | SI | NA |
| MPS VI - Maroteaux-Lamy syndrome | R-HSA-2206285 | 1 | NA | NA | R-HSA-2206281 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | P15848 | ARSB | NA | NA | NA | NA | NA | NA | NA |
| MyD88-independent TLR4 cascade | R-HSA-166166 | NA | NA | 1 | R-HSA-166016 | TRUE | R-HSA-937061 | FALSE | TRUE | TRUE | NA | FALSE | NA | NA | NA | NA | NA | NA | NA | NA | O00206 | TLR4 | NA |
| Platelet degranulation | R-HSA-114608 | 2 | 1 | 6 | R-HSA-76005 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | O00391,P00488 | QSOX1,QSCN6,UNQ2520/PRO6013,F13A1,F13A | NA | P02751 | FN1, FN | NA | P00451,P01009,P01133,P07225,P35609,Q15833 | F8,F8C,SERPINA1,AAT,PI,PRO0684,PRO2209,EGF,PROS1,PROS,ACTN2,STXBP2,UNC18B | NA |
| TICAM1, RIP1-mediated IKK complex recruitment | R-HSA-168927 | 1 | NA | NA | R-HSA-168164 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | P51668 | UBE2D1,SFT,UBC5A,UBCH5,UBCH5A | NA | NA | NA | NA | NA | NA | NA |
| Transcriptional activation of cell cycle inhibitor p21 | R-HSA-69895 | 1 | 1 | 1 | R-HSA-69560 | FALSE | NA | FALSE | FALSE | FALSE | NA | FALSE | NA | NA | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA | P04637 | TP53,P53 | NA |