**Supplementary Table 5. GO enrichment and KEGG pathway of RAS.**

RAS\_GO\_terms

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#Term** | **Database** | **ID** | **Input number** | **Background number** | **P-Value** | **Corrected P-Value** | **Input** | **Hyperlink** |
| regulation of transcription, DNA-dependent | Gene Ontology | GO:0006355 | 56 | 1845 | 0.000219104 | 0.009762097 | Srsf5|Sbno2|Zfp280c|Psip1|Ralgapa1|Nfat5|Paxbp1|Bach2|Parp14|Zmynd11|Osr1|Zfp1|Pura|Hnrnpk|Crem|Cipc|Zbtb49|Pknox2|Arid3a|Irf7|Pmf1|Sp1|Smad6|Jade1|Nfkbiz|Sap130|Mbd3|Tcf12|Smarca2|Meaf6|Nr1h3|Phtf1|Sltm|Nfe2l1|Ubtf|Rpap2|Med24|Men1|Kdm4b|Med7|Tead1|Rlim|Zfp740|Brd2|Snip1|Gtf2h2|Tgif1|Bahd1|Sf1|Srsf10|Med16|Tbp|Wdr61|Mier2|Ncor1|Foxn3 | http://amigo.geneontology.org/amigo/term/GO:0006355 |
| RNA splicing | Gene Ontology | GO:0008380 | 13 | 222 | 0.000320069 | 0.009762097 | Srsf5|Srsf7|Ppil3|U2af1|Arl6ip4|Sf1|U2af1l4|Hnrnpk|Srsf10|Ppih|Thoc2|Ptbp1|Hnrnpf | http://amigo.geneontology.org/amigo/term/GO:0008380 |
| transcription, DNA-dependent | Gene Ontology | GO:0006351 | 52 | 1759 | 0.000709254 | 0.014421505 | Srsf5|Sbno2|Zfp280c|Psip1|Nfat5|Bach2|Parp14|Cipc|Osr1|Zfp1|Pura|Hnrnpk|Crem|Zmynd11|Zbtb49|Tgif1|Arid3a|Irf7|Rlim|Pmf1|Tbp|Mier2|Zfp740|Nfkbiz|Gtf3c2|Sap130|Mbd3|Tcf12|Tead1|Meaf6|Nr1h3|Phtf1|Sltm|Ubtf|Rpap2|Men1|Med24|Kdm4b|Med7|Paxbp1|Smarca2|Brd2|Gtf2h2|Bahd1|Sf1|Jade1|Med16|Sp1|Wdr61|Smad6|Ncor1|Foxn3 | http://amigo.geneontology.org/amigo/term/GO:0006351 |
| mRNA processing | Gene Ontology | GO:0006397 | 14 | 295 | 0.001516767 | 0.023130693 | Srsf5|Srsf7|U2af1|Arl6ip4|Sf1|Hnrnpk|U2af1l4|Ppil3|Srsf10|Ppih|Thoc2|Ptbp1|Papola|Hnrnpf | http://amigo.geneontology.org/amigo/term/GO:0006397 |
| positive regulation of transcription from RNA polymerase II promoter | Gene Ontology | GO:0045944 | 26 | 758 | 0.0025208 | 0.027881678 | Sbno2|Psip1|Strn3|Nfat5|Osr1|Hnrnpk|Crem|Arid3a|Irf7|Traf6|Sp1|Mllt10|Tcf12|Nlrc5|Smarca2|Nr1h3|Nfe2l1|Hax1|Men1|Paxbp1|Tead1|Hras|Mtf2|Senp1|Wdr61|Jade1 | http://amigo.geneontology.org/amigo/term/GO:0045944 |
| mRNA transport | Gene Ontology | GO:0051028 | 6 | 74 | 0.00274246 | 0.027881678 | Srsf7|Myo1c|G3bp2|Thoc2|Ranbp17|Eif5a | http://amigo.geneontology.org/amigo/term/GO:0051028 |
| response to DNA damage stimulus | Gene Ontology | GO:0006974 | 15 | 369 | 0.004586349 | 0.039966755 | Recql5|Zranb3|Rassf1|Gtf2h2|Brcc3|2310003H01Rik|Aplf|Ap5s1|Macrod2|Ikbke|Bbc3|Trip12|Men1|Dclre1c|Fbxo31 | http://amigo.geneontology.org/amigo/term/GO:0006974 |
| cell division | Gene Ontology | GO:0051301 | 14 | 344 | 0.006013197 | 0.045850628 | Recql5|Mapre3|Pmf1|Cdc27|Tacc1|Anapc16|Sgol1|Cdc25c|Sept9|Aurka|Wapal|Chfr|Sept11|Bora | http://amigo.geneontology.org/amigo/term/GO:0051301 |
| protein ubiquitination | Gene Ontology | GO:0016567 | 9 | 180 | 0.00734489 | 0.049782033 | Kctd13|Smurf1|Traf3|Traf6|Anapc16|Wdsub1|March2|Chfr|Rlim | http://amigo.geneontology.org/amigo/term/GO:0016567 |
| mitosis | Gene Ontology | GO:0007067 | 11 | 256 | 0.00968015 | 0.059048915 | Recql5|Mapre3|Pmf1|Cdc25c|Anapc16|Sgol1|Espl1|Aurka|Wapal|Chfr|Bora | http://amigo.geneontology.org/amigo/term/GO:0007067 |
| protein heterooligomerization | Gene Ontology | GO:0051291 | 5 | 77 | 0.015270819 | 0.081596114 | Sept9|Hras|Sept11|Med24|Prkab1 | http://amigo.geneontology.org/amigo/term/GO:0051291 |
| cell cycle | Gene Ontology | GO:0007049 | 19 | 590 | 0.017085342 | 0.081596114 | Recql5|Cdc27|Mapre3|Pmf1|Rassf1|Tacc1|Fbxo31|Anapc16|Sgol1|Cdc25c|Ccndbp1|Sept9|Aurka|Wapal|Pak4|Chfr|Sept11|Bora|Foxn3 | http://amigo.geneontology.org/amigo/term/GO:0007049 |
| regulation of translation | Gene Ontology | GO:0006417 | 6 | 109 | 0.017389336 | 0.081596114 | Mif4gd|Eif4g2|Mknk1|Paip1|Pum1|Eif4ebp2 | http://amigo.geneontology.org/amigo/term/GO:0006417 |
| immune system process | Gene Ontology | GO:0002376 | 12 | 324 | 0.020741619 | 0.090374199 | Otud7b|Irf7|Traf6|Tec|Csf1|Traf3|Ecsit|C8g|Bag6|Nlrc5|Dclre1c|Cadm1 | http://amigo.geneontology.org/amigo/term/GO:0002376 |
| endocytosis | Gene Ontology | GO:0006897 | 7 | 149 | 0.023271634 | 0.094637979 | Gapvd1|Hras|Fcho2|Dnm1|March2|Dnm1l|Ap2b1 | http://amigo.geneontology.org/amigo/term/GO:0006897 |
| chromatin modification | Gene Ontology | GO:0016568 | 10 | 259 | 0.025873348 | 0.09606532 | Bag6|Meaf6|Mtf2|Brcc3|Bahd1|Men1|Kdm4b|Brd2|Zmynd11|Ncor1 | http://amigo.geneontology.org/amigo/term/GO:0016568 |
| intracellular protein transport | Gene Ontology | GO:0006886 | 8 | 188 | 0.026772302 | 0.09606532 | Aspscr1|Tnpo1|Sec23b|Snx10|Ap4b1|Ap2b1|Ranbp17|Snapin | http://amigo.geneontology.org/amigo/term/GO:0006886 |
| protein dephosphorylation | Gene Ontology | GO:0006470 | 6 | 122 | 0.028410917 | 0.09628144 | Ptrhd1|Ppm1e|Cdc25c|Ssh2|Ssh3|Dusp14 | http://amigo.geneontology.org/amigo/term/GO:0006470 |
| protein autophosphorylation | Gene Ontology | GO:0046777 | 7 | 159 | 0.031647465 | 0.101605019 | Ulk3|Ptk2|Ephb4|Wnk1|Mark2|Clk2|Pak2 | http://amigo.geneontology.org/amigo/term/GO:0046777 |
| peptidyl-tyrosine phosphorylation | Gene Ontology | GO:0018108 | 5 | 98 | 0.03828692 | 0.116775107 | Abi1|Clk2|Ptk2|Ephb4|Tec | http://amigo.geneontology.org/amigo/term/GO:0018108 |
| DNA repair | Gene Ontology | GO:0006281 | 10 | 290 | 0.049569392 | 0.143987283 | Recql5|Zranb3|Gtf2h2|Polg2|Brcc3|2310003H01Rik|Aplf|Ap5s1|Trip12|Dclre1c | http://amigo.geneontology.org/amigo/term/GO:0006281 |
| cell proliferation | Gene Ontology | GO:0008283 | 7 | 180 | 0.055275674 | 0.153264367 | Ogfod1|Tacc1|Hras|Bad|Csf1|Scrib|Pura | http://amigo.geneontology.org/amigo/term/GO:0008283 |
| protein transport | Gene Ontology | GO:0015031 | 16 | 557 | 0.064363347 | 0.17070279 | Fam160a2|Tnpo1|C2cd5|Sec23b|Snx10|Myo1c|Sys1|Ap5s1|Stxbp2|Timm10b|Mcfd2|Trim3|Ap4b1|Ap2b1|Ranbp17|Eif5a | http://amigo.geneontology.org/amigo/term/GO:0015031 |
| regulation of apoptotic process | Gene Ontology | GO:0042981 | 5 | 116 | 0.069210717 | 0.175910573 | Bad|Traf3|Bag6|Pak2|Traf6 | http://amigo.geneontology.org/amigo/term/GO:0042981 |
| transcription from RNA polymerase II promoter | Gene Ontology | GO:0006366 | 12 | 398 | 0.076185585 | 0.18588447 | Irf7|Gtf2h2|Tbp|Nfe2l1|Med24|Hnrnpk|Med16|Sp1|Psip1|Smarca2|Jade1|Nr1h3 | http://amigo.geneontology.org/amigo/term/GO:0006366 |
| positive regulation of gene expression | Gene Ontology | GO:0010628 | 7 | 197 | 0.080808424 | 0.18588447 | Nfat5|Prkab1|Cd44|Hras|Csf1|Osr1|Tcf12 | http://amigo.geneontology.org/amigo/term/GO:0010628 |
| translation | Gene Ontology | GO:0006412 | 8 | 240 | 0.086193639 | 0.18588447 | Mrpl24|Eif4g2|Eif2d|Wars|Rps28|Mrps17|Eftud1|Eif5a | http://amigo.geneontology.org/amigo/term/GO:0006412 |
| DNA replication | Gene Ontology | GO:0006260 | 5 | 124 | 0.086352955 | 0.18588447 | Kctd13|Recql5|Polg2|Nol8|Repin1 | http://amigo.geneontology.org/amigo/term/GO:0006260 |
| protein phosphorylation | Gene Ontology | GO:0006468 | 16 | 584 | 0.088838877 | 0.18588447 | Ulk3|Ptk2|Tec|Ephb4|Prkab1|Gtf2h2|Wnk1|Map2k2|Aurka|Mark2|Ikbke|Pak4|Mknk1|Clk2|Mapkapk3|Pak2 | http://amigo.geneontology.org/amigo/term/GO:0006468 |
| dephosphorylation | Gene Ontology | GO:0016311 | 6 | 164 | 0.091418592 | 0.18588447 | Ppap2c|Nt5m|Inpp4a|Ssh2|Ssh3|Dusp14 | http://amigo.geneontology.org/amigo/term/GO:0016311 |

RAS\_KEGG\_pathway

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **#Term** | **Database** | **ID** | **Input number** | **Background**  **number** | **P-Value** | **Corrected P-Value** | **Input** | **Hyperlink** |
| Spliceosome | KEGG PATHWAY | mmu03040 | 8 | 132 | 0.001574191 | 0.248722212 | Srsf5|Srsf7|U2af1|U2af1l4|Hnrnpk|Srsf10|Ppih|Thoc2 | http://www.genome.jp/kegg-bin/show\_pathway?mmu03040/mmu:108121%09red/mmu:331401%09red/mmu:15387%09red/mmu:20384%09red/mmu:225027%09red/mmu:66101%09red/mmu:14105%09red/mmu:233073%09red |
| RIG-I-like receptor signaling pathway | KEGG PATHWAY | mmu04622 | 5 | 69 | 0.00573197 | 0.364549536 | Irf7|Traf3|Cyld|Traf6|Ikbke | http://www.genome.jp/kegg-bin/show\_pathway?mmu04622/mmu:74256%09red/mmu:22031%09red/mmu:56489%09red/mmu:22034%09red/mmu:54123%09red |
| Herpes simplex infection | KEGG PATHWAY | mmu05168 | 9 | 204 | 0.006934073 | 0.364549536 | Srsf5|Srsf7|Traf3|Irf7|Traf6|Tbp|H2-T24|Hnrnpk|Ikbke | http://www.genome.jp/kegg-bin/show\_pathway?mmu05168/mmu:22031%09red/mmu:15387%09red/mmu:22034%09red/mmu:225027%09red/mmu:15042%09red/mmu:54123%09red/mmu:56489%09red/mmu:20384%09red/mmu:21374%09red |
| Viral carcinogenesis | KEGG PATHWAY | mmu05203 | 9 | 228 | 0.013792457 | 0.364549536 | Traf3|Irf7|Gtf2h2|H2-T24|Scrib|Bad|Hnrnpk|Tbp|Vac14 | http://www.genome.jp/kegg-bin/show\_pathway?mmu05203/mmu:22031%09red/mmu:15387%09red/mmu:23894%09red/mmu:21374%09red/mmu:15042%09red/mmu:54123%09red/mmu:12015%09red/mmu:234729%09red/mmu:105782%09red |
| ErbB signaling pathway | KEGG PATHWAY | mmu04012 | 5 | 87 | 0.014877273 | 0.364549536 | Pak4|Map2k2|Bad|Ptk2|Pak2 | http://www.genome.jp/kegg-bin/show\_pathway?mmu04012/mmu:224105%09red/mmu:12015%09red/mmu:70584%09red/mmu:14083%09red/mmu:26396%09red |
| VEGF signaling pathway | KEGG PATHWAY | mmu04370 | 4 | 62 | 0.019607083 | 0.364549536 | Map2k2|Bad|Ptk2|Mapkapk3 | http://www.genome.jp/kegg-bin/show\_pathway?mmu04370/mmu:102626%09red/mmu:26396%09red/mmu:14083%09red/mmu:12015%09red |
| Hepatitis C | KEGG PATHWAY | mmu05160 | 6 | 136 | 0.025952412 | 0.364549536 | Traf3|Irf7|Traf6|Bad|Ikbke|Nr1h3 | http://www.genome.jp/kegg-bin/show\_pathway?mmu05160/mmu:22259%09red/mmu:22031%09red/mmu:22034%09red/mmu:54123%09red/mmu:56489%09red/mmu:12015%09red |
| Toll-like receptor signaling pathway | KEGG PATHWAY | mmu04620 | 5 | 101 | 0.026565741 | 0.364549536 | Map2k2|Traf3|Irf7|Traf6|Ikbke | http://www.genome.jp/kegg-bin/show\_pathway?mmu04620/mmu:22031%09red/mmu:54123%09red/mmu:56489%09red/mmu:22034%09red/mmu:26396%09red |
| Bladder cancer | KEGG PATHWAY | mmu05219 | 3 | 39 | 0.026817017 | 0.364549536 | Rassf1|Map2k2|Mmp2 | http://www.genome.jp/kegg-bin/show\_pathway?mmu05219/mmu:17390%09red/mmu:56289%09red/mmu:26396%09red |
| Ubiquitin mediated proteolysis | KEGG PATHWAY | mmu04120 | 6 | 141 | 0.030279257 | 0.364549536 | Smurf1|Ube4a|Traf6|Cdc27|Uba7|Trip12 | http://www.genome.jp/kegg-bin/show\_pathway?mmu04120/mmu:14897%09red/mmu:217232%09red/mmu:75788%09red/mmu:22034%09red/mmu:74153%09red/mmu:140630%09red |
| Endocytosis | KEGG PATHWAY | mmu04144 | 8 | 220 | 0.030511744 | 0.364549536 | Smurf1|Traf6|Smad6|H2-T24|Dnm1|Git2|Iqsec2|Ap2b1 | http://www.genome.jp/kegg-bin/show\_pathway?mmu04144/mmu:26431%09red/mmu:75788%09red/mmu:22034%09red/mmu:245666%09red/mmu:13429%09red/mmu:15042%09red/mmu:17130%09red/mmu:71770%09red |
| Ether lipid metabolism | KEGG PATHWAY | mmu00565 | 3 | 41 | 0.030541315 | 0.364549536 | Pla2g2e|Ppap2c|Ept1 | http://www.genome.jp/kegg-bin/show\_pathway?mmu00565/mmu:26970%09red/mmu:28042%09red/mmu:50784%09red |
| Transcriptional misregulation in cancer | KEGG PATHWAY | mmu05202 | 7 | 180 | 0.030674244 | 0.364549536 | Aspscr1|Ptk2|Sp1|Golph3l|Men1|Nfkbiz|Ncor1 | http://www.genome.jp/kegg-bin/show\_pathway?mmu05202/mmu:229593%09red/mmu:80859%09red/mmu:17283%09red/mmu:14083%09red/mmu:20683%09red/mmu:68938%09red/mmu:20185%09red |
| Huntington's disease | KEGG PATHWAY | mmu05016 | 7 | 182 | 0.032301858 | 0.364549536 | Atp5c1|Sp1|Ndufs5|Tbp|Bbc3|Ap2b1|Dctn4 | http://www.genome.jp/kegg-bin/show\_pathway?mmu05016/mmu:595136%09red/mmu:170770%09red/mmu:67665%09red/mmu:21374%09red/mmu:11949%09red/mmu:20683%09red/mmu:71770%09red |
| Bacterial invasion of epithelial cells | KEGG PATHWAY | mmu05100 | 4 | 77 | 0.039377071 | 0.410721484 | Dnm1|Ptk2|Sept11|Sept9 | http://www.genome.jp/kegg-bin/show\_pathway?mmu05100/mmu:53860%09red/mmu:13429%09red/mmu:14083%09red/mmu:52398%09red |
| Oocyte meiosis | KEGG PATHWAY | mmu04114 | 5 | 114 | 0.041592049 | 0.410721484 | Cdc25c|Cdc27|Espl1|Aurka|Sgol1 | http://www.genome.jp/kegg-bin/show\_pathway?mmu04114/mmu:217232%09red/mmu:20878%09red/mmu:105988%09red/mmu:12532%09red/mmu:72415%09red |
| Non-small cell lung cancer | KEGG PATHWAY | mmu05223 | 3 | 55 | 0.063656284 | 0.563168546 | Rassf1|Map2k2|Bad | http://www.genome.jp/kegg-bin/show\_pathway?mmu05223/mmu:56289%09red/mmu:12015%09red/mmu:26396%09red |
| Glycerophospholipid metabolism | KEGG PATHWAY | mmu00564 | 4 | 91 | 0.065296868 | 0.563168546 | Pla2g2e|Agpat3|Ppap2c|Ept1 | http://www.genome.jp/kegg-bin/show\_pathway?mmu00564/mmu:28169%09red/mmu:26970%09red/mmu:28042%09red/mmu:50784%09red |
| Axon guidance | KEGG PATHWAY | mmu04360 | 5 | 131 | 0.0677228 | 0.563168546 | Pak4|Ptk2|Ngef|Ephb4|Pak2 | http://www.genome.jp/kegg-bin/show\_pathway?mmu04360/mmu:224105%09red/mmu:53972%09red/mmu:70584%09red/mmu:14083%09red/mmu:13846%09red |
| Regulation of actin cytoskeleton | KEGG PATHWAY | mmu04810 | 7 | 218 | 0.071896512 | 0.567982447 | Ptk2|Map2k2|Ssh2|Ssh3|Pak4|Baiap2|Pak2 | http://www.genome.jp/kegg-bin/show\_pathway?mmu04810/mmu:224105%09red/mmu:26396%09red/mmu:14083%09red/mmu:245857%09red/mmu:237860%09red/mmu:108100%09red/mmu:70584%09red |
| mRNA surveillance pathway | KEGG PATHWAY | mmu03015 | 4 | 97 | 0.078578035 | 0.580578793 | Pcf11|Msi1|Pabpc4|Papola | http://www.genome.jp/kegg-bin/show\_pathway?mmu03015/mmu:17690%09red/mmu:74737%09red/mmu:230721%09red/mmu:18789%09red |
| Thyroid cancer | KEGG PATHWAY | mmu05216 | 2 | 29 | 0.083800753 | 0.580578793 | Map2k2|Ncoa4 | http://www.genome.jp/kegg-bin/show\_pathway?mmu05216/mmu:26396%09red/mmu:27057%09red |
| Synaptic vesicle cycle | KEGG PATHWAY | mmu04721 | 3 | 62 | 0.084514634 | 0.580578793 | Tcirg1|Dnm1|Ap2b1 | http://www.genome.jp/kegg-bin/show\_pathway?mmu04721/mmu:27060%09red/mmu:71770%09red/mmu:13429%09red |
| Nicotinate and nicotinamide metabolism | KEGG PATHWAY | mmu00760 | 2 | 31 | 0.093963925 | 0.618595839 | Nmnat3|Nt5m | http://www.genome.jp/kegg-bin/show\_pathway?mmu00760/mmu:103850%09red/mmu:74080%09red |
| Renal cell carcinoma | KEGG PATHWAY | mmu05211 | 3 | 68 | 0.104406397 | 0.644840961 | Pak4|Map2k2|Pak2 | http://www.genome.jp/kegg-bin/show\_pathway?mmu05211/mmu:224105%09red/mmu:26396%09red/mmu:70584%09red |
| T cell receptor signaling pathway | KEGG PATHWAY | mmu04660 | 4 | 108 | 0.106113069 | 0.644840961 | Pak4|Map2k2|Tec|Pak2 | http://www.genome.jp/kegg-bin/show\_pathway?mmu04660/mmu:224105%09red/mmu:26396%09red/mmu:70584%09red/mmu:21682%09red |
| Prion diseases | KEGG PATHWAY | mmu05020 | 2 | 35 | 0.115259733 | 0.674482885 | Map2k2|C8g | http://www.genome.jp/kegg-bin/show\_pathway?mmu05020/mmu:26396%09red/mmu:69379%09red |
| RNA degradation | KEGG PATHWAY | mmu03018 | 3 | 77 | 0.137277508 | 0.702469863 | Ddx6|Wdr61|Pabpc4 | http://www.genome.jp/kegg-bin/show\_pathway?mmu03018/mmu:13209%09red/mmu:230721%09red/mmu:66317%09red |
| MAPK signaling pathway | KEGG PATHWAY | mmu04010 | 7 | 258 | 0.139691016 | 0.702469863 | Traf6|Mknk1|Map2k2|Ecsit|Dusp14|Mapkapk3|Pak2 | http://www.genome.jp/kegg-bin/show\_pathway?mmu04010/mmu:224105%09red/mmu:26396%09red/mmu:56405%09red/mmu:22034%09red/mmu:26940%09red/mmu:102626%09red/mmu:17346%09red |