

Supplementary Table 2. GO.top.down.

| Id | Term | Category | pval | Enrichment_score | Protein_gene |
|------------|---|--------------------|-------------|-------------------------|-----------------------------|
| GO:0090410 | malonate catabolic process | biological_process | 0 | 23.1066666666667 | Q3URE1:Acsf3 |
| GO:0071577 | zinc II ion transmembrane transport | biological_process | 0 | 23.1066666666667 | Q8C145:Slc39a6 |
| GO:0006622 | protein targeting to lysosome | biological_process | 0 | 23.1066666666667 | O35114:Scarb2 |
| GO:1905123 | regulation of glucosylceramidase activity | biological_process | 0 | 23.1066666666667 | O35114:Scarb2 |
| GO:0010389 | regulation of G2/M transition of mitotic cell cycle | biological_process | 0 | 23.1066666666667 | P51943:Ccna2; Q6PHZ2:Camk2d |
| GO:0044320 | cellular response to leptin stimulus | biological_process | 0 | 23.1066666666667 | P51943:Ccna2 |
| GO:0044843 | cell cycle G1/S phase transition | biological_process | 0 | 23.1066666666667 | P51943:Ccna2 |
| GO:0071314 | cellular response to cocaine | biological_process | 0 | 23.1066666666667 | P51943:Ccna2 |
| GO:0071373 | cellular response to luteinizing hormone stimulus | biological_process | 0 | 23.1066666666667 | P51943:Ccna2 |
| GO:1990314 | cellular response to insulin-like growth factor stimulus | biological_process | 0 | 23.1066666666667 | P51943:Ccna2 |
| GO:1990204 | oxidoreductase complex | cellular_component | 0 | 23.1066666666667 | Q91VT4:Cbr4 |
| GO:0097124 | cyclin A2-CDK2 complex | cellular_component | 0 | 23.1066666666667 | P51943:Ccna2 |
| GO:0000307 | cyclin-dependent protein kinase holoenzyme complex | cellular_component | 0 | 23.1066666666667 | P61025:Cks1b |
| GO:0043194 | axon initial segment | cellular_component | 0 | 23.1066666666667 | Q6PHZ2:Camk2d |
| GO:0042584 | chromaffin granule membrane | cellular_component | 0 | 23.1066666666667 | Q6P069:Sri |
| GO:0020018 | ciliary pocket membrane | cellular_component | 0 | 23.1066666666667 | Q9ERB0:Snap29 |
| GO:0033179 | proton-transporting V-type ATPase, V0 domain | cellular_component | 0 | 23.1066666666667 | P51863:Atp6v0d1 |
| GO:0033181 | plasma membrane proton-transporting V-type ATPase complex | cellular_component | 0 | 23.1066666666667 | P51863:Atp6v0d1 |
| GO:0000220 | vacuolar proton-transporting V-type ATPase, V0 domain | cellular_component | 0 | 23.1066666666667 | P15920:Atp6v0a2 |
| GO:0097413 | Lewy body | cellular_component | 0 | 23.1066666666667 | P11352:Gpx1 |
| GO:0003955 | NAD(P)H dehydrogenase (quinone) activity | molecular_function | 0 | 23.1066666666667 | Q91VT4:Cbr4 |
| GO:0008753 | NADPH dehydrogenase (quinone) activity | molecular_function | 0 | 23.1066666666667 | Q91VT4:Cbr4 |
| GO:0047025 | 3-oxoacyl-[acyl-carrier-protein] reductase (NADH) activity | molecular_function | 0 | 23.1066666666667 | Q91VT4:Cbr4 |
| GO:0070402 | NADPH binding | molecular_function | 0 | 23.1066666666667 | Q91VT4:Cbr4 |
| GO:0016878 | acid-thiol ligase activity | molecular_function | 0 | 23.1066666666667 | Q3URE1:Acsf3 |
| GO:0090409 | malonyl-CoA synthetase activity | molecular_function | 0 | 23.1066666666667 | Q3URE1:Acsf3 |
| GO:0016788 | hydrolase activity, acting on ester bonds | molecular_function | 0 | 23.1066666666667 | Q9D7N9:Apmmap |
| GO:0016844 | strictosidine synthase activity | molecular_function | 0 | 23.1066666666667 | Q9D7N9:Apmmap |
| GO:0097472 | cyclin-dependent protein kinase activity | molecular_function | 0 | 23.1066666666667 | P51943:Ccna2 |
| GO:0061575 | cyclin-dependent protein serine/threonine kinase activator activity | molecular_function | 0 | 23.1066666666667 | P61025:Cks1b |

Supplementary Table 3. GO.top.up.

| Id | Term | Category | pval | Enrichment_score | Protein_gene |
|------------|---|--------------------|----------------------|-------------------------|--|
| GO:0000301 | retrograde transport, vesicle recycling within Golgi | biological_process | 0 | 20.8795180722892 | Q9QYE6:Golga5 |
| GO:0007091 | metaphase/anaphase transition of mitotic cell cycle | biological_process | 0 | 20.8795180722892 | A2A6Q5:Cdc27 |
| GO:0070979 | protein K11-linked ubiquitination | biological_process | 0 | 20.8795180722892 | A2A6Q5:Cdc27 |
| GO:0032410 | negative regulation of transporter activity | biological_process | 0 | 20.8795180722892 | Q99LJ0:Cttnbp2nl |
| GO:0034763 | negative regulation of transmembrane transport | biological_process | 0 | 20.8795180722892 | Q99LJ0:Cttnbp2nl |
| GO:1902525 | regulation of protein monoubiquitination | biological_process | 0 | 20.8795180722892 | Q8BH57:Wdr48 |
| GO:0050806 | positive regulation of synaptic transmission | biological_process | 0 | 20.8795180722892 | Q8BNY6:Ncs1 |
| GO:1903262 | negative regulation of serine phosphorylation of STAT3 protein | biological_process | 0 | 20.8795180722892 | Q99LL5:Pwp1 |
| GO:2000738 | positive regulation of stem cell differentiation | biological_process | 0 | 20.8795180722892 | Q99LL5:Pwp1 |
| GO:0001763 | morphogenesis of a branching structure | biological_process | 0 | 20.8795180722892 | E9Q5F9:Setd2 |
| GO:0033185 | dolichol-phosphate-mannose synthase complex | cellular_component | 0 | 20.8795180722892 | Q9D1Q4:Dpm3; O70152:Dpm1 |
| GO:0030906 | retromer, cargo-selective complex | cellular_component | 0 | 20.8795180722892 | P40336:Vps26a |
| GO:0000243 | commitment complex | cellular_component | 0 | 20.8795180722892 | P62315:Snrpd1 |
| GO:0005666 | DNA-directed RNA polymerase III complex | cellular_component | 0 | 20.8795180722892 | P52432:Polr1c; Q923G2:Polr2h |
| GO:0099053 | activating signal cointegrator 1 complex | cellular_component | 0 | 20.8795180722892 | E9PZJ8:Ascc3 |
| GO:0005960 | glycine cleavage complex | cellular_component | 0 | 20.8795180722892 | Q91WK5:Gcsh |
| GO:0005736 | DNA-directed RNA polymerase I complex | cellular_component | 0.000106104412585285 | 13.9196787148594 | P52432:Polr1c; Q923G2:Polr2h |
| GO:0000788 | nuclear nucleosome | cellular_component | 0.000106104412585285 | 13.9196787148594 | P84244:H3f3a; P84244:H3f3b |
| GO:0005876 | spindle microtubule | cellular_component | 0.000296003570783366 | 7.82981927710843 | A2A6Q5:Cdc27; Q8BHJ5:Tbl1xr1; Q6P9P6:Kif11 |
| GO:0001740 | Barr body | cellular_component | 0.000409697963046072 | 10.4397590361446 | P84244:H3f3a; P84244:H3f3b |
| GO:1990889 | H4K20me3 modified histone binding | molecular_function | 0 | 20.8795180722892 | Q99LL5:Pwp1 |
| GO:0016831 | carboxy-lyase activity | molecular_function | 0 | 20.8795180722892 | Q99K01:Pdxdc1 |
| GO:0070699 | type II activin receptor binding | molecular_function | 0 | 20.8795180722892 | Q9D6K5:Synj2bp |
| GO:0016706 | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors | molecular_function | 0 | 20.8795180722892 | Q9JF3:Riox1; Q80Y84:Kdm5b |
| GO:0051864 | histone demethylase activity (H3-K36 specific) | molecular_function | 0 | 20.8795180722892 | Q9JF3:Riox1 |
| GO:0004827 | proline-tRNA ligase activity | molecular_function | 0 | 20.8795180722892 | Q8CFI5:Pars2 |
| GO:1990050 | phosphatidic acid transporter activity | molecular_function | 0 | 20.8795180722892 | Q9D8Z2:Triap1 |
| GO:0010521 | telomerase inhibitor activity | molecular_function | 0 | 20.8795180722892 | Q9CZX5:Pinx1 |
| GO:0033130 | acetylcholine receptor binding | molecular_function | 0 | 20.8795180722892 | Q9CQU3:Rer1 |
| GO:0047545 | 2-hydroxyglutarate dehydrogenase activity | molecular_function | 0 | 20.8795180722892 | Q91YP0:L2hgdh |