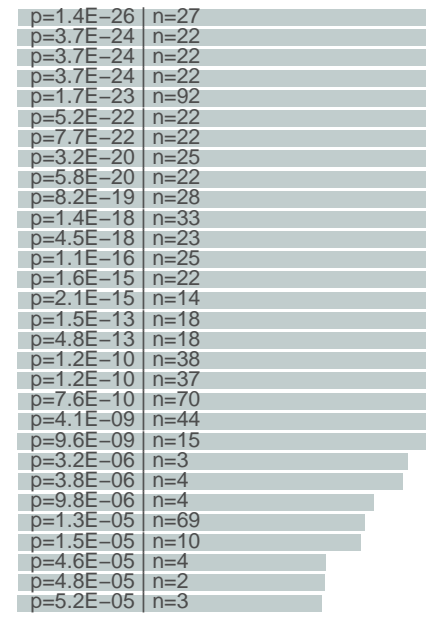


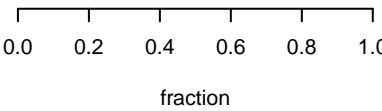
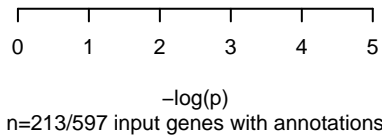
GO:BP
gc006

fraction genes in fg and expected value

| | |
|---|------------|
| activation of adenylate cyclase activity | GO:0007190 |
| thyroid-stimulating hormone signaling pa... | GO:0038194 |
| cellular response to thyrotropin-releasi... | GO:1905229 |
| cellular response to glycoprotein | GO:1904588 |
| G protein-coupled receptor signaling pat... | GO:0007186 |
| dopaminergic neuron differentiation | GO:0071542 |
| cochlea morphogenesis | GO:0090103 |
| positive regulation of multicellular org... | GO:0040018 |
| inner ear receptor cell stereocilium org... | GO:0060122 |
| hormone-mediated signaling pathway | GO:0009755 |
| adenylate cyclase-activating G protein-c... | GO:0007189 |
| adult locomotory behavior | GO:0008344 |
| B cell differentiation | GO:0030183 |
| positive regulation of cold-induced ther... | GO:0120162 |
| epithelial cell proliferation involved i... | GO:2001013 |
| hair follicle development | GO:0001942 |
| oocyte differentiation | GO:0009994 |
| inner ear development | GO:0048839 |
| positive regulation of cell population p... | GO:0008284 |
| regulation of cell population proliferat... | GO:0042127 |
| regulation of locomotion | GO:0040012 |
| positive regulation of canonical Wnt sig... | GO:0090263 |
| actin rod assembly | GO:0031247 |
| cellular response to ATP | GO:0071318 |
| presynaptic dense core vesicle exocytosi... | GO:0099525 |
| cell surface receptor signaling pathway | GO:0007166 |
| adenylate cyclase-inhibiting G protein-c... | GO:0007193 |
| positive regulation of melanin biosynthe... | GO:0048023 |
| cellular response to prostaglandin D sti... | GO:0071799 |
| regulation of axon diameter | GO:0031133 |



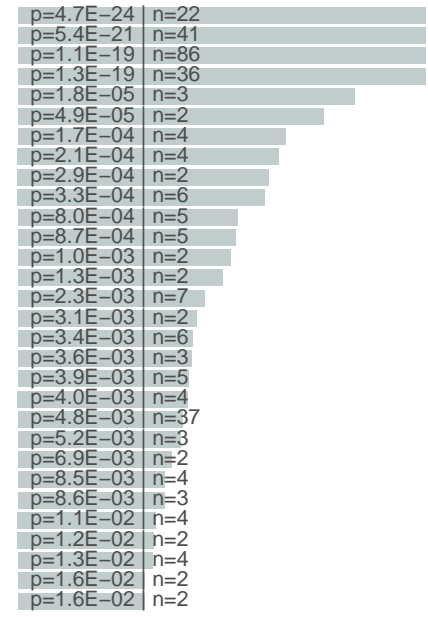
| | |
|---------|---------|
| fg=0.13 | bg=0.01 |
| fg=0.10 | bg=0.00 |
| fg=0.10 | bg=0.00 |
| fg=0.10 | bg=0.00 |
| fg=0.43 | bg=0.07 |
| fg=0.10 | bg=0.01 |
| fg=0.10 | bg=0.01 |
| fg=0.12 | bg=0.01 |
| fg=0.10 | bg=0.01 |
| fg=0.13 | bg=0.01 |
| fg=0.15 | bg=0.02 |
| fg=0.11 | bg=0.01 |
| fg=0.12 | bg=0.01 |
| fg=0.10 | bg=0.01 |
| fg=0.07 | bg=0.00 |
| fg=0.08 | bg=0.01 |
| fg=0.08 | bg=0.01 |
| fg=0.18 | bg=0.02 |
| fg=0.17 | bg=0.05 |
| fg=0.33 | bg=0.10 |
| fg=0.21 | bg=0.06 |
| fg=0.07 | bg=0.01 |
| fg=0.01 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.32 | bg=0.14 |
| fg=0.05 | bg=0.01 |
| fg=0.02 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |



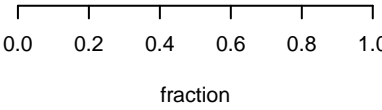
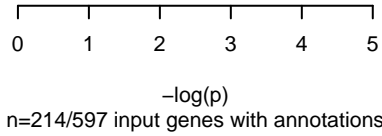
GO:MF
gc006

fraction genes in fg and expected value

| | |
|---|------------|
| thyroid-stimulating hormone receptor act... | GO:0004996 |
| protein-hormone receptor activity | GO:0016500 |
| G protein-coupled receptor activity | GO:0004930 |
| G protein-coupled peptide receptor activ... | GO:0008528 |
| D5 dopamine receptor binding | GO:0031752 |
| prostaglandin F receptor activity | GO:0004958 |
| G-protein beta/gamma-subunit complex bin... | GO:0031683 |
| voltage-gated potassium channel activity | GO:0005249 |
| double-stranded DNA endodeoxyribonucleas... | GO:1990238 |
| substance K receptor activity | GO:0016497 |
| G protein-coupled photoreceptor activity | GO:0008020 |
| myosin binding | GO:0017022 |
| pre-mRNA 5'-splice site binding | GO:0030627 |
| extracellular matrix structural constitu... | GO:0030021 |
| peptide hormone binding | GO:0017046 |
| prostaglandin E receptor activity | GO:0004957 |
| unfolded protein binding | GO:0051082 |
| group II metabotropic glutamate receptor... | GO:0001641 |
| protein phosphatase regulator activity | GO:0019888 |
| protein phosphatase 2A binding | GO:0051721 |
| protein-containing complex binding | GO:0044877 |
| low-density lipoprotein particle recepto... | GO:0050750 |
| D1 dopamine receptor binding | GO:0031748 |
| syntaxin-1 binding | GO:0017075 |
| growth factor activity | GO:0008083 |
| postsynaptic neurotransmitter receptor a... | GO:0098960 |
| G-protein beta-subunit binding | GO:0031681 |
| neurotransmitter receptor activity | GO:0030594 |
| all-trans retinal binding | GO:0005503 |
| Wnt-protein binding | GO:0017147 |



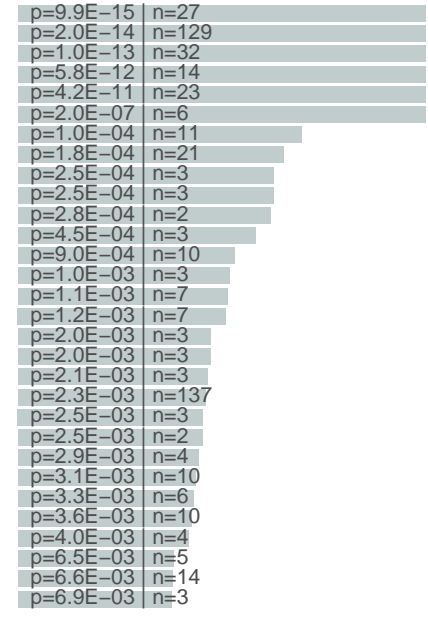
| | |
|---------|---------|
| fg=0.10 | bg=0.00 |
| fg=0.19 | bg=0.01 |
| fg=0.40 | bg=0.06 |
| fg=0.17 | bg=0.02 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.03 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.17 | bg=0.10 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |



GO:CC
gc006

fraction genes in fg and expected value

| | |
|---|------------|
| receptor complex | GO:0043235 |
| plasma membrane | GO:0005886 |
| membrane raft | GO:0045121 |
| trans-Golgi network membrane | GO:0032588 |
| basolateral plasma membrane | GO:0016323 |
| heterotrimeric G-protein complex | GO:0005834 |
| dendritic spine | GO:0043197 |
| glutamatergic synapse | GO:0098978 |
| synaptobrevin 2-SNAP-25-syntaxin-1a-comp... | GO:0070032 |
| synaptobrevin 2-SNAP-25-syntaxin-1a-comp... | GO:0070033 |
| DNA recombinase complex | GO:0097519 |
| synaptobrevin 2-SNAP-25-syntaxin-1a comp... | GO:0070044 |
| Schaffer collateral - CA1 synapse | GO:0098685 |
| cuticular plate | GO:0032437 |
| sperm midpiece | GO:0097225 |
| sperm head | GO:0061827 |
| extrinsic component of presynaptic membr... | GO:0098888 |
| voltage-gated potassium channel complex | GO:0008076 |
| ribbon synapse | GO:0097470 |
| cell periphery | GO:0071944 |
| endoplasmic reticulum chaperone complex | GO:0034663 |
| kinociliary basal body | GO:1902636 |
| sperm plasma membrane | GO:0097524 |
| cluster of actin-based cell projections | GO:0098862 |
| dendritic shaft | GO:0043198 |
| extrinsic component of cytoplasmic side ... | GO:0031234 |
| presynaptic active zone membrane | GO:0048787 |
| photoreceptor outer segment | GO:0001750 |
| presynaptic membrane | GO:0042734 |
| BLOC-1 complex | GO:0031083 |



| | |
|---------|---------|
| fg=0.13 | bg=0.02 |
| fg=0.60 | bg=0.25 |
| fg=0.15 | bg=0.03 |
| fg=0.07 | bg=0.01 |
| fg=0.11 | bg=0.02 |
| fg=0.03 | bg=0.00 |
| fg=0.05 | bg=0.01 |
| fg=0.10 | bg=0.04 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.05 | bg=0.01 |
| fg=0.01 | bg=0.00 |
| fg=0.03 | bg=0.01 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.64 | bg=0.27 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.05 | bg=0.01 |
| fg=0.03 | bg=0.01 |
| fg=0.05 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.01 |
| fg=0.07 | bg=0.02 |
| fg=0.01 | bg=0.00 |

