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| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Table S2-1 KEGG enrichment analysis of CAD-related genes. | | | | |  |  |  |  |
| ID | Description | GeneRatio | BgRatio | pvalue | p.adjust | qvalue | geneID | Count |
| hsa04080 | Neuroactive ligand-receptor interaction | 25/167 | 367/8644 | 3.16E-08 | 6.64E-06 | 6.59E-06 | 117/155/553/680/1133/1392/2563/200959/2690/122876/2901/2902/2916/3060/11255/3375/10022/3814/4544/4987/79957/5731/5733/6754/9287 | 25 |
| hsa04740 | Olfactory transduction | 27/167 | 439/8644 | 7.11E-08 | 7.46E-06 | 7.41E-06 | 81341/81797/138802/347168/26219/392392/144125/338755/120776/26707/254879/8392/81328/256144/390649/441670/390437/79324/390064/338751/120793/219981/392391/26341/390271/219417/283189 | 27 |
| hsa04020 | Calcium signaling pathway | 13/167 | 253/8644 | 0.001208022 | 0.084561523 | 0.083925722 | 108/155/553/1133/1956/2253/2668/2902/3270/5731/5733/7039/10345 | 13 |
| hsa04724 | Glutamatergic synapse | 7/167 | 115/8644 | 0.006773015 | 0.355583264 | 0.352909705 | 108/2901/2902/2916/50944/22941/59345 | 7 |
| hsa04727 | GABAergic synapse | 5/167 | 89/8644 | 0.028674366 | 0.773626336 | 0.767809596 | 108/2563/200959/6538/59345 | 5 |
| hsa04520 | Adherens junction | 5/167 | 93/8644 | 0.0337896 | 0.773626336 | 0.767809596 | 1003/1956/93408/4633/10580 | 5 |
| hsa00430 | Taurine and hypotaurine metabolism | 2/167 | 16/8644 | 0.037284251 | 0.773626336 | 0.767809596 | 2326/2327 | 2 |
| hsa04014 | Ras signaling pathway | 9/167 | 236/8644 | 0.039206785 | 0.773626336 | 0.767809596 | 51378/1956/2253/2902/4254/5322/8437/7039/59345 | 9 |
| hsa04713 | Circadian entrainment | 5/167 | 97/8644 | 0.039439064 | 0.773626336 | 0.767809596 | 108/117/2902/4544/59345 | 5 |
| hsa05033 | Nicotine addiction | 3/167 | 40/8644 | 0.041543461 | 0.773626336 | 0.767809596 | 2563/200959/2902 | 3 |
| hsa00450 | Selenocompound metabolism | 2/167 | 17/8644 | 0.041729348 | 0.773626336 | 0.767809596 | 1491/11185 | 2 |
| hsa04216 | Ferroptosis | 3/167 | 41/8644 | 0.044207219 | 0.773626336 | 0.767809596 | 94033/2730/440738 | 3 |

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| Table S2-2 GO enrichment analysis of CAD-related genes. | | | | | |  |  |  |  |
| ONTOLOGY | ID | Description | GeneRatio | BgRatio | pvalue | p.adjust | qvalue | geneID | Count |
| BP | GO:0007608 | sensory perception of smell | 29/334 | 457/18614 | 4.30E-09 | 7.27E-06 | 6.77E-06 | BEST2/OR10J3/OR10W1/OR12D3/OR13C8/OR1J1/OR1J4/OR1K1/OR2AG1/OR2AG2/OR2D2/OR2J2/OR2T6/OR3A3/OR4A15/OR4C3/OR4F15/OR4M1/OR4N5/OR51G1/OR51I2/OR52L1/OR56A4/OR5A2/OR5C1/OR5H1/OR8B3/OR8U1/OR9G4 | 29 |
| BP | GO:0050911 | detection of chemical stimulus involved in sensory perception of smell | 28/334 | 431/18614 | 4.82E-09 | 7.27E-06 | 6.77E-06 | OR10J3/OR10W1/OR12D3/OR13C8/OR1J1/OR1J4/OR1K1/OR2AG1/OR2AG2/OR2D2/OR2J2/OR2T6/OR3A3/OR4A15/OR4C3/OR4F15/OR4M1/OR4N5/OR51G1/OR51I2/OR52L1/OR56A4/OR5A2/OR5C1/OR5H1/OR8B3/OR8U1/OR9G4 | 28 |
| BP | GO:0050907 | detection of chemical stimulus involved in sensory perception | 28/334 | 479/18614 | 4.67E-08 | 4.69E-05 | 4.37E-05 | OR10J3/OR10W1/OR12D3/OR13C8/OR1J1/OR1J4/OR1K1/OR2AG1/OR2AG2/OR2D2/OR2J2/OR2T6/OR3A3/OR4A15/OR4C3/OR4F15/OR4M1/OR4N5/OR51G1/OR51I2/OR52L1/OR56A4/OR5A2/OR5C1/OR5H1/OR8B3/OR8U1/OR9G4 | 28 |
| BP | GO:0008306 | associative learning | 8/334 | 86/18614 | 0.000155469 | 0.091067487 | 0.084736116 | CSMD1/GRIN1/LRRN4/NEUROD2/NOG/OPRL1/SHANK1/SHANK2 | 8 |
| BP | GO:2000696 | regulation of epithelial cell differentiation involved in kidney development | 4/334 | 16/18614 | 0.000156236 | 0.091067487 | 0.084736116 | GDNF/PAX8/PROM1/WNT9B | 4 |
| BP | GO:0030322 | stabilization of membrane potential | 4/334 | 17/18614 | 0.00020143 | 0.091067487 | 0.084736116 | KCNK1/KCNK18/KCNK4/KCNK9 | 4 |
| BP | GO:0050482 | arachidonic acid secretion | 5/334 | 32/18614 | 0.000244098 | 0.091067487 | 0.084736116 | AVPR1B/OC90/PLA2G5/PLA2R1/SSTR4 | 5 |
| BP | GO:1903963 | arachidonate transport | 5/334 | 32/18614 | 0.000244098 | 0.091067487 | 0.084736116 | AVPR1B/OC90/PLA2G5/PLA2R1/SSTR4 | 5 |
| BP | GO:0071625 | vocalization behavior | 4/334 | 19/18614 | 0.000318872 | 0.091067487 | 0.084736116 | NRXN2/SHANK1/SHANK2/SRPX2 | 4 |
| BP | GO:0007188 | adenylate cyclase-modulating G protein-coupled receptor signaling pathway | 13/334 | 234/18614 | 0.000327976 | 0.091067487 | 0.084736116 | ADCY2/ADCYAP1R1/ADRB3/CHRM5/FFAR3/GPHB5/GRM6/HRH3/IAPP/OPRL1/PTGER1/PTGER3/SSTR4 | 13 |
| BP | GO:0051937 | catecholamine transport | 7/334 | 73/18614 | 0.000332143 | 0.091067487 | 0.084736116 | CHRM5/CRH/FFAR3/GDNF/HRH3/SLC29A4/SYT3 | 7 |
| BP | GO:0072079 | nephron tubule formation | 4/334 | 20/18614 | 0.000392984 | 0.093636689 | 0.087126697 | GDNF/NOG/PAX8/WNT9B | 4 |
| BP | GO:0043010 | camera-type eye development | 16/334 | 338/18614 | 0.000427235 | 0.093636689 | 0.087126697 | BIRC7/CRYAA/CRYBB3/CRYGA/CYP1A1/DLX1/EGFR/GRM6/MEGF11/MTNR1B/MYF5/NES/OPN4/PROM1/TBX2/WNT9B | 16 |
| BP | GO:0006813 | potassium ion transport | 13/334 | 241/18614 | 0.000434653 | 0.093636689 | 0.087126697 | FXYD1/HCRT/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK18/KCNK4/KCNK9/KCNN1/MTNR1B/NALCN/TRPM5 | 13 |
| BP | GO:0048754 | branching morphogenesis of an epithelial tube | 10/334 | 157/18614 | 0.000552147 | 0.107905451 | 0.100403439 | CSMD1/FGF8/GDNF/GLI2/HHIP/HOXA11/NOG/PAX8/TBX2/WNT9B | 10 |
| BP | GO:0061138 | morphogenesis of a branching epithelium | 11/334 | 188/18614 | 0.000606233 | 0.107905451 | 0.100403439 | CSMD1/FGF8/GCM1/GDNF/GLI2/HHIP/HOXA11/NOG/PAX8/TBX2/WNT9B | 11 |
| BP | GO:0072172 | mesonephric tubule formation | 3/334 | 10/18614 | 0.000625667 | 0.107905451 | 0.100403439 | GDNF/NOG/WNT9B | 3 |
| BP | GO:0050890 | cognition | 15/334 | 317/18614 | 0.000643998 | 0.107905451 | 0.100403439 | CRH/CSMD1/EGFR/GRIN1/HRH3/KCNK4/LRRN4/NEUROD2/NOG/NRXN2/OPRL1/SHANK1/SHANK2/TMPRSS11E/TTBK1 | 15 |
| BP | GO:0001658 | branching involved in ureteric bud morphogenesis | 6/334 | 60/18614 | 0.000707031 | 0.11223191 | 0.104429105 | FGF8/GDNF/HOXA11/NOG/PAX8/WNT9B | 6 |
| BP | GO:0098974 | postsynaptic actin cytoskeleton organization | 3/334 | 11/18614 | 0.000848887 | 0.117815239 | 0.109624259 | ACTBL2/CPNE6/SRCIN1 | 3 |
| BP | GO:0042391 | regulation of membrane potential | 18/334 | 433/18614 | 0.000882923 | 0.117815239 | 0.109624259 | BEST2/FXYD1/GABRD/GABRR3/GCLM/GRIK5/GRIN1/HCRT/KCND2/KCNJ11/KCNK1/KCNK18/KCNK4/KCNK9/MTNR1B/NALCN/SHANK1/TRDN | 18 |
| BP | GO:0021983 | pituitary gland development | 5/334 | 42/18614 | 0.000890596 | 0.117815239 | 0.109624259 | FGF8/GLI2/NOG/OTP/PITX1 | 5 |
| BP | GO:0015844 | monoamine transport | 7/334 | 86/18614 | 0.000898458 | 0.117815239 | 0.109624259 | CHRM5/CRH/FFAR3/GDNF/HRH3/SLC29A4/SYT3 | 7 |
| BP | GO:0019226 | transmission of nerve impulse | 6/334 | 65/18614 | 0.00108241 | 0.121990206 | 0.113508966 | CACNG8/CHRM5/HCRT/KCND2/MTNR1B/SPTBN4 | 6 |
| BP | GO:0071715 | icosanoid transport | 6/334 | 65/18614 | 0.00108241 | 0.121990206 | 0.113508966 | AVPR1B/OC90/PLA2G5/PLA2R1/SLC22A8/SSTR4 | 6 |
| BP | GO:0099084 | postsynaptic specialization organization | 5/334 | 44/18614 | 0.001104231 | 0.121990206 | 0.113508966 | NRXN2/PTPRS/SHANK1/SHANK2/SPTBN2 | 5 |
| BP | GO:0003337 | mesenchymal to epithelial transition involved in metanephros morphogenesis | 3/334 | 12/18614 | 0.001116856 | 0.121990206 | 0.113508966 | GDNF/PAX8/WNT9B | 3 |
| BP | GO:0001763 | morphogenesis of a branching structure | 11/334 | 203/18614 | 0.001138605 | 0.121990206 | 0.113508966 | CSMD1/FGF8/GCM1/GDNF/GLI2/HHIP/HOXA11/NOG/PAX8/TBX2/WNT9B | 11 |
| BP | GO:0060675 | ureteric bud morphogenesis | 6/334 | 66/18614 | 0.001172983 | 0.121990206 | 0.113508966 | FGF8/GDNF/HOXA11/NOG/PAX8/WNT9B | 6 |
| BP | GO:0072171 | mesonephric tubule morphogenesis | 6/334 | 67/18614 | 0.001269247 | 0.127601625 | 0.118730257 | FGF8/GDNF/HOXA11/NOG/PAX8/WNT9B | 6 |
| BP | GO:0048568 | embryonic organ development | 18/334 | 453/18614 | 0.001465327 | 0.142562142 | 0.13265066 | COL18A1/EGFR/FGF8/GCM1/GDNF/GLI2/HOXA11/HOXD3/KITLG/LRIG3/MYF5/NES/NOG/OTX1/PAX8/POU3F4/TBX2/WNT9B | 18 |
| BP | GO:0007611 | learning or memory | 13/334 | 276/18614 | 0.001514511 | 0.142742615 | 0.132818585 | CRH/CSMD1/EGFR/GRIN1/KCNK4/LRRN4/NEUROD2/NOG/NRXN2/OPRL1/SHANK1/SHANK2/TTBK1 | 13 |
| BP | GO:0032309 | icosanoid secretion | 5/334 | 48/18614 | 0.001642307 | 0.1442966 | 0.134264532 | AVPR1B/OC90/PLA2G5/PLA2R1/SSTR4 | 5 |
| BP | GO:0001654 | eye development | 16/334 | 385/18614 | 0.001686785 | 0.1442966 | 0.134264532 | BIRC7/CRYAA/CRYBB3/CRYGA/CYP1A1/DLX1/EGFR/GRM6/MEGF11/MTNR1B/MYF5/NES/OPN4/PROM1/TBX2/WNT9B | 16 |
| BP | GO:0072080 | nephron tubule development | 7/334 | 96/18614 | 0.001712093 | 0.1442966 | 0.134264532 | FGF8/GDNF/HOXA11/NOG/PAX8/PROM1/WNT9B | 7 |
| BP | GO:0007612 | learning | 9/334 | 152/18614 | 0.001722373 | 0.1442966 | 0.134264532 | CSMD1/GRIN1/LRRN4/NEUROD2/NOG/NRXN2/OPRL1/SHANK1/SHANK2 | 9 |
| BP | GO:0099188 | postsynaptic cytoskeleton organization | 3/334 | 14/18614 | 0.001799323 | 0.146051983 | 0.135897873 | ACTBL2/CPNE6/SRCIN1 | 3 |
| BP | GO:0150063 | visual system development | 16/334 | 389/18614 | 0.001872706 | 0.146051983 | 0.135897873 | BIRC7/CRYAA/CRYBB3/CRYGA/CYP1A1/DLX1/EGFR/GRM6/MEGF11/MTNR1B/MYF5/NES/OPN4/PROM1/TBX2/WNT9B | 16 |
| BP | GO:0099173 | postsynapse organization | 10/334 | 185/18614 | 0.001922727 | 0.146051983 | 0.135897873 | ACTBL2/CPNE6/GDNF/NRXN2/PTPRS/SHANK1/SHANK2/SHISA6/SPTBN2/SRCIN1 | 10 |
| BP | GO:0071805 | potassium ion transmembrane transport | 11/334 | 217/18614 | 0.001937029 | 0.146051983 | 0.135897873 | KCND2/KCNJ11/KCNJ16/KCNK1/KCNK18/KCNK4/KCNK9/KCNN1/MTNR1B/NALCN/TRPM5 | 11 |
| BP | GO:0061326 | renal tubule development | 7/334 | 100/18614 | 0.00216403 | 0.150907775 | 0.140416072 | FGF8/GDNF/HOXA11/NOG/PAX8/PROM1/WNT9B | 7 |
| BP | GO:0048880 | sensory system development | 16/334 | 395/18614 | 0.00218359 | 0.150907775 | 0.140416072 | BIRC7/CRYAA/CRYBB3/CRYGA/CYP1A1/DLX1/EGFR/GRM6/MEGF11/MTNR1B/MYF5/NES/OPN4/PROM1/TBX2/WNT9B | 16 |
| BP | GO:0072283 | metanephric renal vesicle morphogenesis | 3/334 | 15/18614 | 0.002219441 | 0.150907775 | 0.140416072 | GDNF/PAX8/WNT9B | 3 |
| BP | GO:0072078 | nephron tubule morphogenesis | 6/334 | 75/18614 | 0.002272815 | 0.150907775 | 0.140416072 | FGF8/GDNF/HOXA11/NOG/PAX8/WNT9B | 6 |
| BP | GO:0048706 | embryonic skeletal system development | 8/334 | 129/18614 | 0.002301644 | 0.150907775 | 0.140416072 | DLX1/FGF8/HOXA11/HOXC6/HOXD3/MYF5/NOG/WNT9B | 8 |
| BP | GO:0051928 | positive regulation of calcium ion transport | 8/334 | 129/18614 | 0.002301644 | 0.150907775 | 0.140416072 | ADCYAP1R1/GRIN1/GRM6/HCRT/STAC2/STC1/TRDN/WNK3 | 8 |
| BP | GO:0021536 | diencephalon development | 6/334 | 77/18614 | 0.002597613 | 0.163216673 | 0.151869206 | FGF8/GLI2/NOG/OTP/OTX1/PITX1 | 6 |
| BP | GO:0072088 | nephron epithelium morphogenesis | 6/334 | 77/18614 | 0.002597613 | 0.163216673 | 0.151869206 | FGF8/GDNF/HOXA11/NOG/PAX8/WNT9B | 6 |
| BP | GO:0015671 | oxygen transport | 3/334 | 16/18614 | 0.002695565 | 0.165914779 | 0.154379729 | HBQ1/MB/NGB | 3 |
| BP | GO:0061333 | renal tubule morphogenesis | 6/334 | 79/18614 | 0.002956054 | 0.178309173 | 0.165912416 | FGF8/GDNF/HOXA11/NOG/PAX8/WNT9B | 6 |
| BP | GO:0007193 | adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway | 6/334 | 80/18614 | 0.003148545 | 0.182131273 | 0.169468789 | ADCY2/CHRM5/FFAR3/GRM6/HRH3/OPRL1 | 6 |
| BP | GO:0072028 | nephron morphogenesis | 6/334 | 80/18614 | 0.003148545 | 0.182131273 | 0.169468789 | FGF8/GDNF/HOXA11/NOG/PAX8/WNT9B | 6 |
| BP | GO:0009404 | toxin metabolic process | 3/334 | 17/18614 | 0.003230023 | 0.182131273 | 0.169468789 | CYP1A1/FMO1/FMO2 | 3 |
| BP | GO:0007187 | G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger | 5/334 | 56/18614 | 0.003260971 | 0.182131273 | 0.169468789 | ADRB3/CHRM5/HRH3/MTNR1B/SSTR4 | 5 |
| BP | GO:0035270 | endocrine system development | 8/334 | 137/18614 | 0.003338508 | 0.183071614 | 0.170343754 | CRH/FGF8/GLI2/HOXD3/NOG/OTP/PAX8/PITX1 | 8 |
| BP | GO:0007218 | neuropeptide signaling pathway | 7/334 | 109/18614 | 0.003515179 | 0.183195105 | 0.170458659 | BRS3/HCRT/OPRL1/PCSK1N/PROKR2/SCG5/SSTR4 | 7 |
| BP | GO:0007631 | feeding behavior | 7/334 | 109/18614 | 0.003515179 | 0.183195105 | 0.170458659 | ADRB3/BRS3/HCRT/HELT/IAPP/INSL5/OPRL1 | 7 |
| BP | GO:0050433 | regulation of catecholamine secretion | 5/334 | 57/18614 | 0.003522983 | 0.183195105 | 0.170458659 | CRH/FFAR3/GDNF/HRH3/SYT3 | 5 |
| BP | GO:0007189 | adenylate cyclase-activating G protein-coupled receptor signaling pathway | 8/334 | 140/18614 | 0.003809272 | 0.186065802 | 0.173129774 | ADCY2/ADRB3/GPHB5/IAPP/OPRL1/PTGER1/PTGER3/SSTR4 | 8 |
| BP | GO:0001696 | gastric acid secretion | 3/334 | 18/18614 | 0.00382496 | 0.186065802 | 0.173129774 | CHRM5/OPRL1/PTGER3 | 3 |
| BP | GO:0072077 | renal vesicle morphogenesis | 3/334 | 18/18614 | 0.00382496 | 0.186065802 | 0.173129774 | GDNF/PAX8/WNT9B | 3 |
| BP | GO:0090190 | positive regulation of branching involved in ureteric bud morphogenesis | 3/334 | 18/18614 | 0.00382496 | 0.186065802 | 0.173129774 | GDNF/NOG/PAX8 | 3 |
| BP | GO:1902075 | cellular response to salt | 10/334 | 204/18614 | 0.003889958 | 0.186224023 | 0.173276995 | CHRM5/CPNE6/DPEP1/ECT2/GCLM/HRH3/LY6H/NEUROD2/RASAL1/SYT3 | 10 |
| BP | GO:0050432 | catecholamine secretion | 5/334 | 59/18614 | 0.004091795 | 0.192663841 | 0.179269091 | CRH/FFAR3/GDNF/HRH3/SYT3 | 5 |
| BP | GO:0003002 | regionalization | 16/334 | 422/18614 | 0.004165211 | 0.192663841 | 0.179269091 | DLX1/FGF8/GDNF/GLI2/HELT/HHIP/HOXA11/HOXC6/HOXD3/MEOX1/MYF5/NOG/OTX1/PAX8/RFX4/TBX2 | 16 |
| BP | GO:0010092 | specification of animal organ identity | 4/334 | 37/18614 | 0.004216119 | 0.192663841 | 0.179269091 | FGF8/GDNF/HOXA11/PAX8 | 4 |
| BP | GO:0072087 | renal vesicle development | 3/334 | 19/18614 | 0.004482352 | 0.201772723 | 0.187744688 | GDNF/PAX8/WNT9B | 3 |
| BP | GO:0097106 | postsynaptic density organization | 4/334 | 38/18614 | 0.004646582 | 0.203155079 | 0.189030937 | NRXN2/PTPRS/SHANK1/SHANK2 | 4 |
| BP | GO:0022037 | metencephalon development | 7/334 | 115/18614 | 0.004721017 | 0.203155079 | 0.189030937 | CNTN1/FAIM2/GLI2/NEUROD2/OTX1/PTPRS/SPTBN2 | 7 |
| BP | GO:0010469 | regulation of signaling receptor activity | 9/334 | 177/18614 | 0.004768019 | 0.203155079 | 0.189030937 | CACNG8/CRH/LY6H/NOG/NRXN2/SHANK1/SHISA6/TGFA/WFIKKN1 | 9 |
| BP | GO:0007389 | pattern specification process | 17/334 | 467/18614 | 0.004782497 | 0.203155079 | 0.189030937 | DLX1/FGF8/GDNF/GLI2/HELT/HHIP/HOXA11/HOXC6/HOXD3/MEOX1/MYF5/NOG/OTX1/PAX8/RFX4/STC1/TBX2 | 17 |
| BP | GO:0072009 | nephron epithelium development | 7/334 | 116/18614 | 0.004948972 | 0.20383478 | 0.189663383 | FGF8/GDNF/HOXA11/NOG/PAX8/PROM1/WNT9B | 7 |
| BP | GO:0071277 | cellular response to calcium ion | 6/334 | 88/18614 | 0.005042069 | 0.20383478 | 0.189663383 | CPNE6/DPEP1/ECT2/NEUROD2/RASAL1/SYT3 | 6 |
| BP | GO:0007204 | positive regulation of cytosolic calcium ion concentration | 9/334 | 179/18614 | 0.005127099 | 0.20383478 | 0.189663383 | ADCYAP1R1/AVPR1B/GRIN1/HCRT/IAPP/KISS1/OPRL1/PTGER1/PTGER3 | 9 |
| BP | GO:0042693 | muscle cell fate commitment | 3/334 | 20/18614 | 0.005204005 | 0.20383478 | 0.189663383 | MYF5/MYL2/TBX2 | 3 |
| BP | GO:0060231 | mesenchymal to epithelial transition | 3/334 | 20/18614 | 0.005204005 | 0.20383478 | 0.189663383 | GDNF/PAX8/WNT9B | 3 |
| BP | GO:0071371 | cellular response to gonadotropin stimulus | 3/334 | 20/18614 | 0.005204005 | 0.20383478 | 0.189663383 | EPHA8/GCLM/PAX8 | 3 |
| BP | GO:0099601 | regulation of neurotransmitter receptor activity | 5/334 | 63/18614 | 0.005421201 | 0.209619789 | 0.195046195 | CACNG8/CRH/NRXN2/SHANK1/SHISA6 | 5 |
| BP | GO:0042755 | eating behavior | 4/334 | 40/18614 | 0.005594117 | 0.213567796 | 0.19871972 | ADRB3/HCRT/IAPP/OPRL1 | 4 |
| BP | GO:0032305 | positive regulation of icosanoid secretion | 3/334 | 21/18614 | 0.005991568 | 0.220622725 | 0.205284163 | AVPR1B/PLA2R1/SSTR4 | 3 |
| BP | GO:0090189 | regulation of branching involved in ureteric bud morphogenesis | 3/334 | 21/18614 | 0.005991568 | 0.220622725 | 0.205284163 | GDNF/NOG/PAX8 | 3 |
| BP | GO:0034765 | regulation of monoatomic ion transmembrane transport | 17/334 | 478/18614 | 0.005998363 | 0.220622725 | 0.205284163 | ADCYAP1R1/BPIFA1/FXYD1/GRIN1/GRM6/HRC/KCND2/KCNJ11/KCNJ16/KCNK4/MTNR1B/NALCN/OPRL1/STAC2/TRDN/TRPM5/WNK3 | 17 |
| BP | GO:0006814 | sodium ion transport | 11/334 | 254/18614 | 0.00636514 | 0.229435011 | 0.213483784 | BPIFA1/CNTN1/FXYD1/KCNK1/NALCN/SLC38A8/SLC5A1/SLC6A11/SPTBN4/TRPM5/WNK3 | 11 |
| BP | GO:0048638 | regulation of developmental growth | 13/334 | 328/18614 | 0.006562655 | 0.229435011 | 0.213483784 | ADRB3/BMP10/CPNE6/FGF8/GHR/NOG/PTPRS/RASAL1/SEMA4G/SEMA5B/SPTBN4/SYT3/TBX2 | 13 |
| BP | GO:0010517 | regulation of phospholipase activity | 5/334 | 66/18614 | 0.006600059 | 0.229435011 | 0.213483784 | ADCYAP1R1/AVPR1B/EGFR/PLA2G5/PLA2R1 | 5 |
| BP | GO:0043583 | ear development | 10/334 | 221/18614 | 0.006766212 | 0.229435011 | 0.213483784 | CYTL1/FGF8/LRIG3/NOG/OC90/OTX1/PAX8/PCDH15/POU3F4/TBX2 | 10 |
| BP | GO:0042471 | ear morphogenesis | 7/334 | 123/18614 | 0.006783909 | 0.229435011 | 0.213483784 | FGF8/LRIG3/NOG/OTX1/PAX8/POU3F4/TBX2 | 7 |
| BP | GO:0015669 | gas transport | 3/334 | 22/18614 | 0.006846535 | 0.229435011 | 0.213483784 | HBQ1/MB/NGB | 3 |
| BP | GO:0015874 | norepinephrine transport | 3/334 | 22/18614 | 0.006846535 | 0.229435011 | 0.213483784 | FFAR3/HRH3/SLC29A4 | 3 |
| BP | GO:0032303 | regulation of icosanoid secretion | 3/334 | 22/18614 | 0.006846535 | 0.229435011 | 0.213483784 | AVPR1B/PLA2R1/SSTR4 | 3 |
| BP | GO:0050804 | modulation of chemical synaptic transmission | 17/334 | 487/18614 | 0.007170552 | 0.231324502 | 0.215241911 | CACNG8/GRIK5/GRIN1/GRM6/HCRT/KISS1/LRRTM1/NALCN/NEUROD2/NOG/NRXN2/PTPRS/SHANK1/SHANK2/SHISA6/SV2C/SYN3 | 17 |
| BP | GO:0090278 | negative regulation of peptide hormone secretion | 4/334 | 43/18614 | 0.007243999 | 0.231324502 | 0.215241911 | CRH/FAM3D/KCNJ11/MTNR1B | 4 |
| BP | GO:0009953 | dorsal/ventral pattern formation | 6/334 | 95/18614 | 0.007289776 | 0.231324502 | 0.215241911 | FGF8/GLI2/HHIP/HOXA11/NOG/RFX4 | 6 |
| BP | GO:0048704 | embryonic skeletal system morphogenesis | 6/334 | 95/18614 | 0.007289776 | 0.231324502 | 0.215241911 | FGF8/HOXA11/HOXD3/MYF5/NOG/WNT9B | 6 |
| BP | GO:0099177 | regulation of trans-synaptic signaling | 17/334 | 488/18614 | 0.007311488 | 0.231324502 | 0.215241911 | CACNG8/GRIK5/GRIN1/GRM6/HCRT/KISS1/LRRTM1/NALCN/NEUROD2/NOG/NRXN2/PTPRS/SHANK1/SHANK2/SHISA6/SV2C/SYN3 | 17 |
| BP | GO:0015909 | long-chain fatty acid transport | 5/334 | 68/18614 | 0.007479053 | 0.231324502 | 0.215241911 | AVPR1B/OC90/PLA2G5/PLA2R1/SSTR4 | 5 |
| BP | GO:0048645 | animal organ formation | 5/334 | 68/18614 | 0.007479053 | 0.231324502 | 0.215241911 | FGF8/GDNF/HOXA11/NOG/PAX8 | 5 |
| BP | GO:0030902 | hindbrain development | 8/334 | 157/18614 | 0.007516512 | 0.231324502 | 0.215241911 | CNTN1/FAIM2/GLI2/NEUROD2/NOG/OTX1/PTPRS/SPTBN2 | 8 |
| BP | GO:1903861 | positive regulation of dendrite extension | 3/334 | 23/18614 | 0.007770257 | 0.234650052 | 0.218336255 | CPNE6/RASAL1/SYT3 | 3 |
| BP | GO:0002792 | negative regulation of peptide secretion | 4/334 | 44/18614 | 0.007857976 | 0.234650052 | 0.218336255 | CRH/FAM3D/KCNJ11/MTNR1B | 4 |
| BP | GO:0048512 | circadian behavior | 4/334 | 44/18614 | 0.007857976 | 0.234650052 | 0.218336255 | CRH/KCND2/MTNR1B/OPRL1 | 4 |
| BP | GO:0001657 | ureteric bud development | 6/334 | 97/18614 | 0.00804695 | 0.235627196 | 0.219245464 | FGF8/GDNF/HOXA11/NOG/PAX8/WNT9B | 6 |
| BP | GO:0060993 | kidney morphogenesis | 6/334 | 97/18614 | 0.00804695 | 0.235627196 | 0.219245464 | FGF8/GDNF/HOXA11/NOG/PAX8/WNT9B | 6 |
| BP | GO:0048839 | inner ear development | 9/334 | 193/18614 | 0.008261917 | 0.239595603 | 0.222937972 | CYTL1/FGF8/LRIG3/OC90/OTX1/PAX8/PCDH15/POU3F4/TBX2 | 9 |
| BP | GO:0072163 | mesonephric epithelium development | 6/334 | 98/18614 | 0.008446024 | 0.24029127 | 0.223585274 | FGF8/GDNF/HOXA11/NOG/PAX8/WNT9B | 6 |
| BP | GO:0072164 | mesonephric tubule development | 6/334 | 98/18614 | 0.008446024 | 0.24029127 | 0.223585274 | FGF8/GDNF/HOXA11/NOG/PAX8/WNT9B | 6 |
| BP | GO:0048705 | skeletal system morphogenesis | 10/334 | 229/18614 | 0.00859111 | 0.24029127 | 0.223585274 | FGF8/FREM1/GHR/HHIP/HOXA11/HOXD3/MYF5/NOG/STC1/WNT9B | 10 |
| BP | GO:0001759 | organ induction | 3/334 | 24/18614 | 0.008763939 | 0.24029127 | 0.223585274 | FGF8/GDNF/HOXA11 | 3 |
| BP | GO:0014821 | phasic smooth muscle contraction | 3/334 | 24/18614 | 0.008763939 | 0.24029127 | 0.223585274 | GDNF/PTGER3/TBX2 | 3 |
| BP | GO:0072202 | cell differentiation involved in metanephros development | 3/334 | 24/18614 | 0.008763939 | 0.24029127 | 0.223585274 | GDNF/PAX8/WNT9B | 3 |
| BP | GO:0043270 | positive regulation of monoatomic ion transport | 10/334 | 231/18614 | 0.009101438 | 0.247296727 | 0.230103684 | ADCYAP1R1/CNTN1/FXYD1/GRIN1/GRM6/HCRT/STAC2/STC1/TRDN/WNK3 | 10 |
| BP | GO:0007622 | rhythmic behavior | 4/334 | 46/18614 | 0.009186266 | 0.247373032 | 0.230174684 | CRH/KCND2/MTNR1B/OPRL1 | 4 |
| BP | GO:0010959 | regulation of metal ion transport | 15/334 | 423/18614 | 0.009784178 | 0.25554502 | 0.237778523 | ADCYAP1R1/BPIFA1/CNTN1/FXYD1/GRIN1/GRM6/HCRT/HRC/MTNR1B/OPRL1/SPTBN4/STAC2/STC1/TRDN/WNK3 | 15 |
| BP | GO:0072273 | metanephric nephron morphogenesis | 3/334 | 25/18614 | 0.009828655 | 0.25554502 | 0.237778523 | GDNF/PAX8/WNT9B | 3 |
| BP | GO:2000193 | positive regulation of fatty acid transport | 3/334 | 25/18614 | 0.009828655 | 0.25554502 | 0.237778523 | AVPR1B/PLA2R1/SSTR4 | 3 |
| BP | GO:2000311 | regulation of AMPA receptor activity | 3/334 | 25/18614 | 0.009828655 | 0.25554502 | 0.237778523 | CACNG8/SHANK1/SHISA6 | 3 |
| BP | GO:0048639 | positive regulation of developmental growth | 8/334 | 165/18614 | 0.009992766 | 0.255982023 | 0.238185143 | BMP10/CPNE6/FGF8/GHR/RASAL1/SPTBN4/SYT3/TBX2 | 8 |
| BP | GO:0001823 | mesonephros development | 6/334 | 102/18614 | 0.010184961 | 0.255982023 | 0.238185143 | FGF8/GDNF/HOXA11/NOG/PAX8/WNT9B | 6 |
| BP | GO:0021510 | spinal cord development | 6/334 | 102/18614 | 0.010184961 | 0.255982023 | 0.238185143 | ACTL6B/GDNF/GLI2/NOG/PTPRS/RFX4 | 6 |
| BP | GO:0042472 | inner ear morphogenesis | 6/334 | 102/18614 | 0.010184961 | 0.255982023 | 0.238185143 | FGF8/LRIG3/OTX1/PAX8/POU3F4/TBX2 | 6 |
| BP | GO:0007626 | locomotory behavior | 9/334 | 201/18614 | 0.010610994 | 0.263351395 | 0.245042168 | CNTN1/CRH/GDNF/GRM6/KCND2/LRRTM1/OPRL1/SHANK2/SPTBN4 | 9 |
| BP | GO:0035850 | epithelial cell differentiation involved in kidney development | 4/334 | 48/18614 | 0.010652808 | 0.263351395 | 0.245042168 | GDNF/PAX8/PROM1/WNT9B | 4 |
| BP | GO:0006836 | neurotransmitter transport | 9/334 | 202/18614 | 0.01093661 | 0.264571896 | 0.246177815 | GDNF/GRIK5/HCRT/HRH3/NRXN2/SLC29A4/SLC6A11/SV2C/SYN3 | 9 |
| BP | GO:0031639 | plasminogen activation | 3/334 | 26/18614 | 0.010965347 | 0.264571896 | 0.246177815 | CLEC3B/F11/KLKB1 | 3 |
| BP | GO:1903859 | regulation of dendrite extension | 3/334 | 26/18614 | 0.010965347 | 0.264571896 | 0.246177815 | CPNE6/RASAL1/SYT3 | 3 |
| BP | GO:0051216 | cartilage development | 9/334 | 203/18614 | 0.011269668 | 0.269756503 | 0.251001968 | BMP10/CYTL1/GHR/HOXA11/HOXD3/MYF5/NOG/PITX1/STC1 | 9 |
| BP | GO:0021549 | cerebellum development | 6/334 | 105/18614 | 0.011646078 | 0.276571431 | 0.257343094 | CNTN1/FAIM2/GLI2/NEUROD2/PTPRS/SPTBN2 | 6 |
| BP | GO:0032412 | regulation of monoatomic ion transmembrane transporter activity | 11/334 | 278/18614 | 0.012045095 | 0.28381254 | 0.264080774 | CACNG8/CRH/FXYD1/HRC/MTNR1B/OPRL1/SHANK1/SHISA6/STAC2/TRDN/WNK3 | 11 |
| BP | GO:0048520 | positive regulation of behavior | 3/334 | 27/18614 | 0.012174836 | 0.284645778 | 0.264856082 | CRH/INSL5/MTNR1B | 3 |
| BP | GO:0015872 | dopamine transport | 4/334 | 51/18614 | 0.013122695 | 0.28583656 | 0.265964075 | CHRM5/GDNF/SLC29A4/SYT3 | 4 |
| BP | GO:0048241 | epinephrine transport | 2/334 | 10/18614 | 0.013134029 | 0.28583656 | 0.265964075 | CRH/SLC29A4 | 2 |
| BP | GO:0048840 | otolith development | 2/334 | 10/18614 | 0.013134029 | 0.28583656 | 0.265964075 | LRIG3/OC90 | 2 |
| BP | GO:0060075 | regulation of resting membrane potential | 2/334 | 10/18614 | 0.013134029 | 0.28583656 | 0.265964075 | KCNK1/NALCN | 2 |
| BP | GO:0098953 | receptor diffusion trapping | 2/334 | 10/18614 | 0.013134029 | 0.28583656 | 0.265964075 | CACNG8/SHISA6 | 2 |
| BP | GO:0098970 | postsynaptic neurotransmitter receptor diffusion trapping | 2/334 | 10/18614 | 0.013134029 | 0.28583656 | 0.265964075 | CACNG8/SHISA6 | 2 |
| BP | GO:0098976 | excitatory chemical synaptic transmission | 2/334 | 10/18614 | 0.013134029 | 0.28583656 | 0.265964075 | GRIN1/SHISA6 | 2 |
| BP | GO:0099628 | neurotransmitter receptor diffusion trapping | 2/334 | 10/18614 | 0.013134029 | 0.28583656 | 0.265964075 | CACNG8/SHISA6 | 2 |
| BP | GO:2001054 | negative regulation of mesenchymal cell apoptotic process | 2/334 | 10/18614 | 0.013134029 | 0.28583656 | 0.265964075 | PAX8/POU3F4 | 2 |
| BP | GO:0043271 | negative regulation of monoatomic ion transport | 7/334 | 140/18614 | 0.013289902 | 0.28583656 | 0.265964075 | BEST3/HCRT/HRH3/MTNR1B/OPRL1/STC1/TRDN | 7 |
| BP | GO:0009952 | anterior/posterior pattern specification | 9/334 | 209/18614 | 0.013429942 | 0.28583656 | 0.265964075 | FGF8/HELT/HOXA11/HOXC6/HOXD3/MEOX1/MYF5/NOG/OTX1 | 9 |
| BP | GO:0003272 | endocardial cushion formation | 3/334 | 28/18614 | 0.013457822 | 0.28583656 | 0.265964075 | FGF8/NOG/TBX2 | 3 |
| BP | GO:0098698 | postsynaptic specialization assembly | 3/334 | 28/18614 | 0.013457822 | 0.28583656 | 0.265964075 | NRXN2/PTPRS/SPTBN2 | 3 |
| BP | GO:0048732 | gland development | 15/334 | 441/18614 | 0.013882617 | 0.291621926 | 0.27134722 | CRH/CSMD1/CYP1A1/EGFR/FGF8/GLI2/HOXA11/HOXD3/NOG/OTC/OTP/PAX8/PITX1/TBX2/TGFA | 15 |
| BP | GO:0021695 | cerebellar cortex development | 4/334 | 52/18614 | 0.014020285 | 0.291621926 | 0.27134722 | FAIM2/GLI2/NEUROD2/SPTBN2 | 4 |
| BP | GO:0060425 | lung morphogenesis | 4/334 | 52/18614 | 0.014020285 | 0.291621926 | 0.27134722 | FGF8/HHIP/NOG/TBX2 | 4 |
| BP | GO:0023061 | signal release | 16/334 | 483/18614 | 0.014169955 | 0.291631135 | 0.271355789 | CRH/FAM3D/FFAR3/GDNF/GRIK5/HCRT/HRH3/KCNJ11/KISS1/MTNR1B/NRXN2/PAX8/SCG5/SV2C/SYN3/SYT3 | 16 |
| BP | GO:0001505 | regulation of neurotransmitter levels | 9/334 | 211/18614 | 0.014214117 | 0.291631135 | 0.271355789 | GDNF/GRIK5/HCRT/HRH3/NRXN2/SLC29A4/SLC6A11/SV2C/SYN3 | 9 |
| BP | GO:0030534 | adult behavior | 7/334 | 143/18614 | 0.014787423 | 0.293958667 | 0.273521501 | BRS3/GDNF/NRXN2/SHANK1/SHANK2/SPTBN2/SPTBN4 | 7 |
| BP | GO:0003156 | regulation of animal organ formation | 3/334 | 29/18614 | 0.014814893 | 0.293958667 | 0.273521501 | FGF8/GDNF/HOXA11 | 3 |
| BP | GO:0030431 | sleep | 3/334 | 29/18614 | 0.014814893 | 0.293958667 | 0.273521501 | CRH/HCRT/MTNR1B | 3 |
| BP | GO:0030878 | thyroid gland development | 3/334 | 29/18614 | 0.014814893 | 0.293958667 | 0.273521501 | FGF8/HOXD3/PAX8 | 3 |
| BP | GO:0035640 | exploration behavior | 3/334 | 29/18614 | 0.014814893 | 0.293958667 | 0.273521501 | CRH/LRRTM1/NOG | 3 |
| BP | GO:0022898 | regulation of transmembrane transporter activity | 11/334 | 289/18614 | 0.015675373 | 0.298912147 | 0.278130596 | CACNG8/CRH/FXYD1/HRC/MTNR1B/OPRL1/SHANK1/SHISA6/STAC2/TRDN/WNK3 | 11 |
| BP | GO:0032429 | regulation of phospholipase A2 activity | 2/334 | 11/18614 | 0.015864061 | 0.298912147 | 0.278130596 | AVPR1B/PLA2R1 | 2 |
| BP | GO:0060272 | embryonic skeletal joint morphogenesis | 2/334 | 11/18614 | 0.015864061 | 0.298912147 | 0.278130596 | HOXA11/NOG | 2 |
| BP | GO:0060453 | regulation of gastric acid secretion | 2/334 | 11/18614 | 0.015864061 | 0.298912147 | 0.278130596 | OPRL1/PTGER3 | 2 |
| BP | GO:0072173 | metanephric tubule morphogenesis | 2/334 | 11/18614 | 0.015864061 | 0.298912147 | 0.278130596 | PAX8/WNT9B | 2 |
| BP | GO:1901844 | regulation of cell communication by electrical coupling involved in cardiac conduction | 2/334 | 11/18614 | 0.015864061 | 0.298912147 | 0.278130596 | HRC/TRDN | 2 |
| BP | GO:1903027 | regulation of opsonization | 2/334 | 11/18614 | 0.015864061 | 0.298912147 | 0.278130596 | FCN3/PLA2G5 | 2 |
| BP | GO:0007632 | visual behavior | 4/334 | 54/18614 | 0.01593001 | 0.298912147 | 0.278130596 | GRIN1/LRRN4/NOG/OPN4 | 4 |
| BP | GO:0051048 | negative regulation of secretion | 8/334 | 180/18614 | 0.016198477 | 0.298912147 | 0.278130596 | CRH/FAM3D/HRH3/KCNJ11/MTNR1B/PLA2R1/PTGER3/SRCIN1 | 8 |
| BP | GO:0007202 | activation of phospholipase C activity | 3/334 | 30/18614 | 0.016246528 | 0.298912147 | 0.278130596 | ADCYAP1R1/AVPR1B/EGFR | 3 |
| BP | GO:0034698 | response to gonadotropin | 3/334 | 30/18614 | 0.016246528 | 0.298912147 | 0.278130596 | EPHA8/GCLM/PAX8 | 3 |
| BP | GO:0044344 | cellular response to fibroblast growth factor stimulus | 6/334 | 113/18614 | 0.016253844 | 0.298912147 | 0.278130596 | FGF8/GCLM/HHIP/NOG/SMOC2/TBX2 | 6 |
| BP | GO:0072073 | kidney epithelium development | 7/334 | 146/18614 | 0.016401574 | 0.299800891 | 0.278957551 | FGF8/GDNF/HOXA11/NOG/PAX8/PROM1/WNT9B | 7 |
| BP | GO:0035725 | sodium ion transmembrane transport | 8/334 | 181/18614 | 0.016692889 | 0.301471579 | 0.280512086 | BPIFA1/FXYD1/KCNK1/NALCN/SLC5A1/SLC6A11/TRPM5/WNK3 | 8 |
| BP | GO:0050731 | positive regulation of peptidyl-tyrosine phosphorylation | 8/334 | 181/18614 | 0.016692889 | 0.301471579 | 0.280512086 | ANGPT4/CNTN1/FGF8/GHR/IL20/KITLG/SRCIN1/TGFA | 8 |
| BP | GO:0010518 | positive regulation of phospholipase activity | 4/334 | 55/18614 | 0.016943086 | 0.302368924 | 0.281347045 | ADCYAP1R1/AVPR1B/EGFR/PLA2G5 | 4 |
| BP | GO:0051703 | biological process involved in intraspecies interaction between organisms | 4/334 | 55/18614 | 0.016943086 | 0.302368924 | 0.281347045 | BPIFA1/NRXN2/SHANK1/SHANK2 | 4 |
| BP | GO:0060078 | regulation of postsynaptic membrane potential | 7/334 | 148/18614 | 0.017544639 | 0.309499167 | 0.287981565 | GABRD/GABRR3/GRIK5/GRIN1/HCRT/KCND2/SHANK1 | 7 |
| BP | GO:0048562 | embryonic organ morphogenesis | 11/334 | 294/18614 | 0.017573766 | 0.309499167 | 0.287981565 | FGF8/HOXA11/HOXD3/LRIG3/MYF5/NOG/OTX1/PAX8/POU3F4/TBX2/WNT9B | 11 |
| BP | GO:0043523 | regulation of neuron apoptotic process | 9/334 | 219/18614 | 0.017692288 | 0.309499167 | 0.287981565 | DLX1/FAIM2/FGF8/GCLM/GDNF/GRIK5/MTNR1B/NES/NUPR1 | 9 |
| BP | GO:0095500 | acetylcholine receptor signaling pathway | 3/334 | 31/18614 | 0.017753102 | 0.309499167 | 0.287981565 | CHRM5/HRH3/LY6H | 3 |
| BP | GO:0015908 | fatty acid transport | 6/334 | 116/18614 | 0.018266383 | 0.315230673 | 0.293314593 | AVPR1B/OC90/PLA2G5/PLA2R1/SLC22A8/SSTR4 | 6 |
| BP | GO:0019935 | cyclic-nucleotide-mediated signaling | 5/334 | 85/18614 | 0.018429239 | 0.315230673 | 0.293314593 | ADCY2/ADCYAP1R1/MTNR1B/OPRL1/RUNDC3A | 5 |
| BP | GO:0031644 | regulation of nervous system process | 7/334 | 150/18614 | 0.018742752 | 0.315230673 | 0.293314593 | GRIN1/HCRT/MTNR1B/NRXN2/OPRL1/SHANK1/SHISA6 | 7 |
| BP | GO:0030432 | peristalsis | 2/334 | 12/18614 | 0.018813502 | 0.315230673 | 0.293314593 | GDNF/TBX2 | 2 |
| BP | GO:0071372 | cellular response to follicle-stimulating hormone stimulus | 2/334 | 12/18614 | 0.018813502 | 0.315230673 | 0.293314593 | EPHA8/GCLM | 2 |
| BP | GO:0072182 | regulation of nephron tubule epithelial cell differentiation | 2/334 | 12/18614 | 0.018813502 | 0.315230673 | 0.293314593 | PAX8/PROM1 | 2 |
| BP | GO:0106072 | negative regulation of adenylate cyclase-activating G protein-coupled receptor signaling pathway | 2/334 | 12/18614 | 0.018813502 | 0.315230673 | 0.293314593 | OPRL1/SSTR4 | 2 |
| BP | GO:0051402 | neuron apoptotic process | 10/334 | 259/18614 | 0.018942641 | 0.315640914 | 0.293696313 | DLX1/FAIM2/FGF8/GCLM/GDNF/GRIK5/MTNR1B/NES/NUPR1/SDIM1 | 10 |
| BP | GO:0008543 | fibroblast growth factor receptor signaling pathway | 5/334 | 86/18614 | 0.019288698 | 0.316924103 | 0.29489029 | FGF8/HHIP/NOG/SMOC2/TBX2 | 5 |
| BP | GO:0003338 | metanephros morphogenesis | 3/334 | 32/18614 | 0.019334892 | 0.316924103 | 0.29489029 | GDNF/PAX8/WNT9B | 3 |
| BP | GO:0010765 | positive regulation of sodium ion transport | 3/334 | 32/18614 | 0.019334892 | 0.316924103 | 0.29489029 | CNTN1/FXYD1/WNK3 | 3 |
| BP | GO:1903522 | regulation of blood circulation | 10/334 | 261/18614 | 0.019863597 | 0.317304957 | 0.295244665 | AVPR1B/BMP10/FXYD1/HRC/MTNR1B/MYL2/SPTBN4/STC1/TBX2/TRDN | 10 |
| BP | GO:0072006 | nephron development | 7/334 | 152/18614 | 0.019997147 | 0.317304957 | 0.295244665 | FGF8/GDNF/HOXA11/NOG/PAX8/PROM1/WNT9B | 7 |
| BP | GO:1904064 | positive regulation of cation transmembrane transport | 7/334 | 152/18614 | 0.019997147 | 0.317304957 | 0.295244665 | ADCYAP1R1/FXYD1/GRIN1/GRM6/STAC2/TRDN/WNK3 | 7 |
| BP | GO:0050953 | sensory perception of light stimulus | 9/334 | 224/18614 | 0.020159275 | 0.317304957 | 0.295244665 | COL18A1/CRYAA/CRYBB3/CRYGA/GPR179/GRM6/OPN4/PCDH15/SEMA5B | 9 |
| BP | GO:0008589 | regulation of smoothened signaling pathway | 5/334 | 87/18614 | 0.020174076 | 0.317304957 | 0.295244665 | ACTRT1/GLI2/HHIP/RFX4/SCUBE1 | 5 |
| BP | GO:0001755 | neural crest cell migration | 4/334 | 58/18614 | 0.020220275 | 0.317304957 | 0.295244665 | GDNF/KITLG/SEMA4G/SEMA5B | 4 |
| BP | GO:0061005 | cell differentiation involved in kidney development | 4/334 | 58/18614 | 0.020220275 | 0.317304957 | 0.295244665 | GDNF/PAX8/PROM1/WNT9B | 4 |
| BP | GO:0000096 | sulfur amino acid metabolic process | 3/334 | 33/18614 | 0.02099208 | 0.317304957 | 0.295244665 | CTH/DPEP1/GCLM | 3 |
| BP | GO:0090183 | regulation of kidney development | 3/334 | 33/18614 | 0.02099208 | 0.317304957 | 0.295244665 | GDNF/NOG/PAX8 | 3 |
| BP | GO:1905145 | cellular response to acetylcholine | 3/334 | 33/18614 | 0.02099208 | 0.317304957 | 0.295244665 | CHRM5/HRH3/LY6H | 3 |
| BP | GO:2000191 | regulation of fatty acid transport | 3/334 | 33/18614 | 0.02099208 | 0.317304957 | 0.295244665 | AVPR1B/PLA2R1/SSTR4 | 3 |
| BP | GO:0030326 | embryonic limb morphogenesis | 6/334 | 120/18614 | 0.021206372 | 0.317304957 | 0.295244665 | FGF8/HOXA11/NOG/PITX1/SALL4/TBX2 | 6 |
| BP | GO:0035113 | embryonic appendage morphogenesis | 6/334 | 120/18614 | 0.021206372 | 0.317304957 | 0.295244665 | FGF8/HOXA11/NOG/PITX1/SALL4/TBX2 | 6 |
| BP | GO:0071774 | response to fibroblast growth factor | 6/334 | 120/18614 | 0.021206372 | 0.317304957 | 0.295244665 | FGF8/GCLM/HHIP/NOG/SMOC2/TBX2 | 6 |
| BP | GO:1902074 | response to salt | 13/334 | 383/18614 | 0.021458377 | 0.317304957 | 0.295244665 | CHRM5/CPNE6/CYP1A1/DPEP1/ECT2/GCLM/GHR/HRH3/KCNJ11/LY6H/NEUROD2/RASAL1/SYT3 | 13 |
| BP | GO:0050808 | synapse organization | 15/334 | 466/18614 | 0.021652002 | 0.317304957 | 0.295244665 | ACTBL2/CPNE6/GDNF/LGI2/LRRTM1/NEUROD2/NRXN2/PCDHB11/PTPRS/SHANK1/SHANK2/SHISA6/SPTBN2/SRCIN1/SRPX2 | 15 |
| BP | GO:0006534 | cysteine metabolic process | 2/334 | 13/18614 | 0.021973648 | 0.317304957 | 0.295244665 | CTH/GCLM | 2 |
| BP | GO:0007512 | adult heart development | 2/334 | 13/18614 | 0.021973648 | 0.317304957 | 0.295244665 | BMP10/SCUBE1 | 2 |
| BP | GO:0010524 | positive regulation of calcium ion transport into cytosol | 2/334 | 13/18614 | 0.021973648 | 0.317304957 | 0.295244665 | ADCYAP1R1/GRIN1 | 2 |
| BP | GO:0048853 | forebrain morphogenesis | 2/334 | 13/18614 | 0.021973648 | 0.317304957 | 0.295244665 | FGF8/OTX1 | 2 |
| BP | GO:2001053 | regulation of mesenchymal cell apoptotic process | 2/334 | 13/18614 | 0.021973648 | 0.317304957 | 0.295244665 | PAX8/POU3F4 | 2 |
| BP | GO:0008037 | cell recognition | 7/334 | 155/18614 | 0.021986882 | 0.317304957 | 0.295244665 | CRTAC1/FCN3/FETUB/FUT3/NTM/PLA2G5/ZAN | 7 |
| BP | GO:0043524 | negative regulation of neuron apoptotic process | 7/334 | 155/18614 | 0.021986882 | 0.317304957 | 0.295244665 | DLX1/FAIM2/FGF8/GCLM/GDNF/MTNR1B/NES | 7 |
| BP | GO:0060191 | regulation of lipase activity | 5/334 | 89/18614 | 0.022023659 | 0.317304957 | 0.295244665 | ADCYAP1R1/AVPR1B/EGFR/PLA2G5/PLA2R1 | 5 |
| BP | GO:0051924 | regulation of calcium ion transport | 10/334 | 266/18614 | 0.022308973 | 0.317304957 | 0.295244665 | ADCYAP1R1/GRIN1/GRM6/HCRT/HRC/OPRL1/STAC2/STC1/TRDN/WNK3 | 10 |
| BP | GO:0015695 | organic cation transport | 4/334 | 60/18614 | 0.022607095 | 0.317304957 | 0.295244665 | FFAR3/HRH3/SLC19A3/SLC29A4 | 4 |
| BP | GO:0090497 | mesenchymal cell migration | 4/334 | 60/18614 | 0.022607095 | 0.317304957 | 0.295244665 | GDNF/KITLG/SEMA4G/SEMA5B | 4 |
| BP | GO:1903078 | positive regulation of protein localization to plasma membrane | 4/334 | 60/18614 | 0.022607095 | 0.317304957 | 0.295244665 | EGFR/SORBS1/STAC2/WNK3 | 4 |
| BP | GO:0006536 | glutamate metabolic process | 3/334 | 34/18614 | 0.022724758 | 0.317304957 | 0.295244665 | ATCAY/GCLM/PRODH2 | 3 |
| BP | GO:0009954 | proximal/distal pattern formation | 3/334 | 34/18614 | 0.022724758 | 0.317304957 | 0.295244665 | DLX1/GLI2/HOXA11 | 3 |
| BP | GO:0060351 | cartilage development involved in endochondral bone morphogenesis | 3/334 | 34/18614 | 0.022724758 | 0.317304957 | 0.295244665 | GHR/HOXA11/STC1 | 3 |
| BP | GO:0110110 | positive regulation of animal organ morphogenesis | 3/334 | 34/18614 | 0.022724758 | 0.317304957 | 0.295244665 | FGF8/GDNF/HOXA11 | 3 |
| BP | GO:0022612 | gland morphogenesis | 6/334 | 123/18614 | 0.023610741 | 0.328156661 | 0.305341917 | CSMD1/EGFR/FGF8/NOG/TBX2/TGFA | 6 |
| BP | GO:0043903 | regulation of biological process involved in symbiotic interaction | 4/334 | 61/18614 | 0.023862095 | 0.330128801 | 0.307176945 | BPIFA1/CXCL6/FCN3/TRIM10 | 4 |
| BP | GO:0060079 | excitatory postsynaptic potential | 6/334 | 124/18614 | 0.024451166 | 0.330794296 | 0.307796172 | GABRD/GABRR3/GRIK5/GRIN1/HCRT/SHANK1 | 6 |
| BP | GO:0031128 | developmental induction | 3/334 | 35/18614 | 0.024532932 | 0.330794296 | 0.307796172 | FGF8/GDNF/HOXA11 | 3 |
| BP | GO:0045879 | negative regulation of smoothened signaling pathway | 3/334 | 35/18614 | 0.024532932 | 0.330794296 | 0.307796172 | GLI2/HHIP/RFX4 | 3 |
| BP | GO:0098810 | neurotransmitter reuptake | 3/334 | 35/18614 | 0.024532932 | 0.330794296 | 0.307796172 | GDNF/SLC29A4/SLC6A11 | 3 |
| BP | GO:0001656 | metanephros development | 5/334 | 92/18614 | 0.024998851 | 0.330794296 | 0.307796172 | FGF8/GDNF/HOXA11/PAX8/WNT9B | 5 |
| BP | GO:0002028 | regulation of sodium ion transport | 5/334 | 92/18614 | 0.024998851 | 0.330794296 | 0.307796172 | BPIFA1/CNTN1/FXYD1/SPTBN4/WNK3 | 5 |
| BP | GO:0010752 | regulation of cGMP-mediated signaling | 2/334 | 14/18614 | 0.025336035 | 0.330794296 | 0.307796172 | MTNR1B/RUNDC3A | 2 |
| BP | GO:0014061 | regulation of norepinephrine secretion | 2/334 | 14/18614 | 0.025336035 | 0.330794296 | 0.307796172 | FFAR3/HRH3 | 2 |
| BP | GO:0048243 | norepinephrine secretion | 2/334 | 14/18614 | 0.025336035 | 0.330794296 | 0.307796172 | FFAR3/HRH3 | 2 |
| BP | GO:0050667 | homocysteine metabolic process | 2/334 | 14/18614 | 0.025336035 | 0.330794296 | 0.307796172 | CTH/DPEP1 | 2 |
| BP | GO:0060732 | positive regulation of inositol phosphate biosynthetic process | 2/334 | 14/18614 | 0.025336035 | 0.330794296 | 0.307796172 | ADCYAP1R1/AVPR1B | 2 |
| BP | GO:0072160 | nephron tubule epithelial cell differentiation | 2/334 | 14/18614 | 0.025336035 | 0.330794296 | 0.307796172 | PAX8/PROM1 | 2 |
| BP | GO:0099150 | regulation of postsynaptic specialization assembly | 2/334 | 14/18614 | 0.025336035 | 0.330794296 | 0.307796172 | PTPRS/SPTBN2 | 2 |
| BP | GO:1904427 | positive regulation of calcium ion transmembrane transport | 5/334 | 93/18614 | 0.026045065 | 0.33616979 | 0.31279794 | ADCYAP1R1/GRIN1/GRM6/STAC2/TRDN | 5 |
| BP | GO:0007416 | synapse assembly | 8/334 | 197/18614 | 0.026151265 | 0.33616979 | 0.31279794 | LGI2/LRRTM1/NRXN2/PCDHB11/PTPRS/SHANK2/SPTBN2/SRPX2 | 8 |
| BP | GO:0021696 | cerebellar cortex morphogenesis | 3/334 | 36/18614 | 0.026416525 | 0.33616979 | 0.31279794 | FAIM2/GLI2/SPTBN2 | 3 |
| BP | GO:0097484 | dendrite extension | 3/334 | 36/18614 | 0.026416525 | 0.33616979 | 0.31279794 | CPNE6/RASAL1/SYT3 | 3 |
| BP | GO:1905144 | response to acetylcholine | 3/334 | 36/18614 | 0.026416525 | 0.33616979 | 0.31279794 | CHRM5/HRH3/LY6H | 3 |
| BP | GO:1905332 | positive regulation of morphogenesis of an epithelium | 3/334 | 36/18614 | 0.026416525 | 0.33616979 | 0.31279794 | GDNF/NOG/PAX8 | 3 |
| BP | GO:0010466 | negative regulation of peptidase activity | 9/334 | 236/18614 | 0.027078624 | 0.343147606 | 0.319290632 | BIRC7/DPEP1/FETUB/PCSK1N/SERPINA5/SERPINA7/SPINT4/WFDC2/WFIKKN1 | 9 |
| BP | GO:0061448 | connective tissue development | 10/334 | 275/18614 | 0.027250021 | 0.343874741 | 0.319967214 | BMP10/CYTL1/GHR/HOXA11/HOXD3/MYF5/NOG/PITX1/STC1/UMODL1 | 10 |
| BP | GO:0043648 | dicarboxylic acid metabolic process | 5/334 | 95/18614 | 0.028220497 | 0.345150152 | 0.321153953 | ATCAY/GCLM/HOGA1/ME1/PRODH2 | 5 |
| BP | GO:0071248 | cellular response to metal ion | 8/334 | 200/18614 | 0.0282703 | 0.345150152 | 0.321153953 | CPNE6/CYP1A1/DPEP1/ECT2/EGFR/NEUROD2/RASAL1/SYT3 | 8 |
| BP | GO:0001941 | postsynaptic membrane organization | 3/334 | 37/18614 | 0.028375385 | 0.345150152 | 0.321153953 | GDNF/NRXN2/SHISA6 | 3 |
| BP | GO:0031646 | positive regulation of nervous system process | 3/334 | 37/18614 | 0.028375385 | 0.345150152 | 0.321153953 | HCRT/MTNR1B/OPRL1 | 3 |
| BP | GO:0051051 | negative regulation of transport | 15/334 | 483/18614 | 0.028566885 | 0.345150152 | 0.321153953 | BEST3/CRH/CRYAA/FAM3D/HCRT/HRH3/KCNJ11/LRRTM1/MTNR1B/OPRL1/PLA2R1/PTGER3/SRCIN1/STC1/TRDN | 15 |
| BP | GO:0007567 | parturition | 2/334 | 15/18614 | 0.028892434 | 0.345150152 | 0.321153953 | CRH/CYP1A1 | 2 |
| BP | GO:0010649 | regulation of cell communication by electrical coupling | 2/334 | 15/18614 | 0.028892434 | 0.345150152 | 0.321153953 | HRC/TRDN | 2 |
| BP | GO:0045475 | locomotor rhythm | 2/334 | 15/18614 | 0.028892434 | 0.345150152 | 0.321153953 | KCND2/OPRL1 | 2 |
| BP | GO:0046322 | negative regulation of fatty acid oxidation | 2/334 | 15/18614 | 0.028892434 | 0.345150152 | 0.321153953 | FMO1/FMO2 | 2 |
| BP | GO:0071599 | otic vesicle development | 2/334 | 15/18614 | 0.028892434 | 0.345150152 | 0.321153953 | FGF8/PAX8 | 2 |
| BP | GO:0072498 | embryonic skeletal joint development | 2/334 | 15/18614 | 0.028892434 | 0.345150152 | 0.321153953 | HOXA11/NOG | 2 |
| BP | GO:0097152 | mesenchymal cell apoptotic process | 2/334 | 15/18614 | 0.028892434 | 0.345150152 | 0.321153953 | PAX8/POU3F4 | 2 |
| BP | GO:0106070 | regulation of adenylate cyclase-activating G protein-coupled receptor signaling pathway | 2/334 | 15/18614 | 0.028892434 | 0.345150152 | 0.321153953 | OPRL1/SSTR4 | 2 |
| BP | GO:2000027 | regulation of animal organ morphogenesis | 6/334 | 129/18614 | 0.028953246 | 0.345150152 | 0.321153953 | FGF8/GDNF/HOXA11/NOG/PAX8/WNT9B | 6 |
| BP | GO:0046888 | negative regulation of hormone secretion | 4/334 | 65/18614 | 0.029298842 | 0.346530616 | 0.322438441 | CRH/FAM3D/KCNJ11/MTNR1B | 4 |
| BP | GO:1905330 | regulation of morphogenesis of an epithelium | 4/334 | 65/18614 | 0.029298842 | 0.346530616 | 0.322438441 | GDNF/NOG/PAX8/TBX2 | 4 |
| BP | GO:0006790 | sulfur compound metabolic process | 11/334 | 319/18614 | 0.029719599 | 0.350134023 | 0.325791325 | ACOT12/B3GNT3/CTH/DPEP1/EXTL1/FMO1/GCLM/GHR/PAX8/SLC19A3/SULT4A1 | 11 |
| BP | GO:0034329 | cell junction assembly | 14/334 | 444/18614 | 0.030195679 | 0.352535574 | 0.328025911 | CDH19/CDH5/CLDN11/ECT2/FERMT2/LGI2/LRRTM1/NRXN2/PCDHB11/PTPRS/SHANK2/SORBS1/SPTBN2/SRPX2 | 14 |
| BP | GO:0040036 | regulation of fibroblast growth factor receptor signaling pathway | 3/334 | 38/18614 | 0.030409282 | 0.352535574 | 0.328025911 | HHIP/NOG/SMOC2 | 3 |
| BP | GO:0046676 | negative regulation of insulin secretion | 3/334 | 38/18614 | 0.030409282 | 0.352535574 | 0.328025911 | FAM3D/KCNJ11/MTNR1B | 3 |
| BP | GO:0003205 | cardiac chamber development | 7/334 | 166/18614 | 0.030450011 | 0.352535574 | 0.328025911 | BMP10/FGF8/MYL2/NOG/PAX8/SALL4/TBX2 | 7 |
| BP | GO:0006942 | regulation of striated muscle contraction | 5/334 | 97/18614 | 0.030507886 | 0.352535574 | 0.328025911 | BMP10/HRC/MYBPH/MYL2/STC1 | 5 |
| BP | GO:0045165 | cell fate commitment | 10/334 | 281/18614 | 0.030950369 | 0.356283635 | 0.331513392 | DLX1/FGF8/GCM1/GLI2/HOXA11/MYF5/MYL2/PITX1/TBX2/WNT9B | 10 |
| BP | GO:0051952 | regulation of amine transport | 5/334 | 98/18614 | 0.031694008 | 0.361614349 | 0.336473494 | CRH/FFAR3/GDNF/HRH3/SYT3 | 5 |
| BP | GO:0099565 | chemical synaptic transmission, postsynaptic | 6/334 | 132/18614 | 0.031900093 | 0.361614349 | 0.336473494 | GABRD/GABRR3/GRIK5/GRIN1/HCRT/SHANK1 | 6 |
| BP | GO:0060193 | positive regulation of lipase activity | 4/334 | 67/18614 | 0.032270157 | 0.361614349 | 0.336473494 | ADCYAP1R1/AVPR1B/EGFR/PLA2G5 | 4 |
| BP | GO:0032350 | regulation of hormone metabolic process | 3/334 | 39/18614 | 0.032517919 | 0.361614349 | 0.336473494 | DUOXA2/FFAR3/PAX8 | 3 |
| BP | GO:0098926 | postsynaptic signal transduction | 3/334 | 39/18614 | 0.032517919 | 0.361614349 | 0.336473494 | CHRM5/HRH3/LY6H | 3 |
| BP | GO:0000212 | meiotic spindle organization | 2/334 | 16/18614 | 0.032634844 | 0.361614349 | 0.336473494 | ESPL1/MOS | 2 |
| BP | GO:0010919 | regulation of inositol phosphate biosynthetic process | 2/334 | 16/18614 | 0.032634844 | 0.361614349 | 0.336473494 | ADCYAP1R1/AVPR1B | 2 |
| BP | GO:0045187 | regulation of circadian sleep/wake cycle, sleep | 2/334 | 16/18614 | 0.032634844 | 0.361614349 | 0.336473494 | CRH/MTNR1B | 2 |
| BP | GO:0061101 | neuroendocrine cell differentiation | 2/334 | 16/18614 | 0.032634844 | 0.361614349 | 0.336473494 | FGF8/OTP | 2 |
| BP | GO:0072044 | collecting duct development | 2/334 | 16/18614 | 0.032634844 | 0.361614349 | 0.336473494 | PAX8/WNT9B | 2 |
| BP | GO:0032409 | regulation of transporter activity | 11/334 | 324/18614 | 0.032732333 | 0.361614349 | 0.336473494 | CACNG8/CRH/FXYD1/HRC/MTNR1B/OPRL1/SHANK1/SHISA6/STAC2/TRDN/WNK3 | 11 |
| BP | GO:0007568 | aging | 7/334 | 169/18614 | 0.033091678 | 0.364250009 | 0.338925912 | ADRB3/AVPR1B/CYP1A1/GCLM/HELT/KRTAP4-3/KRTAP4-8 | 7 |
| BP | GO:0035019 | somatic stem cell population maintenance | 4/334 | 68/18614 | 0.033819601 | 0.369564912 | 0.343871302 | NOG/PAX8/SALL4/WNT9B | 4 |
| BP | GO:1904377 | positive regulation of protein localization to cell periphery | 4/334 | 68/18614 | 0.033819601 | 0.369564912 | 0.343871302 | EGFR/SORBS1/STAC2/WNK3 | 4 |
| BP | GO:0050806 | positive regulation of synaptic transmission | 7/334 | 170/18614 | 0.034005152 | 0.370251045 | 0.344509733 | CACNG8/GRIN1/KISS1/LRRTM1/NALCN/NOG/SHANK2 | 7 |
| BP | GO:0043410 | positive regulation of MAPK cascade | 15/334 | 495/18614 | 0.034350602 | 0.372448415 | 0.346554333 | ADRB3/AVPR1B/BIRC7/EGFR/EPHA8/FERMT2/FGF8/GHR/IAPP/KISS1/KITLG/MOS/PLA2G5/SSTR4/TGFA | 15 |
| BP | GO:0010863 | positive regulation of phospholipase C activity | 3/334 | 40/18614 | 0.03470093 | 0.372448415 | 0.346554333 | ADCYAP1R1/AVPR1B/EGFR | 3 |
| BP | GO:0051693 | actin filament capping | 3/334 | 40/18614 | 0.03470093 | 0.372448415 | 0.346554333 | CAPZA3/SPTBN2/SPTBN4 | 3 |
| BP | GO:0099068 | postsynapse assembly | 3/334 | 40/18614 | 0.03470093 | 0.372448415 | 0.346554333 | NRXN2/PTPRS/SPTBN2 | 3 |
| BP | GO:0030858 | positive regulation of epithelial cell differentiation | 4/334 | 69/18614 | 0.035411715 | 0.378729546 | 0.352398775 | GDNF/IL20/PAX8/PROM1 | 4 |
| BP | GO:0006816 | calcium ion transport | 14/334 | 455/18614 | 0.035973491 | 0.381492558 | 0.354969692 | ADCYAP1R1/CACNG8/GRIN1/GRM6/HCRT/HRC/NALCN/OPRL1/PKD1L2/STAC2/STC1/TRDN/TRPM5/WNK3 | 14 |
| BP | GO:0003198 | epithelial to mesenchymal transition involved in endocardial cushion formation | 2/334 | 17/18614 | 0.036555487 | 0.381492558 | 0.354969692 | FGF8/NOG | 2 |
| BP | GO:0008228 | opsonization | 2/334 | 17/18614 | 0.036555487 | 0.381492558 | 0.354969692 | FCN3/PLA2G5 | 2 |
| BP | GO:0031649 | heat generation | 2/334 | 17/18614 | 0.036555487 | 0.381492558 | 0.354969692 | ADRB3/PTGER3 | 2 |
| BP | GO:0051969 | regulation of transmission of nerve impulse | 2/334 | 17/18614 | 0.036555487 | 0.381492558 | 0.354969692 | HCRT/MTNR1B | 2 |
| BP | GO:0090494 | dopamine uptake | 2/334 | 17/18614 | 0.036555487 | 0.381492558 | 0.354969692 | GDNF/SLC29A4 | 2 |
| BP | GO:0097154 | GABAergic neuron differentiation | 2/334 | 17/18614 | 0.036555487 | 0.381492558 | 0.354969692 | DLX1/HELT | 2 |
| BP | GO:0003203 | endocardial cushion morphogenesis | 3/334 | 41/18614 | 0.036957886 | 0.383041184 | 0.356410651 | FGF8/NOG/TBX2 | 3 |
| BP | GO:0072210 | metanephric nephron development | 3/334 | 41/18614 | 0.036957886 | 0.383041184 | 0.356410651 | GDNF/PAX8/WNT9B | 3 |
| BP | GO:0072175 | epithelial tube formation | 6/334 | 138/18614 | 0.038363736 | 0.395454058 | 0.367960533 | FGF8/GDNF/NOG/PAX8/SALL4/WNT9B | 6 |
| BP | GO:0019932 | second-messenger-mediated signaling | 10/334 | 292/18614 | 0.038631189 | 0.395454058 | 0.367960533 | ADCY2/ADCYAP1R1/EGFR/GRIN1/HRC/MTNR1B/NEUROD2/OPRL1/RUNDC3A/TRPM5 | 10 |
| BP | GO:0034767 | positive regulation of monoatomic ion transmembrane transport | 7/334 | 175/18614 | 0.038823942 | 0.395454058 | 0.367960533 | ADCYAP1R1/FXYD1/GRIN1/GRM6/STAC2/TRDN/WNK3 | 7 |
| BP | GO:0008016 | regulation of heart contraction | 8/334 | 213/18614 | 0.038824677 | 0.395454058 | 0.367960533 | BMP10/FXYD1/HRC/MYL2/SPTBN4/STC1/TBX2/TRDN | 8 |
| BP | GO:0071542 | dopaminergic neuron differentiation | 3/334 | 42/18614 | 0.039288299 | 0.395454058 | 0.367960533 | FGF8/OTP/WNT9B | 3 |
| BP | GO:1900274 | regulation of phospholipase C activity | 3/334 | 42/18614 | 0.039288299 | 0.395454058 | 0.367960533 | ADCYAP1R1/AVPR1B/EGFR | 3 |
| BP | GO:0060562 | epithelial tube morphogenesis | 11/334 | 334/18614 | 0.039396803 | 0.395454058 | 0.367960533 | CSMD1/FGF8/GDNF/GLI2/HHIP/HOXA11/NOG/PAX8/SALL4/TBX2/WNT9B | 11 |
| BP | GO:1904888 | cranial skeletal system development | 4/334 | 72/18614 | 0.040444763 | 0.395454058 | 0.367960533 | FGF8/FREM1/NOG/WNT9B | 4 |
| BP | GO:0010522 | regulation of calcium ion transport into cytosol | 2/334 | 18/18614 | 0.040646803 | 0.395454058 | 0.367960533 | ADCYAP1R1/GRIN1 | 2 |
| BP | GO:0021513 | spinal cord dorsal/ventral patterning | 2/334 | 18/18614 | 0.040646803 | 0.395454058 | 0.367960533 | GLI2/RFX4 | 2 |
| BP | GO:0031645 | negative regulation of nervous system process | 2/334 | 18/18614 | 0.040646803 | 0.395454058 | 0.367960533 | HCRT/MTNR1B | 2 |
| BP | GO:0032354 | response to follicle-stimulating hormone | 2/334 | 18/18614 | 0.040646803 | 0.395454058 | 0.367960533 | EPHA8/GCLM | 2 |
| BP | GO:0038128 | ERBB2 signaling pathway | 2/334 | 18/18614 | 0.040646803 | 0.395454058 | 0.367960533 | EGFR/TGFA | 2 |
| BP | GO:0042753 | positive regulation of circadian rhythm | 2/334 | 18/18614 | 0.040646803 | 0.395454058 | 0.367960533 | CRH/MTNR1B | 2 |
| BP | GO:0050665 | hydrogen peroxide biosynthetic process | 2/334 | 18/18614 | 0.040646803 | 0.395454058 | 0.367960533 | CYP1A1/DUOXA2 | 2 |
| BP | GO:0050802 | circadian sleep/wake cycle, sleep | 2/334 | 18/18614 | 0.040646803 | 0.395454058 | 0.367960533 | CRH/MTNR1B | 2 |
| BP | GO:0051917 | regulation of fibrinolysis | 2/334 | 18/18614 | 0.040646803 | 0.395454058 | 0.367960533 | F11/KLKB1 | 2 |
| BP | GO:0090493 | catecholamine uptake | 2/334 | 18/18614 | 0.040646803 | 0.395454058 | 0.367960533 | GDNF/SLC29A4 | 2 |
| BP | GO:0150078 | positive regulation of neuroinflammatory response | 2/334 | 18/18614 | 0.040646803 | 0.395454058 | 0.367960533 | NUPR1/TTBK1 | 2 |
| BP | GO:0015718 | monocarboxylic acid transport | 7/334 | 177/18614 | 0.040870513 | 0.396351983 | 0.368796031 | AVPR1B/OC90/PLA2G5/PLA2R1/SLC22A8/SLC6A11/SSTR4 | 7 |
| BP | GO:0050730 | regulation of peptidyl-tyrosine phosphorylation | 9/334 | 255/18614 | 0.041211789 | 0.397925896 | 0.370260519 | ANGPT4/CNTN1/EGFR/FGF8/GHR/IL20/KITLG/SRCIN1/TGFA | 9 |
| BP | GO:0006739 | NADP metabolic process | 3/334 | 43/18614 | 0.041691621 | 0.397925896 | 0.370260519 | FMO1/FMO2/ME1 | 3 |
| BP | GO:0045494 | photoreceptor cell maintenance | 3/334 | 43/18614 | 0.041691621 | 0.397925896 | 0.370260519 | NXNL1/PCDH15/PROM1 | 3 |
| BP | GO:0045840 | positive regulation of mitotic nuclear division | 3/334 | 43/18614 | 0.041691621 | 0.397925896 | 0.370260519 | ESPL1/FGF8/TGFA | 3 |
| BP | GO:0007269 | neurotransmitter secretion | 6/334 | 141/18614 | 0.041886773 | 0.397925896 | 0.370260519 | GRIK5/HCRT/HRH3/NRXN2/SV2C/SYN3 | 6 |
| BP | GO:0099643 | signal release from synapse | 6/334 | 141/18614 | 0.041886773 | 0.397925896 | 0.370260519 | GRIK5/HCRT/HRH3/NRXN2/SV2C/SYN3 | 6 |
| BP | GO:0050795 | regulation of behavior | 4/334 | 73/18614 | 0.042208128 | 0.397925896 | 0.370260519 | CRH/INSL5/MTNR1B/OPRL1 | 4 |
| BP | GO:0060415 | muscle tissue morphogenesis | 4/334 | 73/18614 | 0.042208128 | 0.397925896 | 0.370260519 | BMP10/MYF5/MYL2/NOG | 4 |
| BP | GO:0046545 | development of primary female sexual characteristics | 5/334 | 106/18614 | 0.042220254 | 0.397925896 | 0.370260519 | ADCYAP1R1/CSMD1/KITLG/NUPR1/UMODL1 | 5 |
| BP | GO:0007219 | Notch signaling pathway | 7/334 | 179/18614 | 0.042986131 | 0.403882152 | 0.375802673 | ANGPT4/CNTN1/DLX1/EGFL7/HOXD3/NEURL1B/TBX2 | 7 |
| BP | GO:0003279 | cardiac septum development | 5/334 | 107/18614 | 0.043667393 | 0.404888865 | 0.376739395 | FGF8/NOG/PAX8/SALL4/TBX2 | 5 |
| BP | GO:0015837 | amine transport | 5/334 | 107/18614 | 0.043667393 | 0.404888865 | 0.376739395 | CRH/FFAR3/GDNF/HRH3/SYT3 | 5 |
| BP | GO:0022600 | digestive system process | 5/334 | 107/18614 | 0.043667393 | 0.404888865 | 0.376739395 | CHRM5/OPRL1/PTGER3/SLC5A1/TFF1 | 5 |
| BP | GO:1902414 | protein localization to cell junction | 5/334 | 107/18614 | 0.043667393 | 0.404888865 | 0.376739395 | CDH5/FERMT2/LRRTM1/NRXN2/SHANK1 | 5 |
| BP | GO:0045927 | positive regulation of growth | 9/334 | 258/18614 | 0.0438267 | 0.404888865 | 0.376739395 | BMP10/CPNE6/EGFR/FGF8/GHR/RASAL1/SPTBN4/SYT3/TBX2 | 9 |
| BP | GO:0021587 | cerebellum morphogenesis | 3/334 | 44/18614 | 0.044167254 | 0.404888865 | 0.376739395 | FAIM2/GLI2/SPTBN2 | 3 |
| BP | GO:0030835 | negative regulation of actin filament depolymerization | 3/334 | 44/18614 | 0.044167254 | 0.404888865 | 0.376739395 | CAPZA3/SPTBN2/SPTBN4 | 3 |
| BP | GO:0071526 | semaphorin-plexin signaling pathway | 3/334 | 44/18614 | 0.044167254 | 0.404888865 | 0.376739395 | GDNF/SEMA4G/SEMA5B | 3 |
| BP | GO:1901215 | negative regulation of neuron death | 8/334 | 219/18614 | 0.044482852 | 0.40654631 | 0.378281608 | DLX1/FAIM2/FGF8/GCLM/GDNF/GHR/MTNR1B/NES | 8 |
| BP | GO:0021692 | cerebellar Purkinje cell layer morphogenesis | 2/334 | 19/18614 | 0.044901444 | 0.406674944 | 0.378401299 | FAIM2/SPTBN2 | 2 |
| BP | GO:0030903 | notochord development | 2/334 | 19/18614 | 0.044901444 | 0.406674944 | 0.378401299 | COL18A1/NOG | 2 |
| BP | GO:1902307 | positive regulation of sodium ion transmembrane transport | 2/334 | 19/18614 | 0.044901444 | 0.406674944 | 0.378401299 | FXYD1/WNK3 | 2 |
| BP | GO:0007601 | visual perception | 8/334 | 220/18614 | 0.0454759 | 0.410644658 | 0.382095022 | COL18A1/CRYAA/CRYBB3/CRYGA/GPR179/GRM6/OPN4/SEMA5B | 8 |
| BP | GO:0048736 | appendage development | 7/334 | 182/18614 | 0.046290336 | 0.415510871 | 0.386622917 | FERMT2/FGF8/HOXA11/NOG/PITX1/SALL4/TBX2 | 7 |
| BP | GO:0060173 | limb development | 7/334 | 182/18614 | 0.046290336 | 0.415510871 | 0.386622917 | FERMT2/FGF8/HOXA11/NOG/PITX1/SALL4/TBX2 | 7 |
| BP | GO:0001504 | neurotransmitter uptake | 3/334 | 45/18614 | 0.046714545 | 0.416837481 | 0.387857296 | GDNF/SLC29A4/SLC6A11 | 3 |
| BP | GO:0009268 | response to pH | 3/334 | 45/18614 | 0.046714545 | 0.416837481 | 0.387857296 | GPR31/KCNK18/KCNK4 | 3 |
| BP | GO:0007224 | smoothened signaling pathway | 6/334 | 146/18614 | 0.048198601 | 0.426296131 | 0.396658344 | ACTRT1/GLI2/HHIP/NOG/RFX4/SCUBE1 | 6 |
| BP | GO:0035107 | appendage morphogenesis | 6/334 | 146/18614 | 0.048198601 | 0.426296131 | 0.396658344 | FGF8/HOXA11/NOG/PITX1/SALL4/TBX2 | 6 |
| BP | GO:0035108 | limb morphogenesis | 6/334 | 146/18614 | 0.048198601 | 0.426296131 | 0.396658344 | FGF8/HOXA11/NOG/PITX1/SALL4/TBX2 | 6 |
| BP | GO:1904062 | regulation of monoatomic cation transmembrane transport | 11/334 | 346/18614 | 0.0485758 | 0.426325836 | 0.396685983 | ADCYAP1R1/BPIFA1/FXYD1/GRIN1/GRM6/HRC/MTNR1B/OPRL1/STAC2/TRDN/WNK3 | 11 |
| BP | GO:0021511 | spinal cord patterning | 2/334 | 20/18614 | 0.049312271 | 0.426325836 | 0.396685983 | GLI2/RFX4 | 2 |
| BP | GO:0035902 | response to immobilization stress | 2/334 | 20/18614 | 0.049312271 | 0.426325836 | 0.396685983 | CYP1A1/TFF1 | 2 |
| BP | GO:0042749 | regulation of circadian sleep/wake cycle | 2/334 | 20/18614 | 0.049312271 | 0.426325836 | 0.396685983 | CRH/MTNR1B | 2 |
| BP | GO:0030517 | negative regulation of axon extension | 3/334 | 46/18614 | 0.049332797 | 0.426325836 | 0.396685983 | PTPRS/SEMA4G/SEMA5B | 3 |
| BP | GO:0034331 | cell junction maintenance | 3/334 | 46/18614 | 0.049332797 | 0.426325836 | 0.396685983 | FERMT2/SHANK1/SHANK2 | 3 |
| BP | GO:0042551 | neuron maturation | 3/334 | 46/18614 | 0.049332797 | 0.426325836 | 0.396685983 | ACTL6B/EPHA8/SPTBN4 | 3 |
| BP | GO:0055010 | ventricular cardiac muscle tissue morphogenesis | 3/334 | 46/18614 | 0.049332797 | 0.426325836 | 0.396685983 | BMP10/MYL2/NOG | 3 |
| BP | GO:0045685 | regulation of glial cell differentiation | 4/334 | 77/18614 | 0.049689592 | 0.428182309 | 0.398413387 | DLX1/NOG/OPALIN/TTBK1 | 4 |
| CC | GO:0005882 | intermediate filament | 17/347 | 214/19518 | 3.04E-07 | 8.89E-05 | 8.36E-05 | CLDN11/EVPL/KRT32/KRT82/KRTAP10-5/KRTAP13-1/KRTAP22-1/KRTAP3-1/KRTAP4-12/KRTAP4-3/KRTAP4-8/KRTAP5-6/KRTAP5-7/KRTAP6-1/KRTAP9-7/NES/SHANK2 | 17 |
| CC | GO:0045111 | intermediate filament cytoskeleton | 17/347 | 253/19518 | 3.11E-06 | 0.000453364 | 0.000426561 | CLDN11/EVPL/KRT32/KRT82/KRTAP10-5/KRTAP13-1/KRTAP22-1/KRTAP3-1/KRTAP4-12/KRTAP4-3/KRTAP4-8/KRTAP5-6/KRTAP5-7/KRTAP6-1/KRTAP9-7/NES/SHANK2 | 17 |
| CC | GO:0045211 | postsynaptic membrane | 15/347 | 277/19518 | 0.000140184 | 0.01364459 | 0.012837916 | CACNG8/CHRM5/CNTN1/FAIM2/GABRD/GABRR3/GRIK5/GRIN1/KCND2/LRRTM1/PTPRS/SHANK1/SHANK2/SHISA6/SLC6A11 | 15 |
| CC | GO:0097060 | synaptic membrane | 18/347 | 390/19518 | 0.000232919 | 0.017003065 | 0.015997837 | CACNG8/CHRM5/CNTN1/FAIM2/GABRD/GABRR3/GRIK5/GRIN1/KCND2/KCNK1/LRRTM1/PTPRS/SHANK1/SHANK2/SHISA6/SLC6A11/SNAP91/SRPX2 | 18 |
| CC | GO:0034702 | ion channel complex | 14/347 | 299/19518 | 0.000984519 | 0.05087168 | 0.047864126 | BEST2/BEST3/CACNG8/GABRD/GABRR3/GRIK5/GRIN1/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK4/KCNN1/SHISA6 | 14 |
| CC | GO:0034705 | potassium channel complex | 7/347 | 89/19518 | 0.001045308 | 0.05087168 | 0.047864126 | GRIK5/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK4/KCNN1 | 7 |
| CC | GO:0043025 | neuronal cell body | 19/347 | 500/19518 | 0.001652384 | 0.063061407 | 0.059333191 | BRS3/CPNE6/CRH/GABRD/GHR/GRIK5/KCND2/KCNK1/KCNN1/KISS1/NGB/OPN4/PTPRS/SHANK2/SPTBN2/SPTBN4/SRCIN1/TRPM5/TTBK1 | 19 |
| CC | GO:0045095 | keratin filament | 7/347 | 97/19518 | 0.00172771 | 0.063061407 | 0.059333191 | KRT82/KRTAP10-5/KRTAP3-1/KRTAP4-12/KRTAP4-3/KRTAP4-8/KRTAP9-7 | 7 |
| CC | GO:1902495 | transmembrane transporter complex | 15/347 | 392/19518 | 0.004631253 | 0.144101472 | 0.135582135 | BEST2/BEST3/CACNG8/FXYD1/GABRD/GABRR3/GRIK5/GRIN1/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK4/KCNN1/SHISA6 | 15 |
| CC | GO:0060076 | excitatory synapse | 5/347 | 64/19518 | 0.005582164 | 0.144101472 | 0.135582135 | GRIN1/SHANK1/SHISA6/SPTBN2/SRPX2 | 5 |
| CC | GO:0097733 | photoreceptor cell cilium | 7/347 | 120/19518 | 0.005667381 | 0.144101472 | 0.135582135 | KIAA1549/KIF17/NXNL1/OPN4/PCDH15/PROM1/SHANK2 | 7 |
| CC | GO:0008328 | ionotropic glutamate receptor complex | 4/347 | 41/19518 | 0.005921978 | 0.144101472 | 0.135582135 | CACNG8/GRIK5/GRIN1/SHISA6 | 4 |
| CC | GO:0001750 | photoreceptor outer segment | 6/347 | 95/19518 | 0.006987471 | 0.156949346 | 0.147670437 | KIF17/NXNL1/OPN4/PCDH15/PROM1/SHANK2 | 6 |
| CC | GO:0062023 | collagen-containing extracellular matrix | 15/347 | 415/19518 | 0.007692485 | 0.159422319 | 0.149997207 | ADAMTS2/ANGPT4/CLEC3B/COL18A1/COL9A1/EGFL7/FCN3/FREM1/KAZALD1/LAMC2/MXRA5/SERPINA5/SMOC2/SRPX2/TINAGL1 | 15 |
| CC | GO:1990351 | transporter complex | 15/347 | 418/19518 | 0.008189503 | 0.159422319 | 0.149997207 | BEST2/BEST3/CACNG8/FXYD1/GABRD/GABRR3/GRIK5/GRIN1/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK4/KCNN1/SHISA6 | 15 |
| CC | GO:0098878 | neurotransmitter receptor complex | 4/347 | 46/19518 | 0.008904852 | 0.161252759 | 0.151719431 | CACNG8/GRIK5/GRIN1/SHISA6 | 4 |
| CC | GO:0097731 | 9+0 non-motile cilium | 7/347 | 132/19518 | 0.009388003 | 0.161252759 | 0.151719431 | KIAA1549/KIF17/NXNL1/OPN4/PCDH15/PROM1/SHANK2 | 7 |
| CC | GO:0034707 | chloride channel complex | 4/347 | 55/19518 | 0.016441753 | 0.266721774 | 0.250953075 | BEST2/BEST3/GABRD/GABRR3 | 4 |
| CC | GO:0043204 | perikaryon | 7/347 | 156/19518 | 0.021719976 | 0.318537677 | 0.299705601 | CPNE6/GRIK5/KCND2/KCNK1/NGB/OPN4/PTPRS | 7 |
| CC | GO:0034703 | cation channel complex | 8/347 | 192/19518 | 0.021817649 | 0.318537677 | 0.299705601 | CACNG8/GRIK5/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK4/KCNN1 | 8 |
| CC | GO:0099634 | postsynaptic specialization membrane | 6/347 | 129/19518 | 0.027869219 | 0.384769823 | 0.362022075 | CACNG8/GRIK5/KCND2/LRRTM1/PTPRS/SHISA6 | 6 |
| CC | GO:0097730 | non-motile cilium | 7/347 | 166/19518 | 0.029197563 | 0.384769823 | 0.362022075 | KIAA1549/KIF17/NXNL1/OPN4/PCDH15/PROM1/SHANK2 | 7 |
| CC | GO:0099572 | postsynaptic specialization | 12/347 | 364/19518 | 0.030307212 | 0.384769823 | 0.362022075 | CACNG8/CPEB1/GRIK5/GRIN1/KCND2/LRRTM1/PTPRS/SHANK1/SHANK2/SHISA6/SRCIN1/SYN3 | 12 |
| CC | GO:0033017 | sarcoplasmic reticulum membrane | 3/347 | 42/19518 | 0.038400338 | 0.442152326 | 0.416012102 | ART1/HRC/TRDN | 3 |
| CC | GO:0016324 | apical plasma membrane | 12/347 | 381/19518 | 0.040680204 | 0.442152326 | 0.416012102 | DPEP1/FRMD1/FXYD1/KCNK1/KISS1/PROM1/SHANK2/SLC22A8/SLC29A4/SLC5A1/SPTBN2/STC1 | 12 |
| CC | GO:0014069 | postsynaptic density | 11/347 | 339/19518 | 0.040819226 | 0.442152326 | 0.416012102 | CACNG8/CPEB1/GRIK5/GRIN1/KCND2/PTPRS/SHANK1/SHANK2/SHISA6/SRCIN1/SYN3 | 11 |
| CC | GO:0016529 | sarcoplasmic reticulum | 4/347 | 73/19518 | 0.041045949 | 0.442152326 | 0.416012102 | ART1/CMYA5/HRC/TRDN | 4 |
| CC | GO:1902711 | GABA-A receptor complex | 2/347 | 19/19518 | 0.044163393 | 0.442152326 | 0.416012102 | GABRD/GABRR3 | 2 |
| CC | GO:0019897 | extrinsic component of plasma membrane | 6/347 | 147/19518 | 0.047776873 | 0.442152326 | 0.416012102 | CDH19/CDH5/FERMT2/SNAP91/STAC2/GNB4 | 6 |
| CC | GO:0031253 | cell projection membrane | 11/347 | 349/19518 | 0.0484806 | 0.442152326 | 0.416012102 | AIF1L/ANTXR1/DPEP1/EGFR/FERMT2/HHIP/KCNK1/PROM1/SHANK2/SHISA6/SLC5A1 | 11 |
| CC | GO:0070382 | exocytic vesicle | 8/347 | 225/19518 | 0.048524401 | 0.442152326 | 0.416012102 | GRIN1/HCRT/KCNK9/PTPRS/RAB3IL1/SNAP91/SV2C/SYN3 | 8 |
| MF | GO:0004984 | olfactory receptor activity | 23/344 | 342/18369 | 1.38E-07 | 7.17E-05 | 6.46E-05 | OR10J3/OR10W1/OR12D3/OR13C8/OR1J1/OR1J4/OR1K1/OR2AG1/OR2AG2/OR2D2/OR2J2/OR2T6/OR3A3/OR4M1/OR51I2/OR52L1/OR56A4/OR5A2/OR5C1/OR5H1/OR8B3/OR8U1/OR9G4 | 23 |
| MF | GO:0022840 | leak channel activity | 5/344 | 19/18369 | 2.10E-05 | 0.003126888 | 0.002817642 | KCNK1/KCNK18/KCNK4/KCNK9/NALCN | 5 |
| MF | GO:0022842 | narrow pore channel activity | 5/344 | 19/18369 | 2.10E-05 | 0.003126888 | 0.002817642 | KCNK1/KCNK18/KCNK4/KCNK9/NALCN | 5 |
| MF | GO:0048018 | receptor ligand activity | 24/344 | 497/18369 | 2.40E-05 | 0.003126888 | 0.002817642 | BMP10/CRH/CXCL6/DEFB103B/DEFB4A/FAM3D/FGF8/GDNF/GPHB5/HCRT/IAPP/IFNA4/IL17B/IL20/IL36B/INSL5/KITLG/NRG2/SEMA4G/SEMA5B/STC1/TFF1/TGFA/WNT9B | 24 |
| MF | GO:0005267 | potassium channel activity | 10/344 | 121/18369 | 9.36E-05 | 0.008709914 | 0.007848514 | GRIK5/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK18/KCNK4/KCNK9/KCNN1/TRPM5 | 10 |
| MF | GO:0005549 | odorant binding | 10/344 | 122/18369 | 0.000100306 | 0.008709914 | 0.007848514 | OR10J3/OR10W1/OR12D3/OR1K1/OR5A2/OR5C1/OR5H1/OR8B3/OR8U1/OR9G4 | 10 |
| MF | GO:0022841 | potassium ion leak channel activity | 4/344 | 16/18369 | 0.000184074 | 0.013700401 | 0.012345446 | KCNK1/KCNK18/KCNK4/KCNK9 | 4 |
| MF | GO:0099186 | structural constituent of postsynapse | 4/344 | 21/18369 | 0.000562156 | 0.036610398 | 0.032989671 | ACTBL2/SHANK1/SHANK2/SPTBN2 | 4 |
| MF | GO:0015079 | potassium ion transmembrane transporter activity | 10/344 | 157/18369 | 0.000766526 | 0.042543379 | 0.038335886 | GRIK5/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK18/KCNK4/KCNK9/KCNN1/TRPM5 | 10 |
| MF | GO:0005244 | voltage-gated monoatomic ion channel activity | 11/344 | 189/18369 | 0.000898229 | 0.042543379 | 0.038335886 | CACNG8/CALHM3/GRIN1/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK18/KCNN1/NALCN/TRPM5 | 11 |
| MF | GO:0022832 | voltage-gated channel activity | 11/344 | 189/18369 | 0.000898229 | 0.042543379 | 0.038335886 | CACNG8/CALHM3/GRIN1/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK18/KCNN1/NALCN/TRPM5 | 11 |
| MF | GO:0005261 | monoatomic cation channel activity | 15/344 | 324/18369 | 0.001233385 | 0.051733519 | 0.046617132 | CACNG8/CALHM3/GRIK5/GRIN1/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK18/KCNK4/KCNK9/KCNN1/NALCN/PKD1L2/TRPM5 | 15 |
| MF | GO:0098918 | structural constituent of synapse | 4/344 | 26/18369 | 0.001304382 | 0.051733519 | 0.046617132 | ACTBL2/SHANK1/SHANK2/SPTBN2 | 4 |
| MF | GO:0005216 | monoatomic ion channel activity | 18/344 | 432/18369 | 0.001390152 | 0.051733519 | 0.046617132 | BEST2/BEST3/CACNG8/CALHM3/FXYD1/GRIK5/GRIN1/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK18/KCNK4/KCNK9/KCNN1/NALCN/PKD1L2/TRPM5 | 18 |
| MF | GO:0005242 | inward rectifier potassium channel activity | 4/344 | 27/18369 | 0.001508853 | 0.052407503 | 0.04722446 | KCNJ11/KCNJ16/KCNK1/KCNN1 | 4 |
| MF | GO:0005344 | oxygen carrier activity | 3/344 | 14/18369 | 0.002032867 | 0.065746532 | 0.059244274 | HBQ1/MB/NGB | 3 |
| MF | GO:0030414 | peptidase inhibitor activity | 10/344 | 180/18369 | 0.00214528 | 0.065746532 | 0.059244274 | BIRC7/DPEP1/FETUB/PCSK1N/SERPINA5/SERPINA7/SPINT4/UMODL1/WFDC2/WFIKKN1 | 10 |
| MF | GO:0030159 | signaling receptor complex adaptor activity | 5/344 | 52/18369 | 0.002827351 | 0.08183609 | 0.073742592 | GAB4/SHANK1/SHANK2/SORBS1/GNB4 | 5 |
| MF | GO:0030297 | transmembrane receptor protein tyrosine kinase activator activity | 3/344 | 16/18369 | 0.003041897 | 0.083412006 | 0.075162652 | ANGPT4/EGFR/TGFA | 3 |
| MF | GO:0015267 | channel activity | 18/344 | 478/18369 | 0.004106576 | 0.099840551 | 0.089966433 | BEST2/BEST3/CACNG8/CALHM3/FXYD1/GRIK5/GRIN1/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK18/KCNK4/KCNK9/KCNN1/NALCN/PKD1L2/TRPM5 | 18 |
| MF | GO:0022803 | passive transmembrane transporter activity | 18/344 | 479/18369 | 0.004195907 | 0.099840551 | 0.089966433 | BEST2/BEST3/CACNG8/CALHM3/FXYD1/GRIK5/GRIN1/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK18/KCNK4/KCNK9/KCNN1/NALCN/PKD1L2/TRPM5 | 18 |
| MF | GO:0099094 | ligand-gated monoatomic cation channel activity | 7/344 | 108/18369 | 0.004215916 | 0.099840551 | 0.089966433 | GRIK5/GRIN1/KCNJ11/KCNJ16/KCNK1/KCNN1/TRPM5 | 7 |
| MF | GO:0004866 | endopeptidase inhibitor activity | 9/344 | 173/18369 | 0.005407405 | 0.114442321 | 0.103124104 | BIRC7/DPEP1/FETUB/PCSK1N/SERPINA5/SERPINA7/SPINT4/WFDC2/WFIKKN1 | 9 |
| MF | GO:0022836 | gated channel activity | 13/344 | 308/18369 | 0.005564818 | 0.114442321 | 0.103124104 | CACNG8/CALHM3/GRIK5/GRIN1/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK18/KCNK4/KCNN1/NALCN/TRPM5 | 13 |
| MF | GO:0022839 | monoatomic ion gated channel activity | 13/344 | 308/18369 | 0.005564818 | 0.114442321 | 0.103124104 | CACNG8/CALHM3/GRIK5/GRIN1/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK18/KCNK4/KCNN1/NALCN/TRPM5 | 13 |
| MF | GO:0008227 | G protein-coupled amine receptor activity | 4/344 | 39/18369 | 0.005930792 | 0.114442321 | 0.103124104 | ADRB3/CHRM5/HRH3/TAAR2 | 4 |
| MF | GO:0019825 | oxygen binding | 4/344 | 39/18369 | 0.005930792 | 0.114442321 | 0.103124104 | CYP1A1/HBQ1/MB/NGB | 4 |
| MF | GO:0005249 | voltage-gated potassium channel activity | 6/344 | 88/18369 | 0.006181359 | 0.115017427 | 0.103642332 | KCND2/KCNJ11/KCNJ16/KCNK1/KCNK18/KCNN1 | 6 |
| MF | GO:0005272 | sodium channel activity | 4/344 | 41/18369 | 0.007092161 | 0.127414337 | 0.114813202 | GRIK5/KCNK1/NALCN/TRPM5 | 4 |
| MF | GO:0004867 | serine-type endopeptidase inhibitor activity | 6/344 | 92/18369 | 0.007645784 | 0.131551706 | 0.11854139 | PCSK1N/SERPINA5/SERPINA7/SPINT4/WFDC2/WFIKKN1 | 6 |
| MF | GO:0005179 | hormone activity | 7/344 | 122/18369 | 0.008125166 | 0.131551706 | 0.11854139 | BMP10/CRH/GPHB5/HCRT/IAPP/INSL5/STC1 | 7 |
| MF | GO:0046873 | metal ion transmembrane transporter activity | 16/344 | 435/18369 | 0.008212242 | 0.131551706 | 0.11854139 | CACNG8/GRIK5/GRIN1/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK18/KCNK4/KCNK9/KCNN1/NALCN/PKD1L2/SLC5A1/SLC6A11/TRPM5 | 16 |
| MF | GO:0001664 | G protein-coupled receptor binding | 12/344 | 289/18369 | 0.008574982 | 0.131551706 | 0.11854139 | ADRB3/CXCL6/DEFB103B/DEFB4A/GPHB5/HCRT/INSL5/KISS1/NES/PTGER1/SHANK1/WNT9B | 12 |
| MF | GO:0005212 | structural constituent of eye lens | 3/344 | 23/18369 | 0.008733279 | 0.131551706 | 0.11854139 | CRYAA/CRYBB3/CRYGA | 3 |
| MF | GO:0061135 | endopeptidase regulator activity | 9/344 | 187/18369 | 0.008837447 | 0.131551706 | 0.11854139 | BIRC7/DPEP1/FETUB/PCSK1N/SERPINA5/SERPINA7/SPINT4/WFDC2/WFIKKN1 | 9 |
| MF | GO:0005227 | calcium activated cation channel activity | 3/344 | 24/18369 | 0.009844483 | 0.142471552 | 0.128381275 | KCNK18/KCNN1/TRPM5 | 3 |
| MF | GO:0030594 | neurotransmitter receptor activity | 6/344 | 98/18369 | 0.010288922 | 0.144879146 | 0.130550761 | CHRM5/GABRD/GABRR3/GRIK5/GRIN1/HRH3 | 6 |
| MF | GO:0035255 | ionotropic glutamate receptor binding | 3/344 | 25/18369 | 0.011034174 | 0.151284332 | 0.136322481 | SHANK1/SHANK2/SHISA6 | 3 |
| MF | GO:0061134 | peptidase regulator activity | 10/344 | 230/18369 | 0.011687611 | 0.15613449 | 0.140692964 | BIRC7/DPEP1/FETUB/PCSK1N/SERPINA5/SERPINA7/SPINT4/UMODL1/WFDC2/WFIKKN1 | 10 |
| MF | GO:0005201 | extracellular matrix structural constituent | 8/344 | 167/18369 | 0.013553242 | 0.172632713 | 0.155559531 | COL18A1/COL9A1/LAMC2/MUC3A/MUC5AC/MXRA5/SRPX2/TINAGL1 | 8 |
| MF | GO:0008066 | glutamate receptor activity | 3/344 | 27/18369 | 0.01365258 | 0.172632713 | 0.155559531 | GRIK5/GRIN1/GRM6 | 3 |
| MF | GO:0004954 | prostanoid receptor activity | 2/344 | 10/18369 | 0.014247997 | 0.172632713 | 0.155559531 | PTGER1/PTGER3 | 2 |
| MF | GO:0004955 | prostaglandin receptor activity | 2/344 | 10/18369 | 0.014247997 | 0.172632713 | 0.155559531 | PTGER1/PTGER3 | 2 |
| MF | GO:0015276 | ligand-gated monoatomic ion channel activity | 7/344 | 140/18369 | 0.016435374 | 0.186148477 | 0.167738601 | GRIK5/GRIN1/KCNJ11/KCNJ16/KCNK1/KCNN1/TRPM5 | 7 |
| MF | GO:0022834 | ligand-gated channel activity | 7/344 | 140/18369 | 0.016435374 | 0.186148477 | 0.167738601 | GRIK5/GRIN1/KCNJ11/KCNJ16/KCNK1/KCNN1/TRPM5 | 7 |
| MF | GO:0022843 | voltage-gated monoatomic cation channel activity | 7/344 | 140/18369 | 0.016435374 | 0.186148477 | 0.167738601 | CACNG8/KCND2/KCNJ11/KCNJ16/KCNK1/KCNK18/KCNN1 | 7 |
| MF | GO:0031731 | CCR6 chemokine receptor binding | 2/344 | 11/18369 | 0.017200719 | 0.186699467 | 0.168235099 | DEFB103B/DEFB4A | 2 |
| MF | GO:0099528 | G protein-coupled neurotransmitter receptor activity | 2/344 | 11/18369 | 0.017200719 | 0.186699467 | 0.168235099 | CHRM5/HRH3 | 2 |
| MF | GO:0005543 | phospholipid binding | 16/344 | 475/18369 | 0.017670356 | 0.18788276 | 0.169301365 | CPNE6/DEFB4A/DPEP1/FERMT2/GLTPD2/OC90/OTC/PLA2G5/RASAL1/SDCBP2/SERPINA5/SNAP91/SPTBN2/SPTBN4/SYT3/TRIM72 | 16 |
| MF | GO:0004869 | cysteine-type endopeptidase inhibitor activity | 4/344 | 54/18369 | 0.018339036 | 0.191092757 | 0.172193898 | BIRC7/DPEP1/FETUB/WFDC2 | 4 |
| MF | GO:0035591 | signaling adaptor activity | 5/344 | 83/18369 | 0.019798434 | 0.200419888 | 0.180598586 | GAB4/SHANK1/SHANK2/SORBS1/GNB4 | 5 |
| MF | GO:0008179 | adenylate cyclase binding | 2/344 | 12/18369 | 0.020388204 | 0.200419888 | 0.180598586 | ADCY2/ADCYAP1R1 | 2 |
| MF | GO:0015269 | calcium-activated potassium channel activity | 2/344 | 12/18369 | 0.020388204 | 0.200419888 | 0.180598586 | KCNK18/KCNN1 | 2 |
| MF | GO:0042923 | neuropeptide binding | 3/344 | 32/18369 | 0.021620573 | 0.208598489 | 0.187968332 | ADCYAP1R1/OPRL1/SSTR4 | 3 |
| MF | GO:0071855 | neuropeptide receptor binding | 3/344 | 33/18369 | 0.0234605 | 0.222234921 | 0.200256137 | HCRT/KISS1/SHANK1 | 3 |
| MF | GO:0030296 | protein tyrosine kinase activator activity | 3/344 | 34/18369 | 0.025382708 | 0.236149834 | 0.21279488 | ANGPT4/EGFR/TGFA | 3 |
| MF | GO:0004953 | icosanoid receptor activity | 2/344 | 14/18369 | 0.027428645 | 0.246384898 | 0.222017708 | PTGER1/PTGER3 | 2 |
| MF | GO:0015271 | outward rectifier potassium channel activity | 2/344 | 14/18369 | 0.027428645 | 0.246384898 | 0.222017708 | KCND2/KCNK18 | 2 |
| MF | GO:0008083 | growth factor activity | 7/344 | 160/18369 | 0.03126448 | 0.272996265 | 0.24599724 | BMP10/FGF8/GDNF/KITLG/NRG2/TFF1/TGFA | 7 |
| MF | GO:0005126 | cytokine receptor binding | 10/344 | 270/18369 | 0.031439109 | 0.272996265 | 0.24599724 | CDH5/CXCL6/DEFB103B/DEFB4A/FERMT2/IFNA4/IL20/IL36B/KITLG/NES | 10 |
| MF | GO:0005125 | cytokine activity | 9/344 | 235/18369 | 0.033427847 | 0.281746284 | 0.253881892 | BMP10/CXCL6/FAM3D/IFNA4/IL17B/IL20/IL36B/KITLG/WNT9B | 9 |
| MF | GO:0030246 | carbohydrate binding | 10/344 | 273/18369 | 0.033528349 | 0.281746284 | 0.253881892 | CLEC2L/CLEC3B/CLEC4G/CNTN1/COL9A1/FCN3/FREM1/LGALS14/PKD1L2/PLA2R1 | 10 |
| MF | GO:0008191 | metalloendopeptidase inhibitor activity | 2/344 | 16/18369 | 0.03529446 | 0.291879584 | 0.26301302 | FETUB/WFIKKN1 | 2 |
| MF | GO:0042056 | chemoattractant activity | 3/344 | 39/18369 | 0.036220459 | 0.294102022 | 0.265015662 | DEFB103B/DEFB4A/GDNF | 3 |
| MF | GO:0019838 | growth factor binding | 6/344 | 132/18369 | 0.038049293 | 0.294102022 | 0.265015662 | EGFR/EPHA8/GHR/KAZALD1/SRPX2/WFIKKN1 | 6 |
| MF | GO:0016709 | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen | 3/344 | 40/18369 | 0.03863069 | 0.294102022 | 0.265015662 | CYP1A1/FMO1/FMO2 | 3 |
| MF | GO:0004857 | enzyme inhibitor activity | 12/344 | 359/18369 | 0.038703221 | 0.294102022 | 0.265015662 | BIRC7/DPEP1/FETUB/PCSK1N/PPP1R1C/SCG5/SERPINA5/SERPINA7/SPINT4/UMODL1/WFDC2/WFIKKN1 | 12 |
| MF | GO:0008201 | heparin binding | 7/344 | 168/18369 | 0.039122225 | 0.294102022 | 0.265015662 | CLEC3B/CXCL6/F11/LAMC2/PTPRS/SERPINA5/SMOC2 | 7 |
| MF | GO:0042165 | neurotransmitter binding | 2/344 | 17/18369 | 0.039514667 | 0.294102022 | 0.265015662 | GRIN1/SLC6A11 | 2 |
| MF | GO:0047498 | calcium-dependent phospholipase A2 activity | 2/344 | 17/18369 | 0.039514667 | 0.294102022 | 0.265015662 | OC90/PLA2G5 | 2 |
| MF | GO:0008391 | arachidonic acid monooxygenase activity | 2/344 | 18/18369 | 0.043915076 | 0.322250061 | 0.290379892 | CYP1A1/CYP4Z1 | 2 |
| MF | GO:0004890 | GABA-A receptor activity | 2/344 | 19/18369 | 0.048487499 | 0.336826493 | 0.30351473 | GABRD/GABRR3 | 2 |
| MF | GO:0004970 | ionotropic glutamate receptor activity | 2/344 | 19/18369 | 0.048487499 | 0.336826493 | 0.30351473 | GRIK5/GRIN1 | 2 |
| MF | GO:0030506 | ankyrin binding | 2/344 | 19/18369 | 0.048487499 | 0.336826493 | 0.30351473 | KCNJ11/SPTBN4 | 2 |
| MF | GO:0033612 | receptor serine/threonine kinase binding | 2/344 | 19/18369 | 0.048487499 | 0.336826493 | 0.30351473 | BMP10/CDH5 | 2 |