Table 1: Top two genes with highest logfoldchanges in each group of genes (original pipeline)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| group | names | scores | logfoldchanges | pvals |
| OPC | AC067968.3 | -2.1378632 | 11.780655 | 0.0331561513661045 |
| OPC | AP001065.7 | -3.0815122 | 12.620021 | 0.00220620599553477 |
| OPC | AC074391.1 | 0.3935949 | 12.64007 | 0.69830241316352 |
| OPC | CTC-365E16.1 | -2.7440376 | 15.8601675 | 0.00634585954480493 |
| astrocytes | XIRP1 | -2.7672293 | 10.793521 | 0.00594664161050909 |
| astrocytes | SPANXD | -1.573144 | 12.030731 | 0.116584453591321 |
| astrocytes | MYBPC3 | -3.1581013 | 13.549382 | 0.00171567660093212 |
| astrocytes | RP11-337C18.7 | -1.6680661 | 14.325747 | 0.096196899373418 |
| endothelial | MPEG1 | -3.7698188 | 11.10753 | 0.000188285211828764 |
| endothelial | PCA3 | -3.5665255 | 11.232262 | 0.000417616282823251 |
| endothelial | FIBIN | -4.294025 | 11.916581 | 2.25356667609239E-05 |
| endothelial | RPL31P52 | 0.6966527 | 13.485387 | 0.497256276553877 |
| fetal\_quiescent | AC069278.4 | -0.18873927 | 10.019977 | 0.850509209265701 |
| fetal\_quiescent | SS18L2P2 | -1.8740529 | 10.044606 | 0.0619140116798568 |
| fetal\_quiescent | RNA5SP295 | -1.4729985 | 10.959235 | 0.141802383199256 |
| fetal\_quiescent | HMGA1P7 | -2.0110362 | 15.701316 | 0.0452042780241364 |
| fetal\_replicating | TMEM139 | -3.2361434 | 11.4475565 | 0.00133916814413786 |
| fetal\_replicating | LRRC32 | -2.0780983 | 11.577548 | 0.0383423958713228 |
| fetal\_replicating | OLFML3 | -2.8367064 | 11.595176 | 0.00479549919943184 |
| fetal\_replicating | AKAP17BP | -2.6104195 | 14.402124 | 0.0094011442335448 |
| hybrid | NONOP2 | -2.4315205 | 9.395579 | 0.0155046680634758 |
| hybrid | RP11-173M11.2 | 0.22313085 | 9.406843 | 0.824560456506841 |
| hybrid | NEUROD4 | -2.34243 | 9.539777 | 0.0196837866147362 |
| hybrid | DDX43 | -2.0059202 | 10.107913 | 0.0455673830251107 |
| microglia | RP11-252E2.2 | -2.0393226 | 11.680095 | 0.0420860844316508 |
| microglia | LDHAL6DP | -3.491122 | 11.795065 | 0.000583267770568372 |
| microglia | RP11-565F19.2 | -1.9596479 | 12.445036 | 0.0508842983117509 |
| microglia | LHX6 | -5.3185034 | 12.736008 | 1.76001392576704E-07 |
| neurons | RP11-36B15.1 | -1.6426461 | 10.175368 | 0.101492890292737 |
| neurons | RP11-129B9.2 | -1.6872222 | 10.914061 | 0.0925129428561722 |
| neurons | KRT18P11 | -1.2490039 | 11.260698 | 0.212446384659299 |
| neurons | RP11-107M16.2 | 0.47737095 | 11.338261 | 0.633865650971954 |
| oligodendrocytes | RP11-809N15.2 | -2.3365471 | 10.29259 | 0.0200025158052678 |
| oligodendrocytes | RP11-509J21.3 | 0.6985042 | 11.062819 | 0.48902017743997 |
| oligodendrocytes | MIR1285-1 | -2.4945097 | 11.308447 | 0.0130464457386572 |
| oligodendrocytes | RP11-122C21.1 | -2.835732 | 14.881016 | 0.00481247196456705 |

Table 2: Top two genes with highest logfoldchanges in each group of genes (Alternative pipeline)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| group | names | scores | logfoldchanges | pvals |
| 0 | GABRA1 | 11.347249 | 6.466964 | 7.65329855404347E-30 |
| 0 | NRIP3 | 12.309119 | 6.7606335 | 8.09015033985811E-35 |
| 0 | DLX6-AS1 | 11.618639 | 7.104732 | 3.31372118914897E-31 |
| 0 | SYNPR | 11.990235 | 7.1212845 | 3.99768105127685E-33 |
| 1 | ARHGDIB | 2.990022 | 5.0897517 | 0.00278957332077441 |
| 1 | HLA-DRB5 | 2.8701782 | 5.169663 | 0.00410240605126794 |
| 1 | ITGAX | 3.1921551 | 5.1974325 | 0.00141215518628865 |
| 1 | C1QA | 2.8386984 | 8.291865 | 0.00452979475839727 |
| 2 | SLA | 9.878982 | 6.8970275 | 5.13522845701713E-23 |
| 2 | SOX11 | 9.071656 | 7.084331 | 1.17221887826011E-19 |
| 2 | SATB2 | 10.56989 | 7.656928 | 4.10976689363691E-26 |
| 2 | NEUROD6 | 10.638222 | 7.729523 | 1.97869957974642E-26 |
| 3 | ATP1A2 | 11.515144 | 8.896854 | 1.10674420885261E-30 |
| 3 | GJA1 | 11.272187 | 9.265508 | 1.80041111568268E-29 |
| 3 | ETNPPL | 11.040619 | 9.699903 | 2.43351172592106E-28 |
| 3 | AQP4 | 10.505355 | 9.732701 | 8.16155630924435E-26 |
| 4 | CNDP1 | 10.382121 | 10.570277 | 2.99055115759377E-25 |
| 4 | OPALIN | 10.391125 | 10.604117 | 2.72123740012828E-25 |
| 4 | ERMN | 10.655007 | 11.40122 | 1.65232299771352E-26 |
| 4 | PLP1 | 10.700719 | 12.617879 | 1.00991761500389E-26 |
| 5 | TMEM155 | 6.308568 | 6.8296595 | 2.81629211237547E-10 |
| 5 | AC018799.1 | 3.2099888 | 7.032055 | 0.00132740175043871 |
| 5 | VSNL1 | 7.9797115 | 7.059061 | 1.46675489332433E-15 |
| 5 | RGS4 | 6.7733545 | 7.5623484 | 1.2582989929704E-11 |
| 6 | B3GNT7 | 7.6155176 | 7.7453737 | 2.62637100018505E-14 |
| 6 | PCDH15 | 7.657918 | 7.7966094 | 1.88971352056656E-14 |
| 6 | PDGFRA | 6.9057684 | 7.9214077 | 4.99324716661086E-12 |
| 6 | TNR | 7.8938866 | 7.9573135 | 2.92918174711517E-15 |
| 7 | BCL11A | 5.781514 | 6.1413164 | 7.4031170867871E-09 |
| 7 | GRIK3 | 5.5944424 | 6.3154774 | 2.21332217502007E-08 |
| 7 | HS3ST4 | 3.9098082 | 6.3758383 | 9.23694552981734E-05 |
| 7 | CRYM | 6.587894 | 7.2529364 | 4.46109526254553E-11 |
| 8 | EDNRB | 4.8094325 | 5.93593 | 1.51359445398048E-06 |
| 8 | VIP | 4.36528 | 5.9491353 | 1.26960014448486E-05 |
| 8 | PROX1 | 5.078102 | 6.214446 | 3.81223448224181E-07 |
| 8 | AQP4 | 4.218843 | 6.725787 | 2.45559353343226E-05 |
| 9 | TOP2A | 4.8660593 | 11.700187 | 1.13845298609385E-06 |
| 9 | HIST1H1B | 5.892612 | 12.114335 | 3.80138782269201E-09 |
| 9 | AURKB | 4.423233 | 12.705043 | 9.72348131186596E-06 |
| 9 | CDK1 | 5.404496 | 13.83896 | 6.49908014879388E-08 |

Table 3: Top two genes with highest logfoldchanges in each group of genes (original pipeline neuron walk community)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| group | names | scores | logfoldchanges | pvals |
| 2 | CNBP | 1.9685829 | 11.513031 | 0.147213532461364 |
| 2 | CCDC132 | -0.91849726 | 11.524325 | 0.515232723766504 |
| 2 | LDOC1L | 5.333736 | 11.876977 | 0.0575001731975791 |
| 2 | NCOA3 | 4.604604 | 12.489227 | 0.075541213062374 |
| 4 | PNMAL1 | -0.16399644 | 6.851855 | 0.870091948892154 |
| 4 | LTB4R | 0.120206095 | 7.0900593 | 0.904602142539595 |
| 4 | GBP3 | -1.469138 | 8.980725 | 0.148805306949905 |
| 4 | PGK1 | -0.08373466 | 10.068966 | 0.933461252327483 |
| 5 | RP11-93H12.4 | -1.3921742 | 9.17577 | 0.167824098601087 |
| 5 | SWAP70 | -0.8791665 | 9.19883 | 0.386910671194865 |
| 5 | APOOL | 0.20049252 | 9.292867 | 0.843301484064998 |
| 5 | GDF11 | 0.2768747 | 10.108558 | 0.784558812933689 |
| 6 | CENPL | 0.36329755 | 10.651517 | 0.726162551816262 |
| 6 | LIMD1 | 0.23336256 | 10.72154 | 0.821607288037178 |
| 6 | NR2C1 | -0.5129308 | 12.142733 | 0.621965921810286 |
| 6 | BCL11A | -1.3827397 | 17.125774 | 0.199688830027597 |
| 7 | APOLD1 | 0.78566027 | 11.426427 | 0.494721895568221 |
| 7 | ZNF527 | 0.4690152 | 11.432625 | 0.684193348996293 |
| 7 | C22orf23 | 0.35368007 | 13.635322 | 0.755439466389421 |
| 7 | RP11-301G7.1 | -3.582349 | 14.621448 | 0.000779490925569853 |
| 8 | GABRE | -0.30749822 | 11.862398 | 0.764272461710009 |
| 8 | SRCRB4D | 0.49853113 | 11.927462 | 0.630270194971468 |
| 8 | RP11-517P14.7 | -1.8875418 | 12.73051 | 0.0629416240277903 |
| 8 | RP11-472I20.1 | 0.48261923 | 14.6521435 | 0.645673362517388 |
| 11 | C6orf100 | 0.3061164 | 11.308491 | 0.773455851200241 |
| 11 | ANO3 | -2.7205718 | 11.982176 | 0.00780907206375892 |
| 11 | RP11-484D2.2 | 0.83043975 | 12.167615 | 0.409095202426047 |
| 11 | ZNF19 | 0.15132678 | 13.351387 | 0.886331680504874 |
| 12 | SNHG1 | -7.975738 | 11.814477 | 4.04237196682801E-12 |
| 12 | THBS1 | -4.5498815 | 12.033528 | 2.63854997084776E-05 |
| 12 | NR2C1 | -1.15949 | 12.246593 | 0.447497642634276 |
| 12 | KBTBD7 | -8.10754 | 13.796643 | 2.0354207032196E-12 |
| 13 | KDELC1 | 0.4844559 | 11.220452 | 0.67488290211416 |
| 13 | RP11-467D6.1 | -3.7623134 | 11.458552 | 0.00106526959471271 |
| 13 | SRGN | 1.4104862 | 12.191781 | 0.177477643451373 |
| 13 | RP11-517P14.7 | -3.872727 | 12.299545 | 0.000350596717701357 |