Supplementary Information

Construction of the Classification Model Using Key Genes Identified between Benign and Malignant Thyroid Nodules from Comprehensive Transcriptomic Data

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Running Title: Classification Model for Thyroid Nodules
**Supplementary Table S1.** The 279 DEGs (differentially expressed genes) identified by student’s t test and fold change method (logFC >0.58 or logFC <-0.58 and adjusted p-value <0.05) from the combined dataset in Table 1.

| ID | Entrez ID | Gene Symbol | Adjusted p-value | logFC  |
|----|-----------|-------------|------------------|--------|
| 1  | 9324      | HMGN3       | 0.035423         | 1.999879 |
| 2  | 515       | ATP5F1      | 0.02562          | 1.907751 |
| 3  | 5800      | PTPRO       | 0.010352         | 1.767712 |
| 4  | 23576     | DDAH1       | 0.003481         | 1.626399 |
| 5  | 9782      | MATR3       | 0.000342         | 1.498593 |
| 6  | 11167     | FSTL1       | 0.000987         | 1.408146 |
| 7  | 4435      | CITED1      | 2.04E-08         | 1.328755 |
| 8  | 301       | ANXA1       | 5.86E-09         | 1.273075 |
| 9  | 1803      | DPP4        | 1.81E-15         | 1.166173 |
| 10 | 55885     | LMO3        | 9.26E-05         | 1.162304 |
| 11 | 10944     | C11orf58    | 0.00016          | 1.162246 |
| 12 | 1001      | CDH3        | 4.16E-14         | 1.155315 |
| 13 | 722       | C4BPA       | 0.000938         | 1.154525 |
| 14 | 10178     | TENM1       | 6.51E-07         | 1.153477 |
| 15 | 439921    | MXRA7       | 0.001287         | 1.117048 |
| 16 | 159       | ADSS        | 0.000106         | 1.113014 |
| 17 | 5627      | PROS1       | 5.72E-10         | 1.104001 |
| 18 | 6447      | SCG5        | 3.80E-06         | 1.081727 |
| 19 | 7360      | UG2         | 7.51E-05         | 1.076941 |
| 20 | 25797     | QPCT        | 5.05E-09         | 1.068464 |
| 21 | 1622      | DBI         | 0.009991         | 1.065552 |
| 22 | 5906      | RAP1A       | 6.06E-05         | 1.055333 |
| 23 | 7991      | TUSC3       | 7.96E-11         | 1.05345  |
| 24 | 7498      | XDH         | 1.86E-05         | 1.04801  |
| 25 | 10981     | RAB32       | 0.000299         | 1.046273 |
| 26 | 4712      | NDUFB6      | 0.003468         | 1.036294 |
| 27 | 2335      | FN1         | 4.05E-06         | 1.035339 |
| 28 | 10289     | EIF1B       | 0.000625         | 1.014718 |
| 29 | 4753      | NELL2       | 2.00E-09         | 1.003549 |
| 30 | 10190     | TXNDC9      | 0.001618         | 0.995109 |
| 31 | 7756      | ZNF207      | 2.64E-05         | 0.976303 |
| 32 | 10551     | AGR2        | 6.43E-06         | 0.96909  |
| 33 | 732       | C8B         | 0.00415          | 0.963064 |
| 34 | 350       | APOH        | 0.014718         | 0.96114  |
| 35 | 892       | CCNC        | 0.001779         | 0.955944 |
| 36 | 3824      | KLRD1       | 0.035056         | 0.95538  |
|   |   |   |   |   |
|---|---|---|---|---|
| 37 | 5378 | PMS1 | 0.001573 | 0.952578 |
| 38 | 4184 | SMCP | 0.006308 | 0.950243 |
| 39 | 9512 | PMPCB | 0.043916 | 0.944831 |
| 40 | 5423 | POLB | 0.002997 | 0.938214 |
| 41 | 11171 | STRAP | 0.007299 | 0.919299 |
| 42 | 1994 | ELAVL1 | 0.01265 | 0.913464 |
| 43 | 5651 | TMPRSS15 | 0.010121 | 0.911664 |
| 44 | 10346 | TRIM22 | 0.000618 | 0.907274 |
| 45 | 90338 | PMPCB | 0.000406 | 0.906331 |
| 46 | 11113 | CIT | 1.64E-05 | 0.898826 |
| 47 | 11321 | GPN1 | 0.039795 | 0.887767 |
| 48 | 967 | CD63 | 0.000659 | 0.879819 |
| 49 | 5597 | MAPK6 | 3.13E-06 | 0.876208 |
| 50 | 7076 | TIMP1 | 3.70E-05 | 0.87375 |
| 51 | 7252 | TSHB | 0.001033 | 0.87295 |
| 52 | 51101 | ZC2HC1A | 0.0133 | 0.870748 |
| 53 | 55023 | PHP | 2.34E-07 | 0.865961 |
| 54 | 2059 | EPS8 | 3.23E-07 | 0.862314 |
| 55 | 9414 | TJP2 | 0.00106 | 0.857954 |
| 56 | 7276 | TTR | 0.000134 | 0.85592 |
| 57 | 2267 | FGL1 | 0.015835 | 0.851886 |
| 58 | 8481 | OFD1 | 0.001143 | 0.846666 |
| 59 | 1278 | COL1A2 | 0.000588 | 0.842995 |
| 60 | 928 | CD9 | 0.000262 | 0.841572 |
| 61 | 55251 | PCMTD2 | 0.000778 | 0.838758 |
| 62 | 7818 | DAP3 | 5.35E-05 | 0.838632 |
| 63 | 9168 | TMSB10 | 4.16E-05 | 0.826025 |
| 64 | 765 | CA6 | 3.89E-05 | 0.825968 |
| 65 | 23095 | KIF1B | 0.000241 | 0.820109 |
| 66 | 1359 | CPA3 | 2.28E-06 | 0.818828 |
| 67 | 5265 | SERPINA1 | 2.31E-05 | 0.817421 |
| 68 | 23362 | PSD3 | 2.28E-07 | 0.811706 |
| 69 | 8846 | ALKBH1 | 0.001502 | 0.811226 |
| 70 | 960 | CD44 | 0.009579 | 0.803231 |
| 71 | 3759 | KCNJ2 | 5.67E-06 | 0.800751 |
| 72 | 7299 | TYR | 0.001273 | 0.799669 |
| 73 | 5858 | PZP | 0.02972 | 0.786161 |
| 74 | 57035 | RSRP1 | 0.000778 | 0.784518 |
| 75 | 6507 | SLC1A3 | 0.000127 | 0.782141 |
| Rank | Gene ID | Gene Symbol | Log2 Fold Change | p-value | FDR | Log10 Fold Change |
|------|---------|-------------|------------------|---------|-----|------------------|
| 78   | 5196    | PF4         | 0.038719         | 0.780987|
| 79   | 6947    | TCN1        | 2.13E-07         | 0.776701|
| 80   | 910     | CD1B        | 6.19E-05         | 0.774637|
| 81   | 51066   | SSUH2       | 0.000158         | 0.773262|
| 82   | 9218    | VAPA        | 0.027383         | 0.767835|
| 83   | 1848    | DUSP6       | 3.32E-05         | 0.762232|
| 84   | 6271    | S100A1      | 0.044205         | 0.758486|
| 85   | 10577   | NPC2        | 1.23E-09         | 0.756935|
| 86   | 7101    | NR2E1       | 0.000264         | 0.752901|
| 87   | 8204    | NRIPI       | 3.71E-05         | 0.752757|
| 88   | 23180   | RFTN1       | 0.006735         | 0.751887|
| 89   | 10099   | TSPAN3      | 0.006228         | 0.748554|
| 90   | 2524    | FUT2        | 0.004373         | 0.74748 |
| 91   | 10050   | SLC17A4     | 6.96E-05         | 0.746404|
| 92   | 8989    | TRPA1       | 0.005963         | 0.741472|
| 93   | 6695    | SPOCK1      | 2.44E-05         | 0.739565|
| 94   | 1044    | CDX1        | 0.004792         | 0.738207|
| 95   | 25976   | TIPARP      | 1.03E-11         | 0.737825|
| 96   | 10205   | MPZL2       | 0.012777         | 0.733413|
| 97   | 1829    | DSG2        | 0.001937         | 0.73068 |
| 98   | 5016    | OVGPI       | 0.001261         | 0.727112|
| 99   | 10409   | BASP1       | 3.57E-07         | 0.72472 |
| 100  | 8754    | ADAM9       | 0.000129         | 0.723038|
| 101  | 5273    | SERPINB10   | 0.001077         | 0.721322|
| 102  | 6385    | SDC4        | 2.79E-12         | 0.718138|
| 103  | 9077    | DIRAS3      | 0.012556         | 0.713309|
| 104  | 689     | BTF3        | 0.005993         | 0.710015|
| 105  | 6281    | S100A10     | 1.35E-07         | 0.702519|
| 106  | 26659   | OR7A5       | 0.011039         | 0.700997|
| 107  | 1809    | DPYSL3      | 0.000475         | 0.700883|
| 108  | 2842    | GPR19       | 3.36E-07         | 0.6965  |
| 109  | 1068    | CETN1       | 0.003572         | 0.695286|
| 110  | 214     | ALCAM       | 0.018923         | 0.694906|
| 111  | 3489    | IGFBP6      | 2.75E-06         | 0.691788|
| 112  | 1315    | COPB1       | 5.26E-06         | 0.690871|
| 113  | 5431    | POLR2B      | 0.000372         | 0.690003|
| 114  | 9648    | GCC2        | 0.000155         | 0.688346|
| 115  | 3426    | CFI         | 0.000175         | 0.685456|
| 116  | 11122   | PTPRT       | 0.000422         | 0.681387|
| 117  | 22948   | CCT5        | 0.002134         | 0.676653|
| 118  | 9969    | MED13       | 7.31E-05         | 0.676161|
|   |   |   |   |   |
|---|---|---|---|---|
| 119 | 8714 | ABCC3 | 1.78E-16 | 0.67522 |
| 120 | 6005 | RHAG | 0.000897 | 0.675176 |
| 121 | 3880 | KRT19 | 2.60E-08 | 0.673278 |
| 122 | 10924 | SMPDL3A | 0.004666 | 0.671237 |
| 123 | 23397 | NCAH | 1.85E-05 | 0.670533 |
| 124 | 8444 | DYRK3 | 0.008629 | 0.66916 |
| 125 | 26716 | OR2H1 | 0.00278 | 0.666886 |
| 126 | 26046 | LTN1 | 0.006889 | 0.666612 |
| 127 | 8288 | EPX | 0.001537 | 0.662731 |
| 128 | 10930 | APOBEC2 | 0.000197 | 0.662694 |
| 129 | 23231 | SEL1L3 | 1.34E-09 | 0.65943 |
| 130 | 4152 | MBD1 | 0.000759 | 0.656896 |
| 131 | 959 | CD40LG | 0.041309 | 0.656646 |
| 132 | 1272 | CNTN1 | 0.003268 | 0.655128 |
| 133 | 1781 | DYNC1I2 | 0.000344 | 0.653878 |
| 134 | 220 | ALDH1A3 | 6.50E-05 | 0.653545 |
| 135 | 9550 | ATP6V1G1 | 3.59E-05 | 0.652118 |
| 136 | 8542 | APOL1 | 4.53E-05 | 0.647395 |
| 137 | 10092 | ARPC5 | 0.00267 | 0.646439 |
| 138 | 5324 | PLAG1 | 4.17E-09 | 0.64433 |
| 139 | 22876 | INPP5F | 0.00184 | 0.644166 |
| 140 | 1267 | CNP | 0.00462 | 0.641788 |
| 141 | 5411 | PNN | 0.008101 | 0.633431 |
| 142 | 8747 | ADAM21 | 0.002226 | 0.630448 |
| 143 | 7472 | WNT2 | 0.001328 | 0.630211 |
| 144 | 9793 | CKAP5 | 0.007447 | 0.627886 |
| 145 | 6554 | SLC10A1 | 0.000755 | 0.623376 |
| 146 | 10782 | ZNF274 | 9.59E-08 | 0.622719 |
| 147 | 5791 | PTPRE | 4.13E-10 | 0.6212 |
| 148 | 8869 | ST3GAL5 | 3.23E-08 | 0.620601 |
| 149 | 9061 | PAPPS1 | 0.000521 | 0.616568 |
| 150 | 5593 | PRKG2 | 0.008555 | 0.614311 |
| 151 | 269 | AMHR2 | 0.041574 | 0.613742 |
| 152 | 671 | BPI | 0.030166 | 0.613295 |
| 153 | 6906 | SERPINA7 | 0.01191 | 0.611129 |
| 154 | 4076 | CAPRIN1 | 0.005785 | 0.609744 |
| 155 | 9407 | TMPRSS11D | 0.020674 | 0.606399 |
| 156 | 64285 | RHBDF1 | 0.002236 | 0.604996 |
| 157 | 3698 | ITIH2 | 0.002248 | 0.604219 |
| 158 | 1545 | CYP1B1 | 2.18E-08 | 0.602743 |
| 159 | 10200 | MPHOSPH6 | 0.013756 | 0.60128 |
| 160 | 7039  | TGFA   | 1.71E-15 | 0.601049 |
|-----|-------|--------|----------|-----------|
| 161 | 2554  | GABRA1 | 0.000197 | 0.600628 |
| 162 | 4077  | NB1R1  | 0.027874 | 0.600467 |
| 163 | 6582  | SLC22A2| 0.04372  | 0.597038 |
| 164 | 2597  | GAPDH  | 0.007192 | 0.596042 |
| 165 | 347902| AMIGO2 | 0.000945 | 0.595924 |
| 166 | 7555  | CNBP   | 0.000618 | 0.593311 |
| 167 | 1826  | DSCAM  | 0.001434 | 0.590168 |
| 168 | 4897  | NRCAM  | 8.57E-08 | 0.5898   |
| 169 | 6716  | SRD5A2 | 0.023964 | 0.587584 |
| 170 | 5251  | PHEX   | 0.035669 | 0.586269 |
| 171 | 129642| MBOAT2 | 7.89E-07 | 0.585995 |
| 172 | 3742  | GALNT8 | 7.60E-05 | 0.585665 |
| 173 | 2887  | GRB10  | 6.85E-05 | -0.58764 |
| 174 | 3712  | IVD    | 2.29E-09 | -0.58911 |
| 175 | 678   | ZFP36L2| 4.57E-07 | -0.58959 |
| 176 | 1040  | CDS1   | 0.010997 | -0.59163 |
| 177 | 90141 | EFCAB11| 0.001098 | -0.59238 |
| 178 | 1059  | CENPB  | 0.000124 | -0.5929  |
| 179 | 3090  | HIC1   | 0.02802  | -0.59372 |
| 180 | 29903 | CCDC106| 0.000434 | -0.597   |
| 181 | 54361 | WNT4   | 2.32E-05 | -0.59749 |
| 182 | 81550 | TDRD3  | 2.77E-06 | -0.59837 |
| 183 | 8898  | MTMR2  | 0.034402 | -0.59882 |
| 184 | 1960  | EGR3   | 0.000616 | -0.6024  |
| 185 | 3339  | HSPG2  | 0.001039 | -0.60691 |
| 186 | 2155  | F7     | 0.028365 | -0.6085  |
| 187 | 11100 | HNRNPUL1| 0.017951| -0.60932 |
| 188 | 7123  | CLEC3B | 5.73E-08 | -0.61301 |
| 189 | 9844  | ELMO1  | 2.74E-05 | -0.62222 |
| 190 | 5989  | HNGC-9982| 0.002238| -0.62388 |
| 191 | 6004  | RGS16  | 9.76E-07 | -0.6241  |
| 192 | 55957 | LIN37  | 9.60E-05 | -0.62709 |
| 193 | 5058  | PAK1   | 0.008696 | -0.62735 |
| 194 | 3298  | HSF2   | 0.006881 | -0.62939 |
| 195 | 50814 | NSDHL  | 0.000144 | -0.63025 |
| 196 | 51668 | HSPB11 | 3.48E-05 | -0.6305  |
| 197 | 6649  | SOD3   | 0.036883 | -0.63255 |
| 198 | 27445 | PCLO   | 0.011926 | -0.63624 |
| 199 | 8676  | STX11  | 0.000467 | -0.63697 |
| 200 | 5277  | PIGA   | 0.006811 | -0.64035 |
|    |   |     |      |        |        |
|----|---|-----|------|--------|--------|
| 201| 2619 | GAS1 | 0.002816 | -0.64075 |
| 202| 4524 | MTHFR | 0.041206 | -0.64918 |
| 203| 27336 | HTATSF1 | 0.00448 | -0.64981 |
| 204| 4493 | MT1E | 2.68E-05 | -0.6512 |
| 205| 7755 | ZNF205 | 0.001924 | -0.66042 |
| 206| 3815 | KIT | 0.042131 | -0.66656 |
| 207| 202 | 4524 | MTHFR | 0.041206 | -0.64918 |
| 208| 209 | EML1 | 4.00E-09 | -0.66977 |
| 209| 2788 | GNG7 | 1.92E-06 | -0.67215 |
| 210| 207 | 10279 | PRSS16 | 1.11E-05 | -0.67225 |
| 211| 208 | 2009 | EML1 | 4.00E-09 | -0.66977 |
| 212| 209 | 2905 | GRIN2C | 5.96E-05 | -0.66707 |
| 213| 210 | 3815 | MT1E | 2.68E-05 | -0.6512 |
| 214| 211 | 7755 | ZNF205 | 0.001924 | -0.66042 |
| 215| 212 | 23092 | ARHGAP26 | 0.005073 | -0.67536 |
| 216| 213 | 28 | ABO | 0.016491 | -0.67557 |
| 217| 214 | 22849 | CPEB3 | 2.33E-07 | -0.67778 |
| 218| 215 | 6480 | ST6GAL1 | 0.000953 | -0.67898 |
| 219| 216 | 4007 | PRICKLE3 | 0.03613 | -0.67985 |
| 220| 217 | 7849 | PAX8 | 6.88E-05 | -0.68524 |
| 221| 218 | 25840 | METTL7A | 0.034275 | -0.68544 |
| 222| 219 | 10425 | ARIH2 | 0.000363 | -0.693 |
| 223| 220 | 10100 | TSPAN2 | 0.00702 | -0.69332 |
| 224| 221 | 5172 | SLC26A4 | 3.62E-11 | -0.69716 |
| 225| 222 | 2273 | FHL1 | 3.36E-09 | -0.69808 |
| 226| 223 | 670 | BPHL | 6.03E-05 | -0.70171 |
| 227| 224 | 84444 | DOT1L | 0.037573 | -0.70555 |
| 228| 225 | 4057 | LTF | 3.57E-10 | -0.71261 |
| 229| 226 | 11193 | WBP4 | 0.001383 | -0.71508 |
| 230| 227 | 3081 | HGD | 9.27E-08 | -0.72673 |
| 231| 228 | 1734 | DIO2 | 1.32E-10 | -0.72726 |
| 232| 229 | 5909 | RAP1GAP | 1.86E-09 | -0.72971 |
| 233| 230 | 26471 | NUPR1 | 0.000304 | -0.73394 |
| 234| 231 | 255057 | C19orf26 | 0.028982 | -0.73829 |
| 235| 232 | 6668 | SP2 | 0.000589 | -0.74243 |
| 236| 233 | 6392 | SDHD | 0.001826 | -0.7456 |
| 237| 234 | 6844 | VAMP2 | 0.018031 | -0.74826 |
| 238| 235 | 3213 | HOXB3 | 0.016098 | -0.75247 |
| 239| 236 | 430 | ASCL2 | 0.014075 | -0.75314 |
| 240| 237 | 5546 | PRCC | 1.43E-06 | -0.76112 |
| 241| 238 | 8857 | FCGBP | 1.18E-05 | -0.76491 |
| 242| 239 | 5897 | RAG2 | 3.87E-05 | -0.76635 |
| 243| 240 | 1147 | CHUK | 0.000761 | -0.76874 |
| 244| 241 | 27350 | APOBEC3C | 8.26E-05 | -0.77319 |
| 245|   | 396 | ARHGDIA | 0.013364 | -0.77533 |
|   |     |       |          |            |            |
|---|-----|-------|----------|------------|------------|
| 242| 7542| ZFPL1 | 0.001336 | -0.77841  |
| 243| 26146| TRAF3IP1 | 0.000189 | -0.78888  |
| 244| 762 | CA4   | 3.05E-10 | -0.79406  |
| 245| 23443| SLC35A3 | 0.000171 | -0.7947   |
| 246| 25802| LMOD1 | 3.89E-08 | -0.80358  |
| 247| 6305| SBF1  | 1.13E-06 | -0.80539  |
| 248| 51232| CRIM1 | 7.84E-05 | -0.81628  |
| 249| 26112| CCDC69 | 0.015341 | -0.82799  |
| 250| 3399| ID3   | 2.91E-11 | -0.83671  |
| 251| 22927| HABP4 | 0.001917 | -0.83713  |
| 252| 2324| FLT4  | 4.54E-05 | -0.83995  |
| 253| 2618| GART  | 0.049823 | -0.84525  |
| 254| 2355| FOSL2 | 0.038951 | -0.85493  |
| 255| 4703| NEB   | 3.90E-06 | -0.8582   |
| 256| 432 | ASGR1 | 2.01E-05 | -0.89599  |
| 257| 1805| DPT   | 0.00018  | -0.8994   |
| 258| 4494| MT1F  | 4.58E-09 | -0.91087  |
| 259| 219333| USP12 | 0.047108 | -0.9167   |
| 260| 2117| ETV3  | 0.000167 | -0.93059  |
| 261| 6722| SRF   | 0.003049 | -0.94275  |
| 262| 1381| CRABP1| 1.48E-06 | -0.95542  |
| 263| 6921| TCEB1 | 0.004592 | -0.98698  |
| 264| 2323| FLT3LG| 0.009582 | -0.98782  |
| 265| 1299| COL9A3| 8.03E-05 | -1.00485  |
| 266| 4713| NDUFB7| 0.000215 | -1.00738  |
| 267| 4495| MT1G  | 1.39E-07 | -1.05177  |
| 268| 9265| CYTH3 | 7.71E-05 | -1.07064  |
| 269| 8458| TTF2  | 0.030282 | -1.09564  |
| 270| 968 | CD68  | 0.007163 | -1.11098  |
| 271| 6624| FSCN1 | 0.003741 | -1.12761  |
| 272| 4920| ROR2  | 3.74E-05 | -1.19808  |
| 273| 2167| FABP4 | 8.24E-10 | -1.24181  |
| 274| 744 | MPPED2| 1.02E-13 | -1.25312  |
| 275| 3292| HSD17B1| 1.63E-05 | -1.28357  |
| 276| 1014| CDH16 | 3.65E-16 | -1.33575  |
| 277| 1733| DIO1  | 8.64E-07 | -1.42927  |
| 278| 7173| TPO   | 3.90E-15 | -1.49917  |
| 279| 9351| SLC9A3R2 | 0.00174 | -1.61953  |
Supplementary Table S2. The Gene Ontology (GO) enrichment analysis was performed to identify the key biological annotations for malignant and benign thyroid nodules, including BP (biological process), MF (molecular function) and CC (cell component).

| GO ID     | Description                                                                 | Raw p-value | Gene Name                                                                 | No. |
|-----------|------------------------------------------------------------------------------|-------------|----------------------------------------------------------------------------|-----|
| GO:0042445| hormone metabolic process                                                    | 1.54E-06    | SCG5/TSHB/TR/SR/XA3/TIPARP/ALDH1A3/CYP1B1/SR/TN4/PAX8/DIO2/CRABP1/HSD17B1/DIO1/TPO | 15  |
| GO:0002576| platelet degranulation                                                       | 1.66E-05    | PROS1/FV/APOH/CD63/TIMP1/CD/9/SERPINA1/PF4/CLEC3B/HABP4                   | 10  |
| GO:0035924| cellular response to vascular endothelial growth factor stimulus            | 5.46E-05    | ANXA1/XDH/CD63/EGR3/GAS1/FLT4/MT1G                                        | 7   |
| GO:0048066| developmental pigmentation                                                  | 5.53E-05    | CITED1/RAB32/RAB27A/CD63/TYR/KIT                                           | 6   |
| GO:0048608| reproductive structure development                                          | 5.74E-05    | CITED1/ANXA1/ALKB1/NRIP1/TIPARP/BASP1/KRT19/PLAG1/WNT2/AMHR2/SR/TN4/NSDHL/KIT/NUP1/ASCL2/COL9A3/ROR2 | 18  |
| GO:0061458| reproductive system development                                             | 6.28E-05    | CITED1/ANXA1/ALKB1/NRIP1/TIPARP/BASP1/KRT19/PLAG1/WNT2/AMHR2/SR/TN4/NSDHL/KIT/NUP1/ASCL2/COL9A3/ROR2 | 18  |
| GO:0006590| thyroid hormone generation                                                  | 8.65E-05    | PAX8/DIO2/DIO1/TPO                                                          | 4   |
| GO:0060231| mesenchymal to epithelial transition                                        | 1.38E-04    | CITED1/BASP1/WNT4/PAX8                                                      | 4   |
| GO:0050931| pigment cell differentiation                                                | 1.56E-04    | CITED1/RAB32/RAB27A/CD63/KIT                                               | 5   |
| GO:0042403| thyroid hormone metabolic process                                           | 2.08E-04    | PAX8/DIO2/DIO1/TPO                                                          | 4   |
| GO:0043312| neutrophil degranulation                                                    | 2.50E-04    | QPCT/RAP1A/RAB27A/CD63/TIPARP/CD44/TCN1/VAPA/NPC2/SERP1/NB1/CPB1/EPX/ARPC5/BPI/METTL7A/LTF/CD68 | 18  |
| GO:0002283| neutrophil activation involved in immune response                          | 2.70E-04    | QPCT/RAP1A/RAB27A/CD63/TIPARP/CD44/TCN1/VAPA/NPC2/SERP1/NB1/CPB1/EPX/ARPC5/BPI/METTL7A/LTF/CD68 | 18  |
GO:0010951  negative regulation of endopeptidase activity  2.88E-04  PROS1/TIMP1/SERPINA1/CD44/PZP/SPOCK1/SERPINB10/SERPINA7/ITIH2/GAPDH/LTF/CRIM1  12
GO:0042119  neutrophil activation  3.44E-04  QPCT/RAP1A/RAB27A/CD63/TTR/SERPINA1/CD44/TCN1/VAPA/NPC2/SERPINB10/COPB1/EPX/ARPC5/BPI/METTL7A/LTF/CD68  18
GO:002446  neutrophil mediated immunity  3.52E-04  QPCT/RAP1A/RAB27A/CD63/TTR/SERPINA1/CD44/TCN1/VAPA/NPC2/SERPINB10/COPB1/EPX/ARPC5/BPI/METTL7A/LTF/CD68  18
GO:0010466  negative regulation of peptidase activity  4.39E-04  PROS1/TIMP1/SERPINA1/CD44/PZP/SPOCK1/SERPINB10/SERPINA7/ITIH2/GAPDH/LTF/CRIM1  12
GO:0031346  positive regulation of cell projection organization  4.69E-04  TENM1/RAP1A/FN1/MAPK6/EP8/DPS3/NCN1/CAPRIN1/DSCAM/PAK1/KIT/CPEB3/ARHGDIA/SRF/FSCN1  15
GO:0008585  female gonad development  4.77E-04  NRIP1/TIPARP/AMHR2/WNT4/KIT/NUPR1/COL9A3  7
GO:0032970  regulation of actin filament-based process  5.36E-04  TENM1/CIT/EP8/TMSB10/KCNJ2/DSG2/SDC4/S100A10/ARPC5/WNT4/PAK1/ARHGDIA/LMOD1/NEB/FSCN1  15
GO:0034754  cellular hormone metabolic process  5.68E-04  TTR/TIPARP/ALDH1A3/CYP1B1/SRD5A2/WNT4/CRABP1/HSD17B1  8
GO:0035019  somatic stem cell population maintenance  5.97E-04  NR2E1/POLR2B/ZFP36L2/KIT/PAX8/ASCL2  6
GO:0046545  development of primary female sexual characteristics  6.48E-04  NRIP1/TIPARP/AMHR2/WNT4/KIT/NUPR1/COL9A3  7
GO:0018958  phenol-containing compound metabolic process  7.28E-04  CITED1/CDH3/TYR/PAX8/DIO2/DIO1/TPO  7
GO:0051491  positive regulation of filopodium assembly  8.60E-04  TENM1/DSL3/ARHGDIA/SRF/FSCN1  4
GO:0034329  cell junction assembly  9.18E-04  PTPRO/CDH3/RAP1A/FN1/CD9/SDC4/S100A10/GABRA1/AMIG02/DSCAM/NRCAM/WNT4/PCLO/SRF/FSCN1  15
GO:0061005  cell differentiation involved in kidney development  1.06E-03  PTPRO/CITED1/BASP1/WNT4/PAX8  5
| GO:0003338 | metanephros morphogenesis | 1.10E-03 | CITED1/BASP1/WNT4/PAX8 | 4 |
| GO:0010273 | detoxification of copper ion | 1.18E-03 | MT1E/MT1F/MT1G | 3 |
| GO:0090136 | epithelial cell-cell adhesion | 1.18E-03 | CYP1B1/KIT/SRF | 3 |
| GO:1990169 | stress response to copper ion | 1.18E-03 | MT1E/MT1F/MT1G | 3 |
| GO:0030282 | bone mineralization | 1.32E-03 | COL1A2/NBR1/PHEX/WNT4/CLEC3B/LTF/ROR2 | 7 |
| GO:0046660 | female sex differentiation | 1.39E-03 | NRIP1/TIPARP/AMHR2/WNT4/KIT/NUPR1/COL9A3 | 7 |
| GO:0048568 | embryonic organ development | 1.44E-03 | CITED1/KRT19/ALDH1A3/WNT2/NSDHL/KIT/PAX8/FOX13/ASCL2/TRAF3IP1/ID3/SRF/FLT3LG/ROR2/TPO | 15 |
| GO:0032956 | regulation of actin cytoskeleton organization | 1.49E-03 | TENM1/CIT/EP8/SMSB10/SDC4/S100A10/ARPC5/WNT4/PAX1/ARHGDIA/LMOD1/NEB/FSCN1 | 13 |
| GO:0042446 | hormone biosynthetic process | 1.52E-03 | SRD5A2/WNT4/DIO2/HSD17B1/DIO1/TPO | 6 |
| GO:0051017 | actin filament bundle assembly | 1.72E-03 | EPS8/SDC4/S100A10/DPYSL3/WNT4/PAX1/ARHGDIA/LMOD1/NEB/FSCN1 | 8 |
| GO:0061687 | detoxification of inorganic compound | 1.73E-03 | MT1E/MT1F/MT1G | 3 |
| GO:0097501 | stress response to metal ion | 1.73E-03 | MT1E/MT1F/MT1G | 3 |
| GO:0071276 | cellular response to cadmium ion | 1.91E-03 | MT1E/CHUK/MT1F/MT1G | 4 |
| GO:0048857 | neural nucleus development | 1.98E-03 | ATP5PB/S100A1/BASP1/ALDH1A3/CNP | 5 |
| GO:0061572 | actin filament bundle organization | 2.02E-03 | EPS8/SDC4/S100A10/DPYSL3/WNT4/PAX1/ARHGDIA/LMOD1/NEB/FSCN1 | 8 |
| GO:0072077 | renal vesicle morphogenesis | 2.06E-03 | CITED1/WNT4/PAX8 | 3 |
| GO:007015 | actin filament organization | 2.08E-03 | TENM1/CIT/EPS8/SMSB10/SDC4/S100A10/DPYSL3/ARPC5/WNT4/PAX1/LMOD1/NEB/SRF/FSCN1 | 14 |
| GO:0048009 | insulin-like growth factor receptor signaling pathway | 2.12E-03 | CDH3/PHIP/IGFBP6/CRIM1 | 4 |
| GO:0046686 | response to cadmium ion | 2.13E-03 | MT1E/KIT/CHUK/MT1F/MT1G | 5 |
| GO:0045861 | negative regulation of proteolysis | 2.17E-03 | PROS1/TIMP1/SERPINA1/CD44/PZP/SPOCK1/SERPINB10/SERPINA7/ITIH2/GAPDH/GAS1/LTF/CRIM1 | 13 |
| GO:0045785 | positive regulation of cell adhesion | 2.23E-03 | ANXA1/DPP4/FN1/AGR2/TFRC/CD44/ADAM9/SDC4/S100A10/CD40LG/WNT4/EGR3/PAK1/CYTH3 | 14 |
| GO:0072087 | renal vesicle development | 2.42E-03 | CITED1/WNT4/PAX8 | 3 |
| GO:0031032 | actomyosin structure organization | 2.45E-03 | CIT/SDC4/S100A10/KRT19/WNT4/PAK1/LMOD1/NEB/SPR | 9 |

**MF (Molecular Function)**

| GO:0004866 | endopeptidase inhibitor activity | 9.45E-05 | PROS1/TIMP1/SERPINA1/PZP/SPOCK1/SERPINB10/SERPINA7/ITIH2/GAPDH/LTF/CRIM1 | 11 |
| GO:0030414 | peptidase inhibitor activity | 1.34E-04 | PROS1/TIMP1/SERPINA1/PZP/SPOCK1/SERPINB10/SERPINA7/ITIH2/GAPDH/LTF/CRIM1 | 11 |
| GO:0061135 | endopeptidase regulator activity | 1.34E-04 | PROS1/TIMP1/SERPINA1/PZP/SPOCK1/SERPINB10/SERPINA7/ITIH2/GAPDH/LTF/CRIM1 | 11 |
| GO:0061134 | peptidase regulator activity | 1.69E-04 | PROS1/FN1/TIMP1/SERPINA1/PZP/SPOCK1/SERPINB10/SERPINA7/ITIH2/GAPDH/LTF/CRIM1 | 11 |
| GO:0005539 | glycosaminoglycan binding | 2.55E-04 | FSTL1/TENM1/FN1/NELL2/ZNF207/APOH/CD44/PF4/DPYSL3/CLEC3B/SOD3/LTF | 12 |
| GO:0008201 | heparin binding | 3.19E-04 | FSTL1/TENM1/FN1/NELL2/ZNF207/APOH/CD44/PF4/DPYSL3/CLEC3B/SOD3/LTF | 10 |
| GO:1901681 | sulfur compound binding | 5.63E-04 | FSTL1/TENM1/DBI/FN1/NELL2/ZNF207/APOH/CD44/PF4/DPYSL3/CLEC3B/SOD3/LTF | 12 |
| GO:0004867 | serine-type endopeptidase inhibitor activity | 6.56E-04 | SERPINA1/PZP/SPOCK1/SERPINB10/SERPINA7/ITIH2/CRIM1 | 7 |
| GO:0005001 | transmembrane receptor protein tyrosine phosphatase activity | 2.15E-03 | PTPRO/PTPRT/PTPRE | 3 |
|-------------|---------------------------------------------------------------|--------------|-------------------|---|
| GO:0019198 | transmembrane receptor protein phosphatase activity          | 2.15E-03     | PTPRO/PTPRT/PTPRE | 3 |
| GO:0005518 | collagen binding                                              | 3.85E-03     | FN1/CD44/SPOCK1/ADAM9/PAK1 | 5 |
| GO:002020  | protease binding                                              | 3.89E-03     | DPP4/FN1/TIMP1/COL1A2/SERPINA1/PZP/KIT | 7 |
| GO:008017  | microtubule binding                                           | 5.27E-03     | ZNF207/POLB/KIF1B/VAPA/CETN1/CKAP5/GAPDH/EML1/TRAFF31P1/CCDC69 | 10 |
| GO:004857  | enzyme inhibitor activity                                     | 6.02E-03     | ANXA1/PROS1/SCG5/TIMP1/SERPINA1/PZP/SPOCK1/SERPINB10/SERPIN7/ITIH2/GAPDH/LTF/CRIM1 | 13 |
| GO:0015631 | tubulin binding                                               | 6.52E-03     | ZNF207/POLB/KIF1B/VAPA/CETN1/CKAP5/GAPDH/EML1/TRAFF31P1/CCDC69 | 12 |
| GO:0035925 | mRNA 3'-UTR AU-rich region binding                            | 7.41E-03     | ELAV1/ZFP362L2/CPEB3 | 3 |
| GO:0098632 | cell-cell adhesion mediator activity                          | 7.50E-03     | ANXA1/DSG2/DSCAM/NRCAM | 4 |
| GO:0019199 | transmembrane receptor protein kinase activity                | 7.73E-03     | AMHR2/KIT/CRIM1/FLT4/ROR2 | 5 |
| GO:0017091 | AU-rich element binding                                       | 9.13E-03     | ELAV1/ZFP362L2/CPEB3 | 3 |
| GO:0033764 | steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | 1.01E-02 | SRD5A2/NSDHL/HSD17B1 | 3 |
| GO:0050839 | cell adhesion molecule binding                                | 1.16E-02     | PTPRO/ANXA1/CDH3/TENM1/FN1/TXNDC9/TJP2/CD9/VAPA/DSG2/ADAM9/PTPRT/CKAP5/FSCN1/SLC9A3R2 | 15 |
| GO:0098631 | cell adhesion mediator activity                               | 1.33E-02     | ANXA1/DSG2/DSCAM/NRCAM | 4 |
| GO:0004126 | cytidine deaminase activity                                   | 1.43E-02     | APOBEC2/APOBEC3C | 2 |
| GO:0008239 | dipeptidyl-peptidase activity | 1.43E-02 | DPP4/PRSS16 | 2 |
| GO:0004714 | transmembrane receptor protein tyrosine kinase activity | 1.57E-02 | KIT/CRIM1/FLT4/ROR2 | 4 |
| GO:0003906 | DNA-(apurinic or apyrimidinic site) endonuclease activity | 1.68E-02 | POLB/ALKBH1 | 2 |
| GO:0052744 | phosphatidylinositol monophosphate phosphatase activity | 1.68E-02 | INPP5F/MTMR2 | 2 |
| GO:0086080 | protein binding involved in heterotypic cell-cell adhesion | 1.68E-02 | DSG2/NRCAM | 2 |
| GO:0016229 | steroid dehydrogenase activity | 1.68E-02 | SRD5A2/NSDHL/HSD17B1 | 3 |
| GO:0004725 | protein tyrosine phosphatase activity | 1.99E-02 | PTPRO/DUSP6/PTPRT/PTPRE/MTMR2 | 5 |
| GO:0019838 | growth factor binding | 2.02E-02 | COL1A2/IGFBP6/AMHR2/RHBDF1/CRIM1/FLT4 | 6 |
| GO:0004089 | carbonate dehydratase activity | 2.21E-02 | CA6/CA4 | 2 |
| GO:0005109 | frizzled binding | 2.25E-02 | WNT2/WNT4/ROR2 | 3 |
| GO:0008236 | serine-type peptidase activity | 2.39E-02 | DPP4/TMPRSS15/CFI/TMPRSS11D/F7/PRSS16/LTF | 7 |
| GO:0008191 | metalloendopeptidase inhibitor activity | 2.50E-02 | TIMP1/SPOCK1 | 2 |
| GO:0016825 | hydrolase activity, acting on acid phosphorus-nitrogen bonds | 2.65E-02 | DPP4/TMPRSS15/CFI/TMPRSS11D/F7/PRSS16/LTF | 7 |
| GO:0017171 | serine hydrolase activity | 2.65E-02 | DPP4/TMPRSS15/CFI/TMPRSS11D/F7/PRSS16/LTF | 7 |
| GO:0015125 | bile acid transmembrane transporter activity | 2.81E-02 | ABCC3/SLC10A1 | 2 |
| GO:0042826 | histone deacetylase binding | 2.96E-02 | NR2E1/NRIP1/HIC1/SP2/SRF | 5 |
| GO:0038024  | cargo receptor activity | 3.06E-02 | TMPRSS15/TFRC/CFI/ASGR1 | 4 |
|------------|-------------------------|----------|-------------------------|---|
| GO:0008138 | protein tyrosine/serine/threonine phosphatase activity | 3.26E-02 | DUSP6/MTMR2/SBF1 | 3 |
| GO:0005086 | ARF guanyl-nucleotide exchange factor activity | 3.46E-02 | PSD3/CYTH3 | 2 |
| GO:0016500 | protein-hormone receptor activity | 3.46E-02 | AMHR2/PAX8 | 2 |
| GO:0031681 | G-protein beta-subunit binding | 3.46E-02 | CCT5/GNG7 | 2 |
| GO:0045296 | cadherin binding | 3.47E-02 | PTPRO/ANXA1/CDH3/TXNDC9/TJP2/VAPA/PTPRT/CKAP5/FSCN1/SLC9A3R2 | 10 |
| GO:0008373 | sialyltransferase activity | 3.80E-02 | ST3GAL5/ST6GAL1 | 2 |
| GO:0030506 | ankyrin binding | 3.80E-02 | RHAG/NRCAM | 2 |
| GO:0004252 | serine-type endopeptidase activity | 3.91E-02 | DPP4/TMPRSS15/CFI/TMPRSS11D/F7/LTF | 6 |
| GO:0030674 | protein-macromolecule adaptor activity | 4.33E-02 | ANXA1/TRIM22/EPS8/TJP2/COL1A2/STX11/FSCN1 | 7 |
| GO:0005158 | insulin receptor binding | 4.53E-02 | PHIP/GRB10 | 2 |

**CC (Cell Component)**

| GO:0062023 | collagen-containing extracellular matrix | 4.69E-06 | ANXA1/MXRA7/FN1/APOH/TIMP1/COL1A2/CPA3/SERPINA1/PZP/PF4/S100A10/WNT2/ITIH2/HSPG2/F7/CLEC3B/SOD3/DPT/COL9A3 | 19 |
| GO:0034774 | secretory granule lumen | 1.23E-05 | PROS1/QPCT/FN1/APOH/RAB27A/TIMP1/TTR/SERPINA1/PF4/TCN1/NPC2/EPX/ARPC5/BPI/CLEC3B/LTF | 16 |
| GO:0060205 | cytoplasmic vesicle lumen | 1.44E-05 | PROS1/QPCT/FN1/APOH/RAB27A/TIMP1/TTR/SERPINA1/PF4/TCN1/NPC2/EPX/ARPC5/BPI/CLEC3B/LTF | 16 |
| GO:0031983 | vesicle lumen | 1.55E-05 | PROS1/QPCT/FN1/APOH/RAB27A/TIMP1/TTR/SERPINA1/PF4/TCN1/NPC2/EPX/ARPC5/BPI/CLEC3B/LTF | 16 |
| GO:0016324 | apical plasma membrane | 5.57E-04 | PTPRO/ANXA1/DPP4/FN1/RAB27A/CD9/CD44/SLC17A4/DSG2/PRKG2/SLC26A4/CA4/SLC9A3R2 | 13 |
|-------------|------------------------|----------|-----------------------------------------------------------------|-----|
| GO:0033162 | melanosome membrane    | 8.72E-04 | RAB32/RAB27A/TYR                                                | 3   |
| GO:0045009 | chitosome              | 8.72E-04 | RAB32/RAB27A/TYR                                                | 3   |
| GO:0090741 | pigment granule membrane | 8.72E-04 | RAB32/RAB27A/TYR                                                | 3   |
| GO:0071437 | invadopodium           | 1.31E-03 | DPP4/PAK1/FSCN1                                                  | 3   |
| GO:0035580 | specific granule lumen | 1.72E-03 | QPCT/RAB27A/TCN1/BPI/LTF                                        | 5   |
| GO:0031091 | platelet alpha granule | 1.73E-03 | PROS1/FN1/TIMP1/CD9/SERPINA1/PF4                                | 6   |
| GO:0031093 | platelet alpha granule lumen | 2.43E-03 | PROS1/FN1/TIMP1/SERPINA1/PF4                                    | 5   |
| GO:0030426 | growth cone            | 2.81E-03 | PTPRO/EPS8/BASP1/DPYSL3/ARPC5/DSCAM/CBARP/FSCN1                 | 8   |
| GO:0042827 | platelet dense granule | 2.96E-03 | APOH/CD63/CLEC3B                                                 | 3   |
| GO:0045177 | apical part of cell    | 3.01E-03 | PTPRO/ANXA1/DPP4/FN1/RAB27A/CD9/CD44/SLC17A4/DSG2/PRKG2/SLC26A4/CA4/SLC9A3R2 | 13 |
| GO:0005796 | Golgi lumen            | 3.07E-03 | PROS1/SDC4/WNT4/HSPG2/F7/SOD3                                   | 6   |
| GO:0030667 | secretory granule membrane | 3.23E-03 | RAP1A/RAB27A/CD63/CD9/CD44/VAPA/SERPINB10/COPB1/VAMP2/CA4/CD68 | 11  |
| GO:0030427 | site of polarized growth | 3.36E-03 | PTPRO/EPS8/BASP1/DPYSL3/ARPC5/DSCAM/CBARP/FSCN1                 | 8   |
| GO:009897  | external side of plasma membrane | 3.66E-03 | ANXA1/KLRD1/TFRC/CD9/CD1B/ADAM9/ALCAM/CD40LG/WNT2/NRCAM/KIT/CA4/FLT3LG | 13 |
| GO:0042470 | melanosome             | 3.72E-03 | RAB32/TFRC/RAB27A/CD63/TYR/CNP                                  | 6   |
| GO:0048770 | pigment granule        | 3.72E-03 | RAB32/TFRC/RAB27A/CD63/TYR/CNP                                  | 6   |
| GO:0005788 | endoplasmic reticulum lumen | 4.24E-03 | FSTL1/DBI/FN1/TIMP1/COL1A2/SERPINA1/APOL1/ITIH2/WNT4/F7/COL9A3 | 11  |
| GO:0031233 | intrinsic component of external side of plasma membrane | 4.37E-03 | ADAM9/CA4/FLT3LG | 3 |
| GO:0072562 | blood microparticle | 4.62E-03 | C4BPA/PROS1/FN1/TFR/C2/ZP/AROL1/ITIH2 | 7 |
| GO:0005925 | focal adhesion | 4.70E-03 | ANXA1/DPP4/C9/CD44/ADAM9/SDC4/ALCAM/ARPC5/HSPG2/PK1/ARHG AP26/FHL1/SCL9A3R2 | 13 |
| GO:0030055 | cell-substrate junction | 5.41E-03 | ANXA1/DPP4/C9/CD44/ADAM9/SDC4/ALCAM/ARPC5/HSPG2/PK1/ARHG AP26/FHL1/SCL9A3R2 | 13 |
| GO:1904724 | tertiary granule lumen | 7.23E-03 | QPCT/TCN1/METTL7A/LTF | 4 |
| GO:0017146 | NMDA selective glutamate receptor complex | 9.81E-03 | EPS8/GRIN2C | 2 |
| GO:0032585 | multivesicular body membrane | 1.17E-02 | RAB27A/C9D3 | 2 |
| GO:0010494 | cytoplasmic stress granule | 1.36E-02 | ELAVL1/DYRK3/CAPRIN1/HABP4 | 4 |
| GO:0030016 | myofibril | 1.36E-02 | S100A1/SDC4/KRT19/NBR1/PK1/LMOD1/HABP4/NEB | 8 |
| GO:0032045 | guanyl-nucleotide exchange factor complex | 1.37E-02 | RAP1A/ELMO1 | 2 |
| GO:0031089 | platelet dense granule lumen | 1.58E-02 | APOH/CLEC3B | 2 |
| GO:0030136 | clathrin-coated vesicle | 1.66E-02 | TFRC/RAB27A/C9/INPP5F/TGFA/VAMP2/ROR2 | 7 |
| GO:0043292 | contractile fiber | 1.72E-02 | S100A1/SDC4/KRT19/NBR1/PK1/LMOD1/HABP4/NEB | 8 |
| GO:0030027 | lamellipodium | 1.89E-02 | PTPRO/DPP4/CD44/DPYSL3/ARPC5/PK1/FSCN1 | 7 |
| GO:0150034 | distal axon | 1.90E-02 | PTPRO/EP8/BASP1/DPYSL3/ARPC5/DSCAM/KCNA6/CARP/FSCN1 | 9 |
| GO:0030135 | coated vesicle | 2.06E-02 | TFRC/RAB27A/C9/SERPINA1/COP1/INPP5F/TGFA/VAMP2/ROR2 | 9 |
| GO:0005766 | primary lysosome | 2.17E-02 | CD63/TTR/VAPA/NPC2/BPI/CD68 | 6 |
| GO          | Term                                 | Score  | Loci                                           | Count |
|-------------|--------------------------------------|--------|------------------------------------------------|-------|
| GO:0042582 | azurophil granule                    | 2.17E-02 | CD63/TTR/VAPA/NPC2/BPI/CD68                    | 6     |
| GO:0030133 | transport vesicle                    | 2.22E-02 | RAB27A/CPA3/OVGP1/DPYSL3/COPB1/TGFA/MTMR2/STX11/CBARP/VAMP2/CA4 | 11    |
| GO:0030665 | clathrin-coated vesicle membrane     | 2.26E-02 | TFRC/CD9/TGFA/VAMP2/ROR2                       | 5     |
| GO:0016607 | nuclear speck                        | 2.41E-02 | TENM1/TRIM22/NRIP1/BASP1/DYRK3/MBD1/PLAG1/PNN/WBP4/PRCC/HABP4 | 11    |
| GO:0030017 | sarcomere                            | 2.47E-02 | S100A1/KRT19/NBR1/PAK1/LMOD1/HABP4/NEB        | 7     |
| GO:0099572 | postsynaptic specialization           | 2.47E-02 | PTPRO/EPS8/PSD3/SPOCK1/GABRA1/NRCAM/MTMR2/PCLO/GRIN2C/CPEB3 | 10    |
| GO:0042581 | specific granule                     | 2.49E-02 | QPCT/RAP1A/RAB27A/TCN1/BPI/LTF                 | 6     |
| GO:0016528 | sarcoplasm                           | 2.56E-02 | XDH/S100A1/SPOCK1/HABP4                       | 4     |
| GO:0031252 | cell leading edge                    | 2.65E-02 | PTPRO/DPP4/EPS8/PSD3/CD44/DPYSL3/ARPC5/GABRA1/PAK1/CYTH3/FSCN1 | 11    |
| GO:0005811 | lipid droplet                        | 2.67E-02 | GAPDH/NSDHL/METTL7A/FABP4                     | 4     |
| GO:0070820 | tertiary granule                     | 2.77E-02 | QPCT/TCN1/SERPINB10/COPB1/METTL7A/LTF         | 6     |
Supplementary Figure S1. The boxplots of the samples before and after batch effect removal for the five transcriptomic datasets (as shown in Table 1).