
Supplementary materials

Supplementary Table 1. differentially expressed genes in set GSE16515

| No. | Row | d.value | stdev | rawp | q.value | R.fold | Name |
|-----|-------|---------|--------|------|---------|---------|-----------|
| 1 | 2584 | 11.19 | 0.2384 | 0 | 0 | 6.3538 | 3914 |
| 2 | 4117 | 11.00 | 0.4471 | 0 | 0 | 30.2398 | 6286 |
| 3 | 7504 | 10.73 | 0.4022 | 0 | 0 | 19.9302 | 11254 |
| 4 | 10489 | 10.62 | 0.1894 | 0 | 0 | 4.0307 | 55359 |
| 5 | 8205 | 10.42 | 0.1893 | 0 | 0 | 3.9235 | 23650 |
| 6 | 10941 | 10.40 | 0.2992 | 0 | 0 | 8.6354 | 56649 |
| 7 | 6725 | 10.38 | 0.3661 | 0 | 0 | 13.9226 | 10232 |
| 8 | 9124 | 10.26 | 0.1722 | 0 | 0 | 3.4041 | 30001 |
| 9 | 14774 | 10.12 | 0.1292 | 0 | 0 | 2.4732 | 130340 |
| 10 | 4286 | 10.05 | 0.1429 | 0 | 0 | 2.7061 | 6513 |
| 11 | 19640 | 9.97 | 0.2130 | 0 | 0 | 4.3595 | 101669762 |
| 12 | 11507 | 9.85 | 0.2357 | 0 | 0 | 4.9952 | 58489 |
| 13 | 15989 | 9.83 | 0.3992 | 0 | 0 | 15.1928 | 195814 |
| 14 | 10730 | 9.77 | 0.1257 | 0 | 0 | 2.3432 | 55785 |
| 15 | 7674 | 9.72 | 0.3533 | 0 | 0 | 10.8002 | 22943 |
| 16 | 431 | 9.67 | 0.2166 | 0 | 0 | 4.2716 | 638 |
| 17 | 2798 | 9.58 | 0.1475 | 0 | 0 | 2.6630 | 4233 |
| 18 | 14529 | 9.39 | 0.2597 | 0 | 0 | 5.4260 | 124220 |
| 19 | 10134 | 9.38 | 0.1434 | 0 | 0 | 2.5407 | 54933 |
| 20 | 5508 | 9.34 | 0.1759 | 0 | 0 | 3.1239 | 8638 |
| 21 | 4186 | 9.28 | 0.1927 | 0 | 0 | 3.4536 | 6382 |
| 22 | 16101 | 9.26 | 0.1812 | 0 | 0 | 3.1988 | 200879 |
| 23 | 7483 | 9.26 | 0.1504 | 0 | 0 | 2.6246 | 11227 |
| 24 | 6618 | 9.22 | 0.2950 | 0 | 0 | 6.5822 | 10103 |
| 25 | 11189 | 9.17 | 0.1903 | 0 | 0 | 3.3494 | 57228 |
| 26 | 9863 | 9.11 | 0.2555 | 0 | 0 | 5.0232 | 54443 |

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|----|-------|-------|--------|---|---|--------|--------|
| 27 | 7204 | 9.09 | 0.3118 | 0 | 0 | 7.1355 | 10874 |
| 28 | 2491 | 9.00 | 0.2009 | 0 | 0 | 3.5008 | 3783 |
| 29 | 11914 | 8.95 | 0.1039 | 0 | 0 | 1.9045 | 64866 |
| 30 | 2587 | 8.83 | 0.3423 | 0 | 0 | 8.1303 | 3918 |
| 31 | 1294 | 8.83 | 0.1481 | 0 | 0 | 2.4758 | 1894 |
| 32 | 15688 | -8.81 | 0.0954 | 0 | 0 | 0.5588 | 158326 |
| 33 | 1768 | 8.76 | 0.1102 | 0 | 0 | 1.9523 | 2707 |
| 34 | 13033 | 8.71 | 0.1416 | 0 | 0 | 2.3516 | 83959 |
| 35 | 16460 | 8.68 | 0.1530 | 0 | 0 | 2.5094 | 253152 |
| 36 | 5798 | 8.65 | 0.2753 | 0 | 0 | 5.2055 | 9052 |
| 37 | 4354 | 8.60 | 0.3218 | 0 | 0 | 6.8133 | 6590 |
| 38 | 1834 | 8.59 | 0.3233 | 0 | 0 | 6.8520 | 2810 |
| 39 | 3788 | 8.56 | 0.1948 | 0 | 0 | 3.1748 | 5753 |
| 40 | 3471 | 8.55 | 0.1792 | 0 | 0 | 2.8921 | 5329 |

Row: lin number of the data entry; d.value: Standardized signal difference values; stdev: Standard deviation; rawp: Raw Pvalue; q.value : adjusted P-value; R.fold: Fold change; Name: entrez id.

Supplementary Table 2. differentially expressed genes in set GSE16515

| No | Row | d.value | stdev | rawp | q.value | R.fold | Name |
|----|------|---------|--------|------|---------|--------|-------|
| 1 | 898 | -11.38 | 0.3994 | 0 | 0 | 0.0428 | 1300 |
| 2 | 7874 | -11.18 | 0.3653 | 0 | 0 | 0.0589 | 23213 |
| 3 | 9229 | -10.28 | 0.1591 | 0 | 0 | 0.3218 | 50863 |
| 4 | 9171 | -10.28 | 0.1748 | 0 | 0 | 0.2878 | 50507 |
| 5 | 6270 | -10.23 | 0.0952 | 0 | 0 | 0.5094 | 9686 |
| 6 | 2364 | -10.22 | 0.2896 | 0 | 0 | 0.1284 | 3624 |
| 7 | 907 | -10.09 | 0.3619 | 0 | 0 | 0.0796 | 1311 |
| 8 | 4691 | -9.99 | 0.3898 | 0 | 0 | 0.0673 | 7058 |
| 9 | 893 | -9.96 | 0.2201 | 0 | 0 | 0.2190 | 1295 |

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|----|-------|-------|--------|---|---|--------|--------|
| 10 | 1606 | -9.89 | 0.2795 | 0 | 0 | 0.1473 | 2335 |
| 11 | 4305 | -9.84 | 0.0986 | 0 | 0 | 0.5105 | 6533 |
| 12 | 1302 | -9.84 | 0.2715 | 0 | 0 | 0.1571 | 1909 |
| 13 | 426 | -9.80 | 0.2174 | 0 | 0 | 0.2284 | 633 |
| 14 | 2136 | -9.68 | 0.1022 | 0 | 0 | 0.5040 | 3213 |
| 15 | 11227 | -9.64 | 0.1716 | 0 | 0 | 0.3177 | 57419 |
| 16 | 14285 | -9.63 | 0.4393 | 0 | 0 | 0.0532 | 115908 |
| 17 | 4706 | -9.56 | 0.3263 | 0 | 0 | 0.1152 | 7076 |
| 18 | 5982 | -9.52 | 0.1477 | 0 | 0 | 0.3775 | 9315 |
| 19 | 2418 | -9.49 | 0.1244 | 0 | 0 | 0.4412 | 3693 |
| 20 | 1014 | -9.46 | 0.3979 | 0 | 0 | 0.0736 | 1462 |
| 21 | 2678 | -9.44 | 0.1761 | 0 | 0 | 0.3158 | 4061 |
| 22 | 1464 | -9.37 | 0.1311 | 0 | 0 | 0.4268 | 2149 |
| 23 | 878 | -9.36 | 0.3613 | 0 | 0 | 0.0959 | 1278 |
| 24 | 568 | -9.30 | 0.2313 | 0 | 0 | 0.2252 | 822 |
| 25 | 887 | -9.26 | 0.3546 | 0 | 0 | 0.1026 | 1289 |
| 26 | 2669 | -9.26 | 0.1573 | 0 | 0 | 0.3644 | 4052 |
| 27 | 117 | -9.25 | 0.2868 | 0 | 0 | 0.1591 | 165 |
| 28 | 4113 | -9.24 | 0.2303 | 0 | 0 | 0.2288 | 6282 |
| 29 | 2400 | -9.23 | 0.2235 | 0 | 0 | 0.2393 | 3673 |
| 30 | 882 | -9.20 | 0.2312 | 0 | 0 | 0.2291 | 1284 |
| 31 | 1767 | -9.19 | 0.3879 | 0 | 0 | 0.0845 | 2706 |
| 32 | 713 | -9.17 | 0.2890 | 0 | 0 | 0.1592 | 1009 |
| 33 | 8759 | -9.12 | 0.1374 | 0 | 0 | 0.4196 | 27122 |
| 34 | 13472 | -9.06 | 0.2493 | 0 | 0 | 0.2091 | 84898 |
| 35 | 888 | -8.98 | 0.3822 | 0 | 0 | 0.0927 | 1290 |
| 36 | 2647 | -8.98 | 0.2565 | 0 | 0 | 0.2027 | 4016 |
| 37 | 9507 | -8.95 | 0.2704 | 0 | 0 | 0.1868 | 51339 |
| 38 | 7241 | -8.94 | 0.0772 | 0 | 0 | 0.6198 | 10916 |

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|----|------|-------|--------|---|---|--------|-------|
| 39 | 3343 | -8.86 | 0.2036 | 0 | 0 | 0.2865 | 5159 |
| 40 | 7330 | -8.82 | 0.3154 | 0 | 0 | 0.1454 | 11031 |

Row: lin number of the data entry; d.value: Standardized signal difference values; stdev: Standard deviation; rawp: Raw Pvalue; q.value : adjusted P-value; R.fold: Fold change; Name: entrez id.

Supplementary Table 3. 347 differentially expressed genes after removing clearly defined genes in the GENE database

| No. | Gene |
|-----|---------|
| 1 | TGFBR1 |
| 2 | PCNA |
| 3 | ANO1 |
| 4 | MYH1 |
| 5 | CAV3 |
| 6 | HCN1 |
| 7 | KCNK6 |
| 8 | USP44 |
| 9 | ADCY1 |
| 10 | IL1A |
| 11 | CACNA1H |
| 12 | KCNA2 |
| 13 | TBC1D7 |
| 14 | PSMD4 |
| 15 | DLG1 |
| 16 | MYRIP |
| 17 | KCNE1 |
| 18 | MT1E |
| 19 | TFAP2B |
| 20 | NOS1 |

| | |
|----|---------|
| 21 | DEDD2 |
| 22 | SPRTN |
| 23 | FASLG |
| 24 | QDPR |
| 25 | PSMB3 |
| 26 | ADAM9 |
| 27 | BIRC3 |
| 28 | EPB41L1 |
| 29 | AMIGO1 |
| 30 | NF1 |
| 31 | TXNL1 |
| 32 | HCN4 |
| 33 | MICALL2 |
| 34 | FMN2 |
| 35 | MNAT1 |
| 36 | GABRB1 |
| 37 | CUL1 |
| 38 | CACNA1E |
| 39 | KCNA7 |
| 40 | EYA1 |
| 41 | ANAPC10 |
| 42 | DIAPH1 |
| 43 | TRPV6 |
| 44 | PPP1R18 |
| 45 | MYO1E |
| 46 | CHRNA2 |
| 47 | KCNH1 |
| 48 | TRIOBP |
| 49 | FEM1A |

| | |
|----|----------|
| 50 | PAAF1 |
| 51 | GGH |
| 52 | GPI |
| 53 | DIXDC1 |
| 54 | CATSPERE |
| 55 | GBP1 |
| 56 | PSMG3 |
| 57 | SPTB |
| 58 | ZER1 |
| 59 | S100A16 |
| 60 | BUB3 |
| 61 | KCNH2 |
| 62 | EGF |
| 63 | STX4 |
| 64 | PSMD8 |
| 65 | S100A4 |
| 66 | GNL3L |
| 67 | SCN10A |
| 68 | SPTAN1 |
| 69 | PAK2 |
| 70 | CDK9 |
| 71 | CACYBP |
| 72 | PSMA5 |
| 73 | SLC25A24 |
| 74 | S100A13 |
| 75 | SHISA9 |
| 76 | TFAP2A |
| 77 | NDRG1 |
| 78 | TAT |

| | |
|-----|---------|
| 79 | MICU1 |
| 80 | GABRQ |
| 81 | FGF10 |
| 82 | ALG2 |
| 83 | MICAL2 |
| 84 | SPOPL |
| 85 | RBCK1 |
| 86 | ARRDC3 |
| 87 | SCN2B |
| 88 | CAT |
| 89 | ARRB1 |
| 90 | N4BP1 |
| 91 | KCNG3 |
| 92 | CPNE1 |
| 93 | HMGB2 |
| 94 | KCNIP1 |
| 95 | PELI1 |
| 96 | AMER1 |
| 97 | SLC6A4 |
| 98 | KCNB2 |
| 99 | ABAT |
| 100 | PPP2R1B |
| 101 | DPP6 |
| 102 | RYR2 |
| 103 | PSMD3 |
| 104 | GRIA1 |
| 105 | AKAP6 |
| 106 | CDC27 |
| 107 | KCNJ8 |

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|-----|-----------|
| 108 | TFF1 |
| 109 | SOX4 |
| 110 | ASCL1 |
| 111 | CORO2A |
| 112 | CACNG3 |
| 113 | GSTP1 |
| 114 | MAD2L1 |
| 115 | CACNG2 |
| 116 | MYO16 |
| 117 | PSMB8 |
| 118 | RET |
| 119 | PSMA7 |
| 120 | FANCI |
| 121 | GPHN |
| 122 | CRIP1 |
| 123 | BEST1 |
| 124 | KCNJ5 |
| 125 | SNTG2 |
| 126 | PSMD13 |
| 127 | PSME3 |
| 128 | PSMB4 |
| 129 | SKP1 |
| 130 | TNFRSF11B |
| 131 | ANXA11 |
| 132 | GRIN2C |
| 133 | CNGB1 |
| 134 | COBLL1 |
| 135 | PSMA4 |
| 136 | UNC5B |

| | |
|-----|---------|
| 137 | CDC23 |
| 138 | UBE2L3 |
| 139 | CPOX |
| 140 | MT1M |
| 141 | GRID2 |
| 142 | KCNH4 |
| 143 | FBXO25 |
| 144 | PSMC6 |
| 145 | IFI6 |
| 146 | PSMD11 |
| 147 | PIN1 |
| 148 | ALOX5AP |
| 149 | KCNIP2 |
| 150 | CLCNKB |
| 151 | SESTD1 |
| 152 | SPATA32 |
| 153 | ANAPC16 |
| 154 | GPX1 |
| 155 | BUB1B |
| 156 | PTTG1IP |
| 157 | DNMT3A |
| 158 | EGLN3 |
| 159 | TRPM4 |
| 160 | CACNB3 |
| 161 | YWHAH |
| 162 | AANAT |
| 163 | ZMYND11 |
| 164 | UBE2C |
| 165 | UBE2S |

| | |
|-----|---------|
| 166 | APBB1 |
| 167 | RFWD2 |
| 168 | GRIN3A |
| 169 | DLG4 |
| 170 | HPCA |
| 171 | FXN |
| 172 | STK3 |
| 173 | CDK1 |
| 174 | MASTL |
| 175 | AKR1C3 |
| 176 | RGN |
| 177 | CLIC1 |
| 178 | CLIC3 |
| 179 | CSRP3 |
| 180 | JUNB |
| 181 | MAP2K5 |
| 182 | CCNB1 |
| 183 | HERPUD1 |
| 184 | IGFBP2 |
| 185 | CBFA2T3 |
| 186 | BEST3 |
| 187 | KCNG1 |
| 188 | KLHL20 |
| 189 | MT1G |
| 190 | SKIL |
| 191 | PSME1 |
| 192 | PTK2B |
| 193 | XRCC4 |
| 194 | UBQLN2 |

| | |
|-----|---------|
| 195 | KCNF1 |
| 196 | CLCN1 |
| 197 | ARPC1A |
| 198 | MT1H |
| 199 | IL7 |
| 200 | PSMC4 |
| 201 | PDCD6 |
| 202 | ZACN |
| 203 | TANK |
| 204 | FKBP1B |
| 205 | STX1A |
| 206 | RUSC1 |
| 207 | SLC34A1 |
| 208 | PAK5 |
| 209 | PSMB9 |
| 210 | T1F |
| 211 | IQGAP1 |
| 212 | MELTF |
| 213 | KCNB1 |
| 214 | GRIK5 |
| 215 | DBN1 |
| 216 | IST1 |
| 217 | ACVR1 |
| 218 | PSMD1 |
| 219 | HAAO |
| 220 | EDN1 |
| 221 | ADAM8 |
| 222 | GABRP |
| 223 | GRIK4 |

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|-----|---------|
| 224 | CROCC |
| 225 | RNF19B |
| 226 | TCF7L2 |
| 227 | SEM1 |
| 228 | KCNA1 |
| 229 | MYOG |
| 230 | P2RX1 |
| 231 | KCNK1 |
| 232 | SMDT1 |
| 233 | SPIRE1 |
| 234 | TNFSF15 |
| 235 | AGTR2 |
| 236 | PSMD7 |
| 237 | G6PD |
| 238 | CLDN1 |
| 239 | KLKB1 |
| 240 | TTYH1 |
| 241 | CACNA1B |
| 242 | LMOD3 |
| 243 | GABRA5 |
| 244 | TRADD |
| 245 | PSMB5 |
| 246 | TNNC1 |
| 247 | DRD2 |
| 248 | RNF19A |
| 249 | CHRNA10 |
| 250 | GRIN1 |
| 251 | CORO1B |
| 252 | TTYH2 |

| | |
|-----|----------|
| 253 | TGFB2 |
| 254 | UBE2D1 |
| 255 | SDC1 |
| 256 | SLC6A1 |
| 257 | PERP |
| 258 | MCU |
| 259 | KCNIP3 |
| 260 | EZR |
| 261 | LRRC8A |
| 262 | SP100 |
| 263 | SVBP |
| 264 | GPLD1 |
| 265 | SLC25A13 |
| 266 | TRIB2 |
| 267 | KCNE3 |
| 268 | CHRNA1 |
| 269 | IMPACT |
| 270 | CACNA1I |
| 271 | GATA1 |
| 272 | PSMD14 |
| 273 | CACNA1G |
| 274 | TPH2 |
| 275 | ENO1 |
| 276 | CNIH2 |
| 277 | KCND2 |
| 278 | MARCKSL1 |
| 279 | GABRA3 |
| 280 | SH3RF1 |
| 281 | CDC20 |

| | |
|-----|----------|
| 282 | GDI1 |
| 283 | ECT2 |
| 284 | ASPH |
| 285 | KCNS2 |
| 286 | FXYD3 |
| 287 | SHROOM3 |
| 288 | GRIK2 |
| 289 | STRADB |
| 290 | PSMA1 |
| 291 | SLC41A1 |
| 292 | PGAM2 |
| 293 | COL4A3 |
| 294 | ANO2 |
| 295 | CACNA1S |
| 296 | VASP |
| 297 | MYH2 |
| 298 | INHBA |
| 299 | PRMT3 |
| 300 | MT1X |
| 301 | GSS |
| 302 | HSPE1 |
| 303 | SHANK1 |
| 304 | CATSPERD |
| 305 | CAPZB |
| 306 | PHACTR3 |
| 307 | GFBR1 |
| 308 | DNAJA1 |
| 309 | CREB1 |
| 310 | ARG1 |

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|-----|--------|
| 311 | CNTN2 |
| 312 | CACNG8 |
| 313 | CHRNA4 |
| 314 | SNTA1 |
| 315 | RP2 |
| 316 | NGF |
| 317 | PSMD2 |
| 318 | KCNMA1 |
| 319 | BMP6 |
| 320 | CTSH |
| 321 | KCNAB1 |
| 322 | CACNB4 |
| 323 | WDR1 |
| 324 | CHRNA3 |
| 325 | IL2 |
| 326 | PSMD6 |
| 327 | TF |
| 328 | KCNK3 |
| 329 | MAPK12 |
| 330 | KCN |

Supplementary Table 4. Clustering Results

| Module | Protein ID |
|--------|---|
| M1 | 51371/5685/5693/5692/5698/991/996/4085/3315/9978/6500/9097/ 57154/11065/5062/7321/9352/5696/5688/9232/5708/51053/990/10 393/6790/26986/10952/701/7979/8697/119504/5886/10213//41430 1/29978/5710/11047/59349/5720/5717/5709/5716/5704/5682/5686 /9184/5719/5707/9861/5714/5713/9520/80227/10197/6185/64326/ |

94056/5706/8454

| | |
|------------|--|
| | 6387/2788/3350/3576/111/115/3627/107/833/5443/5733/58191/10 874/152/2921/57121/10850/2917/4886/9294/9290/10316/8698/271 99/6752/53637/134/6374/6364/165140/1813/727/643/3355/2826/5 6670/3361/2914/2773/23566 |
| M2 | |
| | 5371/3383/3446/3660/3434/3662/3661/3105/3659/9636/4938/3107 /4939/3106/2633/4502/2634/6672/4684/3665/8638/10379/4940/34 33/103/6041/54739/2537/3437/4600/3430/8519/4599/3669 |
| M3 | |
| | 10189/5725/2963/7175/22985/10921/6633/9416/6638/6632/6637/6 629/53981/1478/4686/22916/8731/51692/55746/57122/79902/2363 6/8480/7884/79833/8487/10783/10762/23165/8021/6634/91754/96 31/6636/6628/79023/5438/10907/3185/6626/6627/5436/1479/5440 |
| M4 | |
| | 5744/3375/1392/10267/7253/153/6344/796/3360/5745/1395/155/5 734/797/5739/9340/117/136/2740/79924/7434/3362/799/3363 |
| M5 | |
| | 3751/3737/26251/3754/3743/23415/7881/3736/170850/3788/81033 /9312/3755/3745/3757/3756 |
| M6 | |
| | 57551/7514/991/7272/83540/8379/4085/11130/9793/1062/5885/97 35/22919/22924/701/9184/10403/4928/55746/57122/79902/55166/ 91687/3796/79682/64105/55055/1063/151246/54908/81929/348235 /55920/81930/79023 |
| M7 | |
| | 129642/151056/9663/11145/8398/10434/154141/154141/79887/1090 8/5050/79888/54947/81579/5321/254531 |
| M8 | |
| | 2686/290/2678/1571/2876/2946/1553/9446/2052/2879/2940/2937/ 2950/2877/493869/2944 |
| M9 | |
| | 54552/221078/3692/55661/10813/26156/79039/5822/25879/51388/ 55813/55226/9790/55299/51602 |
| M10 | |
| | 84002/9334/200958/727897/27090/6487/94025/26290/9245/29071/ |
| M11 | |

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|------------|--|
| | 55568/51301/11227/56913 |
| | 6138/51073/29088/6235/6203/79631/140801/51121/5339/6234/513 |
| M12 | 19/6206/10952/1975/6171/6164/8665/6167/116832/6734/6185/907 01/28972/6159 |
| M13 | 84002/9334/200958/727897/55808/94025/26290/9245/29071/64409 /55568/51301/11227/56913 |
| M14 | 26219/4992/81285/26539/26246/124538/26664/26740/26248 |
| M15 | 533/7018/90423/525/529/9296/527/9550/528// /51382 1906/2769/5330/6915/156/2693/10874/57121/10316/2911/23236/2 |
| M16 | 3566/5731/2828/56413/3269/3062/2829/1909/6865/2864/146/887/ 5020/5021/2922 |
| M17 | 1278/1277/3673/1301/1285/1303/64175/1300/1290/22801/1295/12 96/84570/1289 1906/2769/5330/6915/156/2693/10874/57121/10316/2911/23236/2 |
| M18 | 773/23566/85397/5731/5287/79837/138429/2828/56413/3269/3062 /2829/1909/6865/2864/146/887/5020/5021/9455/2922/680 9798/27243/5119/10015/84313/25978/51510/57132/148362/79720/ 128866 |
| M19 | |
| M20 | 9751/11092/284451/27230/51308/65983 |
| M21 | 5351/6419/54904/79709/8985/5352 |
| M22 | 22849/85456/9337/57472/25904/4848/55571/10605/1975 |
| M23 | 9465/779/784/778/859/783/8912/8913/785/8911 |
| M24 | 10243/2566/4337/2557/2560/2558 |
| M25 | 10956/23197/51465/6400/51009/79139 |
| M26 | 2530/11320/11282/146664 |
| M27 | 2593/2628/6470/211/1757/23464/27232/1610 |
| M28 | 4643/60/10109/81873/10095/10552/57180/10092/10094/644150/10 096/10097/4620/10006/4619 |
| M29 | 9487/5277/9091/51227 |

| | |
|------------|---|
| M30 | 8702/2526/2527/11041 |
| M31 | 27443/10042/2186/11177 |
| M32 | 81631/4077/10533/9474/115101/84557 1013/84516/898/1495/8766/4654/10890/8773/6810/5601/26153/22 |
| M33 | 22/6667/83547/55763/4800/6300/7879/79659/1496 |
| M34 | 6723/6303/6611/112483/26 |
| M35 | 5214/2821/6888/5313/5230/7167/2023/5224/2026/5315/2597/226/ 5223/669 |
| M36 | 6097/7376/7068/7421/7067/6258/2104/126382 |
| M37 | 84701/4512/1339/1340 |
| M38 | 10048/54994/79018/80232/63893 |
| M39 | 3052/1352/9997/6834 |
| M40 | 5819/6663/596/835/57161/5077/27022/959/330/4656/973/6585/42 86/5663/5818/57162/9448/91768/1499/3552/2249 |
| M41 | 51208/137075/9069/9075 |
| M42 | 23509/23275/11173/92949 |
| M43 | 3242/4282/6898/7173 |
| M44 | 3212/1959/5469/5468/9325/1051/55588/9443/7480/112950/400569 /10001/90390/219541/688 |
| M45 | 482/53822/5349 |
| M46 | 55967/374291/4710 |
| M47 | 91949/25839/84342 |
| M48 | 91689/10367/90550 |
| M49 | 316/8630/8228/195814/216/8608 |
| M50 | 55364/10985/1819/51389 |
| M51 | 57175/10109/81873/10095/10552/57180/10092/10094/644150/10096 /10097/4620/10006 |
| M52 | 5149/159/1716/2987/4907/56953/5137/205/124583/22978/271/370 4/5145/5138/5148/471 |

| | |
|------------|---|
| M53 | 6425/7474/7976/7480/2535/8321/8323/7479/7475/22943/7472/8326 |
| M54 | 9378/57555/26045 |
| M55 | 4668/8706/53947 |
| M56 | 1137/79608/1141 |
| M57 | 7443/23141/8815 |
| M58 | 6820/1583/412/153642 |
| M59 | 5202/10574/22948/7203/908/5203/5531/3336/84790/6788/25843/29966/10376 |
| M60 | 2160/3818/2815/2811 |
| M61 | 7035/2155/2159/2152/80381 |
| M62 | 28998/51073/29088/64928/55173/6235/6203/79631/140801/63875/51121/7818/64968 |
| M63 | 6879/117143/112869/6878/93624/55689 |
| M64 | 1739/10369/2890/816/59283/2036/9495/10368/729993/2902/2905/815/4646 |
| M65 | 28998/51073/29088/64928/55173/26589/6203/79631/140801/63875/740 |

Supplementary Table 5. GO feature description of clustering modules

| Type | ID | Description |
|------------|------------|---|
| Biological | GO:0016236 | Macroautophagy |
| process | GO:0038096 | Fc-gamma/receptor/signaling/pathway/involved/in/phagocytosis |
| | GO:0002433 | Immune/response-regulating/cell/surface/receptor/signaling/pathway/involved/in/phagocytosis |

| | | |
|----------------|------------|----------------------------|
| | GO:0090382 | Phagosome/maturation |
| | GO:0090383 | Phagosome/acidification |
| Cell component | GO:0030666 | Endocytic/vesicle/membrane |

Supplementary Table 6. KEGG feature description of clustering modules

| module | ID | Description | qvalue | geneID |
|--------|----------|---|----------|--|
| m1 | hsa03050 | Proteasome | 2.69E-44 | 51371/5685/5693/5692/5698/5696/5688/5708/7979/10213/5710/11047/5720/5717/5709/5704/5682/5686/5719/5707/9861/5714/5713/10197/5706 |
| m2 | hsa04062 | Chemokine/signaling/pathway | 3.16E-15 | 6387/2788/3576/111/115/3627/107/2833/58191/2921/10850/6374/6364/643/2826/2773 |
| m3 | hsa05168 | Herpes/simplex/infection | 2.68E-15 | 5371/3446/3434/3661/3105/4938/3107/4939/3106/6672/3665/10379/4940/6041 |
| m4 | hsa03013 | RNA/transport | 3.90E-19 | 10189/7175/22985/10921/4686/22916/55746/57122/79902/23636/8480/79833/8487/10762/23165/8021/9631/79023 |
| m5 | hsa04080 | Neuroactive/ligand-receptor/interaction | 1.12E-20 | 7253/153/6344/3360/5745/1395/155/5734/5739/9340/117/136/2740/7434/3362/799/3363 |
| m6 | hsa04726 | Serotonergic/synapse | NA | 3751 |
| m7 | hsa04110 | Cell/cycle | 1.31E-08 | 991/7272/8379/4085/5885/701/9184 |
| m8 | hsa00564 | Glycerophospholipid/metabolism | 3.82E-25 | 129642/151056/9663/11145/8398/10434/154141/375775/10908/79888/54947/81579/5321/254531 |
| m9 | hsa00480 | Glutathione/metab | 2.65E-25 | 2686/290/2678/2876/2946/9446/2879/2940 |

| | | | | |
|-----|----------|---|----------|--|
| | | olism | | /2937/2950/2877/493869/2944 |
| m10 | hsa03008 | Ribosome/biogenesis/in/eukaryotes | NA | 54552/3692/10813/5822/55813/55226/9790/51602 |
| m11 | hsa00512 | Mucin/type/O-glycan/biosynthesis | 4.31E-17 | 9334/26290/9245/29071/55568/51301/11227/56913 |
| m12 | hsa03010 | Ribosome | 1.80E-16 | 6138/51073/29088/6235/6203/140801/51121/6234/6206/6171/6164/6167/6159 |
| m13 | hsa00512 | Mucin/type/O-glycan/biosynthesis | 5.59E-23 | 9334/55808/26290/9245/29071/64409/55568/51301/11227/56913 |
| m14 | hsa04740 | Olfactory/transduction | NA | 26219/4992/81285/26539/26246/124538/26664/26740/26248 |
| m15 | hsa05110 | Vibrio/cholerae/infection | 5.19E-19 | 533/90423/525/529/9296/527/9550/528/51382 |
| m16 | hsa04020 | Calcium/signaling/pathway | 1.89E-14 | 2769/5330/6915/2911/23236/5731/56413/3269/1909/6865/146/887/5021 |
| m17 | hsa04974 | Protein/digestion/and/absorption | 7.64E-14 | 1278/1277/1301/1285/1303/1300/1290/1289 |
| m18 | hsa04080 | Neuroactive/ligand-receptor/interaction | 5.94E-13 | 6915/2693/10316/2911/23566/5731/56413/3269/3062/1909/6865/146/887/5021/680 |
| m19 | hsa04144 | Endocytosis | NA | 9798/27243/5119/10015/84313/25978/51510/57132/79720/128866 |
| m20 | none | | | |
| m21 | hsa00310 | Lysine/degradation | NA | 5351/6419/54904/79709/8985/5352 |
| m22 | hsa03018 | RNA/degradation | 2.12E-06 | 9337/57472/25904/4848 |
| m23 | hsa04010 | MAPK/signaling/pathway | 1.16E-10 | 779/784/778/783/8912/8913/785/8911 |
| m24 | hsa04727 | GABAergic/synap | 1.47E-09 | 10243/2566/2557/2560/2558 |

| | | | | |
|-----|----------|---------------------|----------|--|
| | | se | | |
| | | Protein/processing | | |
| m25 | hsa04141 | /in/endoplasmic/r | 1.25E-08 | 10956/51465/6400/51009/79139 |
| | | eticulum | | |
| m26 | hsa00510 | N-Glycan/biosynt | 1.94E-09 | 2530/11320/11282/146664 |
| | | hesis | | |
| | | Glycine,/serine/an | | |
| m27 | hsa00260 | d/threonine/meta | 1.29E-18 | 2593/2628/6470/211/1757/23464/27232/1610 |
| | | bolism | | |
| m28 | hsa04144 | Endocytosis | 2.87E-07 | 10109/81873/10095/10552/10092/10094/644150 |
| | | Glycosylphosphati | | |
| m29 | hsa00563 | dylinositol/(GPI)-a | NA | 9487/5277/9091/51227 |
| | | nchor/biosynthesis | | |
| | | Glycosphingolipid | | |
| m30 | hsa00601 | /biosynthesis/-/la | NA | 8702/2526/2527 |
| | | cto/and/neolacto/ | | |
| | | series | | |
| m31 | none | | | |
| m32 | hsa04216 | Ferroptosis | 6.23E-08 | 81631/10533/9474/84557 |
| | | Mitophagy/-/anim | | |
| m33 | hsa04137 | al | 0.006454 | 5601/6667/7879 |
| | | Arginine/and/prol | | |
| m34 | hsa00330 | ine/metabolism | NA | 6723/6303/6611/112483/26 |
| | | Glycolysis//Gluc | | |
| m35 | hsa00010 | oneogenesis | 1.53E-25 | 5214/2821/5313/5230/7167/2023/5224/2026/5315/2597/226/5223/669 |
| | | Thyroid/hormone | | |
| m36 | hsa04919 | /signaling/pathwa | 0.000649 | 7068/7067/6258 |
| | | y | | |

| | | | | |
|-----|----------|--|----------|-------------------------------|
| m37 | hsa04260 | Cardiac/muscle/c ontraction | NA | 84701/4512/1339/1340 |
| m38 | hsa04120 | Ubiquitin/mediate d/proteolysis | NA | 63893 |
| m39 | hsa00860 | Porphyrin/and/ch lorophyll/metaboli sm | 0.000103 | 3052/1352 |
| m40 | hsa04210 | Apoptosis Leukocyte/transen | 0.021628 | 596/835/330 |
| m41 | hsa04670 | dothelial/migratio n Other/types/of/O | NA | 51208/137075/9075 |
| m42 | hsa00514 | -glycan/biosynthes is | NA | 23509/23275 |
| m43 | hsa00350 | Tyrosine/metaboli sm | NA | 3242/4282/6898/7173 |
| m44 | none | Proximal/tubule/b | | |
| m45 | hsa04964 | icarbonate/reclama tion | NA | 482 |
| m46 | hsa00190 | Oxidative/phosph orylation | NA | 55967/374291/4710 |
| m47 | none | NOD-like/receptor | | |
| m48 | hsa04621 | /signaling/pathwa y | NA | 90550 |
| m49 | hsa00830 | Retinol/metabolis m | 8.65E-13 | 316/8630/8228/195814/216/8608 |
| m50 | none | | | |

| | | | | |
|-----|----------|--|----------|--|
| m51 | hsa04144 | Endocytosis | NA | 10109/81873/10095/10552/10092/10094/644150 |
| | | | | 5149/159/1716/2987/4907/56953/5137/205 |
| m52 | hsa00230 | Purine/ metabolism | 6.32E-26 | /124583/22978/271/3704/5145/5138/5148/471 |
| m53 | hsa04310 | Wnt/ signaling/ pat hway | 2.30E-21 | 6425/7474/7976/7480/2535/8321/8323/7479/7475/22943/7472/8326 |
| m54 | hsa04514 | Cell/ adhesion/ mol ecules/ (CAMs) | NA | 9378/57555 |
| | | Glycosphingolipid | | |
| m55 | hsa00603 | /biosynthesis/-/ gl obo/ and/ isoglobo /series | 7.55E-09 | 4668/8706/53947 |
| m56 | hsa05033 | Nicotine/ addiction | NA | 1137/1141 |
| m57 | none | | | |
| m58 | hsa00140 | Steroid/ hormone/ biosynthesis | NA | 6820/1583/412 |
| m59 | hsa05130 | Pathogenic/ Escheri chia/ coli/ infection | 0.001061 | 84790/10376 |
| | | Complement/ and/ | | |
| m60 | hsa04610 | coagulation/ cascades | NA | 2160/3818 |
| | | Complement/ and/ | | |
| m61 | hsa04610 | coagulation/ cascades | 1.36E-07 | 7035/2155/2159/2152 |
| m62 | hsa03010 | Ribosome | 3.45E-18 | 28998/51073/29088/64928/55173/6235/6203/140801/63875/51121/64968 |
| m63 | hsa03022 | Basal/ transcription /factors | 3.97E-05 | 6879/6878 |

| | | | | |
|-----|----------|---------------------|----------|---|
| m64 | hsa04720 | Long-term/potential | 4.43E-08 | 2890/816/2902/2905/815 |
| m65 | hsa03010 | Ribosome | 3.22E-13 | 28998/51073/29088/64928/55173/6203/140801/63875 |

Supplementary Table 7. functional enrichment of LC3 module genes

| ID | Description | qvalue | geneID |
|------------|---------------------------------|----------------------|---|
| GO:0000422 | mitophagy | 9.38675621566875e-10 | MAP1LC3B/ ATG7/ ATG5/ ATG4A/MAP1LC3A |
| GO:0061726 | mitochondrion disassembly | 9.38675621566875e-10 | MAP1LC3B/ ATG7/ ATG5/ ATG4A/MAP1LC3A |
| GO:0016236 | macroautophagy | 9.38675621566875e-10 | MAP1LC3B/NBR1/ ATG7/ ATG5/ ATG4A/MAP1LC3A |
| GO:1903008 | organelle disassembly | 1.99547926407034e-09 | MAP1LC3B/ ATG7/ ATG5/ ATG4A/MAP1LC3A |
| GO:0006914 | autophagy | 1.43099915739969e-08 | MAP1LC3B/NBR1/ ATG7/ ATG5/ ATG4A/MAP1LC3A |
| GO:0007033 | vacuole organization | 3.67582409358148e-06 | MAP1LC3B/ ATG5/ ATG4A/MAP1LC3A |
| GO:0000045 | autophagosome assembly | 3.37660710324853e-05 | ATG5/ ATG4A/MAP1LC3A |
| GO:1905037 | autophagosome organization | 3.37660710324853e-05 | ATG5/ ATG4A/MAP1LC3A |
| GO:0009267 | cellular response to starvation | 0.000132212690697115 | ATG7/ ATG5/MAP1LC3A |

| | | | |
|----------------|--|--------------------------|------------------------|
| GO:00448 04 | nucleophagy | 0.000140965224755 097 | ATG5/ATG4A |
| GO:00064 97 | protein lipidation | 0.000159519882196 554 | ATG7/ATG5/ATG4A |
| GO:00421 58 | lipoprotein biosynthetic process | 0.000178244664904 667 | ATG7/ATG5/ATG4A |
| GO:00425 94 | response to starvation | 0.000206106319631 958 | ATG7/ATG5/MAP1LC3 A |
| GO:00316 69 | cellular response to nutrient levels | 0.000240305176700 272 | ATG7/ATG5/MAP1LC3 A |
| GO:00316 68 | cellular response to extracellular stimulus | 0.000364974986991 163 | ATG7/ATG5/MAP1LC3 A |
| GO:00421 57 | lipoprotein metabolic process | 0.000369322017628 197 | ATG7/ATG5/ATG4A |
| GO:00140 72 | response to isoquinoline alkaloid | 0.000465396270701 896 | ATG7/MAP1LC3A |
| GO:00432 78 | response to morphine | 0.000465396270701 896 | ATG7/MAP1LC3A |
| GO:00973 52 | autophagoso me maturation | 0.000531645925336 373 | MAP1LC3B/MAP1LC3A |
| GO:00975 76 | vacuole fusion | 0.000566984201996 07 | MAP1LC3B/MAP1LC3A |

| | | | |
|----------|-----------------|-------------------|-------------------|
| GO:00714 | cellular | 0.000655522612122 | ATG7/ATG5/MAP1LC3 |
| 96 | response to | 287 | A |
| | external | | |
| | stimulus | | |
| GO:00065 | C-terminal | 0.001641299444545 | ATG5/ATG4A |
| 01 | protein | 7 | |
| | lipidation | | |
| GO:00184 | C-terminal | 0.001926628423660 | ATG5/ATG4A |
| 10 | protein amino | 14 | |
| | acid | | |
| | modification | | |
| GO:00316 | response to | 0.001926628423660 | ATG7/ATG5/MAP1LC3 |
| 67 | nutrient levels | 14 | A |
| GO:00099 | response to | 0.002309270034398 | ATG7/ATG5/MAP1LC3 |
| 91 | extracellular | 25 | A |
| | stimulus | | |
| GO:00436 | post-translatio | 0.002932032671656 | ATG5/ATG4A |
| 87 | nal protein | 51 | |
| | modification | | |
| GO:00603 | response to | 0.004088783298133 | ATG7/MAP1LC3A |
| 59 | ammonium | 94 | |
| | ion | | |
| GO:00057 | autophagoso | 1.04048805353169e | MAP1LC3B/NBR1/ATG |
| 76 | me | -07 | 5/MAP1LC3A |
| GO:00004 | pre-autophag | 4.98402383733435e | NBR1/ATG7/ATG5 |
| 07 | osomal | -07 | |
| | structure | | |
| GO:00059 | axoneme | 9.46719371089602e | MAP1LC3B/ATG7/ATG |
| 30 | | -06 | 5 |

| | | | |
|----------|---------------|-------------------|---------------------------|
| GO:00970 | ciliary plasm | 9.46719371089602e | MAP1LC3B/ ATG7/ ATG |
| 14 | | -06 | 5 |
| GO:00004 | autophagoso | 9.90524908543648e | MAP1LC3B/ MAP1LC3A |
| 21 | me membrane | -05 | |
| GO:00444 | ciliary part | 0.000401400290062 | MAP1LC3B/ ATG7/ ATG |
| 41 | | 242 | 5 |
| GO:00059 | cilium | 0.000788705260923 | MAP1LC3B/ ATG7/ ATG |
| 29 | | 528 | 5 |
| GO:00057 | late endosome | 0.003066559291231 | NBR1/ MAP1LC3A |
| 70 | | 63 | |
| hsa04216 | Ferroptosis | 6.22637299514052e | 81631/ 10533/ 9474/ 84557 |
| | | -08 | |
| hsa04136 | Autophagy - | 4.07669711326647e | 10533/ 9474/ 115201 |
| | other | -06 | |
| hsa04140 | Autophagy - | 0.000181522708473 | 10533/ 9474/ 115201 |
| | animal | 266 | |
| hsa04137 | Mitophagy - | 0.001526817470846 | 4077/ 9474 |
| | animal | 15 | |

Supplementary Table 8. The results of the pathway crosstalk analysis of the
aforementioned clustering modules

| Module | Module | Number | P value | Module | Module | Number | P |
|--------|--------|-----------|---------|--------|--------|-----------|-------|
| 1 | 2 | of | | 1 | 2 | of | value |
| | | crosstalk | | | | crosstalk | |
| m1 | m7 | 126 | 0.0 | m12 | m65 | 38 | 0.0 |
| m1 | m22 | 9 | 0.007 | m16 | m18 | 328 | 0.0 |
| m2 | m16 | 150 | 0.0 | m23 | m64 | 4 | 0.0 |
| m2 | m18 | 170 | 0.0 | m27 | m52 | 1 | 0.044 |

| | | | | | | | |
|-----|-----|-----|-------|-----|-----|----|-------|
| m3 | m23 | 2 | 0.022 | m28 | m51 | 60 | 0.0 |
| m4 | m7 | 135 | 0.0 | m28 | m59 | 5 | 0.001 |
| m5 | m20 | 3 | 0.005 | m33 | m40 | 17 | 0.011 |
| m6 | m64 | 3 | 0.006 | m36 | m44 | 12 | 0.0 |
| m9 | m58 | 1 | 0.01 | m44 | m53 | 8 | 0.0 |
| m11 | m13 | 53 | 0.0 | m52 | m53 | 3 | 0.043 |
| m12 | m22 | 9 | 0.0 | m62 | m65 | 41 | 0.0 |
| m12 | m62 | 67 | 0.0 | | | | |

Supplementary Table 9. The genes involved in the module 33 and module 40 and their functional descriptions

| Gene | Description | Related pathways or functions |
|--------|------------------------------------|---|
| MAPK9 | mitogen-activated protein kinase 9 | Autophagy - animal (KEGG hsa04140) |
| SP1 | Sp1 transcription factor | Direct p53 effectors (from Pathway Interaction Database) |
| RAB7A | member RAS oncogene family | Autophagy - animal (KEGG hsa04140) |
| CTNNA1 | catenin alpha 1 | Adherens junction (KEGG hsa04520) |
| CTNNB1 | catenin beta 1 | Apoptotic cleavage of cell adhesion proteins (from REACTOME) |
| MYOG | myogenin | Regulation of Wnt-mediated beta catenin signaling and target gene transcription (from Pathway Interaction Database) |
| CDH15 | cadherin 15 | Adherens junctions interactions (from REACTOME) |
| CTNNA2 | catenin alpha 2 | Pathways in cancer (KEGG |

| | | | |
|----------|-------------------------------------|--|---|
| | | | hsa05200) |
| STX4 | syntaxin 4 | | Adaptive Immune System (from REACTOME) |
| MAPK12 | mitogen-activated protein kinase 12 | | MAPK (p38) signaling (KEGG hsa_M00689) |
| MYOD1 | myogenic differentiation 1 | | ubiquitin protein ligase binding (GO Molecular Function) |
| CABLES 1 | Cdk5 and Abl enzyme substrate 1 | | Factors involved in megakaryocyte development and platelet production (from REACTOME) |
| NECTIN 2 | nectin cell adhesion molecule 2 | | Adherens junction (KEGG hsa04520) |
| NECTIN 1 | nectin cell adhesion molecule 1 | | Adherens junction (KEGG hsa04520) |
| SLIT1 | slit guidance ligand 1 | | Axon guidance (KEGG hsa04360) |
| CD40LG | CD40 ligand | | tumor necrosis factor receptor binding (GO Molecular Function) |
| PAX3 | paired box 3 | | Transcriptional misregulation in cancer (KEGG hsa05202) |

Supplementary Table 10. modules connected with UBC and their functional information

| modul | KEGG id | Function | P_value |
|-------|----------|-------------|---------------------|
| e | | | |
| m1 | hsa03050 | Proteasome | 9.45E-46 |
| m7 | hsa04110 | Cell cycle | 2.0772854712175E-09 |
| m32 | hsa04216 | Ferroptosis | 1.1830108690767E-08 |

| | | | | | |
|-----|----------|----------------------|------------------|--|----------------------|
| m33 | hsa04137 | Mitophagy - animal | | | 0.000427786394634064 |
| m40 | hsa04210 | Apoptosis | | | 0.00259718975339996 |
| m51 | hsa04144 | Endocytosis | | | 2.057623076858E-08 |
| m59 | hsa05130 | Pathogenic infection | Escherichia coli | | 0.000335866946321112 |
