**Supplementary materials**

**Mitochondria-related core genes and TF-miRNA-hub mrDEGs network in breast cancer**

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**Content:**

**Table S1 GO enrichment analysis of mitochondria-related differential expressed genes**

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| --- | --- | --- | --- |
| **Term ID** | **Term description** | **FDR** | **Genes** |
| GO:0021637 | trigeminal nerve structural organization | 0.0027 | NRP1,SEMA3A,SEMA3F |
| GO:0036486 | ventral trunk neural crest cell migration | 0.0027 | NRP1,SEMA3A,SEMA3F |
| GO:0097490 | sympathetic neuron projection extension | 0.0027 | NRP1,SEMA3A,SEMA3F |
| GO:0097491 | sympathetic neuron projection guidance | 0.0027 | NRP1,SEMA3A,SEMA3F |
| GO:1902287 | semaphorin-plexin signaling pathway involved in axon guidance | 0.0027 | NRP1,SEMA3A,SEMA3F |
| GO:0021612 | facial nerve structural organization | 0.0029 | NRP1,SEMA3A,SEMA3F |
| GO:0021785 | branchiomotor neuron axon guidance | 0.0029 | NRP1,SEMA3A,SEMA3F |
| GO:0001764 | neuron migration | 0.0033 | ASPM,CELSR1,MARK1,MEF2C,NRP1,SEMA3A |
| GO:0014033 | neural crest cell differentiation | 0.0033 | FN1,MEF2C,NRP1,SEMA3A,SEMA3F |
| GO:0040012 | regulation of locomotion | 0.0033 | CXCL2,DDR2,DLC1,EPB41L4B,FN1,LIMCH1,MCTP1,MEF2C,MYLK,NRP1,  PIK3R1,RECK,SEMA3A,SEMA3F,SNCA |
| GO:0048513 | animal organ development | 0.0033 | ANK2,ASPM,BHLHE41,BICC1,CELSR1,COL5A2,COL9A3,CPS1,DDR2,DLC1,  DOCK11,FN1,KRT81,LPIN1,LSR,MECOM,MEF2C,MGST1,MITF,MYLK,NFIB,NRP1,  PIK3R1,PYGO1,SATB1,SEMA3A,SEMA3F,TACC1,VIM,ZEB1 |
| GO:0048731 | system development | 0.0033 | ANK2,ASPM,BHLHE41,BICC1,CELSR1,COL5A2,COL9A3,CPS1,DDR2,DLC1,DOCK11,  EFNA3,FAM126A,FN1,GPC2,HES4,KRT81,LPIN1,LSR,MARK1,MECOM,MEF2C,MGST1,  MITF,MYLK,NAP1L2,NFIB,NRP1,PIK3R1,PYGO1,QKI,RECK,SATB1,SEMA3A,SEMA3F,  TACC1,VIM,ZEB1 |
| GO:0048843 | negative regulation of axon extension involved in axon guidance | 0.0033 | NRP1,SEMA3A,SEMA3F |
| GO:0048846 | axon extension involved in axon guidance | 0.0033 | NRP1,SEMA3A,SEMA3F |
| GO:0051270 | regulation of cellular component movement | 0.0033 | ANK2,CXCL2,DDR2,DLC1,EPB41L4B,FN1,LIMCH1,MCTP1,MEF2C,MYLK,NRP1,PIK3R1,  RECK,SEMA3A,SEMA3F |
| GO:0060600 | dichotomous subdivision of an epithelial terminal unit | 0.0033 | CELSR1,NRP1,SEMA3A |
| GO:0061549 | sympathetic ganglion development | 0.0033 | NRP1,SEMA3A,SEMA3F |
| GO:0016043 | cellular component organization | 0.0039 | ANK2,ASPM,BGN,CCDC136,COL5A2,COL9A3,DDR2,DLC1,EFNA3,EHHADH,EMP1,  EPB41L4B,FGD4,FN1,H2AFJ,JADE1,KCTD12,LIMCH1,LPIN1,LSR,MAP7D3,MARK1,  MECOM,MEF2C,MGST1,MITF,MYLK,NAP1L2,NFIB,NR3C1,NRP1,PADI3,PIK3R1,PYGO1,  RECK,RHOQ,SATB1,SEMA3A,SEMA3F,SNCA,SYNM,TACC1,VIM |
| GO:0051271 | negative regulation of cellular component movement | 0.0046 | DLC1,LIMCH1,MCTP1,MEF2C,NRP1,RECK,SEMA3A,SEMA3F |
| GO:0110020 | regulation of actomyosin structure organization | 0.0056 | DLC1,LIMCH1,MEF2C,NRP1,PIK3R1 |
| GO:0040013 | negative regulation of locomotion | 0.0058 | DLC1,LIMCH1,MCTP1,MEF2C,NRP1,RECK,SEMA3A,SEMA3F |
| GO:0071417 | cellular response to organonitrogen compound | 0.0075 | CACNA2D1,COL5A2,CPS1,LPIN1,MEF2C,PIK3R1,RHOQ,SNCA,ZEB1,ZNF106 |
| GO:0021828 | gonadotrophin-releasing hormone neuronal migration to the hypothalamus | 0.0076 | NRP1,SEMA3A |
| GO:0045664 | regulation of neuron differentiation | 0.0076 | ASPM,EFNA3,FN1,MARK1,MEF2C,NAP1L2,NRP1,SEMA3A,SEMA3F,VIM,ZEB1 |
| GO:0051960 | regulation of nervous system development | 0.0076 | ASPM,CELSR1,EFNA3,FN1,MARK1,MEF2C,NAP1L2,NRP1,SEMA3A,SEMA3F,SNCA,VIM,  ZEB1 |
| GO:1903375 | facioacoustic ganglion development | 0.0076 | NRP1,SEMA3A |
| GO:0007275 | multicellular organism development | 0.0077 | ANK2,ASPM,BHLHE41,BICC1,CELSR1,COL5A2,COL9A3,CPS1,DDR2,DLC1,DOCK11,  EFNA3,EMP1,FAM126A,FN1,GPC2,HES4,KRT81,LPIN1,LSR,MARK1,MECOM,MEF2C,  MGST1,MITF,MYLK,NAP1L2,NFIB,NRP1,PIK3R1,PYGO1,QKI,RECK,SATB1,SEMA3A,  SEMA3F,TACC1,VIM,ZEB1 |
| GO:0150020 | basal dendrite arborization | 0.01 | NRP1,SEMA3A |
| GO:0006928 | movement of cell or subcellular component | 0.0105 | ANK2,ASPM,CACNA2D1,CELSR1,CXCL2,DPP4,EFNA3,FN1,MARK1,MEF2C,NFIB,  NRP1,PIK3R1,PROS1,SEMA3A,SEMA3F,VIM |
| GO:0032970 | regulation of actin filament-based process | 0.0106 | ANK2,CELSR1,DLC1,LIMCH1,MEF2C,NRP1,PIK3R1,RHOQ |
| GO:0032501 | multicellular organismal process | 0.0112 | ANK2,ASPM,BGN,BHLHE41,BICC1,CACNA2D1,CCDC136,CCDC50,CELSR1,COL5A2,  COL9A3,CPS1,DDR2,DLC1,DOCK11,DPP4,EFNA3,EMP1,FAM126A,FN1,GPAM,GPC2,  HES4,KRT81,LPIN1,LSR,MARK1,MECOM,MEF2C,MGST1,MITF,MYLK,NAP1L2,NFIB,  NRP1,PIK3R1,PROS1,PYGO1,QKI,RECK,SATB1,SEMA3A,SEMA3F,SNCA,SYNM,TACC1,  VIM,ZEB1 |
| GO:0032502 | developmental process | 0.0113 | ANK2,ARHGEF28,ASPM,BHLHE41,BICC1,CCDC136,CELSR1,COL5A2,COL9A3,CPS1,  DDR2,DLC1,DOCK11,EFNA3,EMP1,FAM126A,FN1,GPC2,HES4,KRT81,LPIN1,LSR,MARK1,  MECOM,MEF2C,MGST1,MITF,MYLK,NAP1L2,NFIB,NRP1,PIK3R1,PYGO1,QKI,RECK,  SATB1,SEMA3A,SEMA3F,SNCA,TACC1,VIM,ZEB1 |
| GO:0061551 | trigeminal ganglion development | 0.0122 | NRP1,SEMA3A |
| GO:0023051 | regulation of signaling | 0.0128 | AKAP12,ANK2,ARHGEF28,ARHGEF40,ASPM,BGN,BICC1,CXCL2,DEPDC7,DLC1,DPP4,  FAM132A,FGD4,FN1,GPAM,GPC2,JADE1,MAP3K8,MCTP1,MDFIC,MECOM,MEF2C,NRP1,  PIK3R1,PIP5K1B,RHOQ,SEMA3A,SEMA3F,SNCA,ZEB1 |
| GO:0048856 | anatomical structure development | 0.0128 | ANK2,ASPM,BHLHE41,BICC1,CCDC136,CELSR1,COL5A2,COL9A3,CPS1,DDR2,DLC1,  DOCK11,EFNA3,EMP1,FAM126A,FN1,GPC2,HES4,KRT81,LPIN1,LSR,MARK1,MECOM,  MEF2C,MGST1,MITF,MYLK,NAP1L2,NFIB,NRP1,PIK3R1,PYGO1,QKI,RECK,SATB1,  SEMA3A,SEMA3F,TACC1,VIM,ZEB1 |
| GO:0050793 | regulation of developmental process | 0.013 | ASPM,BHLHE41,CELSR1,COL5A2,DDR2,DLC1,EFNA3,FGD4,FN1,GPAM,ISG15,MARK1,  MEF2C,MITF,NAP1L2,NFIB,NRP1,PIK3R1,RHOQ,SEMA3A,SEMA3F,SNCA,VIM,ZEB1 |
| GO:0034764 | positive regulation of transmembrane transport | 0.0131 | ANK2,CACNA2D1,FAM132A,PIK3R1,RHOQ,SNCA |
| GO:0007435 | salivary gland morphogenesis | 0.0141 | NFIB,NRP1,SEMA3A |
| GO:0035023 | regulation of Rho protein signal transduction | 0.0148 | ARHGEF28,ARHGEF40,DLC1,FGD4,NRP1 |
| GO:0051491 | positive regulation of filopodium assembly | 0.0148 | DOCK11,NRP1,RHOQ |
| GO:0060666 | dichotomous subdivision of terminal units involved in salivary gland branching | 0.0148 | NRP1,SEMA3A |
| GO:0016477 | cell migration | 0.0159 | ASPM,CELSR1,CXCL2,DPP4,FN1,MARK1,MEF2C,NRP1,PIK3R1,PROS1,SEMA3A,SEMA3F |
| GO:0032956 | regulation of actin cytoskeleton organization | 0.0175 | CELSR1,DLC1,LIMCH1,MEF2C,NRP1,PIK3R1,RHOQ |
| GO:0051492 | regulation of stress fiber assembly | 0.0175 | DLC1,LIMCH1,NRP1,PIK3R1 |
| GO:0060385 | axonogenesis involved in innervation | 0.0175 | NRP1,SEMA3A |
| GO:0007010 | cytoskeleton organization | 0.0179 | ANK2,ASPM,DLC1,EPB41L4B,FGD4,LIMCH1,MAP7D3,MARK1,NRP1,RHOQ,SYNM,TACC1,  VIM |
| GO:0030029 | actin filament-based process | 0.0179 | ANK2,CACNA2D1,DLC1,EPB41L4B,FGD4,LIMCH1,NRP1,RHOQ,VIM |
| GO:0007411 | axon guidance | 0.0198 | EFNA3,NFIB,NRP1,PIK3R1,SEMA3A,SEMA3F |
| GO:0006644 | phospholipid metabolic process | 0.02 | FAM126A,GPAM,ISYNA1,LPIN1,PIK3R1,PIP5K1B,SERINC2,SNCA |
| GO:0030516 | regulation of axon extension | 0.02 | FN1,NRP1,SEMA3A,SEMA3F |
| GO:0001667 | ameboidal-type cell migration | 0.0201 | DPP4,FN1,NRP1,SEMA3A,SEMA3F |
| GO:0051056 | regulation of small GTPase mediated signal transduction | 0.0201 | ARHGEF28,ARHGEF40,DEPDC7,DLC1,FGD4,NRP1,RHOQ |
| GO:0009966 | regulation of signal transduction | 0.0206 | AKAP12,ARHGEF28,ARHGEF40,ASPM,BGN,BICC1,CXCL2,DEPDC7,DLC1,FAM132A,  FGD4,FN1,GPAM,GPC2,JADE1,MAP3K8,MDFIC,MECOM,MEF2C,NRP1,PIK3R1,PIP5K1B,  RHOQ,SEMA3A,SEMA3F,SNCA,ZEB1 |
| GO:0006638 | neutral lipid metabolic process | 0.0217 | CPS1,GPAM,LPIN1,SNCA |
| GO:0009987 | cellular process | 0.0241 | AKAP12,ANK2,ARHGEF28,ASPM,BGN,BHLHE41,CACNA2D1,CCDC136,CELSR1,CHTF18  ,COL5A2,COL9A3,CPS1,CXCL2,DDR2,DEPDC7,DLC1,DOCK11,DPP4,DSEL,EFNA3,EHHADH,  EMP1,EPB41L4B,FAM126A,FGD4,FIGN,FN1,GPAM,GPC2,H2AFJ,HES4,ISG15,ISYNA1,JADE1,  KCTD12,KRT81,LIMCH1,LPIN1,LRCH2,LSR,MAP3K8,MAP7D3,MARK1,MBNL2,MCTP1,  MDFIC,MECOM,MEF2C,MGST1,MITF,MSRB3,MYLK,NAP1L2,NFIB,NR3C1,NR3C2,NRP1,  NXPH4,OASL,PADI3,PARD3B,PIK3R1,PIP5K1B,PROS1,PTPN21,PYGO1,QKI,RECK,RHOQ,  SACS,SATB1,SEMA3A,SEMA3F,SERINC2,SNCA,SYNM,TACC1,VIM,VKORC1L1,ZDHHC2,  ZEB1,ZNF106 |
| GO:0010604 | positive regulation of macromolecule metabolic process | 0.0246 | ANK2,CHTF18,DDR2,DLC1,EFNA3,EPB41L4B,FN1,JADE1,LIMCH1,LPIN1,MAP3K8,MDFIC,  MECOM,MEF2C,MITF,NAP1L2,NFIB,NR3C1,NRP1,PIK3R1,PYGO1,QKI,RHOQ,SEMA3A,  SNCA,VIM,ZEB1 |
| GO:0030336 | negative regulation of cell migration | 0.0248 | DLC1,LIMCH1,MCTP1,MEF2C,RECK,SEMA3A |
| GO:0040011 | locomotion | 0.0262 | ASPM,CELSR1,CXCL2,DPP4,EFNA3,FN1,MARK1,MEF2C,NFIB,NRP1,PIK3R1,PROS1,  SEMA3A,SEMA3F |
| GO:0051128 | regulation of cellular component organization | 0.0267 | CELSR1,DDR2,DLC1,DOCK11,DPP4,FGD4,FN1,JADE1,LIMCH1,MARK1,MCTP1,  MEF2C,MITF,NAP1L2,NRP1,PIK3R1,RHOQ,SACS,SEMA3A,SEMA3F,SNCA,VIM |
| GO:1901701 | cellular response to oxygen-containing compound | 0.0278 | CACNA2D1,COL5A2,CPS1,LPIN1,MEF2C,MGST1,NR3C1,PIK3R1,RHOQ,SNCA,ZEB1,ZNF106 |
| GO:0046326 | positive regulation of glucose import | 0.0293 | FAM132A,PIK3R1,RHOQ |
| GO:2000026 | regulation of multicellular organismal development | 0.0298 | ASPM,CELSR1,COL5A2,DDR2,EFNA3,FN1,ISG15,MARK1,MEF2C,MITF,NAP1L2,NFIB,  NRP1,PIK3R1,SEMA3A,SEMA3F,SNCA,VIM,ZEB1 |
| GO:0032060 | bleb assembly | 0.0301 | EMP1,MYLK |
| GO:0071679 | commissural neuron axon guidance | 0.0301 | NFIB,NRP1 |
| GO:0048522 | positive regulation of cellular process | 0.0315 | AKAP12,ANK2,ASPM,CHTF18,CXCL2,DDR2,DLC1,DOCK11,DPP4,EFNA3,EPB41L4B,  FAM132A,FGD4,FN1,GPAM,ISG15,JADE1,LIMCH1,LPIN1,MAP3K8,MDFIC,MECOM,  MEF2C,MITF,MYLK,NAP1L2,NFIB,NR3C1,NRP1,PIK3R1,PYGO1,QKI,RHOQ,SEMA3A,  SNCA,VIM,ZEB1 |
| GO:0030335 | positive regulation of cell migration | 0.032 | CXCL2,DDR2,EPB41L4B,FN1,MYLK,NRP1,PIK3R1,SEMA3A |
| GO:0007399 | nervous system development | 0.0324 | ANK2,ASPM,CELSR1,DLC1,EFNA3,FAM126A,FN1,GPC2,HES4,MARK1,MEF2C,NAP1L2,  NFIB,NRP1,PIK3R1,QKI,SEMA3A,SEMA3F,TACC1,VIM,ZEB1 |
| GO:0007165 | signal transduction | 0.0331 | AKAP12,ANK2,ARHGEF28,BGN,CELSR1,CXCL2,DDR2,DEPDC7,DLC1,DOCK11,  EFNA3,FGD4,FN1,GPC2,ISG15,LRCH2,MAP3K8,MARK1,MCTP1,MDFIC,MEF2C,MITF,  NR3C1,NR3C2,NRP1,NXPH4,OASL,PIK3R1,PYGO1,RHOQ,SEMA3A,SEMA3F,SNCA,VIM,  ZEB1,ZNF106 |
| GO:1902531 | regulation of intracellular signal transduction | 0.0339 | AKAP12,ARHGEF28,ARHGEF40,BGN,DEPDC7,DLC1,FAM132A,FGD4,FN1,MAP3K8,  MDFIC,MECOM,MEF2C,NRP1,PIK3R1,PIP5K1B,RHOQ,SEMA3A |
| GO:0001952 | regulation of cell-matrix adhesion | 0.0352 | DLC1,LIMCH1,NRP1,PIK3R1 |
| GO:0048583 | regulation of response to stimulus | 0.0362 | AKAP12,ARHGEF28,ARHGEF40,ASPM,BGN,BICC1,CXCL2,DEPDC7,DLC1,FAM132A,  FGD4,FIGN,FN1,GPAM,GPC2,JADE1,MAP3K8,MCTP1,MDFIC,MECOM,MEF2C,MYLK,  NRP1,PIK3R1,PIP5K1B,PROS1,RHOQ,SEMA3A,SEMA3F,SNCA,ZEB1 |
| GO:0030208 | dermatan sulfate biosynthetic process | 0.0369 | BGN,DSEL |
| GO:0044255 | cellular lipid metabolic process | 0.037 | CPS1,EHHADH,FAM126A,GPAM,GPC2,ISYNA1,LPIN1,PIK3R1,PIP5K1B,QKI,SERINC2,SNCA |
| GO:0021987 | cerebral cortex development | 0.0385 | ASPM,NRP1,SEMA3A,TACC1 |
| GO:0051493 | regulation of cytoskeleton organization | 0.0407 | CELSR1,DLC1,LIMCH1,MEF2C,NRP1,PIK3R1,RHOQ,SNCA |
| GO:0022603 | regulation of anatomical structure morphogenesis | 0.0408 | CELSR1,COL5A2,DLC1,EFNA3,FGD4,FN1,MEF2C,NFIB,NRP1,RHOQ,SEMA3A,SEMA3F |
| GO:0030205 | dermatan sulfate metabolic process | 0.0408 | BGN,DSEL |
| GO:0031295 | T cell costimulation | 0.0408 | DPP4,MAP3K8,PIK3R1 |
| GO:0010810 | regulation of cell-substrate adhesion | 0.0413 | DLC1,FN1,LIMCH1,NRP1,PIK3R1 |
| GO:0045785 | positive regulation of cell adhesion | 0.0413 | DPP4,EPB41L4B,FN1,GPAM,MAP3K8,NRP1,PIK3R1 |
| GO:0051241 | negative regulation of multicellular organismal process | 0.0413 | ASPM,COL5A2,EFNA3,FN1,ISG15,MEF2C,NFIB,NRP1,PIK3R1,PROS1,SEMA3A,SEMA3F,VIM |
| GO:0032989 | cellular component morphogenesis | 0.0427 | ANK2,CCDC136,EFNA3,FN1,MEF2C,NFIB,NRP1,PIK3R1,SEMA3A,SEMA3F |
| GO:0051928 | positive regulation of calcium ion transport | 0.0427 | ANK2,CACNA2D1,MYLK,SNCA |
| GO:0120035 | regulation of plasma membrane bounded cell projection organization | 0.0427 | DOCK11,FN1,MARK1,MEF2C,NRP1,RHOQ,SEMA3A,SEMA3F,VIM |
| GO:0046928 | regulation of neurotransmitter secretion | 0.0442 | MCTP1,MEF2C,SNCA |
| GO:0051173 | positive regulation of nitrogen compound metabolic process | 0.0447 | CHTF18,DDR2,DLC1,EFNA3,FN1,JADE1,LIMCH1,LPIN1,MAP3K8,MDFIC,MECOM,  MEF2C,MITF,NAP1L2,NFIB,NR3C1,NRP1,PIK3R1,PYGO1,QKI,RHOQ,SEMA3A,SNCA,  VIM,ZEB1 |
| GO:0000904 | cell morphogenesis involved in differentiation | 0.0453 | EFNA3,FN1,MEF2C,NFIB,NRP1,PIK3R1,SEMA3A,SEMA3F |
| GO:0010715 | regulation of extracellular matrix disassembly | 0.0453 | DDR2,DPP4 |
| GO:0035239 | tube morphogenesis | 0.0453 | CELSR1,DLC1,FN1,MEF2C,MYLK,NFIB,NRP1,QKI,ZEB1 |
| GO:0045595 | regulation of cell differentiation | 0.0453 | ASPM,BHLHE41,COL5A2,DDR2,EFNA3,FN1,ISG15,MARK1,MEF2C,MITF,NAP1L2,  NRP1,PIK3R1,SEMA3A,SEMA3F,VIM,ZEB1 |
| GO:0051239 | regulation of multicellular organismal process | 0.0453 | ANK2,ASPM,CACNA2D1,CELSR1,COL5A2,DDR2,EFNA3,EPB41L4B,FN1,GPAM,ISG15,  MARK1,MEF2C,MITF,NAP1L2,NFIB,NRP1,PIK3R1,PROS1,SEMA3A,SEMA3F,SNCA,  VIM,ZEB1 |
| GO:0051893 | regulation of focal adhesion assembly | 0.0453 | DLC1,LIMCH1,NRP1 |
| GO:1901653 | cellular response to peptide | 0.0453 | CACNA2D1,CPS1,LPIN1,PIK3R1,RHOQ,ZNF106 |
| GO:0003012 | muscle system process | 0.0455 | ANK2,CACNA2D1,MEF2C,MYLK,SYNM,VIM |
| GO:0051716 | cellular response to stimulus | 0.0475 | AKAP12,ANK2,ARHGEF28,BGN,CACNA2D1,CELSR1,COL5A2,CPS1,CXCL2,DDR2,  DEPDC7,DLC1,DOCK11,EFNA3,FGD4,FN1,GPC2,ISG15,LPIN1,LRCH2,MAP3K8,  MARK1,MCTP1,MDFIC,MEF2C,MGST1,MITF,MYLK,NR3C1,NR3C2,NRP1,NXPH4,  OASL,PIK3R1,PYGO1,RHOQ,SEMA3A,SEMA3F,SNCA,VIM,VKORC1L1,ZEB1,ZNF106 |
| GO:0010243 | response to organonitrogen compound | 0.048 | CACNA2D1,COL5A2,CPS1,LPIN1,MEF2C,MGST1,PIK3R1,RHOQ,SNCA,ZEB1,ZNF106 |
| GO:0023052 | signaling | 0.048 | AKAP12,ANK2,ARHGEF28,BGN,CACNA2D1,CELSR1,CXCL2,DDR2,DEPDC7,  DLC1,DOCK11,EFNA3,FGD4,FN1,GPC2,ISG15,LRCH2,MAP3K8,MARK1,MCTP1,  MDFIC,MEF2C,MITF,NR3C1,NR3C2,NRP1,NXPH4,OASL,PIK3R1,PYGO1,RHOQ,  SEMA3A,SEMA3F,SNCA,VIM,ZEB1,ZNF106 |
| GO:0030155 | regulation of cell adhesion | 0.048 | DLC1,DPP4,EPB41L4B,FN1,GPAM,LIMCH1,MAP3K8,NRP1,PIK3R1 |
| GO:0030198 | extracellular matrix organization | 0.048 | BGN,COL5A2,COL9A3,DDR2,FN1,RECK |
| GO:0045665 | negative regulation of neuron differentiation | 0.048 | ASPM,NRP1,SEMA3A,SEMA3F,VIM |
| GO:0046486 | glycerolipid metabolic process | 0.048 | CPS1,FAM126A,GPAM,LPIN1,PIK3R1,PIP5K1B,SERINC2 |
| GO:0048667 | cell morphogenesis involved in neuron differentiation | 0.048 | EFNA3,MEF2C,NFIB,NRP1,PIK3R1,SEMA3A,SEMA3F |
| GO:0048699 | generation of neurons | 0.048 | ASPM,CELSR1,EFNA3,FN1,GPC2,MARK1,MEF2C,NAP1L2,NFIB,NRP1,  PIK3R1,SEMA3A,SEMA3F,VIM,ZEB1 |
| GO:0065009 | regulation of molecular function | 0.048 | ANK2,ARHGEF28,ARHGEF40,BGN,CACNA2D1,CHTF18,CXCL2,DDR2,  DEPDC7,DLC1,DOCK11,EFNA3,FAM132A,FGD4,FN1,MAP3K8,MDFIC,MEF2C,  NFIB,NRP1,PIK3R1,PROS1,RECK,SEMA3A,SEMA3F,SERINC2,SNCA |
| GO:0051129 | negative regulation of cellular component organization | 0.0489 | DLC1,DPP4,MCTP1,NRP1,SACS,SEMA3A,SEMA3F,SNCA,VIM |
| GO:0048638 | regulation of developmental growth | 0.0494 | FN1,GPAM,MEF2C,NRP1,SEMA3A,SEMA3F |
| GO:0030318 | melanocyte differentiation | 0.0498 | MEF2C,MITF |
| GO:0086012 | membrane depolarization during cardiac muscle cell action | 0.0498 | ANK2,CACNA2D1 |

**Table S2 Enrichment analysis of Modules**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Category** | **Term ID** | **Term description** | **FDR** | **Genes** |
| Module 1 | GO:0048843 | negative regulation of axon extension involved in axon guidance | 3.66E-08 | NRP1,SEMA3A,SEMA3F |
|  | GO:0048846 | axon extension involved in axon guidance | 3.66E-08 | NRP1,SEMA3A,SEMA3F |
|  | GO:0061549 | sympathetic ganglion development | 3.66E-08 | NRP1,SEMA3A,SEMA3F |
|  | GO:0097490 | sympathetic neuron projection extension | 3.66E-08 | NRP1,SEMA3A,SEMA3F |
|  | GO:0097491 | sympathetic neuron projection guidance | 3.66E-08 | NRP1,SEMA3A,SEMA3F |
|  | GO:1901166 | neural crest cell migration involved in autonomic nervous system development | 3.66E-08 | NRP1,SEMA3A,SEMA3F |
|  | GO:1902287 | semaphorin-plexin signaling pathway involved in axon guidance | 3.66E-08 | NRP1,SEMA3A,SEMA3F |
|  | GO:0007411 | axon guidance | 2.81E-07 | EFNA3,NRP1,SEMA3A,SEMA3F |
|  | GO:0021828 | gonadotrophin-releasing hormone neuronal migration to the hypothalamus | 2.10E-06 | NRP1,SEMA3A |
|  | GO:1903375 | facioacoustic ganglion development | 2.10E-06 | NRP1,SEMA3A |
|  | GO:0150020 | basal dendrite arborization | 2.93E-06 | NRP1,SEMA3A |
|  | GO:0061551 | trigeminal ganglion development | 3.68E-06 | NRP1,SEMA3A |
|  | GO:0060666 | dichotomous subdivision of terminal units involved in salivary gland branching | 4.82E-06 | NRP1,SEMA3A |
|  | GO:0045664 | regulation of neuron differentiation | 6.05E-06 | EFNA3,NRP1,SEMA3A,SEMA3F |
|  | GO:0060385 | axonogenesis involved in innervation | 6.05E-06 | NRP1,SEMA3A |
|  | GO:0051093 | negative regulation of developmental process | 2.55E-05 | EFNA3,NRP1,SEMA3A,SEMA3F |
|  | GO:0022603 | regulation of anatomical structure morphogenesis | 3.08E-05 | EFNA3,NRP1,SEMA3A,SEMA3F |
|  | GO:0007413 | axonal fasciculation | 4.05E-05 | NRP1,SEMA3A |
|  | GO:0051241 | negative regulation of multicellular organismal process | 4.84E-05 | EFNA3,NRP1,SEMA3A,SEMA3F |
|  | GO:0050919 | negative chemotaxis | 8.87E-05 | SEMA3A,SEMA3F |
|  | GO:0010469 | regulation of signaling receptor activity | 0.00037 | NRP1,SEMA3A,SEMA3F |
|  | GO:0007166 | cell surface receptor signaling pathway | 0.00055 | EFNA3,NRP1,SEMA3A,SEMA3F |
|  | GO:0018108 | peptidyl-tyrosine phosphorylation | 0.0018 | EFNA3,NRP1 |
|  | GO:0010632 | regulation of epithelial cell migration | 0.0021 | NRP1,SEMA3A |
|  | GO:0065009 | regulation of molecular function | 0.0025 | EFNA3,NRP1,SEMA3A,SEMA3F |
|  | GO:0045765 | regulation of angiogenesis | 0.0035 | EFNA3,NRP1 |
|  | GO:0032270 | positive regulation of cellular protein metabolic process | 0.0049 | EFNA3,NRP1,SEMA3A |
|  | GO:0048880 | sensory system development | 0.0053 | NRP1,SEMA3A |
|  | GO:0050769 | positive regulation of neurogenesis | 0.0077 | NRP1,SEMA3A |
|  | GO:0030335 | positive regulation of cell migration | 0.0086 | NRP1,SEMA3A |
|  | GO:0007169 | transmembrane receptor protein tyrosine kinase signaling pathway | 0.0101 | EFNA3,NRP1 |
|  | GO:0043410 | positive regulation of MAPK cascade | 0.0105 | NRP1,SEMA3A |
|  | GO:0051345 | positive regulation of hydrolase activity | 0.0203 | EFNA3,NRP1 |
|  | GO:0007267 | cell-cell signaling | 0.0378 | EFNA3,NRP1 |
| Module 3 | GO:0043010 | camera-type eye development | 0.0253 | VIM,ZEB1 |
|  | GO:0010975 | regulation of neuron projection development | 0.0316 | FN1,VIM |
|  | GO:0002376 | immune system process | 0.0317 | FN1,VIM,ZEB1 |
|  | GO:0048598 | embryonic morphogenesis | 0.0338 | FN1,ZEB1 |
|  | GO:0035239 | tube morphogenesis | 0.0382 | FN1,ZEB1 |
|  | GO:0044403 | symbiont process | 0.0386 | FN1,VIM |
|  | GO:0048513 | animal organ development | 0.0387 | FN1,VIM,ZEB1 |
|  | GO:0051173 | positive regulation of nitrogen compound metabolic process | 0.0387 | FN1,VIM,ZEB1 |
|  | GO:0045596 | negative regulation of cell differentiation | 0.0393 | VIM,ZEB1 |
|  | GO:0031325 | positive regulation of cellular metabolic process | 0.0409 | FN1,VIM,ZEB1 |
|  | GO:0008022 | protein C-terminus binding | 0.0181 | FN1,VIM |
|  | hsa05206 | MicroRNAs in cancer | 0.00071 | VIM,ZEB1 |