Supplementary materials

Mitochondria-related core genesand TF-miRNA-hub mrDEGs network in breast cancer

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Content:

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

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 musclecell 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

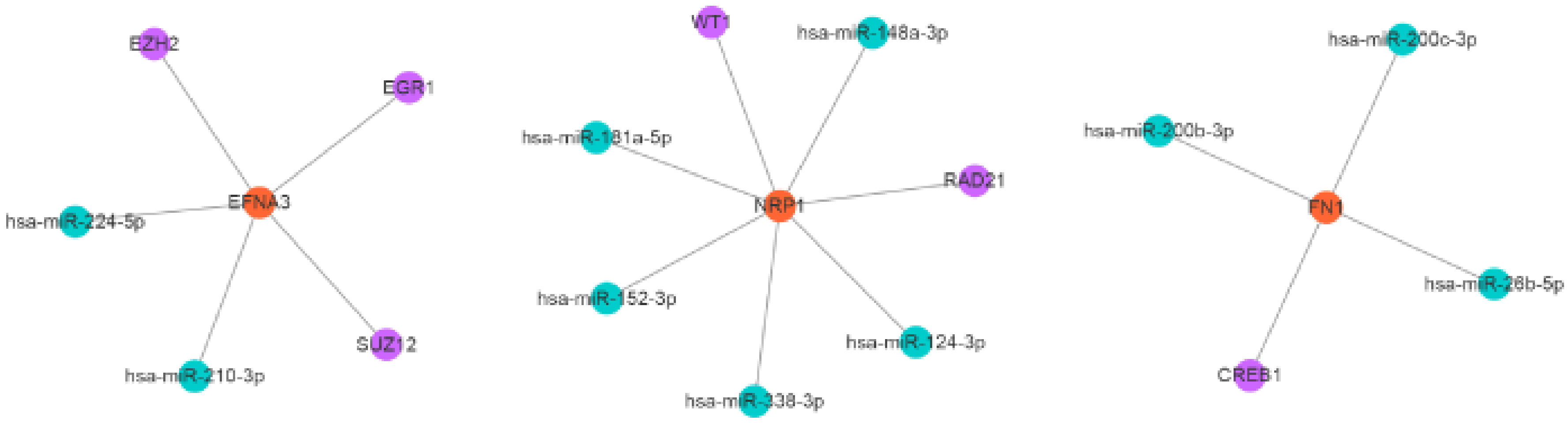

Figure S1: Validation of TF-miRNA-Hub mrDEGs network with starBase database (http://starbase.sysu.edu.cn/starbase2/index.php) and ChEA database with NetworkAnalyst (https://www.networkanalyst.ca/). Red color represented mrDEGs. Blue color represented microRNA and purple color represented TF.mrDEGs, mitochondria-related differential expressed genes; TF, transcription factor.