Table S1. Primer sequences.

Gene Symbol	Forward Primer (5' → 3')	Reverse Primer (5' → 3')
THY1	ATCGCTCTCCTGCTAACAGTC	CTCGTACTGGATGGGTGAACT
BMP2	ACCCGCTGTCTTCTAGCGT	TTTCAGGCCGAACATGCTGAG
LOX	GCCGACCAAGATATTCCTGGG	GCAGGTCATAGTGGCTAAACTC
KDR	GTGATCGGAAATGACACTGGAG	CATGTTGGTCACTAACAGAAGCA
MMP9	GGGACGCAGACATCGTCATC	TCGTCATCGTCGAAATGGGC
ACTB	TTCCTTCCTGGGCATGGAGTCCT	TTGGCGTACAGGTCTTTGCGGAT

Table S2. DEGs between the NERD group and the HC group.

649 upregulated DEGs (NERD vs. HC)					
SLC16A1	KRT16P2	PTPRZ1	KDR	RPS4Y1	MYO1B
KRT1	FAT1	SPRR4	TENM2	KRT14	CAPN6
DDX3Y	KDM5D	HK2	USP9Y	ABCA12	TXLNGY
UTY	S100A7	EIF1AY	KLK5	FMNL2	ZFY
BRCA1	KLK6	CASC19	SERPINB4	FSCN1	TTYH3
SH3PXD2B	PCDHGC3	PRKY	TTTY14	IRS1	TTTY15
CARD18	MYH10	NLGN4Y	MYO5A	LINC00278	MMP12
GALNT18	RAPGEF5	BNC1	TBX3	VANGL2	LAMA1
LRP8	SOX4	TBL1Y	DLX3	MTHFD1L	UBASH3B
COL4A1	NUP210	TMSB4Y	AC011297.1	ST8SIA6	RAB3IP
MYO10	LEF1	NAV1	PTPRD	FOXP3	TRPV3
SPRR2G	QRFPR	FXYD5	SIRPA	LIPN	LIPG
PRSS12	ZNF736P9Y	HMGA2	GLDC	ARAP3	FREM2
CERNA2	PXDN	STEAP1B	ALOX12B	APLNR	RGS20
KIRREL1	GPR153	DLG5	BMP2	LIPK	ENAH
KRTDAP	EPPK1	EPHB2	DMXL2	ABCA1	PCSK9
ADARB1	GABRA4	PITX2	GFPT2	COL14A1	S100A7A

ADGRF5	TNC	NPNT	ZNF827	BRINP1	STEAP4
SRY	GYG2P1	NRG1	NMB	ADAP2	SQLE
MIR31HG	AGPAT4	KRT6A	PGBD5	CDHR1	MMP9
AC011473.4	KRT16P4	CD36	ATP2C2	SLC4A7	CASP1P2
THSD7B	MCM10	ARSFP1	SLC15A1	AP1S3	CHST11
PTPRG	NGFR	THBS2	SPIN4	COL6A5	RNASEH2CP1
EML5	DOC2B	MRLN	MFHAS1	LRRC4	CLSPN
POLR3G	ESYT3	VSIG8	PLA2G4E	SPIRE1	ADAMDEC1
KCNA2	KRT16P3	TTBK2	KRT6C	SDK1	NOTCH1
FAM222A	PIK3R3	LRP12	ELOVL7	CBX2	PFN2
SFXN5	DYNAP	PTHLH	CHML	CEMIP	ARNT2
CCNJL	ELFN1	IQCA1	SEMA3C	KAZALD1	ADAM23
OTOP2	C1orf216	DZIP1	FLVCR2	GDPD2	HOXA7
ANOS2P	WFDC12	FBLIM1	PDPR	NRP2	NKX1-2
PLA2G4D	LINC01886	THSD1	STRA6	LDLR	ZBED9
FAM167A	ABL2	AL157829.1	HSPG2	EPOP	GABRQ
DLC1	ALPL	LTBP1	LOX	MICAL2	SLC36A1
FAM89A	SPRY4	COL4A2	IQGAP2	LRAT	COL27A1
CXCL14	GPRIN1	SLC7A11	CHST2	ERVMER34-1	AC129492.6
TNFSF18	GLI2	TFCP2L1	OLFML2B	PLAT	AVPR1A
EREG	CLSTN2	ADAMTS14	PALM	C1orf226	CPA6
XRCC2	GPR37	SLC26A9	PXDNL	PDE10A	MTCL1
ALOXE3	MAP7D2	AC010889.1	IGFBP6	PHLDB2	FSD1L
B4GALNT3	ANGPTL4	DPF3	HOXC8	AC098864.1	CD163L1
FBN2	SEZ6L2	COL13A1	PLAG1	ADAMTS12	CDC14B
PLPPR4	DDN	CDYL2	KRT16	ZNF704	TCAF1P1
GJA3	COL5A2	KCNS1	NID1	GLT1D1	DUSP9

ADGRL3	TENM3	COL1A1	JCAD	AL161431.1	HEPH
FGF1	AACSP1	TNFRSF10D	AL049767.1	LOXL4	RIMS2
THY1	LAMP5	KRT9	PI3	TMEM178B	RNF183
CEP72	AP001783.1	MYOM3	AC125807.2	CPXM1	CYP24A1
CRYGS	KCNN4	SLAMF7	LINC02580	KRT6B	CCR4
ADAM12	WNT3	CHDH	MMP2	COL5A1	MEX3A
TRPM6	SEZ6L	AL512363.1	BGN	CXCL6	ZFHX4
CICP16	AC007182.1	CHST1	CACNA1D	CRACR2A	AC108010.1
SAA1	FADS1	RASL11B	PKNOX2	TMEM86A	FIGN
ZNF469	BCAN	SCART1	NOS1	PCDHGC4	FAM169A
NUDT11	CPNE8	ATP13A5	FOSL1	ADAMTS9	GJC1
GSDME	C5AR2	ACER2	WDR66	BPIFC	ACP7
PCSK2	TP53TG5	SERPINE1	IFNWP19	IL22RA2	STRIP2
TCERG1L	AC138035.1	HELLPAR	IGFL1P1	HECW1	COL3A1
TFAP2E	SYT12	ITGA11	AL049629.1	OR2A7	HMCN1
GLB1L	PCDHB10	IFNE	TMEM45A	HEPHL1	ADAMTS7
AL355032.1	AC018629.1	ADGRE1	EFR3B	COL6A3	HOXA6
AC009275.1	LINC02188	NOX4	C4B	MT-TR	MIR635
IL36G	GRPEL2-AS1	AC140479.7	DBNDD2	ADAMTS15	HEY1
SNHG28	MAPK10	EGFLAM	DYSF	IRX1	LOXL2
LINC02448	HOXC13	FAM157C	GRIP2	GUCY1A2	AC007319.1
RP1L1	SELE	C1QL3	KLK14	LHFPL2	DEFB4A
PAPPA	KIAA1549	AC012513.3	CCDC150	AC018638.2	FBXL19-AS1
SLC6A17	NKX3-1	AKR1B1	SDK2	PNMA8A	VNN3
AC009053.1	NYAP1	PCDHGB2	NOS1AP	LRRN3	LRRC37A17P
GPR4	IL33	SLAMF9	PRTFDC1	OTX1	KSR2
AC010731.2	AL355336.1	AOC1	TAGLN3	IL1RL1	AC133919.2

AADACL2	TPRG1-AS1	GLDCP1	GPR160	PHLPP2	LINC00346
ABCA13	LCE3E	FABP4	NME9	HRK	ZFY-AS1
NLGN4X	HUNK	PLA2G3	CECR2	TLL2	AL445205.1
SCNN1D	SLC14A1	NRCAM	HAS3	GPLD1	P2RY8
CDH11	AC084337.1	AC093904.3	AC006262.1	MAMLD1	ATP1B3-AS1
HERC2P9	HCAR1	KRT2	CSMD1	LUZP2	OR10H1
AKR1B10	TM4SF19-AS1	ADAMTS1	HS3ST4	KLK1	LINC02159
FAM157B	RIMBP2	LINC00887	MFAP3L	AC021106.1	MTMR7
LYZ	COL4A6	KIF26A	CHRNA3	CLCN4	CORIN
KLK7	BX537318.2	M1AP	PRICKLE1	VDAC1P8	AL590434.1
PROX1	EFCAB2	PCYT1B	IGFL2-AS1	AC105020.1	RBP1
CXCL8	PDE7B	CD22	SLC38A3	AC110285.3	BACH2
AGPAT4-IT1	AC106038.1	ARTN	FER1L6	CYP2C19	PICSAR
AC126474.1	HOXC13-AS	C5orf17	FAM184B	HNF4G	ANK1
PLA2G4E-AS1	GUSBP9	CHODL	WDR63	AL355312.3	AC010761.3
SOS1-IT1	LCE1C	SEMA3G	FBXO16	APOBEC3A	C4A
AC099548.2	SALL4	AC006460.2	CERS3-AS1	ANKRD20A7P	ADCYAP1R1
BLACAT1	ZBTB40-IT1	TAF7L	AL139274.2	COL12A1	KRT18P59
AC006058.1	TSSK4	WNT11	CNTF	AC008764.2	CFAP45
AC106820.4	IL10	TGFB1	AC145138.1	ALOX12P2	U62317.1
U2AF1	AC004706.3	AC092881.1	SNORD17	RHOXF1-AS1	ATP1B2
SAMD12-AS1	SPP1	LINC00462	DACH1	AC138866.1	PTGS2
AP000688.2	STK31	IGHE	GCLM	IGSF1	TMC7
LINC02471	MISP	EGR1	CAPNS1P1	TEX52	CCDC170

NPW	AC027228.2	SAA2	CR786580.1	FAM171B	AC141557.2
PSG4	ABHD12B	SLC9A2	MGC12916	SPRR2F	SLC16A12
AC006480.2	AC091806.1	AL020997.3	SMKR1	SUGCT	SIGLEC6
OR7M1P	CASC15	AC087783.2	BCAT1	TNFRSF10A-AS1	AC025917.1
DLX4	GAL3ST2	TMC5	AC017074.1	AL359922.2	AC011483.1
CYP27C1	SYNPO2L	STEAP3-AS1	LILRA1	HAS2	TNFRSF4
IGSF22	CD177	PDE3B	AL669942.1	EBF2	NID2
AC007785.1	SULT1B1	ZBTB16	SHISAL1	AC100757.1	PRTG
AP000347.1	ZDHHC11B	IL4I1	AC087752.3	RNU6ATAC18P	TPPP3
ARPC3P1	CTH	LINC01152	NAIP	SLC6A14	CALM2P2
COL1A2	HOXC9	GSTA9P	GLI1	NLRP14	PNLDC1
FAM201B	TBC1D3E	AKR1C2	MT-TG	AC073263.1	TSPAN11
SCN2A	AC008610.1	ST8SIA6-AS1	CD44-AS1	POU2AF1	MUC5B
LINC01273					
546 downregulated DEGs (NERD vs. HC)					
KRT4	COX7A1	MUC22	PLEKHG6	ETNK2	CHPT1
RFK	FOXN3-AS1	CRYM	PAX1	C15orf62	RPL9
CDC42EP5	CST3	AC245060.4	FAM3B	TSPAN12	PNPLA4
HES4	NAPRT	CRTAC1	CCDC107	PHYHD1	GYPC
BX255925.3	AC044787.1	NOXA1	KRT79	SNTB1	KRT40
SETD9	HMGCS2	RECQL4	SPINT1-AS1	C8orf82	MYEOV
GCNT3	TMIE	GNG4	ASPG	IL18	LCN2
CIDECP	IL1A	RORC	GPT	CYSLTR1	PAX8
B4GALT1-AS1	AAMDC	HBB	MT1X	KRTAP3-2	LAYN
RRAS	AL365205.1	CAMK2N1	CRISP3	HNMT	AC233266.1

AC087741.3	GGTA1P	ZBED2	FMO9P	MESP1	ZNF683
PRKAA2	LMNTD2	SYT17	TAS1R3	CCDC160	NRTN
BRI3	AL357033.4	PRSS27	METTL24	CYP4F29P	CRISP2
HBA2	ELF5	ADRA2C	LINC01587	RPS20P14	ADRB2
HS3ST1	NDRG2	FNDC4	IL34	AC016739.1	FAHD2B
SOCS2	PET100	LRMP	AP003733.4	AC015912.3	DOCK9-DT
CES1P2	NTN4	LINC01170	ZNF135	AL445524.1	TTYH1
HOTAIRM1	ACOT4	RPL10P9	INSYN1	FTH1P8	MUC1
BCAS1	HSD11B1L	HAAO	AC008969.1	LINC00492	SPINK8
AC016582.3	STRADB	KCNK12	LINC01983	SLURP1	RDH5
KRT33A	GOLGA2P10	IGLV5-52	FAM124B	CYP11A1	AL139384.1
BST1	GNA14	C19orf81	POMC	LYPD2	AC245060.5
GBP3	SCIN	LINC01358	AC116345.1	C5orf66-AS1	ZNF667-AS1
CAMTA1-DT	CLVS1	PKIB	ADAMTSL4-AS1	CXCL17	KRT78
C8orf48	LRFN2	RPL39P3	HIST1H4E	CCDC184	GPIHBP1
PPIAP11	NINJ2	SUSD3	AC116312.1	AL513304.1	AL450992.2
CD55	TNNI2	PAX8-AS1	AL391361.3	NKG7	S1PR4
TMEM171	RASAL2-AS1	CDH20	AP000439.2	LINC01697	SYNE4
PLEKHF1	SYNGR3	AC008105.2	VSIG2	ADAP1	AL357033.3
RPRML	PBX4	BPGM	PART1	HLA-B	DCST2
SYT8	AC027117.2	AC004967.1	CYP2D7	FAM183A	CPNE4
AP000692.2	ATXN2-AS	LENG9	PPP1R1B	PLAC8	FAM181B
CRCT1	AC022613.2	AP002761.1	ADAD2	AC092535.4	AL031777.1
AC233266.2	TREH	TBCAP1	RPL29P11	CIDEA	AP000866.2
FAM171A2	KEL	ZNF714	ZNF671	FTH1P10	LYNX1-SLURP2

AC125232.2	MT1M	TAF10	PDE6A	CD1C	ZNF92
CYP2T1P	TBC1D10C	INSYN1-AS1	TMEM37	FCER1A	ALOX5
AKR7A3	AL161785.1	HCP5	CATSPERG	LINC00857	MYRF
FTH1P11	CYP3A4	LINC02036	AC005523.1	AC144530.1	IRF1
AC116407.1	MT1A	IL12A	BMS1P12	AL161421.1	RNF223
FTH1P2	STXBP6	CYP3A5	ZNF519	ADARB2	CMTM8
AC009414.2	FLJ46906	HBA1	UGT2B7	DUSP14	QPRT
RPL37P6	REN	FGF22	CXCR3	MT1L	FTH1P23
NTF3	AC073046.1	LST1	ZNF582	AC080038.1	DUSP13
AC233280.1	ZCWPW1	AC118754.1	PRR15	LINC02099	AC020659.1
SNAI3	TNNC2	LINC01225	TGFBR3L	HLA-H	KLKP1
HIF3A	AL356867.1	AL662844.4	CD1A	RPL5P4	ACOT1
FSTL4	AC245100.8	AC025539.1	APBA1	LINC01481	AC009299.2
CD1E	NOG	FAM25BP	ZNF503-AS1	CSPG4P10	FTH1
GADD45B	AC008105.3	AC020661.3	AC027117.1	AC011139.1	TCAP
FCGR2B	ADARB2-AS1	AL139246.5	SLC25A41	ZNF835	EEF1A1P11
AL589986.2	OXGR1	TCEAL2	DMRT2	TMEM238	AP006284.1
C2CD4D	AC008972.2	KCNMB1	FTH1P7	AC140479.5	AL139393.1
PHBP11	BEX5	C16orf54	IGLC7	GGACT	AC003973.3
XCL2	GZMH	AC116347.1	CFL2	ZNF382	DUOXA2
NTS	GPR25	ZNF208	SVOPL	RPSAP9	CRIP1
MT1G	COL9A2	AC024592.2	AL139095.2	AP001347.1	HTR3A
TRG-AS1	SH2D1B	MYBPC2	AQP5	CD207	KLRC1
AC010329.1	PLA2G2A	MYOM2	RPS7P10	RPL13AP7	KBTBD11
RPL24P2	MT2A	LINC00933	MAFTRR	LINC01144	NUS1P1
AC093821.1	CYP4F35P	YBX2	EEF1A2	TMEM47	FAM19A3
MATN4	TSPAN32	ICAM3	LINC01978	AC022706.1	BCAP31P2

NEXMIF	EMP3	PPARGC1A	ATP5MC2P4	ADGRE4P	AC243960.1
SLC2A4	RARRES3	RPS3AP25	RHCE	TMEM271	AC016773.1
AC140658.1	CD40LG	CAPN13	PPP1R27	AL606760.1	MT1E
LINC00115	SERHL	FMO8P	LPP-AS2	RAB6B	MIR4787
AP001610.2	DNAAF3	TRBV7-2	VWC2	AC010468.1	MC5R
ITGB2-AS1	MT1B	AP001360.2	CHP2	ADH1C	AKR7L
HLA-DOB	SLAIN1	AC010615.2	RPL7P16	PDXP	AC008608.2
AL592114.1	AL390198.1	KCTD9P4	LRG1	AL645608.7	AC020928.1
AP001412.1	AP006621.5	HRAT5	AC011611.2	KCNJ11	LPAR4
COLEC12	RNF103-CHMP3	AC015908.3	AP000936.3	IL2RG	RPL15P2
AC072061.1	AC093249.6	AC123912.4	LINC01905	PSCA	ADGRD1
CORO6	AC103706.1	AC004264.1	AC005920.1	LINC00892	PTH1R
TMEM178A	FASLG	PKMP3	ISM2	SPINK2	IGLV1-51
TPT1P5	KC6	TNKS2-AS1	LINC01726	MAMDC2	LINC00628
SORD2P	VN1R81P	TMEM52	CKB	KANSL1-AS1	AP001062.1
LINC01011	HSPB1P1	AC024610.2	GAST	SLC5A8	RPL7AP28
RPRM	HEATR4	AP005329.2	PGPEP1L	GABRP	AC006262.4
C16orf86	MNX1-AS1	TBX21	GALR3	AIM2	C2CD4C
DKK2	AC009271.1	NLRP10	LRRC26	ZNF665	PFN4
TMEM156	IL23A	AC142086.1	AC074212.1	AL645608.2	LINC01100
ADM5	FRG2HP	AL645940.1	JARID2-AS1	PPP1R36	HLA-DPB1
ANGPTL1	PROM1	NPIPA7	AL121761.1	LRRC37A7P	AC021087.1
AP006222.1	LINC00513	CCL26	MT1F	CCL5	AL157935.2
GPAT2	LY9	KIF7	SCGB2A1	TRGV2	AL590326.1
KRT34	MT1H	LRRN4CL	AP000553.5	LINC01224	ADRA2B
AL391001.1	GAPDHP65	CRTAM	AC107464.3	AC245033.3	AC106795.1

TFAP2A-AS1	AC026801.2	AC084024.4	AP000553.1	AC233968.1	TNNI3
LINC01970	AL451069.2	CCR2	IFI6	HPGDS	KCTD4
SAMD3	SPTY2D1OS	IGLC2	CYP4B1	FLJ31104	CHAC1

Table S3. Top twenty genes in network ranked by Stress method.

Rank	Name	Score
1	MMP9	363452
2	NOTCH1	334860
3	IL10	238362
4	CXCL8	236866
5	PTGS2	230172
6	MMP2	209894
7	HSPG2	131514
8	BGN	130338
9	SPP1	123834
10	THBS2	117296
11	POMC	106980
12	BMP2	105448
13	LOX	103082
14	HPGDS	101106
15	KDR	96550
16	S100A7	92236
17	SERPINE1	91188
18	THY1	89584
19	COL1A1	89354
20	MUC1	86354

Table S4. The interactions between miRNA and hub genes, TFs and miRNAs, and miRNAs and hub genes in the regulatory network.

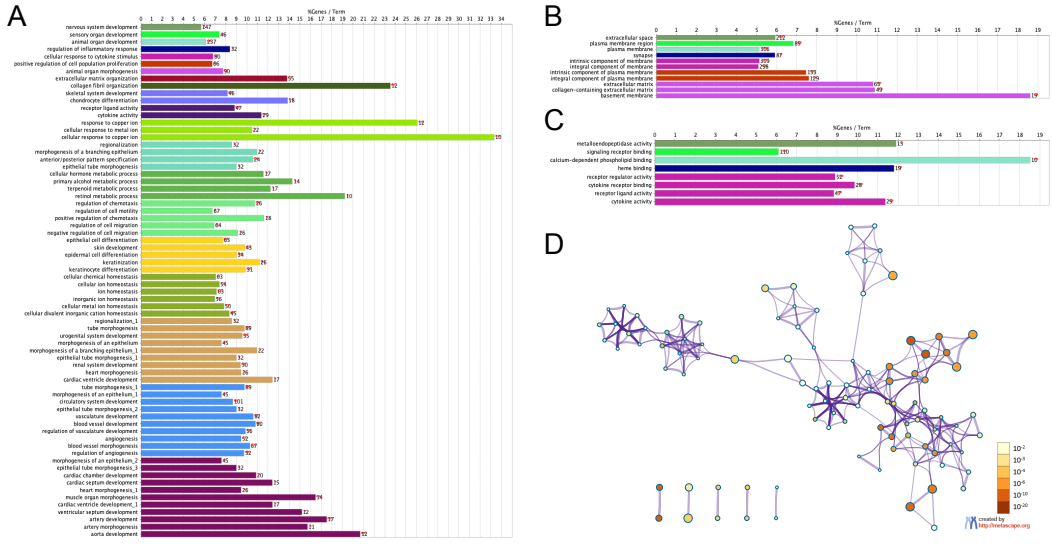
TF/miRNA regulatory pairs		
DNMT1/hsa-miR-200b	DNMT1/hsa-miR-429	DNMT1/hsa-miR-27b
DNMT1/hsa-miR-30a	DNMT1/hsa-miR-30c	SMAD3/hsa-miR-200b
SMAD3/hsa-miR-20a	SMAD3/hsa-miR-17	SMAD3/hsa-miR-30d
SMAD3/hsa-miR-27a	SMAD3/hsa-miR-140	SMAD3/hsa-miR-29b
HDAC4/hsa-miR-429	HDAC4/hsa-miR-200b	HDAC4/hsa-miR-29c
HDAC4/hsa-miR-29a	NFKB1/hsa-miR-200b	NFKB1/hsa-miR-17
NFKB1/hsa-miR-106b	NFKB1/hsa-miR-429	NFKB1/hsa-miR-27b
NFKB1/hsa-miR-93	NFKB1/hsa-miR-29b	NFKB1/hsa-miR-30c
NFKB1/hsa-miR-29c	NFKB1/hsa-miR-29a	E2F3/hsa-miR-200b
E2F3/hsa-miR-20a	E2F3/hsa-miR-27b	E2F3/hsa-miR-106b
E2F3/hsa-miR-17	ASCL2/hsa-miR-200b	ASCL2/hsa-miR-200c
ASCL2/hsa-miR-429	EPAS1/hsa-miR-24	EPAS1/hsa-miR-27a
EPAS1/hsa-miR-30d	EPAS1/hsa-miR-29c	NFE2L2/hsa-miR-200c
NFE2L2/hsa-miR-106b	NFE2L2/hsa-miR-140	NFE2L2/hsa-miR-93
NFE2L2/hsa-miR-29b	NFE2L2/hsa-miR-29c	NFE2L2/hsa-miR-29a
TP53/hsa-miR-200b	TP53/hsa-miR-200c	TP53/hsa-miR-17
TP53/hsa-miR-106a	TP53/hsa-miR-27a	TP53/hsa-miR-429
TP53/hsa-miR-27b	TP53/hsa-miR-20a	TP53/hsa-miR-519d
TP53/hsa-miR-29a	TWIST1/hsa-miR-200b	TWIST1/hsa-miR-200c
TWIST1/hsa-miR-27a	TWIST1/hsa-miR-429	TAF15/hsa-miR-20a
TAF15/hsa-miR-17	AP-1/hsa-miR-27b	AP-1/hsa-miR-30a
AP-1/hsa-miR-29a	ZEB2/hsa-miR-429	ZEB2/hsa-miR-200b
ZEB2/hsa-miR-200c	FOXF2/hsa-miR-429	FOXF2/hsa-miR-200b
E2F7/hsa-miR-27b	E2F7/hsa-miR-106b	E2F7/hsa-miR-93

SNAI1/hsa-miR-429	SNAI1/hsa-miR-200b	SNAI1/hsa-miR-200c
EZH2/hsa-miR-429	EZH2/hsa-miR-200b	EZH2/hsa-miR-200c
EZH2/hsa-miR-30a	EZH2/hsa-miR-27a	EZH2/hsa-miR-30d
MITF/hsa-miR-106a	MITF/hsa-miR-20b	MITF/hsa-miR-338
MITF/hsa-miR-140	MITF/hsa-miR-29a	SIX1/hsa-miR-200b
SIX1/hsa-miR-200c	SLUG/hsa-miR-200b	SLUG/hsa-miR-200c
SMAD2/hsa-miR-27a	SMAD2/hsa-miR-30d	HDAC1/hsa-miR-200b
HDAC1/hsa-miR-429	HDAC1/hsa-miR-30d	HDAC1/hsa-miR-140
ESR2/hsa-miR-30a	ESR2/hsa-miR-27b	MEN1/hsa-miR-27a
MEN1/hsa-miR-27b	MNT/hsa-miR-20a	MNT/hsa-miR-17
TLX3/hsa-miR-20a	TLX3/hsa-miR-17	HES1/hsa-miR-20a
HES1/hsa-miR-17	E2F2/hsa-miR-20a	E2F2/hsa-miR-17
NKX2-5/hsa-miR-20a	NKX2-5/hsa-miR-17	ARNT/hsa-miR-93
ARNT/hsa-miR-106b	ATF4/hsa-miR-93	ATF4/hsa-miR-106b
HDAC2/hsa-miR-200b	HDAC2/hsa-miR-200c	HDAC2/hsa-miR-30d
HDAC2/hsa-miR-429	HDAC2/hsa-miR-29c	AHR/hsa-miR-93
AHR/hsa-miR-106b	HNF4A/hsa-miR-200b	HNF4A/hsa-miR-200c
HNF4A/hsa-miR-410	HNF4A/hsa-miR-485	HNF4A/hsa-miR-543
ZEB1/hsa-miR-200b	ZEB1/hsa-miR-200c	ZEB1/hsa-miR-429
ZEB1/hsa-miR-140	GRHL2/hsa-miR-200b	GRHL2/hsa-miR-200c
GRHL2/hsa-miR-429	DNMT3B/hsa-miR-29b	DNMT3B/hsa-miR-29a
TLX1/hsa-miR-20a	TLX1/hsa-miR-17	HIF1A/hsa-miR-200c
HIF1A/hsa-miR-24	HIF1A/hsa-miR-106b	HIF1A/hsa-miR-429
HIF1A/hsa-miR-27a	HIF1A/hsa-miR-140	HIF1A/hsa-miR-20a
HIF1A/hsa-miR-30a	HIF1A/hsa-miR-93	HIF1A/hsa-miR-30d
HIF1A/hsa-miR-29c	TP73/hsa-miR-429	TP73/hsa-miR-200b
KLF4/hsa-miR-429	KLF4/hsa-miR-200b	KLF4/hsa-miR-200c

TEAD1/hsa-miR-93	TEAD1/hsa-miR-106b	
TF/hub gene pairs		
SMAD3/THY1	SMAD3/BMP2	SMAD3/LOX
SMAD3/KDR	SMAD3/MMP9	NFKB1/THY1
NFKB1/MMP9	EPAS1/THY1	EPAS1/LOX
NFE2L2/LOX	NFE2L2/KDR	NFE2L2/MMP9
TP53/THY1	TP53/BMP2	TP53/LOX
TP53/MMP9	TWIST1/THY1	TWIST1/MMP9
TAF15/MMP9	AP-1/THY1	AP-1/BMP2
AP-1/LOX	AP-1/KDR	AP-1/MMP9
E2F7/THY1	EZH2/THY1	EZH2/BMP2
EZH2/LOX	EZH2/KDR	EZH2/MMP9
MITF/THY1	MITF/BMP2	MITF/LOX
MITF/KDR	MITF/MMP9	SIX1/LOX
SLUG/THY1	SLUG/BMP2	SLUG/LOX
SLUG/KDR	SLUG/MMP9	SMAD2/THY1
SMAD2/BMP2	SMAD2/LOX	SMAD2/KDR
SMAD2/MMP9	HDAC1/THY1	HDAC1/BMP2
HDAC1/LOX	HDAC1/KDR	HDAC1/MMP9
ESR2/THY1	ESR2/LOX	ARNT/THY1
ARNT/BMP2	ARNT/LOX	ARNT/MMP9
ATF4/BMP2	ATF4/LOX	HDAC2/BMP2
HDAC2/LOX	HDAC2/KDR	HDAC2/MMP9
AHR/BMP2	AHR/LOX	AHR/KDR
HNF4A/LOX	HNF4A/MMP9	ZEB1/LOX
ZEB1/MMP9	GRHL2/THY1	DNMT3B/THY1
TLX1/MMP9	HIF1A/THY1	HIF1A/BMP2

HIF1A/LOX	HIF1A/KDR	HIF1A/MMP9
KLF4/THY1	KLF4/LOX	KLF4/KDR
TEAD1/THY1	TEAD1/KDR	
miRNA/hub gene pairs		
hsa-miR-485/THY1	hsa-miR-543/BMP2	hsa-miR-374a/BMP2
hsa-miR-106b/BMP2	hsa-miR-519d/BMP2	hsa-miR-140/BMP2
hsa-miR-106a/BMP2	hsa-miR-374b/BMP2	hsa-miR-410/BMP2
hsa-miR-20a/BMP2	hsa-miR-17/BMP2	hsa-miR-526b/BMP2
hsa-miR-93/BMP2	hsa-miR-20b/BMP2	hsa-miR-29b/LOX
hsa-miR-29c/LOX	hsa-miR-29a/LOX	hsa-miR-30d/LOX
hsa-miR-30c/LOX	hsa-miR-27b/LOX	hsa-miR-30a/LOX
hsa-miR-27a/LOX	hsa-miR-429/LOX	hsa-miR-200b/LOX
hsa-miR-200c/LOX	hsa-miR-24/LOX	hsa-miR-338/KDR
hsa-miR-665/KDR		

Figure S1. ClueGO identified clusters of significantly enriched GO terms in BP (A), CC (B), and MF (C). (D) Network of KEGG enriched terms colored by p-value, where terms containing more genes tend to have a more significant p-value.



Supplementary Figure 2. (A) Heatmap illustrating the gene expression network. The brighter color indicates lower overlap, and the comparatively darker red color indicates higher overlap. Modules are defined as branch-like structures on the dendrogram. (B) A hierarchical clustering dendrogram and heatmap of module eigengene correlations. The hierarchical clustering dendrogram is overlaid with symbols identifying gene subnetworks, while the heatmap in the lower panel shows the eigengene adjacency.