

Figure S1. Network topology analysis of various soft threshold powers. The left panel displays the scale-free fit index (y-axis) as a function of soft threshold power (x-axis). The panel on the right shows the average connectivity (degrees, y-axis) as a function of soft threshold power (x-axis).

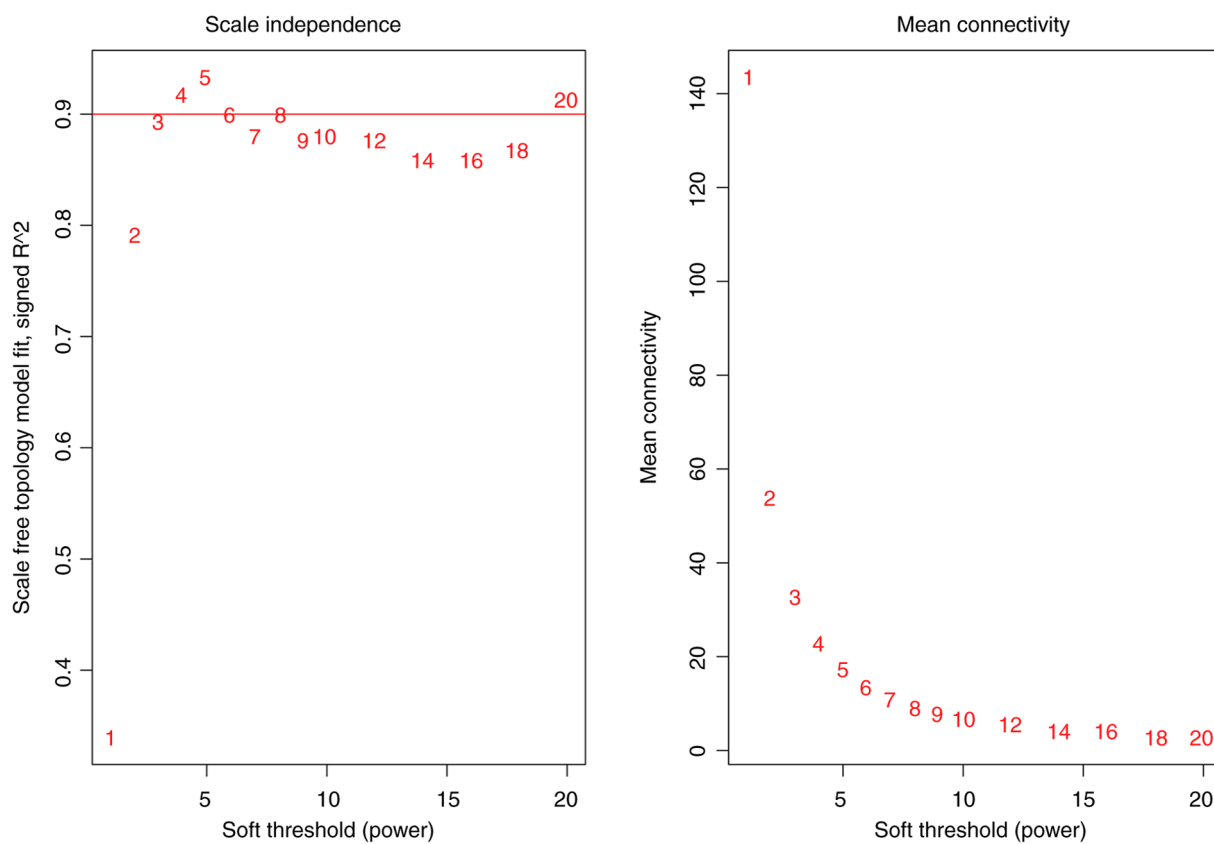


Figure S2. Heat map visualization of the genetic network. The heat map depicts the topological overlap matrix among all genes in the analysis. Light colors indicate low overlap, and red that gradually darkens indicates a higher overlap. Gene dendrogram and module assignments are shown on the left hand side and top of the figure.

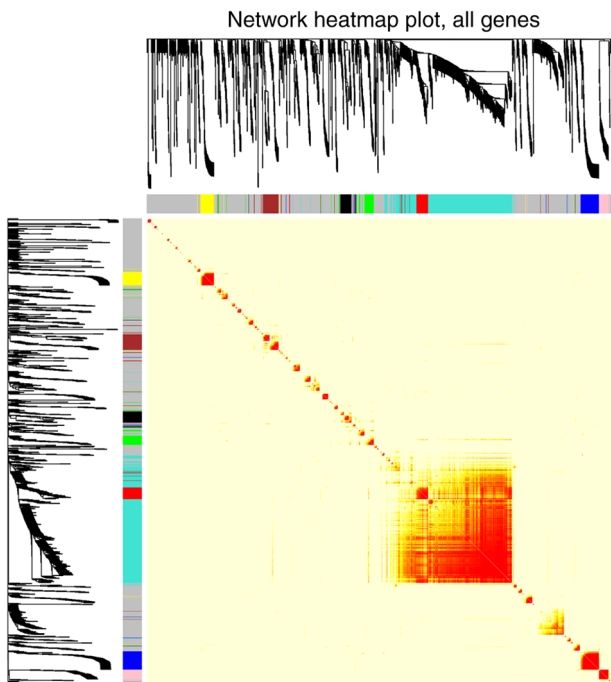


Table S1. Co-expression analysis of the 1,400 genes was performed using weighted correlation network analysis.

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A, Black module

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OR5G5P CEMIP CA6 TTPA AC007608.2 AXIN2 GSX1 DLX4 KRT40 FGF3 INHBB SP7 STRA6 KRT39 NKD1 SNORC COL9A3 AC004231.1 HSD3BP5 IGDCC3 AC007608.4 GLDC NFIA-AS2 LHX1 NOTUM RNF2P1 XAGE2 KRTAP4-12 LY6G6E OR7E5PLY6G6FCNTFR-AS1 AL662899.1 NKD2 KRTAP3-1 HOXD13 KRT23 AP002992.1 SLC22A11 AP000785.1

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B, Blue module

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LCN1 S100A2 GYS2 CIR1P3 LY6D ATP12A PSG9 RDH12 SH3GL3 UPK1A AL356867.1 FAM83C PRR9 S100A7A FETUB EPGN AC103563.2 BNC1 PNLIPRP3 PSG2 RPTN LY6G6C KRTAP4-1 KRT5 FLG2 PSG1 KRT15 GH2 LINC01214 PSG3 IL36RN SERPINB11 KRT4 KRT75 CLDN17 LCE3A WFDC5 LINC01527 SPRR2E CSH1 KRT16 DSG1 SPINK7 CSH2 LCE3E LCE3D GBP6 VSIG8 CALML3 TGM1 KPRP KRT13 ATP6V0A4 KRT32 DSC1 KRTAP3-2 AC133485.2 MUC21 WFDC12 HCG22 POU3F1

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C, Brown module

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MEIS1-AS3 C3orf56 ERVW-1 PRR23C BPIFA1 PDCL2 SPANXB1 FAM9B LINC01419 NR0B1 LINC01254 GAGE12J AC004987.3 VCX2 DSCR4-IT1 VCX LUZP4 SOHLH1 CER1 SPATA31D1 PRSS38 MAGEC1 DSCR4 ZFP42 LINC01287 HDGFL1 AC022616.1 IFNL4P1 PNMA6E DDX4 MAEL BANF2 SYCN CETN1 AARD AC117500.1 DMRTB1 UNC5D VCX3A PLA2G1B AC016710.1 RNF17 AC087277.1 AC010385.2 MAGEC2 RHOXF2 TEX11 AP001547.1 INSL6 TMEM207 RBPJL CTAG1A AL691420.1 AC073347.1 CT45A1 HSD3BP4

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D, Green module

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TDRG1 SYT7 AC074237.1 MYH7B TSPY10 LINC02492 FREM2-AS1 TACR1 DLX1 DLX2 OTX2 AC036222.1 CAMTA1-IT1 CTBP2P1 BMP3 AC026336.3 PRB4 CU104787.1 AC024230.1 TSPY6P DCAF8L2 AC106785.2 C2orf69P1 AL356364.1 HS3ST6 AC003669.1 CHL1-AS2 LINC01019 GABRA3 LINC01194 AC010894.3 AC026336.4 ASCL5 MED15P9 LINC00200 DLL3 SHISAL2B PENK HOXD10 PAGE5 FAM181A-AS1 NAA11 HOXD11 NRXN1

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E, Grey module

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AC237221.1 AP1B1P1 C22orf42 IL17C IGLV7-46 IGLC3 MIR4539 ACTBL2 CTXND1 LINC00922 AC025470.2 MAGEB10 AC007950.1 PRSS56 IGFBL1 IGLV3-22 LINC01497 GNMT AL356108.1 TFAP2B LGR6 OLFM4 MTCO3P38 CSN1S1 MTND2P31 PLEKHD1 NXPH1 GRIN3B SST SLC6A3 ALPI TLR8-AS1 ALPL2 CALCA MTND4P5 LRRC53 LINC01986 LINC01894 PLAC4 AC022034.2 MARK2P11 AC036111.2 AC022034.4 AP003110.1 PRB2 KLHDC7B ASCL1 AC026780.2 AC095350.1 AC243829.4 LINC00523 RPS17P15 AC108865.2 KCNK16 CASR H2BFWT MIR4527HG IGLV1-36 AC108865.1 NMS OVAAL AC005307.1 AP003108.5 MIR7515HG AC113349.1 PSKH2 ESX1 AC106875.1 MT3 AC004944.1 HMGN2P34 AL023754.1 AC011754.1 IGFN1 AC006484.1 HHLA1 AC012501.2 LINC02544 AC139491.3 BTG4 AL121892.1 LINC01241 AC090340.1 OR7E145P AC007920.1 PRR27 MTND4P27 AL133284.1 LINC02052 LINC01048 AC011124.1 AP001284.1 AC091173.1 PRR4 GADL1 HTN3 AC126763.1 SBK2 ZNF716 ACTBP13 AC138915.2 REG3A AL033397.1 AC027369.1 AC144450.1 AL391358.1 AL080248.1 IGLJ1 PTPRO DSCR10 CPE FMO1 AC105411.1 TCF23 ERP27 KRTAP3-3 U62317.1 AC011124.2 C8orf87 ADAACL2 LINC00534 GSTA3 AC007277.1 SUCNR1 AP000997.2 LINC01152 FAR2P1 NOL4L-DT IGHD3-3 AL139002.1 AC108174.1 LINC02312 AL139384.2 SLC6A4 AL513185.3 TRBV5-5 CCT7P2 LINC01088 AZGP1P1 SLCO4A1-AS1 AL354984.1 LINC02526 AC106774.4 SCNN1G PTCHD1-AS MAGEA10 BCAT1 TRIM48 LYPD8 AL589745.1 INHA IDO2 POU6F2-AS2 CUZD1 AC109454.3 TRIM43 AL162511.1 FABP4 LINC02365 HTR3D CYP24A1 AC126915.2 AL161908.1 LINC00319 LBP LINC01257 MUC12 KLF2P1 AC128707.1 AC010145.1 CNTN1 LINC01105 ANKRD33 NOX3 FAM205BP DDX53 GNG13 TMEM211 AC011525.1 AC079098.1 LINC01925 AC027088.3 AC004233.2 NTS AC148476.1 SYNGR4 RGS21 LINC02485 AC107398.3 AC104958.1 CRYBA2 AC023866.2 PDILT SSX4 TMEM255A CD27 GIMD1 SLC24A5 AC007422.1 DSCAML1 FMO9P DGCR5 AC091987.1 DSCR8 AC026797.1 AC131254.1 LINC00284 AC079466.1 RNU6-1238P DPPA3 AL160287.1 AC009229.1 COL6A6 SLC30A2 AC119751.4 AP000842.3 ATP4A LETM1P2 TRIM43B MEP1AP4 CCKBR IGKV6D-21 RAG2 SLC13A1 AC021074.3 KCNE2 MRGPRX2 AC012558.1 AC010998.1 OR7E4P LINC00945 AC034228.3 CIDEA AC118658.1 MIR4538 PCSK2 AP000851.1 LINC02532 LINC02582 PGM5P4-AS1 GTF2IP6 AP001858.2 AQP12B PNMT POU3F2 TEK4 KLKP1 LINC02461 CD19 LINC01029 CD79A LINC02278 AC023469.2 GTF3AP6 IGHD3-16 THRSP AC021534.1 AC090957.1 AC023824.3 AL512638.2 PPP1R27 RERGL AL138826.1 AC007923.1 AC011298.1 LINC01204 NCR3 OR8D1 TRIM42 KLK4 TRIML2 LINC00454 IGLV3-24 VWA5B1 NEUROD4

Table S1. Continued.

## E, Grey module

HPGDS HLA-DPB2 P2RY12 VEGFD RNASE2 TRDV3 AC090809.1 DPPA3P2 AC003092.1 MMP20 MTATP6P3 AC093772.1 AL163953.1 PNMA6F MYBPHL AC245100.6 AC003988.1 C10orf53 LY6L TBC1D3P7 GLYATL3 LCE1E AC069061.2 PARAL1 AC023310.4 AC121342.1 NBEAP1 CCDC190 MTCO1P25 STMND1 ATP4B C17orf77 PPY SERPINB10 AC092593.1 MMP8 TFDP3 SLC25A47P1 CXorf67 MTND2P13 ITGAD CRH HSD3B1 AC118273.1 BAALC AC009646.2 AL133330.2 AC025263.3 OPRK1 CLDN6 LINC02154 IGLL1 TEX35 AC010609.1 AC126323.6 HSPA8P17 MTND3P1 LINC01511 FAM9C LIPF KRT81 TRBJ2-2P ADIPOQ PHEX-AS1 AC105460.1 MUCL1 PRAC1 DLX2-AS1 KRTAP1-5 GP2 AC005840.3 MAN1A2P1 AC007671.1 KRT89P DPP3P2 AC006557.2 AL499627.1 DIRAS1 AC007099.1 AC104958.2 RORB-AS1 MTATP6P25 FGL1 AC100860.1 AC011900.1 AP002358.2 LINC02434 AC015911.3 IGKV1D-16 ETNPPL CLSTN2-AS1 TSPY9P DAZL AL138900.2 COL11A2 LINC00508 AC187653.1 IGHV1-18 AQP2 MS4A3 CXCL11 GKN1 GDF10 LINC01742 NEUROD2 AC008517.1 AC106794.1 OR8K5 ELANE RNASE3 AC022167.4 AZU1 TM4SF1-AS1 PRTN3 SSX2 MPO IGFL1 HOXC12 CT45A5 MYH1 DNAH9 AACSP1 DEFA4 TMEM196 NOBOX TKTL1 SH3GL2 DRD2 GACAT3 LINC01501 CYP4F30P AC099552.4 BEST2 AC112206.3 PGC AC008753.2 CRYGB DLGAP1-AS5 LCT KCN3 TMT1 LINC02563 CMA1 KCN2 MAP1LC3C SERTM2 TRAJ35 IGHV3-13 AC108482.1 AC021351.1 UROC1 CRP TSPY1 AL450267.1 SLC5A5 AL162384.1 RNU1-120P BCAR4 GFRA4 LINC01632 AL591468.1 CYP17A1 CXCR2P1 SAMD7 CALB1 ACTRT2 CT45A10 LINC01209 CYP11B1 ALOX15B DHRS2 COX7B2 PRH2 AP003037.1 AC004147.4 FMR1NB HOXA9 QRSL1 REG3G AL138974.1 AL139247.1 LINC00326 AC011474.2 CFD CCDC166 AC133561.1 LINC02152 AC108752.1 FADS2P1 SEZ6 SIT1 AC011474.4 AC239859.2 USP24P1 AL445209.1 AC055748.1 TSPY2 PHF2P2 AC244107.1 AC012322.1 GMCL1P2 KRT9 IGHV3-6 BFSP2-AS1 KRTAP9-12P PRSS1 IGLV7-43 AL121748.1 CHIT1 MIR567 LINC01667 PGA4 ADH4 AC092674.1 AC022893.2 ASB4 AC093583.1 AC117402.1 KRTAP1-4 CAV1 IGHV1-3 AVIL OBP2A GAL3ST3 PLD5 KRT35 TDRD9 PRSS3P1 DMP1 FCRLA IGKV2OR2-7D PGA3 OBP2B RBM22P12 GBP4 AC090283.1 RSPO4 KRT28 AC007991.4 VSTM2B CTHRC1P1 C20orf204 ELF5 AL133325.3 SMC01 KRT43P OSTN-AS1 UGT2A1 SAMSN1-AS1 LINC01346 DOC2A CR392039.3 AC012103.1 IGHJ1P HAO1 IGKV2D-40 LAMP5-AS1 TRAJ38 AC244502.1 EVA1A PLIN1 C6orf223 MSLNL MTCO1P42 FAR2P4 TRAJ34 LINC02542 PNPLA3 AC069287.3 OTUD6A ARHGDI WARS AL096828.1 CXCL10 PRLH TUSC5 IFNG IGKV6D-41 PPP4R3C TMED6 ADAM20P3 GOLGA2P11 PROS2P OR56A3 SNRPCP19 AF279873.2 AC139720.2 AC009988.1 MAGEA4 AC008619.1 BSND GIF AF274855.1 AL353747.3 HSD3BP3 DDX11L8 VPRES3 BPIFB2 LY6G6D IGF2-AS CRYBB2 AL355376.1 BX510359.5 CALML3-AS1 NPTX1 AQP12A AC147651.2 GGT4P IGKV2OR2-7 TCL1A ERAS CD300LG PROKR2 AL139099.3 LINC02424 LINC02404 AC087379.1 AC104051.2 AC093063.1 RNF182 AC025254.1 BANC1 AL354919.1 DPYS BLK BLACE AL121974.1 CSAG3 AC044839.3 CNTNAP2 PSAPL1 PINCR PDIA2 ARRDC5 CTRB1 IGHV3-53 NPBWR2 AC025244.1 VAX1 NKX6-2 AC128689.1 AL137078.1 AC104823.1 MAGEB6 NAALADL2-AS2 LINC01448 CRYGD STAP1 AC007991.2 AC090709.1 ALDOB BHMGI LCN12 AC007923.3 SLC22A31 KLF2P4 RARRES2P6 AF131216.3 AL162582.1 AC008163.1 AC022559.1 MYBPH MPZ AC105109.1 CTRB2 LINC00112 AC132825.4 CYP4F24P MEP1A AL445238.1 CLPS AC005357.1 LINC01854 IGLC5 LY6G6F-LY6G6D ASB11 PAQR9 CXCL9 FAM71E2 IGLV8-61 SLC17A8 LINC02051 AC110772.1 AC084128.1 PTF1A PPP1R2P10 AC023824.6 CEL LINC01781 AC115220.1 ADRA1D ACTG1P22 AC011507.1 SP8 BAAT MYCNUT DDX43P3 LINC00552 PNMA5 AC008514.1 SLC6A18 ASCL3 SFTA3 PNLIPRP1 TRAJ23 HEPACAM PGBD5 GLRA2 SPACA3 AC112518.2 AL133467.1 CD5L DLK1 AC005515.1 AC253536.4 BPIFA2 RNA5-8S5 DSCAM-AS1 AC090502.1 SCGB2A1 IGLC7 AC090680.1 NDUFA5P6 IDO1 SAGE1 MC4R CD79B CHAT AL390763.2 GUCA2B AC245100.3 FADS6 AC022126.1 AL078621.2 SFRP5 PGA5 LEP SFTPB MYH8 AC124290.1 CEACAM20 AC006065.1 LINC01087 IGHV1-68 LINC00661 GBP5 GBX2 AC209154.2 NF1P8 AC105254.2 IGLVI-63 AC016642.1 IGLVI-70 AC007848.2 MTND4P13 SERPINA3 POU4F1 AC110741.1 PHF21B

## F, Pink module

AL160408.4 DUSP13 GPR87 AL365356.5 AC244230.1 AC093627.1 LINC00973 AP000542.1 CGB8 ZNF72P APCDD1L-AS1 AC008687.6 ANXA8L1 AP000542.2 AC087258.1 KCNJ18 CKM ANXA8 LINC01711 CGB3 BNIP3P2 MYOSLID DCLK1 MIR205HG CGB5 GPR78 AL390755.1 LINC01468 LINC01940 FAT2 ZBED2 AL355607.1 CPA4 TP63

## G, Red module

AC008268.1 AC114786.1 AC104407.1 TGM4 CST4 MLNR SERPINA6 CHODL AC044784.1 KCNA1 VWC2 SMYD1 RYR3 AC068722.1 MIR4269 AC006007.1 NPAS4 CLVS2 EPHA7 AC092598.1 AC078925.1 AC005906.2 SLC5A7 BCHE AC078925.2 CISTR AC078925.3 RERG-IT1 AC006019.2 AC055874.1 HAND2-AS1 AC103770.1 AC093775.1 TAC1 AC093702.1 RN7SKP268 AC073862.3 CACNA1C-IT2 LINC01625 AC093390.1 AC114786.2 SPHKAP AC080100.1 SLC7A13

Table S1. Continued.

## H, Turquoise module

TMEM252 FRMD6-AS2 LINC01412 KCTD8 LMO3 ABCC9 PTGIS GRPR AC036108.2 MIR1-1HG PPP2R2B ABCA6 AL359633.2 RYR2 C2orf71 AC036108.3 SLIT2 LINC00561 LINC01489 AC008878.3 AP000722.1 MIR1-1HG-AS1 ABCA9 FRZB INMT AFF3 KCNA4 PRIMA1 GLP2R HLF LCN10 LINC01354 AC079411.2 CNKSR2 RBM24 MIR770 AC008808.1 CNR1 C7 GHR ADCYAP1R1 AC009229.2 FAT3 AC074131.1 AC119396.1 KCNN3 CARTPT NFASC POPDC2 DPT SHISAL1 AC005165.1 MIR100HG PSD CHRDL1 SFRP1 SLC7A3 PTCHD1 CRTAC1 MAPK10 RN7SKP208 AL008707.1 AL445426.1 KLHL4 AC106789.1 INMT-MINDY4 FAM19A4 NTRK3 MORN5 FLRT1 DNAJB5 SYNM LMO1 FGF2 BOC ABCA8 AC024651.1 LGI1 WISP2 OGN AC007495.1 CADM3-AS1 LDB3 ADRB3 SLC2A4 NEXMIF ANGPTL1 C1QTNF7 NRXN3 PIRT ABI3BP GAP43 DPP6 AF001548.1 AP000721.2 METTL24 FGF10-AS1 KCNA5 NCAM1 PMP2 PRKCB BVES PGR AL132642.1 AC009549.1 AC093787.1 SLC18A3 ACTG2 GRIK5 AP001107.5 LINC00891 AP000894.2 AL136369.2 C8orf46 FXDY1 AL513217.1 VIP ARPP21 ADAMTS8 CILP PDZD4 AC005180.1 SPARCL1 FLNC COL19A1 SPEG ZNF385D MYOC PDZRN4 AC103740.1 RN7SL334P SVILP1 ADH1B NGB SRPX PLIN4 ACTN2 PGM5 AC053503.6 ZBTB16 AOC3 AC005180.2 TMEM35A PYGM ANK2 SCN7A MAS1L AF001548.3 AC012636.1 HSPB6 AC005358.1 AL390783.1 ATP1A2 CASQ1 PHOX2B MYH11 CNN1 MKX-AS1 CTNNA3 AC008676.2 CLEC10A ANGPTL7 TMOD1 MYOZ2 AL662860.1 FAM129A DMD AC092667.1 SORCS1 PGM5-AS1 GRIA1 ADGRB3 CARMN NSG2 AL161457.1 SYNPO2 MSRB3 FP325317.1 C2orf40 PCDH10 AC079313.2 AC090531.1 AC002546.1 LINC00710 RGMANMRK2 NPPC RNF165 AC012055.1 AC005344.1 ASB5 RPL7P3 MYOCD MBNL1-AS1 DES FOXP2 FCER1A KCNK3 AC009102.2 AC092691.1 FGF10 FOXI2 MYLK MRGPRF-AS1 CHRM2 TNXB FGF14 STMN2 PRELP CMTM5 ANKS1B LINC00163 SNAP91 JAM2 TMEM100 GNAO1 FBXL22 MAP6 ACTA2-AS1 AL357936.1 ACKR1 MYLK1 NR5A1 CASQ2 AC008808.2 KCNMA1 AC053503.4 CADM2 PPP1R12B STUM FGL2 UNC45B MYL9 AKAP6 ASB2 AC096745.2 PCA3 AOC4P JPH2 TRBV26OR9-2 PTGDS AC110491.1 STMN4 RBMS3-AS3 AC009102.3 NT5C1A SCN2B GALR1 AL355974.2 AC011247.3 GPM6A NECAB1 AC024337.2 LMOD1 AP003071.3 SLITRK5 PI16 FILIP1 CNTN2 HAND2 CPED1 AJ011932.1 AC069437.1 PHOX2A AC087641.1 RSPO1 AL391807.1 TCEAL6 C8orf88 CFL2 TNS1 NEGR1 PCP4L1 CHRNA3 PLP1 C1QTNF4 FLNA CRHBP PLN SORBS1 FRRS1L HSPB7 NEXN KCNMB1 AL356489.2 ELAVL4 CPXM2 CNGA3 PRUNE2 LINC02106 KCNB1 VIT RERG RBPMS2 OLFM3 TACR2 SYNC AC116917.1 AC124891.1 PART1 LINC02557 RNF150 CALD1 AP000892.3 MRGPRF CALY AP003071.4 PCDH9 LINC00702 PDLIM3 AF106564.1 BVES-AS1 ADAMTSL3 ADCY5 ATP2B3 TRIM55 MRGPRD BHMT2 AC090044.1 SHISA3 ADAM33 MEF2C-AS1 PPP1R1A ADAMTS9-AS2 HSPB8 AP002518.2 TAGLN PGM5P4 HPSE2 FHL1 AC002398.2 AC027306.1 FAM180B AL359314.1 SLITRK3 INA CADM3 KIAA0408 AC025594.1

## I, Yellow module

ALLC F10 AQP8 AL162574.2 SERPINA10 AGT APCS CSN2 ITIH2 HP SERPINA5 CPN1 APOA1 FGB AC079414.2 CACNG3 PAGE4 RBP4 SLC38A4 AC115619.1 CFHR5 APOC3 ACSM2B FGG RNU1-70P SERPIND1 AFM AFP CPN2 PAH LINC02499 CCL16 ALB AHSG SLC2A2 APOA2 VTN CPB2 UGT2B4 AC023511.1 PLPPR1 ITIH1 AL355096.1 TRIM50 IGF2 ASGR2 SLC22A8 KNG1

Table SII. List of the top GO terms and Kyoto Encyclopedia of Genes and Genomes pathways in the black module.

Category	Term	Count	Genes	P- value	False discovery rate
GOTERM_BP_DIRECT	GO:0090090~negative regulation of canonical Wnt signaling pathway	4	NKD1, NKD2, NOTUM, AXIN2	6.58x10 <sup>-04</sup>	0.84007
GOTERM_BP_DIRECT	GO:0016055~Wnt signaling pathway	4	NKD1, NKD2, NOTUM, AXIN2	9.80x10 <sup>-04</sup>	1.248817
GOTERM_BP_DIRECT	GO:0061205~paramesonephric duct development	2	LHX1, STRA6	0.003213	4.038584
GOTERM_MF_DIRECT	GO:0005198~structural molecule activity	4	KRT39, KRTAP3-1, KRT40, KRT23	0.004414	4.351465
GOTERM_BP_DIRECT	GO:0051180~vitamin transport	2	TTPA, STRA6	0.005349	6.640331
KEGG_PATHWAY	hsa04310:Wnt signaling pathway	3	NKD1, NKD2, AXIN2	0.007786	5.775713
GOTERM_CC_DIRECT	GO:0005882~intermediate filament	3	KRT39, KRT40, KRT23	0.010416	9.135425
GOTERM_BP_DIRECT	GO:0060322~head development	2	LHX1, STRA6	0.010671	12.84151
GOTERM_BP_DIRECT	GO:0021527~spinal cord association neuron differentiation	2	LHX1, GSX1	0.013851	16.36353
GOTERM_CC_DIRECT	GO:0071944~cell periphery	2	INHBB, NKD2	0.052183	38.75752

GO, Gene Ontology.

Table SIII. Intramodular connectivity of the black module as calculated by Cytoscape software.

Node_	MCC	DMNC	MNC	Degree	EPC	Bottle neck	Eccentricity	Closeness	Radiality	Betweenness	Stress	Clustering coefficient
GSX1	7	0.309	3	6	14.1	12	0.15	14.466	5.767	263.147	696	0.13333
KRTAP4-12	7	0.309	3	6	13.9	4	0.125	13.55	5.483	98.591	294	0.13333
DLX4	9	0.379	4	5	13.6	3	0.125	13.016	5.48	41.955	114	0.4
KRT40	5	0.308	2	5	13.4	1	0.125	13.433	5.560	123.13	420	0.1
NFIA-AS2	5	0	1	5	13.2	2	0.1071	12.662	5.224	97.360	338	0
SP7	4	0	1	4	13.1	3	0.125	12.683	5.482	61.078	204	0
GLDC	5	0.309	3	4	12.9	1	0.1071	11.195	4.991	6.2666	28	0.33333
KRT39	4	0	1	4	12.4	1	0.1071	12.045	5.224	60.152	108	0
OR5G5P	4	0.309	3	3	12.2	2	0.125	11.05	5.224	7.179	36	0.66667
AC007608.2	3	0	1	3	12	2	0.1071	11.162	5.094	24.971	122	0
FGF3	5	0	1	5	11.8	30	0.15	13.7	5.767	410.498	822	0
IGDCC3	4	0.308	2	4	11.6	5	0.125	12.433	5.457	131.695	196	0.16667
RNF2P1	3	0.308	2	3	11.4	16	0.15	12.1	5.560	114.792	212	0.33333
OR7E5P	2	0	1	2	10.5	1	0.1071	10.461	5.043	5	10	0
COL9A3	2	0	1	2	9.73	1	0.0938	9.2702	4.551	1.667	6	0
NOTUM	3	0	1	3	9.7	3	0.1071	11.295	5.147	123.152	172	0
CA6	2	0	1	2	8.38	1	0.125	9.883	5.043	11.0778	22	0
AXIN2	2	0	1	2	8.22	2	0.15	10.283	5.198	24.282	38	0
AC007608.4	2	0	1	2	7.88	8	0.125	11.1	5.405	308	574	0
CEMIP	1	0	1	1	7.49	1	0.0938	8.604	4.5	0	0	0
LY6G6E	4	0.308	2	4	6.6	7	0.1071	10.926	4.991	286	514	0.16667
AP002992.1	1	0	1	1	6.24	1	0.125	9.283	5.043	0	0	0
STRA6	2	0	1	2	6.1	2	0.0938	8.770	4.474	56	72	0
LY6G6F	4	0.308	2	4	5.68	3	0.0938	9.787	4.422	110	186	0.16667
LHX1	3	0.308	2	3	5.48	2	0.0938	9.287	4.397	56	94	0.33333
CNTFR-AS1	1	0	1	1	3.77	1	0.0938	7.787	4.267	0	0	0
INHBB	1	0	1	1	3.72	1	0.0833	6.784	3.75	0	0	0
TTPA	1	0	1	1	3.6	1	0.0833	7.059	3.698	0	0	0

Table SIII. Continued.

Node_	MCC	DMNC	MNC	Degree	EPC	Bottle neck	Eccentricity	Closeness	Radiality	Betweenness	Stress	Clustering coefficient
AP000785.1	1	0	1	1	3.58	1	0.0833	6.893	3.672	0	0	0
AL662899.1	1	0	1	1	3.55	1	0.0833	7.059	3.698	0	0	0
SLC22A11	0	0	0	0	1	0	0	0	0	0	0	0
HSD3BP5	0	0	0	0	1	0	0	0	0	0	0	0
XAGE2	0	0	0	0	1	0	0	0	0	0	0	0
NKD2	0	0	0	0	1	0	0	0	0	0	0	0
KRT23	0	0	0	0	1	0	0	0	0	0	0	0
HOXD13	0	0	0	0	1	0	0	0	0	0	0	0
SNORC	0	0	0	0	1	0	0	0	0	0	0	0
NKDI	0	0	0	0	1	0	0	0	0	0	0	0
AC004231.1	0	0	0	0	1	0	0	0	0	0	0	0
KRTAP3-1	0	0	0	0	1	0	0	0	0	0	0	0



Table SIV. Association of black module genes with TNM stages using one-way ANOVA.

Gene	Mean	Standard error of the mean	F	P-value
AP002992.1	3.996	0.421	7.164	<0.001
OR5G5P	3.346	1.424	6.015	0.001
IGDCC3	123.986	49.893	5.594	0.001
NOTUM	13547.104	7010.246	5.967	0.001
RNF2P1	7.143	1.331	6.135	0.001
OR7E5P	3.070	0.982	5.995	0.001
FGF3	127.735	69.405	5.077	0.002
GLDC	571.514	206.991	5.267	0.002
NKD1	2451.413	850.316	4.624	0.004
KRT39	13.068	6.112	4.188	0.007
CA6	21.439	8.567	3.954	0.009
DLX4	127.662	27.929	3.939	0.010
NFIA-AS2	11.551	2.538	3.825	0.011
AC004231.1	12.217	2.858	3.825	0.011
AC007608.4	22.154	4.378	3.769	0.012
AC007608.2	4.779	1.273	3.511	0.017
SP7	8.130	4.912	3.460	0.018
KRT40	77.085	54.880	3.113	0.028
KRTAP4-12	0.538	0.133	3.091	0.029
GSX1	2.660	1.427	2.886	0.037
NKD2	934.876	163.325	2.841	0.040
CEMIP	5368.009	1092.622	1.700	0.169
SNORC	492.833	56.975	1.601	0.191
KRTAP3-1	12.217	2.858	1.581	0.196
CNTFR-AS1	3.109	0.825	1.576	0.197
TTPA	93.652	19.901	1.423	0.238
AL662899.1	0.718	0.185	1.414	0.241
HOXD13	85.384	26.588	1.280	0.283
KRT23	1949.286	524.721	1.255	0.292
STRA6	1058.823	244.069	1.178	0.320
INHBB	1089.960	248.176	1.155	0.329
AP000785.1	6.435	1.389	0.916	0.435
AXIN2	1967.154	435.111	0.463	0.708
SLC22A11	40.279	9.445	0.425	0.735
LHX1	58.605	24.828	0.409	0.747
LY6G6E	3.724	1.229	0.379	0.768
LY6G6F	2.891	0.936	0.365	0.778
COL9A3	1414.299	423.891	0.329	0.804
HSD3BP5	15.959	1.603	0.294	0.830
XAGE2	21.012	9.554	0.180	0.910