Table S6. Gene networks identified in Ingenuity Pathway Analysis

	Molecules in Network	Score	Top Functions
1	**AKAP12, ALOX5**, **ARPP21**, **BLNK**, CD3, **CD79A**, **CDH1**, Creb, CSRP3, **EBF1**, **EMP1**, ERK1/2, **GFRA1**, GFRA2, Histone h3, **HLA DRB1**, IgG1, IgG, **IGLL1/IGLL5**, IgM, Immunoglobulin, **LEF1**, MHC Class II (complex), **MID1 (includes EG:100330952)**, **P2RX7**,P38 MAPK, **PDE4B**, **RFX5**, SCRT1, **SIGLEC10**, SYK/ZAP, **TCF4**, TCR, **TLR3**, Vegf	52	Hematological System Development and Function
2	BEGAIN, CDH3, **CECR2**, **CLIP4**, CTNNAL1, D glucose, DDR1, **DGKE**, **EGFL7**, EHBP1, EHD1, **EHD3**, Histone h3, IGF1R, IP6K1, **KIAA0284**, **KIAA0930**, LOXL4, LRPPRC, **Mcpt8**, **NEK1**, NEURL4, PACSIN2, **PRG2**, PTPRF, **RAB3IL1**, RALY, **SHPRH**, SMARCA5, SNAP29, **TP53I11**, UBC, UQCRC1, XRCC3, **ZNHIT3**	29	Organ Morphology, Development and Function
3	**AKAP12**, **ASXL2**, BANP, **C15orf48**, CDKN1A, CLCA2, **CPA3**, DDR1, **DLGAP1**, EZH2, FER, **FOXA3**, indican, ITSN1, KIT, MAPK1, **MYOM1**, MZF1, **NUAK1**, PTPRU, PVRL1, **RAB27B**, **Serpina3g** (includes others), SHANK2, SHANK3, SMARCA4, SRF, **SRGAP3**, STAT3, TACC3, TBX1, TEC/BTK/ITK/TXK/BMX, TP53 (includes EG:22059), TTK	21	Cell Cycle
4	**AMOT**, ARG1, **Camk2b**, CBR4, CPEB3, CREBBP, CTNND2, DPAGT1, DYNLL2, **EEF1D**, FCGR3A, FER, GAD2, GRIN2A, GRIP1, **HSD17B8**, HTATIP2, IFNG (includes EG:15978), IL10, LAT2, LATS1, **LOH12CR1**, LRPPRC, MLANA, MPP7, **MS4A2**, NEURL, NFKBID, **NSFL1C**, PHF23, RAD21, SREBF1, **SSTR2**, UBC, **VLDLR**	17	Gene Expression
5	AANAT, **ACSL5**, Akt,B-cell receptor, **BLNK**, Ccl9, CD72 (includes EG:100427076), Cg, Ck2,D glucose, ERK, **GNE**, GRIN1, Histone h3, HMGA2, Il8r, indican, ITSN1, Jnk, **KCNIP3**, NFkB (complex), NOS1, **NUAK1**, PI3K (complex), Pkc(s), PPP4R4, PRKD3, **Prss34**, RNA polymerase II, SLPI, SORBS2, **SUB1** (includes EG:10923), TBC1D4, TEC/BTK/ITK/TXK/BMX, **TRAF4**	17	Cell Death and Survival

Bold font indicates genes that are found to be up- or down-regulated in RNAseq data; non-bold genes are directly associated with bold genes.