

Category	Term	Count	p-value	Genes
BP	GO:0001570~vasculogenesis	5	0.01	GJC1, ACKR3, PTK2, TEAD2, VEGFA
BP	GO:0050900~leukocyte migration	7	0.011	SELP, CXADR, ITGA4, PDE4B, SIRPA, SLC16A3, NKX2-3
BP	GO:0051607~defense response to virus	7	0.04	DNAJC3, RNASEL, CXADR, OAS1, STAT1, NCBP3, IFIT1
BP	GO:0007507~heart development	7	0.06	GJA1, CXADR, LOX, TRPS1, XIRP2, BCOR, FBN1
BP	GO:0009311~oligosaccharide metabolic process	3	0.056	ST6GAL2, ST8SIA4, ST3GAL6
BP	GO:0007159~leukocyte cell-cell adhesion	3	0.056	SELP, ITGA4, EZR
BP	GO:0009615~response to virus	4	0.09	GJA1, STMN1, TRIM13, GNG11
BP	GO:0030198~extracellular matrix organization	7	0.084	ITGA4, LOX, ABI3BP, ITGA2, SPP1, PTK2, FBN1
CC	GO:0005662~DNA replication factor A complex	4	1.4E-3	PURB, PURA, RPA4, ERCC5
CC	GO:0005654~nucleoplasm	60	0.7E-2	NUMA1, C2ORF88, ZBTB20, EFCAB13, AHR, CLINT1, PTPDC1, CDC14A, DCAF7, CDC14B, SPRED1, METTL14, TRPS1, NAMPT, UBXN7, TEAD2, C8ORF44, KDM6A, FBNP4, CXADR, RMI1, GTF3A, HCFC2, CDC25A, EMSY, SGO2, ZC3H11A, MORF4L2, BMP2K, AAGAB, ANAPC5, MCTP2, CASZ1, XIAP, NMD3, TGOLN2, CAND1, NAA25, E2F1, SRSF11, SCAI, TCF7L2, RBM39, NFYB, STAT1, PCIF1, ANKRD23, BTBD8, SMARCA2, SCAF4, FOSL2, SELP, RAD52, NFIA, RPA4, ZNF217, ERCC5, NANOG, RAD18, FERMT2
CC	GO:0005925~focal adhesion	14	0.8E-2	TPM4, ITGA4, ITGA2, LPP, TRIOBP, PTK2, GJA1, NFASC, NCSTN, CSRP2, ATP6V0A2, P4HB, EZR, FERMT2
CC	GO:0043197~dendritic spine	6	1.9E-2	FARP1, ARHGAP32, PDE4B, CRIPT, STRN, SHANK2
CC	GO:0045177~apical part of cell	5	2.9E-2	SRR, NUMA1, FAT4, EZR, ATP6V1C1
KEGG	hsa05160:Hepatitis C	7	1.4E-2	RNASEL, OAS1, PPP2R1B, PPP2R2B, STAT1, PPP2R2D, IFIT1
KEGG	hsa04390:Hippo signaling pathway	6	7.5E-2	TCF7L2, PPP2R1B, PPP2R2B, PPP2R2D, BMPR1B, TEAD2
KEGG	hsa05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC)	4	7.8E-2	TCF7L2, GJA1, ITGA4, ITGA2

Note. BP: biological process; CC: cell component; GO: gene ontology; KEGG: Kyoto Encyclopedia of Genes and Genomes; MF: molecular function (as ranked by the p-value)