



Research article

Machine learning–based approach for efficient prediction of diagnosis, prognosis and lymph node metastasis of papillary thyroid carcinoma using adhesion signature selection

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Abstract: The association between adhesion function and papillary thyroid carcinoma (PTC) is increasingly recognized; however, the precise role of adhesion function in the pathogenesis and prognosis of PTC remains unclear. In this study, we employed the robust rank aggregation algorithm to identify 64 stable adhesion-related differentially expressed genes (ARDGs). Subsequently, using univariate Cox regression analysis, we identified 16 prognostic ARDGs. To construct PTC survival risk scoring models, we employed Lasso Cox and multivariate + stepwise Cox regression methods. Comparative analysis of these models revealed that the Lasso Cox regression model (LPSRSM) displayed superior performance. Further analyses identified age and LPSRSM as independent prognostic factors for PTC. Notably, patients classified as low-risk by LPSRSM exhibited significantly better prognosis, as demonstrated by Kaplan-Meier survival analyses. Additionally, we investigated the potential impact of adhesion feature on energy metabolism and inflammatory responses. Furthermore, leveraging the CMAP database, we screened 10 drugs that may improve prognosis. Finally, using Lasso regression analysis, we identified four genes for a diagnostic model

of lymph node metastasis and three genes for a diagnostic model of tumor. These gene models hold promise for prognosis and disease diagnosis in PTC.

Keywords: adhesion; bioinformatics; immune cell infiltration; machine learning; papillary thyroid carcinoma

1. Supplementary figures

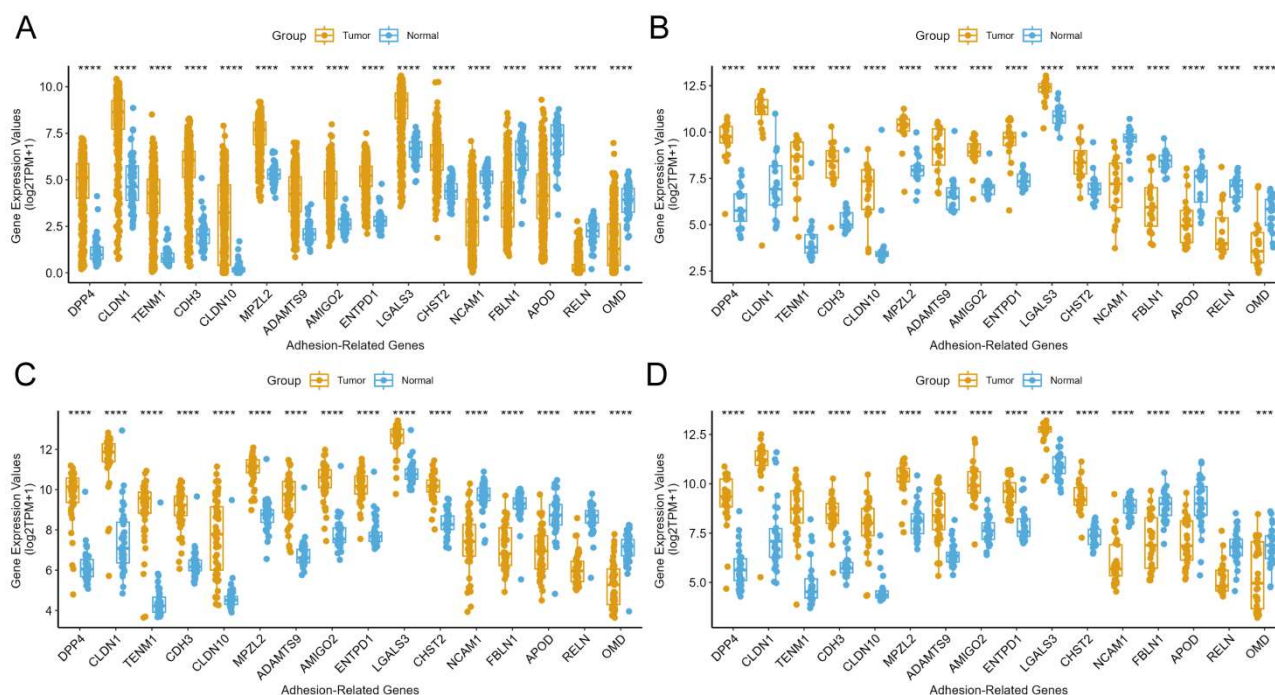


Figure S1. The box plots and dot plots show significant differences in the expression of prognostic ARDGs between tumor and normal tissues in different databases, including TCGA cohort (A), GSE29265 (B), GSE33630 (C), and GSE60542 (D). Statistical significance is shown as follows: * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; **** $P < 0.0001$.

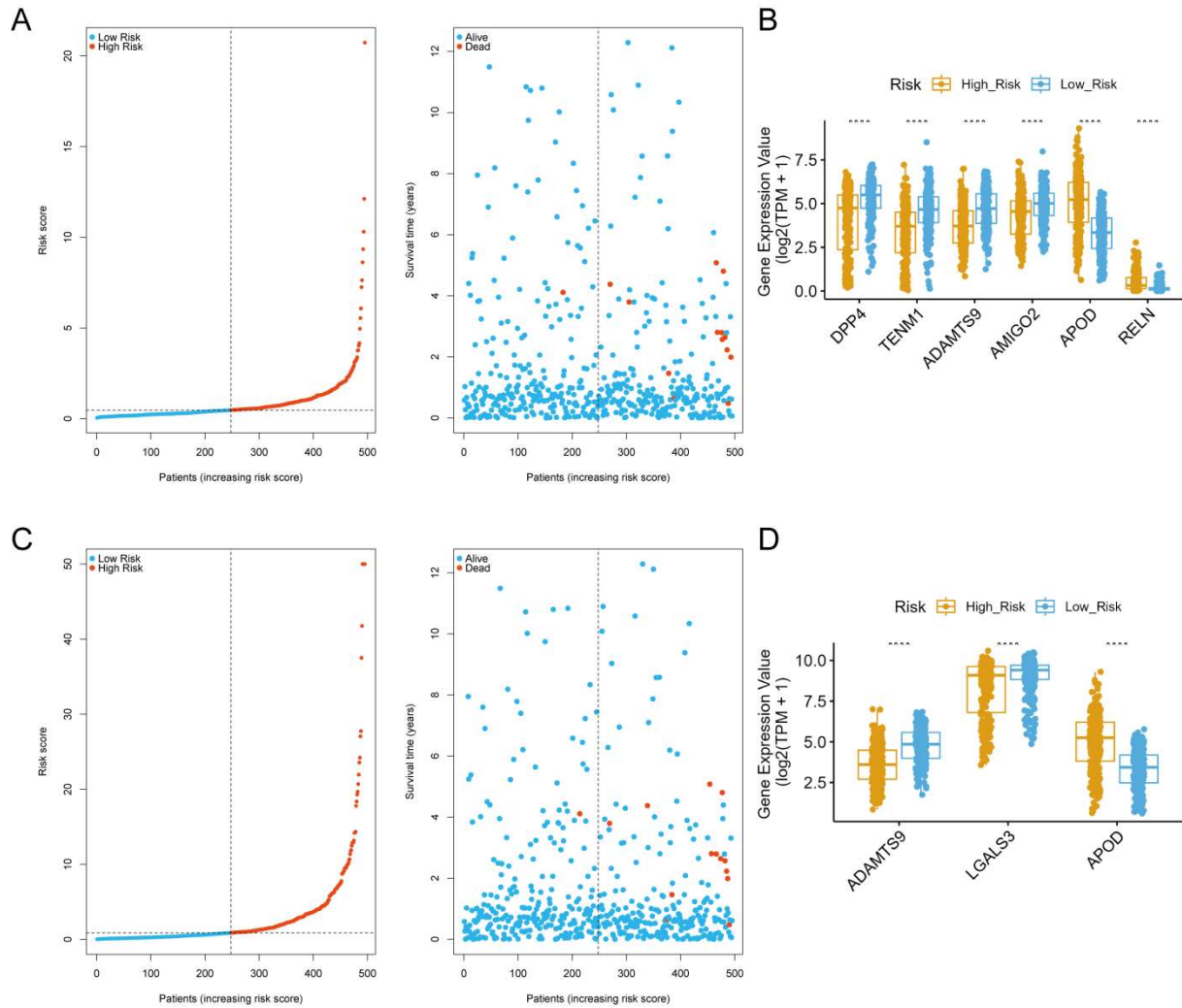


Figure S2. A Distribution of survival status, survival time and risk score in LPSRSM. B Differential expression of the six prognostic ARDGs in LPSRSM in high-risk and low-risk groups. C Distribution of survival status, survival time and risk score in MPSRSM. D Differential expression of four prognostic ARDGs in MPSRSM in high-risk and low-risk groups. Statistical significance is shown as follows: $*P < 0.05$; $**P < 0.01$; $***P < 0.001$; $****P < 0.0001$.

2. Supplementary tables

Table S1. Adhesion-related genes from the MSigDB database.

ACE2	CHST10	GPC6	MUC1	RGMB
BPIFA1	CHST2	GPM6B	MUC16	RHOA
CD209	CHST4	GPNMB	MUC21	RHOB
CD81	CIB1	GPR4	MUC4	RHOD
CLEC4M	CITED2	GREM1	MXRA8	RHOH
GAS6	CLASP1	GRHL2	MYADM	RIC8A
HSP90AB1	CLASP2	GRID2	MYB	RIN2
HSPD1	CLCA2	GSK3B	MYBPC1	RIPK2
ICAM1	CLDN1	GTPBP4	MYBPC2	RIPOR2
INHBB	CLDN10	HABP2	MYBPC3	RNASE10
LRRC15	CLDN11	HAPLN1	MYBPH	RND1
LTF	CLDN12	HAPLN2	MYF5	RND3
NECTIN1	CLDN14	HAPLN3	MYH10	ROBO1
NECTIN2	CLDN15	HAPLN4	MYH9	ROBO2
SCARB1	CLDN16	HAS1	MYL12A	ROBO3
SFTPD	CLDN17	HAS2	MYL9	ROBO4
AATF	CLDN18	HAVCR2	MYO10	ROCK1
ABAT	CLDN19	HBB	MYO1G	ROCK2
ABCA12	CLDN2	HCK	MYOC	ROM1
ABI3BP	CLDN20	HEPACAM	MYOT	ROPN1B
ABL1	CLDN22	HES1	MYPN	RPS3
ABL2	CLDN23	HES5	NCAM1	RPSA
ACAN	CLDN24	HFE	NCAM2	RRAS
ACER2	CLDN25	HHLA2	NCAN	RREB1
ACHE	CLDN3	HLA-A	NCK1	RS1
ACKR3	CLDN34	HLA-DMA	NCK2	RSU1
ACTB	CLDN4	HLA-DMB	NCKAP1L	RUNX1
ACTG1	CLDN5	HLA-DOA	NDFIP1	RUNX3
ACTN1	CLDN6	HLA-DOB	NDNF	S100A10
ACTN2	CLDN7	HLA-DPA1	NECTIN3	S100A11
ACTN3	CLDN8	HLA-DPB1	NECTIN4	S100A8
ACTN4	CLDN9	HLA-DQA1	NEDD9	S100A9
ACVR1	CLEC4A	HLA-DQA2	NEGR1	S1PR1
ACVRL1	CLEC4G	HLA-DQB1	NEO1	SAA1
ADA	CLEC7A	HLA-DQB2	NEXMIF	SART1
ADAM10	CLECL1	HLA-DRA	NEXN	SASH3
ADAM12	CLIC1	HLA-DRB1	NF1	SCARF1
ADAM15	CLSTN1	HLA-DRB3	NF2	SCARF2
ADAM17	CLSTN2	HLA-DRB4	NFASC	SCGB1A1
ADAM18	CLSTN3	HLA-DRB5	NFAT5	SCN1B
ADAM19	CNN3	HLA-E	NFKBID	SCRIB
ADAM2	CNTN1	HLA-G	NFKBIZ	SDC4
ADAM22	CNTN2	HLX	NID1	SDK1
ADAM23	CNTN3	HMCN1	NID2	SDK2
ADAM32	CNTN4	HMGB1	NINJ1	SELE

ADAM5	CNTN5	HOXA7	NINJ2	SELENOK
ADAM8	CNTN6	HOXD3	NKAP	SELL
ADAM9	CNTNAP1	HPSE	NLGN1	SELP
ADAMDEC1	CNTNAP2	HRG	NLGN2	SELPLG
ADAMTS12	CNTNAP3	HSD17B12	NLGN3	SEMA3E
ADAMTS13	CNTNAP3B	HSPB1	NLGN4X	SEMA4D
ADAMTS18	CNTNAP4	HSPH1	NLGN4Y	SEMA5A
ADAMTS9	CNTNAP5	HYAL1	NLRP3	SEMA6A
ADD2	COL12A1	IBSP	NME2	SERPINB8
ADGRB1	COL13A1	ICAM2	NOD2	SERPINE1
ADGRE1	COL14A1	ICAM3	NODAL	SERPINE2
ADGRE2	COL15A1	ICAM4	NOTCH1	SERPINF2
ADGRE5	COL16A1	ICAM5	NOTCH4	SERPINI1
ADGRG1	COL17A1	ICOS	NPHP1	SERPINI2
ADGRL1	COL18A1	ICOSLG	NPHP4	SFRP1
ADGRL3	COL19A1	ID1	NPHS1	SFRP2
ADGRV1	COL1A1	IDO1	NPNT	SGCE
ADIPOQ	COL26A1	IFNA2	NPTN	SH2B3
ADORA2A	COL28A1	IFNB1	NPY	SHC1
ADTRP	COL3A1	IFNG	NR4A3	SHH
AFDN	COL4A3	IFNL1	NRARP	SIGLEC1
AGER	COL4A6	IFT74	NRCAM	SIGLEC10
AGGF1	COL5A1	IGDCC3	NRP1	SIGLEC11
AGR2	COL5A3	IGDCC4	NRP2	SIGLEC12
AIF1	COL6A1	IGF1	NRXN1	SIGLEC14
AJAP1	COL6A2	IGF2	NRXN2	SIGLEC16
AJUBA	COL6A3	IGFALS	NRXN3	SIGLEC5
AKIP1	COL6A5	IGFBP2	NT5E	SIGLEC6
AKNA	COL6A6	IGFBP7	NTM	SIGLEC7
AKT1	COL7A1	IGFN1	NTN1	SIGLEC8
ALCAM	COL8A1	IGSF11	NTN4	SIGLEC9
ALOX12	COL8A2	IGSF21	NTNG1	SIGLECL1
ALOX15	COMP	IGSF5	NTNG2	SIPA1
ALOX5	CORO1A	IGSF9	NUAK1	SIRPA
AMBN	CORO1C	IGSF9B	OBSCN	SIRPB1
AMBP	CORO2B	IHH	OBSL1	SIRPG
AMBRA1	CR1	IL10	OLFM4	SKAP1
AMELX	CRB1	IL12A	OLR1	SLAMF1
AMIGO1	CRB2	IL12B	OMD	SLAMF7
AMIGO2	CRK	IL12RB1	OMG	SLC39A8
AMIGO3	CRKL	IL15	ONECUT1	SLC7A1
AMTN	CRNN	IL18	ONECUT2	SLC7A11
ANGPT1	CRTAM	IL1A	OPCML	SLC9A1
ANGPT2	CSF1	IL1B	OTOA	SLITRK1
ANGPTL3	CSF3R	IL1RAP	P2RY12	SLITRK2
ANK3	CSK	IL1RAPL1	P4HB	SLITRK3
ANOS1	CSPG5	IL1RL2	PAG1	SLK
ANTXR1	CSRP1	IL1RN	PAK4	SLURP1
ANXA1	CSTA	IL2	PALLD	SMAD3

ANXA2	CTLA4	IL20RB	PARD3	SMAD6
ANXA9	CTNNA1	IL21	PARD3B	SMAD7
AOC3	CTNNA2	IL23A	PARVA	SNAI2
AP1AR	CTNNA3	IL23R	PARVB	SNED1
AP3B1	CTNNAL1	IL27RA	PARVG	SOCS1
AP3D1	CTNNB1	IL2RA	PAWR	SOCS5
APBA1	CTNND1	IL32	PBXIP1	SOCS6
APBB1IP	CTNND2	IL36B	PCDH1	SORBS1
APC	CTSG	IL4	PCDH10	SORBS3
APLP1	CTTN	IL4I1	PCDH11X	SOX12
APOA1	CUZD1	IL4R	PCDH11Y	SOX13
APOA4	CX3CL1	IL6	PCDH12	SOX2
APOD	CX3CR1	IL6ST	PCDH15	SOX4
APP	CXADR	IL7	PCDH17	SOX9
AQP4	CXCL12	IL7R	PCDH18	SPACA4
ARF6	CXCL13	ILDR2	PCDH19	SPAM1
ARG1	CXCL8	ILK	PCDH20	SPARCL1
ARG2	CXCR3	INPPL1	PCDH7	SPECC1L
ARHGAP5	CXCR4	IRAK1	PCDH8	SPI1
ARHGAP6	CYFIP2	IRF1	PCDH9	SPINK5
ARHGDIA	CYP1B1	ISLR	PCDHA1	SPINT2
ARHGDIB	CYRIB	ITCH	PCDHA10	SPN
ARHGDIG	CYTH1	ITGA1	PCDHA11	SPOCK1
ARHGEF7	CYTH3	ITGA10	PCDHA12	SPOCK2
ARL2	CYTIP	ITGA11	PCDHA13	SPON1
ARPC2	DAB1	ITGA2	PCDHA2	SPON2
ARVCF	DAB2	ITGA2B	PCDHA3	SPP1
ASS1	DACT2	ITGA3	PCDHA4	SPRY4
ASTL	DAG1	ITGA4	PCDHA5	SPTA1
ASTN1	DAPK3	ITGA5	PCDHA6	SRC
ASTN2	DCC	ITGA6	PCDHA7	SRCIN1
ATM	DCHS1	ITGA7	PCDHA8	SRF
ATP1B1	DCHS2	ITGA8	PCDHA9	SRGAP2
ATP1B2	DDR1	ITGA9	PCDHAC1	SRPX
ATP2A2	DDR2	ITGAD	PCDHAC2	SRPX2
ATP2C1	DEFB118	ITGAE	PCDHB1	SSPN
ATP4B	DENND6A	ITGAL	PCDHB10	SSPOP
ATP5F1B	DGCR2	ITGAM	PCDHB11	SSX2IP
ATRNL1	DGCR6	ITGAV	PCDHB12	ST3GAL4
ATRN	DHPS	ITGAX	PCDHB13	ST6GAL1
ATXN3	DISC1	ITGB1	PCDHB14	STAB1
AXL	DLC1	ITGB1BP1	PCDHB15	STAB2
AZGP1	DLG1	ITGB2	PCDHB16	STAT5B
AZU1	DLG2	ITGB3	PCDHB18P	STK10
B2M	DLG3	ITGB3BP	PCDHB2	STK4
B4GALNT2	DLG4	ITGB4	PCDHB3	STRC
B4GALT1	DLG5	ITGB5	PCDHB4	STRCP1
BAD	DLL1	ITGB6	PCDHB5	STX3
BAG4	DMP1	ITGB7	PCDHB6	STX4

BAIAP2	DMTN	ITGB8	PCDHB7	STXBP1
BAIAP2L1	DNAJA3	ITGBL1	PCDHB8	STXBP3
BCAM	DNAJB6	ITPKB	PCDHB9	STXBP6
BCAN	DNM2	IZUMO1	PCDHGA1	SUSD5
BCAR1	DOCK1	IZUMO1R	PCDHGA10	SVEP1
BCAS3	DOCK5	JAG1	PCDHGA11	SWAP70
BCL10	DOCK8	JAG2	PCDHGA12	SYK
BCL2	DPP4	JAK1	PCDHGA2	SYMPK
BCL2L11	DPT	JAK2	PCDHGA3	SYNJ2BP
BCL6	DSC1	JAK3	PCDHGA4	TACSTD2
BCR	DSC2	JAM2	PCDHGA5	TAOK2
BGLAP	DSC3	JAM3	PCDHGA6	TARM1
BLK	DSCAM	JAML	PCDHGA7	TBCD
BLOC1S4	DSCAML1	JCAD	PCDHGA8	TBX21
BMP10	DSG1	JUP	PCDHGA9	TECTA
BMP2	DSG2	KANK1	PCDHGB1	TEK
BMP4	DSG3	KDR	PCDHGB2	TENM1
BMP5	DSG4	KIF14	PCDHGB3	TENM2
BMP6	DSP	KIF26B	PCDHGB4	TENM3
BMP7	DST	KIFAP3	PCDHGB5	TENM4
BMX	DUSP1	KIFC3	PCDHGB6	TESC
BOC	DUSP10	KIRREL1	PCDHGB7	TESK1
BSG	DUSP22	KIRREL2	PCDHGC3	TESK2
BST1	DUSP26	KIRREL3	PCDHGC4	TESPA1
BTN2A2	DUSP3	KIT	PCDHGC5	TFE3
BVES	EBI3	KITLG	PCK1	TFRC
C1QBP	ECM2	KLF4	PDCD1LG2	TGFB1
C1QTNF1	EDA	KLRC4-KLRK1	PDE3B	TGFB1I1
C2CD4A	EDIL3	KLRK1	PDE5A	TGFB2
C2CD4B	EFEMP2	KNG1	PDGFB	TGFB1
CADM1	EFNA1	KRT18	PDGFRA	TGFBR2
CADM2	EFNA5	L1CAM	PDLIM1	TGM2
CADM3	EFNB1	LAG3	PDLIM5	THBS1
CADM4	EFNB2	LAMA1	PDPN	THBS2
CALR	EFNB3	LAMA2	PDZD2	THBS3
CAMSAP3	EFS	LAMA3	PEAK1	THBS4
CARD11	EGFL6	LAMA4	PEAR1	THEMIS2
CARMIL1	EGFL7	LAMA5	PECAM1	THSD1
CASK	EGFLAM	LAMB1	PELI1	THY1
CASP3	EGFR	LAMB2	PERP	TIAM1
CASS4	EGR3	LAMB3	PGM5	TIGIT
CAV1	ELANE	LAMB4	PHLDB2	TIMM10B
CBFB	ELMO2	LAMC1	PIEZO1	TINAG
CBLB	EMB	LAMC2	PIK3CA	TJP1
CBLL1	EMILIN1	LAMC3	PIK3CB	TJP2
CBLL2	EMILIN2	LAPTM5	PIK3CG	TJP3
CBLN1	EMP2	LAX1	PIK3R1	TLN1
CCDC80	ENG	LCK	PIK3R6	TLN2
CCDC88B	ENSG00000278817	LDB1	PIP5K1A	TM9SF4

CCL11	ENTPD1	LEF1	PIP5K1C	TMEFF2
CCL19	EPB41L4B	LEP	PKD1	TMEM102
CCL2	EPB41L5	LGALS1	PKD1L1	TMEM131L
CCL21	EPCAM	LGALS2	PKHD1	TMEM47
CCL25	EPDR1	LGALS3	PKN2	TMEM8B
CCL28	EPHA1	LGALS3BP	PKP1	TMIGD2
CCL4	EPHA2	LGALS4	PKP2	TMOD3
CCL5	EPHA3	LGALS7B	PKP3	TNC
CCN1	EPHA4	LGALS9	PKP4	TNF
CCN2	EPHA7	LGALS9B	PLA2G2D	TNFAIP6
CCN3	EPHA8	LGALS9C	PLA2G2F	TNFAIP8L2
CCN4	EPHB1	LIF	PLAU	TNFRSF12A
CCN5	EPHB2	LILRB1	PLAUR	TNFRSF13C
CCN6	EPHB3	LILRB2	PLEK	TNFRSF14
CCR1	EPHB4	LILRB4	PLEKHA2	TNFRSF18
CCR2	EPO	LIMCH1	PLEKHA7	TNFRSF21
CCR3	ERBB2	LIMS1	PLET1	TNFSF11
CCR7	ERBB3	LIMS2	PLG	TNFSF13B
CCR8	ERBIN	LMLN	PLPP3	TNFSF14
CD151	ESAM	LMLN2	PLXNA1	TNFSF18
CD160	ETS1	LMO7	PLXNA2	TNFSF4
CD164	EXT1	LOXL2	PLXNA3	TNFSF9
CD177	EZR	LOXL3	PLXNA4	TNIP1
CD1D	F11R	LPP	PLXNB1	TNN
CD2	FADD	LPXN	PLXNB2	TNR
CD200	FAF1	LRFN3	PLXNB3	TNXB
CD200R1	FAM107A	LRFN4	PLXNC1	TOR1A
CD22	FAP	LRFN5	PLXND1	TPBG
CD226	FARP2	LRP6	PML	TPM1
CD24	FAT1	LRRC32	PNN	TRAF6
CD27	FAT2	LRRC4	PNP	TRIM29
CD274	FAT3	LRRC4B	PODXL	TRIOBP
CD276	FAT4	LRRC4C	PODXL2	TRIP6
CD28	FBLIM1	LRRC7	POLDIP2	TRO
CD2AP	FBLN1	LRRN2	POSTN	TROAP
CD300A	FBLN2	LSAMP	PPARA	TRPM7
CD33	FBLN5	LY6D	PPARD	TRPV4
CD34	FBLN7	LY9	PPFIA1	TSC1
CD36	FBN1	LYN	PPFIA2	TSPAN32
CD3E	FCGR2B	LYPD3	PPFIBP1	TTYH1
CD4	FCHO1	LYVE1	PPIA	TWSG1
CD40LG	FER	MACF1	PPM1F	TYK2
CD44	FERMT1	MAD1L1	PPP1CA	TYRO3
CD46	FERMT2	MAD2L2	PPP1CB	UBASH3B
CD47	FERMT3	MADCAM1	PPP1R12A	UMOD
CD5	FES	MAEA	PPP2CA	UNC13D
CD55	FEZ1	MAG	PPP2R1A	UNC5D
CD58	FGA	MAGI1	PPP3CA	USH2A
CD6	FGB	MALT1	PRDX2	UTRN

CD63	FGFRL1	MAP2K5	PREX1	VAMP3
CD70	FGG	MAP3K8	PRKAR1A	VAV1
CD72	FGL1	MAP4K4	PRKCA	VAV3
CD74	FGL2	MAPK14	PRKCD	VCAM1
CD80	FIBCD1	MAPK7	PRKCE	VCAN
CD83	FIBP	MARCHF7	PRKCC	VCL
CD84	FLCN	MBP	PRKCCZ	VEGFA
CD86	FLG2	MCAM	PRKD2	VEZT
CD9	FLNA	MDGA1	PRKG1	VIT
CD93	FLOT1	MDK	PRKX	VMP1
CD96	FLOT2	MEGF10	PRLR	VNN1
CD99	FLRT1	MEGF11	PRNP	VSIG10
CD99L2	FLRT2	MEGF9	PRPH2	VSIG10L2
CDC42	FLRT3	MELTF	PRSS2	VSIG4
CDC42EP1	FMN1	MEN1	PSEN1	VSIR
CDH1	FN1	MERTK	PSTPIP1	VSTM2L
CDH10	FNDC3A	METAP1	PTAFR	VTCN1
CDH11	FOLR1	METTL3	PTEN	VTN
CDH12	FOLR2	MFAP4	PTK2	VWA2
CDH13	FOLR3	MFGE8	PTK2B	VWC2
CDH15	FOXA1	MIA3	PTK7	VWF
CDH16	FOXA2	MICALL2	PTPN11	WASHC2C
CDH17	FOXC2	MILR1	PTPN2	WDPCP
CDH18	FOXF1	MINK1	PTPN22	WHAMM
CDH19	FOXJ1	MIP	PTPN23	WNK1
CDH2	FOXO3	MIR10A	PTPN6	WNT1
CDH20	FOXP3	MIR125A	PTPRA	WNT3A
CDH22	FPR2	MIR128-1	PTPRC	WNT4
CDH23	FREM1	MIR138-1	PTPRD	WNT5A
CDH24	FREM2	MIR141	PTPRF	WNT7B
CDH26	FREM3	MIR146A	PTPRG	XBP1
CDH3	FRMD5	MIR181C	PTPRJ	XCL1
CDH4	FSTL3	MIR183	PTPRK	XG
CDH5	FUT1	MIR192	PTPRM	YES1
CDH6	FUT2	MIR21	PTPRO	YTHDF2
CDH7	FUT3	MIR221	PTPRR	ZAN
CDH8	FUT4	MIR222	PTPRS	ZAP70
CDH9	FUT7	MIR27A	PTPRT	ZBTB1
CDHR1	FUT9	MIR27B	PTPRU	ZBTB16
CDHR2	FXYD5	MIR29C	PVR	ZBTB7B
CDHR3	FYB2	MIR30B	PXN	ZC3H12A
CDHR4	FYN	MIR31	PYCARD	ZC3H8
CDHR5	FZD4	MIR503	RAB10	ZDHHC2
CDK5	FZD7	MIR519D	RAB1A	ZDHHC21
CDK5R1	GATA1	MIR675	RAC1	ZFH3
CDK6	GATA3	MIR9-1	RAC2	ZFP36L1
CDKN2A	GATA5	MIR92A1	RAC3	ZMIZ1
CDON	GBP1	MIR939	RADIL	ZNF703
CDSN	GCNT1	MIRLET7E	RAG1	ZP3

CEACAM1	GCNT2	MIRLET7G	RAG2	ZP4
CEACAM5	GFUS	MKLN1	RAP2B	ZYX
CEACAM6	GLDN	MMP12	RARA	COLEC12
CEACAM8	GLI2	MMP14	RASA1	MIR101-1
CEBPB	GLI3	MMP2	RASAL3	MIR1298
CEL	GLMN	MMP24	RASGRP1	MIR144
CELA2A	GNAS	MMRN1	RC3H1	MIR206
CELSR1	GNE	MOG	RC3H2	MIR20A
CELSR2	GOLPH3	MPL	RCC2	MIR374A
CELSR3	GP1BA	MPZ	RDX	MIR506
CERCAM	GP1BB	MPZL2	REG3A	MIR520C
CFDP1	GP5	MPZL3	RELA	MYOCD
CGREF1	GP6	MSLN	RELL2	IQSEC1
CHL1	GP9	MSLNL	RELN	
CHRD	GPAM	MSN	RET	
MAPRE2	GPC4	MTSS1	RGCC	

Table S2. DEGs obtained based on RRA algorithm (Score < 0.05).

	TCGA	GSE29265	GSE33630	GSE60542	Score
ZCCHC12	5.87	4.873	5.576	4.197	0
PRR15	5.018	3.731	4.82	4.634	0
LRP4	3.772	4.011	4.429	3.831	0
HMGA2	2.897	4.937	5.376	4.539	0
SERPINA1	3.687	3.352	3.566	4.13	0
GABRB2	3.488	5.121	4.416	5.563	0
CHI3L1	3.462	3.152	4.661	4.115	0
DPP4	3.441	3.662	3.53	3.464	0
SCEL	3.334	3.706	3.899	3.785	0
METTL7B	3.862	2.785	3.239	3.078	0
ARHGAP36	4.424	4.424	4.322	2.879	0
SLC34A2	4.084	2.793	3.034	4.111	0
TACSTD2	3.259	2.744	3.509	4.091	0
LRRK2	3.254	3.801	4.26	3.591	0
CLDN1	3.238	3.776	4.17	3.748	0
PDZK1IP1	3.271	2.529	3.562	2.741	0
SYTL5	3.136	3.676	4.218	3.957	0
LAMB3	3.535	2.783	2.909	2.678	0
TENM1	3.094	4.059	4.614	3.77	0
LPAR5	3.003	2.925	3.16	2.652	0
FN1	4.369	2.426	2.853	3.143	0
QPCT	2.983	3.301	3.019	3.212	0
AGR2	3.036	3.181	2.983	2.523	0
CDH3	3.517	2.893	2.772	2.585	0
TUSC3	2.728	2.96	2.925	2.926	0
CAMK2N1	2.768	2.395	2.652	2.872	0
IGSF1	3.458	3.592	3.075	2.341	0
CLDN10	2.699	3.001	3.018	3.241	0
KCNJ2	2.651	3.093	3.822	3.462	0
SFTPB	3.202	2.181	3.011	3.396	0
KLHDC8A	4.1	2.16	2.582	2.503	0
SLC27A6	2.583	2.784	3.314	3.193	0
CITED1	2.307	3.482	4.032	3.251	0
GDF15	3.794	2.749	2.487	2.943	0
DCSTAMP	4.444	2.931	2.429	4.062	0
RXRG	4.707	2.077	3.73	3.211	0
PLAU	2.587	2	3.54	2.333	0
TIAM1	2.349	2.135	2.502	2.253	0
GALE	2.728	2.162	2.217	2.155	0
ABCC3	2.294	2.483	2.378	2.509	0
STK32A	2.541	2.543	2.402	2.018	0
CYP1B1	2.288	2.127	3.014	3.658	0
COMP	2.813	1.927	2.482	2.011	0
DTX4	2.581	1.967	2.12	2.318	0.001
TGFA	2.245	2.654	2.564	2.585	0.001

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	TCGA	GSE29265	GSE33630	GSE60542	Score
PROS1	2.897	1.905	2.632	2.816	0.001
TESC	2.561	2.202	2.721	1.99	0.001
TMEM163	2.231	2.129	2.946	2.306	0.001
LIPH	4.535	3.37	2.095	2.053	0.001
KLK10	3.573	1.872	2.284	3.518	0.001
CLDN16	4.222	2.097	2.08	2.272	0.001
ALOX5	2.21	2.328	2.941	2.693	0.001
DUSP4	2.178	2.683	2.183	2.197	0.001
NGEF	3.519	1.822	2.274	2.559	0.001
PDLIM4	2.774	1.797	2.069	2.798	0.001
TIMP1	2.451	1.785	2.178	2.283	0.001
MET	2.158	2.072	2.144	2.371	0.001
PCSK2	2.941	3.04	3.611	1.9	0.001
ITGA2	2.245	2.468	1.996	2.498	0.001
AHNAK2	2.132	2.001	2.252	2.303	0.001
MPZL2	2.128	2.193	2.302	2.197	0.001
GOLT1A	3.289	2.257	1.966	2	0.001
PDZRN4	1.286	2.487	3.1	2.72	0.001
FRMD3	2.107	2.298	2.783	2.291	0.001
ECM1	2.637	1.971	3.729	1.827	0.001
NMU	2.988	2.608	1.498	2.728	0.001
NRCAM	2.071	2.422	2.393	2.375	0.001
FAM20A	2.067	1.904	2.887	2.548	0.001
ADAMTS9	2.062	2.39	2.784	2.01	0.002
SLPI	2.058	1.75	2.09	1.919	0.002
THRSP	2.941	2.568	3.515	1.027	0.002
EVA1A	2.029	1.859	1.908	1.858	0.002
SLIT1	3.338	2.377	3.114	1.72	0.002
TNFRSF12A	2.172	1.577	1.915	2.363	0.002
LEMD1	2.165	1.986	1.887	2.199	0.002
TCRDV2	NA	2.355	2.823	2.752	0.002
AMIGO2	1.997	1.905	2.623	2.401	0.002
SDC4	1.989	1.741	2.273	2.297	0.002
DUSP6	2.177	1.528	2.055	1.738	0.003
PRSS2	2.915	0.986	2.959	2.418	0.003
TRDV3	NA	2.305	3.026	3.047	0.003
PDE5A	1.968	2.06	2.338	2.282	0.003
ALOX15B	2.409	1.498	1.94	2.122	0.003
GALNT7	1.963	2.141	1.935	2.047	0.003
ENTPD1	2.296	1.932	2.329	1.662	0.003
C4orf48	2.115	1.992	1.815	1.701	0.003
CEACAM6	2.107	1.582	1.939	1.652	0.004
UBE2QL1	1.944	1.943	1.883	2.02	0.004
RUNX2	1.489	2.209	2.867	2.492	0.004
NFE2L3	1.973	1.428	2.636	2.566	0.004
GABBR2	1.933	1.94	2.546	2.432	0.004
HEY2	1.929	1.595	2.644	2.159	0.004

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	TCGA	GSE29265	GSE33630	GSE60542	Score
LGALS3	2.075	1.4	1.733	1.736	0.005
MAMLD1	1.948	1.392	1.831	1.705	0.005
SCG5	1.905	2.343	2.539	2.054	0.005
APOE	1.934	1.359	2.598	2.375	0.005
PRSS23	1.881	1.533	2.195	1.876	0.006
CTSH	2.102	1.381	1.696	2.061	0.006
KCNN4	2.8	1.352	1.917	2.034	0.006
CST6	2.225	2.224	1.694	2	0.006
PLXNC1	1.874	2.158	2.286	2.737	0.006
FAXC	1.742	2.244	2.543	2.465	0.006
NELL2	1.671	2.129	2.606	2.574	0.006
HS6ST2	1.47	3.338	3.643	2.204	0.007
RYR1	1.971	1.333	2.849	2.519	0.007
ULBP2	2.024	1.918	1.713	1.534	0.007
GLT1D1	2.268	1.668	1.979	1.511	0.007
CHST2	1.842	1.364	1.803	1.965	0.007
MDK	2.143	1.324	1.753	1.923	0.007
CDH6	2.262	2.09	3.133	1.507	0.008
LAMP5	2.04	2.006	1.646	1.779	0.008
SYTL1	1.821	1.617	2.046	1.818	0.008
KCNQ3	2.413	1.822	1.63	1.61	0.008
CDH2	2.29	2.325	2.654	1.483	0.009
CBLN1	2.123	1.304	1.886	1.539	0.009
DIRAS3	1.81	2.287	1.613	1.8	0.009
KRT19	1.796	1.984	2.169	2.722	0.009
MRC2	2.582	1.297	2.003	1.653	0.009
TMPRSS4	3.126	1.599	1.606	2.017	0.01
SFN	2.799	1.848	1.863	1.47	0.01
SPOCK1	1.781	1.292	1.987	1.775	0.01
MIR31HG	NA	2.088	2.566	2.135	0.01
EPS8	1.774	1.623	1.891	1.605	0.011
BID	1.772	1.565	1.671	1.701	0.011
PSD3	1.727	2.118	2.282	2.161	0.011
ALDH1A3	1.756	2.857	2.688	1.859	0.012
DUSP5	1.99	1.615	1.568	2.129	0.012
IL1RAP	1.739	1.96	1.818	1.643	0.013
ETV5	1.715	1.715	1.795	1.547	0.014
AX748273	NA	2.024	2.187	2.193	0.014
NOD1	1.96	1.233	1.688	1.982	0.014
C19orf33	NA	1.945	2.278	2.337	0.015
MMP7	1.816	1.75	1.5	1.515	0.015
NPC2	2.208	1.306	1.628	1.398	0.016
CFI	1.685	1.602	2.022	1.86	0.017
LCN2	3.283	1.296	1.483	2.145	0.017
PHLDA2	1.736	1.942	1.846	1.388	0.017
FOXQ1	1.68	2.197	1.782	2.026	0.017
TMC6	2.226	1.194	1.921	1.79	0.019

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	TCGA	GSE29265	GSE33630	GSE60542	Score
LONRF2	1.667	2.094	1.542	2.079	0.019
ZMAT3	1.655	1.687	1.911	1.431	0.02
APOC1	1.651	1.28	2.68	2.296	0.021
LPL	1.984	1.445	2.754	1.348	0.021
EDIL3	1.643	1.24	1.974	1.35	0.022
TREM1	1.639	1.344	1.886	1.541	0.022
CTSC	1.625	1.329	1.786	1.652	0.025
SPOCK2	1.873	1.14	1.873	1.449	0.026
CORO2A	1.601	1.569	1.634	1.848	0.028
FAM230B	NA	2.412	1.979	1.979	0.029
SHROOM4	2.356	1.108	2.077	1.456	0.031
TMEM100	1.571	1.681	2.325	2.121	0.031
SPP1	1.153	1.685	2.347	1.969	0.031
ICAM1	1.823	1.101	1.667	1.391	0.033
ADM	1.881	1.092	1.89	1.751	0.035
TNFRSF21	1.559	1.201	1.404	1.271	0.035
MXRA8	1.722	1.088	1.429	1.877	0.037
NAB2	1.66	1.14	1.361	1.559	0.037
LOC100506403	NA	1.649	2.135	1.808	0.037
PRDM1	1.545	1.752	1.933	1.49	0.038
PHEX	1.087	2.374	2.419	1.785	0.04
UPP1	1.828	1.072	1.572	1.576	0.04
PLAG1	1.539	2.119	1.477	1.845	0.04
EMILIN2	1.523	1.329	1.927	1.474	0.043
LOC100507165	NA	2.018	2.004	1.763	0.044
GGCT	1.906	1.215	1.325	1.761	0.045
TRPC5	2.156	2.372	1.258	1.751	0.045
MMP16	1.509	1.498	1.852	1.921	0.046
CDKN2B	2.025	0.064	2.275	1.798	0.047
CD109	1.496	1.128	1.665	1.496	0.048
TFF3	-6.008	-3.96	-4.108	-4.423	0
PKHD1L1	-3.832	-3.146	-3.637	-4.321	0
TPO	-4.375	-3.493	-3.187	-4.788	0
IPCEF1	-3.509	-3.183	-3.162	-3.834	0
DPP6	-3.245	-3.582	-3.055	-3.539	0
PLA2R1	-3.168	-2.966	-3.056	-3.505	0
DIO1	-3.895	-2.631	-3.201	-4.82	0
TFCP2L1	-3.477	-2.683	-2.807	-3.296	0
IGFBPL1	-3.254	-2.632	-2.774	-2.879	0
SLC4A4	-2.942	-2.892	-3.015	-3.606	0
DPT	-3.913	-3.113	-3.028	-2.755	0
AOX1	-2.894	-2.89	-2.909	-2.788	0
MMRN1	-3.082	-3.141	-4.249	-2.721	0
TCEAL2	-2.845	-2.935	-2.816	-2.982	0
KIT	-2.991	-2.334	-2.854	-3.056	0
ADH1B	-2.459	-3.071	-3.49	-3.807	0
CHRDL1	-3.679	-3.154	-2.502	-2.776	0

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	TCGA	GSE29265	GSE33630	GSE60542	Score
MPPED2	-2.779	-3.051	-2.93	-3.949	0
CWH43	-3.06	-2.781	-2.642	-2.572	0
RGS8	-2.743	-2.474	-2.842	-2.591	0
BEX1	-2.738	-2.254	-3.187	-2.555	0
DGKI	-2.695	-2.448	-2.885	-3.369	0
HGD	-2.871	-2.77	-2.393	-2.823	0
CDH16	-4.461	-2.215	-2.93	-2.461	0
PAPSS2	-2.637	-2.573	-2.396	-2.709	0
CRABP1	-3.587	-1.83	-3.465	-3.369	0
GPM6A	-2.37	-3.05	-3.199	-3.269	0
ZMAT4	-3.114	-2.795	-2.347	-2.437	0
SMOC2	-2.844	-2.146	-2.518	-2.606	0
OGN	-2.567	-2.734	-2.423	-2.459	0
CCL21	-5.735	-2.076	-3.432	-2.403	0
LRP1B	-2.512	-2.735	-3.44	-3.525	0
MRO	-2.507	-2.636	-2.571	-2.438	0
FAM167A	-2.612	-2.051	-2.234	-2.7	0
WSCD2	-3.8	-2.16	-2.316	-2.248	0
WDR72	-2.433	-2.073	-2.572	-2.64	0
GLT8D2	-2.345	-2.204	-2.347	-2.396	0
SPX	-2.328	-2.584	-2.91	-3.667	0.001
NCAM1	-2.335	-2.534	-2.275	-2.775	0.001
FABP4	-2.712	-3.095	-2.005	-3.261	0.001
COL9A3	-2.317	-1.925	-2.662	-2.329	0.001
SERTM1	-2.287	-2.67	-2.754	-2.873	0.001
COL23A1	-2.849	-1.992	-1.991	-2.211	0.001
PPARGC1A	-2.317	-2.277	-2.564	-2.752	0.001
RYR2	-2.445	-1.854	-2.371	-2.202	0.001
LIFR	-2.278	-1.902	-2.057	-2.54	0.001
ELMO1	-2.254	-1.868	-2.035	-2.184	0.001
DGKI	NA	-2.566	-2.631	-3.073	0.001
AVPR1A	-2.194	-1.869	-2.019	-2.571	0.001
LYVE1	-2.805	-2.487	-3.338	-1.902	0.001
CSGALNACT1	-2.187	-1.815	-2.275	-2.233	0.001
DLG2	-2.219	-2.057	-1.927	-1.891	0.001
CFD	-2.41	-2.488	-2.137	-1.876	0.002
FBLN1	-2.51	-2.295	-2.087	-1.866	0.002
OGDHL	-2.162	-1.726	-2.237	-1.985	0.002
PID1	-2.074	-2.223	-1.958	-1.923	0.002
EPHB1	-2.001	-2.551	-2.693	-2.337	0.002
APOD	-2.925	-2.068	-1.742	-1.868	0.002
TNFRSF11B	-2.771	-1.713	-2.156	-2.497	0.002
ANK2	-1.994	-2.35	-2.302	-2.544	0.002
LOC100506558	NA	-2.301	-2.453	-2.766	0.002
MUM1L1	NA	-2.291	-2.8	-2.631	0.002
RASSF6	-1.99	-2.186	-2.469	-1.916	0.003
TDRD9	-1.98	-2.286	-2.524	-2.869	0.003

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	TCGA	GSE29265	GSE33630	GSE60542	Score
ABI3BP	-2.286	-2.03	-1.986	-1.816	0.003
RAP1GAP	-1.988	-1.861	-2.02	-2.041	0.003
LOC646736	NA	-2.267	-2.412	-3.069	0.003
RASSF9	-1.947	-1.916	-1.814	-2.144	0.003
OCA2	-2.669	-2.089	-2.227	-1.781	0.004
LINGO2	-1.943	-1.99	-1.886	-1.876	0.004
EFEMP1	-2.24	-1.821	-1.689	-1.968	0.004
CLCNKB	-2.377	-1.87	-2.123	-1.771	0.004
MT1M	-2.132	-1.637	-2.335	-2.907	0.004
DEPTOR	-2.125	-1.688	-1.663	-2.343	0.004
LMOD1	-2.578	-1.624	-1.762	-1.783	0.004
RNF150	-1.915	-2.237	-1.822	-1.787	0.004
FIBIN	-1.9	-2.204	-2.39	-1.942	0.005
OTOS	-2.452	-1.71	-1.646	-2.639	0.005
SMAD9	-1.861	-1.562	-1.816	-2.059	0.006
TMEM139	-1.851	-2.055	-2.249	-1.971	0.006
ANGPTL1	-2.205	-1.683	-1.599	-1.884	0.007
EDN3	-2.52	-1.48	-2.416	-2.539	0.007
SLC26A4	-3.141	-2.045	-1.585	-2.75	0.007
LAYN	-1.973	-1.579	-1.834	-1.659	0.008
SORBS2	-2.221	-1.482	-1.751	-2.028	0.008
C8orf88	-1.782	-1.628	-1.595	-2.285	0.008
SCARA5	-3.126	-2.133	-1.789	-1.641	0.009
ARHGAP24	-1.953	-1.764	-1.555	-2.016	0.009
IP6K3	-2.145	-1.457	-2.16	-2.323	0.01
RELN	-1.875	-2.411	-2.54	-1.629	0.01
HBB	-2.627	-1.695	-1.548	-1.797	0.01
ZFPM2	-1.743	-1.801	-1.833	-1.929	0.01
CCDC146	-1.739	-1.726	-1.931	-1.649	0.011
BMP8A	-3.814	-1.177	-2.15	-2.499	0.011
SLITRK5	-1.212	-2.216	-2.411	-2.236	0.011
PLCH1	-2.122	-1.895	-1.532	-1.813	0.011
SGCD	-1.696	-1.815	-1.941	-1.594	0.012
MT1F	-2.651	-1.415	-1.558	-2.498	0.013
PROM1	-1.733	-2.43	-2.668	-1.584	0.013
CITED2	-1.963	-1.714	-1.725	-1.576	0.013
CUX2	-1.94	-1.41	-2.234	-1.673	0.013
DIRAS2	-1.675	-1.766	-2.423	-1.832	0.014
MYOC	-3.202	-1.752	-1.556	-1.559	0.014
SLC25A15	-1.665	-1.508	-2.226	-1.863	0.014
LOC440934	NA	-1.911	-2.621	-2.173	0.015
GDF10	-2.614	-1.396	-1.798	-1.744	0.015
DCN	-2.87	-1.784	-1.712	-1.537	0.016
FMOD	-1.91	-1.426	-1.494	-1.575	0.017
OMD	-2.196	-1.723	-1.79	-1.531	0.017
PCOLCE2	-1.611	-2.268	-1.756	-1.754	0.018
AGR3	-2.413	-1.442	-2.501	-1.522	0.018

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	TCGA	GSE29265	GSE33630	GSE60542	Score
SYNDIG1	-1.937	-1.409	-1.493	-1.508	0.02
GPR83	-1.603	-1.643	-2.252	-1.517	0.02
SLC26A4-AS1	NA	-2.191	-1.995	-3.208	0.02
CPXM1	-2.506	-1.827	-1.634	-1.506	0.021
PDLIM3	-1.95	-1.734	-1.938	-1.502	0.021
AIF1L	-1.728	-1.353	-1.827	-1.618	0.021
CAPSL	-1.572	-1.661	-1.712	-1.71	0.022
CDON	-1.98	-1.515	-1.453	-1.817	0.022
FRAS1	-1.557	-1.749	-1.55	-1.595	0.023
GLDC	-1.544	-1.947	-1.536	-1.956	0.024
BMP2	-1.761	-1.53	-1.435	-1.5	0.025
TMEM171	-2.623	-2.366	-1.432	-1.517	0.026
BCL2	-1.744	-1.32	-1.716	-1.88	0.026
GPC3	-3.084	-2.19	-1.528	-1.468	0.027
GHR	-1.334	-1.815	-1.989	-2.188	0.027
PLA2G7	-1.615	-1.312	-1.652	-1.648	0.027
FCGBP	-1.823	-1.311	-1.543	-2.04	0.028
HKDC1	-1.518	-1.339	-1.717	-1.894	0.028
STXBP5L	-2.157	-0.843	-2.725	-3.142	0.029
FOSB	-2.918	-1.677	-1.41	-2.318	0.029
CA4	-2.219	-2.181	-1.298	-2.506	0.03
TPPP	-2.164	-1.915	-1.998	-1.435	0.032
MAMDC2	-1.494	-1.286	-1.501	-1.784	0.034
FAM3B	-1.48	-1.796	-1.552	-1.904	0.034
ENPP1	-1.613	-1.282	-1.526	-1.534	0.035
SLC26A7	-3.472	-1.271	-1.686	-2.582	0.037
CRYAB	-1.749	-1.293	-1.516	-1.397	0.037
PBX4	-2.243	-1.845	-1.357	-1.498	0.038
KY	-1.462	-1.412	-1.418	-1.773	0.039
PRTG	-1.459	-1.644	-1.492	-1.86	0.04
FOXP2	-1.457	-1.746	-2.336	-2.124	0.041
ATP2C2	-2.245	-1.366	-1.336	-1.807	0.042
GJB6	-1.457	-1.473	-2.443	-2.341	0.042
SCUBE3	-1.842	-1.256	-2.03	-2.008	0.043
ALDH1A1	-1.743	-1.254	-1.637	-1.796	0.043
GNA14	-1.746	-1.244	-1.839	-2.378	0.046
PRKX	-1.439	-1.385	-1.495	-1.492	0.05

Table S3. ARDGs in the TCGA cohort.

gene	logFC	AveExpr	t	P	adj.P	B
DPP4	3.441	4.244	15.058	0	0	87.377
TACSTD2	3.259	7.819	8.766	0	0	28.464
CLDN1	3.238	7.751	12.858	0	0	64.748
LAMB3	3.535	5.684	12.188	0	0	58.219
TENM1	3.094	3.64	14.929	0	0	86.006
FN1	4.369	9.448	12.023	0	0	56.643
AGR2	3.036	5.155	12.726	0	0	63.445
CDH3	3.517	5.204	17.343	0	0	112.395
CLDN10	2.699	2.646	9.61	0	0	35.179
PLAU	2.587	6.099	11.02	0	0	47.35
TIAM1	2.349	3.658	14.747	0	0	84.076
CYP1B1	2.288	4.557	8.664	0	0	27.683
COMP	2.813	3.935	9.209	0	0	31.931
TESC	2.561	6.414	12.248	0	0	58.797
CLDN16	4.222	5.189	14.242	0	0	78.783
ALOX5	2.21	4.795	7.602	0	0	19.983
ITGA2	2.245	4.368	12.208	0	0	58.408
MPZL2	2.128	7.188	16.287	0	0	100.681
NRCAM	2.071	4.444	16.733	0	0	105.599
ADAMTS9	2.062	3.97	12.67	0	0	62.897
TNFRSF12A	2.172	7.671	11.764	0	0	54.197
AMIGO2	1.997	4.417	13.253	0	0	68.673
SDC4	1.989	9.683	12.13	0	0	57.661
PRSS2	2.915	2.909	9.117	0	0	31.205
PDE5A	1.968	5.737	10.065	0	0	38.984
ENTPD1	2.296	4.874	19.173	0	0	133.18
CEACAM6	2.107	2.307	7.625	0	0	20.144
LGALS3	2.075	8.431	10.23	0	0	40.389
PLXNC1	1.874	4.006	10.913	0	0	46.382
CHST2	1.842	6.014	12.789	0	0	64.061
MDK	2.143	7.414	11.437	0	0	51.148
CDH6	2.262	3.18	14.549	0	0	81.997
CDH2	2.29	3.664	10.206	0	0	40.187
CBLN1	2.123	3.315	7.974	0	0	22.591
SPOCK1	1.781	3.945	8.508	0	0	26.501
IL1RAP	1.739	3.009	11.425	0	0	51.04
EDIL3	1.643	3.214	15.21	0	0	89
SPOCK2	1.873	6.328	7.472	0	0	19.097
SPP1	1.153	5.049	4.646	0	0	3.116
ICAM1	1.823	5.785	10.024	0	0	38.631
TNFRSF21	1.559	4.865	10.115	0	0	39.407
MXRA8	1.722	7.354	8.727	0	0	28.163
EMILIN2	1.523	4.503	11.662	0	0	53.244
DPT	-3.913	2.116	-18.988	0	0	131.052
MMRN1	-3.082	2.059	-21.884	0	0	164.631

Continued on next page

gene	logFC	AveExpr	t	P	adj.P	B
KIT	-2.991	3.671	-13.998	0	0	76.259
CDH16	-4.461	2.907	-16.569	0	0	103.784
CCL21	-5.735	4.322	-14.821	0	0	84.864
NCAM1	-2.335	3.028	-11.435	0	0	51.138
LYVE1	-2.805	2.165	-22.006	0	0	166.063
DLG2	-2.219	1.473	-18.234	0	0	122.447
FBLN1	-2.51	4.03	-11.742	0	0	53.99
EPHB1	-2.001	2.194	-15.36	0	0	90.612
APOD	-2.925	4.45	-13	0	0	66.154
ABI3BP	-2.286	3.183	-13.391	0	0	70.068
RELN	-1.875	0.552	-28.913	0	0	246.44
HBB	-2.627	5.876	-12.753	0	0	63.709
CITED2	-1.963	7.75	-14.255	0	0	78.922
MYOC	-3.202	1.212	-17.984	0	0	119.611
OMD	-2.196	1.876	-11.444	0	0	51.213
CDON	-1.98	2.658	-12.822	0	0	64.386
BMP2	-1.761	4.646	-12.894	0	0	65.096
BCL2	-1.744	4.224	-14.741	0	0	84.02
PRKX	-1.439	5.136	-13.902	0	0	75.267

Table S4. The univariate Cox regression analysis of ARDGs for OS in the TCGA tumor cohort.

gene	HR	HR.95L	HR.95H	<i>P</i>
DPP4	0.679686237	0.536122941	0.861692992	0.001424702
CLDN1	0.767363543	0.60822997	0.968131851	0.025542792
TENM1	0.67299445	0.497728976	0.909976214	0.010086446
CDH3	0.745592147	0.560566135	0.991689677	0.043663502
CLDN10	0.752114678	0.584456408	0.967867717	0.026844444
MPZL2	0.591360577	0.382979442	0.913122984	0.017788883
ADAMTS9	0.534460754	0.335353671	0.851782229	0.008423827
AMIGO2	0.625595321	0.40505346	0.966216917	0.034436586
ENTPD1	0.559406123	0.350713584	0.892281406	0.014752456
LGALS3	0.741530747	0.551635442	0.996795722	0.047565773
CHST2	0.68774816	0.479845111	0.985729607	0.041527392
NCAM1	1.391813893	1.009386281	1.919132397	0.043699647
FBLN1	1.420118098	1.040907246	1.937478504	0.026903139
APOD	1.798450211	1.305453997	2.477623238	0.000329854
RELN	3.868804513	1.800017914	8.315277446	0.000528987
OMD	1.536448479	1.153171081	2.047115097	0.003353083

Table S5. Correlation coefficients for co-expression of prognostic ARDGs in the TCGA tumor cohort.

	DPP4	CLDN1	TENM 1	CDH3	CLDN10	MPZL2	ADAMTS 9	AMIGO 2	ENTPD1	LGALS3	CHST2	NCAM 1	FBLN1	APOD	RELN	OMD
DPP4	1	0.807	0.388	0.681	0.599	0.774	0.341	0.616	0.363	0.799	0.587	-0.482	0.131	0.258	-0.06	0.194
CLDN1	0.807	1	0.485	0.728	0.593	0.769	0.424	0.669	0.466	0.76	0.566	-0.501	0.176	0.286	-0.05	0.219
TENM1	0.388	0.485	1	0.487	0.199	0.439	0.688	0.513	0.52	0.315	0.356	-0.435	-0.121	-0.004	-0.122	-0.067
CDH3	0.681	0.728	0.487	1	0.683	0.727	0.461	0.756	0.406	0.763	0.665	-0.649	0.177	0.345	-0.119	0.174
CLDN10	0.599	0.593	0.199	0.683	1	0.662	0.225	0.622	0.128	0.675	0.574	-0.515	0.332	0.441	-0.018	0.334
MPZL2	0.774	0.769	0.439	0.727	0.662	1	0.409	0.659	0.38	0.774	0.587	-0.525	0.125	0.269	-0.115	0.199
ADAMTS9	0.341	0.424	0.688	0.461	0.225	0.409	1	0.558	0.482	0.258	0.39	-0.481	-0.052	0.064	-0.027	-0.009
AMIGO2	0.616	0.669	0.513	0.756	0.622	0.659	0.558	1	0.415	0.631	0.693	-0.61	0.194	0.318	-0.054	0.209
ENTPD1	0.363	0.466	0.52	0.406	0.128	0.38	0.482	0.415	1	0.262	0.398	-0.377	-0.158	-0.035	-0.144	-0.124
LGALS3	0.799	0.76	0.315	0.763	0.675	0.774	0.258	0.631	0.262	1	0.617	-0.576	0.243	0.417	-0.096	0.26
CHST2	0.587	0.566	0.356	0.665	0.574	0.587	0.39	0.693	0.398	0.617	1	-0.579	0.096	0.259	-0.091	0.124
NCAM1	-0.482	-0.501	-0.435	-0.649	-0.515	-0.525	-0.481	-0.61	-0.377	-0.576	-0.579	1	0.005	-0.193	0.195	-0.007
FBLN1	0.131	0.176	-0.121	0.177	0.332	0.125	-0.052	0.194	-0.158	0.243	0.096	0.005	1	0.742	0.486	0.882
APOD	0.258	0.286	-0.004	0.345	0.441	0.269	0.064	0.318	-0.035	0.417	0.259	-0.193	0.742	1	0.458	0.716
RELN	-0.06	-0.05	-0.122	-0.119	-0.018	-0.115	-0.027	-0.054	-0.144	-0.096	-0.091	0.195	0.486	0.458	1	0.494
OMD	0.194	0.219	-0.067	0.174	0.334	0.199	-0.009	0.209	-0.124	0.26	0.124	-0.007	0.882	0.716	0.494	1

Table S6. The changes in hallmark pathway between high-risk and low-risk groups (*adj.P* < 0.05).

pathway	logFC	<i>adj.P</i>
HALLMARK_PROTEIN_SECRETION	-0.083108003	0.002034736
HALLMARK_ALLOGRAFT_REJECTION	0.034329353	0.020568439
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	0.041540717	0.025550503
HALLMARK_GLYCOLYSIS	0.04211261	0.001355689
HALLMARK_UV_RESPONSE_DN	0.04864657	0.025550503
HALLMARK_APICAL_JUNCTION	0.052028391	0.003629686
HALLMARK_APOPTOSIS	0.052487621	0.005741702
HALLMARK_PANCREAS_BETA_CELLS	0.05350985	0.00134948
HALLMARK_INTERFERON_GAMMA_RESPONSE	0.054038862	0.010673227
HALLMARK_UV_RESPONSE_UP	0.054134733	2.80×10^{-7}
HALLMARK_ADIPOGENESIS	0.054164019	0.000693943
HALLMARK_IL6_JAK_STAT3_SIGNALING	0.054283135	0.038951488
HALLMARK_KRAS_SIGNALING_DN	0.054826736	1.74×10^{-8}
HALLMARK_XENOBIOTIC_METABOLISM	0.055017189	2.20×10^{-7}
HALLMARK_COAGULATION	0.055878011	0.000878813
HALLMARK_FATTY_ACID_METABOLISM	0.057590725	0.002187247
HALLMARK_CHOLESTEROL_HOMEOSTASIS	0.05891604	8.25×10^{-5}
HALLMARK_COMPLEMENT	0.059619231	0.002243366
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	0.060925363	9.60×10^{-5}
HALLMARK_IL2_STAT5_SIGNALING	0.063800693	0.003069629
HALLMARK_ESTROGEN_RESPONSE_EARLY	0.064675231	0.000120989
HALLMARK_MTORC1_SIGNALING	0.065827924	0.000771177
HALLMARK_ESTROGEN_RESPONSE_LATE	0.067864783	2.33×10^{-5}
HALLMARK_MYC_TARGETS_V2	0.082325198	0.001752676
HALLMARK_KRAS_SIGNALING_UP	0.084093022	0.000117849
HALLMARK_INFLAMMATORY_RESPONSE	0.090120767	0.001442109
HALLMARK_APICAL_SURFACE	0.094535486	7.27×10^{-8}
HALLMARK_MYOGENESIS	0.094958571	6.86×10^{-10}
HALLMARK_TNFA_SIGNALING_VIA_NFKB	0.099613225	0.000333822
HALLMARK_HYPOXIA	0.103356177	3.67×10^{-10}
HALLMARK_OXIDATIVE_PHOSPHORYLATION	0.10801343	0.000452316
HALLMARK_ANGIOGENESIS	0.160379145	2.08×10^{-8}
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	0.198197731	6.66×10^{-10}

Table S7. Clinicopathological features of high-risk and low-risk groups.

Characterisitcs	High-risk group	Low-risk group	X^2	P
Patients	247	248		
Gender			0.548	0.459
Male	69 (13.94%)	62 (12.53%)		
Female	178 (35.96%)	186 (37.58%)		
Age (years)			8.056	0.005
>= 46	146 (29.49%)	115 (23.23%)		
< 46	101 (20.40%)	133 (26.87%)		
N stage			0.385	0.535
N0	111 (24.94%)	115 (25.84%)		
N1	114 (25.62%)	105 (23.60%)		
T stage			1.489	0.222
T1 + 2	146 (29.61%)	161 (32.66%)		
T3 + 4	99 (20.08%)	87 (17.65%)		
M stage			1.145×10^{-30}	1
M0	148 (51.75%)	129 (45.10%)		
M1	5 (1.75%)	4 (1.40%)		
Total stage			5.224	0.022
I + II	153 (34.85%)	176 (40.09%)		
III + IV	65 (14.81%)	45 (10.25%)		



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