

154 Up-regulated

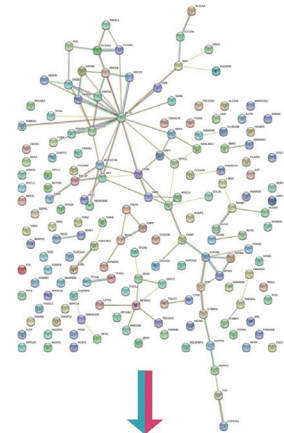
GAS6 NCCRP1 KCNIP5 FBLN1 DPP4 LSS MAP1LC5A
 TOM1 C6orf48 CIQTNF1 REC8 FAM53B TSC2D3 TSPO
 C15orf59 CTNS PQLC1 ILVBL LG3 FAM69C DPP7
 LIMS2 MFS012 NAGLU CYP1B1 NICN1 TPCN2 PALM
 CCL18 HS1BP3 AGPAT2 BMP1 CYB561A3 FOXO3
 VEGFB RTN2 CYB5R3 GRN OSBP15 IFI271 MARCKSL1
 SYNCR1 TBC1D16 POR KIAA0930 FOXO4 PIPRU
 TANGO2 SERP1 WFS1 TMEM120A STATA5A FAM234A
 HMG20B CRYL1 CYBA NAALADL1 BSG WDR81 CHPF
 CHKB KIAA0556 EPHX1 EFCAB1 PRKCB PLBD2 AKT1
 GSTM2 TOLLIP HERC2 QPRT UAP1L1 MICAL1 CTSD
 PLXNA1 DKK3 ANKRD9 OR7A5 OCA2 THNSL2 ERBB3
 SLC04A1-AS1 TMEMBA HTT GSN IFI272 ST5 MSC
 CFAPB1 TMEM184B MAL ACSF2 TNFSF12 CD79B
 TABBP COMT H2AF3 FCGRT UCHL1 NUDT11 CSRP9
 FXVD6 PRUNE2 SELENBP1 NINJ1 HSD17B14 ADCY9
 MCF2L PLXNB1 AHNAK TTYH2 PYCARD MGAT1
 CYP27A1 GAPDH5 HLA-G TFF3 APH1B CIQTNF5
 TUBB4A GPAT4 KLHDC8B TMEM140 BCAN SPSB1 GBA
 PLTP RETSAT FAM101B STXB2 SLC2A8 SYNC CDH3
 SLC1A4 IL17D ARMC9 CLEC11A MRPL44 FEZ1
 ADORA2 ITPKB PES NYNDIN LZTSL1 4400B SERPINF1
 SLC16A6 SLC7A8 PIK3CD CECR1 IRX5 TMEM204
 TTYH3 RASIP1

A

6 Down-regulated

ISM1 PLA2R1 SPATA18 LINC01279 DST FOXQ1

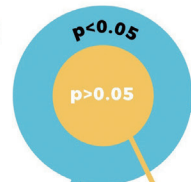
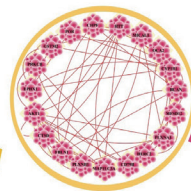
B1



B3



19 core genes



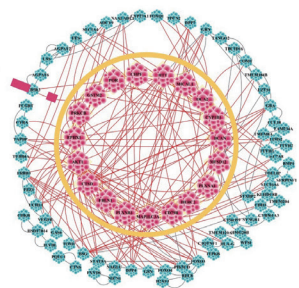
8 Genes with significantly worse survival

CYP1B1 POR BCAN PRKCB
 OCA2 MFS012 CD79B FBLN1

11 Genes without significantly worse survival

EPHX1 CTSD HTT AKT1 MICAL1 PLXNB1
 PLXNA1 HERC2 GSTM2 CHPF MAP1LC5A

B2



2 Genes without expressed in melanoma tissues (p > 0.05)

BACN FBLN1

6 Genes with high expressed in melanoma tissues (p < 0.05)

CYP1B1 POR PRKCB CD79B MFS012 OCA2

C

Two significant up-regulated DEGs with poor prognosis in SKCM

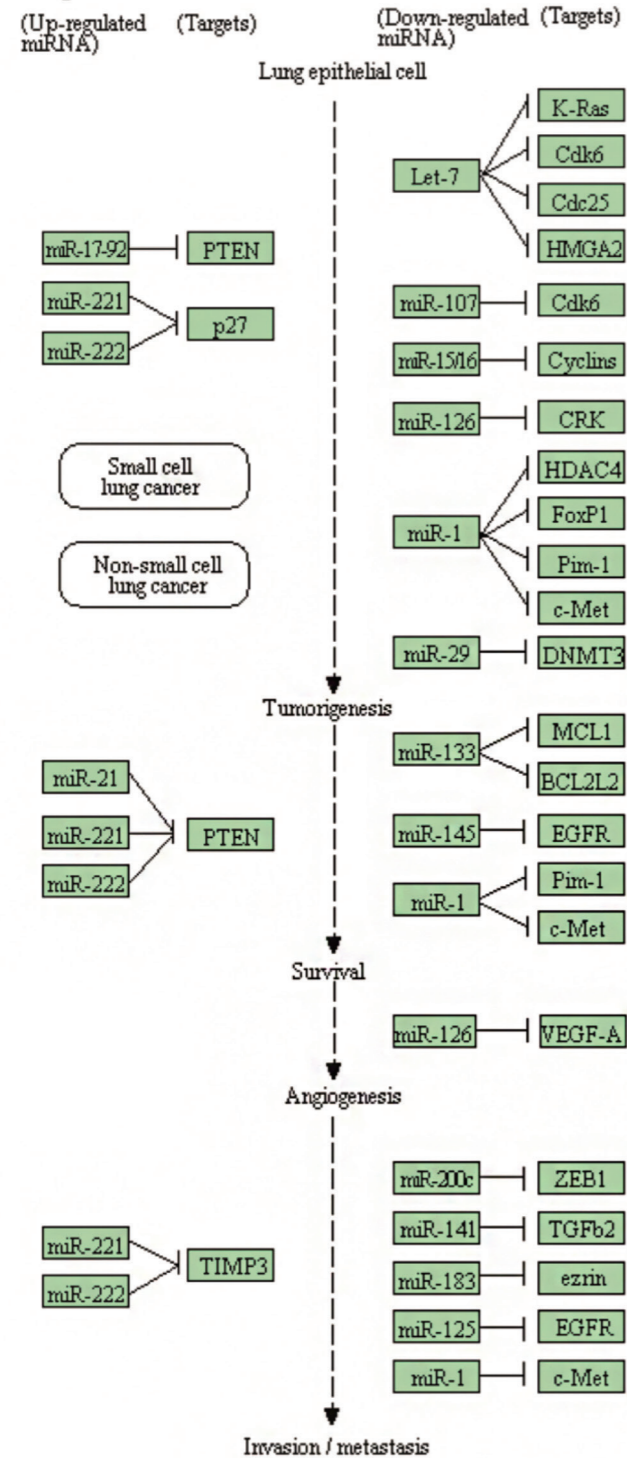
PRKCB CYP1B1

D

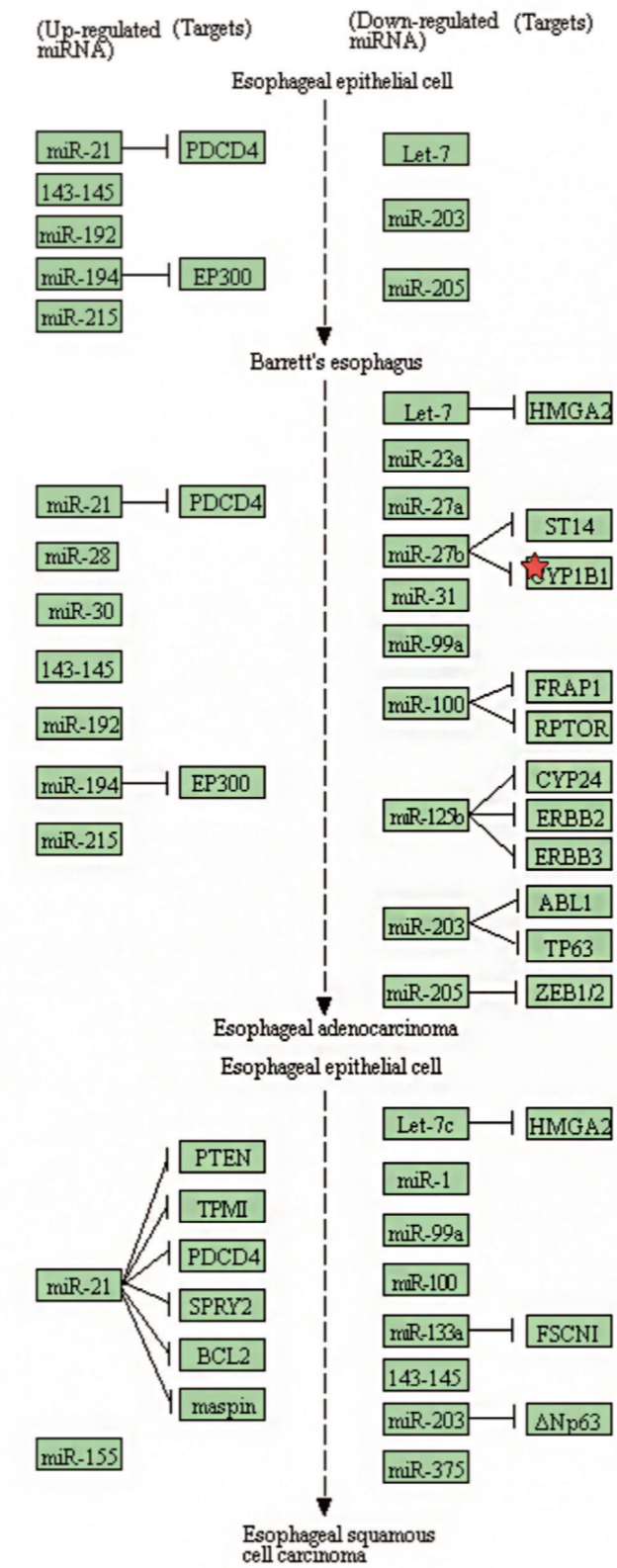
Figure S1 Data preprocessing. (A) All 160 common DEGs (154 upregulated genes and 6 downregulated genes). (B1) 89 DEGs are selected from 160 genes following a module analysis of the PPI network. (B2) The Cytoscape MCODE plug-in selected 19 genes. The red-gene models denote the selected genes. (B3) The prognostic information of the 19 key candidate genes. (C) Validation of 8 genes via R package. (D) 2 DEGs (*PRKCB* and *CYP1B1*) were identified and significantly enriched in the microRNAs in the cancer pathway. DEG, differentially expressed gene; PPI, protein-protein interaction; SKCM, skin cutaneous malignant melanoma.

MicroRNAs IN CANCER

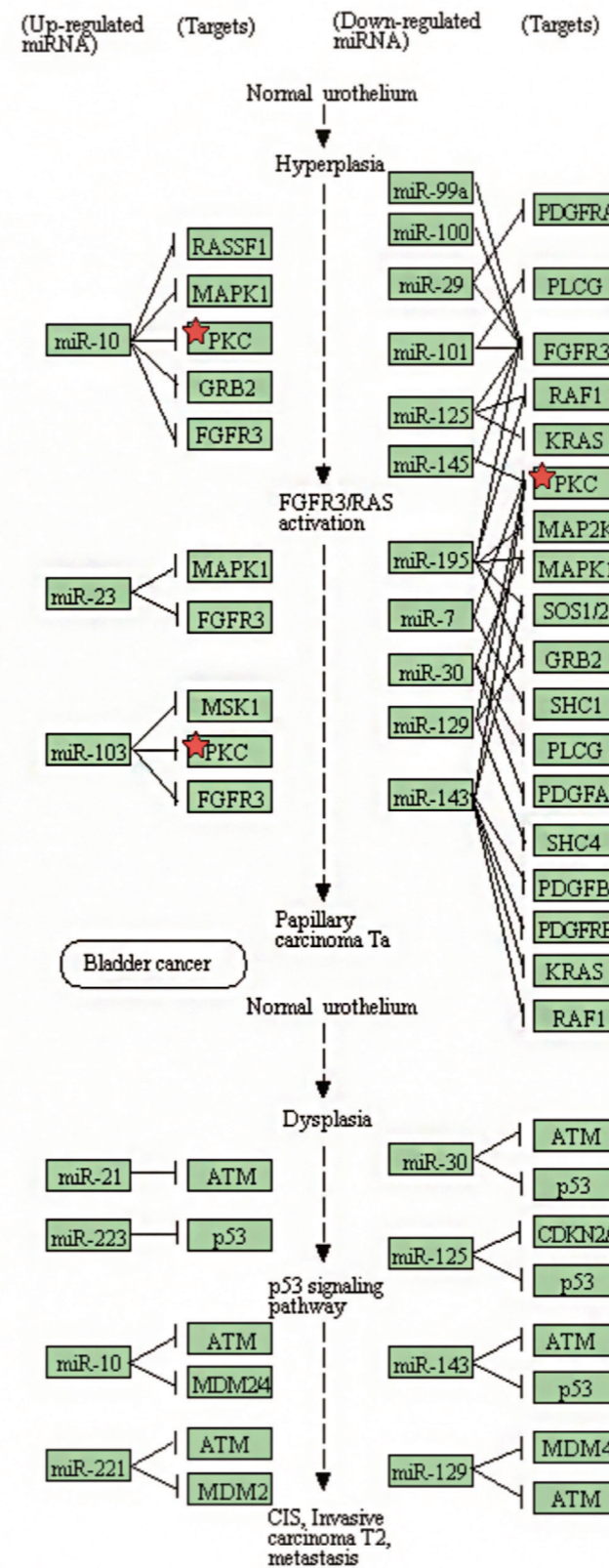
Lung cancer



Esophageal cancer



Bladder cancer



Prostate cancer

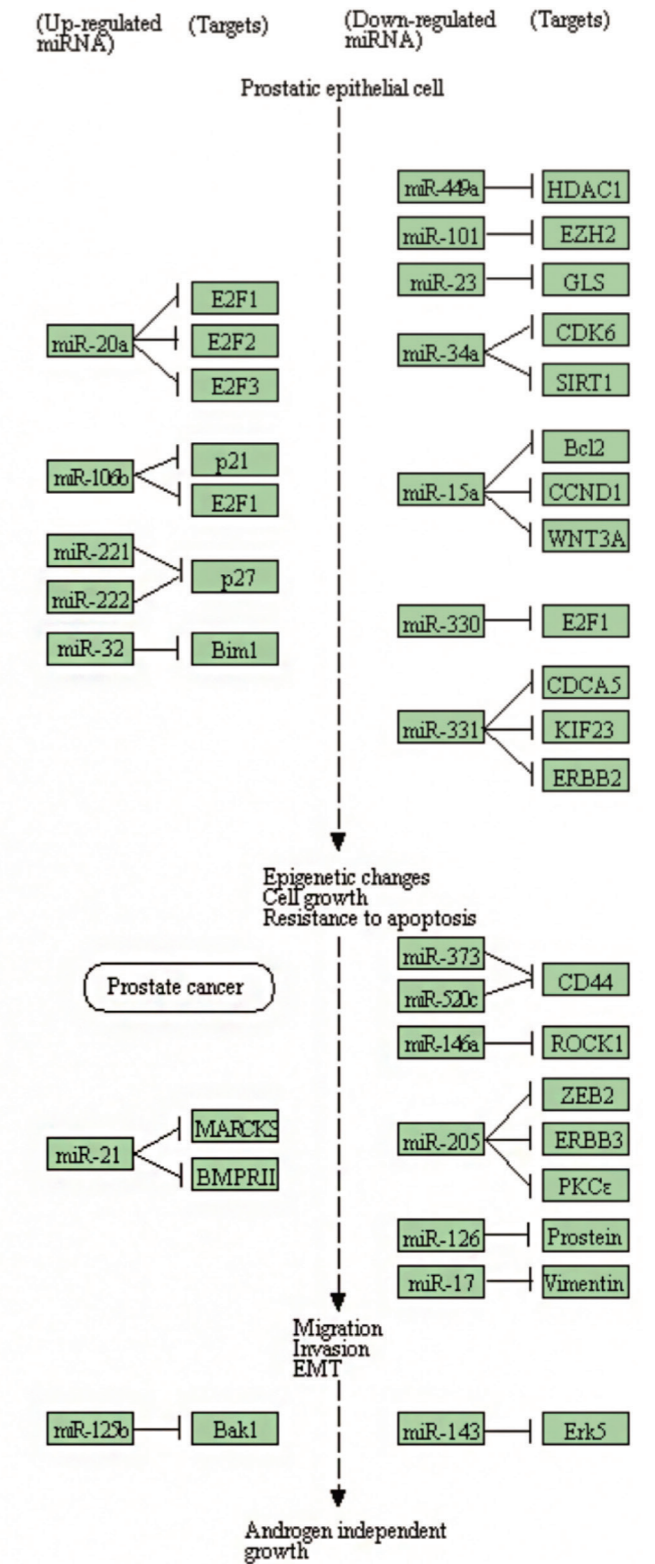


Figure S2 PRKCB and CYP1B1 were enriched in microRNAs in the cancer pathway. PKC refers to PRKCB.