

**Table S1** The survival-related programmed cell death (PCD) genes (P<0.1 in 3 cohorts)

Gene symbol	(log_rank_p)GSE72094	(log_rank_p)GSE68465	(log_rank_p)TCGA
<i>CCNB2</i>	2.84E-05	0.005654841	0.033803887
<i>HMGA1</i>	3.84E-05	0.001597858	0.041492281
<i>TPX2</i>	5.03E-05	0.002562288	0.061037328
<i>NEK2</i>	5.09E-05	0.010897718	0.007801333
<i>AGER</i>	0.000126312	0.04507162	0.029615087
<i>PLK1</i>	0.000129184	0.059669692	0.004148606
<i>KIF23</i>	0.000185082	0.013417401	0.066899943
<i>CDC25C</i>	0.00019753	0.020963128	0.065879425
<i>CACNA2D2</i>	0.000321476	0.001916941	0.021866302
<i>BUB1B</i>	0.000367861	0.000118066	0.005372506
<i>MKI67</i>	0.000454237	0.06374044	0.025609505
<i>CDC45</i>	0.000469767	0.015299836	0.066335821
<i>MCM4</i>	0.000585974	0.001005206	0.027355433
<i>CCNA2</i>	0.000688165	0.013456951	0.020412708
<i>SFTPD</i>	0.000706024	0.015252519	0.047214081
<i>CX3CR1</i>	0.001046449	0.052707861	0.026179317
<i>KIF20A</i>	0.001096336	0.058720132	0.012952189
<i>CCNB1</i>	0.001108929	0.002791029	0.017818945
<i>DAPK2</i>	0.001152561	0.011751125	0.033862096
<i>RRM2</i>	0.001304365	0.00298777	0.009092745
<i>CHEK1</i>	0.001337828	0.005171351	0.047904683
<i>MAD2L1</i>	0.001629227	0.000763495	0.075083932
<i>BTG2</i>	0.002516053	0.00450642	0.013038883
<i>KIF14</i>	0.003453479	0.0000158	0.002403165
<i>BUB1</i>	0.004244291	0.006373378	0.05978903
<i>PLK4</i>	0.006377572	0.016701634	0.04851904
<i>PTGDS</i>	0.007929071	0.008264632	0.05256148
<i>KPNA2</i>	0.008511015	0.066562233	0.017601079
<i>SERPINB5</i>	0.010962214	0.000442857	0.000841564
<i>CDK1</i>	0.011107966	0.025131225	0.033238859
<i>KIF11</i>	0.018668047	0.004697073	0.074222135
<i>ECT2</i>	0.019635342	0.003845668	0.043179083
<i>RAD51</i>	0.020251926	0.010973893	0.085608289
<i>PCSK1</i>	0.025327198	0.083934677	0.024585121
<i>GDF15</i>	0.04632371	0.030608418	0.055560909
<i>BRCA1</i>	0.05534496	0.000110963	0.015815775
<i>TFAP2A</i>	0.058265981	0.047342194	0.018369627
<i>TTK</i>	0.064580205	0.003778702	0.054457703
<i>NLRP2</i>	0.076085821	0.087124789	0.000288338

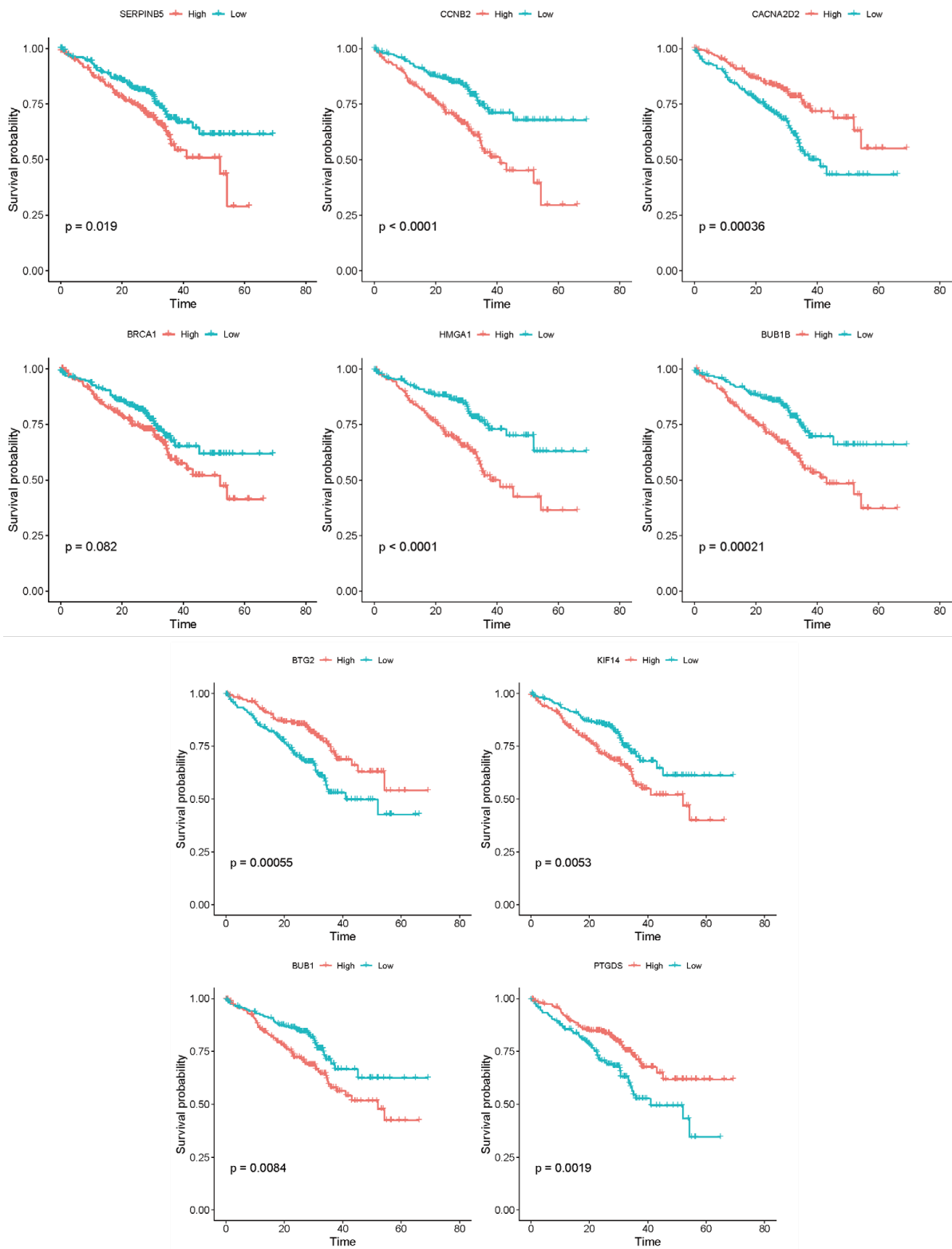
**Table S2** The survival-related programmed cell death genes (P<0.02 in at least 2 cohorts)

Gene symbol	(log_rank_p)GSE72094	(log_rank_p)GSE68465	(log_rank_p)TCGA
<i>CCNB2</i>	0.0000284	0.005654841	0.033803887
<i>HMGA1</i>	0.0000384	0.001597858	0.041492281
<i>TPX2</i>	0.0000503	0.002562288	0.061037328
<i>CACNA2D2</i>	0.000321476	0.001916941	0.021866302
<i>BUB1B</i>	0.000367861	0.000118066	0.005372506
<i>MCM4</i>	0.000585974	0.001005206	0.027355433
<i>CCNB1</i>	0.001108929	0.002791029	0.017818945
<i>RRM2</i>	0.001304365	0.00298777	0.009092745
<i>CHEK1</i>	0.001337828	0.005171351	0.047904683
<i>MAD2L1</i>	0.001629227	0.000763495	0.075083932
<i>BTG2</i>	0.002516053	0.00450642	0.013038883
<i>KIF14</i>	0.003453479	0.0000158	0.002403165
<i>BUB1</i>	0.004244291	0.006373378	0.05978903
<i>PTGDS</i>	0.007929071	0.008264632	0.05256148
<i>SERPINB5</i>	0.010962214	0.000442857	0.000841564
<i>KIF11</i>	0.018668047	0.004697073	0.074222135
<i>ECT2</i>	0.019635342	0.003845668	0.043179083
<i>BRCA1</i>	0.05534496	0.000110963	0.015815775

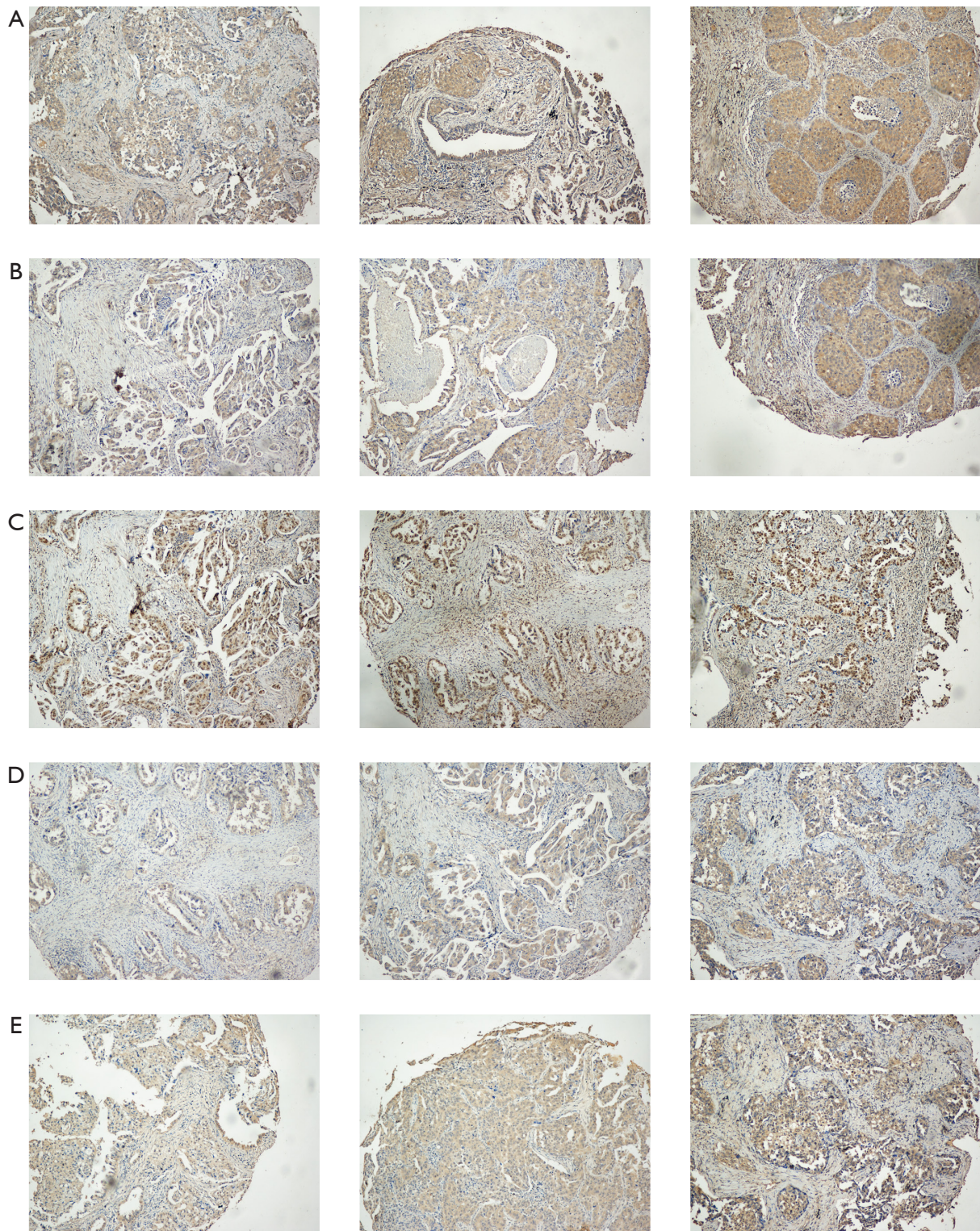
**Table S3** Cox regression in FUSCC-LUAD training cohort using IRS of the 10 candidate genes and overall survival data

Gene symbol	Coefficient	Exponential of the coefficient	Standard error of the coefficient
<i>BUB1</i>	-1.026E-02	9.025E-01	1.842E-01
<i>KIF14</i>	8.816E+01	1.929E+38	3.215E+04
<i>BUB1B</i>	-4.959E+02	4.323E-216	1.813E+05
<i>BRCA1</i>	-2.849E+02	1.823E-124	1.043E+05
<i>HMGA1</i>	6.706E+02	1.803E+291	2.452E+05
<i>CCNB2</i>	4.263E+02	1.399E+185	1.558E+05
<i>CACNA2D2</i>	-2.741E+02	9.147E-120	1.002E+05
<i>BTG2</i>	-9.306E+01	3.847E-41	3.416E+04
<i>PTGDS</i>	-4.085E+01	1.813E-18	1.495E+04
<i>SERPINB5</i>	5.627E+01	2.748E+24	2.049E+04

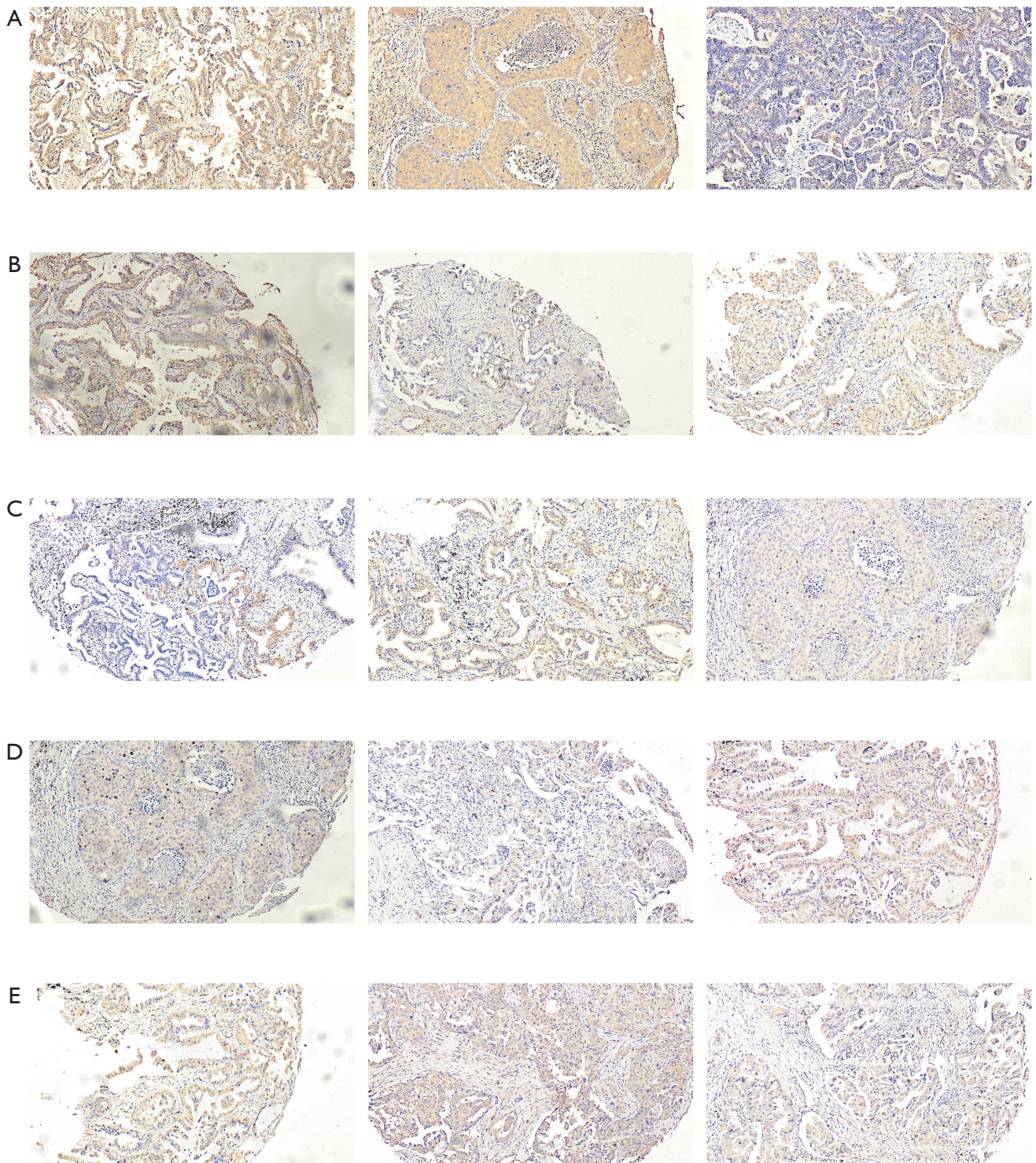
FUSCC, Fudan University Shanghai Cancer Center; LUAD, lung adenocarcinoma; IRS, immunoreactivity score.



**Figure S1** Kaplan-Meier survival analysis of RNA-seq of each model gene in GSE72094 cohort (green: low-expression group; orange: high-expression group).



**Figure S2** The protein expression levels of the model genes in LUAD tumor tissues ( $\times 100$ ). (A) IHC staining of *KIF14* (antibody: 26000-1-AP). (B) IHC staining of *CCNB2* (antibody: 21644-1-AP). (C) IHC staining of *HMGAI* (antibody: 29895-1-AP). (D) IHC staining of *BUB1B* (antibody: 11504-2-AP). (E) IHC staining of *BTG2* (antibody: 22339-1-AP). IHC, immunohistochemistry; LUAD, lung adenocarcinoma.



**Figure S3** The protein expression levels of the model genes in LUAD tumor tissues ( $\times 100$ ). (A) IHC staining of *BUB1* (antibody: 13330-1-AP). (B) IHC staining of *PTGDS* (antibody: 10754-2-AP). (C) IHC staining of *SERPINB5* (antibody: 11722-1-AP). (D) IHC staining of *BRCA1* (antibody: 22362-1-AP). (E) IHC staining of *CACNA2D2* (antibody: 46384-1, Sabbiotech). IHC, immunohistochemistry; LUAD, lung adenocarcinoma.