

Table S1 Clinical information of LUAD patients with EGFR mutations in the TCGA database

Samples	Gender	Age (years)	TNM stage	Futime (days)	Fustat
TCGA-05-4382	Male	68	T1	607	Alive
TCGA-05-4425	Female	70	T4	669	Alive
TCGA-05-5423	Male	65	T2	151	Alive
TCGA-38-4627	Female	64	T2	1,147	Dead
TCGA-38-4628	Female	65	T2	1,492	Dead
TCGA-38-4629	Male	68	T2	864	Dead
TCGA-38-6178	Female	70	T3	448	Alive
TCGA-44-5645	Female	61	T1	852	Alive
TCGA-44-A4SU	Female	67	T1	409	Dead
TCGA-49-4490	Female	45	T3	385	Dead
TCGA-49-4494	Male	77	T3	1,081	Dead
TCGA-49-4501	Female	67	T1	1,421	Dead
TCGA-49-6743	Female	81	T3	1,621	Alive
TCGA-50-5933	Male	72	T3	2,393	Dead
TCGA-50-6595	Female	74	T3	189	Dead
TCGA-55-6979	Female	59	T2	237	Dead
TCGA-55-6980	Male	56	T1	2,109	Alive
TCGA-55-6981	Female	53	T3	1,379	Dead
TCGA-55-7570	Male	60	T1	824	Alive
TCGA-55-8087	Female	59	T1	462	Alive
TCGA-55-8096	Female	67	T1	719	Dead
TCGA-55-8206	Male	56	T1	888	Alive
TCGA-55-8616	Female	58	T1	48	Alive
TCGA-55-A48Z	Female	60	T3	651	Alive
TCGA-62-8394	Female	65	T3	139	Dead
TCGA-62-8397	Female	70	T2	1,289	Alive
TCGA-62-8402	Female	73	T3	1,498	Dead
TCGA-64-1681	Female	61	T1	1,167	Dead
TCGA-67-3770	Female	70	T1	610	Alive
TCGA-67-3772	Female	82	T1	573	Alive
TCGA-67-6217	Female	73	T2	422	Alive
TCGA-69-7760	Male	73	T2	202	Alive
TCGA-69-7765	Male	56	T1	165	Alive
TCGA-71-6725	Female	48	T1	256	Alive
TCGA-71-8520	Female	60	T1	210	Dead

Table S1 (continued)

Table S1 (*continued*)

Samples	Gender	Age (years)	TNM stage	Futime (days)	Fustat
TCGA-75-7025	Male	75	T1	3,305	Alive
TCGA-78-7147	Female	67	T2	586	Dead
TCGA-78-7155	Male	68	T1	1,171	Dead
TCGA-78-7158	Female	59	T3	179	Dead
TCGA-86-8055	Male	79	T2	124	Dead
TCGA-86-8075	Female	66	T1	694	Dead
TCGA-86-8280	Female	54	T2	701	Alive
TCGA-86-8668	Female	61	T1	423	Alive
TCGA-91-8496	Female	63	T1	505	Alive
TCGA-95-7039	Female	54	T2	1,272	Alive
TCGA-95-7947	Male	67	T1	477	Alive
TCGA-97-8171	Male	81	T4	568	Alive
TCGA-97-8177	Female	59	T1	499	Alive
TCGA-97-8552	Female	55	T1	626	Alive
TCGA-97-A4M1	Female	52	T1	601	Alive
TCGA-97-A4M6	Female	45	T1	568	Alive
TCGA-97-A4M7	Male	74	T1	629	Alive
TCGA-J2-8192	Female	65	T2	739	Alive
TCGA-L9-A50W	Male	75	T2	442	Dead
TCGA-MP-A4SW	Male	53	T2	1,778	Dead
TCGA-MP-A4T6	Female	76	T3	1,790	Dead
TCGA-MP-A4T9	Female	54	T3	1,265	Dead
TCGA-O1-A52J	Female	74	T1	1,798	Dead

EGFR, epidermal growth factor receptor; LUAD, lung adenocarcinoma; T, tumor; TCGA, The Cancer Genome Atlas; TNM, tumor-node-metastasis.

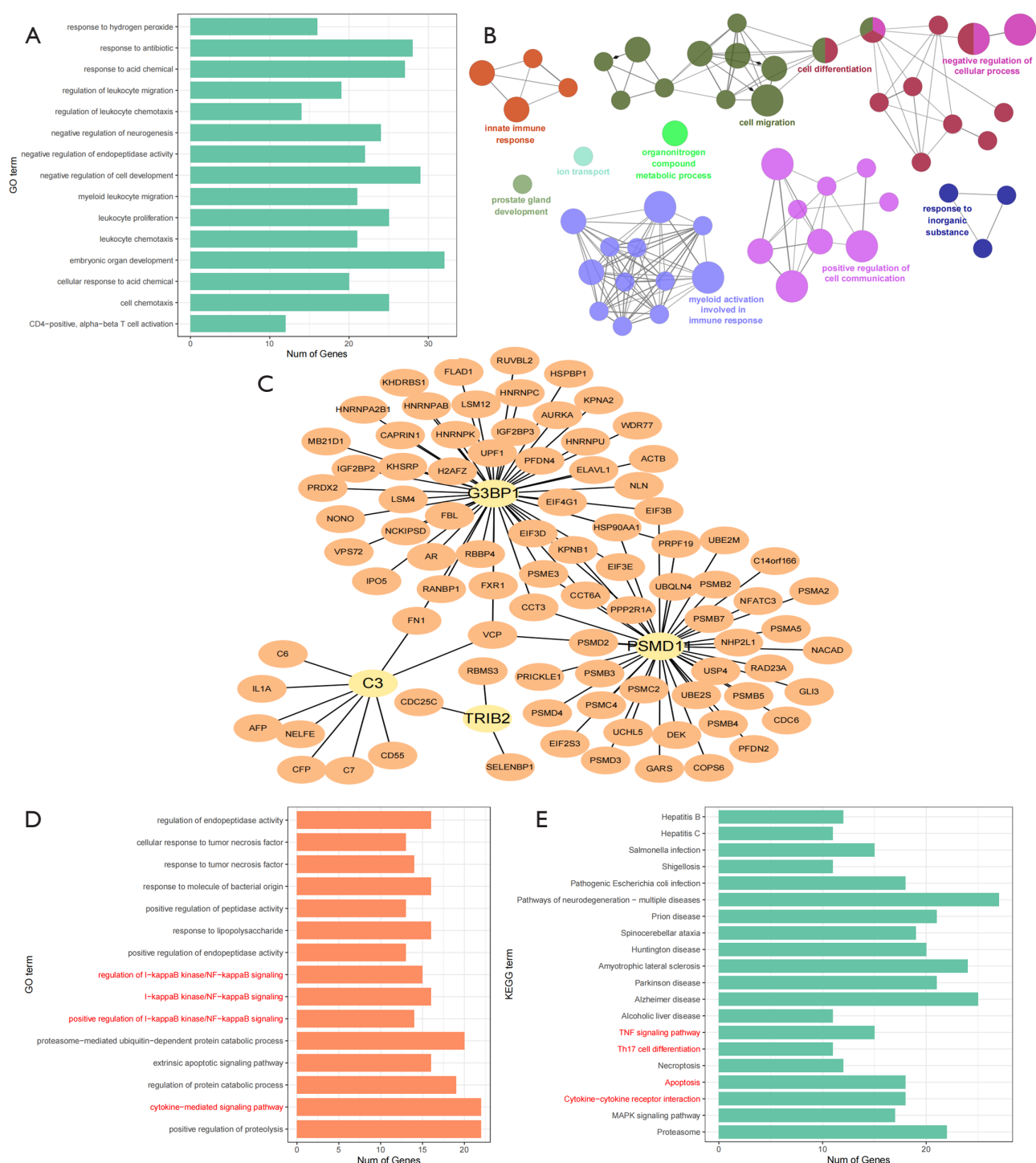


Figure S1 Functional analysis of DEGs and four hub genes. (A,B) GO and KEGG functional enrichment analysis of DEGs. (C) PPI network analysis revealed genes directly associated with four hub genes. (D,E) GO and KEGG functional enrichment analysis was conducted on four hub genes and their directly related genes. DEGs, differentially expressed genes; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; PPI, protein-protein interaction.

Table S2 Analysis of GSEA pathway enrichment in high- and low-risk groups

Description	Set size	Enrichment score	NES	P value	Core enrichment
High-risk group					
KEGG_ECM_RECEPTOR_INTERACTION	73	0.690546276	1.98145	2.67E−06	COL2A1/LAMA1/IBSP/COL11A1/ITGB8/CHAD/THBS2/ITGA11/COL5A2/SPP1/TNC/ITGB3/LAMC2/ITGA6/COL5A3/COL3A1/COL5A1/SV2A/COL1A2/FN1/LAMC1/COL1A1/COMP/HMMR/COL6A3/ITGAV/LAMB1/LAMB3/COL6A2/ITGA1/SDC3/COL4A2/COL4A1/COL6A1/ITGA2
KEGG_CELL_CYCLE	121	0.618151204	1.87411	9.19E−06	BUB1B/CCNE1/ESPL1/CDC45/CDC25A/ORC1/CCNA2/CDC6/TTK/BUB1/CDC20/CHEK1/E2F2/MAD2L1/CDK1/CCNB1/SKP2/CDC25C/PLK1/MCM4/CCNB2/CDK6/PKMYT1/MCM2/ORC6/MCM6/MCM7/E2F1/CHEK2/E2F3/PTTG1/MCM3/PRKDC/CDC7/CCNE2/CDKN2A/DBF4/MCM5/RBL1/PCNA/ANAPC1/YWHAG/CDK2/ORC5/WEE1/SMC1A/TGFB3/TFDP1/ATR/HDAC2/GSK3B/TGFB2/MYC/ABL1/GADD45A/SFN/CDC27/BUB3
KEGG_DNA_REPLICATION	35	0.682282395	1.76462	0.001766	MCM4/MCM2/POLE2/DNA2/MCM6/FEN1/RFC4/MCM7/MCM3/POLE/MCM5/PCNA/RFC3/PRIM2/RNASEH2A/RNASEH1/POLA2/POLD2/RFC5/POLA1/RFC2
KEGG_P53_SIGNALING_PATHWAY	65	0.554448297	1.5701	0.011085	SERPINB5/RPRM/CCNE1/GTSE1/CHEK1/RRM2/CDK1/CCNB1/CCNB2/CDK6/CHEK2/PMAIP1/ADGRB1/CCNE2/CDKN2A/SERPINE1/IGFBP3
KEGG_SMALL_CELL_LUNG_CANCER	80	0.541065728	1.56374	0.012659	LAMA1/CCNE1/NOS2/E2F2/SKP2/PTGS2/CDK6/LAMC2/ITGA6/FN1/LAMC1/E2F1/E2F3/CCNE2/ITGAV/LAMB1/LAMB3/COL4A2/COL4A1/ITGA2/ITGB1/CDK2/CYCS/PIAS3
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	103	0.515221378	1.54334	0.008815	CHRNA9/GABRA3/F2/GRIK5/PRSS3/NTSR1/PRLR/HTR1D/PRSS2/KISS1R/BDKRB1/AVPR1A/CHRNA1/GABRP/CHRNA5/F2RL2/GPR35/HTR2B/PRSS1/GRIN2D/P2RY6/ADORA1
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	12	0.730654308	1.5425	0.030339	NEUROD1/HNF4A/PDX1/HNF4G/BHLHA15/HES1/FOXA3
KEGG_HOMOLOGOUS_RECOMBINATION	26	0.631626407	1.53723	0.04235	RAD54L/BLM/RAD51/XRCC2/EME1/BRCA2/XRCC3/RAD54B/POLD2/TOP3A/RAD51C/SEM1
KEGG_GAP_JUNCTION	71	0.530669486	1.52008	0.027059	TUBA3C/TUBB2B/ADCY5/TUBB4A/CDK1/PLCB1/TUBB3/PLCB4/HTR2B/TUBB/EGF/SRC/PDGFC/GNAI1/TUBA1C/PDGFB/NRAS/TUBA4A/PRKX/PDGFRB/GU-CY1A1/PDGFD/SOS1/GUCY1B1/EGFR/MAPK7/KRAS
KEGG_OOCYTE_MEIOSIS	94	0.497249934	1.47168	0.021651	CCNE1/ESPL1/SGO1/BUB1/ADCY5/CDC20/CALML3/MAD2L1/CDK1/CCNB1/CDC25C/PLK1/CCNB2/PKMYT1/AURKA/PTTG1/CALML5/CCNE2/ANAPC1/YWHAG/FBXO5/CDK2/PPP2R1B/SMC1A
KEGG_FOCAL_ADHESION	179	0.4660114	1.4673	0.010064	COL2A1/LAMA1/IBSP/COL11A1/ITGB8/CHAD/THBS2/ITGA11/COL5A2/SPP1/TNC/ITGB3/LAMC2/FLNC/ITGA6/COL5A3/COL3A1/COL5A1/COL1A2/FN1/LAMC1/ACTN1/COL1A1/COMP/ERBB2/COL6A3/ITGAV/VEGFA/VEGFC/LAMB1/LAMB3/COL6A2/ITGA1/COL4A2/COL4A1/COL6A1/ITGA2/AV3/TLN2/EGF/SRC/ITGB1/PDG-FC/ITGB5/ARHGAP5/SHC1/ITGA5/VAV2/PDGFB/THBS3/GSK3B/ITGB4
KEGG_SPLICEOSOME	125	0.451726264	1.37517	0.040975	HSPA2/PRPF4/SNRPD1/PPIL1/EFTUD2/SNRPA1/ALYREF/PRPF40A/ACIN1/SNRPB/PRPF40B/SF3B4/THOC1/SNRNP200/U2SURP/LSM5/NCBP1/SNRPE/NCBP2/SNRPB2/PRPF19/TCERG1/DDX39B/CRNKL1/CHERP/PRPF3/DHX8/THOC3/LSM8/SRSF1/PLRG1/HSPA6/SNW1/DHX15/HNRNPC/AQR/RBM8A/SNRPF/SNRPD3/HNRNPK/DDX23/HNRNPU/HSPA1L/HSPA1A/EIF4A3/SMNDC1/HNRNPM/WBP11/U2AF2/SNRNP40/CDC5L/CTNBNL1/PUF60/SNRPC/HSPA1B/THOC2/RBM25/LSM4/SRSF10/SNRNP27/ISY1/BUD31/PCBP1/SRSF2/HNRNPA1L2/SRSF9/HSPA8/DDX46/HNRNPA1/RBMX/SF3B2/SART1/LSM2/SNRPG/TRA2B/DDX42/SNRPA/SF3B6/TXNL4A/DHX16/SF3B3
KEGG_PATHWAYS_IN_CANCER	288	0.406927131	1.31058	0.027692	MMP1/LAMA1/WNT16/FGF19/EGLN3/SLC2A1/CCNE1/NOS2/FZD10/E2F2/SMO/MMP9/RAD51/SKP2/PTGS2/CDK6/LEF1/FZD1/LAMC2/ITGA6/BIRC5/FGF18/FN1/LAMC1/FGF1/E2F1/E2F3/ERBB2/HHIP/CCNE2/AXIN2/CDKN2A/ITGAV/GLI3/TGFA/MSH2/CXCL8/VEGFA/VEGFC/LAMB1/LAMB3/COL4A2/FGFR1/COL4A1/STAT1/MSH6/BRCA2/ITGA2/BMP4/WNT5B/EGF/TFG/ITGB1/CDK2/GLI2/CYCS/WNT7A/PML/PIAS3/TGFB3/WNT5A/FASLG/HDAC2/DVL3/PDGFB/PPARD/NRAS/GSK3B/HSP90B1/CKS1B/FZD8/TRAF2/MMP2/TGFB2/BID/MYC/ABL1/RALA/ARNT2/CBLB
Low-risk group					
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	36	−0.715211359	−2.3193	4.13E−06	CD86/CXCR4/TNFRSF13C/HLA-DQB1/CD40/HLA-DQA1/CXCL12/CD40LG/ICOS/PIGR/HLA-DRB5/HLA-DMA/TNFSF13/HLA-DMB/HLA-DOB/CCR10/HLA-DRB1/HLA-DRA/HLA-DOA/HLA-DPA1/HLA-DPB1/HLA-DQA2/IL6
KEGG_ASTHMA	20	−0.761960494	−2.1369	5.76E−05	HLA-DQB1/CD40/HLA-DQA1/CD40LG/HLA-DRB5/TNF/HLA-DMA/HLA-DMB/MS4A2/HLA-DOB/HLA-DRB1/HLA-DRA/HLA-DOA/HLA-DPA1/HLA-DPB1/HLA-DQA2/FCER1A
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	49	−0.624152957	−2.1098	1.70E−05	HLA-DRB5/TNF/C2/HLA-DMA/HLA-DMB/C5/HLA-DOB/C3/HLA-DRB1/HLA-DRA/HLA-DOA/HLA-DPA1/HLA-DPB1/FCGR3B/CTSG/HLA-DQA2/C7/C6/ELANE
KEGG_AUTOIMMUNE_THYROID_DISEASE	30	−0.637211634	−1.9686	0.000864	HLA-DQB1/CD40/HLA-DQA1/CD40LG/FAS/HLA-E/HLA-DRB5/HLA-DMA/HLA-DMB/HLA-DOB/HLA-DRB1/HLA-DRA/HLA-DOA/HLA-DPA1/HLA-DPB1/HLA-DQA2/CGA
KEGG_HEMATOPOIETIC_CELL_LINEAGE	71	−0.530851902	−1.9103	0.000111	CD34/IL11RA/CD44/CD36/CSF1/HLA-DRB5/TNF/CD9/CD37/CD22/CD59/CD33/ITGAM/CD38/CR1/MS4A1/CD1D/IL6R/HLA-DRB1/HLA-DRA/FCER2/CSF2/CSF3R/CD55/CD1E/CD1B/CD1C/ANPEP/IL6/CD1A/CSF3
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	43	−0.558358116	−1.8751	0.001007	ALDH3A1/MGST1/GSTM5/UGT2B7/UGT1A10/FMO2/MAOA/CYP2D6/UGT2B15/ALDH3B1/ADH1B/GSTA1/ADH7/GSTA2
KEGG_VIRAL_MYOCARDITIS	58	−0.527220897	−1.7978	0.000872	HLA-DQB1/CD40/MYH14/HLA-DQA1/FYN/CCND1/CD40LG/MYH11/SGCA/HLA-E/ITGAL/HLA-DRB5/ITGB2/DMD/HLA-DMA/HLA-DMB/ICAM1/CAV1/HLA-DOB/HLA-DRB1/HLA-DRA/HLA-DOA/HLA-DPA1/HLA-DPB1/SGCG/HLA-DQA2/CD55
KEGG_ALLOGRAFT_REJECTION	30	−0.573226944	−1.7709	0.00613	HLA-DQB1/CD40/HLA-DQA1/CD40LG/FAS/HLA-E/HLA-DRB5/TNF/HLA-DMA/HLA-DMB/HLA-DOB/HLA-DRB1/HLA-DRA/HLA-DOA/HLA-DPA1/HLA-DPB1/HLA-DQA2
KEGG_GRAFT_VERSUS_HOST_DISEASE	31	−0.530611814	−1.669	0.007957	FAS/HLA-E/HLA-DRB5/TNF/KIR2DL1/HLA-DMA/HLA-DMB/HLA-DOB/HLA-DRB1/HLA-DRA/HLA-DOA/HLA-DPA1/HLA-DPB1/HLA-DQA2/IL6
KEGG_RIBOSOME	85	−0.402022953	−1.4915	0.006941	RPS7/RPS4X/RPS17/RPL31/RPL27A/RPL27/RPL34/FAU/RPL10A/RPL39/RPS27L/RPS24/RSL24D1/RPL26L1/RPL15/RPS13/RPL5/RPS27/RPS29/RPL22/RPL13A/RPS23/RPL41/RPL10/RPS16/RPS11/RPL13/RPS9/RPL21/RPLP1/RPS5/RPS8/RPL11/RPS6/RPS12/RPS21/RPS15A/RPS3A
KEGG_FATTY_ACID_METABOLISM	36	−0.456253111	−1.4795	0.037402	ACOX3/CPT2/HADHB/ECI2/CPT1B/GCDH/ACSL1/ALDH7A1/ACSL5/ACAA1/ECI1/ACAT1/HADH/ACADVL/ALDH3A2/ACADL/ACADSB/ALDH2/ADH1B/ADH7
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	43	−0.436614797	−1.4662	0.034707	ALDH3A1/MGST1/DHDH/GSTM5/UGT2B7/UGT1A10/EPHX1/UGT2B15/ALDH3B1/ADH1B/GSTA1/ADH7/GSTA2/CYP2F1
KEGG_LEISHMANIA_INFECTION	66	−0.383812056	−1.3598	0.0299	NCF1/HLA-DRB5/TNF/ITGB2/TLR2/ITGAM/PRKCB/IFNGR1/CR1/HLA-DMA/HLA-DMB/FOS/HLA-DOB/C3/HLA-DRB1/HLA-DRA/HLA-DOA/HLA-DPA1/HLA-DPB1/FCGR3B/HLA-DQA2
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	57	−0.385004006	−1.3061	0.040187	HLA-DQB1/HLA-DQA1/CD4/IFI30/HLA-E/CIITA/HLA-DRB5/KIR2DL1/HLA-DMA/HLA-DMB/CD74/HLA-DOB/HLA-DRB1/HLA-DRA/HLA-DOA/HLA-DPA1/HLA-DPB1/HLA-DQA2
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	69	−0.366158877	−1.3	0.047643	FYN/PRKCE/PLA2G2A/MAPK3/INPP5D/VAV1/PLA2G3/GAB2/PRKCD/TNF/PIK3R5/PLCG2/PIK3CG/PRKCB/BTK/MS4A2/MAPK10/PLA2G1B/CSF2/PLA2G10/FCER1A/PLA2G12B
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	97	−0.331923906	−1.2472	0.044948	NCR3/PRKCA/PTPN6/PPP3CB/PPP3CC/TNFRSF10C/TNFSF10/HCST/FYN/NFATC3/MAPK3/ICAM2/SH2D1A/CHP1/MICA/VAV1/FAS/PTK2B/NFATC2/HLA-E/TNFRS-F10D/ITGAL/TNF/TYROBP/PIK3R5/PLCG2/NFATC1/ITGB2/CD244/PIK3CG/KIR2DL1/PRKCB/CD48/IFNGR1/ICAM1/CSF2/FCGR3B/SHC3

GSEA, gene set enrichment analysis; KEGG, Kyoto Encyclopedia of Genes and Genomes; NES, normalized enrichment score.

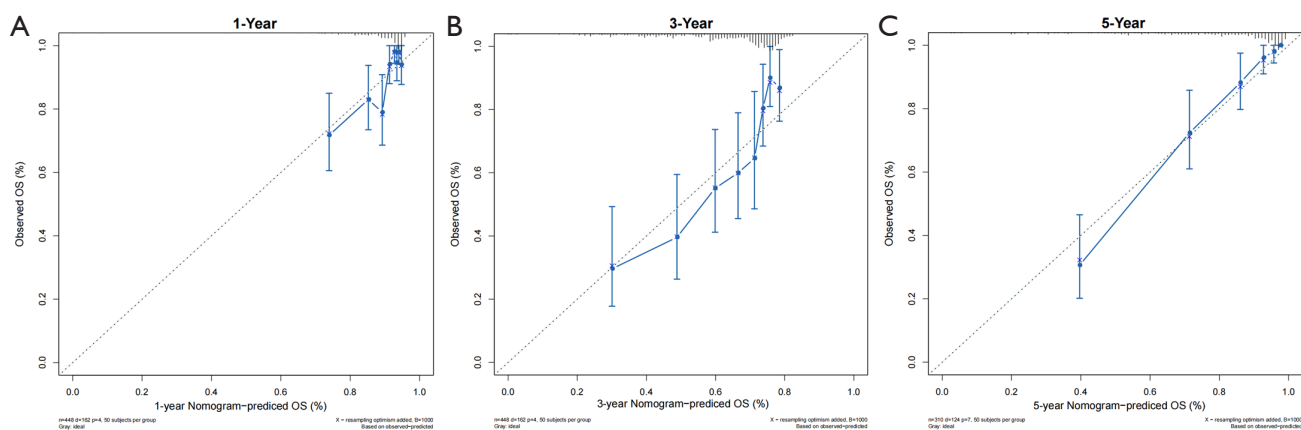
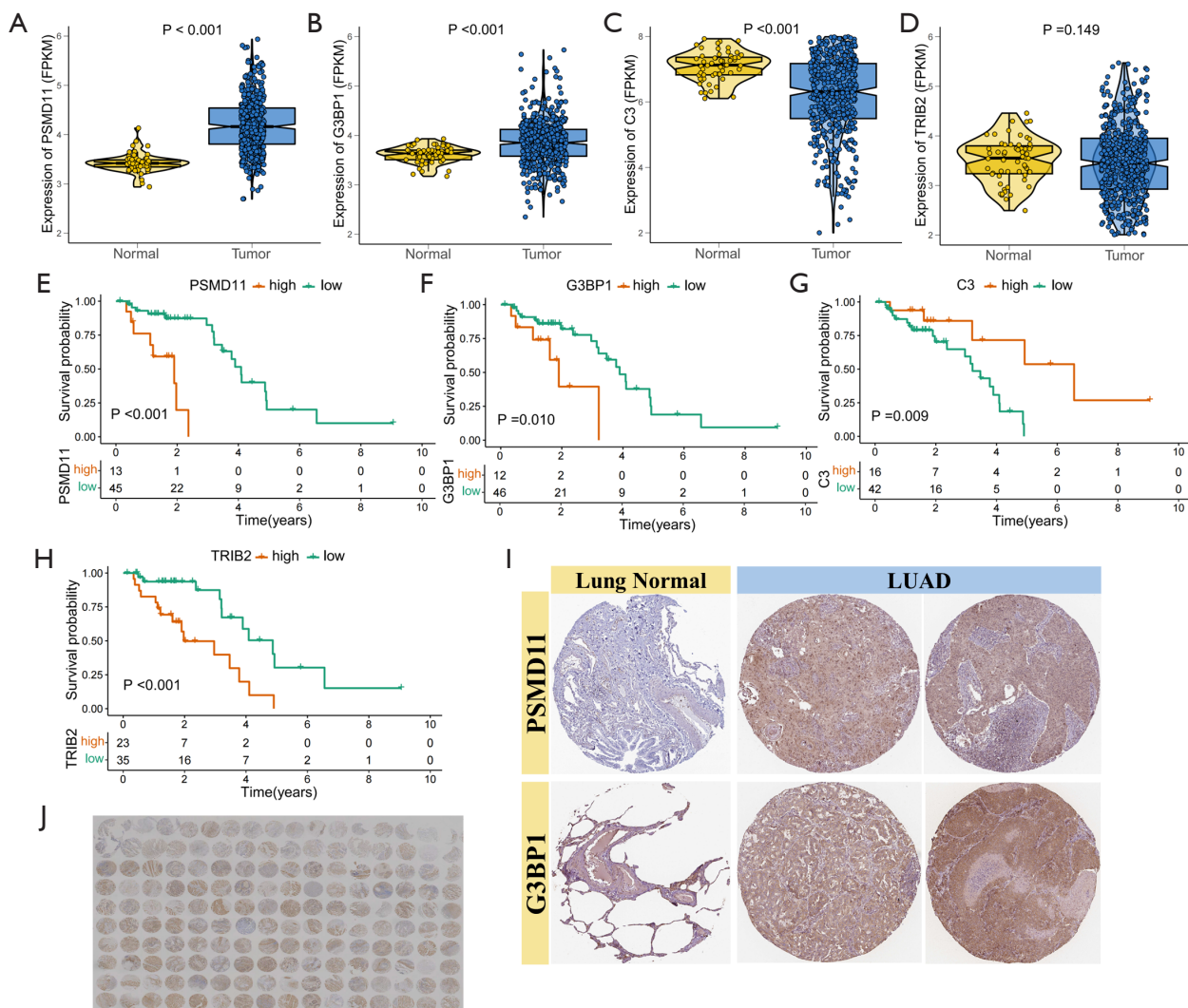


Figure S2 The nomogram model has high predictive consistency. (A-C) Draw calibration plot to verify the accuracy of the nomogram model in predicting 1-, 3-, and 5-year survival rates. OS, overall survival.



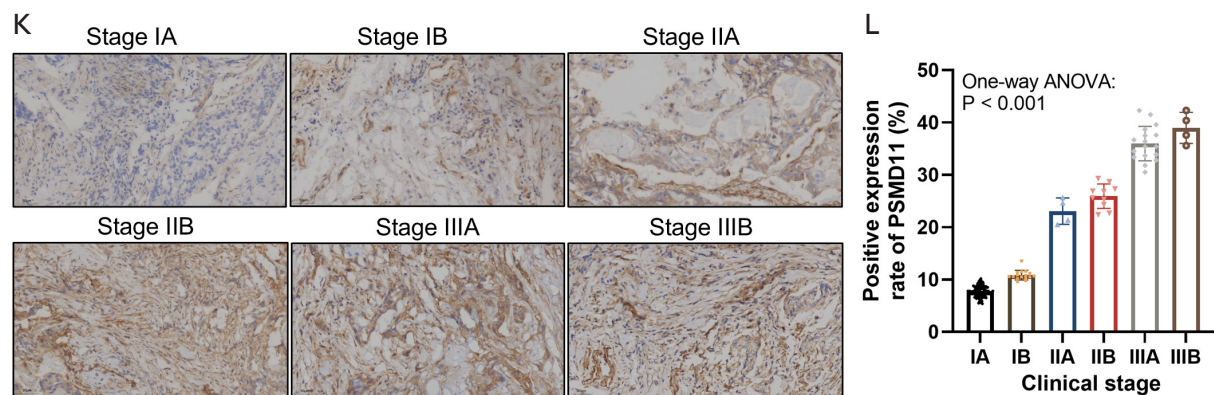


Figure S3 The value of four hub genes in predicting OS in LUAD. (A-D) Based on the LUAD cohort of TCGA database, analyze the expression differences of four hub genes in LUAD and normal lung tissues. (E-H) The prognostic differences of four hub genes in LUAD patients with EGFR mutation. (I) Immunohistochemistry showed the expression levels of PSMD11 and G3BP1 in normal lung and LUAD tissues through HPA database. (J) PSMD11 immunohistochemical staining of a 160-spot LUAD tissue microarray. (K,L) The protein expression of PSMD11 in LUAD samples of different clinical stages (magnification: 400×) was shown by histogram. ANOVA, analysis of variance; EGFR, epidermal growth factor receptor; FPKM, fragments per kilobase of transcript per million fragments mapped; HPA, Human Protein Atlas; LUAD, lung adenocarcinoma; OS, overall survival; TCGA, The Cancer Genome Atlas.

Table S3 Site information of LUAD tissue microarray

ID	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
A	1	3	5	7	9	11	13	15	17	19	21	23	25	27	29	31
B	33	35	37	39	41	43	45	47	49	51	53	321	57	59	61	63
C	65	67	69	71	73	75	77	79	81	83	85	87	89	91	93	323
D	97	99	101	103	105	107	109	111	113	115	117	119	121	123	125	127
E	129	131	133	135	137	139	141	143	145	147	149	151	153	155	157	159
F	161	163	165	167	169	171	173	175	177	179	181	183	185	187	189	191
G	193	195	197	199	325	203	205	207	209	211	213	215	217	219	221	223
H	225	227	229	231	233	235	237	239	241	243	245	247	249	251	253	255
I	257	259	261	263	265	267	269	271	273	275	277	279	281	283	285	287
J	289	291	293	295	297	299	301	303	305	307	309	311	313	315	317	319

LUAD, lung adenocarcinoma.

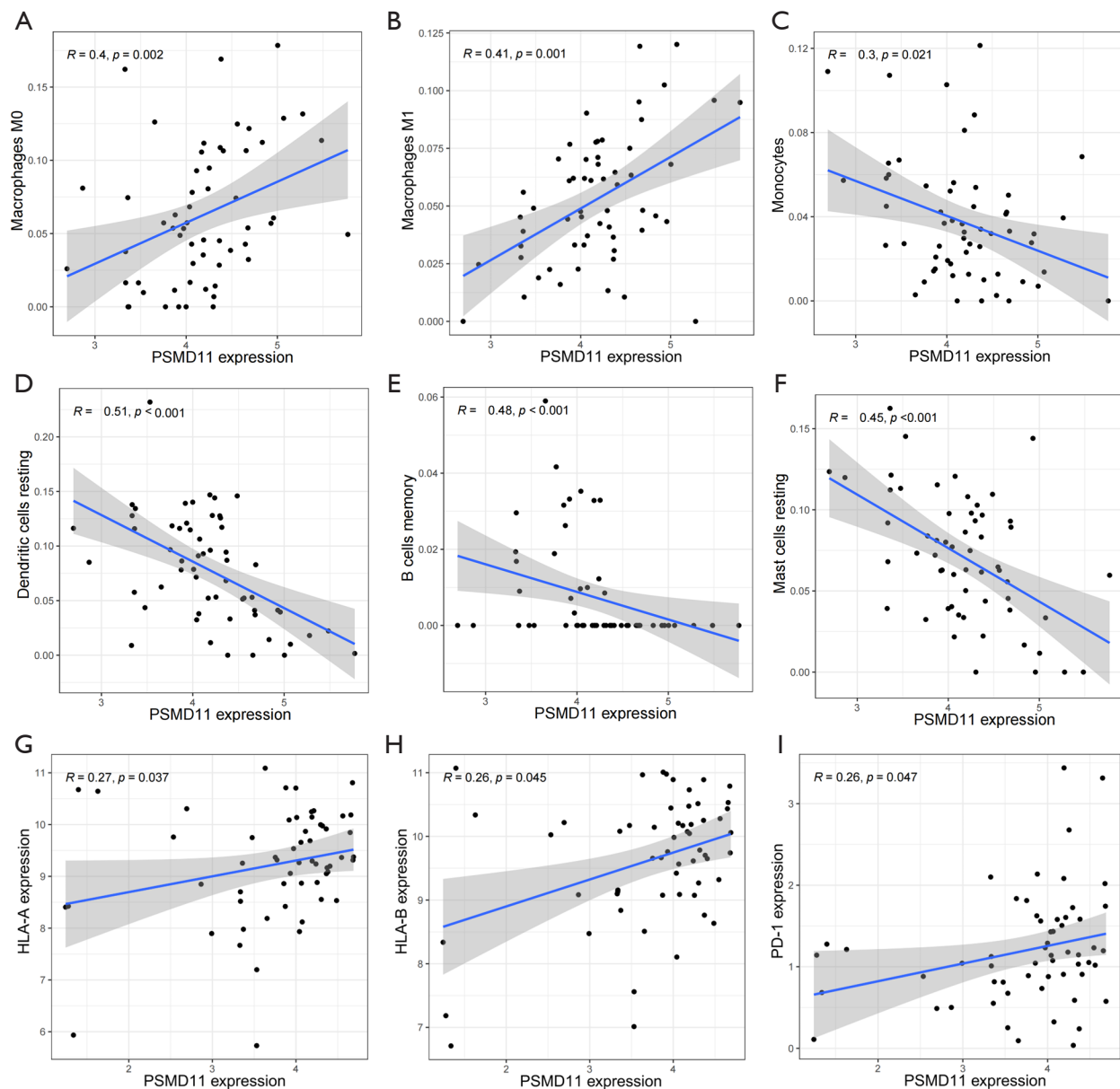


Figure S4 The correlation between PSMD11 and infiltrating immune cells and immune related molecules. (A,B) The expression of PSMD11 was positively correlated with the proportion of M0/M1 macrophages. (C-F) The expression of PSMD11 was negatively correlated with the proportion of monocytes, memory B cells, resting dendritic cells, and resting mast cells. (G-I) The expression of PSMD11 is positively correlated with immune related molecules HLA-A, HLA-B, and PD-1.

Table S4 Correlation between PSMD11 and 22 types of immune cells

Immune cells	P value	Correlation
B cells memory	<0.001*	Negative
Plasma cells	0.93	Negative
T cells CD4 memory resting	0.88	Negative
Tregs	0.76	Positive
NK cells resting	0.79	Negative
Monocytes	0.021*	Negative
Macrophages M2	0.88	Negative
Dendritic cells resting	<0.001*	Negative
Dendritic cells activated	0.6	Positive
Mast cells resting	<0.001*	Negative
Eosinophils	0.059	Negative
Neutrophils	0.42	Negative
B cells naive	0.16	Positive
T cells CD8	0.86	Positive
T cells CD4 memory activated	0.25	Positive
T cells follicular helper	0.63	Positive
T cells gamma delta	0.52	Positive
NK cells activated	0.47	Positive
Macrophages M0	0.0017*	Positive
Macrophages M1	0.0013*	Positive
Mast cells activated	0.32	Positive

*, P<0.05. NK, natural killer; Tregs, regulatory T cells.

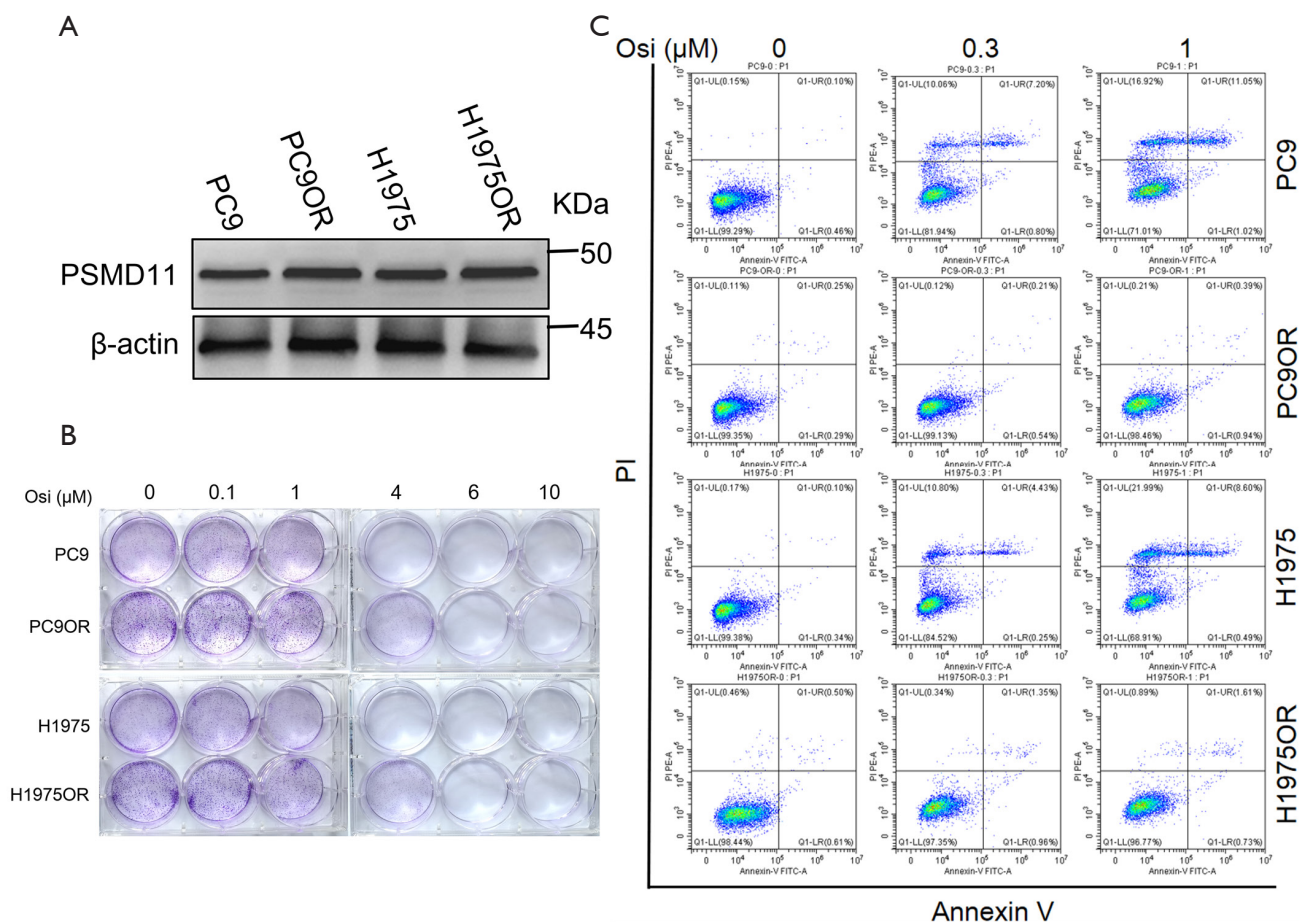


Figure S5 The drug-resistant cells PC9OR and H1975OR have a higher resistance to OSI. (A) Western blot was used to detect the protein expression of PSMD11 in OSI-sensitive cells (PC9, H1975) and OSI-resistant cells (PC9OR, H1975OR). (B) Colony formation assay (crystal violet staining) was used to detect the cell proliferation of PC9, PC9OR, H1975, and H1975OR cells treated with six different concentrations of OSI. (C) Flow cytometry was used to detect the apoptosis of PC9, PC9OR, H1975, and H1975OR cells treated with three different concentrations of OSI. FITC, fluorescein isothiocyanate; OSI, osimertinib; PE, phycoerythrin; PI, propidium iodide.

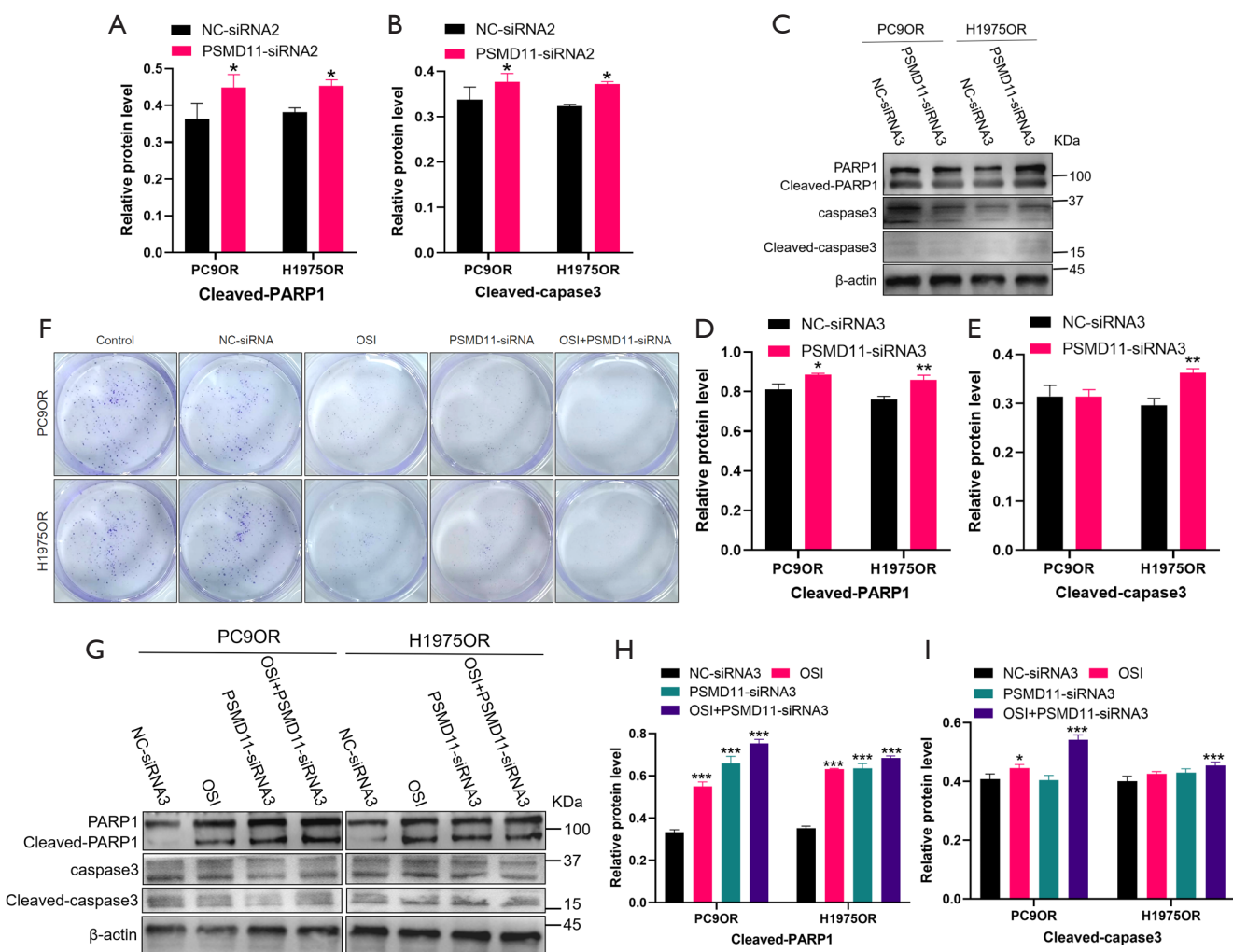


Figure S6 Knocking down PSMD11 in OSI-resistant cells could inhibit cell proliferation and promote cell apoptosis. (A,B) The bar chart shows the effect of knocking down PSMD11 on the expression of apoptosis-related molecules in PC9OR and H1975OR cells (corresponding to Figure 4F). (C-E) Western blotting was used to detect the effect of transfection of PSMD11-siRNA3 into PC9OR and H1975OR cells on the expression of apoptosis-related molecules, and a gray-scale analysis graph was drawn. (F) Colony formation assay (crystal violet staining) was used to detect the effects of individual or combined treatment with PSMD11-siRNA and OSI on the cell proliferation of PC9OR and H1975OR cells. (G-I) Western blotting was used to detect the expression of apoptosis-related molecules in PC9OR and H1975OR cells after treatment with PSMD11-siRNA3 and OSI, and a gray-scale analysis graph was drawn. *, $P < 0.05$ compared with control group; **, $P < 0.01$ compared with control group; ***, $P < 0.001$ compared with control group. NC, negative control; OSI, osimertinib; siRNA, small interfering RNA.