

Table S1 Ferroptosis, necroptosis, and pyroptosis-related genes

Ferroptosis-gene				Necroptosis-gene		Pyroptosis-gene
<i>PTG</i>	<i>STMN1</i>	<i>NEDD4L</i>	<i>IFNG</i>	<i>BRD7</i>	<i>ALK</i>	<i>BAK1</i>
<i>DUSP1</i>	<i>RRM2</i>	<i>BRD2</i>	<i>ANO6</i>	<i>SLC25A28</i>	<i>APP</i>	<i>BAX</i>
<i>NOS2</i>	<i>CAPG</i>	<i>BRD3</i>	<i>LPIN1</i>	<i>MFN2</i>	<i>ATRX</i>	<i>CASP1</i>
<i>NCF2</i>	<i>HNF4A</i>	<i>BRDT</i>	<i>TNFAIP3</i>	<i>SLC11A2</i>	<i>AXL</i>	<i>CASP3</i>
<i>MT3</i>	<i>NGB</i>	<i>DECR1</i>	<i>TLR4</i>	<i>ZFAS1</i>	<i>BACH2</i>	<i>CASP4</i>
<i>UBC</i>	<i>YWHAE</i>	<i>GLRX5</i>	<i>ATM</i>	<i>TSC1</i>	<i>BCL2</i>	<i>CASP5</i>
<i>ALB</i>	<i>GABPB1</i>	<i>NCOA3</i>	<i>YY1AP1</i>	<i>TGFB1</i>	<i>BCL2L11</i>	<i>CHMP2A</i>
<i>TXNRD1</i>	<i>AURKA</i>	<i>NR5A2</i>	<i>EGLN2</i>	<i>SNCA</i>	<i>BIRC2</i>	<i>CHMP2B</i>
<i>SRXN1</i>	<i>MIR4715</i>	<i>PANX2</i>	<i>MIOX</i>	<i>CGAS</i>	<i>BIRC3</i>	<i>CHMP3</i>
<i>GPX2</i>	<i>RIPK1</i>	<i>RHEBP1</i>	<i>TAZ</i>	<i>STING1</i>	<i>BNIP3</i>	<i>CHMP4A</i>
<i>BNIP3</i>	<i>PRDX1</i>	<i>TFAP2A</i>	<i>MTDH</i>	<i>HDCC3</i>	<i>BRAF</i>	<i>CHMP4B</i>
<i>OXSRI</i>	<i>MIR30B</i>	<i>CP</i>	<i>IDH1</i>	<i>MIR761</i>	<i>CASP8</i>	<i>CHMP4C</i>
<i>SELENOS</i>	<i>MMP13</i>	<i>ARF6</i>	<i>SIRT1</i>	<i>MDM2</i>	<i>CD40</i>	<i>CHMP6</i>
<i>ANGPTL7</i>	<i>LRRFIP1</i>	<i>ABHD12</i>	<i>FBXW7</i>	<i>MDM4</i>	<i>CDC37</i>	<i>CHMP7</i>
<i>CHAC1</i>	<i>AKR1C1</i>	<i>PPP1R13L</i>	<i>PANX1</i>	<i>DLD</i>	<i>CDKN2A</i>	<i>CYCS</i>
<i>SLC7A11</i>	<i>AKR1C2</i>	<i>TFAM</i>	<i>DNAJB6</i>	<i>WWTR1</i>	<i>CFLAR</i>	<i>ELANE</i>
<i>DDIT4</i>	<i>AKR1C3</i>	<i>KDM3B</i>	<i>BACH1</i>	<i>PRKCA</i>	<i>CXCL8</i>	<i>GSDMD</i>
<i>LOC284561</i>	<i>RB1</i>	<i>RNF113A</i>	<i>LONP1</i>	<i>EPAS1</i>	<i>CYLD</i>	<i>GSDME</i>
<i>ASNS</i>	<i>HSF1</i>	<i>AHCY</i>	<i>CD82</i>	<i>HILPDA</i>	<i>DDX58</i>	<i>GZMB</i>
<i>TSC22D3</i>	<i>GCLC</i>	<i>circ-TTBK2</i>	<i>IL1B</i>	<i>CircL4R</i>	<i>DIABLO</i>	<i>HMGB1</i>
<i>DDIT3</i>	<i>SQSTM1</i>	<i>MIR522</i>	<i>CTSB</i>	<i>CDH1</i>	<i>DNMT1</i>	<i>IL18</i>
<i>JDP2</i>	<i>NQO1</i>	<i>IDH2</i>	<i>POR</i>	<i>MIR214</i>	<i>EGFR</i>	<i>IL1A</i>
<i>SESN2</i>	<i>MUC1</i>	<i>PPARA</i>	<i>CYB5R1</i>	<i>HIC1</i>	<i>FADD</i>	<i>IL1B</i>
<i>SLC1A4</i>	<i>MT1G</i>	<i>SIAH2</i>	<i>ELOVL5</i>	<i>DRD5</i>	<i>FAS</i>	<i>IRF1</i>
<i>PCK2</i>	<i>CISD1</i>	<i>PRKAA2</i>	<i>FADS1</i>	<i>DRD4</i>	<i>FASLG</i>	<i>IRF2</i>
<i>TXNIP</i>	<i>FANCD2</i>	<i>VDR</i>	<i>FBW7</i>	<i>MAP3K5</i>	<i>FLT3</i>	<i>TP53</i>
<i>VLDLR</i>	<i>FTMT</i>	<i>NEDD4</i>	<i>PTEN</i>	<i>MAPK14</i>	<i>GATA3</i>	<i>TP63</i>
<i>GPT2</i>	<i>HSPA5</i>	<i>AR</i>	<i>NR1D1</i>	<i>SLC2A1</i>	<i>HAT1</i>	<i>AIM2</i>
<i>PSAT1</i>	<i>TP53</i>	<i>MTF1</i>	<i>NR1D2</i>	<i>SLC2A3</i>	<i>HDAC9</i>	<i>CASP6</i>
<i>LURAP1L</i>	<i>HELLS</i>	<i>CS</i>	<i>TBK1</i>	<i>SLC2A6</i>	<i>HMGB1</i>	<i>CASP8</i>
<i>SLC7A5</i>	<i>SCD</i>	<i>EMC2</i>	<i>USP7</i>	<i>SLC2A8</i>	<i>HSP90AA1</i>	<i>CASP9</i>
<i>HERPUD1</i>	<i>FADS2</i>	<i>NOX1</i>	<i>miR-182-5p</i>	<i>SLC2A12</i>	<i>HSPA4</i>	<i>GPX4</i>
<i>XBP1</i>	<i>SRC</i>	<i>CYBB</i>	<i>miR-378a-3p</i>	<i>GLUT13</i>	<i>ID1</i>	<i>GSDMA</i>
<i>ATF3</i>	<i>STAT3</i>	<i>NOX3</i>	<i>AQP3</i>	<i>SLC2A14</i>	<i>IDH1</i>	<i>GSDMB</i>
<i>SLC3A2</i>	<i>PML</i>	<i>NOX4</i>	<i>AQP5</i>	<i>EIF2AK4</i>	<i>IDH2</i>	<i>GSDMC</i>

Table S1 (continued)

Table S1 (continued)

Ferroptosis-gene				Necroptosis-gene		Pyroptosis-gene
CBS	MTOR	NOX5	AQP8	ALOX5	IPMK	IL6
ATF4	NFS1	DUOX1	LINC00618	ALOX12	ITPK1	NLRC4
ZNF419	TP63	DUOX2	MT1DP	ALOX15	KLF9	NLRP1
KLHL24	CDKN1A	G6PD	PEX10	ACSF2	LEF1	NLRP2
TRIB3	MIR137	PGD	PEX12	IREB2	MAP3K7	NLRP3
ZFP69B	ENPP2	FLT3	CHP1	HMGB1	MAPK8/JNK	NLRP6
ATP6V1G2	VDAC2	SCP2	GPAT4	ELAVL1	MLKL	NLRP7
VEGFA	FH	ACSL4	BRPF1	TFAP2C	MPG	NOD1
GDF15	CISD2	LPCAT3	OSBPL9	SP1	MYC	NOD2
TUBE1	MIR9-1	NRAS	INTS2	HBA1	MYCN	PJVK
ARRDC3	MIR9-2	KRAS	MMD	NNMT	NLRP3	PLCG1
CEBPG	MIR9-3	HRAS	CYP4F8	PIR	OTULIN	PRKACA
SNORA16A	ISCU	TFR2	MLLT1	HCAR1	PANX1	PYCARD
RGS4	ACSL3	SLC38A1	TTPA	SLC16A1	PLK1	SCAF11
BLOC1S5-TXNDC5	OTUB1	SLC1A5	GRIA3	NR4A1	RIPK1	TIRAP
LOC390705	CD44	GLS2	EPT1	PIK3CA	RIPK3	TNF
EIF2S1	LINC00336	GOT1	POM121L12	RPTOR	RNF31	GZMA
KIM-1	BRD4	CARS1	LIG3	SREBF1	SIRT1	
IL6	PRDX6	KEAP1	AEBP2	SREBF2	SIRT2	
CXCL2	MIR17	ATG5	AGPS	FZD7	SIRT3	
RELA	NF2	ATG7	CDCA3	P4HB	SLC39A7	
HSD17B11	ARNTL	NCOA4	PEX2	NT5DC2	SPATA2	
AGPAT3	HIF1A	ALOX12B	PEX6	BCAT2	SQSTM1	
SETD1B	JUN	ALOX15B	TIMM9	PLA2G6	STAT3	
HMOX1	CA9	ALOXE3	DCAF7	MIR424	STUB1	
TF	TMBIM4	PHKG2	LCE2C	PARK7	TARDBP	
FTL	PLIN2	ACO1	FAR1	FXN	TERT	
RPL8	MIR212	G6PDX	PHF21A	SUV39H1	TLR3	
ATP5MC3	Fer1HCH	ULK1	SMAD7	ATF2	TLR4	
TFRC	AIFM2	ATG3	LYRM1	ACOT1	TNF	
MAFG	LAMP2	ATG4D	AMN	ALDH3A2	TNFRSF1A	
IL33	ZFP36	BECN1	PEX3	STK11	TNFRSF1B	
FTH1	PROM2	MAP1LC3A	MTCH1	FNDC5	TNFRSF21	
SLC40A1	CHMP5	GABARAPL2	ACADSB	PLIN4	TNFSF10	
GPX4	CHMP6	GABARAPL1	PVT1	ATG13	TRAF2	

Table S1 (continued)

Table S1 (continued)

Ferroptosis-gene			Necroptosis-gene		Pyroptosis-gene
<i>HAMP</i>	<i>CAV1</i>	<i>ATG16L1</i>	<i>hsa_circ_0008367</i>	<i>ULK2</i>	<i>TRIM11</i>
<i>HSPB1</i>	<i>GCH1</i>	<i>WIPI1</i>	<i>SLC39A14</i>	<i>SAT1</i>	<i>TSC1</i>
<i>NFE2L2</i>	<i>SIRT3</i>	<i>WIPI2</i>	<i>MAP3K11</i>	<i>EGFR</i>	<i>USP22</i>
<i>STEAP3</i>	<i>DAZAP1</i>	<i>SNX4</i>	<i>GSK3B</i>	<i>MAPK3</i>	<i>ZBP1</i>
<i>ABCC1</i>	<i>MAPK9</i>	<i>SOCS1</i>	<i>DPP4</i>	<i>MAPK1</i>	
<i>MIR6852</i>	<i>LINC00472</i>	<i>CDO1</i>	<i>CDKN2A</i>	<i>BID</i>	
<i>ACVR1B</i>	<i>PRKAA1</i>	<i>MYB</i>	<i>PEBP1</i>	<i>ZEB1</i>	
<i>TGFBR1</i>	<i>BAP1</i>	<i>MAPK8</i>			

Table S2 39 DEFNPRlncRNAs associated with LUAD prognosis obtained by univariate COX analysis in the training set

DEFNPRlncRNA	HR	HR.95L	HR.95H	P value
AC097634.1	0.296376	0.094248	0.931993	0.037484
AL590729.1	0.291248	0.100106	0.847355	0.023577
AC092145.1	0.034597	0.001569	0.762938	0.033056
NFYC-AS1	0.47964	0.279161	0.824092	0.007801
AL031600.2	0.108891	0.015971	0.742409	0.023569
AC105429.1	0.177735	0.031802	0.993337	0.049117
MIR155HG	0.682905	0.472497	0.987011	0.042404
AC018529.1	0.242293	0.068714	0.854359	0.02747
AC006017.1	0.401667	0.202982	0.79483	0.008809
AC090559.1	0.684617	0.481068	0.974291	0.035323
AC109809.1	0.185872	0.042222	0.81826	0.026067
AC018682.1	0.199326	0.057332	0.692994	0.011187
AL109811.1	0.054517	0.005913	0.502668	0.010263
AC107021.2	2.647579	1.399005	5.010472	0.002775
AC068724.2	0.211498	0.055408	0.80731	0.023017
AC006033.2	0.341857	0.129464	0.902689	0.030264
DHDDS-AS1	0.435714	0.204082	0.930247	0.031809
AP005131.2	0.269848	0.101001	0.720959	0.008989
MIR223HG	0.503342	0.320803	0.789749	0.002817
AC091132.2	0.21853	0.061051	0.782221	0.019415
AC010999.2	0.187356	0.043307	0.810541	0.025023
AC025917.1	0.420113	0.217394	0.811869	0.00988
AP003170.3	0.571583	0.357632	0.913527	0.019387
AC027277.2	0.524044	0.278345	0.986625	0.04532

Table S2 (continued)

Table S2 (continued)

DEFNPRIncRNA	HR	HR.95L	HR.95H	P value
C1orf147	0.166485	0.033105	0.837257	0.029593
AC008764.8	0.312561	0.126694	0.771103	0.011598
LINC01281	0.279087	0.089226	0.872948	0.028271
EML4-AS1	0.476838	0.23088	0.984813	0.045358
AC025287.3	0.472404	0.244941	0.911099	0.025235
AL117379.1	0.650785	0.432726	0.978728	0.039091
AC012676.4	0.251232	0.072115	0.875234	0.030065
LINC01150	0.477776	0.266014	0.858112	0.013431
AC245060.5	0.429378	0.193997	0.950354	0.037017
AL513327.2	0.401946	0.184328	0.876482	0.021939
AC084876.1	0.260184	0.090495	0.748058	0.012466
AL662844.3	0.522568	0.277015	0.985785	0.045051
AP000692.1	0.501546	0.260109	0.967089	0.039412
AC013731.1	0.481349	0.23431	0.988846	0.046536
VIPR1-AS1	0.199942	0.051756	0.772406	0.019571

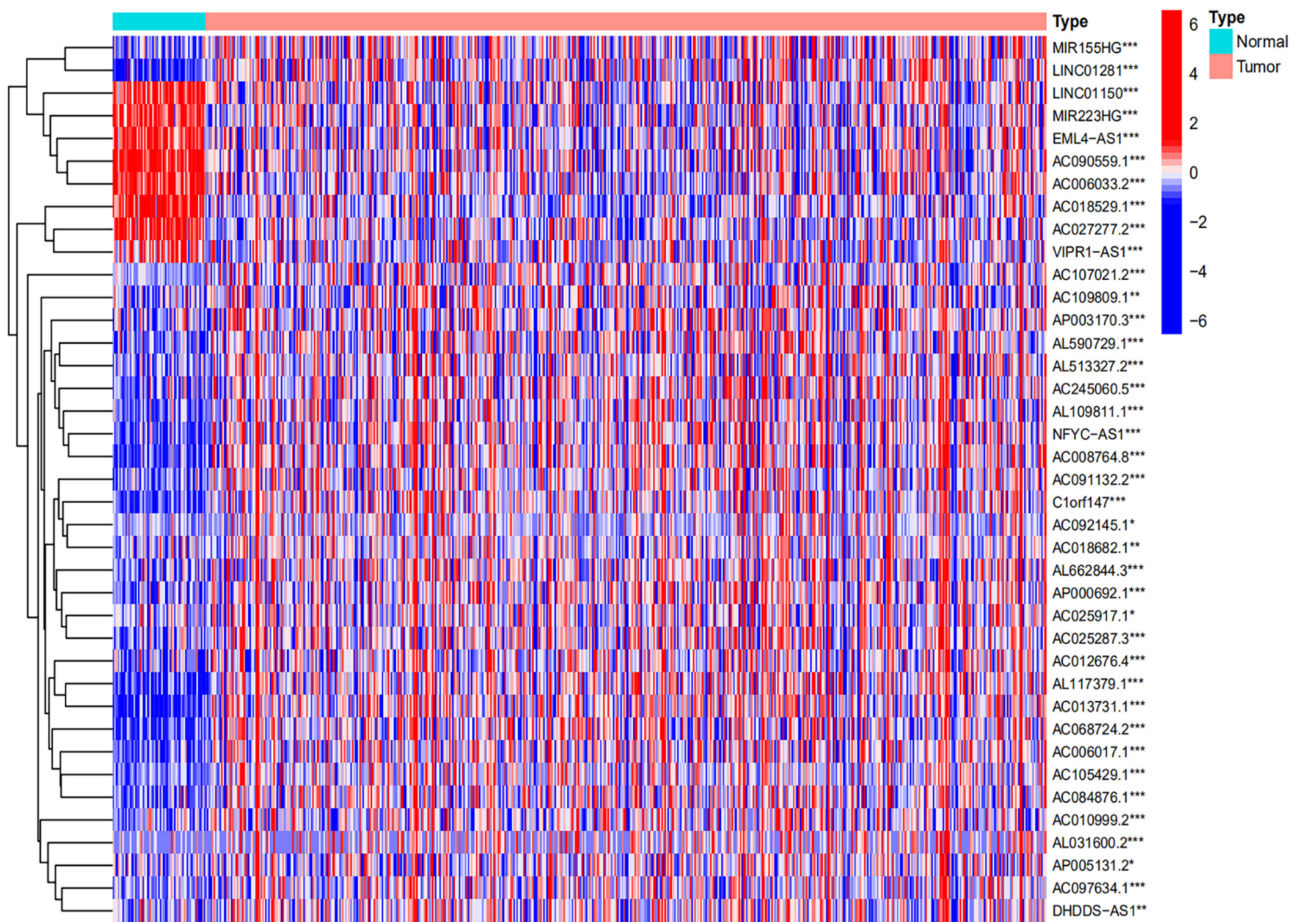


Figure S1 Differential expression of these 39 lncRNAs between LUAD and normal tissues in TCGA samples. P values are shown as *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$. lncRNAs, long non-coding RNAs; LUAD, lung adenocarcinoma; TCGA, The Cancer Genome Atlas.

Table S3 Enriched pathways of differentially expressed ferroptosis, necroptosis, and pyroptosis-related lncRNAs (DEFNPRlncRNAs) in gene set enriched analysis (GSEA)

ID	Set Size	Enrichment Score	NES	P value	p adjust
KEGG_RIBOSOME	85	0.677049994	2.558504478	1.00E-10	9.05E-09
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	108	-0.710980228	-1.940372173	1.00E-10	9.05E-09
KEGG_CELL_CYCLE	121	0.559875559	2.154064866	2.91E-09	1.75E-07
KEGG_DNA_REPLICATION	35	0.641143892	2.140640245	6.20E-05	0.002804636
KEGG_ASTHMA	20	-0.803197454	-1.830787777	8.16E-05	0.002952227
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	0.588704243	2.018529945	0.000136213	0.004109084
KEGG_CITRATE_CYCLE_TCA_CYCLE	29	0.67867263	2.177369713	0.000217309	0.005619
KEGG_PYRIMIDINE_METABOLISM	89	0.457786397	1.752069557	0.000264636	0.005987391
KEGG_SPLICEOSOME	125	0.409563054	1.566276565	0.00036966	0.007394432
KEGG_PRIMARY_IMMUNODEFICIENCY	29	-0.732827137	-1.753412404	0.000408532	0.007394432
KEGG_INTESTINAL_IMMUNE_NETWORK_FOR_IGA_PRODUCTION	36	-0.690646242	-1.702073234	0.000722683	0.011891416
KEGG_ALLOGRAFT_REJECTION	30	-0.711852723	-1.713228272	0.001016874	0.014210596
KEGG_OOCYTE_MEIOSIS	94	0.424173544	1.627900154	0.001020651	0.014210596
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	193	-0.497543103	-1.388818348	0.002841718	0.034029241
KEGG_ALZHEIMERS_DISEASE	147	0.341875523	1.366955603	0.002960375	0.034029241
KEGG_VIRAL_MYOCARDITIS	58	-0.606481286	-1.578814224	0.003284403	0.034029241
KEGG_PROTEIN_EXPORT	24	0.615399897	1.897058724	0.003411975	0.034029241
KEGG_GLYCOLYSIS_GLUCCONEOGENESIS	47	0.478586351	1.687567289	0.003680804	0.034029241
KEGG_MISMATCH_REPAIR	22	0.632328294	1.896171814	0.003692683	0.034029241
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	99	-0.546019223	-1.47874917	0.003843622	0.034029241
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	59	0.44309512	1.654682605	0.004057957	0.034029241
KEGG_RNA_POLYMERASE	25	0.585514379	1.808411381	0.004136151	0.034029241
KEGG_PPAR_SIGNALING_PATHWAY	55	0.448860752	1.646820579	0.005289291	0.041624424
KEGG_ECM_RECEPTOR_INTERACTION	71	0.41407957	1.543053061	0.008267676	0.058901251
KEGG_PENTOSE_PHOSPHATE_PATHWAY	23	0.584395533	1.772135306	0.008370941	0.058901251
KEGG_HEMATOPOIETIC_CELL_LINEAGE	71	-0.571172228	-1.511124688	0.008460953	0.058901251
KEGG_CHEMOKINE_SIGNALING_PATHWAY	164	-0.488582964	-1.358997298	0.010019056	0.067164784
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	26	0.552550408	1.696486906	0.010776746	0.068703656
KEGG_P53_SIGNALING_PATHWAY	65	0.416548859	1.536827287	0.011143915	0.068703656
KEGG_HISTIDINE_METABOLISM	25	0.536139069	1.655911499	0.011387346	0.068703656
KEGG_ALANINE_ASPARTATE_AND_Glutamate_METABOLISM	26	0.537372693	1.649887004	0.014252989	0.083219064

Table S3 (continued)

Table S3 (continued)

ID	Set Size	Enrichment Score	NES	P value	p adjust
KEGG_PHENYLALANINE_METABOLISM	17	0.591573754	1.648799193	0.01786944	0.097530211
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	58	0.407681044	1.518451847	0.018093584	0.097530211
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	12	0.694483253	1.834497263	0.018320592	0.097530211
KEGG_PENTOSE_AND_GLUCURONATE_INTERCONVERSIONS	14	0.63069687	1.736192036	0.01939764	0.10031351
KEGG_ARGININE_AND_PROLINE_METABOLISM	48	0.427683217	1.514219157	0.023241572	0.116853459
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	72	-0.532316586	-1.409059675	0.025850661	0.126458637
KEGG_LEISHMANIA_INFECTION	67	-0.528980578	-1.396374238	0.026567481	0.126545109
KEGG_AUTOIMMUNE_THYROID_DISEASE	30	-0.616239394	-1.483114018	0.031233858	0.144957138
KEGG_HUNTINGTONS_DISEASE	163	0.280222792	1.10915853	0.03296712	0.146783239
KEGG_BASE_EXCISION_REPAIR	34	0.446751238	1.481943392	0.033762234	0.146783239
KEGG_STARCH_AND_SUCROSE_METABOLISM	26	0.499610957	1.533947734	0.034060199	0.146783239
KEGG_FOLATE_BIOSYNTHESIS	10	0.663879399	1.636170894	0.035020611	0.147412338
KEGG_STEROID_HORMONE_BIOSYNTHESIS	29	0.468512046	1.503116366	0.038622509	0.158878958
KEGG_PARKINSONS_DISEASE	119	0.322653761	1.256049595	0.041881111	0.168455137
KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	14	0.575479075	1.584187643	0.044692133	0.175853827
KEGG_PURINE_METABOLISM	135	0.303960534	1.197877609	0.049660037	0.191243972

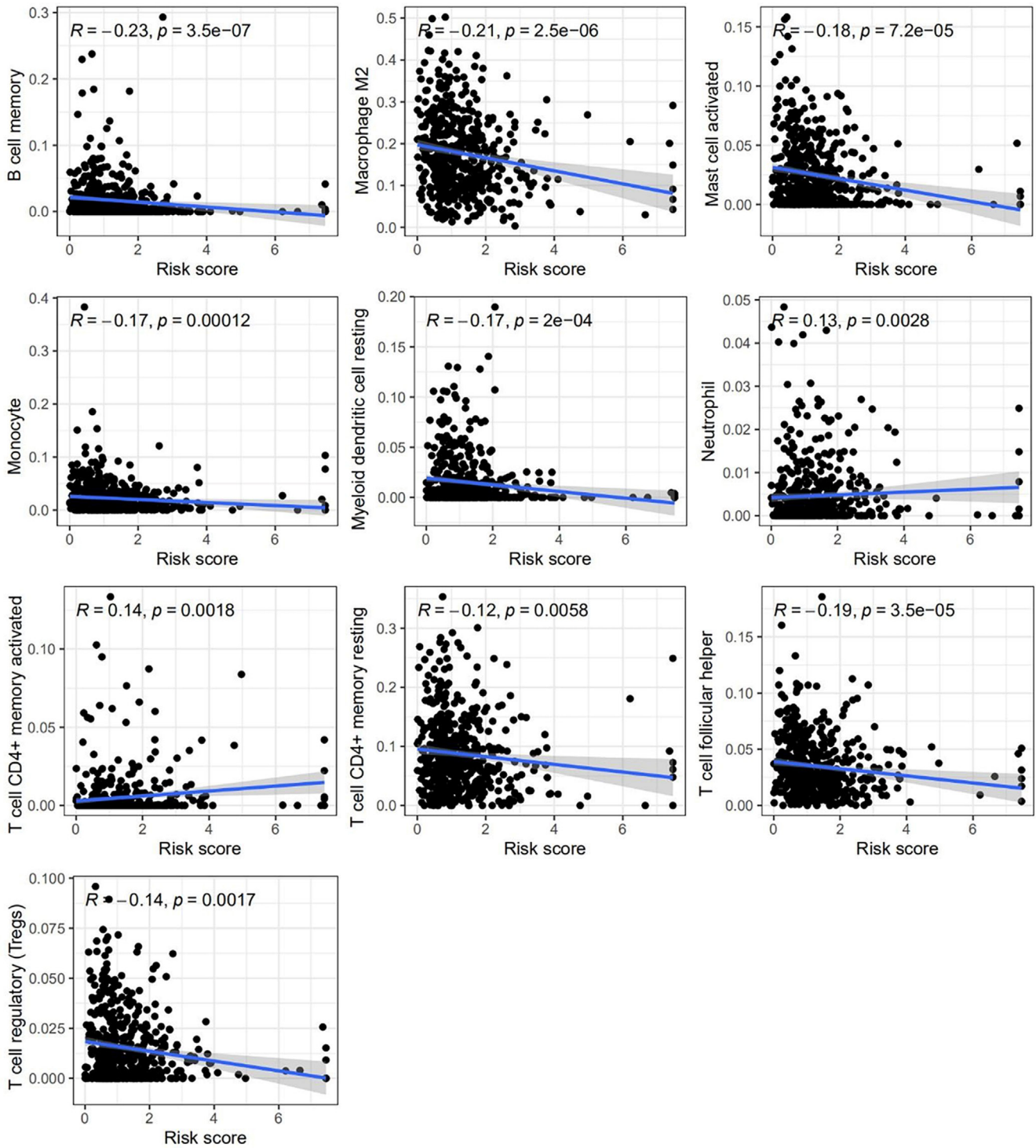


Figure S2 Immune-infiltrating cells significantly associated with risk score calculated by CIBERSORT-ABS ($P < 0.05$).

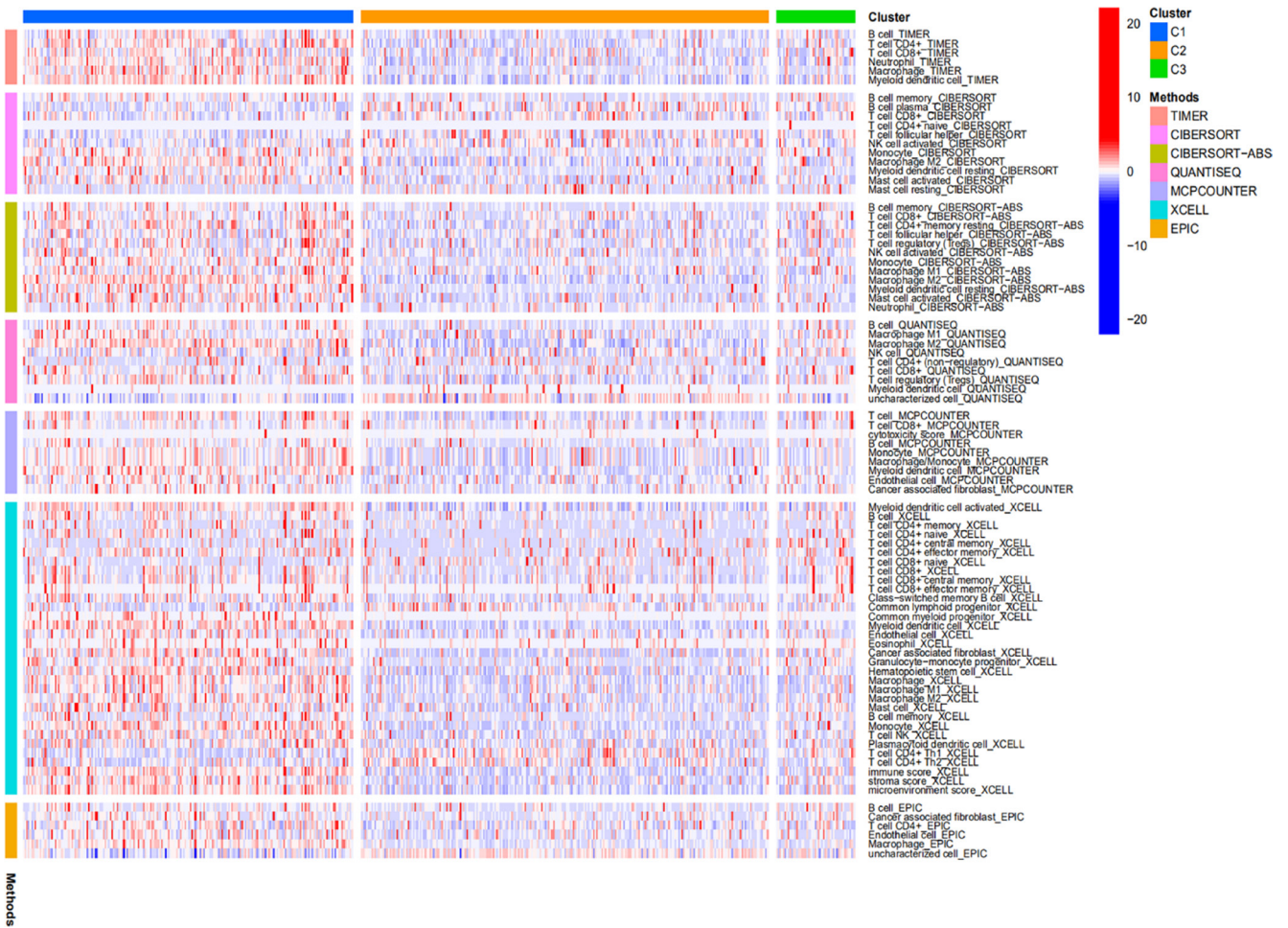


Figure S3 Heatmap for immune cell infiltration landscape based on the CIBERSORT, CIBERSORT-ABS, QUANTISEQ, XCELL, MCPCOUNTER, EPIC, and TIMER algorithms among LUAD clusters (C1, C2, and C3). LUAD, lung adenocarcinoma.