

Table S1 The primers sequences for mRNAs of the telomere-related signature

Genes	Forward primer sequence	Reverse primer sequence
<i>TPX2</i>	GCAAGAGCTGGAGAAGAGTATG	TCTTCACAGGTTGCCCTATTC
<i>ACACB</i>	GGCTGAGGTCAAGATCAACA	AGGCTGATGTCCAGGTAGTA
<i>CD36</i>	GGCTGTGTTTGGAGGTATTCTA	TTGTACCTTCTTCGAGGACAAC
<i>SRPX</i>	ACAGTGTGGCCTTGATCTTC	GGGCTGGAGGCATAATCTTT
<i>MMP1</i>	CTCTGACATTCACCAAGGTCTC	GATTTCTCCAGGTCCATCAAA
<i>MMP3</i>	CTCGTTGCTGCTCATGAAATTG	TCAGGTCTGTGAGTGAGTGATA
<i>MMP10</i>	GGCCCTCTCTCCATCATATTT	CCTGCTTGACCTCATTTCCT
<i>NAT2</i>	GACCATTGACGGCAGGAATTA	GGCTGATCCTTCCCAGAAATTA
<i>HIGD1A</i>	ATTCGTACCCGTTGGAATAGC	CCAACAGTCATTGCTCCTACA
<i>PPARGC1A</i>	TGAACTGAGGGACAGTGATTC	CCCAAGGGTAGCTCAGTTTATC

Table S2 GSEA enrichment analysis results of TCGA-COADREAD dataset

ID	Enrichment Score	NES	p.adjust	q.value
REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_PHOSPHORYLATION	-0.53684	-1.8185	0.024931	0.019299
REACTOME_EXTENSION_OF_TELOMERES	-0.57764	-1.77255	0.024931	0.019299
BIOCARTA_IL17_PATHWAY	-0.73969	-1.76086	0.024931	0.019299
PID_IL23_PATHWAY	-0.59675	-1.7429	0.04771	0.036933
REACTOME_PROGRAMMED_CELL_DEATH	-0.43533	-1.66258	0.024931	0.019299
WP_CYTOKINES_AND_INFLAMMATORY_RESPONSE	-0.74339	-2.01703	0.024931	0.019299

GSEA, gene set enrichment analysis; TCGA, The Cancer Genome Atlas; COADREAD, colorectal adenocarcinoma; NES, normalized enrichment score.

Table S3 mRNA-miRNA interaction network nodes

miRNA	mRNA	miRNA	mRNA	miRNA	mRNA
hsa-miR-141-3p	CD36	hsa-miR-107	MMP3	hsa-miR-19a-3p	SRPX
hsa-miR-141-3p	CD36	hsa-miR-182-5p	MMP3	hsa-miR-19b-3p	SRPX
hsa-miR-200a-3p	CD36	hsa-miR-15a-5p	PPARGC1A	hsa-miR-103a-3p	SRPX
hsa-miR-200a-3p	CD36	hsa-miR-15a-5p	PPARGC1A	hsa-miR-107	SRPX
hsa-miR-135b-5p	CD36	hsa-miR-15a-5p	PPARGC1A	hsa-miR-15b-5p	SRPX
hsa-miR-382-5p	HIGD1A	hsa-miR-16-5p	PPARGC1A	hsa-miR-15b-5p	SRPX
hsa-miR-382-5p	HIGD1A	hsa-miR-16-5p	PPARGC1A	hsa-miR-141-3p	SRPX
hsa-miR-576-5p	HIGD1A	hsa-miR-146a-5p	PPARGC1A	hsa-miR-186-5p	SRPX
hsa-miR-576-5p	HIGD1A	hsa-miR-424-5p	PPARGC1A	hsa-miR-186-5p	SRPX
hsa-miR-455-3p	HIGD1A	hsa-miR-424-5p	PPARGC1A	hsa-miR-200a-3p	SRPX
hsa-let-7c-5p	MMP1	hsa-miR-146b-5p	PPARGC1A	hsa-miR-130b-3p	SRPX
hsa-let-7f-5p	MMP1	hsa-miR-3613-5p	PPARGC1A	hsa-miR-576-5p	SRPX
hsa-miR-181c-5p	MMP1	hsa-miR-3613-5p	PPARGC1A	hsa-miR-454-3p	SRPX
hsa-let-7g-5p	MMP1	hsa-miR-3613-5p	PPARGC1A	hsa-miR-301b-3p	SRPX
hsa-miR-361-5p	MMP1	hsa-miR-3613-5p	PPARGC1A	hsa-miR-29a-3p	TPX2
hsa-miR-361-5p	MMP1	hsa-miR-15a-5p	SRPX	hsa-miR-29b-3p	TPX2
hsa-miR-181d-5p	MMP1	hsa-miR-15a-5p	SRPX	hsa-miR-181c-5p	TPX2
hsa-miR-488-3p	MMP1	hsa-miR-16-5p	SRPX	hsa-miR-29c-3p	TPX2
hsa-miR-103a-3p	MMP3	hsa-miR-16-5p	SRPX	hsa-miR-628-5p	TPX2

Table S4 mRNA-TF interaction network nodes

mRNA	TF	mRNA	TF	mRNA	TF
ACACB	ELF1	HIGD1A	ETS1	TPX2	CEBPB
ACACB	EP300	HIGD1A	FLI1	TPX2	CREB1
ACACB	ESR1	HIGD1A	FOXA1	TPX2	CTCF
ACACB	FLI1	HIGD1A	FOXA2	TPX2	E2F1
ACACB	FOXA1	HIGD1A	FOXP1	TPX2	ELF1
ACACB	FOXA2	HIGD1A	GABPA	TPX2	ELK1
ACACB	GABPA	HIGD1A	GATA1	TPX2	ELK4
ACACB	GATA3	HIGD1A	GATA4	TPX2	ERG
ACACB	HNF4G	HIGD1A	GRHL2	TPX2	ETS1
ACACB	MAX	MMP1	FOSL1	TPX2	ETV1
ACACB	MED1	MMP10	JUN	TPX2	GABPA
ACACB	mxi1	MMP10	FOSL1	TPX2	GTF2B
ACACB	RUNX1T1	PPARGC1A	AR	TPX2	HDAC1
ACACB	SPI1	PPARGC1A	CREB1	TPX2	MYBL2
ACACB	TFAP4	PPARGC1A	EP300	TPX2	NFYA
ACACB	YY1	PPARGC1A	FOXA1	TPX2	NFYB
ACACB	CEBPA	PPARGC1A	GATA4	TPX2	NOTCH1
HIGD1A	HDAC1	PPARGC1A	MITF	TPX2	POLR2A
HIGD1A	KLF5	PPARGC1A	MYOD1	TPX2	PPARG
HIGD1A	MAX	PPARGC1A	USF1	TPX2	RAD21
HIGD1A	MAZ	PPARGC1A	USF2	TPX2	SMC3
HIGD1A	NFIC	SRPX	MAX	TPX2	SP1
HIGD1A	NR2F2	TPX2	BRD2	TPX2	SPI1
HIGD1A	BRD4	TPX2	BRD4	TPX2	STAG1
HIGD1A	E2F1	TPX2	CDK9	TPX2	TBP
HIGD1A	ESR1	TPX2	CEBPA	TPX2	ZBTB7A

TF, transcription factor.

Table S5 mRNA-RBP interaction network nodes

mRNA	RBP	mRNA	RBP	mRNA	RBP
ACACB	ALYREF	PPARGC1A	U2AF1	TPX2	HNR NPC
ACACB	CSTF2T	PPARGC1A	U2AF2	TPX2	IGF2BP1
ACACB	ELAVL1	PPARGC1A	UPF1	TPX2	IGF2BP2
ACACB	HNR NPC	SRPX	HDLBP	TPX2	IGF2BP3
ACACB	PRPF8	SRPX	SRSF7	TPX2	ILF3
ACACB	RBM10	TPX2	ALYREF	TPX2	LIN28B
ACACB	RBMX	TPX2	AQR	TPX2	MTDH
ACACB	RNPS1	TPX2	BCLAF1	TPX2	NUDT21
ACACB	SCAF4	TPX2	CPSF6	TPX2	PRPF8
ACACB	SCAF8	TPX2	CPSF7	TPX2	RBFOX2
ACACB	TARDBP	TPX2	CSTF2	TPX2	RBM10
ACACB	U2AF1	TPX2	CSTF2T	TPX2	RBM15
ACACB	U2AF2	TPX2	CTCF	TPX2	RBM20
CD36	CSTF2	TPX2	DDX3X	TPX2	RBMX
CD36	CSTF2T	TPX2	DDX54	TPX2	RNPS1
CD36	ELAVL1	TPX2	EIF4A3	TPX2	SCAF4
HIGD1A	CSTF2T	TPX2	ELAVL1	TPX2	SCAF8
HIGD1A	ELAVL1	TPX2	EWSR1	TPX2	SRSF1
HIGD1A	HNRNPC	TPX2	FIP1L1	TPX2	SRSF7
HIGD1A	RBMX	TPX2	FMR1	TPX2	TARDBP
PPARGC1A	CSTF2	TPX2	FXR1	TPX2	TRA2A
PPARGC1A	CSTF2T	TPX2	FXR2	TPX2	U2AF1
PPARGC1A	ELAVL1	TPX2	G3BP1	TPX2	U2AF2
PPARGC1A	EWSR1	TPX2	GRWD1	TPX2	WDR4
PPARGC1A	HNRNPC	TPX2	HDLBP	TPX2	YBX1
PPARGC1A	HNRNPL	TPX2	HNRNPA2B1	TPX2	YTHDC1

RBP, RNA-binding protein.

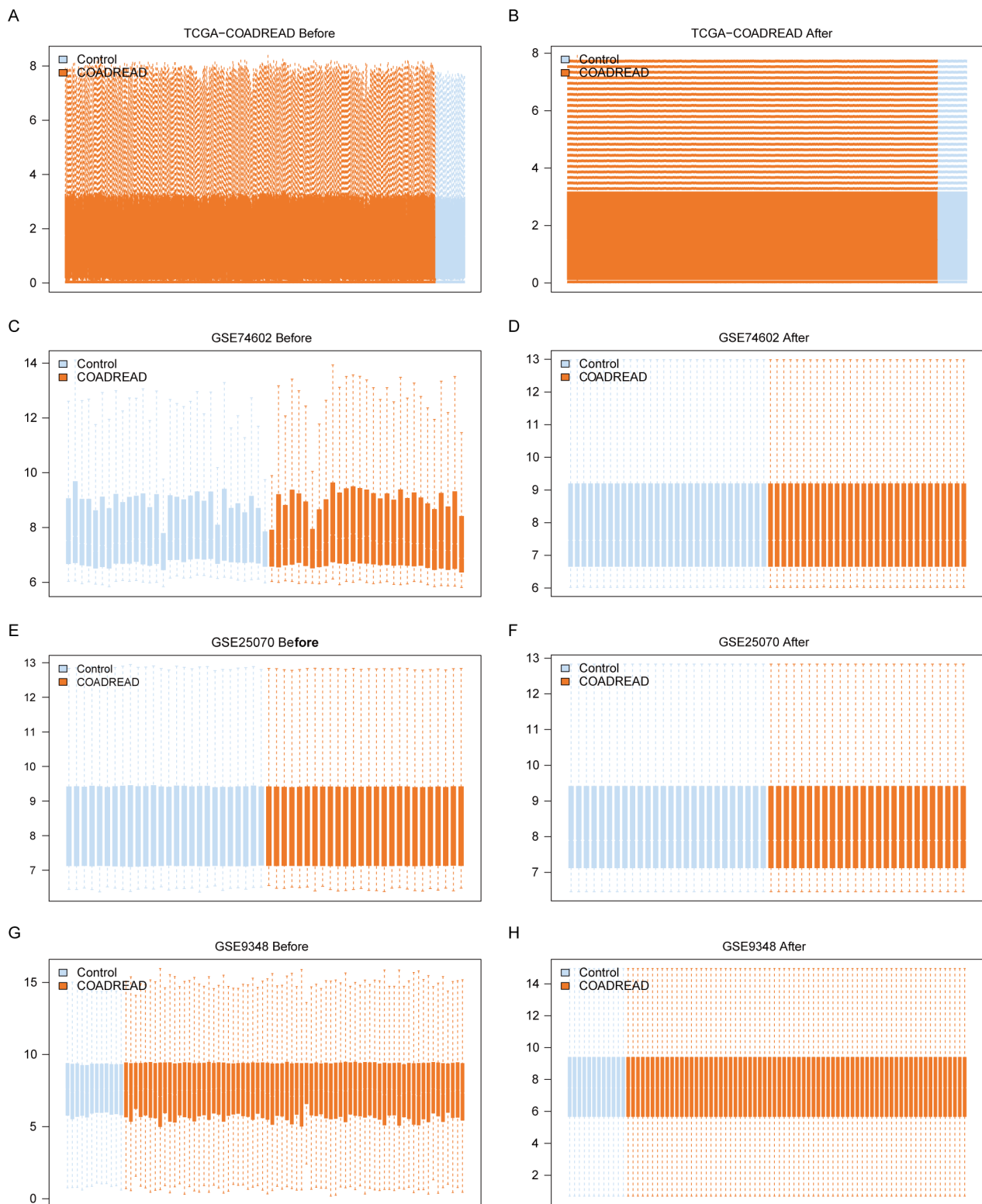
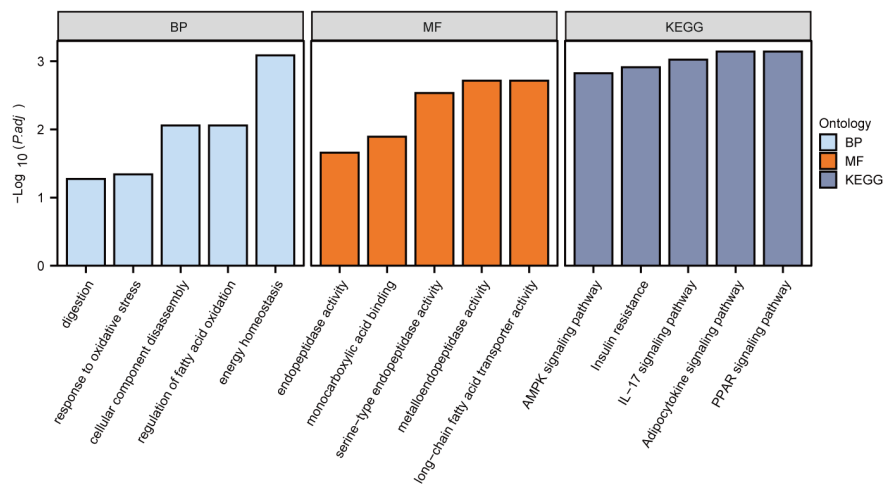
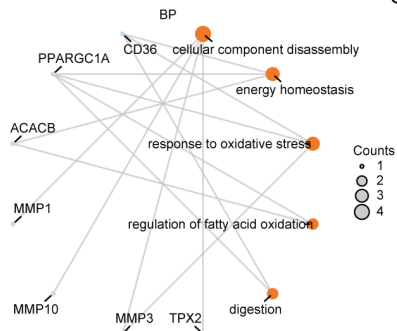


Figure S1 Datasets standardization processing. Boxplots of TCGA-COADREAD before (A) and after (B) processing. Boxplots of GSE74602 before (C) and after (D) processing. Boxplots of GSE25070 before (E) and after (F) processing. Boxplots of GSE9348 before (G) and after (H) processing. TCGA, The Cancer Genome Atlas; COADREAD, colorectal adenocarcinoma.

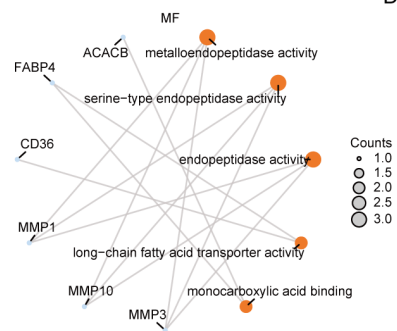
A



B



C



D

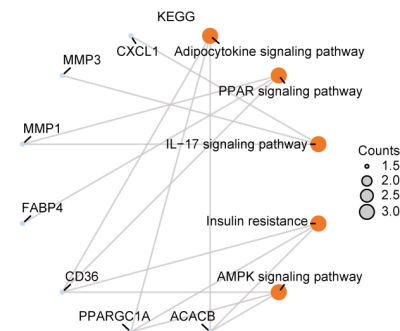


Figure S2 Functional enrichment analysis of TRDEGs. (A) GO and KEGG enrichment analysis. Circular network diagram of BP (B), MF (C) and KEGG (D). TRDEGs, telomere-related differentially expressed genes; GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; BP, biological process; MF, molecular function.

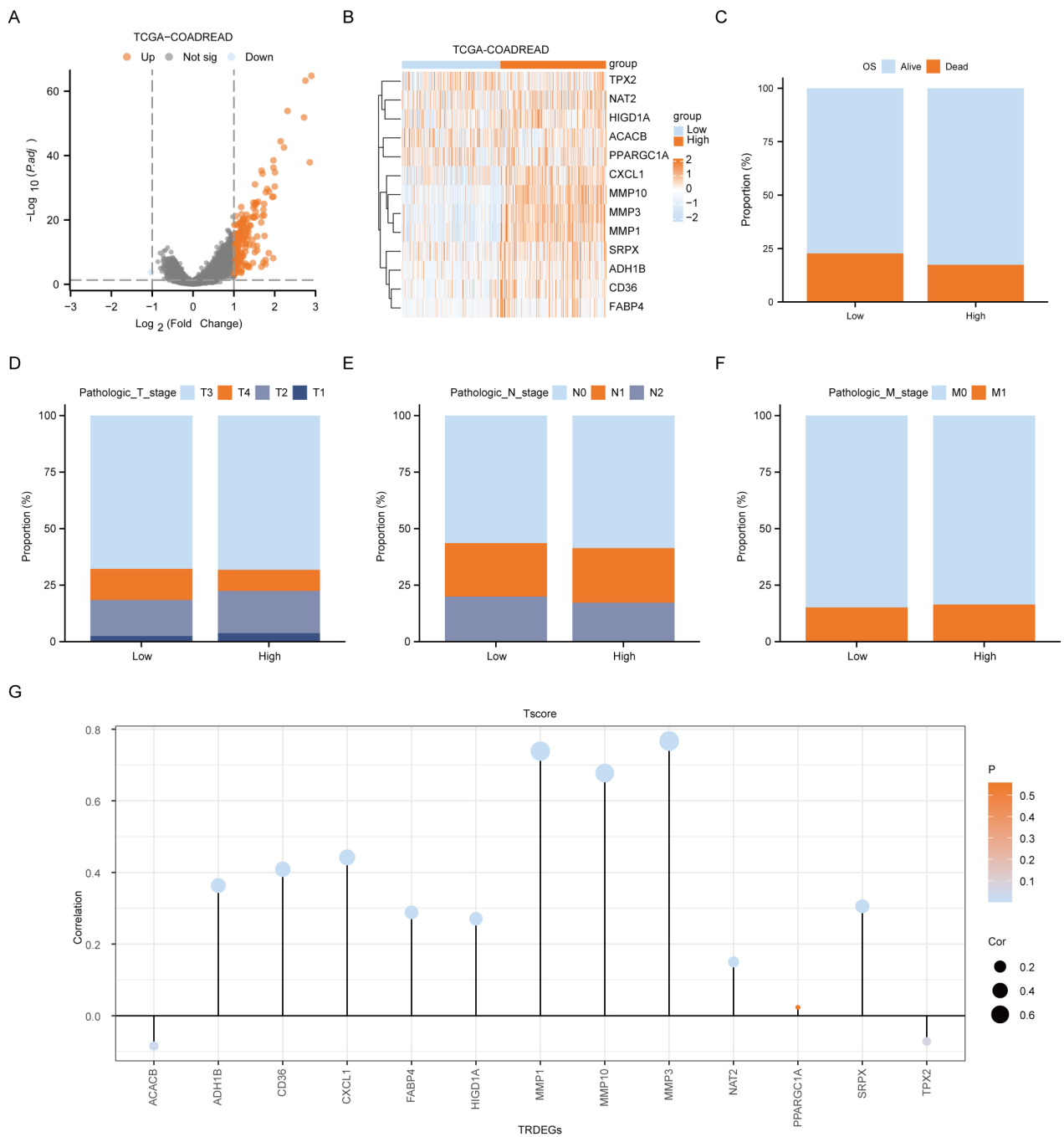


Figure S3 Tscore construction and clinical correlation analysis. (A) The volcano map of the high- and low-scoring groups in the TCGA-COADREAD dataset. (B) Heatmap of expression of TRDEGs between high- and low-scoring groups. The stacked histograms of (C) OS, (D) T stage, (E) N stage and (F) M stage between high- and low-scoring groups. (G) Correlation lollipop graph of Tscore and TRDEGs. TCGA, The Cancer Genome Atlas; COADREAD, colorectal adenocarcinoma; TRDEGs, telomere-related differentially expressed genes; OS, overall survival.

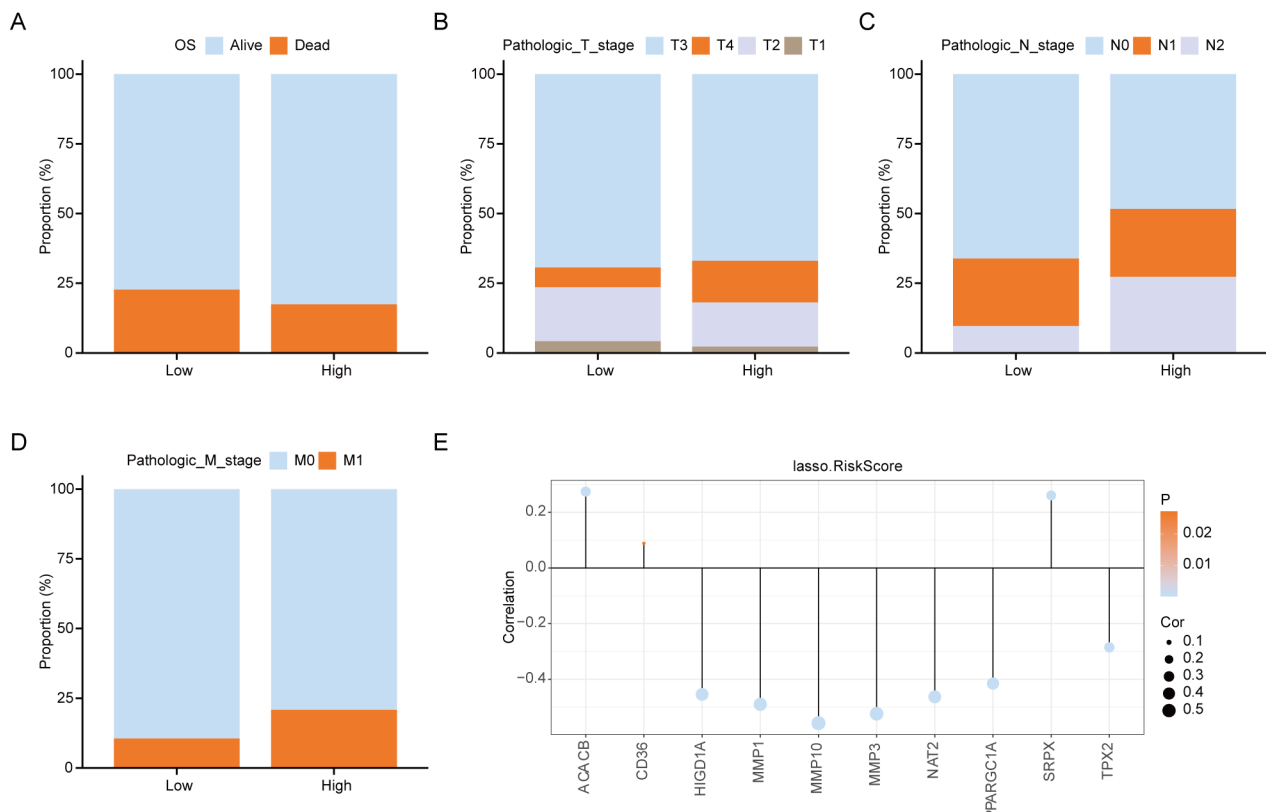


Figure S4 Clinical correlation analysis between high- and low-risk groups. The stacked histograms of (A) OS, (B) T stage, (C) N stage and (D) M stage between high- and low-risk groups. (E) Correlation lollipop graph of riskscore and TRDEGs. OS, overall survival; TRDEGs, telomere-related differentially expressed genes; LASSO, least absolute shrinkage and selection operator.

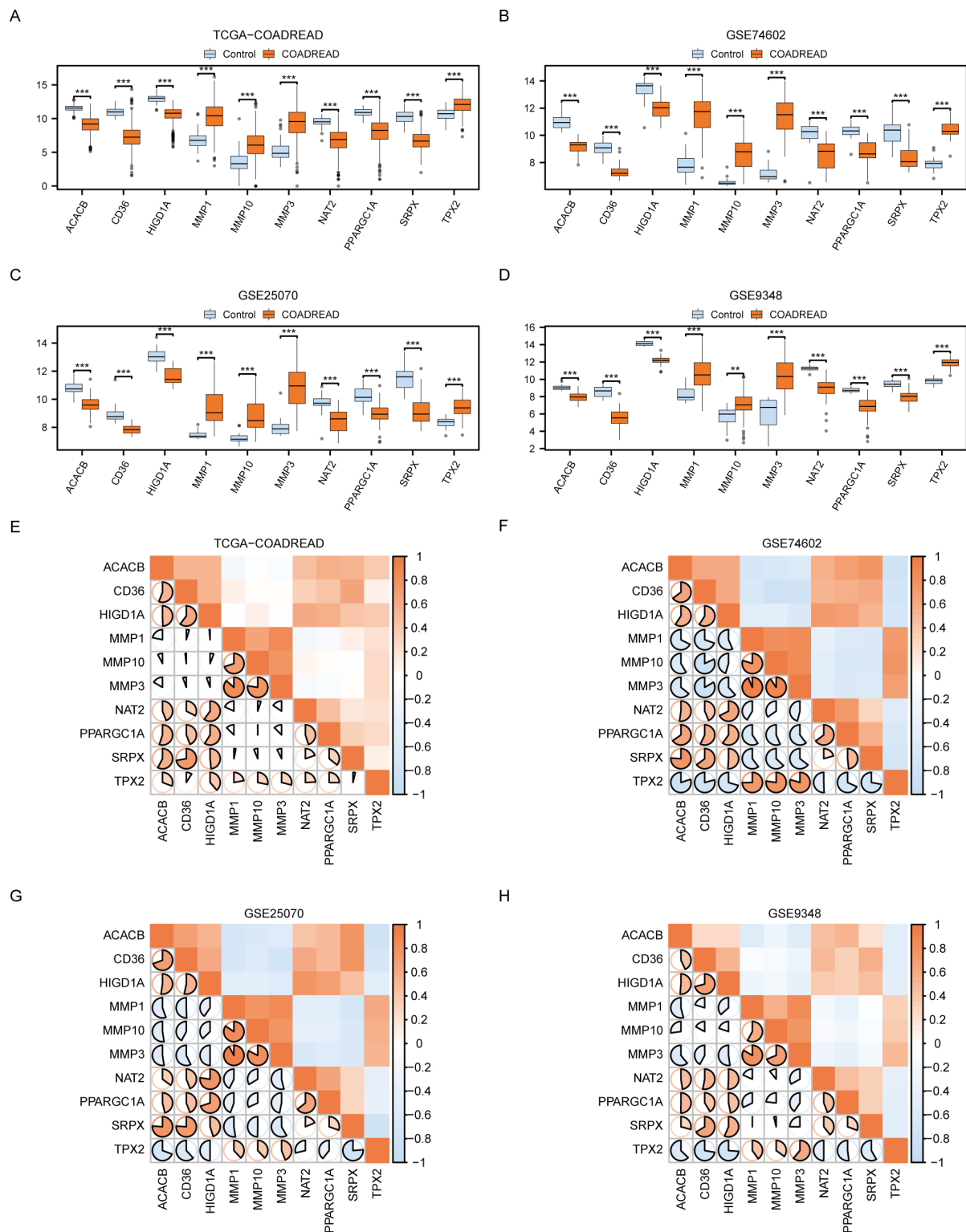


Figure S5 Differential and correlation analysis of prognostic TRDEGs. Grouping comparison chart of prognostic TRDEGs in (A) TCGA-COADREAD, (B) GSE74602, (C) GSE25070, (D) GSE9348. Correlation display of prognostic TRDEGs in (E) TCGA-COADREAD, (F) GSE74602, (G) GSE25070, (H) GSE9348. **, $P < 0.01$; ***, $P < 0.001$. TRDEGs, telomere-related differentially expressed genes; TCGA, The Cancer Genome Atlas; COADREAD, colorectal adenocarcinoma.

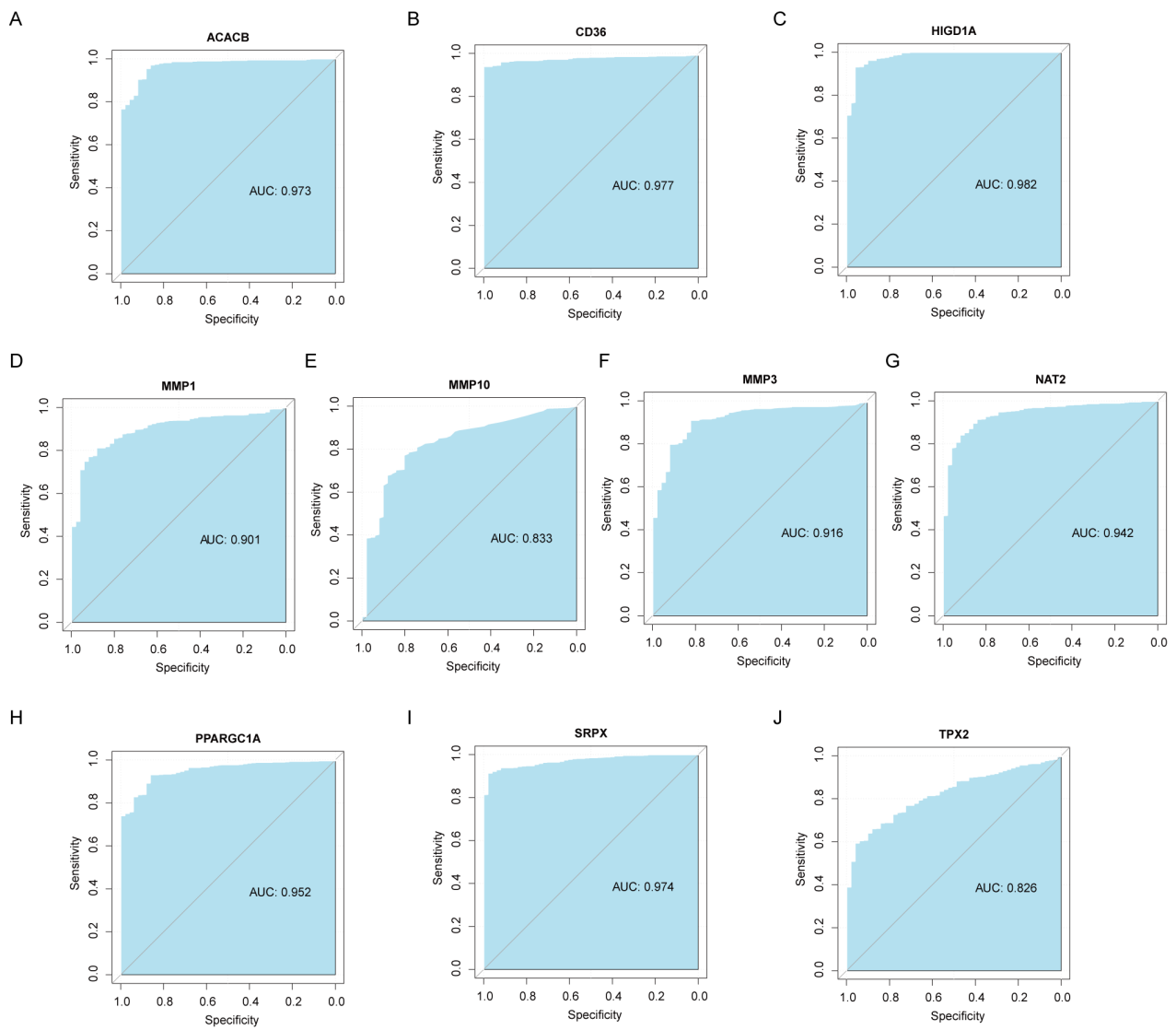


Figure S6 ROC curve analysis of prognostic TRDEGs. ROC curves of (A) ACACB, (B) CD36, (C) HIGD1A, (D) MMP1, (E) MMP10, (F) MMP3, (G) NAT2, (H) PPARGC1A, (I) SRPX, (J) TPX2 in the TCGA-COADREAD dataset. ROC, receiver operating characteristic curve; AUC, area under the curve; TRDEGs, telomere-related differentially expressed genes; TCGA, The Cancer Genome Atlas; COADREAD, colorectal adenocarcinoma.

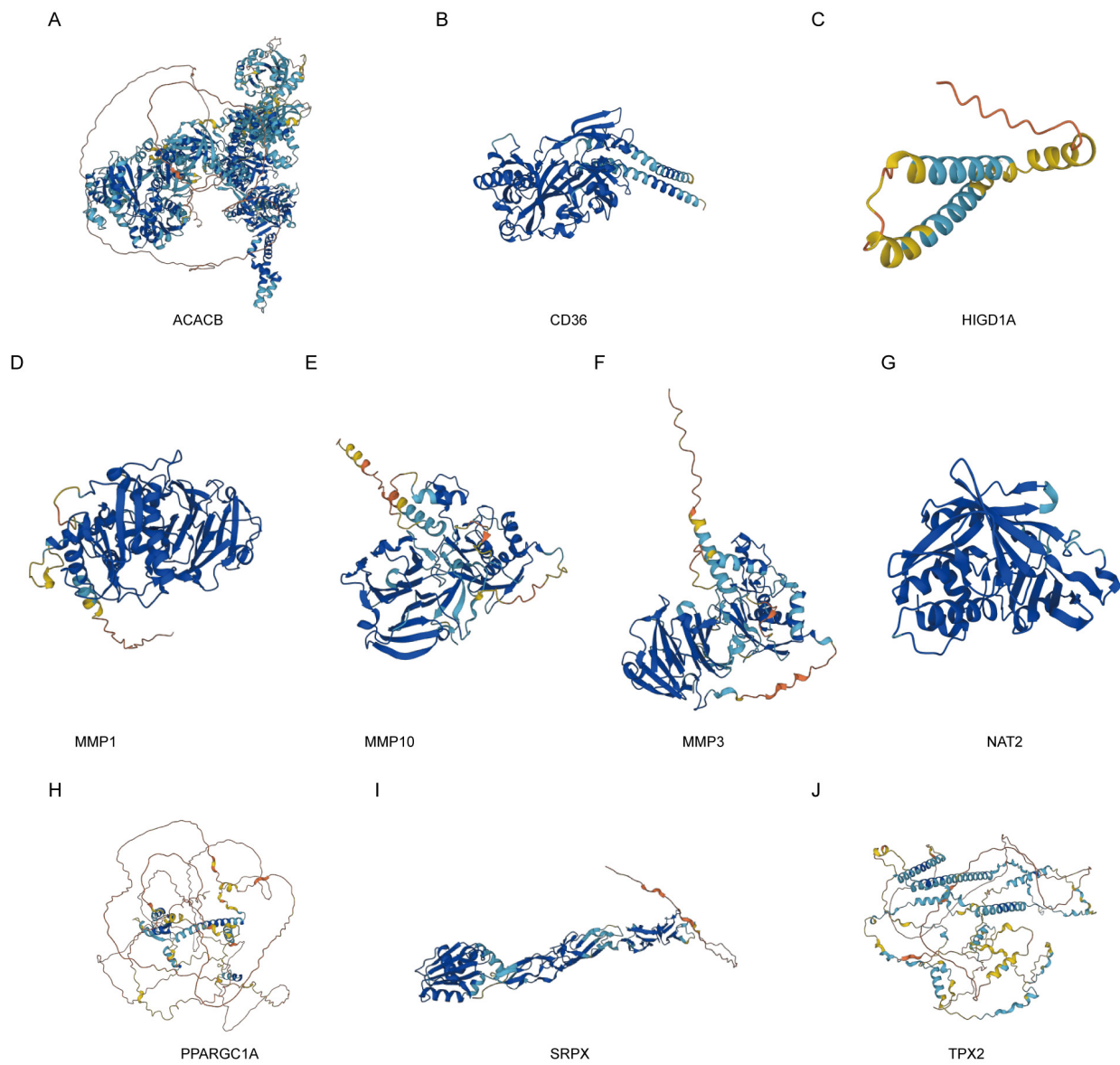


Figure S7 Protein structures of prognostic TRDEGs. Protein structure display of (A) ACACB, (B) CD36, (C) HIGD1A, (D) MMP1, (E) MMP10, (F) MMP3, (G) NAT2, (H) PPARGC1A, (I) SRPX, (J) TPX2. TRDEGs, telomere-related differentially expressed genes.