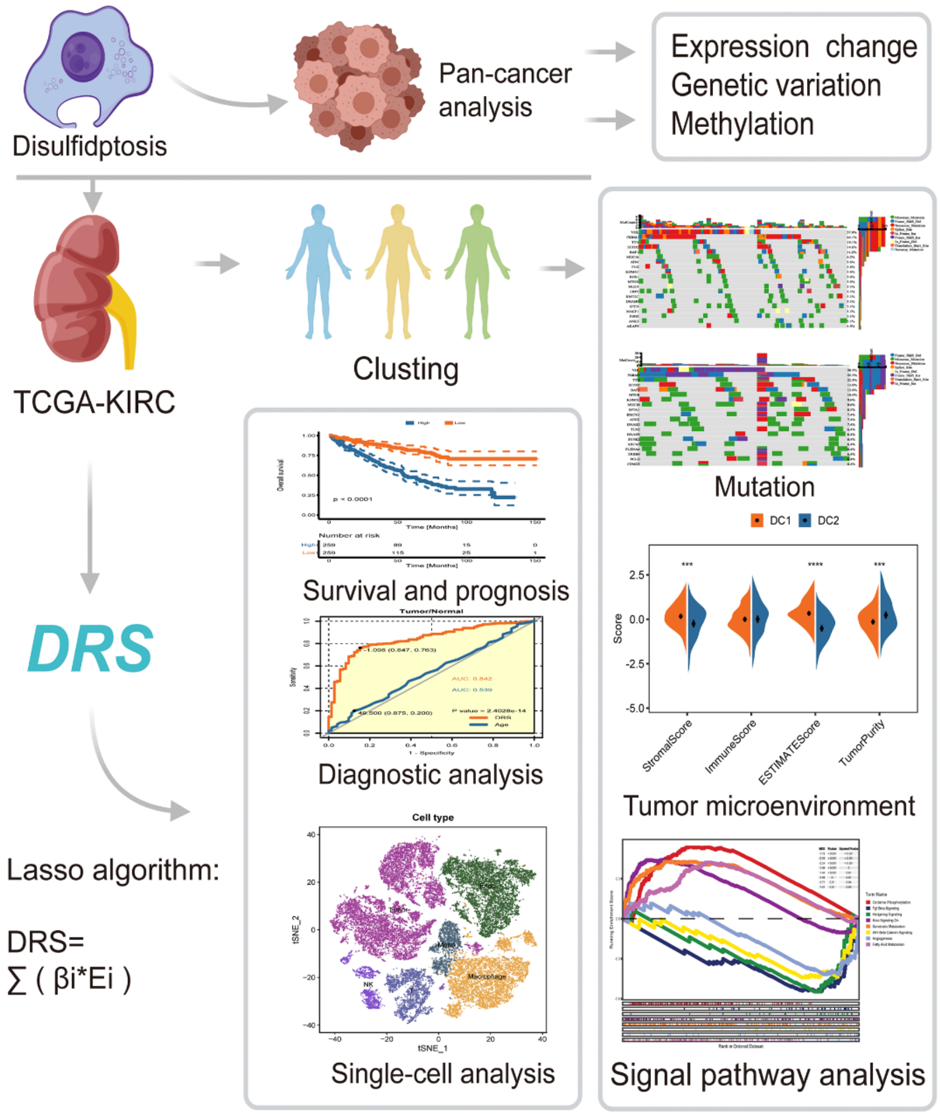
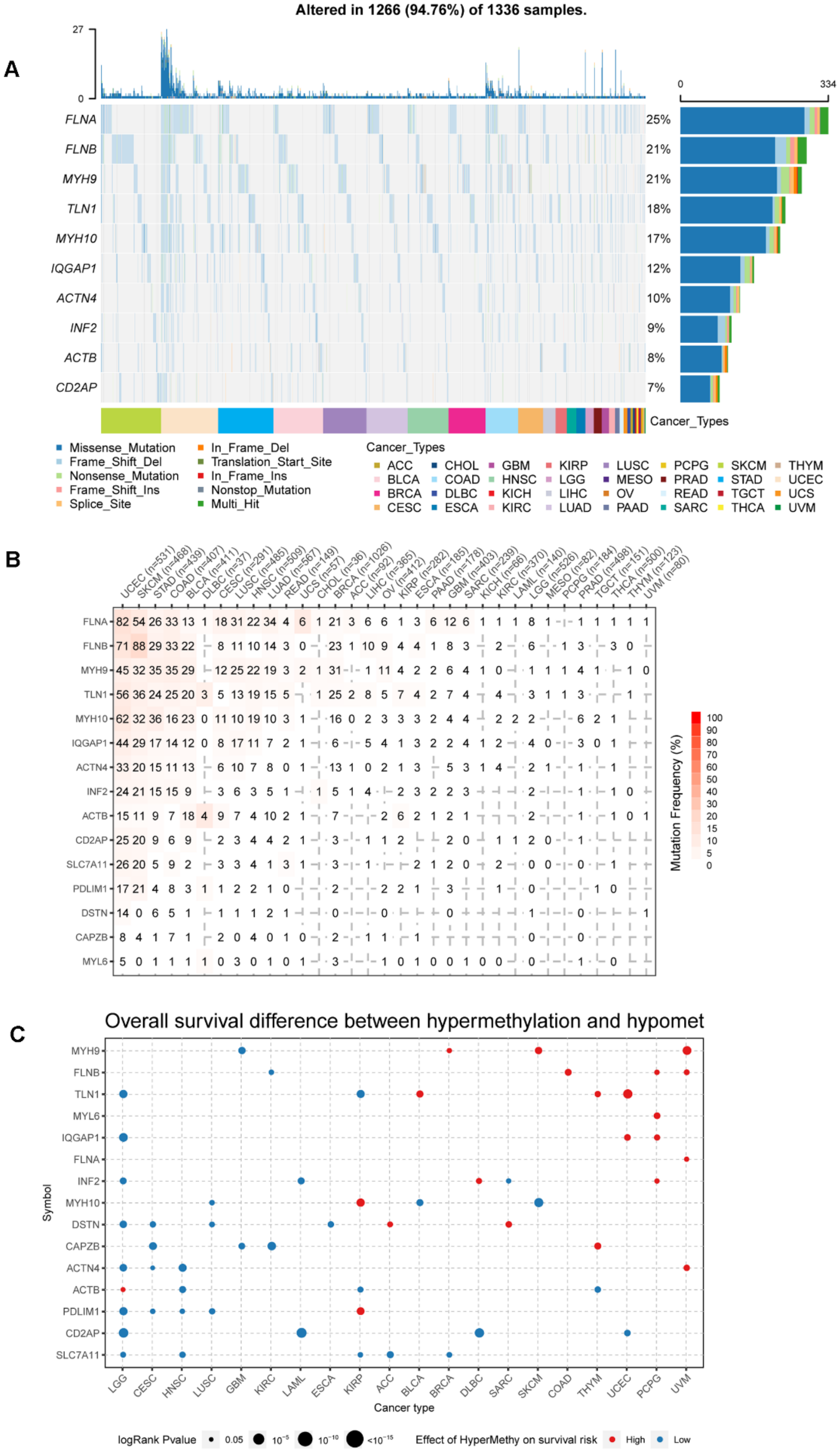
SUPPLEMENTARY FIGURES

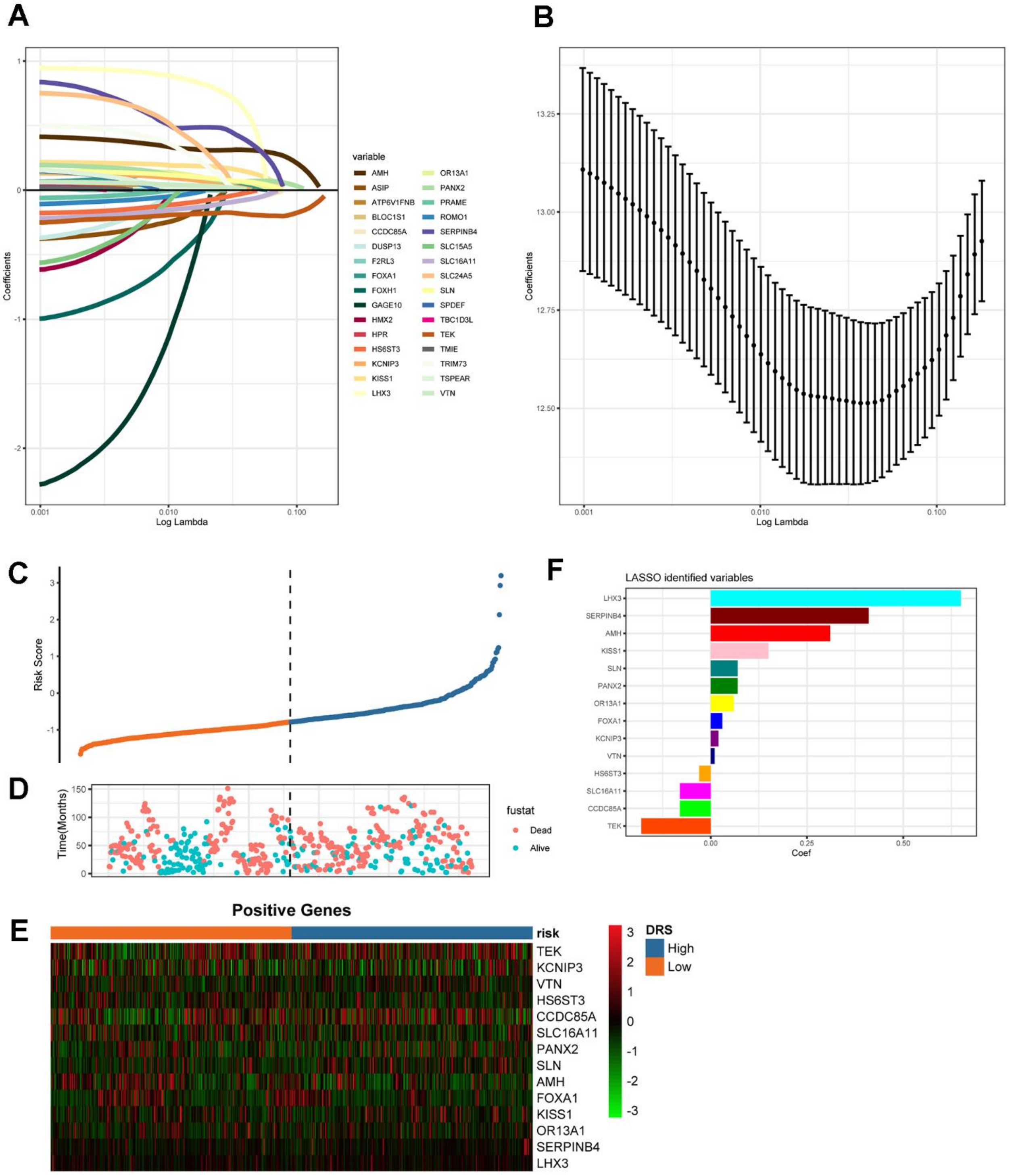


Supplementary Figure 1. Workflow of our research.

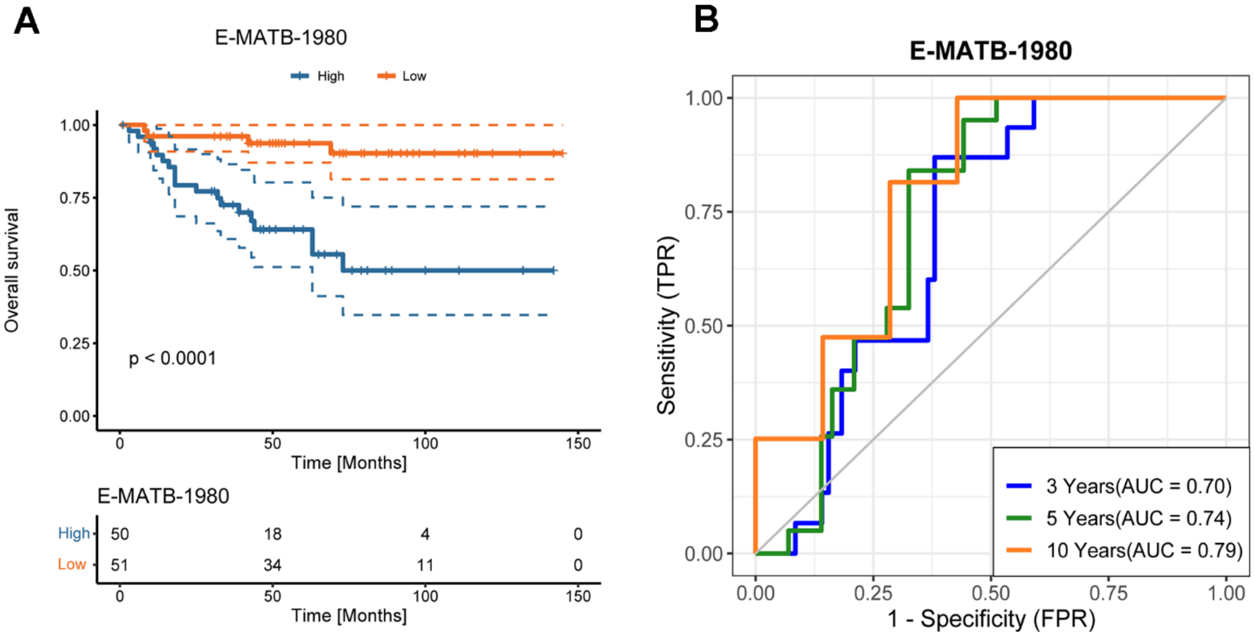


	UCEC (n=531)	SKCM (n=468)	STAD (n=439)	COAD (n=407)	BLCA (n=411)	DLBC (n=37)	CESC (n=291)	LUSC (n=485)	HNSC (n=509)	LUAD (n=567)	READ (n=149)	UCS (n=57)	CHOL (n=36)	BRCA (n=1026)	ACC (n=92)	LIHC (n=365)	OV (n=412)	KIRP (n=282)	ESCA (n=185)	PAAD (n=178)	GBM (n=403)	SARC (n=239)	KICH (n=66)	KIRC (n=370)	LAML (n=140)	LGG (n=526)	MESO (n=82)	PCPG (n=184)	PRAD (n=498)	TGCT (n=151)	THCA (n=500)	THYM (n=123)	UVM (n=80)
FLNA	82	54	26	33	13	1	18	31	22	34	4	6	1	21	3	6	6	1	3	6	12	6	1	1	1	8	1		1	1	1	1	1
FLNB	71	88	29	33	22		8	11	10	14	3	0		23	1	10	9	4	4	1	8	3		2		6		1	3		3	0	
MYH9	45	32	35	35	29		12	25	22	19	3	2	1	31		1	11	4	2	2	6	4	1	0		1	1	1	4	1		1	0
TLN1	56	36	24	25	20	3	5	13	19	15	5		1	25	2	8	5	7	4	2	7	4		4		3	1	1	3			1	
MYH10	62	32	36	16	23	0	11	10	19	10	3	1		16	0	2	3	3	3	2	4	4		2	2	2			6	2	1		
IQGAP1	44	29	17	14	12	0	8	17	11	7	2	1		6		5	4	1	3	2	2	4	1	2		4	0		3	0	1		
ACTN4	33	20	15	11	13		6	10	7	8	0	1		13	1	0	2	1	3		5	3	1	4		2	1		1		1		
INF2	24	21	15	15	9		3	6	3	5	1		1	5	1	4		2	3	2	2	3				2			1		1	0	
ACTB	15	11	9	7	18	4	9	7	4	10	2	1		7			2	6	2	1	2	1				2			1		1	0	1
CD2AP	25	20	9	6	9		2	3	4	4	2	1		3		1	1	2			2	0		1	1	2	0		1				
SLC7A11	26	20	5	9	2		3	3	4	1	3	1		3		1			2	1	2	0		2		0	0		0		1		
PDLIM1	17	21	4	8	3	1	1	2	2	1	0			2			2	2	1		3			1		0				1	0		
DSTN	14	0	6	5	1		1	1	1	2	1			0			0				0					1			0				1
CAPZB	8	4	1	7	1		2	0	4	0	1	0		2		1	1		1							0			0				
MYL6	5	0	1	1	1	1	0	3	0	1	0	1		3			1	0	1	0	0	1	0	0		0			1		0		

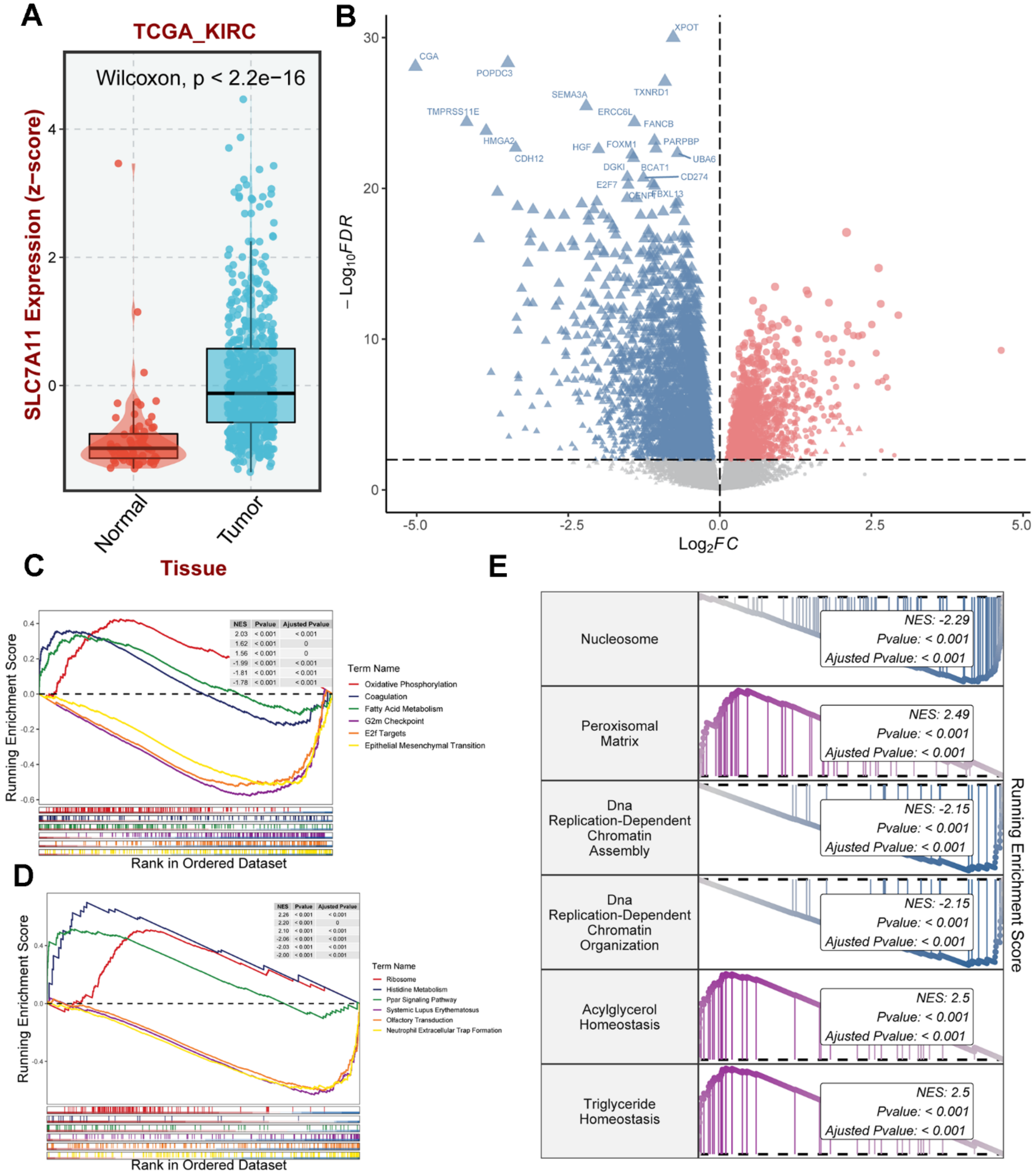
Supplementary Figure 2. Landscape of mutation and methylation of 15 disulfide-related molecules. (**A**) Waterfall diagram showing the mutation types of disulfidation-related genes in multiple cancers. (**B**) Heatmap showing the mutation frequency of 15 disulfide-related molecules in pan-cancer. (**C**) Bubble chart showing the correlation between methylation of 15 disulfide-related molecules and overall survival.



Supplementary Figure 3. Establishment of DRS by LASSO regression analysis. (**A**) LASSO coefficient profiles of the 32 DEGs in ccRCC. (**B**) Tenfold cross-validation LASSO regression analysis to estimate the optimal LASSO regularization parameter. (**C**, **D**) DRS distribution, survival status, and survival time of patients with ccRCC in the TCGA-KIRC dataset. (**E**) Heatmap of the mRNA expression of 14 DRS model-related genes in patients with ccRCC from TCGA-KIRC (n = 518) dataset. (**F**) Coefficients for 14 modeled genes.



Supplementary Figure 4. Verify the prognostic value of DRS in the E-MATB-1980 cohort. (**A**) Survival analysis for overall survival of the two DRS groups in the E-MATB-1980 cohort. (**B**) Time-dependent ROC analysis of the predictive value of the DRS in the overall survival of patients at 1, 3, 5, and 10 years based on the E-MATB-1980 cohort.



NES	Pvalue	Ajusted Pvalue
2.03	< 0.001	< 0.001
1.62	< 0.001	0
1.56	< 0.001	0
-1.99	< 0.001	< 0.001
-1.81	< 0.001	< 0.001
-1.78	< 0.001	< 0.001

NES	Pvalue	Ajusted Pvalue
2.26	< 0.001	< 0.001
2.20	< 0.001	0
2.10	< 0.001	< 0.001
-2.06	< 0.001	< 0.001
-2.03	< 0.001	< 0.001
-2.00	< 0.001	< 0.001

NES: -2.29
Pvalue: < 0.001
Ajusted Pvalue: < 0.001

NES: 2.49
Pvalue: < 0.001
Ajusted Pvalue: < 0.001

NES: -2.15
Pvalue: < 0.001
Ajusted Pvalue: < 0.001

NES: -2.15
Pvalue: < 0.001
Ajusted Pvalue: < 0.001

NES: 2.5
Pvalue: < 0.001
Ajusted Pvalue: < 0.001

NES: 2.5
Pvalue: < 0.001
Ajusted Pvalue: < 0.001

Supplementary Figure 5. Functional enrichment indicates that SLC7A11 is potentially associated with EMT and the TME in ccRCC. (**A**) The box plot compares the expression levels of the SLC7A11 gene between tumor and normal tissues. (**B**) Volcano plot of SLC7A11-related DEGs in ccRCC. Red and blue points indicate the upregulated and downregulated genes, respectively. (**C**) GSEA Hallmark analysis. (**D**) GSEA KEGG analysis. (**E**) GSEA GO analysis.