



**Figure S1** *VDAC3* expression and survival analysis by Gepia2. (A) Pan-cancer analysis of *VDAC3* expression by Gepia2. (B) Relationship between *VDAC3* expression and clinicopathological parameters by Gepia2. (C) Kaplan-Meier analysis of *VDAC3* expression by Gepia2. *VDAC3*, voltage-dependent anion channel 3.

**Table S1** Univariate and multivariate Cox risk regression analysis of *VDAC3* in the TCGA-COAD dataset

Characteristics	Univariate analysis				Multivariate analysis			
	Exp(B)	HR.95L	HR.95H	P value	Exp(B)	HR.95L	HR.95H	P value
Age	1.031	1.011	1.052	0.002**	1.048	1.027	1.07	<0.001***
M	4.098	2.618	6.415	<0.001***	2.577	1.482	4.481	<0.001***
N	2.437	1.581	3.756	<0.001***	0.446	0.167	1.189	0.11
T	5.968	1.882	18.923	0.002**	3.365	1.033	10.96	0.04*
Stage	2.961	1.892	4.633	<0.001***	4.431	1.428	13.751	0.009**
<i>VDAC3</i>	0.638	0.413	0.985	0.04*	0.609	0.391	0.95	0.03*

\*, P<0.05; \*\*, P<0.01; \*\*\*, P<0.001. *VDAC3*, voltage-dependent anion channel 3; TCGA, The Cancer Genome Atlas; COAD, colorectal adenocarcinoma; HR, hazard ratio.

**Table S2** Correlation analysis between *VDAC3* and genes markers of prognostic models

Description	Gene marker	Cor	P
Prognostic Model 1	<i>CYP4A11</i>	-0.032	0.57
	<i>PGM2</i>	0.25	<0.001***
	<i>PKLR</i>	0.12	0.029*
	<i>PPARGC1A</i>	-0.022	0.7
	<i>CPT2</i>	0.033	0.56
	<i>ACAT2</i>	0.11	0.048*
Prognostic Model 2	<i>LARS2</i>	0.1	0.06
	<i>PARS2</i>	0.21	<0.001***
	<i>ETHE1</i>	-0.045	0.42
	<i>LRPPRC</i>	0.19	<0.001***
	<i>TMEM70</i>	0.49	<0.001***
	<i>AARS2</i>	0.064	0.26
	<i>ACAD9</i>	0.093	0.1
	<i>VARS2</i>	0.087	0.12
	<i>ATP8A2</i>	-0.067	0.24
Prognostic Model 3	<i>CDC25C</i>	0.24	<0.001***
	<i>KCNJ11</i>	0.066	0.24
	<i>NOL3</i>	-0.048	0.4
	<i>P4HA1</i>	0.15	0.01*
	<i>QSOX2</i>	-0.0084	0.88
	<i>Trap1</i>	0.24	<0.001***
	<i>DNAJC28</i>	-0.051	0.37
	<i>ATCAY</i>	-0.053	0.35

\*, P<0.05; \*\*\*, P<0.001. *VDAC3*, voltage-dependent anion channel 3.