

Table SI. Primer sequences for quantitative RT-PCR.

Gene name	Direction	Primer sequence
<i>GAPDH</i>	Forward	<i>GCACCGTCAAGGCTGAGAAC</i>
	Reverse	<i>ATGGTGGTGAAGACGCCAGT</i>
<i>PMM2</i>	Forward	<i>GAGCAACTGGGAAATGATGTG</i>
	Reverse	<i>TTTCGCAATGTAGCTCAGACA</i>
<i>ACOXI</i>	Forward	<i>ATT CGCT CAG ATG CT GT GC</i>
	Reverse	<i>TTC GT GG AC CT CT G C T T GT</i>
<i>KDM3A</i>	Forward	<i>TGT GCG AC ACC ACC AT CT TC</i>
	Reverse	<i>CAC CCT GT GG CA ATT C T T T</i>
<i>HSPB1</i>	Forward	<i>AG CT GAC GGT CAAG ACC AAG</i>
	Reverse	<i>TGG GAT GGT GAT CTC GT TT GG</i>
<i>PPARGC1A</i>	Forward	<i>CCC ACC ACT C C T C C T C A T A A A</i>
	Reverse	<i>GC AT ACA ACT C G G A T T G C T CC</i>
<i>UPK3B</i>	Forward	<i>CC CT GCT GG AGT GATT GG A</i>
	Reverse	<i>GG AG AAG GT GG T GG C T GT GA</i>
<i>EPHB2</i>	Forward	<i>CG CCG T GCG TG T C T C T A</i>
	Reverse	<i>AG CC ACC AG CG AT GT G C T</i>

Table SII. Multivariate Cox regression analysis of prognostic genes in colon adenocarcinoma.

Gene	Coefficient	HR	95%CI	P-value
<i>PMM2</i>	-0.34559	0.70780	0.48650-1.02978	0.07083
<i>ACOX1</i>	-0.44662	0.63979	0.44133-0.92748	0.01841
<i>KDM3A</i>	0.79297	2.20996	1.61007-3.03335	9.22x10 ⁻⁷
<i>HSPB1</i>	0.14968	1.16146	0.97045-1.39007	0.10252
<i>PPARGC1A</i>	-0.20650	0.81342	0.66362-0.99705	0.04677
<i>UPK3B</i>	0.19863	1.21973	1.00828-1.47552	0.04087
<i>EPHB2</i>	-0.14950	0.86113	0.70764-1.04792	0.13553

HR, hazard ratio; CI, confidence interval.