

**S2 Table.** Genes (methylations) selected and entered into the prognostic model

Genes associated with lymphatic invasion	Probe	Fold change	FDR	OR (95% CI)	Weight
<i>ITGBL1</i>	cg03386869	-0.09	0.006	7.13 (1.33-41.46)	1.9637
<i>CAPN9</i>	cg06585893	-0.08	0.005	15.29 (2.27-117.35)	2.7273
<i>LOC84931</i>	cg07412254	-0.07	0.001	14.08 (0.76-355.94)	2.6450
<i>ACAP1</i>	cg25671438	0.05	0.001	0.01 (0.00-1.27)	-4.3617
<i>ADORA3</i>	cg02947253	-0.09	0.010	0.31 (0.07-1.34)	-1.1581
<i>FBN3</i>	cg14156381	-0.04	0.004	0.01 (0.00 -0.89)	-4.4722
<i>CD37</i>	cg10037005	0.07	< 0.001	12.06 (0.42-417.18)	2.4902

FDR, false discovery rate; OR, odds ratio; CI, confidence interval.