

Supplemental Materials

S1 Table. mRNA selected and entered into the prognostic model

mRNA associated with lymphatic invasion	Fold change	FDR	OR (95% CI)	Weight
HTR3A	-1.61	0.014	1.35 (0.93-2.06)	0.2983
PCP4	1.31	0.031	0.53 (0.30-0.80)	-0.6302
CAPN9	1.15	0.017	0.42 (0.20-0.76)	-0.8574
MASP1	1.11	0.020	0.49 (0.24-0.88)	-0.7095
CYP8B1	-1.05	0.011	3.74 (1.77-10.48)	1.3189
GDF5	1.02	0.015	0.61 (0.34-1.02)	-0.4935
AOAH	-0.97	0.017	5.96 (1.43-29.79)	1.7850
ADORA3	-0.92	0.013	5.77 (1.60-28.78)	1.7531
CLCNKB	0.90	0.029	0.62 (0.34-1.03)	-0.4757
EBI3	-0.90	0.020	2.20 (0.84-6.95)	0.7888
LILRB3	-0.85	0.014	2.88 (1.01-8.93)	1.0577
C16orf54	-0.84	0.014	6.70 (2.20-31.84)	1.9022
PODNL1	-0.82	0.029	1.71 (0.90-3.73)	0.5381
DCN	-0.77	0.026	16.30 (3.29-165.00)	2.7914
USH2A	-0.75	0.017	1.74 (0.95-3.87)	0.5553
FGD2	-0.73	0.020	8.57 (1.75-69.85)	2.1488
TNFAIP8L2	-0.71	0.029	0.00 (0.00-0.04)	-5.9484
SP140	-0.71	0.030	0.37 (0.10-1.04)	-1.0032
WISP1	-0.68	0.021	0.04 (0.00-0.26)	-3.1931
SH2D4B	0.67	0.026	0.45 (0.22-0.85)	-0.7937
RUNX1	-0.67	0.016	0.14 (0.02-0.57)	-1.9687

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