

S3 Table. Meta-analysis of genes selected for overall survival

mRNA associated with lymphatic invasion	HR	95% CI
HTR3A	0.95	0.89-1.00
PCP4	1.03	0.98-1.09
CAPN9	0.93	0.88-0.98
MASP1	1.00	0.94-1.06
CYP8B1	0.99	0.91-1.07
GDF5	1.04	0.98-1.10
AOAH	1.02	0.96-1.08
ADORA3	1.05	1.00-1.11
CLCNKB	1.05	0.98-1.12
EBI3	0.96	0.90-1.01
LILRB3	0.95	0.83-1.10
C16orf54	0.94	0.87-1.02
PODNL1	1.10	1.04-1.17
DCN	1.18	1.12-1.25
USH2A	1.04	0.98-1.10
FGD2	0.97	0.91-1.02
TNFAIP8L2	0.96	0.89-1.03
SP140	0.94	0.89-1.00
WISP1	1.12	1.06-1.19
SH2D4B	1.00	0.93-1.08
RUNX1	1.07	1.01-1.13

HR, hazard ratio; CI, confidence interval.