Supplementary Table 1. Primer Sequences

Name	Sequence
AMT_F	TGGGAATGACATTGATGAACA
AMT_R	CTCCAGGGAAGTCCATAGCA
C2CD4A_F	GGTGCAGAGACCCATCTGAC
C2CD4A_R	GCTCCAGGCACCACATCT
FOXA1_F	AGGGCTGGATGGTTGTATTG
FOXA1_R	ACCGGGACGGAGGAGTAG
LYZ_F	CCGCTACTGGTGTAATGATGG
LYZ_R	CATCAGCGATGTTATCTTGCAG
MMP1_F	CAGAGATGAAGTCCGGTTTTTC
MMP1_R	GGGGTATCCGTGTAGCACAT
MMP9_F	GAACCAATCTCACCGACAGG
MMP9_R	GCCACCCGAGTGTAACCATA
PIGR_F	ACTGCAGCCGTCTATGTGG
PIGR_R	CTTCGCTAGGCTGACATCG
RCC1_F	CGATGATGGCCGTGTCTT
RCC1_R	TCCAACAGTCCAATCACACC
Actin Beta_F	CCTTTGCCGATCCGCCG
Actin Beta_R	GATATCATCCATGGTGAGCTGG

F, forward; R, reverse

Supplementary Table 2: Model performance in estimating the risk of LNM in the training cohort using each panel

Variable	Value (95% CI)		
	4-miRNA panel	5-mRNA panel	Combination panel (4-miRNA and 5-mRNA)
Cutoff value	0.08	0.05	0.08
Sensitivity, %	80.0 (28.4–99.5)	80.0 (28.4–99.4)	80.0 (28.4–99.5)
Specificity, %	70.7 (54.5–83.9)	78.1 (62.4–89.4)	92.7 (80.1–98.5)
AUC, %	78.4 (63.9–89.3)	77.1 (62.3–88.2)	85.5 (71.8–94.0)
PPV, %	25.0 (14.9–38.9)	30.8 (17.7–47.8)	57.1 (29.2–81.2)
NPV, %	96.7 (83.2–99.4)	97.0 (84.6–99.5)	97.4 (86.8–99.5)

AUC, area under the curve; PPV, positive predictive value; NPV, negative predictive value; LNM, lymph node metastasis; CI, confidence interval

Supplementary Table 3: Univariate logistic regression analysis for LNM

Variable	4-miRNA panel	5-mRNA panel	Combination panel (4-miRNA and 5-mRNA)
OR	8.62	8.44	14.22
95% CI	0.87–84.90	0.99–71.83	1.41–143.67
P value	0.06	0.05	0.02

OR, odds ratio; CI, confidence interval; LNM, lymph node metastasis

Supplementary Figure 1