Meta-Analysis

The roles of ncRNAs in the diagnosis, prognosis and clinicopathological features of breast cancer: a systematic review and meta-analysis

Shihui Tang¹, Wei Fan^{1,2}, Jiang Xie³, Qiaoling Deng¹, Ping Wang¹, June Wang¹, Peipei Xu¹, Zheng Zhang¹, Yirong Li¹ and Mingxia Yu¹

¹Department of Clinical Laboratory & Center for Gene Diagnosis, Zhongnan Hospital of Wuhan University, Wuhan, Hubei, 430071, China

²Department of Pathology, Zhongnan Hospital of Wuhan University, Wuhan, Hubei, 430071, China

³Department of Otorhinolaryngology and Head & Neck Surgery, Hunan Children's Hospital, University of South China Hengyang, Hunan, 421000, China

Correspondence to: Mingxia Yu, email: dewrosy520@163.com Yirong Li, email: YirongLi_Whu@163.com

Keywords: noncoding RNA, breast cancer, meta-analysis, prognosis, diagnosis

Received: November 07, 2016 Accepted: April 12, 2017 Published: August 10, 2017

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ABSTRACT

Background: A number of studies have shown that noncoding RNAs (ncRNAs) are abnormally expressed in breast cancers. However, the roles of ncRNAs remain unclear in breast cancer. Here, we aim to investigate the potential diagnostic and prognostic roles of ncRNAs in breast cancer.

Methods: Comprehensive literature search in Medline and Web of Science and a meta-analysis were performed to identify the association between ncRNAs and diagnosis, prognosis, and clinicopathological features of breast cancer.

Results: A total of 103 eligible studies, involving16, 828 independent participants, were included in the meta-analysis. In total, there were 98 individual and 11 grouped ncRNAs. 51 studies were eligible for survival analysis, 27 studies were eligible for diagnostic analysis, and 46 studies were eligible for clinicopathological features analysis. The abnormal expression of ncRNAs is associated with OS, RFS and PFS in breast cancer patients. For the diagnosis value of ncRNAs, the pooled OR and 95% CI for sensitivity, specificity, DOR and AUC on all ncRNAs were 0.83 [95% CI: 0.82- 0.84], 0.80 [95% CI: 0.79- 0.82], 24.77 [95% CI: 17.44- 35.16] and 0.9037, respectively. The analysis showed that downregulation of ncRNAs in breast cancer was associated with decreased risk of LNM, increased tumor size and PR expression, whereas, upregulation of ncRNAs was associated with increased HER2 expression.

Conclusions: High expression of ncRNAs was associated with poor OS, RFS, and PFS, while low expression of ncRNAs was related to favorable OS and RFS. Meanwhile, ncRNAs have potential diagnostic value for breast cancer.

INTRODUCTION

Breast cancer is the leading cause of cancer death in women. Early diagnosis and treatment are crucial to improve survival rate and quality of life of breast cancer patients [1]. However, because the primary breast cancers often lack typical clinical manifestations, many patients have been in advanced stage at the time of diagnosis [2]. Therefore, it is very important to find good breast cancer biological markers.

NcRNAs regulate cell differentiation, polarity, and epithelial to mesenchymal transition in breast cancer [3]. In recent years, it is known that ncRNAs served as prognosis factors in breast cancer [1, 4]. For example, Yu et al. found that down-regulation of miR-129-5p induced EMT in breast cancer cells and is associated with poor prognosis [5]. However, whether or not and how ncRNAs could be used in diagnosing and predicting prognosis of breast cancer patients remain to be determined. Systematic review and meta-analysis of data from individual studies can help to evaluate the potential clinical value of ncRNAs. This study aimed to assess the association between ncRNAs (miRNAs and long noncoding RNAs (lncRNAs)) and prognosis, diagnosis, and clinicopathological features of breast cancer.

RESULTS

Description of studies

The PRISMA flow chart (Figure 1) summaries the selected studies in the review. We followed the PRISMA writing specification [6]. Our search yielded a total of 8981 reports. This was reduced to 6283 after removal of 2698 duplicates. 6055 were excluded after screening the titles and abstracts. Full-text articles were obtained for 138 studies, of which 103 were eligible for meta-analysis. 51 studies included survival data, 27 studies included diagnostic data, and 46 studies included clinicopathological features which included age, lymph node metastasis, tumor size, ER, PR, HER2, and menopausal. Low expression of ncRNAs was found in 30 studies while high expressions of ncRNAs were found in 64 studies. 32 articles investigated lncRNA, and 71 articles studied microRNA.

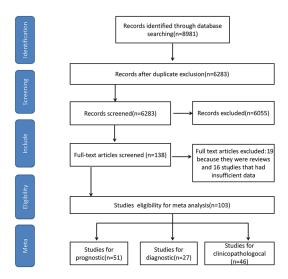
Micro-21 is the most commonly studied ncRNA [7–17], and all of these studies investigated its diagnostic and prognostic values in breast cancer. However, other ncRNAs showed opposite role. Madhavan [18] deemed the upregulation of miR-200b and miR-22 as unfavorable prognostic factors, while both Yao [19] and Chen [20] demonstrated that these two had potential favorable effect on breast cancer. Besides, Lu [21] proposed that breast

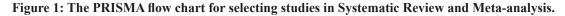
cancer patients with high expression of HOX transcript antisense RNA (HOTAIR) had lower risks of relapse and mortality than those with lower expression. On the contrary, Gupta [22] considered that HOTAIR could reprogram chromatin state to promote breast cancer metastasis and death.

Prognosis

51 studies reporting survival analysis were eligible for the meta-analyses (Supplementary Table 1). 44 studies reported overall survival (OS), 9 studies reported recurrence-free survival (RFS), and 4 studies reported progression/event/disease-free survival (PFS) (Table 1). Summarized hazard ratio (HR) was used as effect size to estimate the relationship between expression of ncRNAs and breast cancer survival. Random-effects model was used for the pooled analysis to detect heterogeneity. In the 44 studies reporting OS, high expression of 19 ncRNAs was associated with improved breast cancer survival rates (HR=0.33, 95% confidence interval (95% CI) : 0.23-0.47) (Supplementary Figure 1B) and 21 ncRNAs were associated with an increased risk of death (HR=2.63, 95% CI: 2.27-3.05) (Supplementary Figure 1A).

Seven ncRNAs were investigated in more than two studies: miR-21 (n=8 studies), miR-200a (n=2 studies), miR-200b (n=2 studies), miR-200c (n=2 studies), miR-22 (n=2 studies), miR-124 (n=2 studies), miR-210 (n=2 studies), and HOTAIR (n=2 studies). By combining these studies, the pooled HR and 95% CI were as follows: miR-21 (HR=1.97, 95% CI: 1.55-2.44); miR-200a (HR=3.24, 95% CI: 1.30-8.07); miR-200b (HR=2.08, 95% CI: 0.54-8.01); miR-200c (HR=3.41, 95% CI: 1.91-6.09); miR-22 (HR=0.88, 95% CI: 0.36-2.19); miR-124 (HR=0.71, 95% CI: 0.55-0.92); miR-210 (HR=0.71, 95% CI: 0.55-0.92); HOTAIR (HR=1.21, 95% CI:0.16-8.93) (Supplementary Figure 3).





Survival analysis		No. of studies	No. of patients	Pooled HR	Heterogeneity
OS	Down	19	4472	0.33[0.23-0.47]	79%
	Up	25	6854	2.63[2.27-3.05]	53%
RFS	Down	4	2605	0.68[0.53,0.87]	67%
	Up	5	7447	2.70[1.91,3.81]	0%
PFS	Down	1	57	0.40[0.17,0.94]	/
	Up	3	442	2.09[1.41,3.11]	64%

Table 1: Summary HR of ncRNAs for breast cancer

Similarly, 9 studies were eligible for the RFS, with 4 down-regulated ncRNAs (HR=0.71, 95% CI: 0.55-0.92) and 5 up-regulated ncRNAs (HR=2.70, 95% CI: 1.91-3.81) were associated with risk of recurrence (Supplementary Figure 1D). After combining two studies, the result for MALAT1 showed a pooled HR of 2.36 (95% CI: 1.55-3.60) in terms of RFS. For the PFS, three studies addressed 4 up-regulated ncRNAs (HR=2.09, 95% CI: 1.41-3.11) and one down regulated (Supplementary Figure 1C).

Diagnosis

Analysis of data from diagnostic accuracy studies including 27 original studies reported 1 lncRNA and 47 miRNAs (Supplementary Table 2). 13 ncRNAs are down regulated and the others are up regualted. All articles including 2287 patients and 1644 healthy control were published between 2010 and 2016. Significant heterogeneity was observed among the 27 studies in sensitivity and specificity analyses (I²=86.1% and 93.8%, respectively). The pooled estimates for sensitivity, specificity, positive likelihood ratios (PLR), negative likelihood ratios (NLR), diagnostic odds ratios (DOR) and Area Under Curve (AUC) of all ncRNAs were 0.83 [95% CI: 0.82-0.84], 0.80 [95% CI: 0.79-0.82], 4.51 [95% CI: 3.62-5.62], 0.21 [95% CI: 0.17-0.25], 24.77 [95% CI: 17.44-35.164] and 0.9037, respectively.

The most commonly studied ncRNA is miR-21 (n=9 studies). Pooled estimates of sensitivity, specificity, PLR, NLR, DOR and AUC associated with miR-21 were 0.77 [95% CI: 0.74-0.82], 0.84 [95% CI: 0.78-0.88], 4.25 [95% CI: 2.40-7.52], 0.23 [95% CI: 0.12-0.46], 18.141 and 0.8982 (Supplementary Figure 4; Supplementary Figure 5; Supplementary Figure 6).

Clinicopathological features

46 studies including 24 microRNAs and 15 lncRNAs were included in analyses of the relationship between ncRNA and clinicopathological features (Supplementary Table 3), such as age, lymph node metastasis (LNM), tumor size, estrogen receptor (ER), progesterone receptor (PR), human epidermalgrowth factor receptor-2 (HER2), and menopausal factors (Table 2). 24 ncRNAs were up-regulated and 15 ncRNAs were down-regulated in breast cancer. The results suggested that upregulation of ncRNAs was positively correlated with the expression of HER2 (odd ratio (OR)=1.36, 95% CI: 1.10- 1.82). Meanwhile, an inverse correlation between downregulated ncRNAs and LNM (OR=0.53, 95% CI: 0.36-0.78), positive correlation between down-regulated ncRNAs and tumor size (OR=1.47, 95% CI: 1.19- 1.82) and the expression of PR (OR=1.33, 95% CI: 1.05- 1.68) was noted (Figure 2). There were no other statistically significant associations between ncRNA and other factors (Supplementary Figure 7-Supplementary Figure 14).

Subgroup analyses and meta-regression

Prognosis

We performed meta-regression analysis but didn't found the publication year and RNA type which can explain the heterogeneity in up regulation ncRNAs [Chi²=79.90, df=36 (P<0.0001); I²=55%]. Then, we performed subgroup analysis based on races and sample type. There was no significant heterogeneity in the tissue microarrays subgroup [Chi²=2.60, df =4 (P=0.63); I²=0%] and blood subgroup [Chi²=2.57, df=7 (P=0.28); I²=22%]. But significant heterogeneity [Chi²=62.74, df=30 (P=0.0004); I²=52%] was observed in fresh tissue subgroup (Figure 3B).

Diagnosis

To study the diagnostic value, we performed subgroup analysis based on sample type. We found that the ncRNAs extracted from blood have higher sensitivity, specificity and AUC than those from tissue (Figure 4). Furthermore, diagnosis based on multiple ncRNAs showed higher accuracy than signle ncRNA (Table 3, and Figure 5). This information revealed a high potential diagnostic value of multiple ncRNAs from blood for breast cancer detection.

Influence analysis and publication bias

In influence analysis for studies on highly expressed ncRNA, pooled results were not substantially altered

Table 2: Summary diagnostic accuracy of ncRNAs for breast cancer

Analysis	No.	Pooled Sen	Pooled Spe	PLR	NLR	AUC
Sum	27	0.83(0.82-0.84)	0.80(0.79- 0.82)	4.51(3.62-5.62)	0.21(0.17-0.25)	0.9037
ncRNA profile	es					
combine	7	0.86(0.84- 0.89)	0.87(0.84- 0.89)	7.22(4.26-12.23)	0.16(0.11- 0.24)	0.9240
single	24	0.82(0.80- 0.83)	0.79(0.77-0.80)	4.16(3.28-5.26)	0.22(0.18-0.27)	0.8951
Sample types						
tissue	7	0.81(0.79-0.83)	0.77(0.74-0.80)	3.75(2.48- 5.67)	0.26(0.18-0.39)	0.8744
blood	22	0.83(0.82-0.84)	0.82(0.80- 0.84)	4.93(3.838-6.34)	0.18(0.15-0.23)	0.9147

Sen: sensitivity, Spe: specificity, PLR: Positive likelihood ratio, NLR: negative likelihood ratio, AUC: area under concentration-time curve

after removing any one of the studies, suggesting that the pooled result is stable. In contrast, in down regulated part, we found an outlier and once this outlier was excluded [23], I² went down from 79% to 0% [Chi²=13.21, df =17 (P=0.72); I²=0%] (Figure 6B).

Risk of publication bias is a significant concern in prognostic studies [24]. Begg's funnel plot and Egger's test were used to evaluate the publication bias in the published literature [25]. For OS, Begg's funnel plot (P=0.045) and Egger's test (P=0.053) showed certain publication bias (Supplementary Figure 1; Supplementary Figure 2A). By using trim-and-fill Method, a symmetrical funnel plot was produced.

Α

Hypothetical negative unpublished studies imputed to mirror the positive studies that cause funnel plot asymmetry (Figure 3B) [26]. The pooled analysis showed a negative relationship between high expression ncRNA and OS (HR, 0.82 [95% CI, 0.65-0.99]), and the result has good stability (Supplementary Figure 1B). For low expression ncRNA, the result of Begg's funnel plot is opposite to Egger's test. After excluded the outlier as mentioned above, funnel plot transformed to symmetry.

The Deek's funnel plot asymmetry test was used to evaluate the publication bias in diagnostic analysis [25]. The result (P=0.12) confirmed that there was no significant publication bias (Supplementary Figure 6).

udy or Subaroup	HER2		HER2		Valabt	Odds Ratio M-H, Random, 95% CI	Odds Ratio M-H. Random, 95%	Cl	<=2 cr		>2 cm			Odds Ratio	Odds Ratio
ten 2015	Events 6	19	36	103	4.9%	0.86 [0.30, 2.45]	M-H. Kanoom, 957	CI Study or Subgroup Dong 2015	Events 43	70	Events 24	63	Weight 5.8%	M-H. Fixed. 95% C 2.59 [1.28, 5.21]	M-H. Fixed, 95% Cl
ni 2014	34	66	41	85	8.1%	1.14 [0.60, 2.17]	+	Jang 2013	43	144	63	163	19.1%	1.34 [0.85, 2.12]	-
2015	94	370	63		11.1%	1.45 [1.01, 2.09]	h	Li 2014		44	41	85	8.0%		
2016	30	58	50	103	8.1%	1.14 [0.60, 2.16]	+		23					1.18 [0.57, 2.44]	
Jang 2009	66	144	63	163	10.1%	1.34 [0.85, 2.12]		P Liu 2015	10	31	20	84	4.4%	1.52 [0.62, 3.77]	
en-Polar 2015	8	47	7	47	4.6%	1.17 [0.39, 3.54]		Tang 2014	5	18	9	33	2.7%	1.03 [0.28, 3.71]	
e 2011	19	41	12	67	6.1%	3.96 [1.65, 9.50]		Wang 2013	32	54	42	74	8.6%	1.11 [0.54, 2.26]	
ta D 2011	15	32	22	138	6.5%	4.65 [2.03, 10.68]		Wang 2014	32	76	12	34	5.7%	1.33 [0.58, 3.08]	T-
ang 2012	25	67	16	35	6.5%	0.71 [0.31, 1.62]	-+	Yang a 2016	7	15	5	49	0.7%	7.70 [1.95, 30.39]	
uomarila 2014	15	26	66	133	6.3%	1.38 [0.59, 3.24]	+	Yang b 2016	108	193	248	520	35.3%	1.39 [1.00, 1.94]	-
nao 2011	15	27	30	66	5.9%	1.50 [0.61, 3.69]	+	Zhou 2016	35	69	40	99	9.7%	1.52 [0.82, 2.82]	
eng 2015	20	36	59	137	7.2%	1.65 [0.79, 3.46]									
teng s 2015	19	36	52	137	7.2%	1.83 [0.87, 3.83]		Total (95% CI)		714		1204	100.0%	1.46 [1.20, 1.78]	•
ou 2014	46	93	37	51	7.3%	0.37 [0.18, 0.77]		Total events	361		504				
00 2014	40	35	31	51	1.3%	0.57 [0.10, 0.77]		Heterogeneity: Chi ² =	9.68, df = 9	P = 0	38); I ² =	7%			0.01 0.1 1 10
stal (95% CI)		1062		1597	00.0%	1.36 [1.01, 1.82]	•	Test for overall effect:	Z = 3.83 (F	= 0.00	01)				0.01 0.1 1 10 Favours [=2 cm] Favours [>2 c
otal events	412		554				1.								Pavours (=2 cm) Pavours (>2 c
st for overall effect: 2	= 2.04 (P	= 0.04)					Favours [HER2 +] Favour	[HER2 ·] D							
est for overall effect: 2	= 2.04 (P	= 0.04)					Favours (HER2 +) Favour	[HER2-] D	PR		PR -			Odds Ratio	Odds Ratio
est for overall effect: 2	: = 2.04 (P	= 0.04)					Favours [HER2 +] Favour	[HER2 ·] D	PR		PR -	Total	Weight	Odds Ratio M-H. Random. 95% C	Odds Ratio
est for overall effect: 2	. = 2.04 (P	= 0.04)					Favours [HER2 +] Favour	D				Total 45	Weight	M-H. Random, 95% C	M-H. Random. 95% CI
est for overall effect: 2	LNM	•	LNN			Odds Ratio	Odds Ratio	Study or Subgroup Arabkheradmand 2015 Cao 2016	Events	Total	Events				M-H. Random, 95% CI
C tudy or Subgroup	LNM	+ Total	Events	Total		Odds Ratio M-H. Random. 95% C	Odds Ratio	Study or Subgroup Arabkheradmand 2015 Cao 2016	Events 30	Total 55	Events 19	45	4.7%	M-H. Random. 95% C 1.64 [0.74, 3.64]	M-H. Random, 95% CI
C tudy or Subgroup rabkheradmand 2015	LNM Events 8	+ Total 34	Events 48	Total 66	5.9%	Odds Ratio	Odds Ratio	Study or Subgroup Arabkheradmand 2015 Cao 2016	Events 30 111	Total 55 133	Events 19 118	45 242	4.7% 6.7%	M-H. Random, 95% C 1.64 [0.74, 3.64] 5.30 [3.15, 8.94]	H. Random. 95% CI
C tudy or Subgroup rabhheradmand 2015 so 2016	LNM Events 8 124	+ <u>Total</u> 34 163	Events 48 171	Total 66 212	5.9% 8.3%	Odds Ratio <u>M-H. Random, 95% C</u> 0.12 [0.04, 0.30] 0.76 [0.46, 1.25]	Odds Ratio		Events 30 111 48	Total 55 133 94	19 118 28	45 242 56	4.7% 6.7% 5.6%	M-H. Random. 95% C 1.64 [0.74, 3.64] 5.30 [3.15, 8.94] 1.04 [0.54, 2.02]	I M-H. Random, 95% Cl
Ludy or Subgroup abkheradmand 2015 so 2016 ong 2015	LNM Events 8 124 18	+ Total 34 163 59	Events 48 171 49	Total 66 212 74	5.9% 8.3% 7.1%	Odds Ratio MH. Random, 95% C 0.12 (0.04, 0.30) 0.76 (0.46, 1.25) 0.22 (0.11, 0.47)	Odds Ratio	Study or Subgroup Arabheradmand 2015 Col Chi 2014 Dong 2015	Events 30 111 48 34 54 105	Total 55 133 94 59 98 460	Events 19 118 28 33 88 46	45 242 56 74 202 221	4.7% 6.7% 5.6% 5.4% 7.0% 7.8%	M-H. Random. 95% C 1.64 [0.74, 3.64] 5.30 [3.15, 8.94] 1.04 [0.54, 2.02] 1.69 [0.85, 3.37]	I M.H. Random, 95% CL
ady or Subgroup abkheradmand 2015 bio 2016 bing 2015 bioh 2014	LNM Events 8 124 18 91	* 34 163 59 199	Events 48 171 49 51	Total 66 212 74 101	5.9% 8.3% 7.1% 8.4%	Odds Ratio M-H. Random. 95% C 0.12 [0.04, 0.30] 0.76 [0.46, 1.25] 0.22 [0.11, 0.47] 0.83 [0.51, 1.33]	Odds Ratio		Events 30 111 48 34 54 54 105 62	Total 55 133 94 59 98 460 152	Events 19 118 28 33 88 46 63	45 242 56 74 202 221 149	4.7% 6.7% 5.6% 5.4% 7.0% 7.8% 7.2%	M-H. Random, 95% C 1.64 [0.74, 3.64] 5.30 [3.15, 8.94] 1.04 [0.54, 2.02] 1.69 [0.85, 3.37] 1.59 [0.98, 2.58]	H.H. Random. 95% Cl
udy or Subgroup abkheradmand 2015 to 2016 ong 2015 tieh 2014 2015	LNM Events 8 124 18 91 94	+ <u>Total</u> 34 163 59 199 370	Events 48 171 49 51 63	Total 66 212 74 101 332	5.9% 8.3% 7.1% 8.4% 9.0%	Odds Ratio M-H. Random. 95% C 0.12 [0.04, 0.30] 0.76 [0.46, 1.25] 0.22 [0.11, 0.47] 0.83 [0.51, 1.33] 1.45 [1.01, 2.09]	Odds Ratio	Study or Subgroup Anabheradmand 2015 Cao 2016 Chi 2014 Dong 2015 Hsien 2014 Hu 2015	Events 30 111 48 34 54 54 105 62 31	Total 55 133 94 59 98 460	Events 19 118 28 33 88 46 63 33	45 242 56 74 202 221	4.7% 6.7% 5.6% 5.4% 7.0% 7.8%	M-H. Random, 95% C 1.64 [0.74, 3.64] 5.30 [3.15, 8.94] 1.04 [0.54, 2.02] 1.69 [0.85, 3.37] 1.59 [0.98, 2.58] 1.13 [0.76, 1.66]	HH. Random. 95% Cl
udy or Subgroup abkheradmand 2015 so 2016 sigh 2014 u 2015 sign 2013	LNM Events 124 18 91 94 65	+ <u>Total</u> 34 163 59 199 370 136	Events 48 171 49 51 63 64	Total 66 212 74 101 332 171	5.9% 8.3% 7.1% 8.4% 9.0% 8.5%	Odds Ratio M-H. Random. 95% C 0.12 [0.04, 0.30] 0.76 [0.46, 1.25] 0.22 [0.11, 0.47] 0.83 [0.51, 1.33] 1.45 [1.01, 2.09] 1.53 [0.97, 2.42]	Odds Ratio	Study or Subgroup Arabheradmand 2015 Cao 2016 Hisin 2015 Hisin 2014 Hu 2015 Jang 2013 Li 2014 SHINDEN 2015	Events 30 111 48 34 54 105 62 31 51	Total 55 133 94 59 98 460 152 59 117	Events 19 118 28 33 88 46 63 33 54	45 242 56 74 202 221 149 60 111	4.7% 6.7% 5.6% 5.4% 7.0% 7.8% 7.2% 5.2% 6.7%	M-H. Random. 95% C 1.64 [0.74, 3.64] 5.30 [3.15, 8.94] 1.04 [0.54, 2.02] 1.69 [0.85, 3.37] 1.59 [0.98, 2.58] 1.13 [0.76, 1.66] 0.94 [0.59, 1.49] 0.91 [0.44, 1.86] 0.82 [0.48, 1.37]	3 M.H. Random. 95% GL
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udy or Subgroup. abhheradmand 2015 to 2016 to 2016 tein 2014 2015 tein 2014 2015 tein 2015 tein 2015 tein 2015 tein 2015 tein 2015 tein 2015 tein 2015 tein 2015	LNM Events 124 18 91 94 65 13 48 4	+ <u>Total</u> 34 163 599 199 370 136 76 101 30	Events 48 171 49 51 63 64 17 58 10	Total 66 212 74 101 332 171 39 129 21	5.9% 8.3% 7.1% 8.4% 9.0% 8.5% 6.4% 8.2% 4.2%	Odds Ratio M-H. Random. 95% C 0.12 [0.04, 0.30] 0.76 [0.046, 1.25] 0.22 [0.11, 0.47] 0.33 [0.51, 1.209] 1.53 [0.97, 2.42] 0.27 [0.11, 0.64] 1.11 [0.66, 1.87] 0.77 [0.04, 0.66]	Odds Ratio	Study or Subgroup Anabheradmand 2015 Cao 2016 Chi 2014 Dong 2015 Hsiah 2014 Hu 2015 Jang 2013 Li 2014 SHINDEN 2015 Wang 2013 Wang 2014 Wu 2016	Events. 30 111 48 34 54 105 62 31 51 24 56 11	Total 55 133 94 59 98 460 152 59 117 66 99 34	Events 19 118 28 33 88 46 63 33 54 20 18 16	45 242 56 74 202 221 149 60 111 44 29 56	4.7% 6.7% 5.6% 5.4% 7.0% 7.8% 7.2% 5.2% 6.7% 4.8% 4.4% 4.0%	M-H. Random. 95% C 1.64 (0.74, 3.64) 5.30 (3.15, 8.64) 1.04 (0.54, 2.02) 1.69 (0.85, 3.37) 1.59 (0.98, 2.58) 1.13 (0.76, 1.66) 0.94 (0.59, 1.49) 0.91 (0.44, 1.86) 0.82 (0.48, 1.37) 0.69 (0.32, 1.49) 0.80 (0.34, 1.86) 1.20 (0.47, 3.01)	MHL Random 95% CL
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C tudy or Subgroup. tabheradmand 2015 tab 2016 tab 2015 tab 2014 12015 tab 2015 tab 2015 tab 2015 tab 2014 tab 2016 tab 2016 tab 2016	LNM Events 8 124 18 91 94 65 13 48 4 18 13 48 13 4 225	+ Total 34 163 59 199 370 136 76 101 30 59 61 400 430	Events 48 171 63 64 17 58 10 26 14 8 201	Total 66 212 74 101 332 171 39 129 21 51 29 24 353	5.9% 8.3% 7.1% 8.4% 9.0% 8.5% 6.4% 8.2% 4.2% 6.8% 6.0% 4.3% 9.3%	Odds Ratio MH Random. 35% C 012 (0.04, 0.03) 0.76 (0.46, 1.25) 0.22 (0.11, 0.47) 0.83 (0.51, 1.33) 1.45 (1.01, 2.09) 1.53 (0.97, 2.42) 0.27 (0.11, 0.64) 1.11 (0.66, 1.87) 0.27 (0.11, 0.64) 0.42 (0.19, 0.82) 0.22 (0.01, 0.75) 0.22 (0.06, 0.85) 0.83 (0.63, 1.10)	Odds Ratio	Study of Subgroup Arabheradmand 2015 Cao 2016 Chi 2014 Dong 2015 Haien 2014 Hu 2015 Jang 2013 Li 2014 SHINDEN 2015 Wang 2013 Wang 2014 Wu 2010 Xu 2016 Yang 2016 Yang 2015	Events. 30 111 48 34 54 54 54 55 62 31 51 51 24 56 111 83 6 248 66 66 248 66 248 66 248 66 838 66 248 75 75 75 75 75 75 75 75 75 75	Total 55 133 94 59 98 460 152 59 117 66 99 34 147 38 479 115	Events 19 118 28 28 33 88 46 63 33 54 20 18 16 42 6 108 72	45 242 56 74 202 221 149 60 111 44 29 56 103 26 234 163	4.7% 6.7% 5.6% 5.6% 5.4% 7.8% 7.2% 5.2% 6.7% 4.8% 4.8% 4.4% 6.8% 8.4% 7.0%	M-H. Random 35% G 1.64 (0.74, 3.64) 5.30 (3.15, 6.84) 1.04 (0.54, 202) 1.09 (0.85, 3.37) 1.59 (0.85, 3.37) 1.59 (0.85, 3.37) 1.59 (0.82, 1.34) 0.54 (0.59, 1.49) 0.51 (0.44, 1.37) 0.69 (0.32, 1.40) 0.62 (0.44, 1.37) 0.69 (0.32, 1.40) 1.20 (0.47, 3.01) 1.58 (1.13, 3.14) 0.63 (0.16, 2.21) 1.50 (0.92, 1.71) 1.70 (10.5, 2.76)	
C tudy or Subgroup. tabheradmand 2015 tab 2016 tab 2015 tab 2014 12015 tab 2015 tab 2015 tab 2015 tab 2014 tab 2016 tab 2016 tab 2016	LNM Events 8 124 18 94 94 65 13 48 4 4 13 4 8 13 4	+ Total 34 163 59 199 370 136 76 101 30 59 61 400 430	Events 48 171 49 51 63 64 17 58 10 26 14 8	Total 66 212 74 101 332 171 39 129 21 51 29 24 353	5.9% 8.3% 7.1% 8.4% 9.0% 8.5% 6.4% 8.2% 4.2% 6.8% 6.0% 4.3%	Odds Ratio MH. Random, 95% C 0.12 [0.04, 0.30] 0.76 [0.46, 1.25] 0.22 [0.11, 0.47] 1.53 [0.07, 2.42] 0.27 [0.11, 0.64] 1.51 [0.06, 1.87] 0.17 [0.04, 0.66] 0.42 [0.19, 0.52] 0.29 [0.01, 0.75] 0.22 [0.06, 0.85]	Odds Ratio	<u>Study of Subgroup</u> Arabheradmand 2015 Cao 2016 Huain 2015 Huain 2014 Jang 2013 Li 2014 SHINDEN 2015 Wang 2013 Wang 2013 Wang 2014 Wu 2016 Yang 2016	Events. 30 111 48 34 105 62 31 51 51 51 24 56 11 83 6 248	Total 55 133 94 59 98 460 152 59 117 66 99 34 147 38 479	Events 19 118 28 28 33 88 46 63 33 54 20 18 16 42 6 108 108	45 242 56 74 202 221 149 60 111 44 29 56 103 26 234	4.7% 6.7% 5.6% 5.4% 7.8% 7.2% 5.2% 6.7% 4.8% 4.4% 4.6% 6.8% 2.6% 8.4%	M-H. Random. 955:C 1.64 (0.74, 3.64) 5.30 (3.15, 8.94) 1.04 (0.54, 2.02) 1.69 (0.85, 3.37) 1.59 (0.98, 2.58) 0.91 (0.44, 1.86) 0.91 (0.44, 1.86) 0.82 (0.48, 1.37) 0.69 (0.32, 1.49) 0.80 (0.34, 1.86) 1.20 (0.47, 3.01) 1.88 (1.13, 3.14) 0.63 (0.18, 2.21) 1.25 (0.92, 1.71) 1.25 (0.92, 1.71) 1.25 (0.92, 1.71)	
C ab/heredmand 2015 to 2016 to 2016 to 2016 to 2015 to 2015 to 2015 to 2015 to 2015 to 2015 to 2014 to 2010 to 2010 to 2016 to 2016 to 2016 to 2016	LNM Events 8 124 18 91 94 65 13 48 4 18 13 48 13 4 225	+ Total 34 163 59 199 370 136 76 101 30 59 61 400 430	Events 48 171 63 64 17 58 10 26 14 8 201	Total 66 212 74 101 332 171 39 129 21 51 29 24 353 69	5.9% 8.3% 7.1% 8.4% 9.0% 8.5% 6.4% 8.2% 4.2% 6.8% 6.0% 4.3% 9.3%	Odds Ratio MH Random. 35% C 012 (0.04, 0.30) 0.76 [0.46, 1.25] 0.22 [0.11, 0.47] 0.33 [0.51, 1.33] 1.45 [1.01, 2.09] 1.53 [0.97, 2.42] 0.27 [0.11, 0.64] 1.11 [0.66, 1.87] 0.27 [0.11, 0.65] 0.42 [0.10, 0.68] 0.42 [0.10, 0.55] 0.22 [0.00, 0.68] 0.22 [0.00, 0.68] 0.23 [0.30, 1.10] 1.32 [0.71, 2.46]	Odds Ratio	Study of Subgroup Arabheradmand 2015 Cao 2016 Chi 2014 Dong 2015 Huine 2014 Hu 2015 Jang 2013 Li 2014 SHINDEN 2015 Wang 2013 Li 2014 SHINDEN 2015 Wang 2013 Wang 2014 Wu 2010 Xu 2016 Yang 2016	Events. 30 111 48 34 54 54 54 55 62 31 51 51 24 56 111 83 6 248 66 66 248 66 248 66 248 66 838 66 248 75 75 75 75 75 75 75 75 75 75	Total 55 133 94 59 98 460 152 59 117 66 99 34 147 38 479 115 86	Events 19 118 28 28 33 88 46 63 33 54 20 18 16 42 6 108 72	45 242 56 74 202 221 149 60 111 44 29 56 103 26 234 163 82	4.7% 6.7% 5.6% 5.4% 7.2% 5.2% 6.7% 4.8% 4.8% 4.8% 4.6% 2.6% 8.4% 7.0% 5.9%	M-H. Random 355: C 1.64 (0.74, 3.64) 1.64 (0.74, 3.64) 1.64 (0.54, 2.02) 1.69 (0.85, 3.37) 1.59 (0.96, 2.58) 1.13 (0.76, 1.66) 0.94 (0.24, 1.86) 0.92 (0.44, 1.37) 0.96 (0.22, 1.49) 0.96 (0.24, 1.86) 1.20 (0.47, 3.01) 1.88 (1.13, 3.14) 0.63 (0.16, 2.21] 1.25 (0.92, 1.71) 1.72 (0.93, 3.19) 1.72 (0.93, 3.19)	
C tudy or Subgroup tabkhreidmand 2015 ao 2016 sieh 2014 u 2015 u 2015 u 2015 u 2015 ung 2014 turg 2014 turg 2014 turg 2016 ung 2015 ung 2014 ung 2016 ung 2016	LNM Events 1244 18 91 945 13 48 48 13 48 13 4 4 225 47	+ Total 34 163 59 370 136 76 76 76 76 76 76 76 76 70 130 59 61 101 30 59 61 40 430 99 1857	Events 48 171 49 51 63 64 17 58 10 26 14 8 201 28	Total 666 212 74 101 332 171 399 129 21 51 29 24 353 69 1671	5.9% 8.3% 7.1% 8.4% 9.0% 8.5% 6.4% 8.2% 4.2% 6.8% 6.0% 4.3% 9.3% 7.7%	Odds Ratio MH Random. 35% C 012 (0.04, 0.03) 0.76 (0.46, 1.25) 0.22 (0.11, 0.47) 0.83 (0.51, 1.33) 1.45 (1.01, 2.09) 1.53 (0.97, 2.42) 0.27 (0.11, 0.64) 1.11 (0.66, 1.87) 0.27 (0.11, 0.64) 0.42 (0.19, 0.82) 0.22 (0.01, 0.75) 0.22 (0.06, 0.85) 0.83 (0.63, 1.10)	Odds Ratio	Study of Subgroup Arabheradmand 2015 Cao 2016 Dong 2015 Haieh 2015 Jang 2013 Li 2014 SHINDEN 2015 Wang 2013 Wang 2013 Wang 2013 Wang 2016 Yang 2016	Events 30 111 48 34 54 105 62 31 51 51 51 51 51 83 6 6 248 83 6 6 248 83 6 44	Total 55 133 94 59 98 460 152 59 117 66 99 34 147 38 479 115	Events 19 118 28 283 38 46 63 334 20 18 16 42 6 108 72 31	45 242 56 74 202 221 149 60 111 44 29 56 103 26 234 163 82	4.7% 6.7% 5.6% 5.6% 5.4% 7.8% 7.2% 5.2% 6.7% 4.8% 4.8% 4.4% 6.8% 8.4% 7.0%	M-H. Random 35% G 1.64 (0.74, 3.64) 5.30 (3.15, 6.84) 1.04 (0.54, 202) 1.09 (0.85, 3.37) 1.59 (0.85, 3.37) 1.59 (0.85, 3.37) 1.59 (0.82, 1.34) 0.54 (0.59, 1.49) 0.51 (0.44, 1.37) 0.69 (0.32, 1.40) 0.62 (0.44, 1.37) 0.69 (0.32, 1.40) 1.20 (0.47, 3.01) 1.58 (1.13, 3.14) 0.63 (0.16, 2.21) 1.50 (0.92, 1.71) 1.70 (10.5, 2.76)	
tudy or Subgroup rabkheradmand 2015 ao 2016 ao 2016 ao 2016 ao 2016 ao 2016 ang 2013 a 2013 ang 2013 ang 2014 ang 2014 ang 2014 ang 2014 to 2016 ang 2016 ang a 2016 ang	LNM Events 124 18 91 94 65 13 14 8 4 4 18 13 48 13 48 13 47 772	+ <u>Total</u> 34 163 59 370 136 76 101 30 59 61 140 430 99 1857	Eventa 48 171 49 51 63 64 175 8 10 26 14 8 201 28 808	Total 66 212 74 101 332 171 39 21 51 29 24 353 69 1671	5.9% 8.3% 7.1% 8.4% 9.0% 8.5% 6.4% 8.2% 4.2% 6.8% 4.2% 6.0% 4.3% 9.3% 7.7%	Odds Ratio M-H. Random. 35% C 0.12 (0.04, 0.35) 0.76 (0.46, 1.25) 0.23 (0.11, 0.47) 1.55 (0.07, 2.42) 1.55 (0.07, 2.42) 0.27 (0.11, 0.64) 1.51 (0.07, 2.42) 0.42 (0.19, 0.32) 0.42 (0.40, 0.44)	Odds Ratio	Study of Subgroup Arabheradmand 2015 Cao 2016 Chi 2014 Dong 2015 Huine 2014 Hu 2015 Jang 2013 Li 2014 SHINDEN 2015 Wang 2013 Li 2014 SHINDEN 2015 Wang 2013 Wang 2014 Wu 2010 Xu 2016 Yang 2016	Events. 30 1111 48 34 34 34 56 62 311 511 24 56 61 24 56 62 31 51 24 56 62 48 66 44 56 10 111 111 111 111 111 111 111	Total 55 133 94 59 98 460 152 59 117 66 99 34 147 38 479 115 86 2291	Events 19 118 28 28 33 88 46 63 33 54 20 18 16 42 6 108 72 31 795	45 242 56 74 202 221 149 60 111 44 29 56 103 26 234 163 82 1897	4.7% 6.7% 5.6% 5.4% 5.2% 6.7% 4.8% 4.4% 6.8% 2.6% 8.4% 5.9% 100.0%	M-H. Random 355: C 1.64 (0.74, 3.64) 1.04 (0.54, 2.02) 1.09 (0.85, 3.37) 1.09 (0.85, 3.37) 1.39 (0.96, 2.56) 0.34 (0.76, 1.66) 0.34 (0.74, 1.86) 0.32 (0.44, 1.36) 0.32 (0.44, 1.36) 0.32 (0.44, 1.36) 0.42 (0.44, 1.86) 0.42 (0.44, 1.86) 0.43 (0.16, 0.27) 1.20 (0.47, 3.01) 1.30 (1.65, 2.76) 1.72 (0.33, 3.19) 1.33 (1.05, 1.68)	

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Figure 2: Forest plots for Clinicopathological features. Up-regulated ncRNAs : (A) Her2; down-regulated ncRNAs: (B) Tumor size; (C) Lymph node metastasis; (D) PR.

Influence analysis and publication bias examination were implemented for every clinicopathological feature, in highly and lowly expressed ncRNAs, respectively.

Α

P-values from Begg's funnel plot and Egger's test were all larger than 0.05. Since the studies of down-regulated ncRNAs were less than twenty, we performed the Begg's

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			Odds Ratio	Odds Ratio				Odds Ratio	Odds Ratio
Udy or Subgroup 5.1.1 Wstern countries	log[Odds Ratio] SE	Weight	IV. Random, 95% CI	IV. Random, 95% Cl	Study or Subgroup 14.1.1 microarrays	log[Odds Ratio] Si	E Weight	IV. Random, 95% Cl	IV. Random, 95% CI
tolin b 2015	1.2499 0.4624	1.8%			JANG 2013	0.257 0.288	9 3.1%	1.29 [0.73, 2.28]	+
			3.49 [1.41, 8.64]	-	MacKenzie 2014	0.6729 0.17		1.96 [1.38, 2.78]	-
ota 2010	1.1969 0.2859		3.31 [1.89, 5.80]	-	Peng DSE22220 2016	0.6471 0.310	1 2.9%	1.91 [1.04, 3.51]	
Kenzie 2014	0.6729 0.179		1.96 [1.38, 2.78]		Peng GSE19536	1.3913 0.8433	2 0.7%	4.02 [0.77, 20.99]	+
dhavan a 2016	1.1663 0.2238	3.8%	3.21 [2.07, 4.98]		Peng TCGA 2016	1.4609 0.409	9 2.1%	4.31 [1.93, 9.62]	
dhavan b 2016	1.7783 0.3434	2.6%	5.92 [3.02, 11.60]		Subtotal (95% CI)		13.1%	2.05 [1.43, 2.94]	•
dhavan c 2016	1.2698 0.2207	3.8%	3.56 [2.31, 5.49]		Heterogeneity: Tau ² = 0.	06; Chi ² = 6.50, df = 4 (P =	0.16); l2 = :	38%	
dhavan d 2016	2.0373 0.3451	2.6%	7.67 [3.90, 15.08]		Test for overall effect: Z	= 3.90 (P < 0.0001)			
dhavan e 2016	0.4511 0.2353		1.57 [0.99, 2.49]	-					
dhavan f 2016	0.0488 0.3994	2.2%	1.05 [0.48, 2.30]	-	14.1.2 fresh tissue				
dhavan g 2016	0.571 0.2335	3.7%	1.77 [1.12, 2.80]		Cai 2015	1.1506 0.533		3.16 [1.11, 9.00]	
dhavan h 2016	1.1756 0.3537	2.5%	3.24 [1.62, 6.48]		CHEN 2012	1.0228 0.134		2.78 [2.13, 3.62]	-
dhavan i 2016	0.8416 0.2225	3.8%	2.32 [1.50, 3.59]	-	Dong 2014	0.8416 0.319		2.32 [1.24, 4.34]	÷-
dhavan j 2016	1.7263 0.3429	2.6%	5.62 [2.87, 11.01]		Guo a 2016	1.008 0.192		2.74 [1.88, 3.99]	
Iter 2011	0.6981 0.2342	3.7%	2.01 [1.27, 3.18]		Guo b 2016	0.6881 0.16		1.99 [1.44, 2.75]	
ototal (95% CI)		44.1%	2.81 [2.18, 3.62]	◆	Gupta 2010	1.1969 0.2859 0.9357 0.342		3.31 [1.89, 5.80]	
	5; Chi ² = 41.45, df = 13 (P				HU 2016 Lee 2011	0.9357 0.342		2.55 [1.30, 4.99]	
t for overall effect: Z = 7					Lee 2011 Li 2015	2.6542 1.205		14.21 [1.34, 151.01] 2.75 [1.23, 6.18]	·
	1.00 (1 . 0.00001)				Madhavan a 2016	1.1663 0.223			
1.2 Asian countries					Madhavan b 2016	1.7783 0.343		3.21 [2.07, 4.98] 5.92 [3.02, 11.60]	
2015	1.1506 0.5338	1.5%	3.16 [1.11, 9.00]		Madhavan c 2016	1.2698 0.220		3.56 [2.31, 5.49]	-
				-	Madhavan d 2016	2.0373 0.345		7.67 [3.90, 15.08]	· · · ·
EN 2012	1.0228 0.1349		2.78 [2.13, 3.62]		Madhavan e 2016	0.4511 0.235		1.57 [0.99, 2.49]	-
g 2014	0.8416 0.3196	2.8%	2.32 [1.24, 4.34]	-	Madhavan f 2016	0.0488 0.399		1.05 [0.48, 2.30]	+
o a 2016	1.008 0.1922		2.74 [1.88, 3.99]		Madhavan g 2016	0.571 0.233		1.77 [1.12, 2.80]	
b 2016	0.6881 0.165		1.99 [1.44, 2.75]	<u> </u>	Madhavan h 2016	1.1756 0.353		3.24 [1.62, 6.48]	
2016	0.9357 0.3424	2.6%	2.55 [1.30, 4.99]		Madhavan i 2016	0.8416 0.222		2.32 [1.50, 3.59]	
NG 2013	0.257 0.2889	3.1%	1.29 [0.73, 2.28]	T .	Madhavan j 2016	1.7263 0.342		5.62 [2.87, 11.01]	
2011	2.6542 1.2057	0.4%	14.21 [1.34, 151.01]	· · · · ·	Ota D 2011	0.8502 0.4493	3 1.9%	2.34 [0.97, 5.65]	
015	1.0131 0.4125		2.75 [1.23, 6.18]	 -	Qian 2008	0.1906 0.533	8 1.5%	1.21 [0.43, 3.44]	
D 2011	0.8502 0.4493	1.9%	2.34 [0.97, 5.65]		Qian 2009	0.0296 0.320	1 2.8%	1.03 [0.55, 1.93]	+
ng DSE22220 2016	0.6471 0.3101	2.9%	1.91 [1.04, 3.51]		Toyama 2012	1.4793 0.754	8 0.8%	4.39 [1.00, 19.27]	
ng GSE19536	1.3913 0.8432	0.7%	4.02 [0.77, 20.99]	<u> </u>	Walter 2011	0.6981 0.234		2.01 [1.27, 3.18]	-
g TCGA 2016	1.4609 0.4099	2.1%	4.31 [1.93, 9.62]		X Xu a 2016	0.5068 0.37		1.66 [0.79, 3.48]	<u>+</u>
n 2008	0.1906 0.5338	1.5%	1.21 [0.43, 3.44]	_ <u> </u>	X Xu b 2016	1.2641 0.461		3.54 [1.43, 8.75]	
n 2009	0.0296 0.3201	2.8%	1.03 [0.55, 1.93]	+	Xu 2015	0.6921 0.256		2.00 [1.21, 3.30]	-
ama 2012	1.4793 0.7548	0.8%	4.39 [1.00, 19.27]		YAN 2008	1.419 0.424		4.13 [1.80, 9.50]	
u a 2016	0.5068 0.378	2.3%	1.66 [0.79, 3.48]	+	Yu 2014	0.8809 0.38		2.41 [1.13, 5.16]	
b 2016	1.2641 0.4619	1.8%	3.54 [1.43, 8.75]		Zhang 2015	1.0616 0.340		2.89 [1.48, 5.64]	
015	0.6921 0.2567	3.4%	2.00 [1.21, 3.30]		Zheng 2015 Subtotal (95% Cl)	2.4376 0.75	4 0.8% 83.1%	11.45 [2.61, 50.17] 2.63 [2.25, 3.08]	
2008	1,419 0,4244	2.0%	4.13 [1.80, 9.50]			00- CHR - 60 74 - 4 - 20 /			
2014	0.8809 0.388	2.0%	2.41 [1.13, 5.16]	——		09; Chi ² = 62.74, df = 30 (i	-= 0.0004);	r = 52%	
ng 2015	1.0616 0.3406	2.5%	2.89 [1.48, 5.64]		Test for overall effect: Z	= 12.02 (F < 0.00001)			
o 2011	1.9273 0.6382	1.1%			14.1.3 serum				
		0.8%	6.87 [1.97, 24.00]		Antolin b 2015	1.2499 0.462	4 1.8%	3.49 [1.41, 8.64]	
ng 2015	2.4376 0.754		11.45 [2.61, 50.17]		Zhao 2011	1.9273 0.638		6.87 [1.97, 24.00]	
ng s 2015	2.6225 0.754	0.8%	13.77 [3.14, 60.36]	•	Zheng s 2015	2.6225 0.75		13.77 [3.14, 60.36]	
total (95% CI)			2.48 [2.08, 2.97]	· ·	Subtotal (95% CI)		3.8%	5.82 [2.71, 12.51]	
	r; Chi ² = 38.83, df = 24 (P	= 0.03); l ²	= 38%			11; Chi ² = 2.57, df = 2 (P =			
t for overall effect: Z = 9	9.95 (P < 0.00001)				Test for overall effect: Z				
al (95% CI)		100.0%	2.63 [2.27, 3.05]		Total (95% CI)		100.0%	2.63 [2.27, 3.05]	
); Chi ² = 80.99, df = 38 (P	< 0.0001)	; I ² = 53% 0.01	0.1 1 10 100		10; Chi ² = 80.99, df = 38 (f	<pre>< 0.0001);</pre>	l² = 53%	0.01 0.1 1 10
t for overall effect: Z = "	12.86 (P < 0.00001)				Test for overall effect: Z	= 12.86 (P < 0.00001)			
	ces: Chi ² = 0.60, df = 1 (P			s [experimental] Favours [control]		nces: Chi ² = 5.94. df = 2 (F		F	avours [experimental] Favours [control

Figure 3: Subgroup analyses for OS of breast cancer patients. (A) Subgroup analyses based on races for up-regulated ncRNAs; **(B)** Subgroup analyses based on sample types for up-regulated ncRNAs.

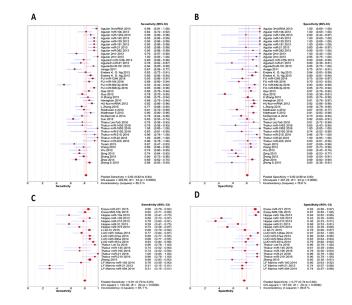


Figure 4: Sensitivity and specificity in subgroup analysis based on sample type. (A) the pooled sensitivity for blood; (B) the pooled specificity for blood; (C) the pooled sensitivity for tissues; (D) the pooled specificity for tissues.

funnel plot and founded the funnel is asymmetric. Meanwhile, influence analysis results manifested the stability of results. In the high expression series, only HER2 group existed significant publication bias.

DISCUSSION

According to the GLOBOCAN estimates, about 14.1 million new cancer cases and 8.2 million deaths occurred in 2012 worldwide [27]. Human breast carcinoma is one of the most frequent cancers in the female and deeply threatens woman health and life quality. In this review, we gathered published papers to study the relationship between ncRNAs and prognosis, diagnosis, and clinicopathological features in breast cancer. By systematically analyzing published original studies, we found that ncRNA have predictive value for prognosis in breast cancer. Combined HRs suggest that ncRNA are independent risk factors for OS in breast cancer patients. In addition, ncRNAs appear to be independent prognostic risk factors for RFS and PFS in breast cancer patients. However, these analyses had significant heterogeneity in terms of sample type and multivariable models. Large sample microarrays subgroup showed no significant heterogeneity but the effect size (HR=1.83) was weaker than others, indicating the possibility of overestimating effect size. Besides, our finding also suggest that some ncRNAs alone (miR-124, miR-210, miR-21, miR-200a, miR-200c) are independent risk factors for OS in breast cancer.

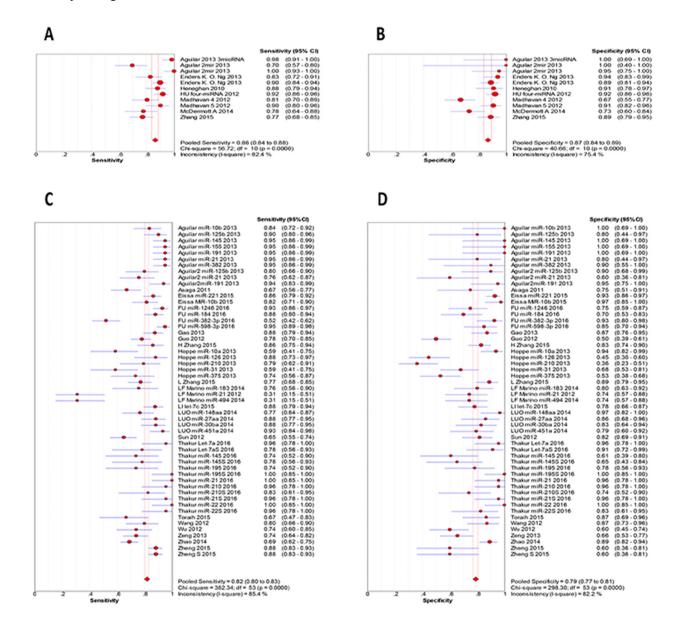


Figure 5: Sensitivity and specificity in subgroup analysis based on constituent. (A) the pooled sensitivity for single ncRNA; **(B)** the pooled specificity for single ncRNA; **(C)** the pooled sensitivity for multiple ncRNAs; **(D)** the pooled specificity for multiple ncRNAs.

Table 3: Relationship between clinicopathol	logical features and ncRNAs in breast cancer
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Survival analys	is	No. of studies	No. of patients/ controls	Pooled HR	Heterogeneity
Age	Down	10	881/788	1.05[0.80-1.38]	37%
	Up	15	934/1022	1.01[0.84-1.22]	0%
LNM	Down	13	1721/1500	0.58[0.40,0.84]	81%
	Up	17	1480/1441	1.00[0.73,1.36]	70%
Tumor Size	Down	9	714/1204	1.47[1.19,1.82]	7%
	Up	18	1265/1596	0.80[0.60,1.05]	65%
ER	Down	15	2499/1535	1.25[0.98,1.61]	66%
	Up	25	2133/1818	0.91[0.73,1.14]	59%
PR	Down	16	2291/1897	1.33[1.05,1.68]	65%
	Up	23	1964/1981	1.15[0.94,1.41]	50%
HER2	Down	11	849/1389	0.68[0.42,1.11]	85%
	Up	14	1062/1597	1.36[1.10,1.82]	58%
Menopausal	Down	2	166/159	1.11[0.72,1.69]	0%
	Up	11	866/917	1.13[0.93,1.36]	15%

The detection methods for breast cancer such as imaging examination and pathological examination had certain limitations, including radiation, invasion and low diagnostic accuracy. Noninvasive biomarkers, such as CEA and CA15-3, are widely used in clinic. However, these markers have low sensitivity and specificity for breast screening [9, 28]. Zeng et al [29] have demonstrated that these markers may be more suitable for advanced breast cancer. Thus, it is important to identify effective and noninvasive tumor biomarkers for early detection and diagnosis. In this meta-analysis, the overall AUC of SROC is 0.9037, indicating a high accuracy of ncRNAs. The DOR value also evaluates the accuracy of a diagnostic test, with higher values indicating better performance[30]. DOR value less than 1.0 does not approve its competent role as a biomarker in the diagnostic test [31]. Nevertheless, the pooled DOR in this work reached up to 24.767, suggesting ncRNA can be used as a non-invasive indicator for breast

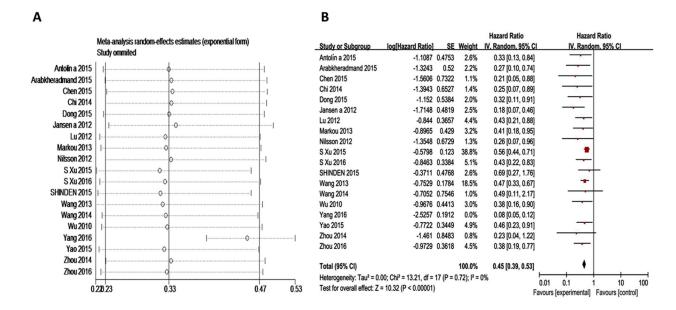


Figure 6: Subgroup analyses for OS of breast cancer patients. (A) Influence analysis for down-regulated ncRNAs; (B) Forest plots for down-regulated ncRNAs after excluding the outlier.

cancer diagnosis. Besides, the sensitivity and specificity of multiple ncRNAs [18, 32–37] are higher than the single ones, suggesting combined ncRNAs could be useful for the diagnosis of breast cancer.

The threshold effect is one of the leading causes of heterogeneity in a diagnostic meta-analysis [38], and mainly caused by the different cut-off values used in individual studies [39]. Heterogeneity generated by non-threshold effect is usually addressed via pooled DOR [30]. The P values in Cochran's Q test were all less than 0.01 in our study, accompanied by I² more than 50 %, suggesting that heterogeneity in the overall and subgroup analyses was attributed to threshold effect and non- threshold effect. Deek's funnel plot asymmetry test indicated no significant publication bias in the diagnostic analysis.

In the clinicopathological features part, downregulated ncRNAs were negatively related to tumor size and LNM, but positively related to the expression of PR; and up-regulated ncRNAs were positively related to the expression of HER2. However, the result of the relationship between down-regulated ncRNAs and HER2 exist significant heterogeneity, and after excluding the article [19] that stood out in the influence analysis, heterogeneity no longer has significance (Supplementary Figure 10). The LNM group showed large heterogeneity as well, and subgroup analyses by ncRNA type and sample type failed to locate the source of heterogeneity. Influence analyses for other aspects showed fine stability.

Three ncRNAs (miR-2 (n=6), MALAT 1 (n=4), miR-124 (n=2)) were studied in more than two studies. Our comprehensively analyzed data suggested that the expression of miR-21 was positively related to HER2 (OR=2.74, 95% CI: 1.13-6.62), negatively related to ER (OR=0.57, 95% CI: 0.34-0.96) and positively related to age (OR=0.57, 95% CI: 0.35-0.95). Meanwhile, the expression of MALAT1 was negatively related to tumor size (OR=1.29, 95% CI: 1.05-1.59). The expression of mir-124 was negatively related to LNM (OR=0.17, 95% CI: 0.10-0.31).

Most of the meta-analysis only evaluated the relationship between a type of ncRNA and many cancers. In our study, data were pooled rationally. We have analyzed the role of all ncRNAs in breast cancer including prognosis, diagnosis, and clinicopathological features. Besides, single ncRNA was also estimated. In diagnosis, we analyzed single ncRNA and multiple ncRNAs, respectively. The results suggested joint detection is better than single detection.

Limitations

Most of the included ncRNAs have been studied only once previously, making it difficult to systematically evaluate the clinical value of one specific ncRNA. There are several other limitations in our study. First, this review is only based on the results of databases of published studies, and did not include study registers or gray literature. This could be the source of publication bias. Second, our meta-analysis combines multiple studies, which contains different types, samples, cutoff values, and HRs, all of which may cause statistical heterogeneity. Third, many potential biomarkers being analyzed in our study are not used in clinical practice yet.

CONCLUSION

Taken together, our results indicated the potential value of ncRNAs in the prognosis and diagnosis of breast cancer. But considerable shortcoming might influence our final estimates. Therefore, future standardized researches with high quality are needed to verify these results.

MATERIALS AND METHODS

Study strategy and eligibility criteria

We conducted comprehensive literature searches in Medline and Web of Science for eligible studies up to Sep, 2016, using the keywords[(ncRNAs or microRNAs or miRNAs or long non-coding RNAs) AND (breast or breast cancer)], with publication language limited to English.

Case-control reports were identified that explored the association of any single or combination of relevant ncRNAs with one or more of the following aspects: survival, diagnosis and clinical features of breast cancer patients.

In order to be eligible for inclusion in meta-analysis, studies had to provide the effect size and CI for the association of ncRNAs with outcomes, or appropriate data for the effect size and CI could be calculated. For survival analysis, we extracted the HRs and 95% CI [40] for overall survival (OS, duration of time from day of diagnosis to the day of death due to any cause), recurrence-free survival (RFS, duration of time from day of cure from cancer to the day evidence of cancer progression/recurrence is identified), progression/event/disease-free survival (PFS, duration of time from the day of first treatment to the day evidence of cancer progression are identified or the patient dies of any cause). In diagnostic articles, the sensitivity and specificity are extracted to construct twoby-two tables. ORs and 95% CI were used to investigate the relationship between expression levels of ncRNAs and clinicopathological features. At the same time, we excluded review, letters, case reports, guidelines, and some studies without complete data.

Two reviewers independently screened titles and abstracts of all identified records according to prespecified inclusion and exclusion criteria. Disagreements were resolved by a third reviewer. Full text articles were obtained for all included studies and were screened again for inclusion or exclusion by two reviewers independently, with disagreements resolved by discussion.

Quality assessment

Three researchers independently reviewed and evaluated eligible studies assessed by the Newcastle-Ottawa quality assessment scale (NOS)[41, 42]. The methodological quality of diagnosis part in this study was performed with Quality Assessment of Diagnostic Accuracy Studies (QUADAS-2) criteria [41].

Data extraction

Data were extracted from eligible articles as follow. General information: first author's name, year of publication, country of the study, type of ncRNAs, sample size; characteristics of participants: (1) HRs and 95% CI were extracted for survival effect size. Since effect estimates extracted from multivariate analysis (e.g. Cox regression) that are affected by other variables, HR and 95% CI were not directly extracted [10, 43–46]; approximations of HRs were indirectly calculated based on the correlative statistics using the methods described by Tierney et al [28]. When ncRNA expression levels were subdivided into low versus medium versus high groups, only data for the comparison between high versus low expression levels were extracted [14, 21, 47, 48]; (2) For diagnostic studies data were extracted relating to: sensitivity and specificity (two-by-two tables); (3) clinicopathological characteristics are age, tumor size, menopausal, lymph node metastasis, and the expression of growth factor receptors (estrogen receptor, ER; progesterone receptor, PR; epidermal growth factor receptor 2, HER2).

Statistical analysis

Data syntheses were conducted using Review Manager 5.2 and Meta-Disc 1.4. Publication bias examination, and influence analyses were performed using STATA 11.0. The HR with the corresponding 95% CI for OS, RFS and PFS were calculated to evaluate the prognostic value of ncRNA [49, 50]. HR>1 imply that patients with lower expression of the ncRNA had better prognosis than patients with higher expression. The true positive (TP), false positive (FP), false negative (FN), true negative (TN) based on two-by-two tables, that were used to consider sensitivity (SE), specificity (SP), positive likelihood ratio (PLR), negative likelihood ratio (NLR), and summary receiver operator characteristic (SROC) curve. These data were used to assess the diagnosis value of ncRNAs in breast cancer. Odds ratios (ORs) and the 95% CI were calculated to analyze the relationship between ncRNA and clinicopathological features. P<0.05 was considered statistically significant. Heterogeneity was analyzed using the Q and I² statistics [41, 42]. P < 0.1 indicated presence of heterogeneity. I² > 50% was defined as significant heterogeneity.

ACKNOWLEDGMENTS

This study was supported by National Natural Science Funds (No. 81472033 and No. 30901308), the National Science Foundation of Hubei Province (No. 2013CFB233, No. 2013CFB235 and No.2016CFB672), the Scientific and technological project of Wuhan City (No. 2014060101010045), Hubei Province health and family planning scientific research project (WJ2015Q021), and Training Program of the science and technology innovation from Zhongnan Hospital of Wuhan University (cxpy20160054).

CONFLICTS OF INTEREST

All authors declare that there is no conflicts of interests.

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