Prognostic significance of long intergenic non-protein-coding RNA 511 expression in malignant tumors
A systematic review and meta-analysis
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Abstract
Background: A growing number of studies have suggested that the Long intergenic noncoding RNA 00511 (LINC00511) is aberrantly expressed in multiple malignancies and is related to patient survival. Herein, we conducted a systematic review and meta-analysis to comprehensively evaluate the prognostic significance of LINC00511 in human malignancies.

Methods: Eligible studies published by March 11, 2020 were identified in 4 electronic databases including PubMed, EMBASE, Web of Science, and the Chinese National Knowledge Infrastructure. Hazard ratios and 95% confidence intervals (CIs) were used to evaluate the prognostic significance of LINC00511 expression in malignant tumors. The association between LINC00511 expression and cancer clinicopathologic features were assessed using Odds ratios (ORs) and CIs.

Results: A total of 13 studies, comprising 1,053 patients, were included in the meta-analysis. The calculated hazard ratio was 2.00 (95% CI: 1.59–2.52, P < .000), suggesting that higher LINC00511 expression could predict poorer overall survival in patients with malignancies. Additionally, our statistical analysis indicated that elevated LINC00511 expression closely associated with bigger tumours (OR=2.92, 95% CI 1.65–5.18, P < .000), higher incidence of lymph node metastasis (OR=3.46, 95% CI 2.11–5.66, P < .000) and distant metastasis (OR=2.40, 95% CI 1.14–5.05, P = .02), poorer differentiation (OR=1.55, 95% CI 1.11–2.16, P = .01), as well as more advanced TNM stage (OR=3.90, 95% CI 2.70–5.63, P < .000).

Conclusions: High LINC00511 expression may predict unfavorable prognosis in patients with malignancies. It should be further explored as a potential prognostic and therapeutic biomarker for human cancer.

Abbreviations: CC = cervical cancer, CI = confidence interval, HCC = hepatocellular carcinoma, HR = hazard ratio, LINC00511 = lnRNA long intergenic non-protein-coding RNA 511, OC = ovarian cancer, OR = odds ratio, OS = overall survival.

Keywords: long intergenic non-protein-coding RNA 511, long non-coding RNA, prognosis, tumor

1. Introduction
Malignant tumors are the major cause of death globally, representing a severe public health problem with its incidence and mortality rapidly rising in recent years.[1] In 2018, 18.1 million newly diagnosed cancer cases and 9.6 million cancer-associated deaths were reported.[2] Several diagnostic and therapeutic advances were reported in the past decades, but the 3- and 5-year survival rates of patients with malignancies remain unsatisfying.[3] Thus, it is imperative and urgent to identify new diagnostic biomarkers and therapeutic targets to improve the prognosis of these patients.

Long noncoding RNAs consist of more than 200 nucleotides RNA sequences[4] that were previously considered as genetic “junk.” However, increasing evidence shows that many long noncoding RNA are dysregulated in tumor tissues and play a vital role in tumor progression, which suggests that they may serve as prognostic and therapeutic biomarkers for tumors.[5–7] The long intergenic noncoding RNA 00511 (LINC00511) was firstly identified in 2015 by Cabanski et al.[8] Subsequently, several studies reported that abnormal LINC00511 expression was correlated with prognosis in patients with malignancies. Moreover, most studies suggested that LINC00511 could act as an oncogene and its high expression was predictive of poor prognosis in various malignancies, such as cervical cancer.
with favorable prognosis of some cancer patients.[28] Some studies also reported that LINC00511 could be a tumor suppressor, with high LINC00511 expression being associated with favorable prognosis of some cancer patients.[24]

To better understand the prognostic significance of LINC00511 in human malignancies, we performed a comprehensive systematic review and meta-analysis. Additionally, we also explored the association between LINC00511 expression and several clinicopathological features of cancer that are closely associated with prognosis.

2. Materials and methods

This study was performed following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines.[29] The ethical approval is not necessary, since this study is a review article.

2.1. Literature search

Relevant studies available by March 11, 2020, were selected upon a systematic review of the PubMed, EMBASE, Web of Science, and Chinese National Knowledge Infrastructure databases. The search strategy was established by the following keywords:

(i) (Long intergenic noncoding RNA 00511) or (LINC00511);
(ii) (cancer) or (neoplasm) or (tumor) or (carcinoma) or (adenocarcinoma);
(iii) We also manually searched through the references to identify potentially eligible studies.

2.2. Inclusion and exclusion criteria

The inclusion criteria were as follows:

(i) cohort studies that explored the association of LINC00511 expression with overall survival (OS) or clinicopathological features of cancer;
(ii) LINC00511 expression was detected using quantitative real-time PCR (RT-qPCR); and
(iii) Odds ratios (ORs) or hazard ratios (HRs), which assessed the relationship of LINC00511 expression with OS or clinicopathological features, were presented directly or could be calculated indirectly.

The exclusion criteria were:

(i) studies performed only at the cellular level;
(ii) case reports, letters, reviews, or summaries of conferences or discussions;
(iii) studies that evaluated tumor specimens collected before radiotherapy or chemotherapy; or
(iv) sample size < 30. If 2 or more studies analyzed the same cohort of patients, the most recent or complete study was selected.

2.3. Data extraction and quality assessment

Two authors extracted data from all the selected studies in an independent manner and inconsistencies between them were resolved through discussion. The collected data were as followings: first author’s name, year of publication, patient source, sample size, median age, gender, TNM stage, tumor size, cut-off value for high LINC00511 expression, detection method, follow-up time, HRs with 95% confidence interval (CIs) (presented directly or obtained indirectly from Kaplan-Meier survival curve), ORs with 95% CIs, and analysis type. Methodological quality of the included studies was assessed using Newcastle-Ottawa Scale,[30] with the maximum score of 9. In our study, we considered a score ≥ 6 as high quality, as previously reported.[31]

2.4. Statistical analysis

Review Manager (RevMan) 5.3 software was used to calculate the HRs or ORs, whereas publication bias assessment and sensitivity analysis were performed by Stata 14 software. The predicted effect size was calculated using a random-effects model when there was significant heterogeneity among the included studies.[32] Otherwise, a mixed-effects model was adopted. Heterogeneity studies were assessed using the Q value and I² statistic values. A predicted HR > 1 indicated that high LINC00511 expression was closely associated with poor prognosis of patients with malignancy. Statistical differences were considered when P value in Q statistics was < .05 or P was > 50%. Publication bias was determined by Begg funnel plot.[32]

3. Results

3.1. Basic characteristics and information of eligible studies

The preliminary search yielded 179 potential studies from PubMed, EMBASE, Web of Science and Chinese National Knowledge Infrastructure databases. First of all, we removed duplicated records using EndNote X9 software with 73 studies left for further identification. Next, these 73 studies were carefully screened by the titles, abstracts, and full texts. Finally, a total of 13 eligible studies comprising 1053 cancer patients were included according to the inclusion and exclusion criteria in this meta-analysis[9,10,16,17,21,22,25,28,33–35] (Fig. 1). All the eligible studies were from China and reported the association between LINC00511 expression and OS. A total of 9 cancer types were referred in these included studies, including pancreatic ductal adenocarcinoma, CC, OC, glioma, HCC, osteosarcoma, clear cell renal cell carcinoma, and lung cancer. Each eligible study was given no less than 6 points based on Newcastle-Ottawa Scale score system, which suggested that these studies were high-quality and proper for the synthesized analysis. The basic characteristics and information of the included studies were shown in Table 1.

3.2. Association between LINC00511 expression and OS

The association between LINC00511 expression and OS was explored in all the included studies with 1053 cancer. The HRs were synthesized using a random effect model due to the significant heterogeneity ($I^2=77\%$, $P=.000$). The synthesized HR was 2.00 (95% CI 1.59–2.52, $P<.000$) (Fig. 2), which indicated that increased LINC00511 expression may predict unfavorable OS. To determine the prognostic significance of LINC00511 expression in different cancer types, we conducted
the subgroup analysis by malignancy type. As illustrated in Figure 3, higher \( \text{LINC00511} \) expression was associated with poorer OS in lung cancer, breast cancer, glioma, and CC. Additionally, the subgroup analysis by analysis type (univariate vs multivariate) showed that there was a tight relationship between high \( \text{LINC00511} \) expression and short OS regardless of analysis type (Fig. 4). This result implied that high \( \text{LINC00511} \) expression may be an independent prognostic factor in cancer patients.

3.3. Association between \( \text{LINC00511} \) expression and clinicopathological features

Cancer clinicopathological features closely correlate with prognosis of patients, so we further explored the association between \( \text{LINC00511} \) expression and several clinicopathological features. As shown in Figure 5 and Table 2, the elevated \( \text{LINC00511} \) expression was closely associated with larger tumor size (OR = 2.92, 95% CI 1.65–5.18, \( P < .000 \)), higher incidence of lymph node metastasis (OR = 3.46, 95% CI 2.11–5.66,
and distant metastasis (OR = 2.40, 95% CI 1.14–5.05, \( P < .02 \)), poorer differentiation (OR = 1.55, 95% CI 1.11–2.16, \( P = .01 \)) as well as more advanced TNM stage (OR = 3.90, 95% CI 2.70–5.63, \( P < .000 \)).

3.4. Publication bias assessment and sensitivity analysis

Begg test was conducted to assess the publication bias of this meta-analysis. As a result, no significant publication bias for OS (\( P = .890 \)) was detected (Fig. 6A). The sensitivity analysis showed that sequential deletion of single study did not obviously alter the synthesized HRs for OS indicating that our synthesized analysis was stable and reliable (Fig. 6B).

4. Discussion

Growing evidence suggests that LINC00511 may act as an oncogene and could be a prognostic biomarker for several malignancies. Nevertheless, the prognostic significance of LINC00511 expression in cancer remains inconclusive. Most data suggested that increased LINC00511 expression was significantly correlated with shorter OS. In contrast, some studies reported that LINC00511 may be a tumor suppressor and that high LINC00511 expression may correlate with favorable prognosis of cancer patients. Therefore, we performed this meta-analysis and systematic review of current literature to comprehensively evaluate the prognostic value of LINC00511 in patients with malignant tumors. To the best of our knowledge, the present study is the first meta-analysis to evaluate the relationship between LINC00511 expression and prognosis in patients with malignant tumors. A total of 13 eligible studies, comprising 1053 patients, were included in this meta-analysis. The results showed that higher LINC00511 expression was significantly associated with worse OS. Additionally, our analyses indicated that high LINC00511 expression was significantly correlated with larger tumor size, positive metastasis, low tumor differentiation, and advanced TNM stage. Notably, in our subgroup and sensitivity analyses, the calculated HR for OS did not fluctuate dramatically, indicating the robustness of our meta-analysis.

LINC00511 plays an important role in the progression of multiple malignancies, which may account for the prognostic significance of LINC00511. Liu et al.\(^{[21]}\) and Lu et al.\(^{[22]}\) reported that LINC00511 contributed to the proliferation, stemness,

| Table 1 |
|---|
| The main characteristics of the eligible literatures included in the meta-analysis. |
| First author | Publication year | Region | Tumor type | Detection method | Cut-off value | Sample size | HRs (95% CIs) for OS | Analysis type | NOS score |
| Deng HH | 2019 | China | RCC | qRT-PCR | Median | 49 | 1.43 (1.09–1.88) | Univariate | 6 |
| Du XL | 2020 | China | Glioma | qRT-PCR | Median | 36 | 3.28 (1.33–8.09) | Univariate | 6 |
| Liu L | 2019 | China | BC | qRT-PCR | Median | 98 | 1.67 (1.23–2.27) | Univariate | 6 |
| Lu GM | 2018 | China | BC | qRT-PCR | Median | 39 | 1.57 (1.20–2.05) | Univariate | 6 |
| Mao BD | 2019 | China | CC | qRT-PCR | Median | 84 | 1.44 (1.13–1.84) | Univariate | 6 |
| Qiao SC | 2019 | China | Osteosarcoma | qRT-PCR | Median | 45 | 0.04 (0.00–0.29) | Univariate | 6 |
| Sun CC | 2016 | China | NSCLC | qRT-PCR | Median | 124 | 7.19 (5.33–14.65) | Multivariate | 7 |
| Wang B | 2019 | China | Glioma | qRT-PCR | Median | 82 | 2.53 (1.53–4.18) | Multivariate | 7 |
| Wang J | 2019 | China | OC | qRT-PCR | Median | 60 | 1.76 (1.14–2.72) | Univariate | 6 |
| Wang RP | 2019 | China | CC | qRT-PCR | Median | 127 | 3.02 (2.22–7.48) | Multivariate | 7 |
| Yu CL | 2019 | China | CC | qRT-PCR | Median | 92 | 2.90 (1.45–5.80) | Multivariate | 7 |
| Zhao XH | 2018 | China | PDAC | qRT-PCR | Median | 140 | 2.26 (1.99–2.56) | Multivariate | 7 |
| Zhu FY | 2019 | China | NSCLC | qRT-PCR | Median | 57 | 2.54 (1.05–6.17) | Univariate | 6 |

BC = breast cancer; CC = cervical cancer; CIs = confidence intervals; HCC = hepatocellular carcinoma; HRs = hazard ratios; NOS = Newcastle-Ottawa Scale; NSCLC = non–small-cell Lung cancer; OC = ovarian cancer; OS = overall survival; PDAC = pancreatic ductal adenocarcinoma; RCC = renal cell carcinoma.

Figure 2. Forest plot for the association of LINC00511 expression with overall survival (OS) in patients with malignancies.
Figure 3. Subgroup analysis by tumor type of the association between LINC00511 expression and overall survival (OS).

| Study or Subgroup | Hazard Ratio (95% CI)       | Weight | Hazard Ratio (95% CI)       |
|-------------------|-----------------------------|--------|-----------------------------|
| 1.8.1 Lung cancer |                             |        |                             |
| Sun CC 2016       | 1.9727 [0.363, 10.61]       | 5.6%   | 7.16 [3.53, 14.65]          |
| Zhu FY 2019       | 0.9341 [0.457, 1.98]        | 4.5%   | 2.54 [1.05, 6.17]           |
| Heterogeneity: $\tau^2 = 0.37; \chi^2 = 3.21, df = 1 (P = 0.07); P = 69\%$ |
| Total (95% CI)    |                             |        |                             |
| 1.8.2 Breast cancer |                            |        |                             |
| Liu L 2016        | 0.5218 [0.296, 0.94]        | 10.7%  | 1.67 [1.23, 2.27]           |
| Lu GM 2016        | 0.4511 [0.1371, 1.46]       | 11.1%  | 1.87 [1.33, 2.65]           |
| Heterogeneity: $\tau^2 = 0.00; \chi^2 = 0.09, df = 1 (P = 0.77); P = 0\%$ |
| Total (95% CI)    |                             |        |                             |
| 1.8.3 Glioma      |                             |        |                             |
| Du JL 2020        | 1.1878 [0.4606, 3.28]       | 4.3%   | 3.28 [1.33, 8.09]           |
| Wang B 2019       | 0.9286 [0.2596, 2.33]       | 8.1%   | 2.33 [1.33, 4.11]           |
| Heterogeneity: $\tau^2 = 0.00; \chi^2 = 0.24, df = 1 (P = 0.62); P = 0\%$ |
| Total (95% CI)    |                             |        |                             |
| 1.8.4 Cervical cancer |                           |        |                             |
| Mao BD 2019       | 0.3646 [0.1237, 1.15]       | 11.5%  | 1.44 [1.13, 1.84]           |
| Yu CL 2019        | 1.083 [0.3642, 3.28]        | 8.0%   | 3.28 [1.33, 8.09]           |
| Heterogeneity: $\tau^2 = 0.17; \chi^2 = 3.47, df = 1 (P = 0.08); P = 71\%$ |
| Total (95% CI)    |                             |        |                             |
| 1.8.5 Other cancers |                             |        |                             |
| Deng HH 2019      | 0.3577 [0.1385, 1.11]       | 11.1%  | 1.43 [1.09, 1.88]           |
| Qiao SC 2019      | -3.792 [0.7034, 1.32]       | 11.2%  | 1.32 [0.70, 2.45]           |
| Wang J 2019       | 0.5853 [0.2833, 1.46]       | 8.6%   | 1.46 [1.23, 2.23]           |
| Wang RP 2019      | 1.1039 [0.4635, 2.33]       | 4.3%   | 2.33 [1.33, 4.11]           |
| Zhao XH 2018      | 0.8148 [0.3647, 2.33]       | 12.6%  | 2.33 [1.33, 4.11]           |
| Heterogeneity: $\tau^2 = 0.17; \chi^2 = 25.01, df = 4 (P < 0.00001); P = 84\%$ |
| Total (95% CI)    |                             |        |                             |

Figure 4. Subgroup analysis by analysis type of the association between LINC00511 expression and overall survival (OS).
radio-resistance, and growth of breast cancer cells by inhibiting miR-185-3p. In HCC, LINC00511 promoted the proliferation, colony formation, migration, and invasion of cancer cells by targeting miR-424 and miR-29c, and regulating the miR-195/eyes absent homolog 1 axis.[14-16] Jiang et al[36] also suggested that silencing LINC00511 would suppress the proliferation, migration, and epithelial-mesenchymal transition of lung cancer cells by modulating the PTEN/AKT/FOXO1 axis. Moreover, Li et al[37] found that overexpression of LINC00511 enhanced the proliferation and invasion of glioma cells through inhibition of

Figure 5. Forest plots for the correlation between LINC00511 expression and clinicopathological characteristics of cancer. A: Tumor size; B: Lymph node metastasis; C: Tumor differentiation; D: TNM staging; E: Distant metastasis.
miR-124-3p and concomitant upregulation of cyclin D2.\textsuperscript{[37]} In OC, LINC00511 was found to interact with enhancer of zeste homologue 2 to repress P21 expression, thereby augmenting the viability and invasive ability of cancer cells.\textsuperscript{[16]} Yu et al.\textsuperscript{[10]} and Mao et al.\textsuperscript{[9]} also demonstrated that LINC00511 could promote the proliferation, migration, invasion, and resistance to paclitaxel in CC cells by upregulating matrix metalloproteinase-9, P-glycoprotein, Bcl-2, and a multidrug resistance protein. In pancreatic cancer, overexpression of LINC00511 could significantly contribute to tumor cell proliferation, migration, invasion, and angiogenesis via the miR-29b-3p/vascular endothelial growth factor A axis.\textsuperscript{[17]} In thyroid cancer, Chen et al.\textsuperscript{[37]} revealed that LINC00511 could bind to TATA-box binding protein-associated factor 1 to activate Janus kinase 2/signal transducer and activator of transcription 3 signaling pathway, which remarkably decreased the radio-sensitivity of malignant cells. In renal cell cancer cells, Deng et al.\textsuperscript{[25]} found that LINC00511 was capable of promoting the proliferation, colony formation, in vitro invasion, and in vivo tumor growth, as well as inhibit apoptosis of cancer cells, by repressing the miR-625 and consequently upregulating CCND1.\textsuperscript{[25]} Collectively, these studies provide extensive evidences that LINC00511 may act as an oncogene in human malignancies, which strongly supported the findings of our meta-analysis.

There are several limitations in our meta-analysis. First, significant inter-study heterogeneity was observed, which may have resulted in overestimation of the calculated effect size. Second, all the studies included in the analysis were conducted in Chinese populations; therefore the meta-analysis results may not fully reflect the cellular and molecular features of other ethnic populations. Third, we applied an indirect method to obtain HRs and 95% CI from the survival curves, which was likely accompanied by some operating errors, thereby leading to the overestimation of the association between LINC00511 expression and prognosis in malignancies. Fourth, less than 2 studies reported the prognostic value of LINC00511 in the same malignancy, so our predictive analysis of the association between LINC00511 expression and prognosis in a particular type of malignancy may not be reliable, which may limit the prognostic value of LINC00511 in human cancer. Lastly, there was significant publication bias in our meta-analysis. Usually, researchers tend to publish studies with positive results but not those with negative results, which may partially explain the publication bias.

In summary, high LINC00511 expression may predict unfavorable prognosis in patients with malignancies and it should be explored as a potential prognostic and therapeutic biomarker for malignant tumors. More homogeneous studies enrolling multiracial populations are needed to further confirm our conclusions.

**Author contributions**

Ming Chen and Ping Qi performed literature search, identified the eligible studies and extracted the data independently. Wen-wen Jiang helped to resolve the disagreements in the literature assessment and data extraction, and conducted the statistical analysis. Besides, Ming Chen wrote the original manuscript and the other authors reviewed and corrected it. All the authors read and approved the final manuscript.

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References

[1] Siegel RL, Miller KD, Jemal A. Cancer statistics, 2020. Cancer J Clin 2020;70:7–30.
[2] Bray F, et al. Global cancer statistics 2018: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. Cancer J Clin 2018;68:394–424.
[3] Li S, et al. Prognostic value of long noncoding RNA ROR in patients with cancer in China: a systematic review and meta-analysis. Medicine (Baltimore) 2019;98:e15758.
[4] Yin S, Dou J, Yang G. Long non-coding RNA XIST expression as a prognostic factor in human cancers: a meta-analysis 2019;34:327–33.
[5] Zhou X, et al. Prognostic and clinical significance of long non-coding RNA HNF1A-AS1 in solid cancers: a systematic review and meta-analysis. Medicine (Baltimore) 2019;98:e18264.
[6] Yu H, et al. The prognostic value of long non-coding RNA H19 in various cancers: a meta-analysis based on 15 studies with 1584 patients and the Cancer Genome Atlas data. Medicine (Baltimore) 2020;99:e18533.
[7] Zeng J, et al. Prognostic value of long non-coding RNA SNHG20 in cancer: a meta-analysis. Medicine (Baltimore) 2020;99:e19204.
[8] Cabanski CR, et al. Pan-cancer transcriptome analysis reveals long noncoding RNAs with conserved function. RNA Biol 2015;12:628–42.
[9] Mao B-DI, et al. LINC00511 knockdown prevents cervical cancer cell proliferation and reduces resistance to paclitaxel. J Biosci 2019;44:44.
[10] Yu C-L, Xu X-L, Yuan F. LINC00511 is associated with the malignant status and promotes cell proliferation and motility in cervical cancer. Biosci Rep 2019;39:BSR20190903.
[11] Wang J, et al. Expressions clinical signification and prognostic analysis of linc00511 in ovarian cancer tissues. The J Pract Med 2019;35:2584–91.
[12] Wang J, et al. An integrated analysis reveals the oncogenic function of lncRNA LINC00511 in human ovarian cancer. Cancer Med 2019;8:3026–35.
[13] Wang K, et al. Long non-coding RNA LINC00511 mediates the effects of esr1 on proliferation and invasion of ovarian cancer through miR-424-5p and miR-370-5p. Cancer Manag Res 2019;11:10807–19.
[14] Hu P, et al. Linc00511 indicates a poor prognosis of liver hepatocellular carcinoma. Onco Targets Ther 2019;12:9367–76.
[15] Hu W-Y, et al. LINC00511 as a ceRNA promotes cell malignant behaviors and correlates with progression of hepatocellular carcinoma patients by modulating miR-195/EYA1 axis. Biomed Pharmacother 2020;121:109642–109642.
[16] Wang RP, et al. Increased long noncoding RNA LINC00511 is correlated with poor prognosis and contributes to cell proliferation and metastasis by modulating miR-424 in hepatocellular carcinoma. Eur Rev Med Pharmacol Sci 2019;23:3291–3301.
[17] Zhao X, et al. Linc00511 acts as a competing endogenous RNA to regulate VEGFA expression through sponging hsa-miR-29b-3p in pancreatic ductal adenocarcinoma. J Cell Mol Med 2018;22:653–67.
[18] Jiang L, et al. Silencing LINC00511 inhibits cell proliferation, migration, and EMT via PTEN/AKT/FOXO1 signaling pathway in lung cancer. Biochem Cell Biol 2019;1:1–8. doi: 10.1139/bcb-2018-0364.
[19] Zhu FY, et al. LINC00511 promotes the progression of non-small cell lung cancer through downregulating LAT52 and KLF2 by binding to EZH2 and LSD1. Eur Rev Med Pharmacol Sci 2019;23:3877–90.
[20] Long noncoding RNA LINC00511 contributes to breast cancer cell growth by regulating the miR-185-3p/E2F1/Retraction. Cancer Manag Res 2019;11:8603–18603.
[21] Liu L, et al. Long noncoding RNA LINC00511 involves in breast cancer recurrence and radioresistance by regulating STXBP4 expression via miR-185. Eur Rev Med Pharmacol Sci 2019;23:7457–68.
[22] Lu G, et al. Long noncoding RNA LINC00511 contributes to breast cancer tumourigenesis and stemness by inducing the miR-185-3p/E2F1/Nanog axis. J Exp Clin Cancer Res 2018;37:289–1289.
[23] Zhang H, et al. LINC00511 knockdown enhances paclitaxel cytotoxicity in breast cancer via regulating miR-29c/CDK6 axis. Life Sci 2019;228:133–44.
[24] Zhang J, et al. The transcriptional landscape of lncRNAs reveals the oncogenic function of LINC00511 in ER-negative breast cancer. Cell Death Dis 2019;10:599–1599.
[25] Deng H, et al. LINC00511 promotes the malignant phenotype of clear cell renal cell carcinoma by sponging microRNA-625 and thereby increasing cyclin D1 expression. Aging 2019;11:5975–91.
[26] Li C, et al. Long noncoding RNA LINC00511 induced by SP1 accelerates the glioma progression through targeting miR-124-3p/CCND2 axis. J Cell Mol Med 2019;23:4386–94.
[27] Wang B, et al. Expression and clinical significance of lincRNA LINC00511 in plasma exosome of glioma patients. Chin J Pract Nerv Dis 2019;22:1548–53.
[28] Qiao S, et al. Long intergenic non-coding RNA 511 correlates with improved prognosis, and hinders osteosarcoma progression both in vitro and in vivo. J Clin Lab Anal 2020;24:1364–123164.
[29] Liberati A, et al. The PRISMA statement for reporting systematic reviews and meta-analyses of studies that evaluate healthcare interventions: explanation and elaboration. BMJ (Clinical research ed) 2009;339:b2700.
[30] Shao Q, et al. Prognostic role of galectin expression in patients with hepatic cancer: a meta-analysis. Medicine (Baltimore) 2020;99:e19622.
[31] Li R, et al. GLI1 expression in pancreatic ductal adenocarcinoma correlates the clinical significance and prognosis: a meta-analysis. Medicine 2020;99:e20950.
[32] Zhang X, et al. Prognostic significance of E-cadherin expression in prostatic carcinoma: a protocol for systematic review and meta-analysis. Medicine (Baltimore) 2020;99:e19707.
[33] Du X, et al. LINC00511 contributes to glioblastoma tumorigenesis and epithelial-mesenchymal transition via LINC00511/miR-524-5p/YB1/ZEBl positive feedback loop. J Cell Mol Med 2020;24:1474–87.
[34] Sun C-C, et al. Long intergenic noncoding RNA 00511 acts as an oncogene in non-small-cell lung cancer by binding to EZH2 and suppressing p57. Molecular therapy. Nucleic acids 2016;5:90.
[35] Deng H, et al. Long non-coding RNA LINC00511 promotes radiosensitivity of thyroid carcinoma cells via suppressing JAK2/STAT3 signaling pathway. Cancer Biol Ther 2019;20:1249–57.