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ORIGINAL ARTICLE

A Pooled Analysis of The Clinical Utilities of Long Non-Coding RNA Based Molecular Signature for Diffuse Large B Cell Lymphoma

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SUMMARY

Background: **Long non-coding RNAs (lncRNAs) have been highlighted as promising biomarkers for several types of malignancies. The current meta-analysis sought to investigate the clinical value of lncRNA-based molecular signatures as biomarkers for diagnosis, subtype classification, and prognosis in diffuse large B cell lymphoma (DLBCL).**

Methods: **A systematic search of the online databases was carried out and data were retrieved by pairs of independent reviewers. Effect sizes of the diagnostic parameters were combined using a quantitative meta-analysis. In the prognostic analysis, hazard ratio (HR) with 95% confidence interval (CI) for the primary endpoints of overall survival (OS) and progression-free survival (PFS) were meta-analyzed.**

Results: **Our data exhibited that lncRNA expression profiling harvested a pooled sensitivity of 0.87 (95% CI: 0.78 - 0.92), specificity of 0.84 (95% CI: 0.75 - 0.90), and AUC of 0.92 in distinguishing DLBCL cases from cancer-free participants. For subtype classification, lncRNA signature could discriminate germinal center B-cell-like (GCB) and activated B-cell-like (ABC) DLBCL cases with an estimated sensitivity of 0.92 (95% CI: 0.89 - 0.95), specificity of 0.89 (95% CI: 0.83 - 0.93) and AUC of 0.96. Prognostic analysis manifested that altered lncRNA profiles predicted unfavorable clinical outcomes of DLBCL in OS (univariate analysis: HR = 1.45, 95% CI: 1.14 - 1.83, $p < 0.001$). Further subgroup study stratified by clinicopathological features revealed that the LDH level, IPI score, subtype, and testing pattern of lncRNAs were markedly correlated with the OS in DLBCL.**

Conclusions: **Collectively, our data uncover that lncRNA expression profiling retains a relatively high accuracy in the diagnosis and classification of DLBCL. Altered levels of lncRNAs are also closely associated with worse OS and appeared to be powerful predictors in forecasting prognosis in DLBCL.**

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Supplementary Figures

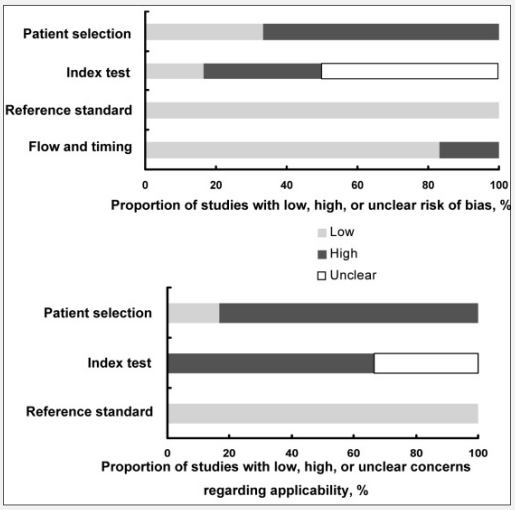

Figure 1. Risk of bias for the diagnostic studies evaluated by the QUADAS II checklist.

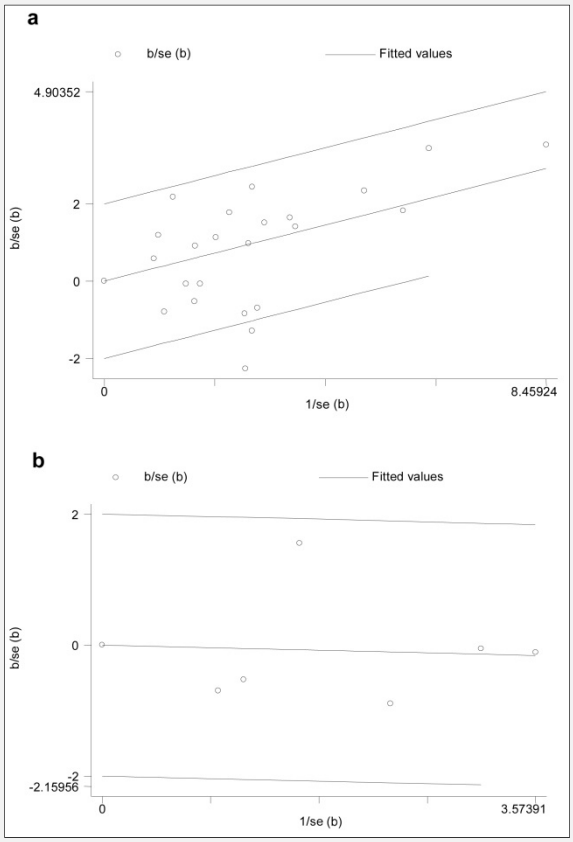

Figure 2. Study heterogeneity assessed by the Galbraith plot for pooled OS (A) and PFS (B).

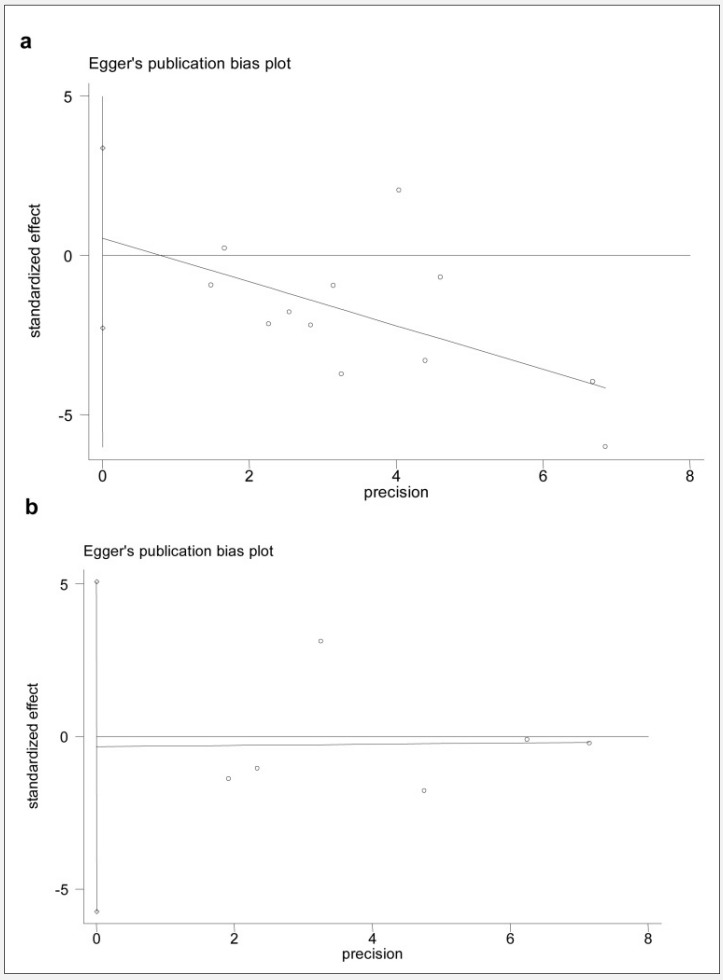

Figure 3. Publication bias examined by the Egger's linear regression assay (A, the usage of lncRNAs in the prediction of OS in DLBCL, p = 0.454; B, the usage of lncRNAs in the prediction of PFS in DLBCL, p = 0.380).