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### DIAGNOSTIC VALUE AND RELATED MECHANISMS OF PLASMA EXOSOMAL LNCRNAs IN STROKE

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**Background and aims:** Acute ischemic stroke (AIS) and hypertensive intracerebral hemorrhage (HICH) are neurological diseases with high incidence and disability rates. Current therapeutic approaches remain limited, and there is an urgent clinical need for highly specific, convenient, and efficient biomarkers as well as novel diagnostic and therapeutic strategies.

**Methods:** The study first collected plasma samples from AIS patients, HICH patients, and healthy controls. After extracting exosomes, differential expression lncRNAs were screened using lncRNA microarray sequencing, and the expression characteristics of these differentially expressed genes were validated by qRT-PCR. The diagnostic efficacy of differential lncRNAs in early detection of the two diseases was analyzed using ROC curve analysis, combined with NHSS score and mRS typing to evaluate their association with disease severity and prognosis. Bioinformatics techniques were employed to predict target genes of differential lncRNAs, and their involvement in biological functions and signaling pathways was revealed through GO and KEGG analysis. The molecular regulatory mechanisms were further validated at the cellular level using siRNA interference technology.

**Results:** Multiple differentially expressed lncRNAs were identified, with some genes (e.g., AIS-associated NONHSAT016392 and HICH-associated NONHSAG074724) demonstrating favorable diagnostic value (AUC values 0.7898-0.9524).

**Conclusions:** These findings are expected to identify specific plasma exosomal lncRNAs that can serve as early diagnostic and prognostic biomarkers for AIS and HICH, clarify the key signaling pathways through which they regulate disease occurrence and progression, and provide a theoretical basis and experimental evidence for the development of novel diagnostic and therapeutic strategies for cerebrovascular diseases.

**Conflict of interest:** Li Jiangmin: nothing to disclose