

lncRNAs [ZFAS1](#) and [MALAT1](#) were significantly upregulated ($p < 0.05$), whereas lncRNAs [LINC00261](#) and [LINC01619](#) were significantly downregulated in [SAH](#) patients with [CVS](#) ($p < 0.05$) compared to SAH patients without CVS. Pan et al. applied this lncRNA signature to retrospectively predict CVS in SAH patients ($n = 38$ for SAH patients without CVS, and $n = 27$ for SAH patients with CVS). The 4-lncRNA signature was found to be predictive in $>40\%$ of samples and the 2-lncRNA comprising MALAT1 and LINC01619 accurately predicted CVS in $\sim 90\%$ cases. These results are initial steps toward personalized management of SAH patients in clinics and provide novel [CSF biomarkers](#) that can substantially improve the clinical management of SAH patients ¹⁾.

¹⁾

Pan CY, Tian M, Zhang LL, et al. lncRNA Signature for Predicting Cerebral Vasospasm in Patients with SAH: Implications for Precision Neurosurgery [published online ahead of print, 2020 Jul 25]. *Mol Ther Nucleic Acids*. 2020;21:983-990. doi:10.1016/j.omtn.2020.07.028

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Last update: **2024/06/07 02:54**

