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 ~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].

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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