ASO Author Reflections: A Novel Three-lncRNA Signature Predictive of Prognoses of HNSCC Patients

Hongyi Jiang, MM^{1,2}, Ben Ma, MD^{1,2}, Weibo Xu, MM^{1,2}, Yi Luo, MM^{1,2}, Zhongwu Lu, MD^{1,2}, Tian Liao, MM^{1,2}, Xiao Wang, MD^{1,2}, Shishuai Wen, MD^{1,2}, Shuwen Yang, MD^{1,2}, and Yu Wang, MD^{1,2}

¹Department of Head and Neck Surgery, Fudan University Shanghai Cancer Center, Shanghai, China; ²Department of Oncology, Shanghai Medical College of Fudan University, Shanghai, China

Recently, the prognostic role of long noncoding RNAs (lncRNAs) has been increasingly noted in various cancer types including head and neck squamous cell carcinoma (HNSCC). However, the published work is mostly limited to public databases, lacking an independent cohort to further validate the utility of the identified lncRNA signatures.

In this study, we identified several disease-associated lncRNAs from The Cancer Genome Atlas (TCGA) dataset to develop an independent prognosis prediction model and further validated the utility of identified lncRNA signatures in cases from our center, the Fudan University Shanghai Cancer Center (FUSCC).

Though the three lncRNAs were observed to be a potent biomarker for prognosis, the related mechanisms in HNSCC have not yet been clarified. It will be intriguing to investigate the biological roles of aberrant molecular pathways caused by these three lncRNAs in HNSCC^{1–5}.

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