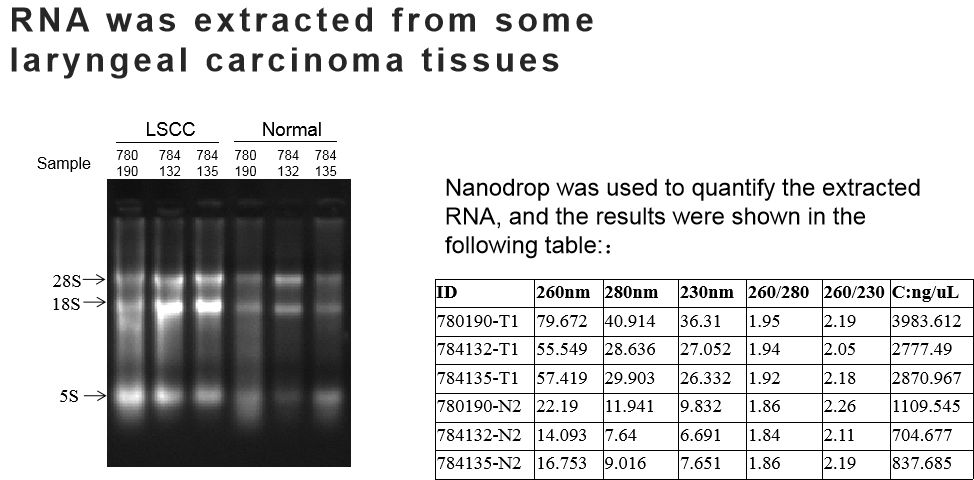
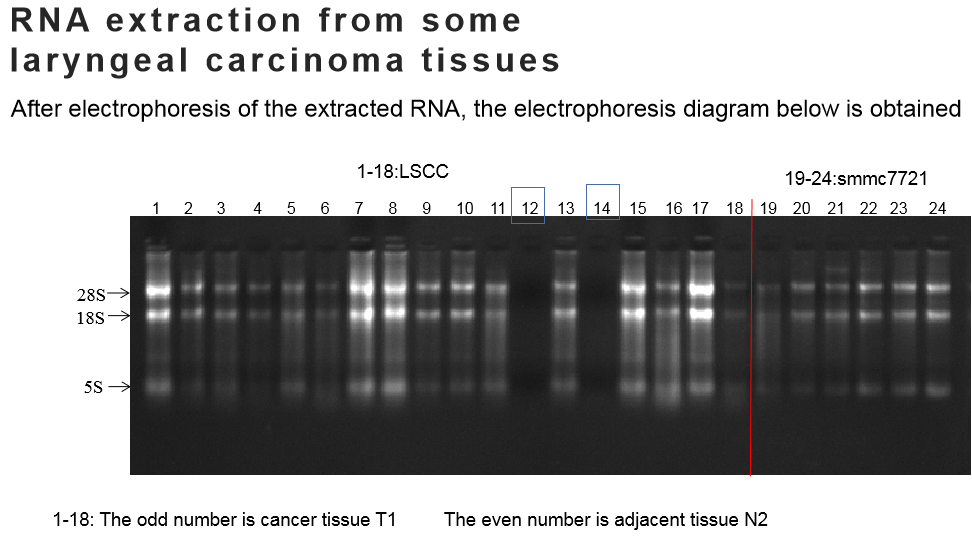
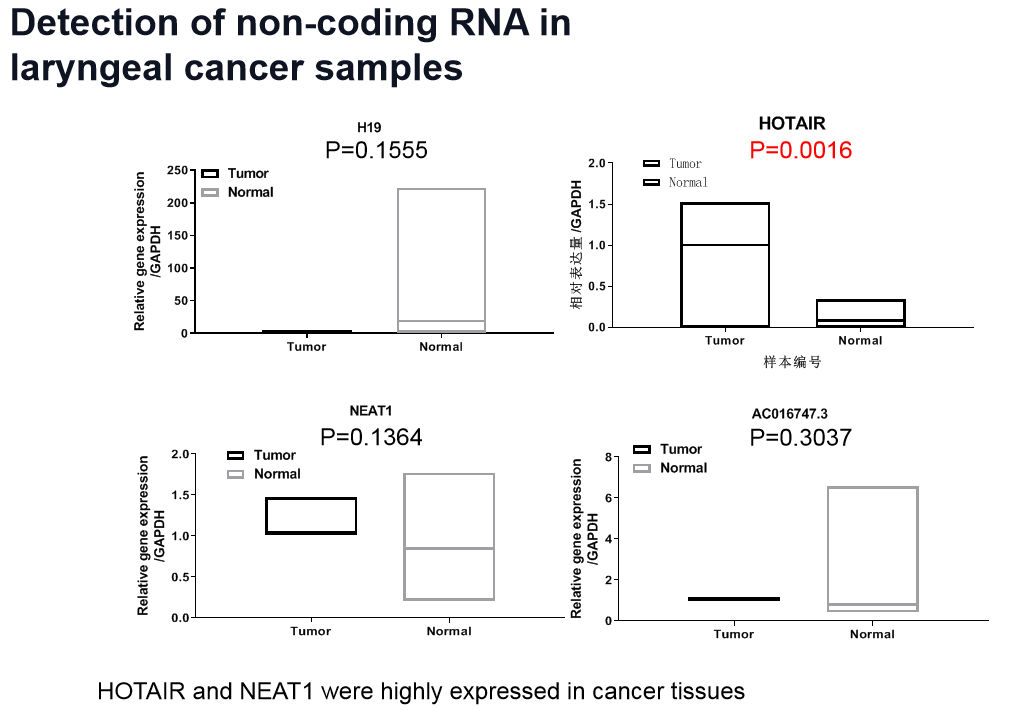
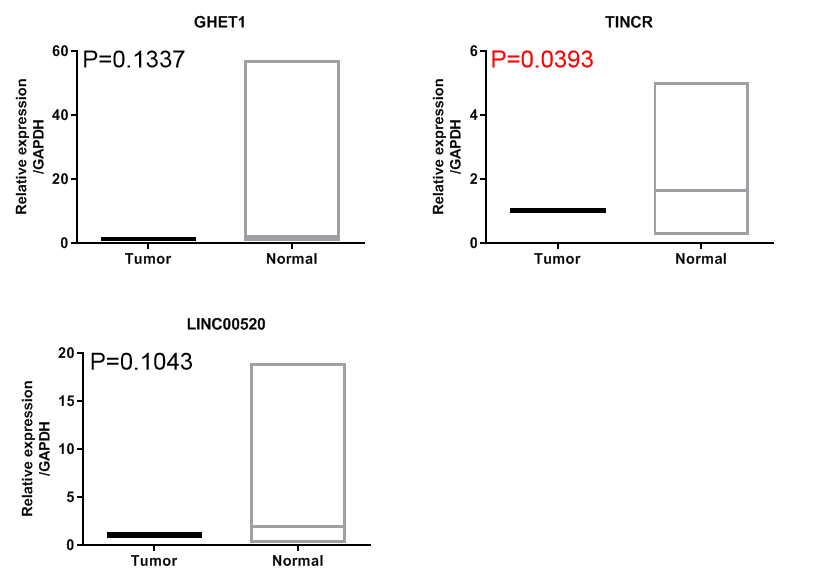
**Fig S1A. Gel electrophoresis of mRNA extracted from tissue of a patient with laryngeal squamous cell carcinoma.**



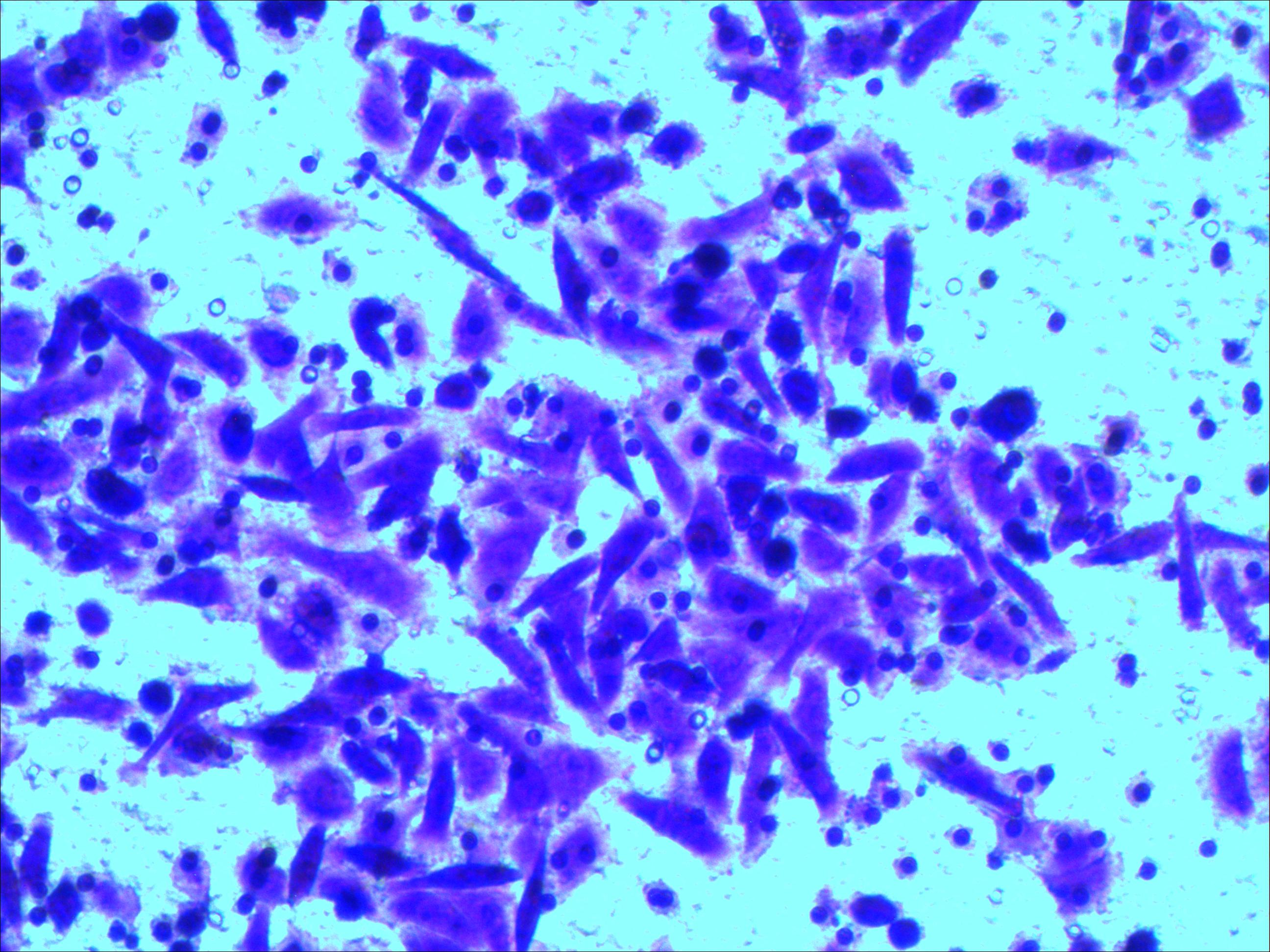
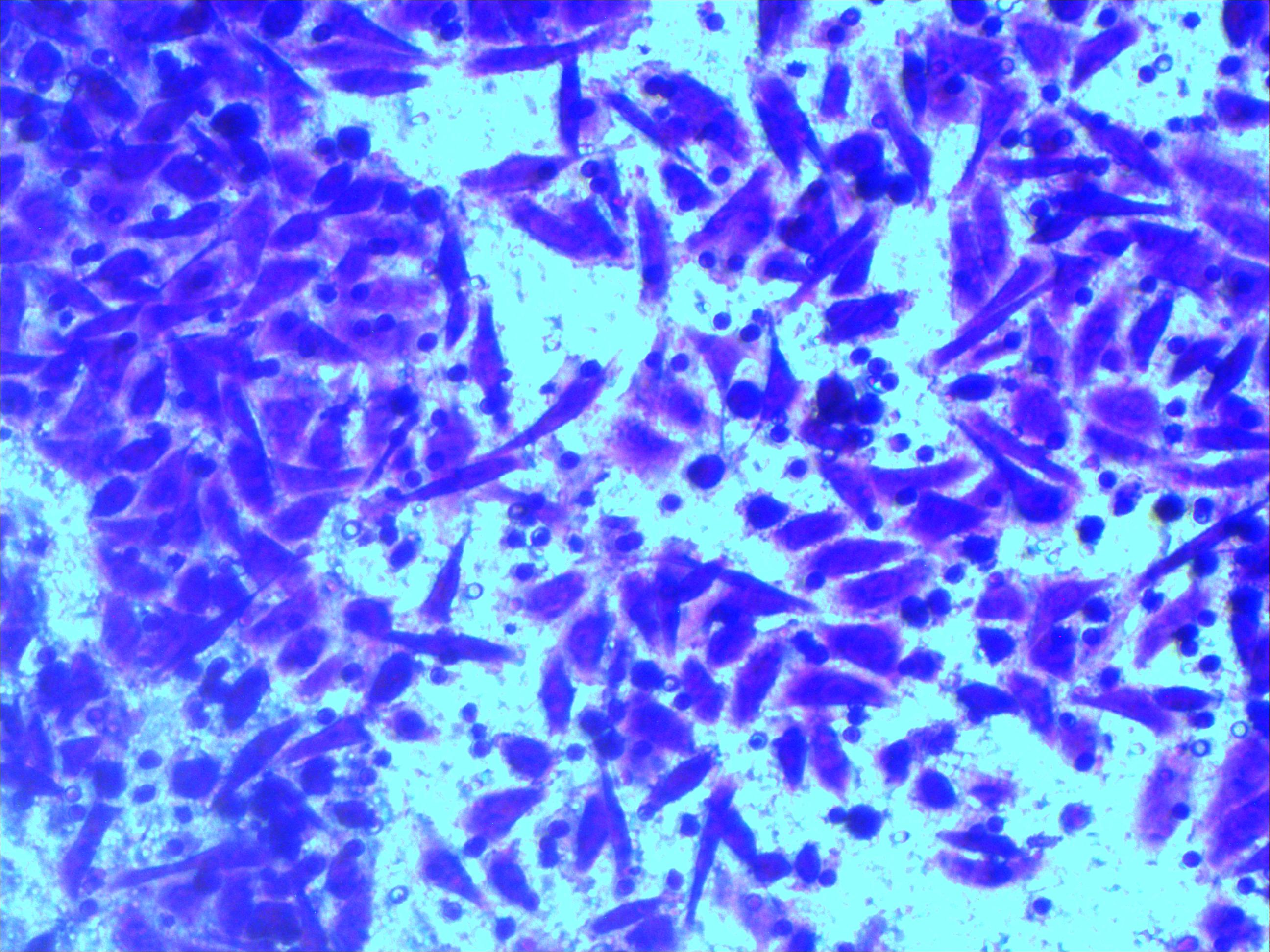
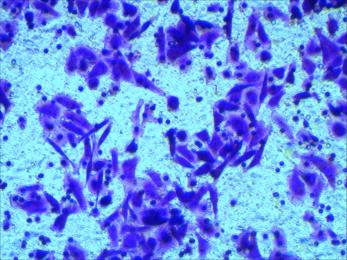


**Fig S1B. The relative expression levels of lncRNA genes were detected by qPCR.**





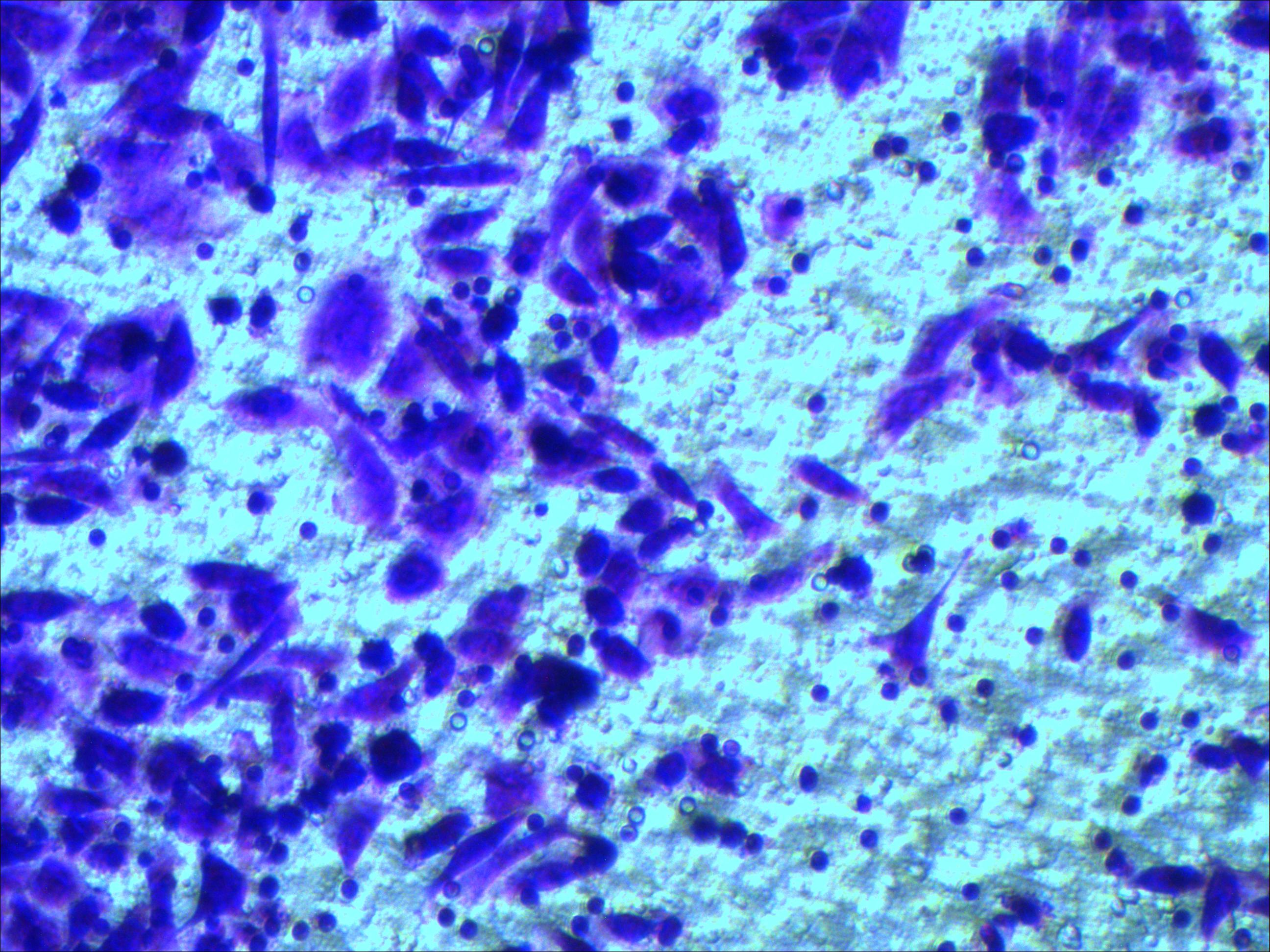
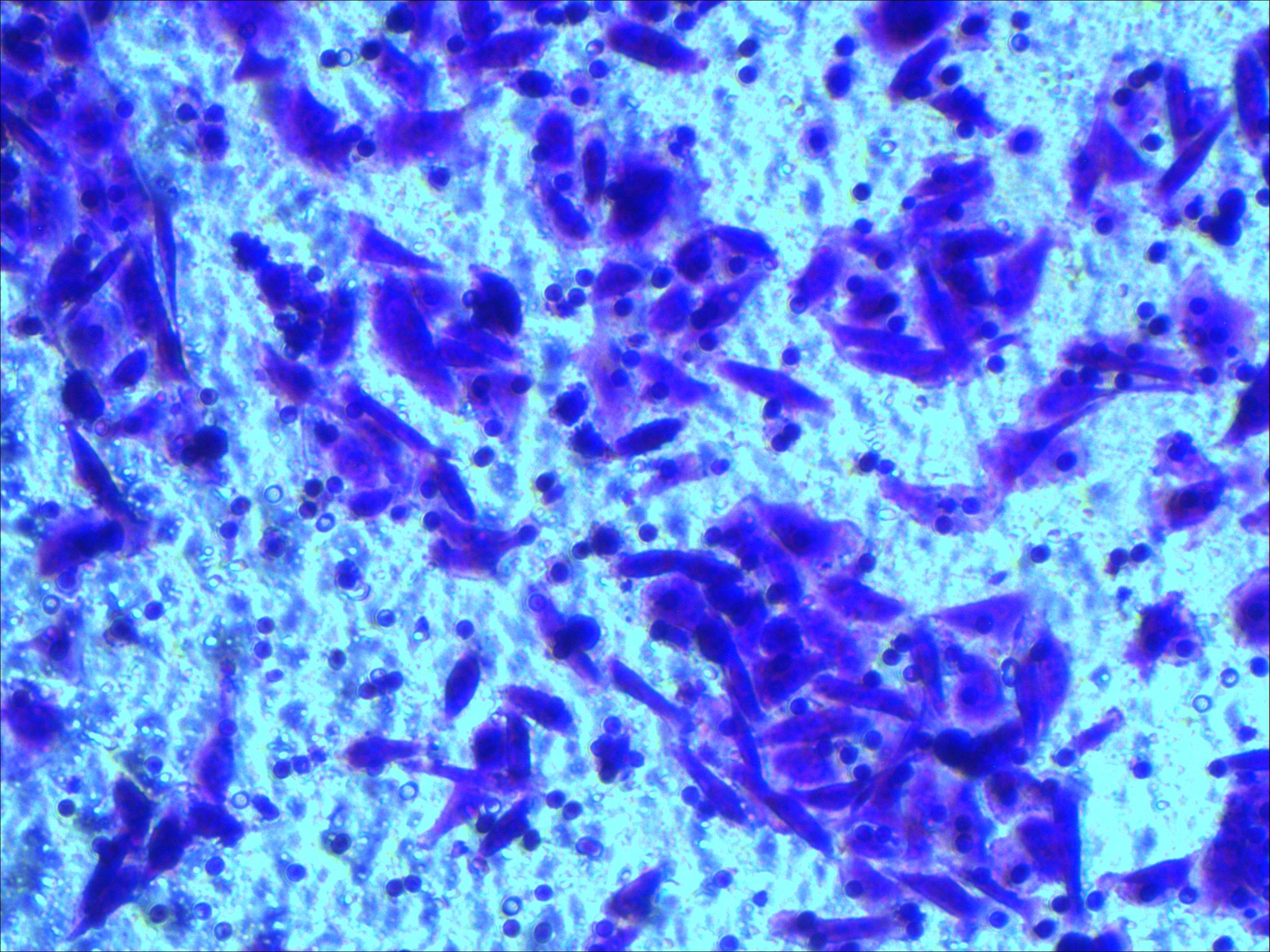
**Fig S1C. Transwell detects the invasion ability of different laryngeal squamous cell carcinoma cell lines.**

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TU686

TU212

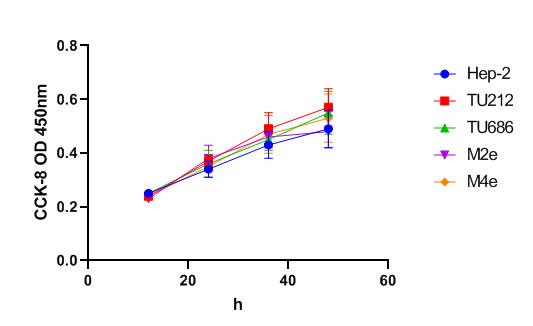
Hep-2

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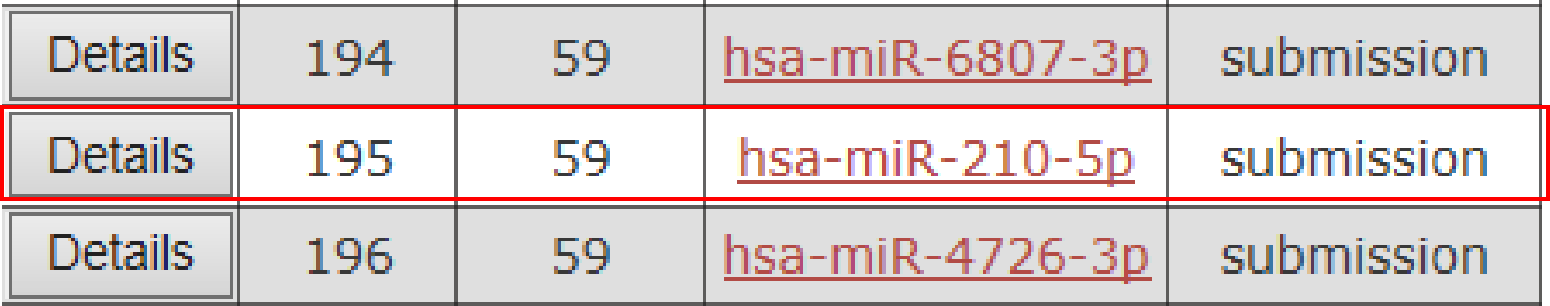
M4e

M2e

**Fig S1D.** **CCK-8 detects the proliferation ability of different laryngeal squamous cell carcinoma cell lines.**

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**Fig S1E. Bioinformatics Web sites predict the targeted binding of TINCR to miRNA.**

The miRDB online website predicted the sequences of binding sites between hsa-miR-210-5p and Tincr sequences. The sequence segments in the figure below are the nucleotide sequences of Tincr, and the blue sites are the binding nucleotide sites 

TargetScan predict result1

**Fig S1F. Bioinformatics Web sites predict the targeted binding of hsa-miR-210-5p to miRNA**

TargetScan predicted that hsa-miR-210-5p had targeted binding sites with 7 consecutive binding nucleotide sites in the 3’UTR sequence of BTG2.TargetScanpredict result2