Supplementary Figures and Tables

Supplementary Figure Legends

A.

B.

C.
**Supplementary Figure 1.**

A. A Heat map plot of immune-related functions calculated by ssGSEA.

B. The location of CNV alteration for OS-associated methylated and autophagy associated genes on 23 chromosomes using the TCGA cohort.

C. Heapmap from TIDE used to rank pRS genes (TSC2, DAPK2, CFLAR, CAPN10, PEX14, ST13, FADD and MBTPS2) based on dysfunction and risk score.
Supplementary Figure 2.

A. Heat map of differentially expressed circ-RNAs from GSE117001;

B. The regulatory network between pRS-related mRNAs and pRS-related miRNAs.
A. nFeature_RNA | nCount_RNA | percent_mt

B. IGKC

C. PC: p-value

D. Standard Deviation

E. Identity

F. cell_type3

Expression
Supplementary Figure 4. RNA-seq data analysis reveal the high heterogeneity of laryngocarcinoma single cells.

A. 1229 laryngocarcinoma cells were included for analysis;

B. ANOVA plots revealed 2000 corresponding genes in all laryngocarcinoma cells. Red dots indicate highly variable genes and black dots represent non-variable genes. The top 20 marker genes were labeled;

C-D. PCA identified 20 PCs with an estimated P value < 0.05;

E. The top 20 marker genes for each cell cluster were revealed in the heat map.
Supplementary Figure 5.

A. Correlation analysis of HAS2 with BMP4, CXCL2, IL1B and SELE respectively based on TCGA database;

B. Correlations among INHBA, IL-1B, CXCL2, BMP4, EGFR, SELE, PEX14, FADD, DAPK2, TSC2, CFLAR, CAPN10, ST13, MBTPS and HAS2 in the scRNA-seq data.
Supplementary Figure 3. An TIDE analysis of compare HAS2 with existed biomarkers.
Supplementary Tables

**Supplementary Table 1.** Baseline characteristics of 6058 patients from SEER database

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<th>Alive (n=6058)</th>
<th>Dead with tumor (n=3526)</th>
<th>Total (n=9584)</th>
<th>P Value</th>
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<td>Overlapping lesion</td>
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<td>Subglottis</td>
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<td>* significant different</td>
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**Supplementary Table 2. Data sources**

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<th>Data Source</th>
<th>Source Information</th>
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<tr>
<td>Laryngocarcinoma data from authors’ hospital</td>
<td>Shanghai ninth people’s Hospital</td>
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<td>TCGA-HNCS RNA-seq files</td>
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<td>TCGA-HNCS Copy Number Variation data</td>
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<td>circRNAs data of laryngocarcinoma</td>
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