

Supplementary materials

Transcriptomic analysis reveals key lncRNAs associated with ribosomal biogenesis and epidermis differentiation in head and neck squamous cell carcinoma

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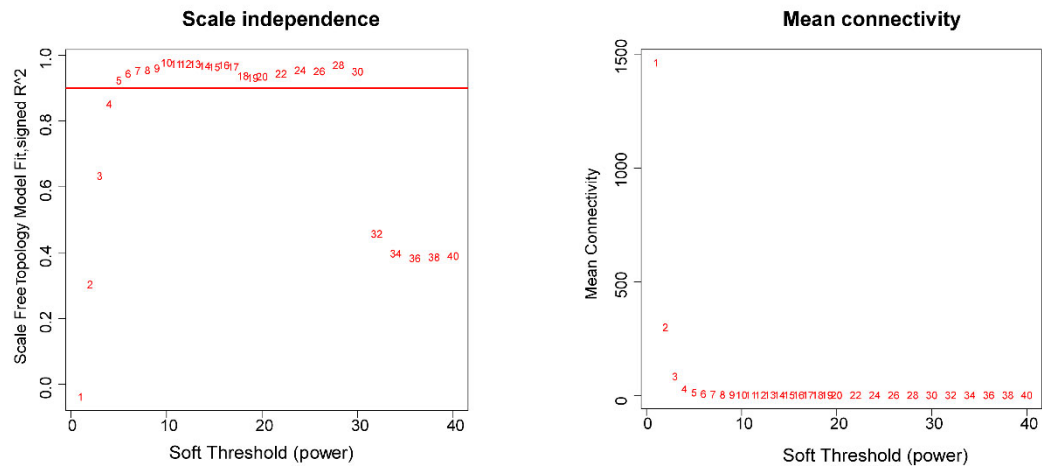


Fig. S1 Determination of parameter β of the adjacency function in the WGCNA algorithm

The weighted parameter β of the adjacency function was determined by a minimum value of β constructing a scale-free network which follows the power law distribution. According to the criteria $R^2 > 0.9$ and the mean connectivity of the network becoming smooth, $\beta = 6$ was chosen for the downstream analysis

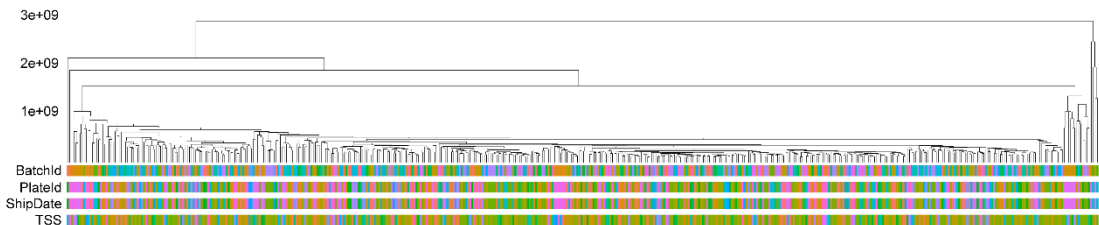


Fig. S2 Hierarchical clustering of samples based on the gene expression profile

Hierarchical clustering of samples based on the gene expression profile suggests that there is no significant batch effect. The bars at bottom are BatchID, PlateID, Ship Date, and Tissue Source Site, respectively

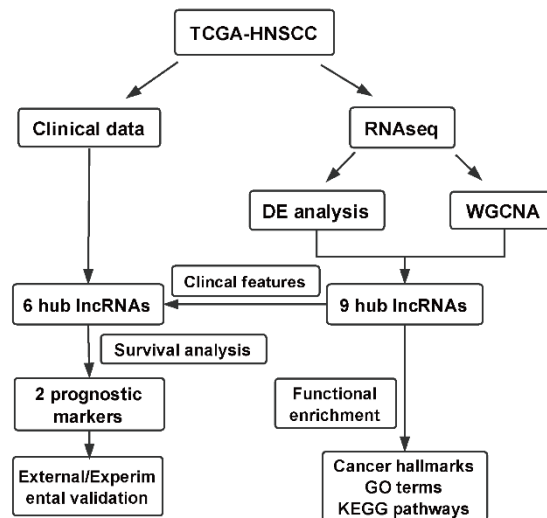


Fig. S3 Overview of the workflow of the study design

The differential expression (DE) analysis was performed using edgeR and co-expression network was constructed by Weighted Correlation Network Analysis (WGCNA). Six clinical-relevant hub lncRNAs were discovered, of which two were identified as prognostic marker lncRNAs based on TCGA dataset and external dataset from Oncomine

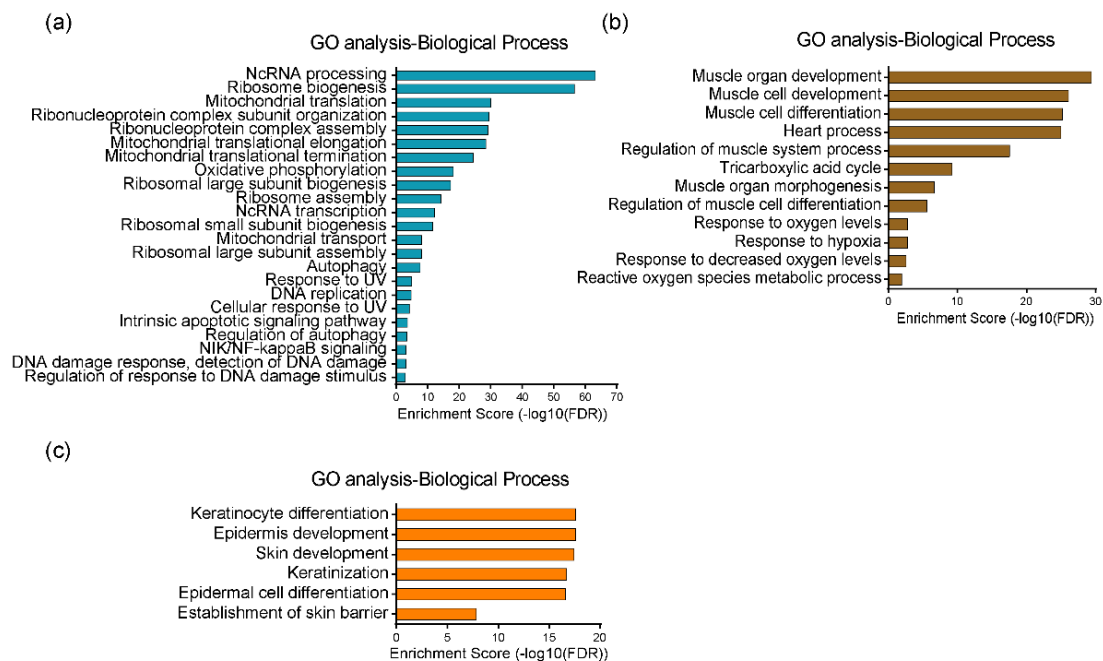


Fig. S4 Functional profiling of modules identified by WGCNA

The GO terms of biological process enriched in module M1 (turquoise) genes (a), M3 (brown) genes (b), M4 (yellow) (c). The terms with $FDR \leq 0.05$ are considered significantly enriched. The negative log of FDR (base 10) is plotted on the X-axis

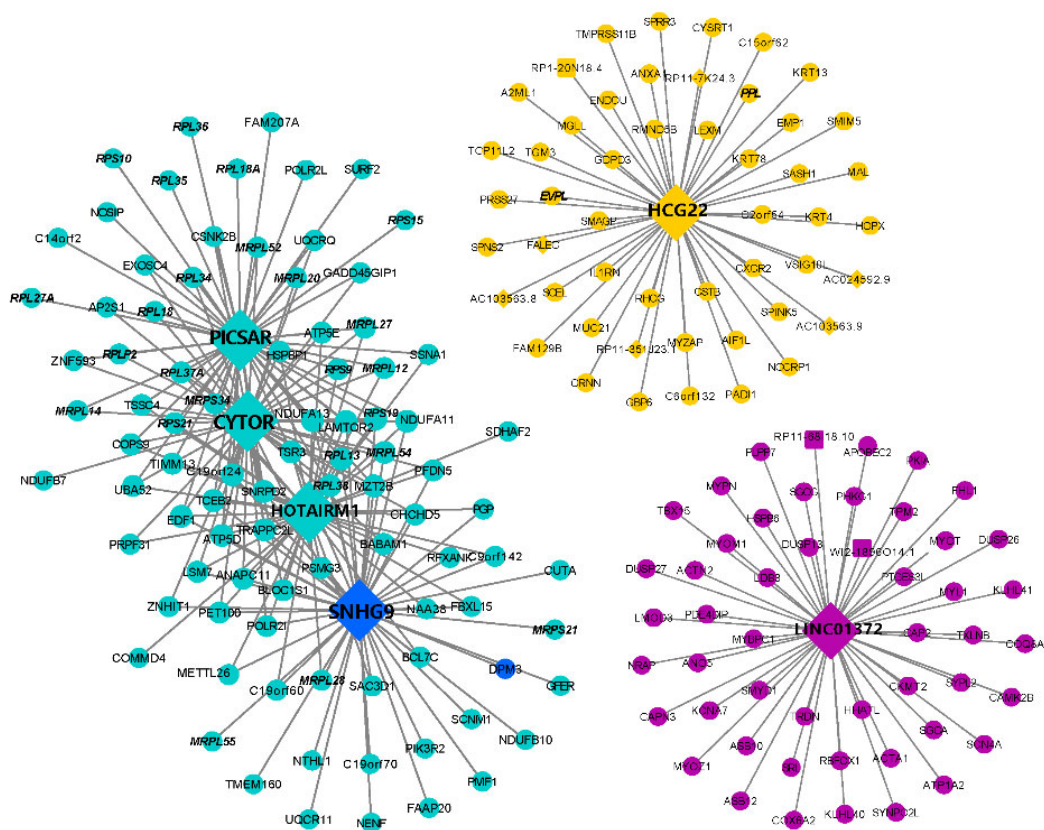


Fig. S5 Co-expression of six hub lncRNAs visualized using Cytoscape software based on the top 50 most connected genes of each given lncRNA

These six hub lncRNAs are in the center of each sub-network. The size of the node indicates the connectivity. The color denotes which network module a certain gene belongs to

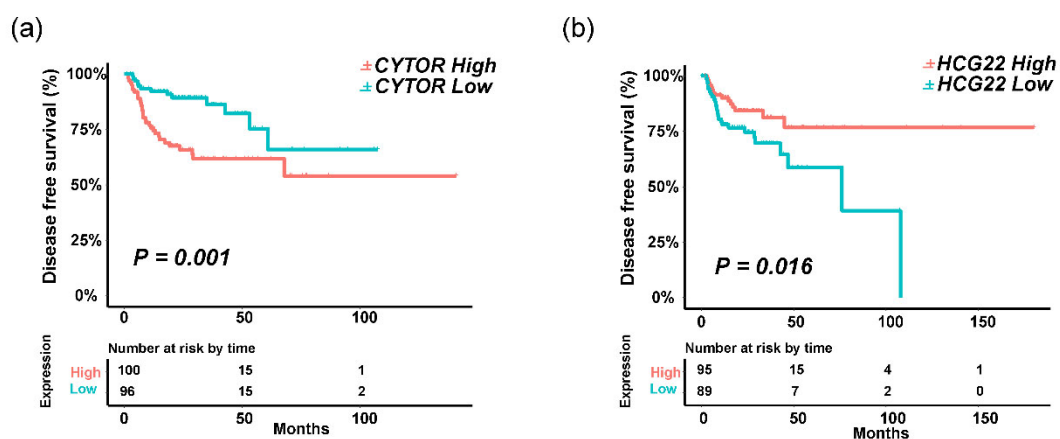


Fig. S6 Kaplan-Meier analysis of disease free survival in HNSCC patients

Kaplan-Meier analysis of disease free survival in HNSCC patients with *CYTOR* (a) and *HCG22* (b) expression.

HNSCC patients with higher *HCG22* and lower *CYTOR* expression have a better disease free survival. *P*-values were calculated by log-rank test

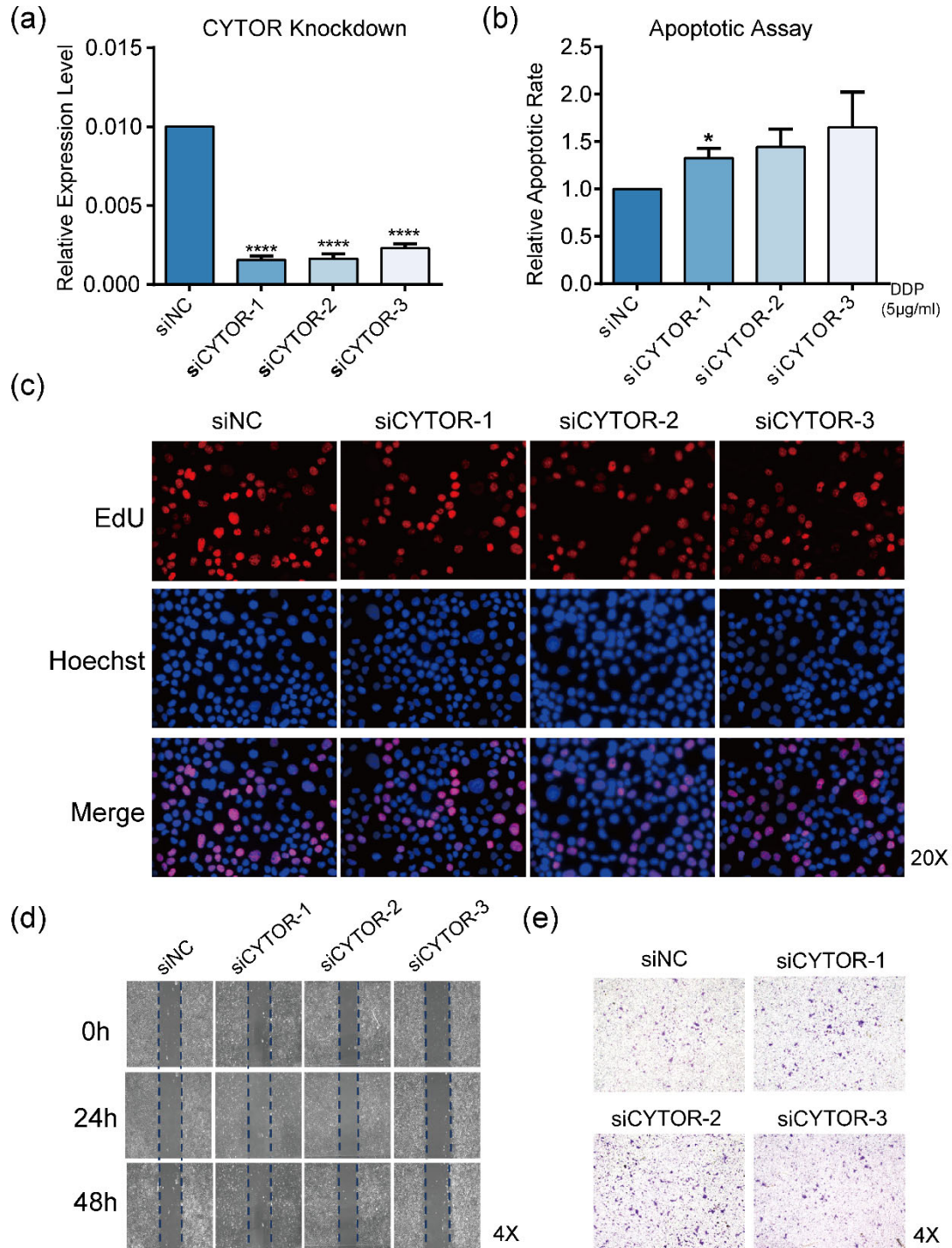


Fig. S7 Effects of *CYTOR* knockdown on cell apoptosis, proliferation, and migration in TSCC15 cells

(a) qRT-PCR analysis of *CYTOR* knockdown efficiency ($n=3$ independent biological experiments; * $P<0.05$, **** $P<0.0001$, vs. siNC). (b) Apoptosis analysis of *CYTOR* knockdown with DDP treatment (5 µg/ml). (c) Cell proliferation was determined with EdU incorporation assay after knocking down *CYTOR*. Red fluorescence (EdU) stands for cells with DNA synthesis, and blue fluorescence (Hoechst) shows cell nuclei. Magnification: $\times 20$. (d) Cell mobility was detected by wound-healing assay after knocking down *CYTOR*. Images were captured at 0, 24 and 48 h. Magnification: $\times 4$. (e) Cell migration was detected by Transwell assay after knocking down *CYTOR* for 24 h. Magnification: $\times 4$