

# A Global Genome-wide Scan with Optimal Cutoff Mining for Emerging Biomarkers in Head and Neck Squamous Cell Carcinoma

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## Supplementary figure legends

### Supplementary Figure S1

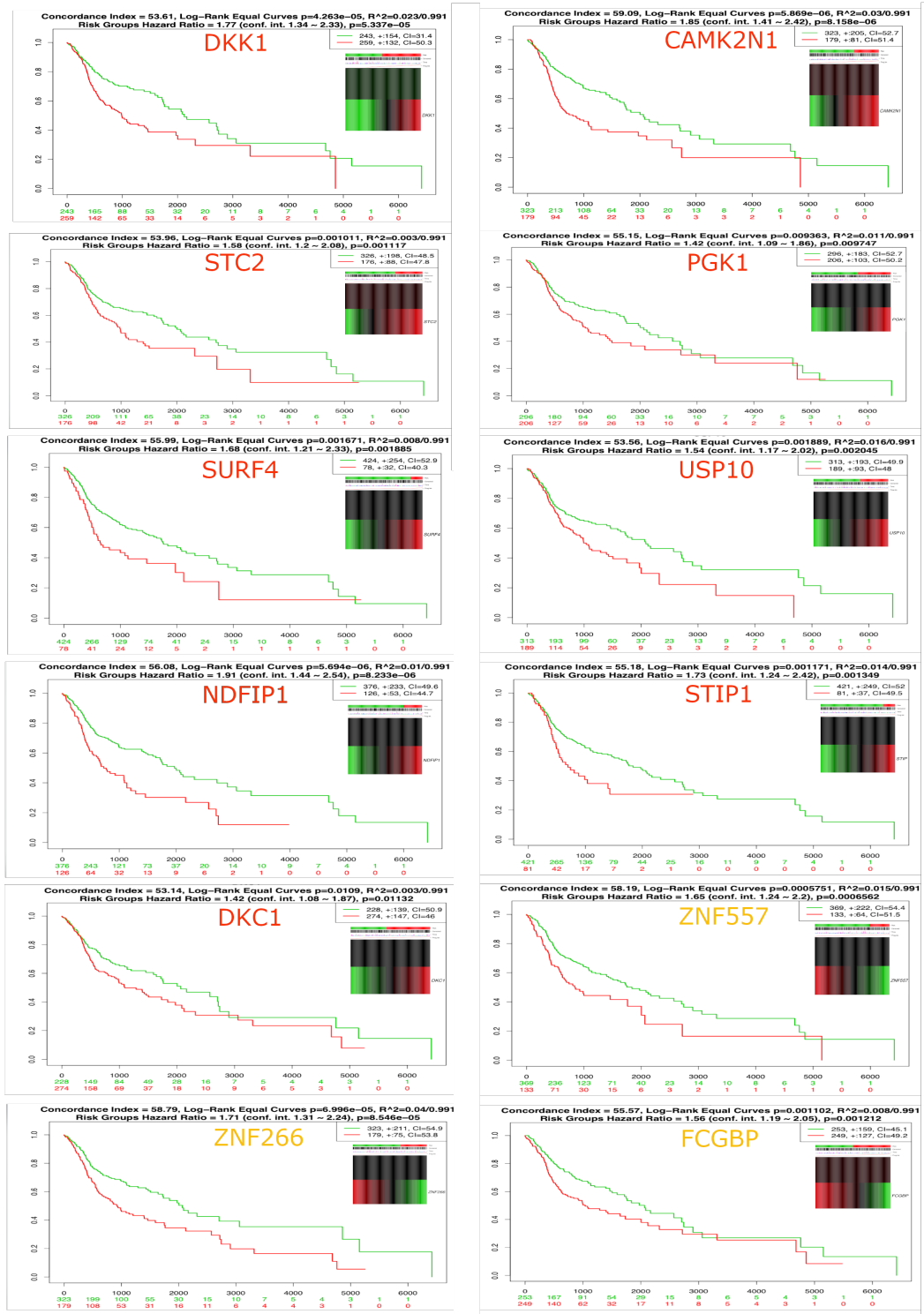
The query results from SurvExpress: Kaplan-Meier plots of 12 genes (the cutoff of high risk and low risk groups, which is derived from risk groups optimization. Inset color scale shows risk groups (high/low) and corresponded RNA expression in high/low. Thus, the poor prognostic genes are marked as red; the better prognostic genes are marked as orange.

### Supplementary Figure S2

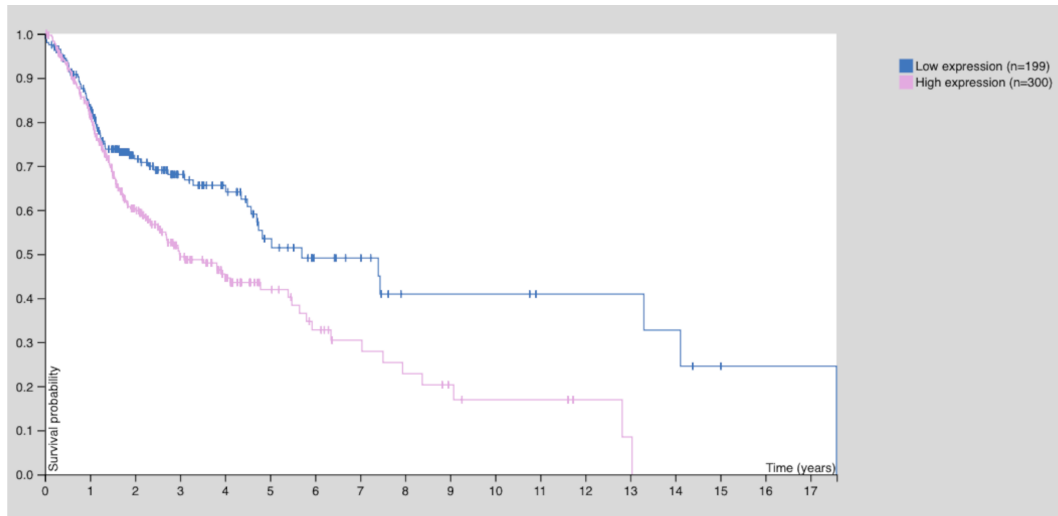
The query results from HPA: Kaplan-Meier plots of ubiquitin-specific peptidase 10 (USP10) with cutoff by mRNA high expression and low expression groups (P-value = 0.0018). Over-expression of USP10 has poor prognosis on HNSCC.

### Supplementary Figure S3

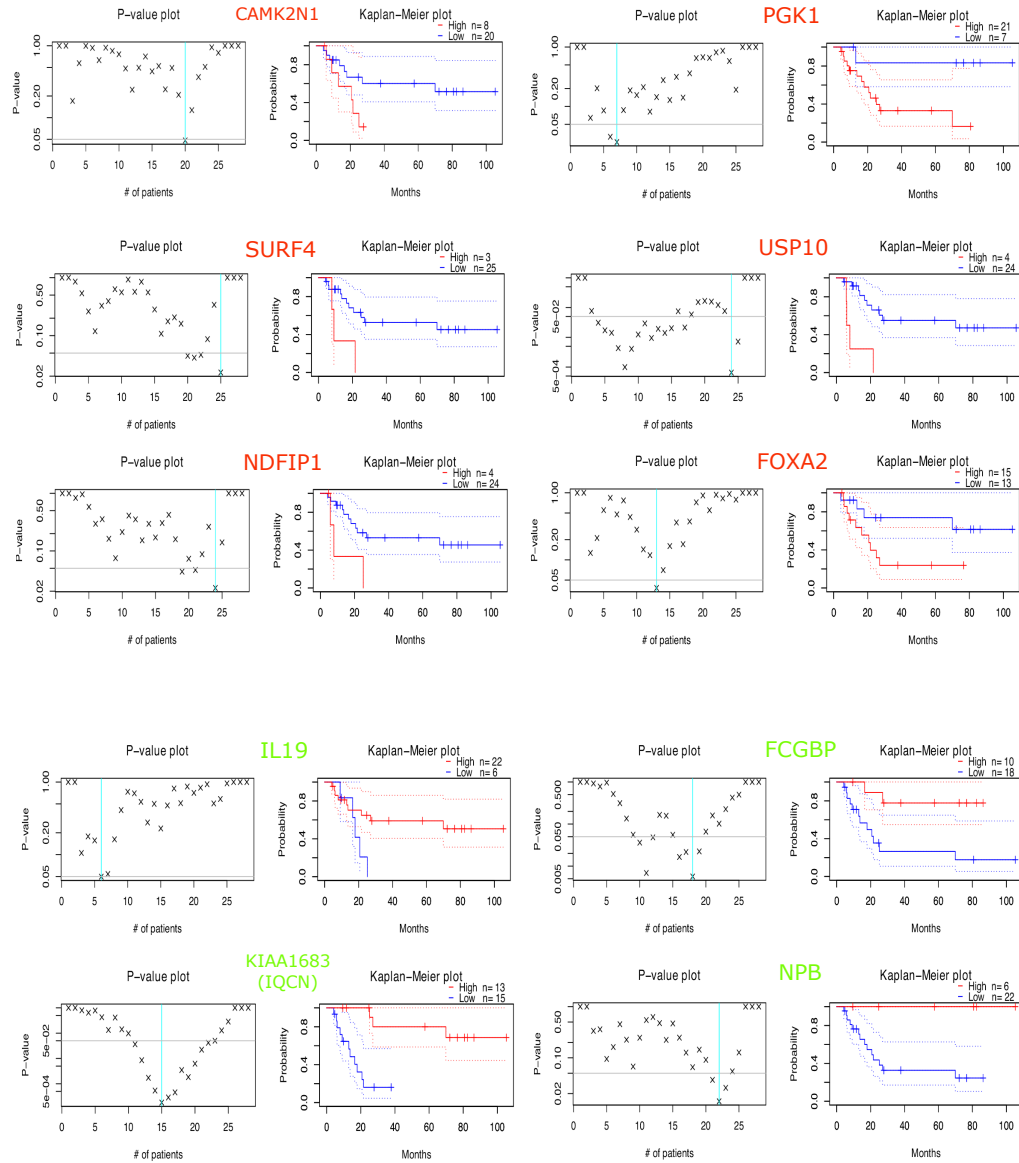
GSE2837 query results from Prognoscan: Kaplan-Meier plots of 10 genes (the cutoff of high risk and low risk groups, which is derived from cumulative P-value plots). The poor prognostic genes are marked as red; the better prognostic genes are marked as green.



Supplementary Figure S 1: The query results from SurVExpress: Kaplan-Meier plots of 12 genes (the cutoff of **high risk** and **low risk** groups, which is derived from risk groups optimization. Inset color scale shows risk groups (**high/low**) and corresponded RNA expression in **high/low**. Thus, the poor prognostic genes are marked as **red**; the better prognostic genes are marked as **orange**.



Supplementary Figure S 2: The query results from HPA: Kaplan-Meier plots of ubiquitin specific peptidase 10 (USP10) with cutoff by mRNA **high expression** and **low expression** groups (P-value = 0.0018). Overexpression of USP10 has poor prognosis on HNSCC.



Supplementary Figure S 3: GSE2837 query results from Prognoscan: Kaplan-Meier plots of 10 genes (the cutoff of **high risk** and **low risk** groups, which is derived from cumulative P-value plots). The poor prognostic genes are marked as **red**; the better prognostic genes are marked as **green**.