

Figure S1. An expression heatmap showed 202 serum miRNAs (117 upregulated and 85 downregulated) that exhibited significantly different levels between patients and healthy individuals with a fold change > 3 or < 0.33 and a P value < 0.01 . Clinicopathological characteristics of patients were indicated. (OSCC patients, $n=25$; healthy controls, $n=15$).

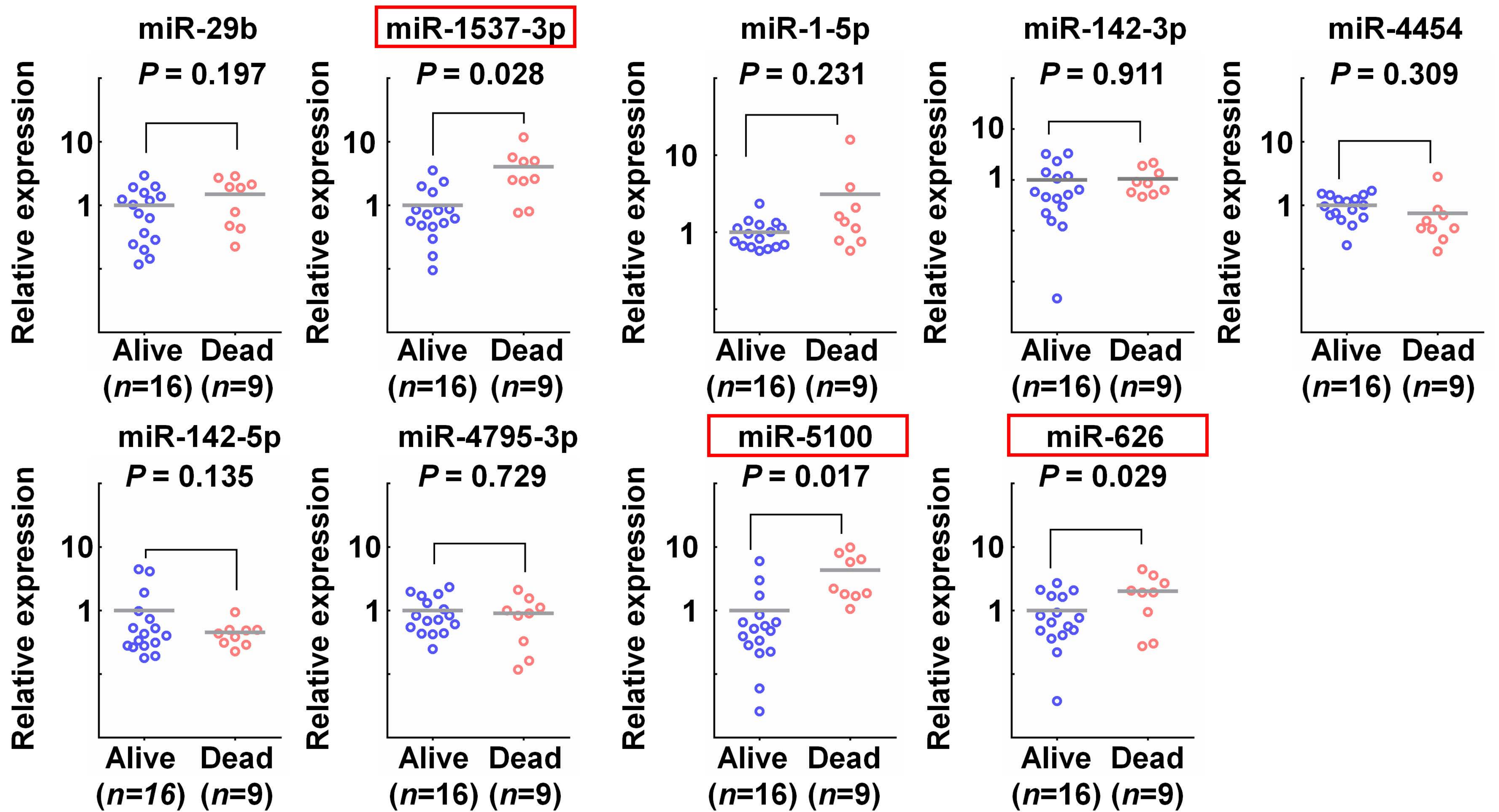


Figure S2. Comparison of indicated miRNAs levels in the serum of patients had died ($n=9$) and those were still alive ($n=16$) in the screening cohort. miR-1537-3p, miR-626 and miR-5100 were elevated in the serum of patients had died compared with those were alive.

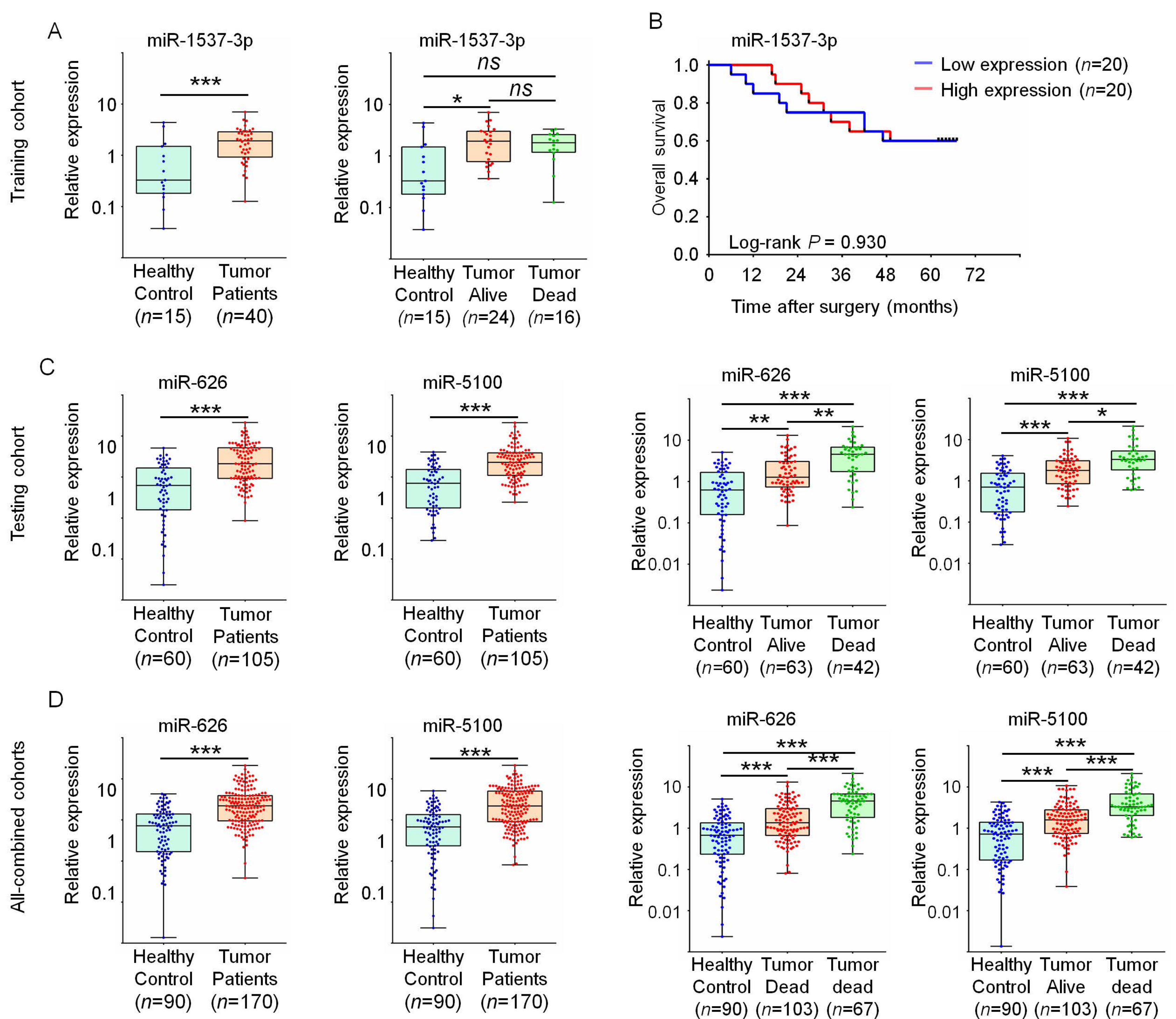


Figure S3. Expression levels of indicated miRNAs in patients with OSCC. (A), Comparison of the expression of serum miR-1537-3p between healthy controls and OSCC patients (unpaired two-tailed Student's t test, $***P < 0.001$), as well as among healthy controls and patients with different survival status. (one-way ANOVA, $*P < 0.05$) in the training cohort. (OSCC patients, $n=40$; HC, healthy controls, $n=15$). (B), Kaplan–Meier analysis of OS of patients with OSCC with higher levels ($n=20$) or low levels ($n=20$) expression of serum miR-1537-3p. (C, D), Comparison of the expression of serum miR-626 and miR-5100 between healthy controls and OSCC patients (unpaired two-tailed Student's t test, $***P < 0.001$), as well as among healthy controls and patients with different survival status. (one-way ANOVA, $*P < 0.05$, $**P < 0.01$, $***P < 0.001$) in both the testing cohort (C) (OSCC patients, $n=105$; healthy controls, $n=60$) and all-combined cohorts (D) (OSCC patients, $n=170$; healthy controls, $n=90$).

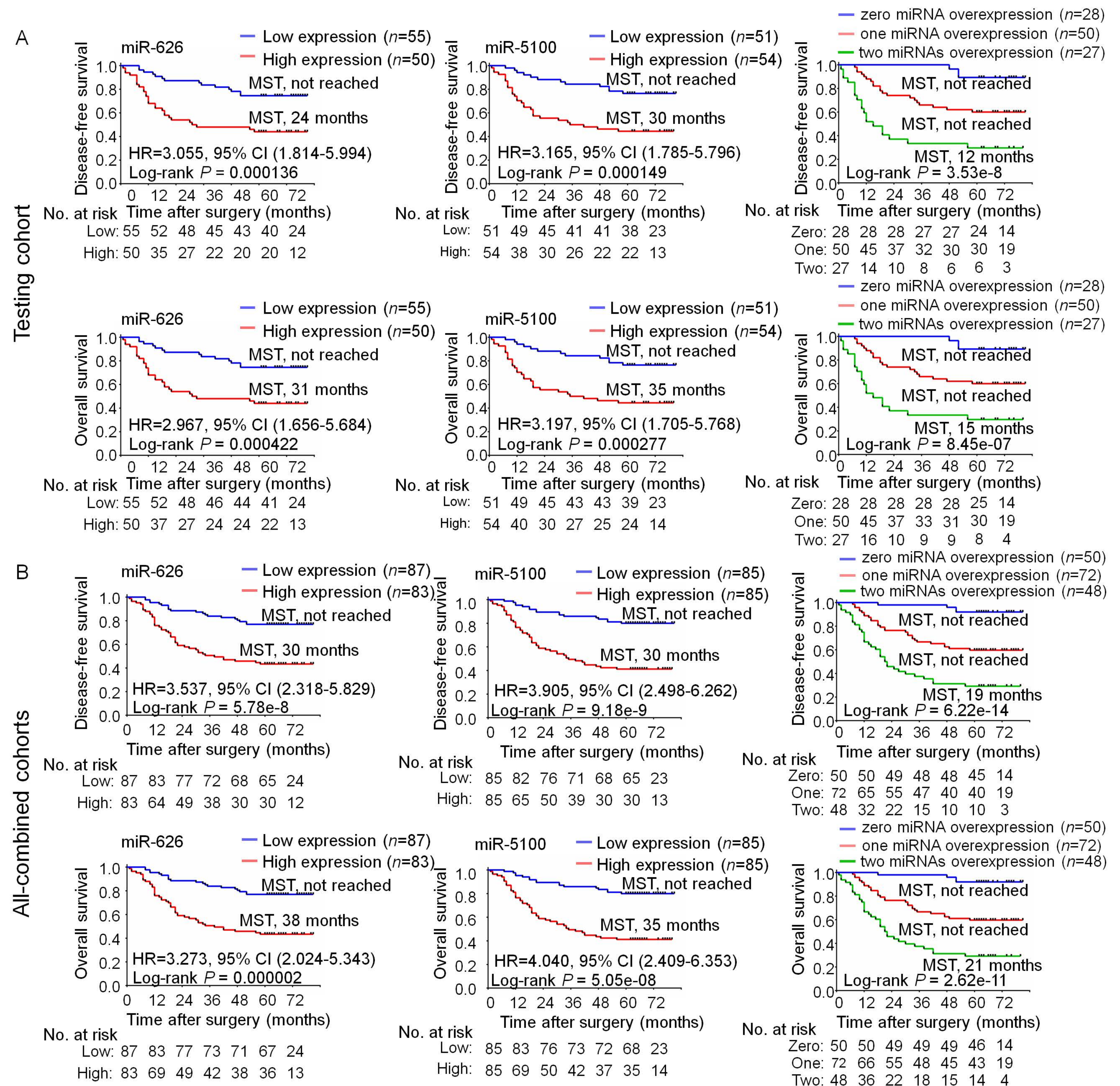


Figure S4. The two-miRNA signature showed greater performance than one-single-miRNA. (A), Comparisons of DFS (upper) and OS (below) in patients with OSCC according to miR-626 (left) and miR-5100 (middle) expression levels and their combination (right) in the testing cohort. (OSCC patients, $n = 105$, Log-rank test, $P < 0.001$). (B), Comparisons of DFS (upper) and OS (below) in patients with OSCC according to miR-626 (left) and miR-5100 (middle) expression levels and their combination (right) in all-combined cohorts. (OSCC patients, $n = 170$, Log-rank test, $P < 0.001$).

miR-626 expression in 32 tumors from TCGA data base

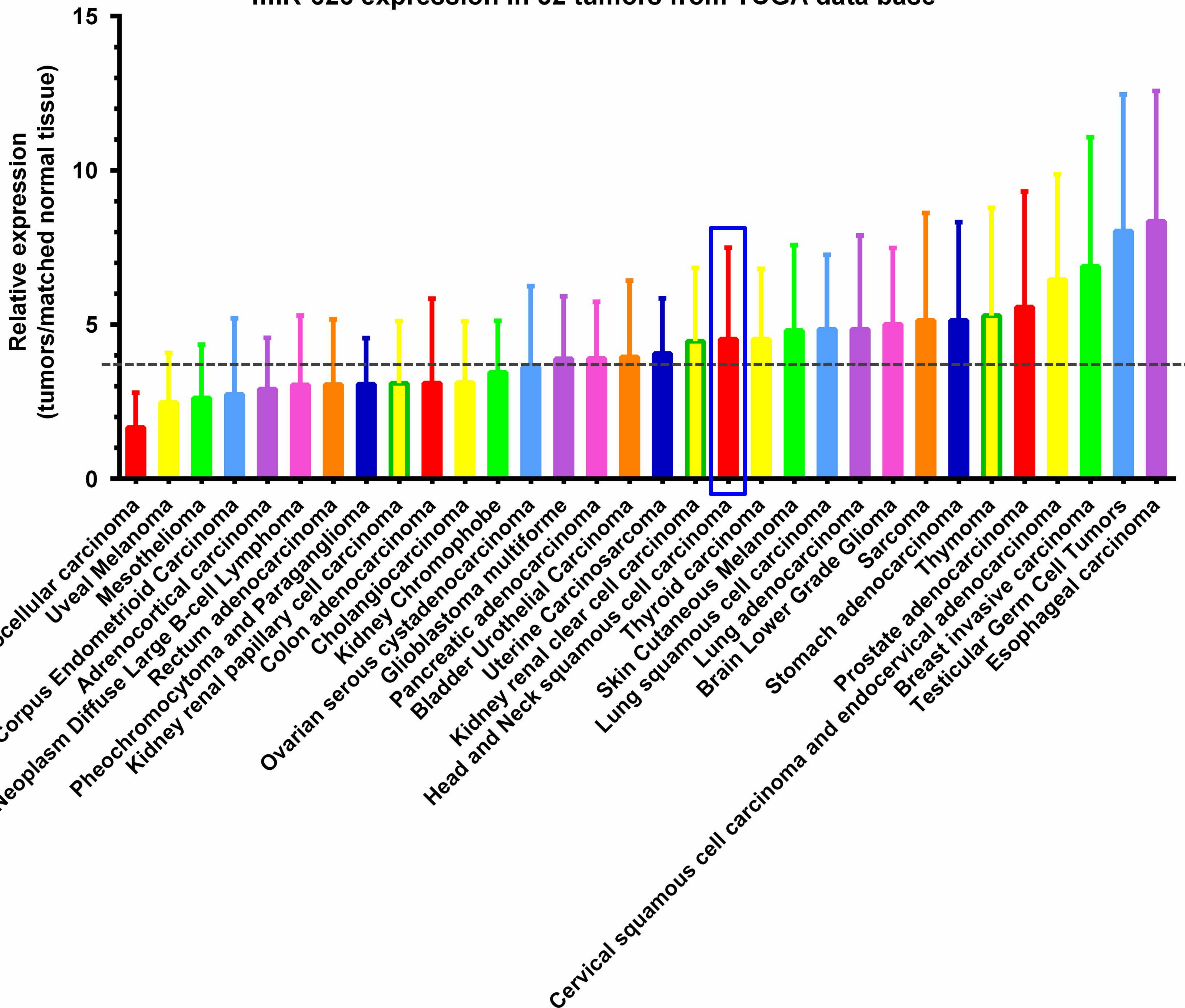


Figure S5. miR-626 is significantly overexpressed in TCGA-HNSCC samples.