Supplementary materials

Table S1. Basic elements of included datasets for differential expression analysis.

Figure S1. Correlations between HOXA4 or HOXA5 expression and SIRT1 expression in LUAD. A: Scatter plot of HOXA4-SIRT1 expression pair in TCGA-GTEx dataset; B: Scatter plot of HOXA4-SIRT1 expression pair in GPL6884 dataset; C: Scatter plot of HOXA5-SIRT1 expression pair in TCGA-GTEx dataset; D: Scatter plot of HOXA5-SIRT1 expression pair in ArrayExpress_Affymetrix dataset.

Figure S2. The co-expressed modules clustered by HOXA4, HOXA5 and all significant differentially expressed genes from RNA-seq dataset of LUAD. The node graph displayed the hierarchy of the co-expressed modules.

Figure S3. The comparisons of expression of HOXA4 and HOXA5 in LUAD cell lines after transfection with negative control or lv-HOXA4 and lv-HOXA5 lentiviruses. A: Bar graph of expression values for A549 cell line; B: Bar graph of expression values for HCC827 cell line. *: P<0.05.

Figure S4. The effect of over-expression of HOXA4 and HOXA5 on the migration ability of HCC827 cells detected by wound healing test. Photos for scratch and healing areas were taken at 0h, 24, 48h and 72h after transfection with negative control or lv-HOXA4 and lv-HOXA5 lentiviruses.

Figure S5. The scratch healing ability of A549 and HCC827 cell lines after over-expression of HOXA4 and HOXA5. A. Line chart of scratch healing area values for different groups of A549 cells. B. Line chart of scratch healing area values for different groups of HCC827 cells. C. Bar chart of scratch healing area values for different groups of A549 cells. D. Bar chart of scratch healing area values for different groups of HCC827 cells. *: P<0.05. **: P<0.01. ***: P<0.001.