



Supplementary Figure 3. Scatter plot shows the expression signature of differentially expressed genes between cervical squamous cell carcinoma (SCC) and adenocarcinoma (ADC) samples from our study (x-axis) and from the cancer genome atlas (TCGA) consortium (y-axis). Quadrant II shows 126 genes upregulated in SCC, while 166 genes downregulated in SCC samples in both cohorts (Quadrant III). FC: fold change (log₂); False discovery rate (FDR) < 0.01 was defined as the limit of significance.