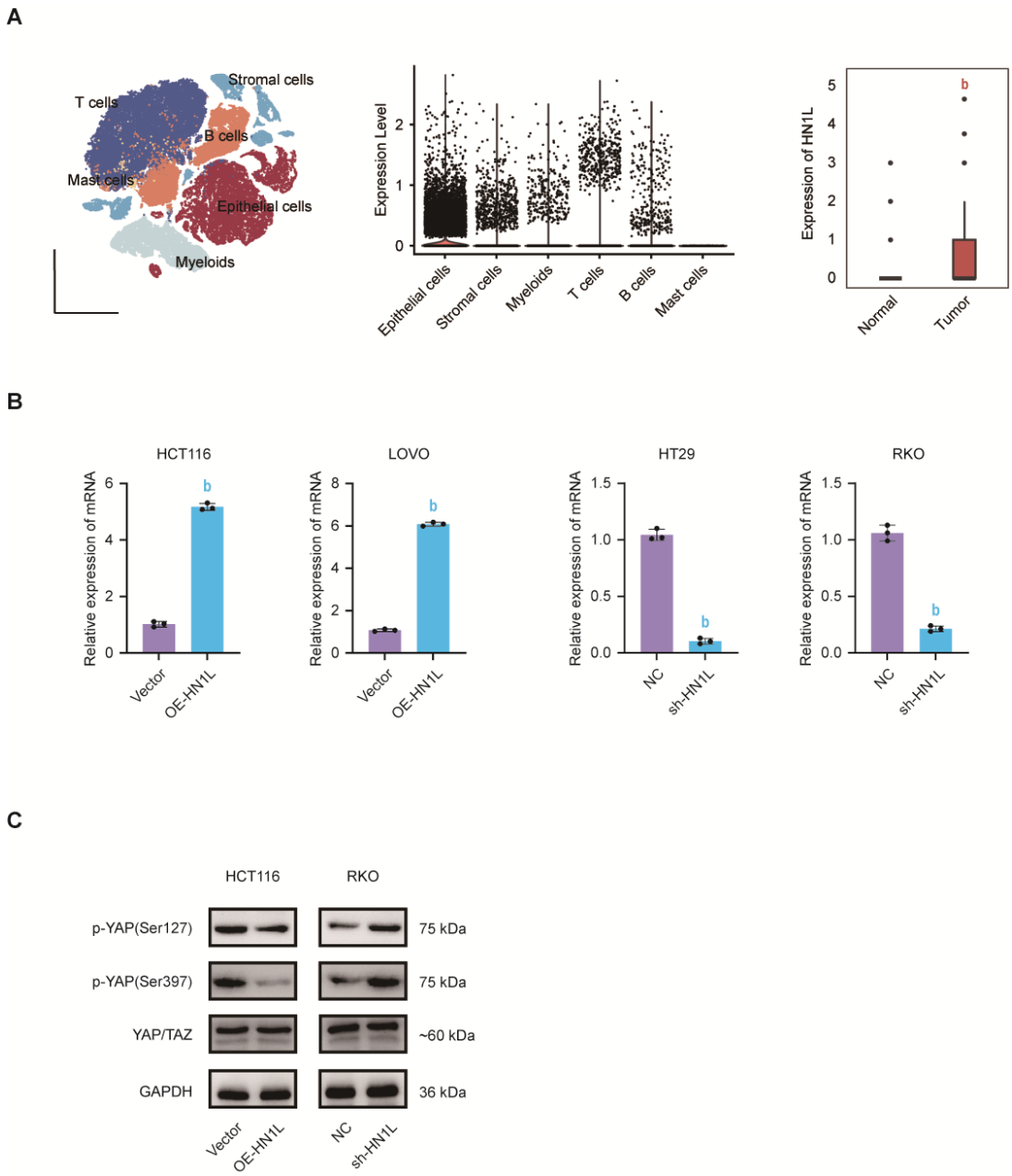


Supplementary Figure 1

A, Reanalysis of the GSE132465 scRNA-seq dataset using a stricter mitochondrial transcript threshold (<10%), showing the major cell populations, HN1L expression across different cell types, and HN1L expression in normal and tumor epithelial cells. **B,** qRT-PCR validation of HN1L overexpression in

HCT116 and LOVO cells and HN1L knockdown in HT29 and RKO cells. **C,** WB analysis of p-YAP (Ser127), p-YAP (Ser397), and total YAP/TAZ in HCT116 cells with HN1L overexpression and RKO cells with HN1L knockdown. In A, $^{b}P < 0.01$ vs normal epithelial cells. In B, $^{a}P < 0.05$ and $^{b}P < 0.01$ vs the corresponding control group (Vector or NC).

Abbreviations: **scRNA-seq**, single-cell RNA sequencing; **qRT-PCR**, quantitative real-time polymerase chain reaction; **WB**, Western blotting; **HN1 L**, hematological and neurological expressed 1-like; **OE**, overexpression; **NC**, negative control; **YAP**, Yes-associated protein; **TAZ**, transcriptional coactivator with PDZ-binding motif; **GAPDH**, glyceraldehyde-3-phosphate dehydrogenase.