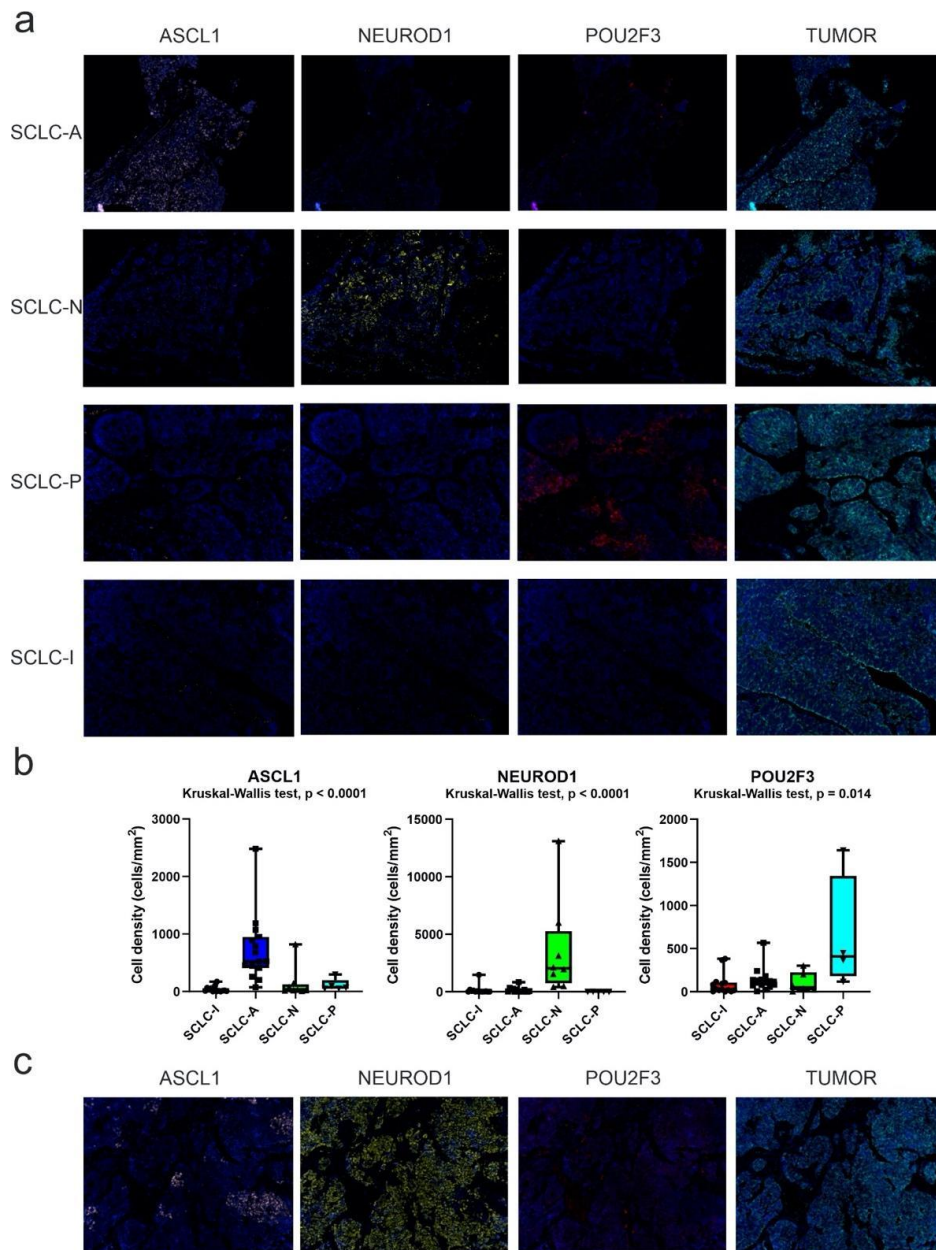
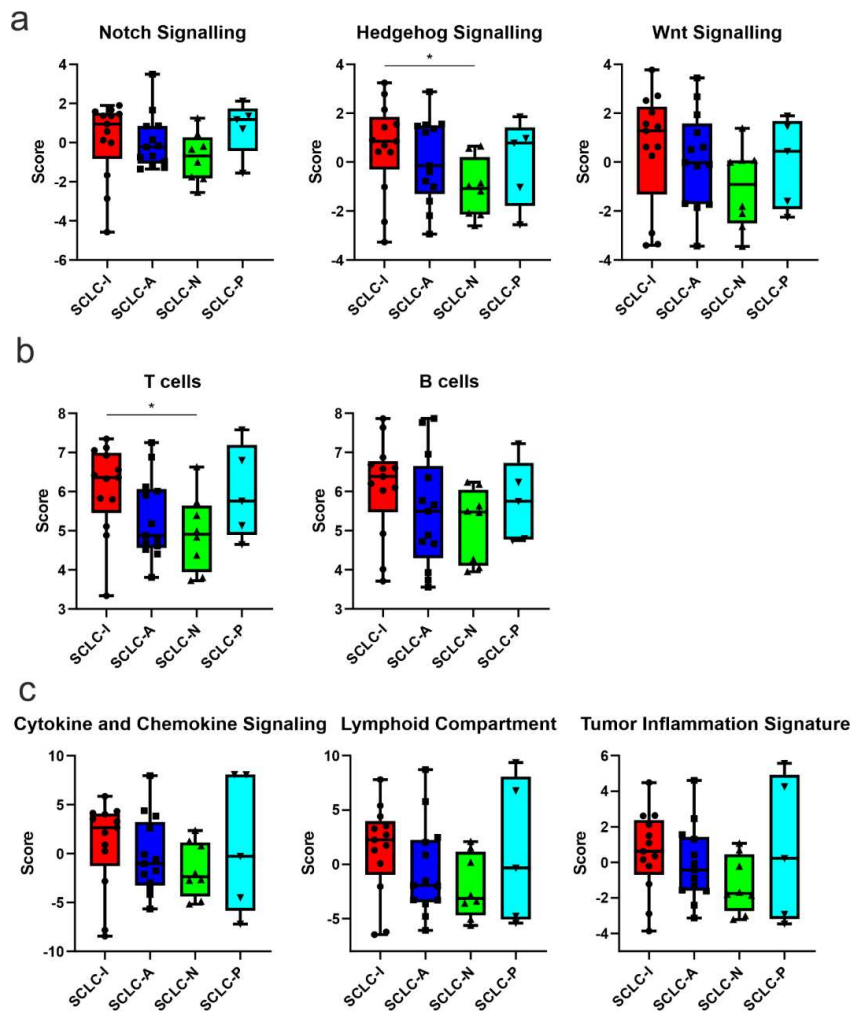


Supplementary Figure 1. Immune microenvironment characterization. a) Left: Representative image of ES-SCLC sample stained with the first mIF panel. Markers and color codes are delineated under the picture. Original magnification $\times 20$. Right: Percentage of HLA-class I negative tumor cells in ES-SCLC samples. b) Quantification of immune cells infiltrating the ES-SCLC microenvironment. c) Quantification of M1-like (CD68+CD163-) and M2-like (CD68+CD163+) macrophages infiltrating the ED-SCLC microenvironment.



Supplementary Figure 2. Identification of four SCLC subtypes. a) Four SCLC subtypes were identified by mIF according to the differential expression of the transcription factors ASCL1, NEUROD1 and POU2F3. b) Quantification by mIF of ASCL1, NEUROD1 and POU2F3 transcription factors in SCLC subtypes. c) Representative images of the co-expression of different transcription factors by tumor cells within the same SCLC sample. Original magnification x20.



Supplementary Figure 3. Gene-based signalling analysis in SCLC subtypes.