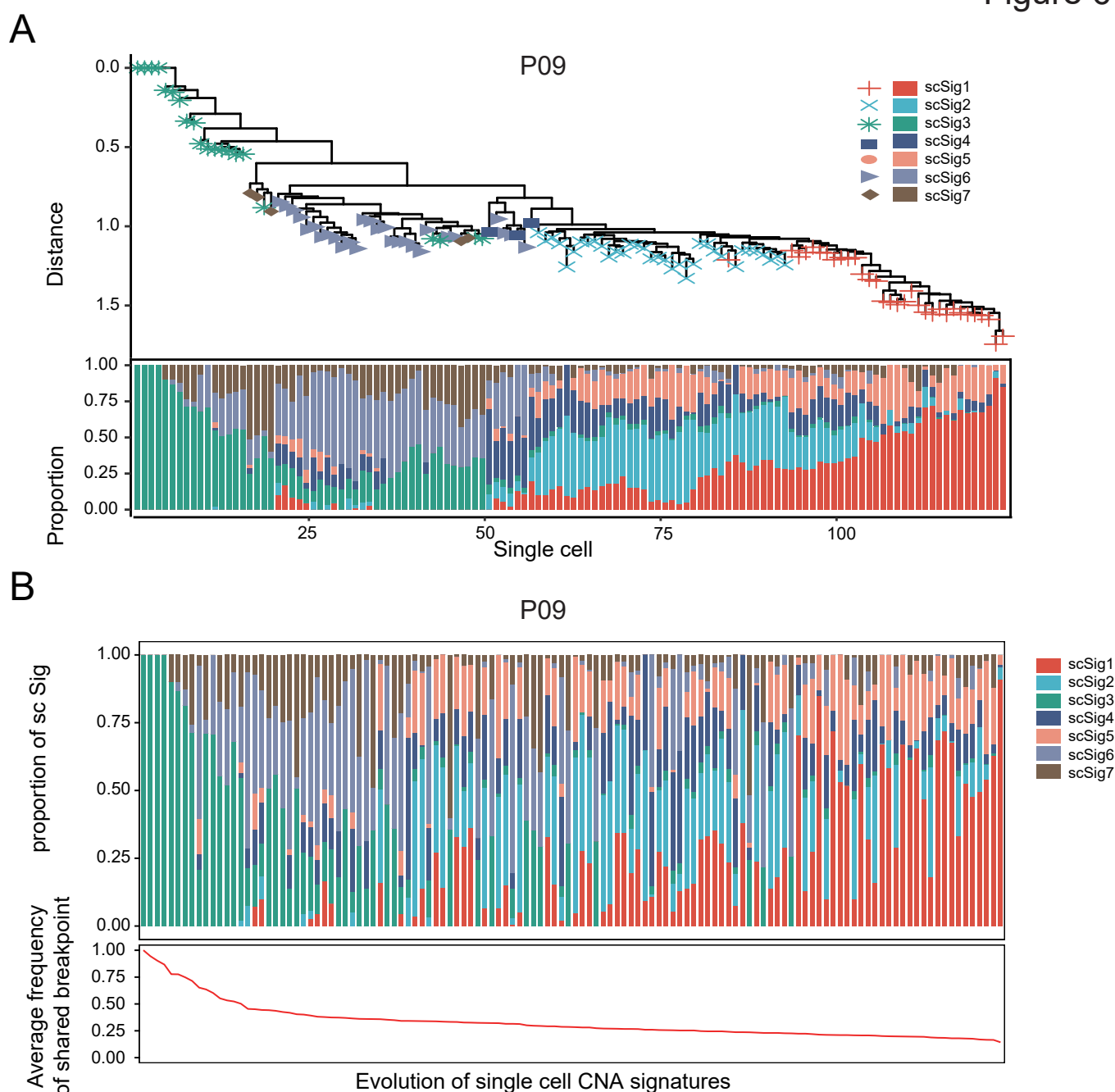


Figure 6



**Figure 6. CNA signature evolution analysis in HCC.**

A, Evolutionary tree analysis of scSig. Calculate the distance between cells based on scSig, infer the evolutionary relationship based on the distance, and then draw an evolutionary tree. Symbols on each branch represent the most prevalent scSig within that lineage.

B, Evolutionary trajectory analysis of scSig. The average number of shared breakpoints per cell within the sample is calculated, and cells are ranked according to the number. Cells with a higher ratio of shared breakpoints are positioned early in the clonal evolution, as subsequent subclones retain the breakpoints of earlier cells.