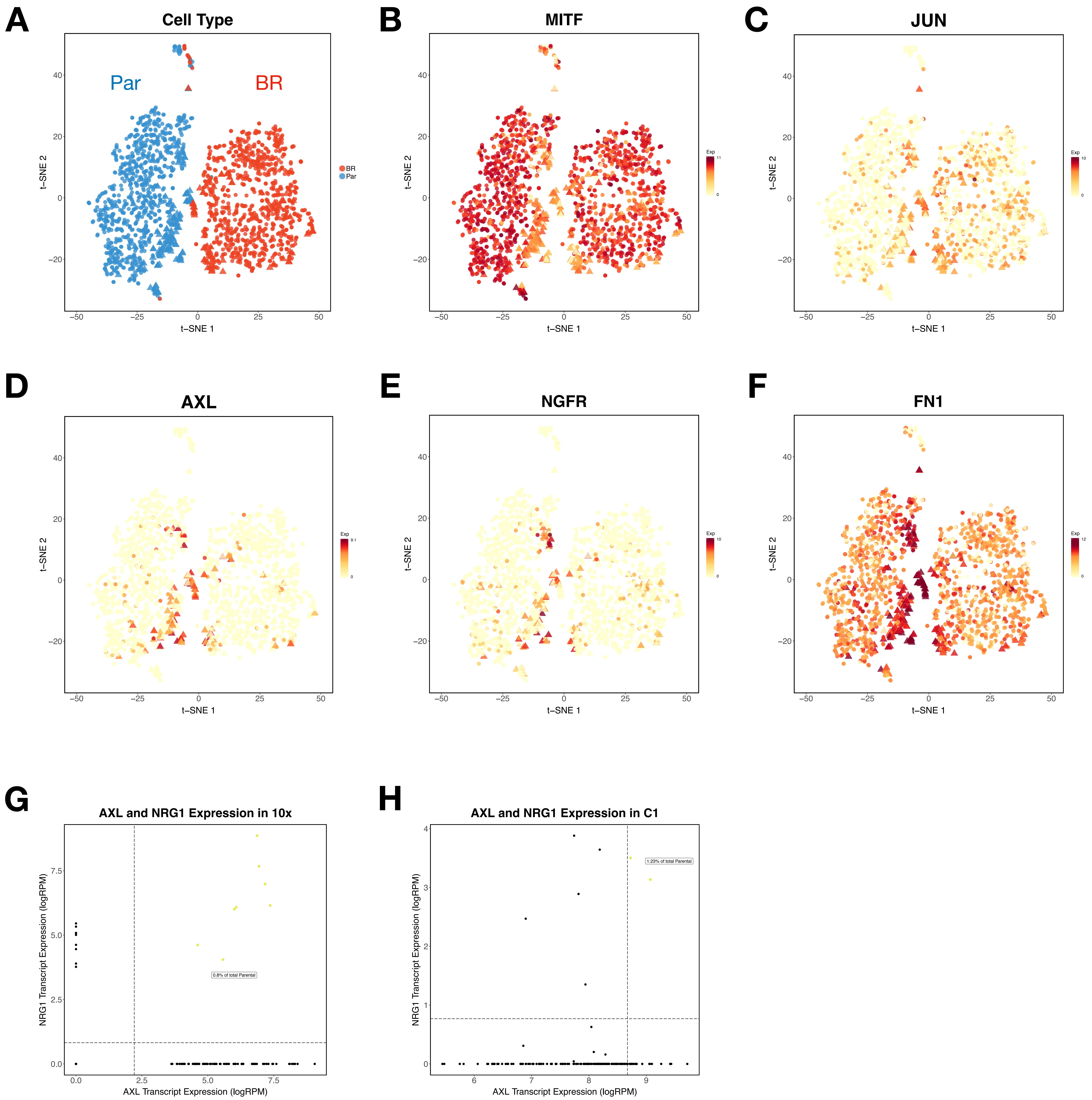

Supplemental Fig. S9 | Genes that showed distinct expression patterns in the intermediate transitional state during BRAF drug treatments. t-SNE maps were used to display the scRNA-seq data from 10x Genomics datasets, colored by **A)** whether the cells were derived from the parental population (blue) or the BRAFi resistant population (red) or by the expression levels of **B)** MITF, **C)** JUN, **D)** AXL, **E)** NGFR, and **F)** FN1. These five genes show the greatest degree of differential expression at the interface between the parental and BRAFi resistant cells, where SAKE had identified a third cluster of cells marked in yellow (triangle shape) in Figure 5 of the main text. This yellow cluster of cells showed the greatest enrichment for differentially expressed genes marking a "transitional state" between drug sensitivity and resistance in a recent publication by Shaffer et al (2017). The percentage of parental cells in that have both AXL and NRG1 high expression, which indicating the property of transitional state to resistance, was around 1% of the population in **G)** 10x and **H)** C1 data.