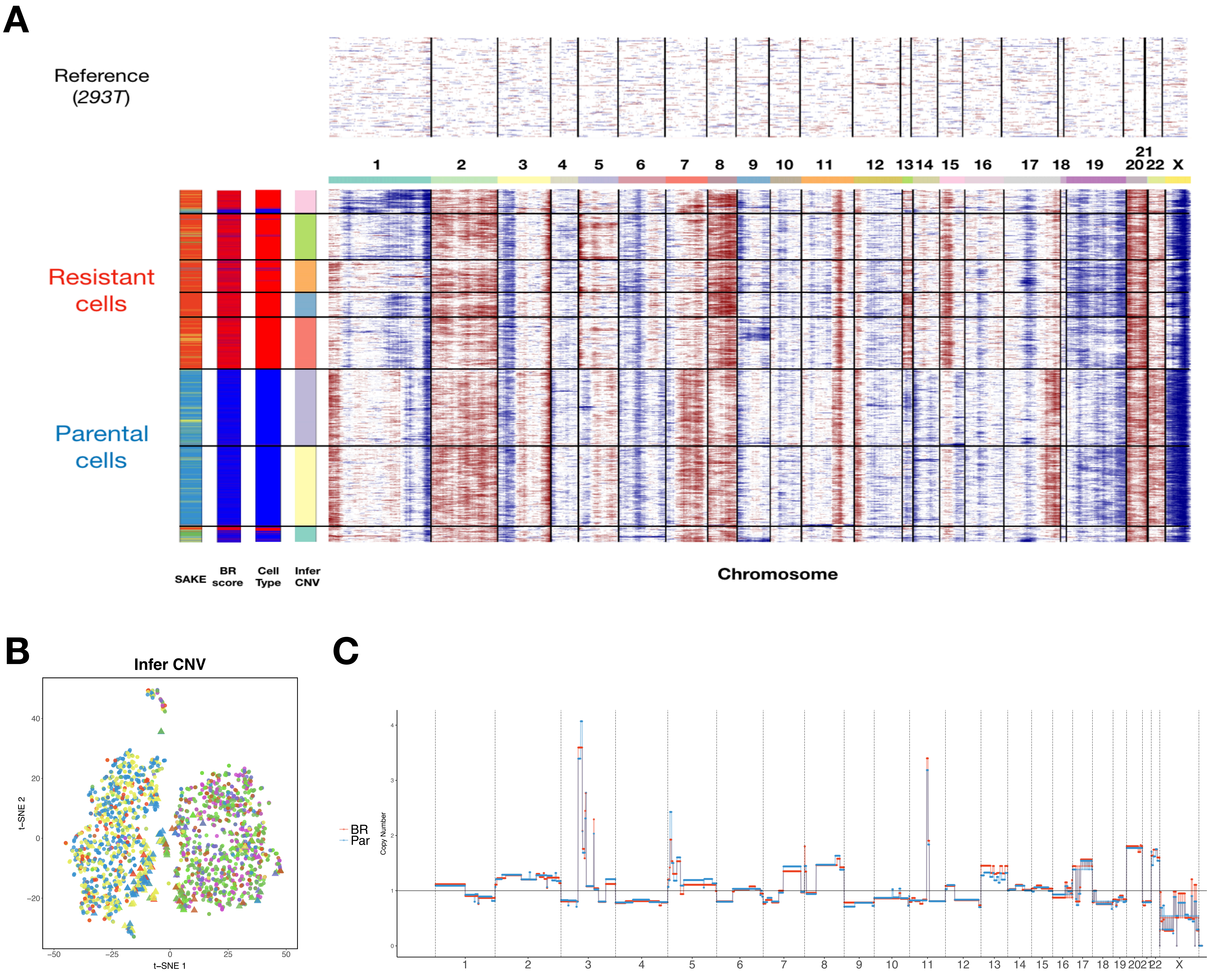

Supplemental Figure S13 | CNV and transcriptomic profiles identified an intermediate state between parental and resistant cells. **A)** Inferred CNV profiles (scRNA-Seq) were used as a proxy to assess the clonal states among parental and resistant cells via the inferCNV method (Tirosh et al., 2016). InferCNV identified 8 sub clonal populations in the 10x 451Lu dataset that largely segregated the Parental (blue) and BRAFi resistant (red) population, but showed no sub clustering of the candidate Transitional State cells (yellow). **B)** A t-SNE map was used to display the inferred clonality among the single-cells, with no apparent sub clusters separate from the Parental/BR groups. Each circle represents a cell and is colored by inferred CNV groups. **C)** Copy number profiles from bulk DNA samples were used to support the patterns observed from the inferred CNV profiles, which show good agreement for large-scale alterations.