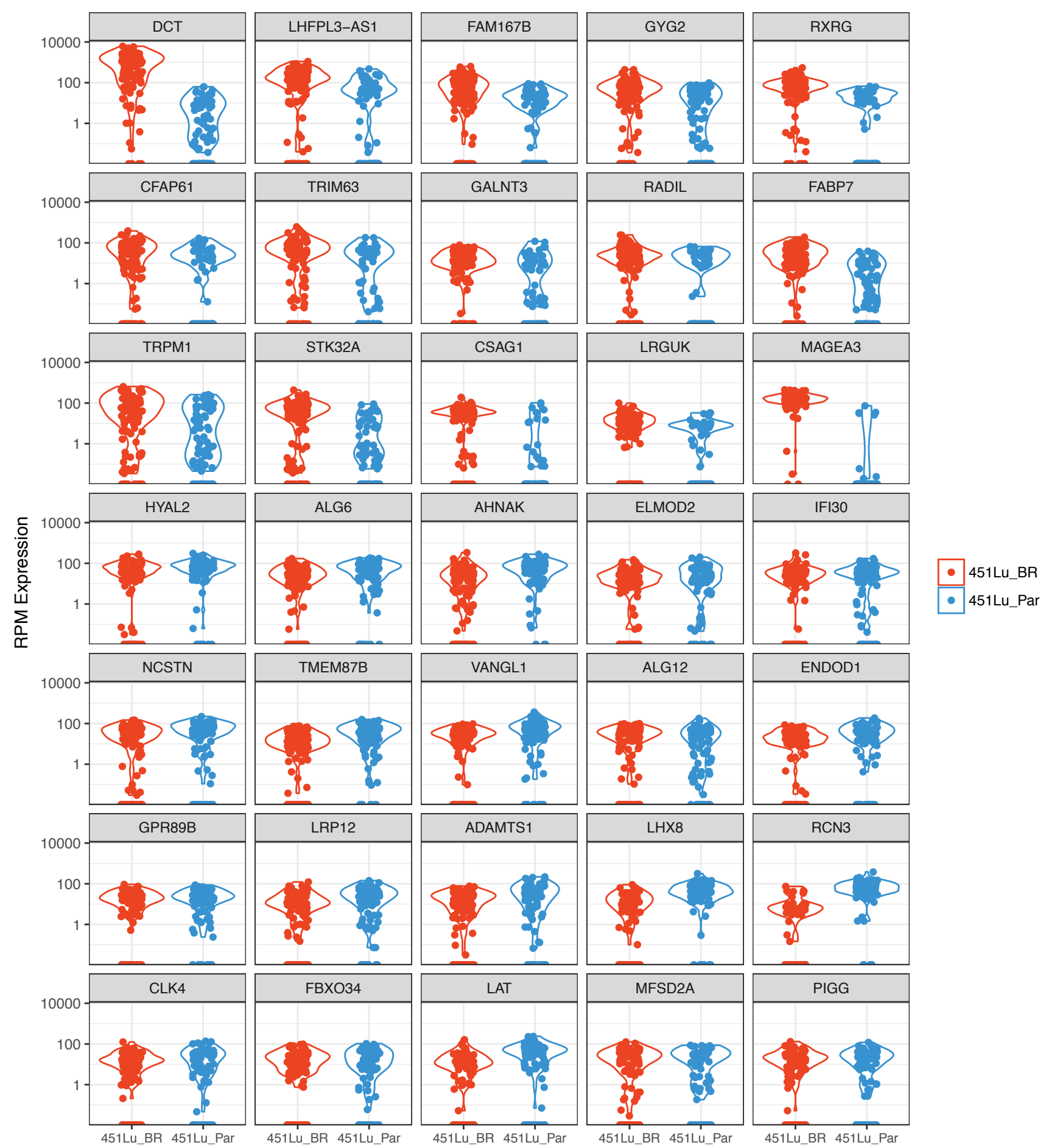
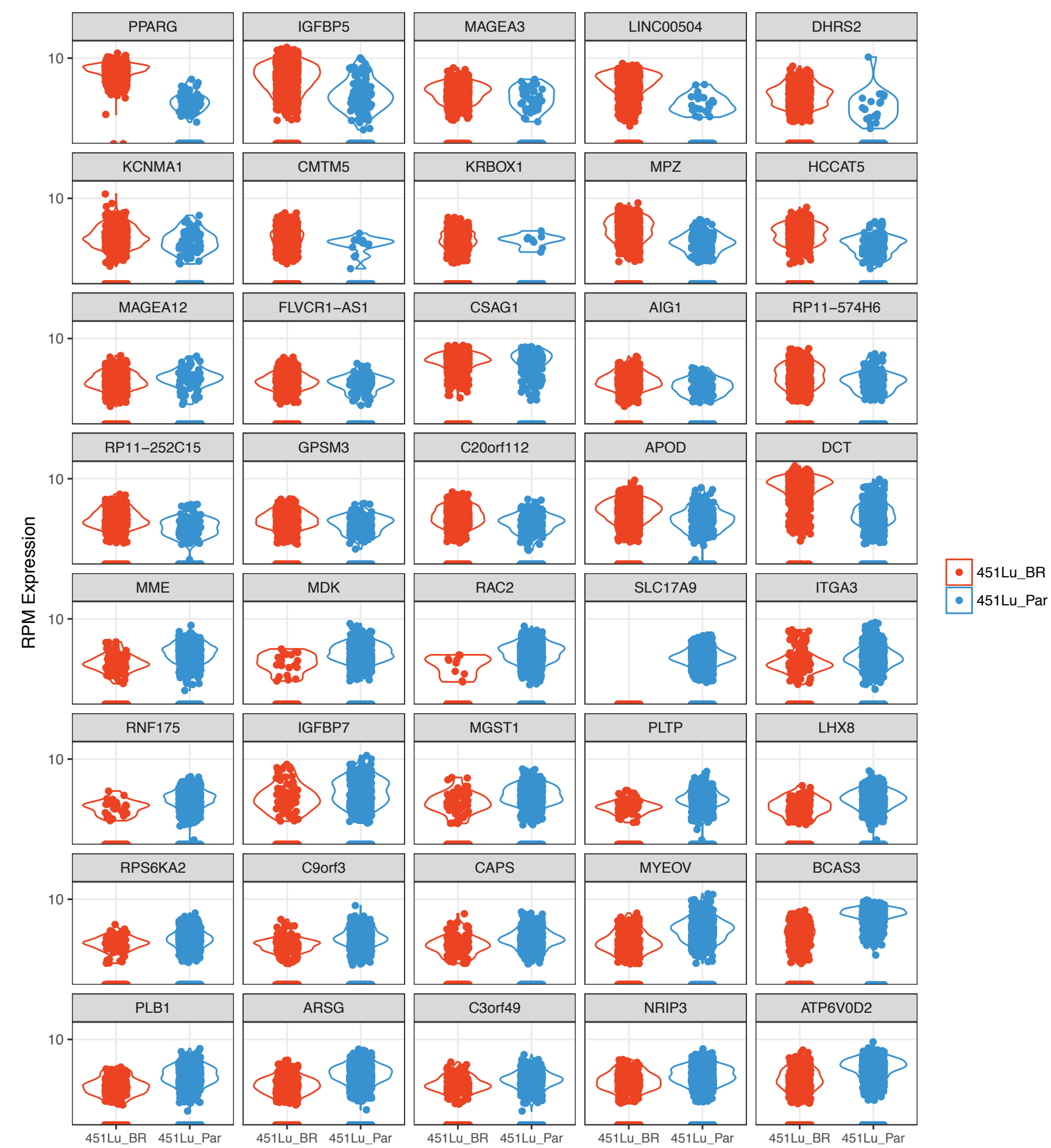


A



B



Supplemental Fig. S7 | Candidates genes that mark cells intrinsically resistant to BRAFi drug treatments from C1 and 10X data. SAKE was used to identify genes that could mark the BRAFi intrinsically resistant cells from the naïve parental cell populations. Top enriched markers in parental and resistant cells were identified in A) Fluidigm C1 and B) 10X data. The y-axis is the RPM normalized log expression value in the BRAFi resistant cells (red) and the parental cell population (blue). DCT is one of the most highly differentially expressed candidate markers for BRAFi resistant cells in both platforms.