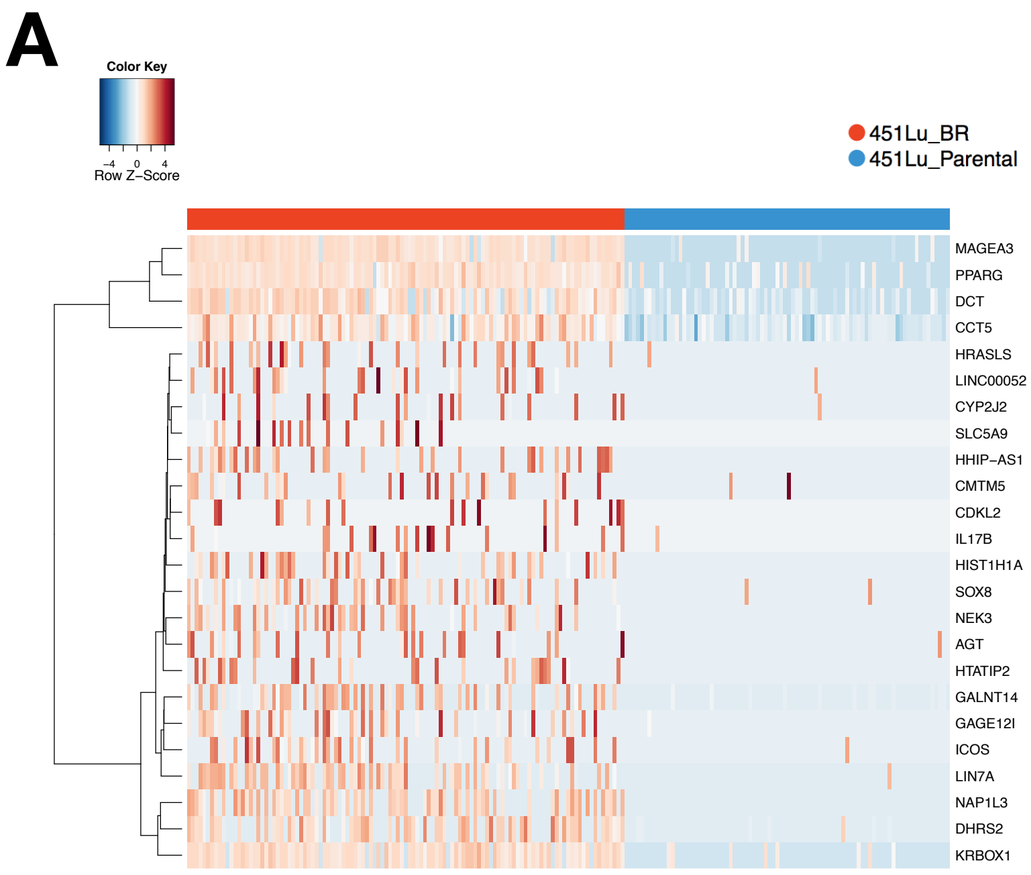

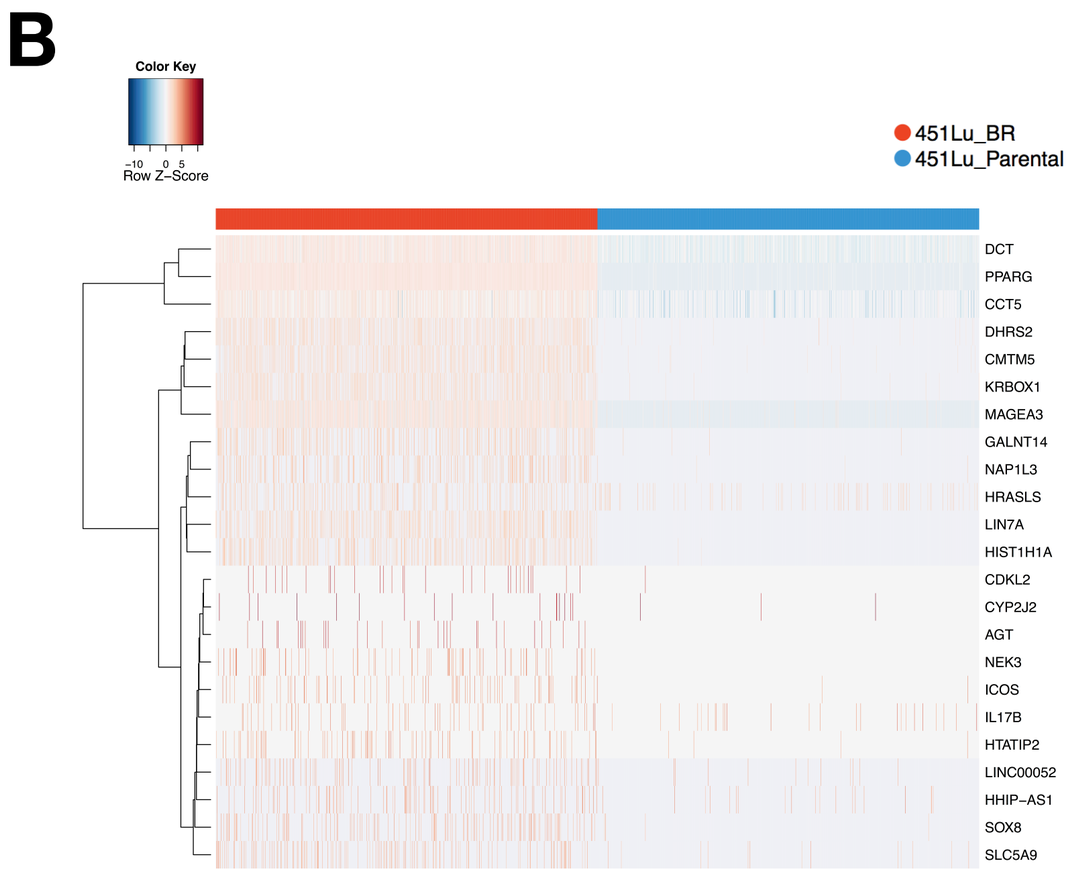

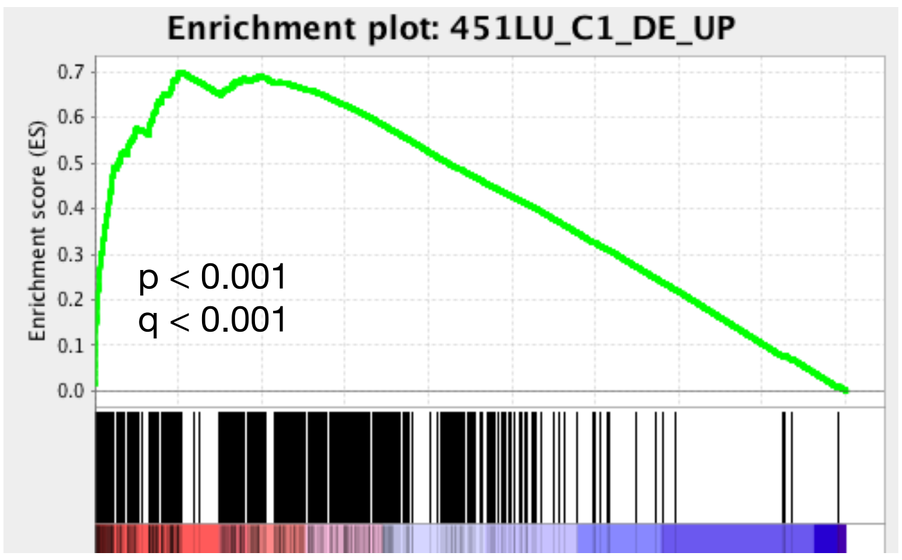

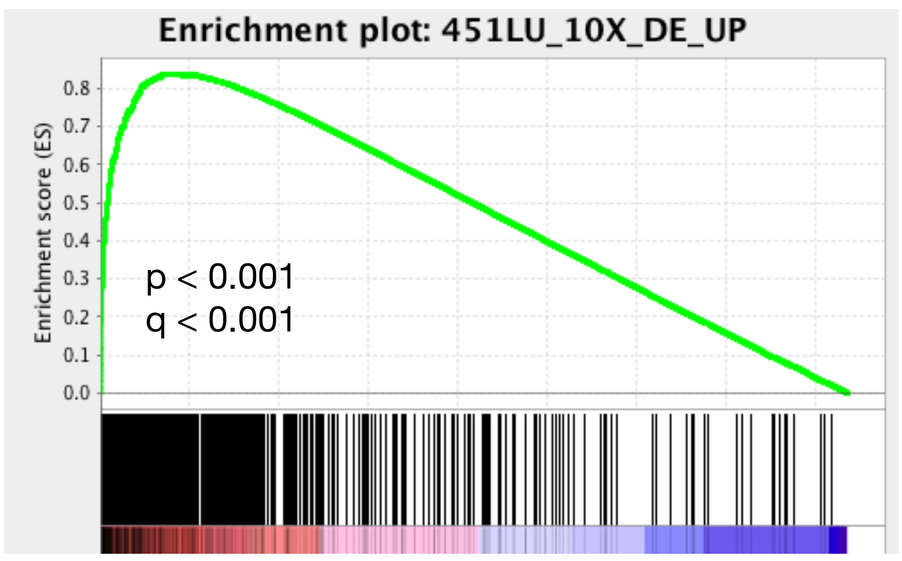

Supplemental Fig. S6 | High concordance between the Fluidigm C1 and 10X clustering results. Differential expression analysis was performed using DESeq2 (C1 data) and 10x Cell Ranger suite (10x data). Log2FoldChange between 451Lu-BR and 451Lu-Par from C1 data was plotted on the horizontal axis with Log2FoldChange(BR/Par) for the 10x data on the vertical axis. Genes that have adjusted p-value less than 1e-50 were highlighted in red, with all statistically significant genes (P<0.01) shown in black. These highly significant (red) genes were used to generate a heat map for **A)** C1 data and **B)** 10x data. Many of these genes showed stochastic expression across single cells, despite the very low P values, possibly due to transcript dropout artefacts. **C)** Genes identified as differentially expressed (DE) between 451Lu-BR and 451Lu-Par in Fluidigm C1 data, with a pvalue less than 0.001, were used for gene set enrichment analysis (GSEA) on 10x data sets. GSEA was performed using a pre-ranked file generated using log2FoldChange. **D)** The same analysis as **C)** was performed using DE genes identified from 10x and run GSEA on C1 log2FoldChange data. The significant GSEA results demonstrates a high concordance between the data sets generated across the C1 and 10x platforms.