



Supplemental Fig. S4 | Quality check and clustering results from single-cell RNA-Seq data from Fluidigm C1 system. A) Fluidigm C1 and bulk RNA-Seq data were mixed and clustered using SAKE. Single-cell data clustered together with its bulk counterparts and did not show platform specific batch effects. **B)** Single-cell RNA-Seq data from 451Lu and A375 cell lines were sequenced in Fluidigm C1 system. Each circle in the t-SNE map represents a cell and is colored by SAKE assigned groups. Four major groups were identified and occupied different quadrant in the t-SNE map. More SAKE3 cells were localized with SAKE4 cells suggesting higher level of heterogeneity between these two groups. These two groups (SAKE3 and SAKE4) correspond to cells from the 451Lu cell line. **C)** Genes that are reported to be expressed in each of the cell cycle stage were downloaded from QIAGEN. A Heatmap of these cell cycle markers shows no clear correlation between SAKE identified groups and cell cycle stage.