

Figure Legend

- **A.** The number of genes detected using CEL-Seq in 33 single mouse fibroblast cells processed in the C1 and 20 single cells processed manually.
- **B.** Data for ERCC Spike-in showing a linear relationship between levels of addition and detection. For this analysis all cells C1 collected (left) and manually collected (right) were pooled.
- **C.** Principal component analysis distinguished between GFP- and GFP+ cells processed in C1, using the fibroblast primary cells previously published by Klochender et al. (*Dev Cell* **23**:681-690, 2012) where GFP distinguishes between the cell cycle stages G1/G0 and S/G2/M.

