



Suppl. Figure 11. Assessment of deconvolution performance of synthetic chimeric cell populations in in-silico mixing experiments. A Identification of maternally inherited mtDNA variants that distinguish single cell chromatin profiles of CLL4 and CLL5 reanalyzed from Pentter & Gohil et al., Cancer Discovery 2021 (3) (informative mtDNA variants) using variance-to-mean ratio (VMR) and strand concordance. B Deconvolution of single cells from CLL4 (orange) and CLL5 (purple) based on mean heteroplasmy of 29 (CLL4) and 8 (CLL5) maternal mtDNA variants. Black dots indicate cells which cannot be assigned to either individual. C Number of unannotated cells from CLL4 cells after mtDNA-based deconvolution of mixed data for conditions from 1 to 1,000 CLL4 cells spiked into 7,579 CLL5 cells. D Single cell mtDNA coverage in CLL4 (orange), CLL5 (purple) and cells that could not be annotated. E UMAP projection of single cell chromatin accessibility profiles of CLL4 and CLL5 annotated by cell types (left) and by cells that could not be annotated using maternal mtDNA variants (right). F Spike-in experiment with single cells from AML1011 spiked into AML1012. G Germline-free deconvolution of mixed single cell RNA sequencing (scRNA-seq) profiles with vireo leads to random annotation for fewer than 300 (3%) CLL4 cells into 10,000 CLL5 cells (left). Number of unassigned cells (middle) and cells detected as doublets (right) for spike-in experiment of scRNA-seq profiles of CLL4 and CLL5 reanalyzed from Pentter & Gohil et al., Cancer Discovery 2021 using vireo without a germline reference. H Number of unassigned cells (left) and cells detected as doublets (right) for spike-in data using souporcell without a germline reference. I Number of unassigned cells (left) and cells detected as doublets (right) for spike-in data using vireo with a germline reference.