



Suppl. Fig. 12. Deconvolution of chimeric populations using mitochondrial DNA mutations and germline single nucleotide polymorphisms. A Identification of maternal mitochondrial DNA (mtDNA) variants from in-silico mixing experiment of CLL4 and CLL5 mtscATAC-seq profiles reanalyzed from Pentter & Gohil et al., Cancer Discovery 2021 (3) at a ratio of 10 (CLL4) to 7,579 (CLL5). After filtering of potential maternal mtDNA variants based on strand-concordance >0.8, variants are clustered using k-means clustering with k=3 and filtered for mtDNA variants that are mutually exclusive across both CLL populations. B-C Concordance of single nucleotide polymorphisms (SNP)-based germline-free donor-recipient deconvolution with souporecell and SNP-based whole-exome sequencing (WES) germline-based donor-recipient deconvolution with vireo across single cell RNA sequencing (scRNA-seq) profiles of 5 AML patients (4) for recipient- (B) and donor-derived cells (C). D-E Mutual exclusive detection of sex-specific genes XIST and RPS4Y1 in AML1010 following donor-recipient deconvolution with vireo (D) and souporecell (E) confirms the donor-recipient annotations. F Number of unassigned cells following SNP-based germline-free donor-recipient deconvolution with souporecell and SNPbased whole-exome sequencing germline-based donor-recipient deconvolution with vireo across scRNA-seq profiles of 5 AML patients. G Effect of T cell expansion protocol on chromatin profiles of CD4+ (G) and CD8+ T cells (H) demonstrated by differential chromatin accessibility of transcription factor binding motifs. H Surface marker expression of TSA and TSB oligotags across cell types. SAV: streptavidin, mTcrβ: murinized Tcrβ I Detection of MART1-specific T cells using TSA SAV:HLA-monomer conjugates. The color indicates the expression of the murinized Tcrβ sequence.