



Suppl. Fig. 9. Co-segregation of mitochondrial and somatic nuclear DNA mutations in AML bone marrow. A Donor-recipient deconvolution of AML1026 using mtDNA mutations or germline single nucleotide polymorphisms are highly consistent. B Donor-recipient deconvolution with mitochondrial DNA (mtDNA) (left) and single nucleotide polymorphisms (SNPs) (right). C Identification of hematopoietic stem cell (HSC)-like, progenitor-like, monocyte-like, erythroid, CD4+ T cell, CD8+ T cell and B cell populations with 45 Total-seq D antibodies in AML1026. D UMAP projections of surface marker expression data obtained from AML1026 annotated by cell types (top left), donorrecipient annotation (bottom left), apparent variant allele frequencies (VAFs) of NRASG13R (top right) and SF3B1P775Q (bottom right). E Apparent VAFs per cell of NRASG13R (top) and SF3B1P775Q (bottom) cell types for recipient- and donor-derived cells. F Apparent single cell VAF of NRASG13R and SF3B1P775Q in AML1026 across all scDNA-seq profiles (left) or only cells with coverage of both loci with at least 10x (right), demonstrating the relevance of drop-out for analysis of scDNA-seq data. G Co-occurrence of 11736T>C with NRASG13R and SF3B1P775Q in AML1026 (top). Heteroplasmy of 11736T>C across cell populations in AML1026 (bottom). H Identification of T cell subpopulations with surface marker expression (Total-seq D) (left). Donor chimerism across T cell subpopulations. (right)