



Suppl. Fig. 16. Deconvolution and identification of AML phenotypes in bone marrow using ASAP-seq. A-F Deconvolution of pooled samples using mean expression Total-seq A hashtags (HTA) measured with ASAP-seq. Numbers indicate the number of cells that could be assigned to HTA1 and HTA2 (HTA12) and HTA3 and HTA4 (HTA34), or that could not be deconvoluted (unassigned). G Chromatin accessibility profiles (top) and surface marker expression (bottom) across hematopoietic stem cell (HSC)-like, granulocyte macrophage progenitor (GMP)-like, monocytic (Mono) and erythroid cells in AML1010, AML1026 and AML1012. H Donor-recipient deconvolution using maternal mtDNA variants in AML1010 (left) and AML1026 (right). Orange and purple indicate donor and recipient-derived cells, while cells without clear annotation (i.e. doublets or low-quality cells) are indicated in grey. I, J Identification of copy number changes del(5q) and amp(22q) in AML1012 across cell types indicated by the color key. T cells do not harbor any copy number change, while myeloid and progenitor cells have del(5q) (I – bottom left) or del(5q) and amp(22q) (I – top left). Amp(22q) is not detected in isolation (I – top right).