



Suppl. Fig. 8. Co-segregation of mitochondrial and somatic nuclear DNA mutations in CLL. A Single-cell variant allele frequencies (VAFs) and heteroplasmy of mitochondrial DNA (mtDNA) mutations in CLL5335 preFCR and post-HSCT, in recipient-derived (rec.) and donor-derived (donor) immune cells. The fish plot (bottom) summarizes the results, with outgrowth of a resistant clone (purple) that co-existed beside two subclones marked by 2332C>T and 5979G>A. B Single-cell VAFs and heteroplasmy of mtDNA mutations in CLL5327 pre-FCR and post-HSCT, in recipient-derived (R) and donor-derived (D) immune cells. CLL clones relapse at a ratio which is shifted towards the subclone marked by TP53V272M, 3830T>C and 3526G>A (fish plot bottom). C Co-occurrence of 2332C>T, 5979G>A, ASLY321C, MMEK525N and KCKNV197I pre-FCR (blue) and post-HSCT (red) in CLL5335. Both mtDNA mutations are lost at relapse post-HSCT. The arrows indicate that ASLY321C and MMEK525N do not always co-occur with KCKNV197I pre-FCR but almost always co-occur at relapse post-HSCT, indicating outgrowth of CLL5335 from a subclone that harbors all three mutations at relapse post-HSCT. D Mutual exclusivity of a subclone in CLL5327 marked by PKDREJV245P versus a subclone marked by TP53V272L, 3830T>C and 3526G>A. Further, 3526G>A and 3830T>C are mutually exclusive, as demonstrated by the insets that show the number of cells that are positive (heteroplasmy >5%) for 3526G>A (top left), 3830T>C (bottom right), both (top right) or none (bottom left). E Distribution of 3526G>A (left) or 3830T>C (right) in cells that are PKDREJV245P (grey) or TP53V272L (red), illustrating that 3526G>A and 3830T>C cooccur with TP53 mutated cells in CLL5327. F Heteroplasmy of three mtDNA mutations with expansion in donor-derived immune cells of CLL5328.