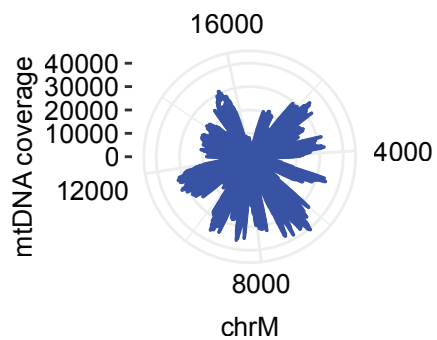
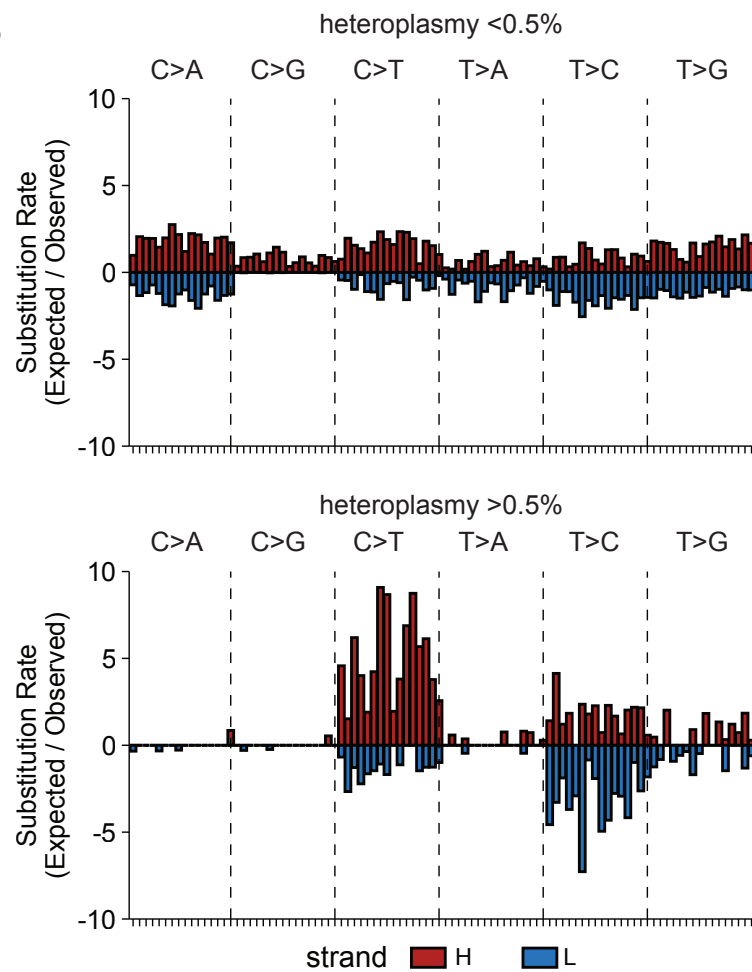
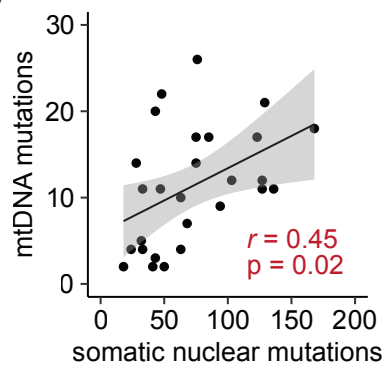
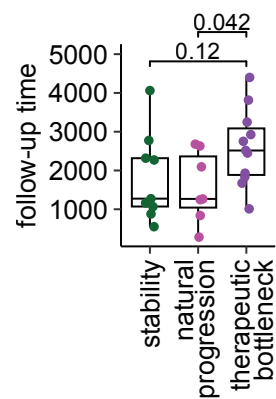
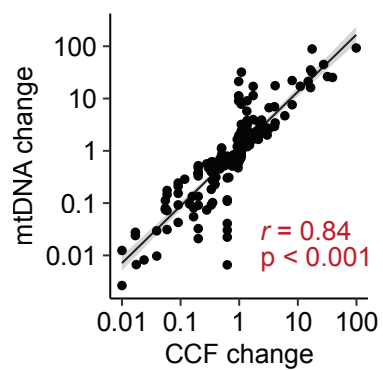


**A****B****C****D****E**

Suppl. Fig. 1. Extraction of mitochondrial DNA mutations from bulk RNA-seq data in CLL. A Coverage of mitochondrial transcripts in bulk RNA-seq data of CLL. B Mutational profiles in mitochondrial DNA (mtDNA) mutations extracted from bulk RNA-seq data. Those mtDNA mutations with heteroplasmy  $<0.5\%$  (top) were excluded due to their unspecific mutational profiles, while mtDNA mutations with a heteroplasmy  $>0.5\%$  in at least one sample (bottom) showed a characteristic profile and were used for further analyses. C Association of somatic nuclear and mitochondrial DNA mutations. Statistical testing using Pearson's correlation coefficient. D Follow-up time from first to last sample across genetic CLL subgroups in cohort. E Correlation of change in mtDNA mutations and CCF values. Statistical testing using Pearson's correlation coefficient.