



Suppl. Fig. 2. Longitudinal changes of somatic nuclear and mitochondrial DNA mutations in naturally progressing CLL. Cancer cell fractions (CCF) of CLL subclones were calculated from whole-exome sequencing (WES) data. Heteroplasmies were calculated from mitochondrial DNA mutations extracted from matched bulk RNA-seq data. Colors in CCF plots indicate CLL subclones identified from WES data, while colors in heteroplasmy plots indicate the closest-matching CLL subclone for each mitochondrial DNA mutation.