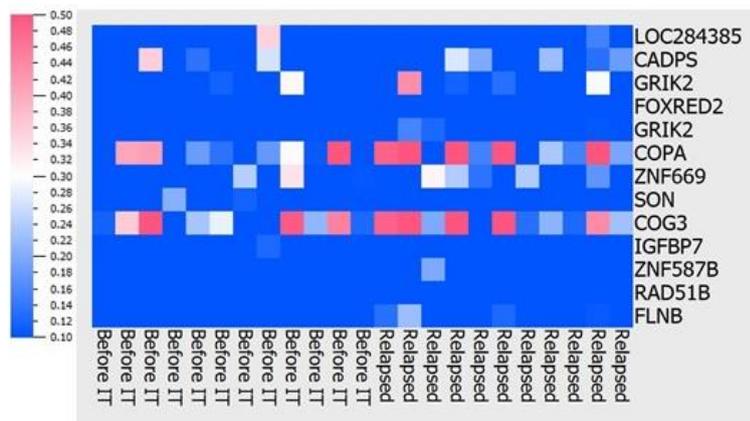


Supplementary Figure S1. Analysis of gene expression. The graph in A symbolizes the level of gene expression for the 50 genes most differentially expressed between cell lines made from tumours before IT and cell lines made from tumours relapsing during immunotherapy (“relapsed”). Cell lines are organized via gene expression pattern hierarchical clustering. Genes are ranked based on q values obtained through multivariate analysis using limma and voom test. The scale on the left represents the q-value. The scale on the right represents the log2 scale of gene expression where red denotes high expression and blue denotes low expression. In B a 3D PCA plot representation of samples based on top 50 genes differentially expressed.



Supplementary Figure S2. Heat map representation of all recoding editing events. Thirteen editing recoding events were evidenced in cell lines made from tumours before immunotherapy (“Before IT”) and from relapses occurring during immunotherapy (“Relapsed”). Editing is observed in the majority of cell lines for only COG3 and COPA. The scale on the left indicates the level of editing observed per site.