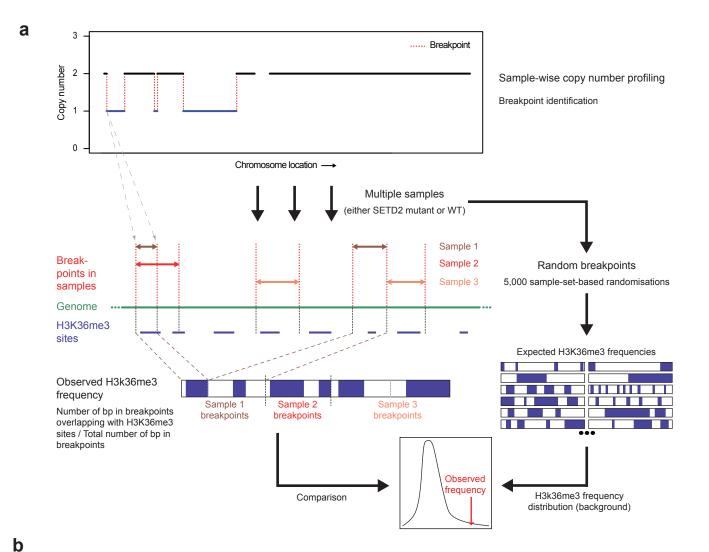
Figure S1. Schematic diagram illustrating analysis of H3K36me3 frequency within defined breakpoint regions and analysis of chromosomal complexity of SETD2 mutant tumors in the TCGA ccRCC dataset.



P = 0.33