



Supplementary Figure 6. Analysis of tumour ploidy for xenografts evaluated in the preclinical trial that were not whole genome sequenced. (a) The allele-specific copy number analysis of tumors (ASCAT) algorithm was used to infer tumour ploidy (top) and tumour purity (bottom) for the HR-proficient xenografts (Q133, Q155, Q66). Q70LM was determined to be polyploid. As a proof of principle, the ploidy determined using the ASCAT algorithm for Q70P and Q70AM was concordant with the ploidy estimated by whole genome sequencing. **(b)** The polyploidy of Q70LM was further verified using propidium iodide staining. Shown is flow cytometric quantification of DNA content using PE-A histograms.