



Supplementary Figure S4: Absence of *ARID1A* variant in targeted panel sequencing of Biopsy 1 despite adequate depth

Top panel shows Biopsy 1 targeted panel sequencing. Bottom panel shows representative tumor sampled at autopsy (Sc6) with heterozygous deletion in *ARID1A*, clearly absent from Biopsy 1 sequencing despite adequate depth (7240 unique molecules). The probability of not sampling the *ARID1A* variant in Biopsy 1 due to chance alone was calculated assuming tumor cellularity of 80% and the heterozygous *ARID1A* variant being present in 50% of tumor reads. 7240 unique molecules covered this genomic position. The binomial distribution in R was used to calculate the probability of not sampling this variant: $\text{dbinom}(7240, \text{size}=7240, \text{prob}=0.6)$.