# Supplementary Tables

**Table S1**. We provide ten representative phylogenies and cellularity matrices used in our simulations summarised in Manica et. al.

**Table S2**. We provide mutations and inferences based on 10 profiles of the same CRPC tumor. Each mutation, in the tab “Mutation” is given in terms of coordinates in hg19. For each mutation, we provide the biopsy index (from Biopsy 1 to Biopsy 10), the number of reads with the reference allele in that biopsy, the number of reads with the mutated allele, predicted copy number at the allele, and the ratio of reference to alternative (read fraction). We also describe the association between mutations and subclones (Subclones tab), and the mutation frequencies (Frequencies tab) and subclone cellularities (Cellularities tab).