



Supplementary Figure 5. Somatic mutation trinucleotide contexts. Bar plots illustrating the proportion of single nucleotide variants (SNVs) in each trinucleotide context, from whole exome sequencing of patients within the 95th percentile of tumor mutation burden by initial targeted sequencing. Each row represents a different category of patient (e.g. mismatch repair defective (MMRd) etiology versus homologous recombination repair defects (HRRd)). For patients with >1 cfDNA sample subjected to whole exome sequencing, proportions of SNVs used in the calculation are from the sample with the highest calculated ctDNA fraction.