



Figure 3 – figure supplement 1: The distance between a somatic substitution and the nearest somatic indel (top left), substitution (top right), repeat (bottom left) or homopolymer (bottom right) in the individual MMR-deficient genomes, and the expected distance based on 200 random models. The substitutions located nearby indels and substitutions were enriched respectively within a range of ~30bp and ~200bp, whereas substitutions near repeats were enriched only at the base immediately flanking the repeat.