



Figure 4 – figure supplement 2: The fraction of indels (left panel) and substitutions (right panel) identified by whole-exome sequencing, as observed in microsatellites, homopolymers (length over 5 bp), short homopolymers (length of 3 to 5 bp) and 'not in repeat regions' compared to their expected fraction in these regions. Indels mainly affected homopolymers (59.0%), whereas microsatellites and short homopolymers were affected at a frequency that was expected based on their genome-wide occurrence. In contrast, indels were depleted in non-repeat regions. Substitutions affected the exome independent of repeat composition. These distributions mirror our observations in the MMR-deficient tumors undergoing whole-genome sequencing.