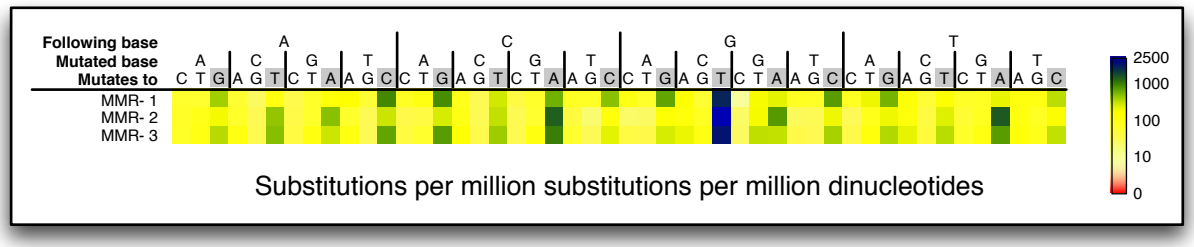

Figure 2 – figure supplement 1: Somatic substitution frequency per million dinucleotides and per million substitutions for the individual MMR-deficient genomes. The first row lists the base following the mutated base, the second row the base that was mutated and the third row the new base. Transitions are indicated by grey boxes. Frequencies are depicted color-coded following a logarithmic distribution as shown by the gradient on the right. The average R^2 between the MMR-deficient tumors is 0.75.