



Figure 2 – figure supplement 2: Multivariate linear regression modeling of genome features predicting substitutions frequencies per 1Mb window in the individual MMR-deficient genomes. T-values resulting from the linear model are displayed for each genome feature in the bar plots and indicate significance (shaded grey box equals $P > 0.05$, Bonferroni-corrected per model) and direction of the correlation. High concordance between the individual tumors is observed.