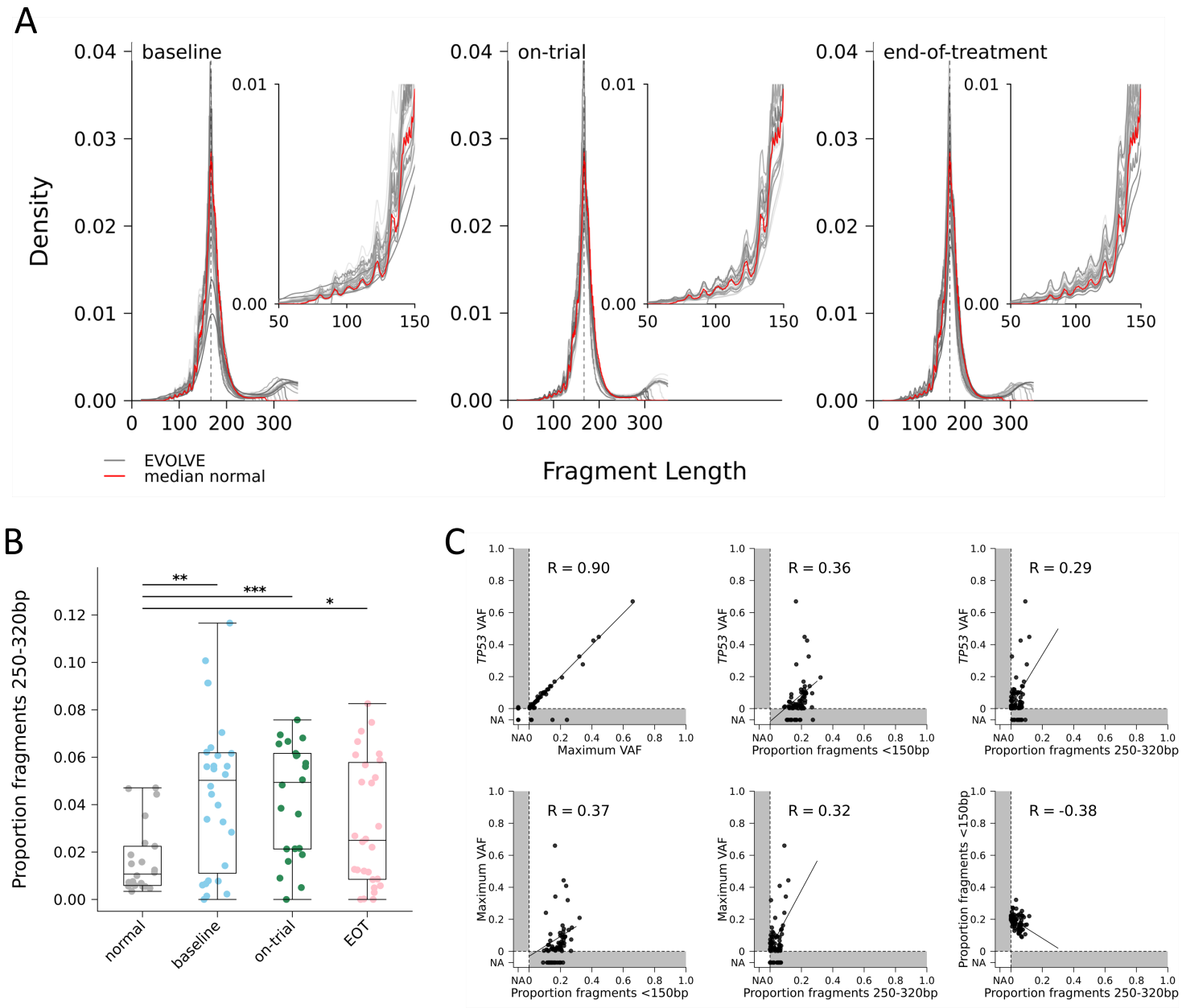

Supplementary Figure 4: A) Distribution of fragment length among patient derived cfDNA samples collected at baseline, cycle 2 of treatment and end of treatment, and a panel of healthy control cfDNA; inserts highlight increased frequency of short fragments in patient-derived samples. B) Proportion of long (250-320bp) fragments was significantly higher in patient cfDNA collected at baseline and at cycle 2 of treatment than cfDNA from healthy controls (two-sample Wilcoxon test: * $p < 0.1$; ** $p < 0.01$; *** $p < 0.001$). C) Comparison of tumour content estimation methods including TP53 VAF (based on known high-frequency somatic mutations), maximum VAF (of all high-confidence somatic mutations), proportion of short (<150bp) and long (250-320bp) fragments.