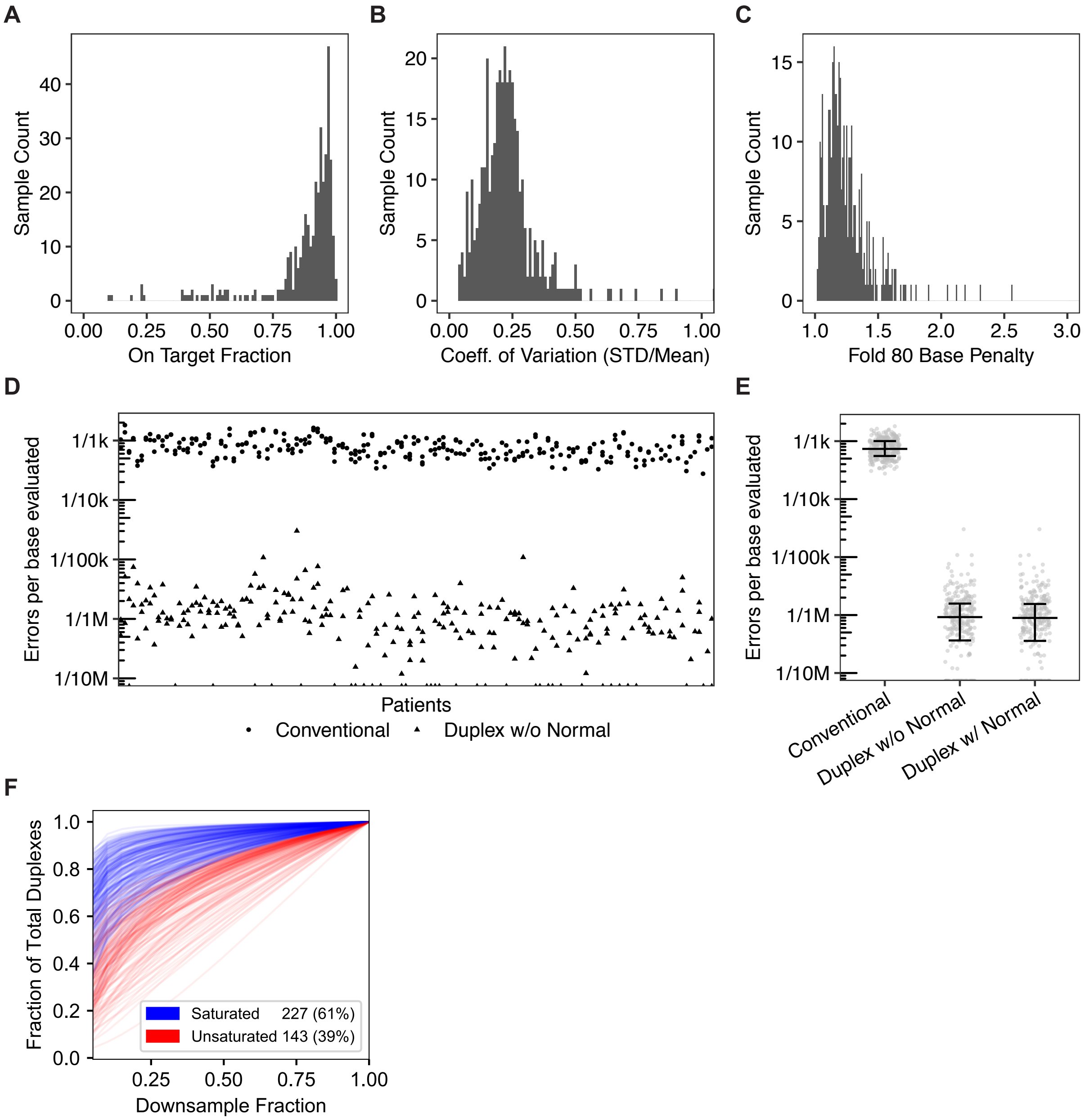

Supplementary Figure 9: **Technical performance of the MRD Assay.** All samples from early stage breast cancer cohort. Includes plasma cfDNA and buffy coat gDNA samples. Samples from the same patient and probed with the same panel are represented independently. (A) On target fraction calculated from Picard CollectHsMetrics and using pct_selected_bases. (B) Coefficient of variation of duplex fragment depth across fingerprint sites. (C) Fold 80 base penalty score for duplex fragment depth across fingerprint sites. (D, E) Error rate comparison between conventional sequencing (requiring Q20 base quality and removing duplicate fragments) and our duplex sequencing with added filters (see methods). (F) Fraction of total duplexes after downsampling raw reads. We considered a sample to be saturated if it still contained at least 95% of its duplexes after downsampling to 80% of its raw reads.