Libraries were generated using the KAPA HyperPrep Kit and the KAPA Universal UMI Adapter from either 10 ng or 50 ng of plasma cfDNA or fragmented reference cell-line DNA as input, and individually captured using the KAPA HyperPETE Reagent Kit and the respective panel.

Final libraries were sequenced on an Illumina NextSeq™ 550 System with 6M – 14M (median: 8M) high-quality read pairs (2 x 150 bp) allocated per sample for the KAPA HyperPETE Hot Spot Panel, and 55M – 81M (median: 66M) high-quality read pairs allocated per sample for the KAPA HyperPETE Pan Cancer Panel.

Two (2) Seraseq® ctDNA Mutation Mix samples in duplicates and sixteen (16) healthy donor plasma cfDNA samples were used to assess the performance.

Data was analyzed using the NAVIFY® Mutation Caller.