

High specificity was demonstrated by the high percent of reads on-target when starting from 10 ng or 50 ng of various quality (low, medium, high) input FFPE RNA.

On-target rate was 92% to 97% (includes housekeeping and fusion targets) with good performance across all sample input amounts, qualities, and types. The on-target rate was calculated following rRNA read removal (0.8% to 11% of all reads).

Two (2) cell-line samples (in duplicates) and fourteen (14) normal adjacent FFPE samples were used to assess performance.

RNA was extracted with the Roche High Pure FFPE RNA Isolation Kit and quality was determined with the DV200 score using the Agilent RNA 6000 Pico Assay on the Bioanalyzer.

The KAPA HyperPETE Workflow for Tissue RNA Fusion Transcript Preparation using the KAPA HyperPETE LC Fusion Panel was followed.

Libraries were generated using the KAPA RNA HyperPrep Kit in combination with the KAPA Universal UMI Adapter and either 10 ng or 50 ng of RNA while adjusting PCR cycles based on the input amount and DV200 score. Libraries were captured using the KAPA HyperPETE Reagent Kit and sequenced on an Illumina NextSeq™ 550 System.

Total read pairs (2 x 150 bp) per sample ranged from 3.6M to 17M and data was analyzed using NAVIFY® Mutation Caller to assess enrichment and variant detection performance.