

# KAPA Total Prep FFPE workflow

Get more out of your paired sequencing with a combined, single-tube library preparation for DNA and RNA

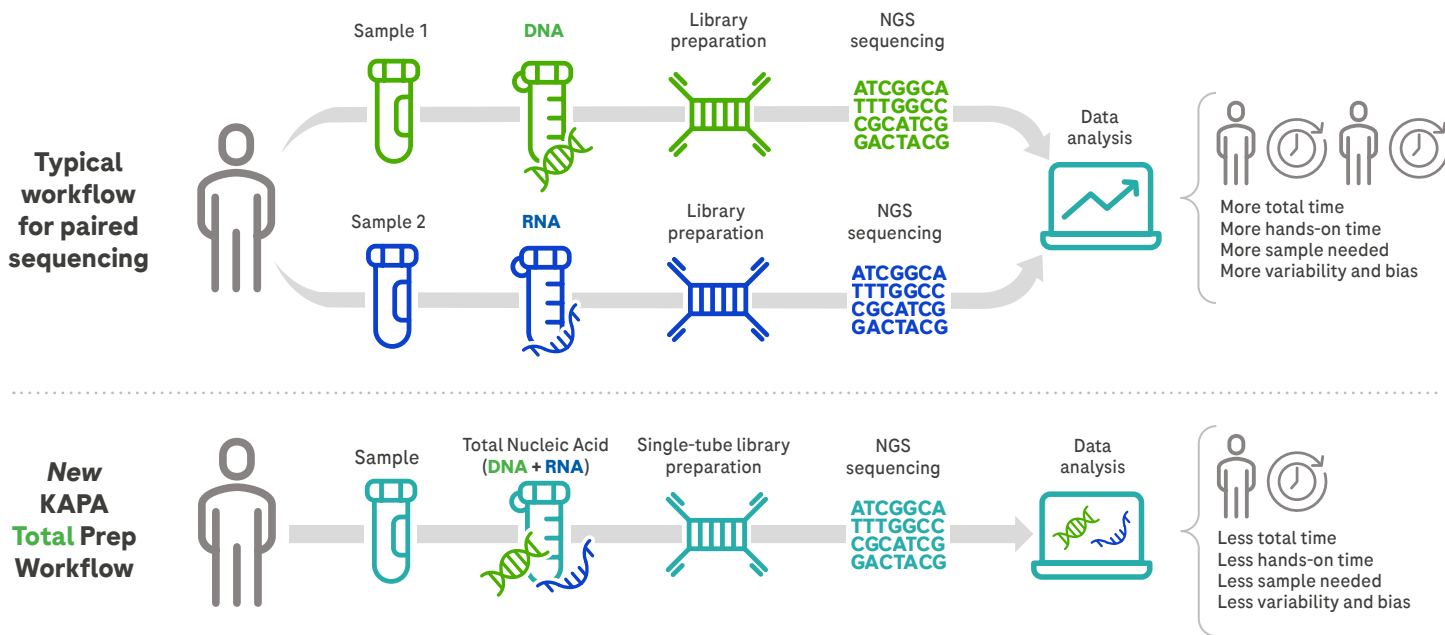


**KAPA Total Prep FFPE workflow** simultaneously generates DNA and RNA libraries from a single input FFPE sample.

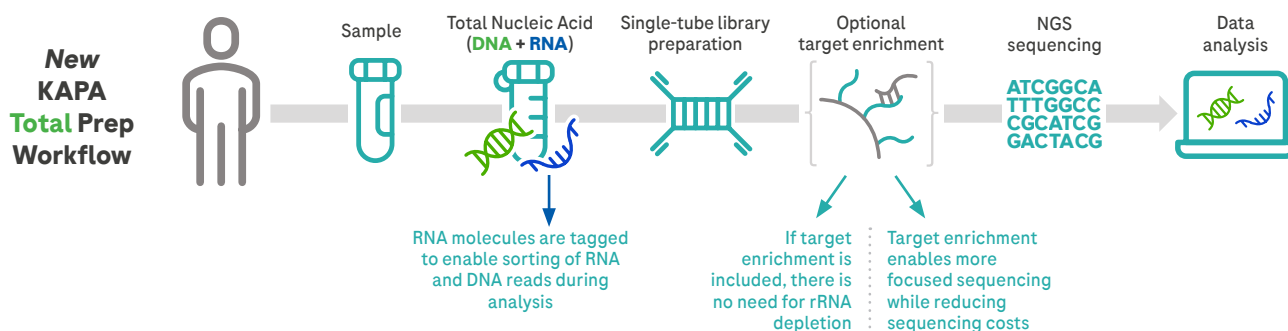
### Advantages over separate DNA and RNA library prep:

- Saves time, resources, and labware
- Conserves often-limited FFPE sample
- Enables more reliable tumor profiling by reducing bias caused by FFPE sample variability

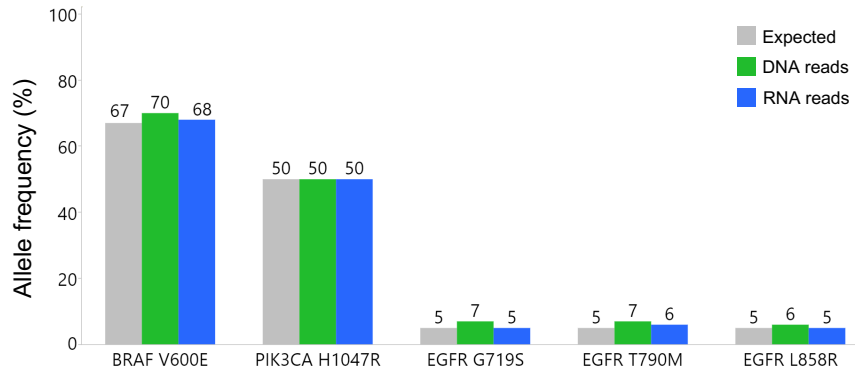
Save time and resources compared to parallel or sequential library preparation



Simultaneously capture regions of interest from the genome and corresponding transcripts with optional target enrichment

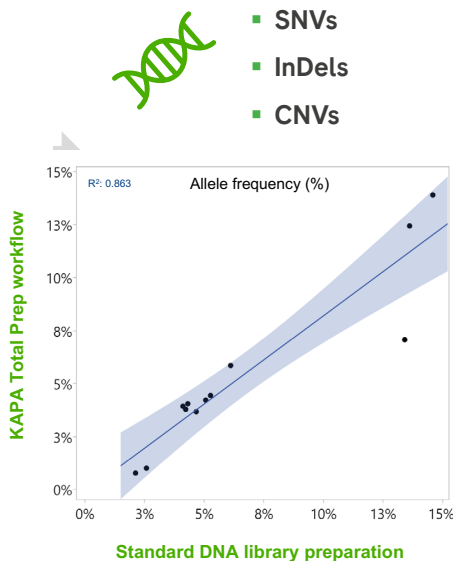


# Conserve sample while detecting both genomic variants and expressed transcripts

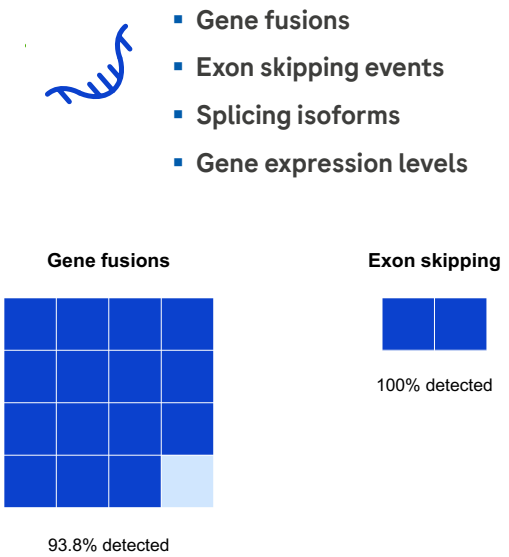


**SNV allele frequency is consistent between DNA and RNA reads.** SNVs were detected in an FFPE sample with known expected allele frequencies using the KAPA Total Prep FFPE workflow, with the KAPA HyperCap Oncology Panel. Results for both DNA and RNA reads were compared to the expected allele frequencies.

## Detect DNA & RNA biomarkers from the same total nucleic acid input



**SNV and InDel allele frequency in the DNA reads is concordant between manual and KAPA Total Prep library preparation workflows.** Both workflows included target enrichment with the KAPA HyperCap Oncology Panel.



**The KAPA Total Prep workflow enables the detection of RNA fusions and exon-skipping events.** Detection of 16 RNA known fusions and 2 exon-skipping events was analyzed with the KAPA Total Prep FFPE workflow.

### Learn more

about the **KAPA Total Prep FFPE workflow** and how it can help you at [go.roche.com/TotalPrep](https://go.roche.com/TotalPrep) or by scanning the QR code.

