

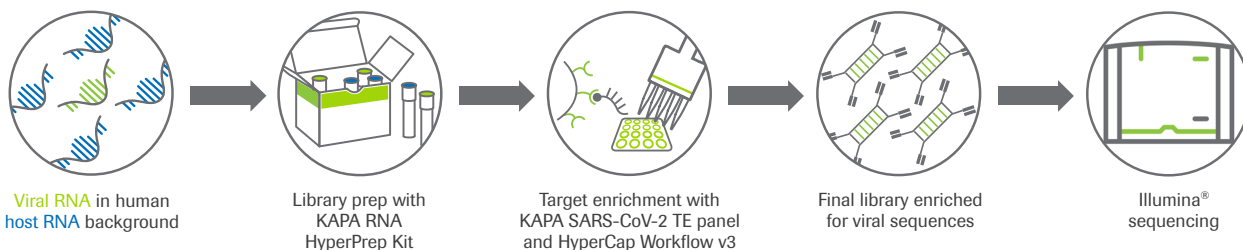


KAPA SARS-CoV-2 Target Enrichment Panel

Better by Design

Monitor the presence of the SARS-CoV-2 virus and the emergence of new strains with the **KAPA SARS-CoV-2 Target Enrichment Panel**. Prepare libraries from input RNA using the robust **KAPA RNA HyperPrep Kit** and then enrich for viral sequences; this panel targets 100% of the reference SARS-CoV-2 genome (NC_045512) and >99.7% of another 183 publicly available SARS-CoV-2 genomes (GenBank, March 2020).

- **Identify multiple variants of SARS-CoV-2 in a single reaction***
- **Achieve 1X coverage of >97% of the SARS-CoV-2 genome down to 1000 viral copies** and obtain genomic sequence from as few as 10 viral copies (in a background of 20 ng or 100 ng RNA with 1 million 2x75 bp reads)
- **Save valuable time with hybridization as short as 1 hour**



Project: Analyzing the SARS-COV-2 Genome with Target Enriched RNA-Seq, Wilmington, MA 2021.

For Research Use Only. Not for use in diagnostic procedures.

*World Health Organization. (2021). Genomic sequencing of SARS-CoV-2: a guide to implementation for maximum impact on public health, 8 January 2021.

World Health Organization: <https://apps.who.int/iris/handle/10665/338480>. License: CC BY-NC-SA 3.0 IGO.

Identify multiple variants of SARS-CoV-2 in a single reaction

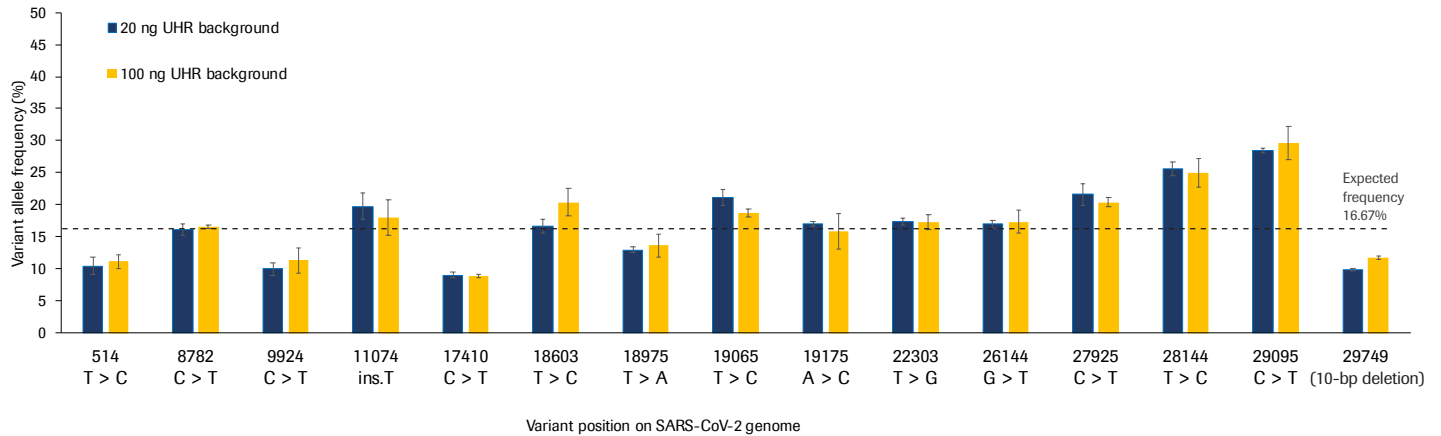


Figure 1. Variants from six strains of SARS-CoV-2 are identified from within a single sample. A total of 1,000,000 SARS-CoV-2 genome copies from 6 different strains was combined with either 20 ng (dark blue) or 100 ng (yellow) of human RNA and processed in triplicate using KAPA RNA HyperPrep and the KAPA SARS-CoV-2 Target Enrichment Panel. Alternate allele frequency analysis shows that all expected variants from the six SARS-CoV-2 strains were identified at close to the expected frequency. Datasets downsampled to 1 million reads prior to analysis.

Cover more of the SARS-CoV-2 genome and identify viral sequence from low viral copy numbers

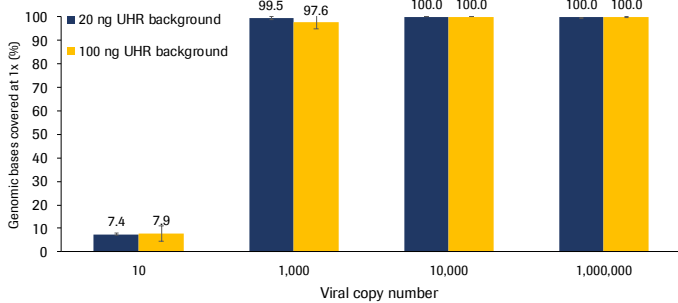


Figure 2. The KAPA SARS-CoV-2 Target Enrichment Panel achieves 1X coverage of >97% of the SARS-CoV-2 genome down to 1000 viral copies and genomic sequence from as few as 10 viral copies. Samples containing the indicated number of viral copies in a background of either 20 ng or 100 ng of human RNA were processed in triplicate using KAPA RNA HyperPrep and the KAPA SARS-CoV-2 Target Enrichment Panel. Datasets were downsampled to 1 million reads prior to analysis.

Save valuable time with hybridization as short as 1 hour

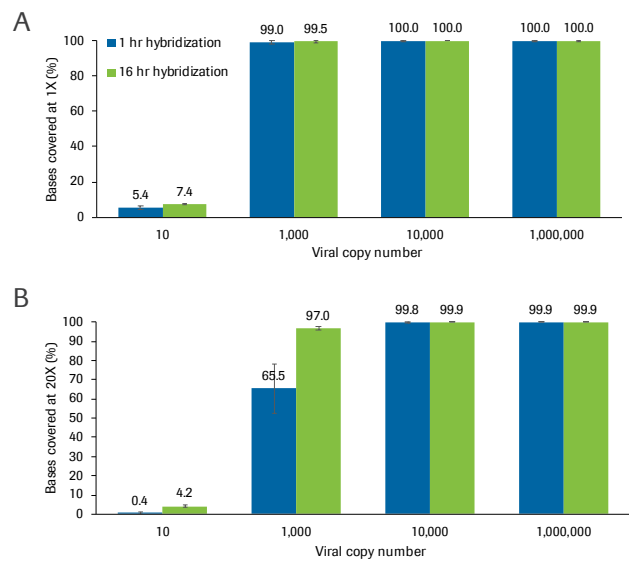


Figure 3. Shortening the hybridization time to 1 hour yields equivalent 1X SARS-CoV-2 genome coverage compared to 16-hour hybridization. Libraries generated from samples containing the indicated number of viral copies in a background of 20 ng of human RNA were hybridized to the SARS-CoV-2 TE panel for 1 hour or 16 hours and processed through the HyperCap v3 workflow in triplicate. **A.** The 1-hour hybridization time and 16-hour hybridization time yield similar SARS-CoV-2 genome coverage at 1X for all viral copy levels. **B.** Samples with higher viral loads also yield similar genome coverage at 20X for the 1-hour and 16-hour hybridization times, with somewhat reduced coverage for lower viral loads. 1 million Illumina NextSeq reads (2x75 bp).

KAPA HyperExplore MAX 0.5MB
IRN: 1000004753



Roche cat no.	Kit size
09062815001	12 rxn
09062823001	24 rxn
09062831001	48 rxn
09062840001	96 rxn
09062858001	192 rxn
09062866001	384 rxn



Learn more at:

<https://go.roche.com/SARS-CoV2-Panel>

Request a no-charge evaluation of the SARS-CoV-2 Enrichment Panel at:

<https://go.roche.com/SARS-CoV2-Eval>