ONETest™ Coronaviruses *Plus*

The **ONETest™ Coronaviruses** *Plus* offers full genome capture of the SARS-CoV-2 [1] from total nucleic acid extracts and up to 10,000-fold increase in viral reads compared to whole metagenome sequencing.

In addition, it provides simultaneous sequence chracterization of a diverse range of common viruses associated with respiratory infections.

[1] Target Capture Sequencing of SARS-CoV-2 Genomes from COVID-19 Patients in Florida, USA, Zhan & Alamouti et al. (under review). https://www.fusiongenomics.com/onetest-platform/coronavirusesplus/

1. Targets regions of interest with up to 25% dissimilarity to reference sequences
2. Provides up to 20% better sequence coverage than commonly used amplicon assays for a wide range of viral genome input
3. Captures nucleic acids from co-occurring genotypes, subtypes and strains in highly complex samples
4. Determine the relative abundance of viral target genes

Pathogen	Type/Subtype/Lineage	Target	Target coverage (%)
SARS-CoV-2	whole genome	whole genome	100
Coronaviruses (other)	229E, HKU1, NL63, OC43, SARS-CoV-1, MERS	Spike protein, Nucleo-protein	51 to 91 31 to 80
Influenza virus	A/H1N1, A/H3N2, B/Yam, B/Vic	Haemagglutinin, Neuraminidase & Matrix protein	100, 100, 30
Respiratory syncytial virus	RSV A, RSV B	Glycoprotein Fusion protein	50, 70
Human metapneumovirus	hMPV A, hMPV B	Fusion protein, Nucleoprotein	98, 88
Parainfluenza virus 1 and 3	hPIV 1, hPIV 3	Hemagglutinin-neuraminidase, Nucleoprotein	35, 85
Parainfluenza virus 2 and 4	hPIV 2, hPIV 4	Hemagglutinin-neuraminidase, Nucleoprotein	50, 75
Enterovirus/ rhinovirus	EV A to EV D & RV A to RV C	VP1 capsid protein	40 to 70
Parechovirus	PeV 1 to PeV 6	VP1 capsid protein	60 to 70
Adenovirus	AdV A to AdV G	Hexon, Fiber	45 to 75, 40 to 60
Bocavirus	hBoV 1 to hBoV 4	VP1, NS1, NP1	30 to 51

Table 1: Viral targets captured by the **ONE**Test Coronaviruses *Plus* assay.

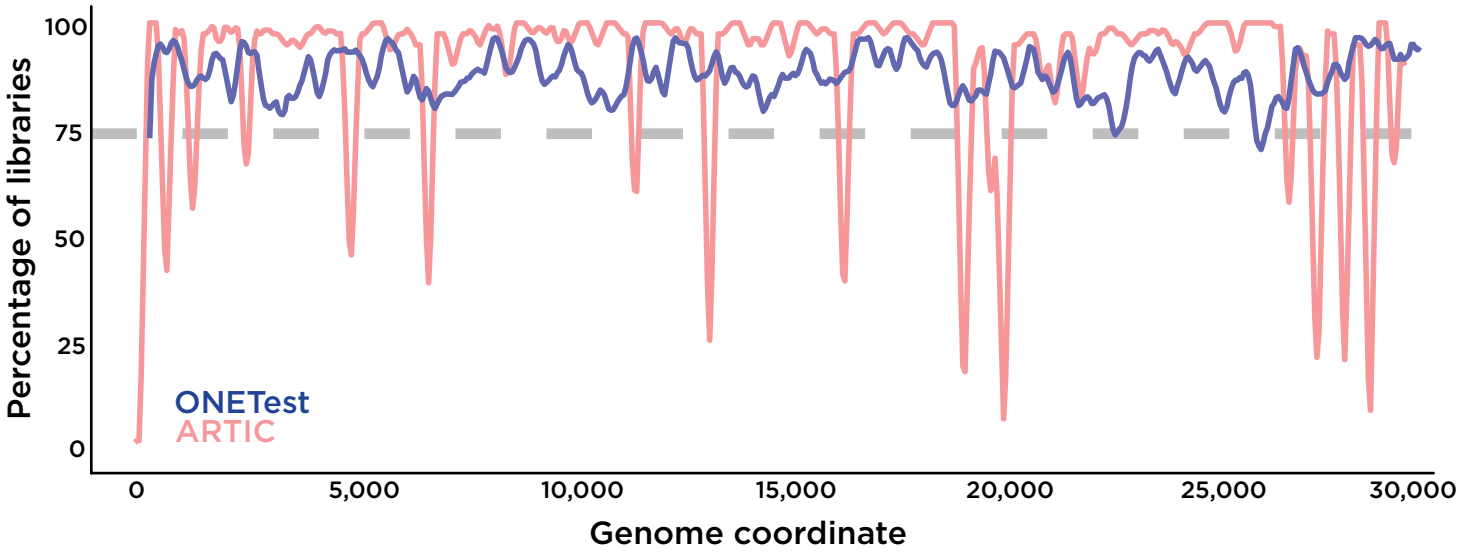

Figure 1: SARS-CoV-2 genome sequence coverage of the ONETest and ARTIC libraries from 39 respiratory specimens. The libraries were sequenced as 2x150 nucleotide reads on an Illumina sequencer. For each position in the reference SARS-CoV-2 genome sequence (MN996528.1), we computed the percentage of the specimens in which its depth of coverage is ≥ 10. This percentage was averaged across the positions of each 200 nucleotide partially overlapping window (skip size of 50 nucleotides) across the genome. There were fewer poorly covered regions in the SARS-CoV-2 genome (shown by the troughs below the dashed line) in the ONETest libraries than in the ARTIC libraries. Figure reproduced from "Target Capture Sequencing of SARS-CoV-2 Genomes from COVID-19 Patients in Florida, USA" by Zhan & Alamouti et al. (under review).

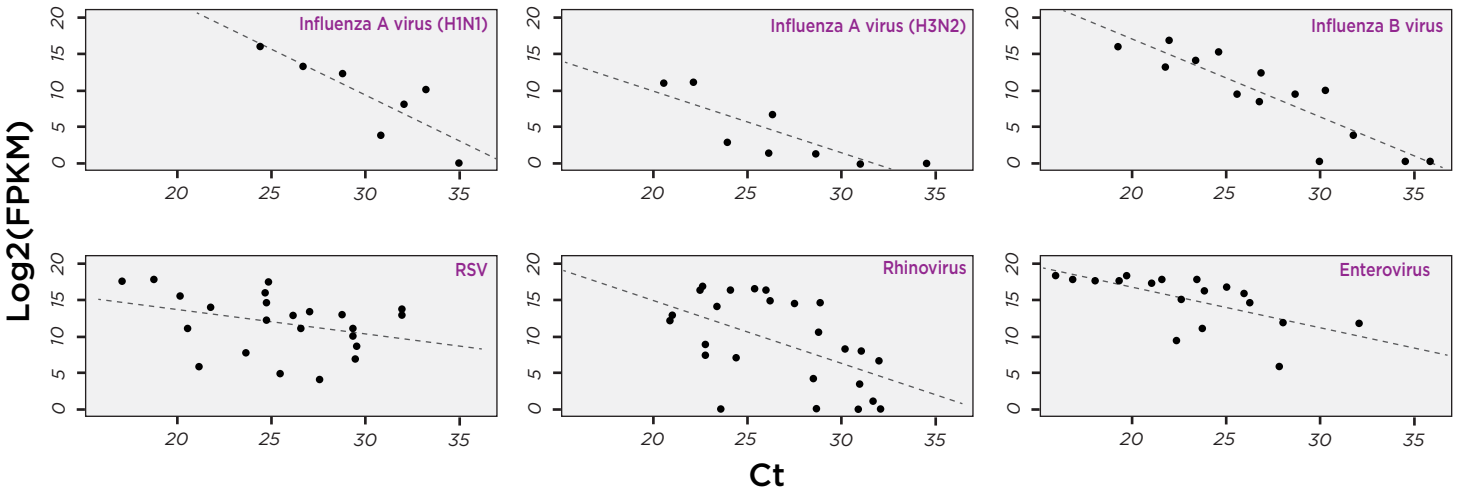

Figure 2: Correlation between FPKM values from ONETest libraries and Ct values for select respiratory pathogens. The target genes analyzed were the following: the hemagglutinin gene of influenza A and B viruses; the fusion protein gene of RSV and hMPV; the VP1 capsid protein gene of rhinovirus and enterovirus. The ONETest libraries were sequenced as 2x150 nucleotide reads on an Illumina sequencer, and the Ct values were obtained using various qPCR assays. An estimate of the quantity of a target gene was calculated as FPKM, or Fragments per Kilobase of the target gene per a Million paired-end reads. Figure reproduced from "A target hybridization-based next-generation sequencing assay enhances surveillance of seasonal respiratory pathogens: a retrospective assessment (ERVINGS)" by Janssens et al. (2019), European Congress of Virology.

Learn more

For more information about the **ONE**Test™ Coronaviruses *Plus* assay and the **ONE**Test™ system, please visit: **WWW.FUSIONGENOMICS.COM**

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