

Comprehensive Respiratory Virus Panel

Research and Diagnosis of Respiratory viruses

DESCRIPTION

The CRV Panel is designed for the comprehensive analysis of clinically significant respiratory viruses that are widely assessed by medical institutions around the globe. The panel validation test with clinical samples showed superior whole genome sequencing (WGS) success rates compared to other competitor kits on the market. The panel tests for multiple infections by assessing all types of respiratory viruses including SARS-CoV-2. The panel includes all required kits including the RNA-to-cDNA Kit and cDNA-to-Captured Library Kit. The hybridization enhancer technology is used for rapid one-day workflow. Our customers can receive stand-alone bioinformatics software, 'Celemics Virus Verifier', which provides in-depth analysis information while ensuring the security of client sequence information.

KEY FEATURES

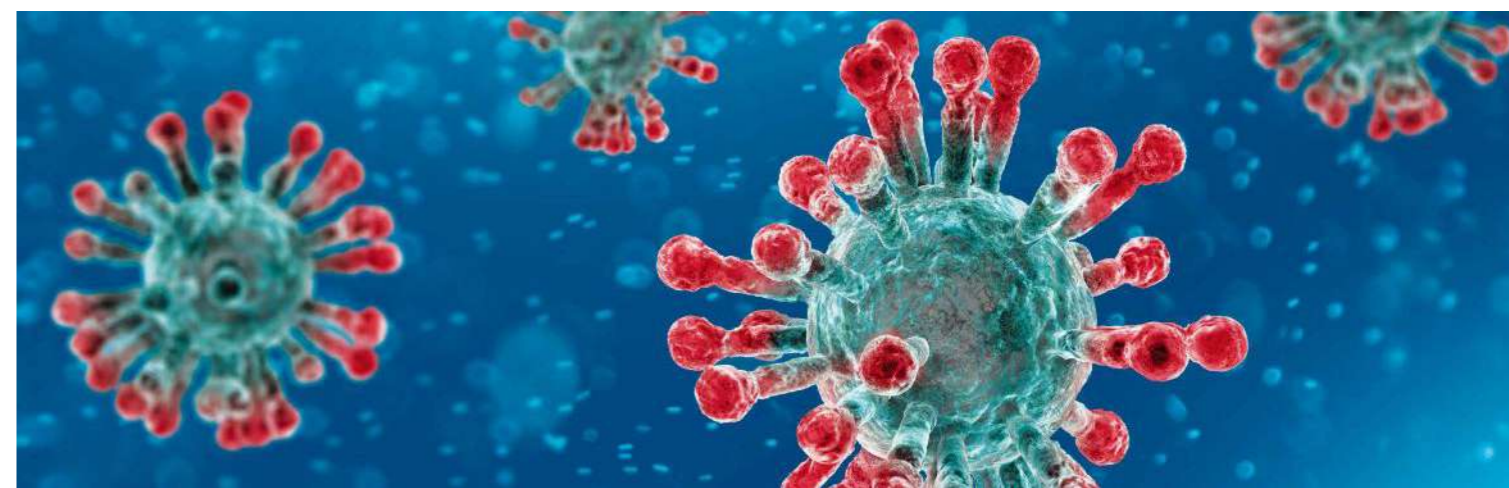
1. Coverage of wide range of respiratory pathogens	Assess WGS of 39 variants for 9 different virus types (SARS-CoV-2 solo analysis also available) Includes all types of respiratory viruses that are assessed by medical institutions around the globe
2. Superior WGS success rate even with poor quality specimen	Able to detect pathogens from patient specimens as well as poor quality environmental specimens Exceptional success rate of variant detection and WGS Significantly reduced gap formation
3. Double pandemic / coinfection detection	Detect all relevant viral strains in a single assay and test for multiple infections
4. Inclusion of Celemics Virus Verifier or bioinformatics analysis	Receive stand-alone bioinformatics SW Protect your easily-compromised data with our EU-GDPR compliant cloud system

SPECIFICATION

Target viruses*	9 types / 39 virus strains, including SARS-CoV-2
Target size	706 kb
Mutation type	Viral variants detection, Viral mutation (SNV, Indel) from generated Whole Genome Sequence
Sample type	Upper respiratory tract, Nasopharyngeal, Oropharyngeal specimens, and others
Platform	All sequencers from Illumina and Thermo Fisher
Kit composition	Provides all required reagents, including RNA to cDNA kit, cDNA to captured library kit, and bioinformatics software
Bioinformatics pipeline	Provides stand-alone bioinformatics software 'Celemics Virus Verifier' (FASTQ to Report)
Related publication	Evidence of long-distance droplet transmission of SARS-CoV-2 by direct air flow in a restaurant in Korea, J Korean Med Sci. (2020)

PATHOGEN LIST

Human Adenovirus	Coronavirus	Parainfluenza Virus	Respiratory Syncytial Virus
Human Adenovirus Type 1 (HAdV-C1)	Coronavirus HKU1	Parainfluenza 1 (PIV 1)	Respiratory Syncytial Virus A (RSV A)
Human Adenovirus Type 2 (HAdV-C2)	Coronavirus NL63	Parainfluenza 2 (PIV 2)	Respiratory Syncytial Virus B (RSV B)
Human Adenovirus Type 3 (HAdV-B3)	Coronavirus 229E	Parainfluenza 3 (PIV 3)	Human Metapneumovirus
Human Adenovirus Type 4 (HAdV-E4)	Coronavirus OC43	Parainfluenza 4 (PIV 4) A	
Human Adenovirus Type 5 (HAdV-C5)	SARS-CoV-2	Parainfluenza 4 (PIV 4) B	
Human Adenovirus 7 (HAdV-B7)			
Human Adenovirus 14 (HAdV-B14)			
Human Adenovirus 21 (HAdV-B21)			
	Influenza A		
	Influenza A Virus (Flu A)	EV-C104	Human Rhinovirus A
		EV-C105	Human Rhinovirus B
Bocavirus 1/2/3/4 (HBoV)	Influenza A-H1 Virus (Flu A-H1)	EV-C109	Human Rhinovirus C
Human Bocavirus 1	Influenza A-H3 Virus (Flu A-H3)	EV-C117	
Human Bocavirus 2		EV-C118	
Human Bocavirus 3	Influenza B	CV-A21	
Human Bocavirus 4	Influenza B Virus (Flu B)	EV-D68	
			Human Enterovirus
			Human Rhinovirus (A/B/C)

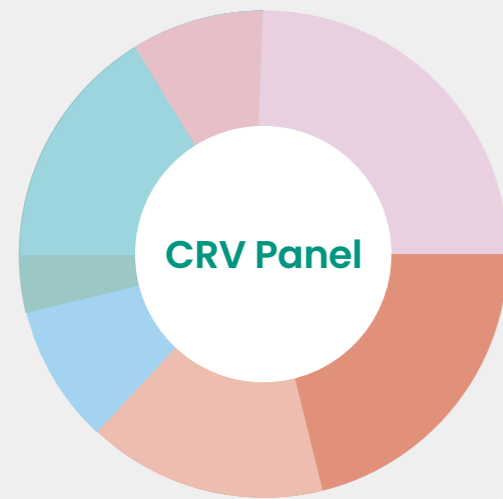


PERFORMANCE

High coverage of whole genome from reference samples using CRV Panel

Sample Type	Coverage [1X]	Coverage [10X]	Coverage [100X]
Reference sample (Illumina 2x75 bp)	99.95%	99.87%	98.95%

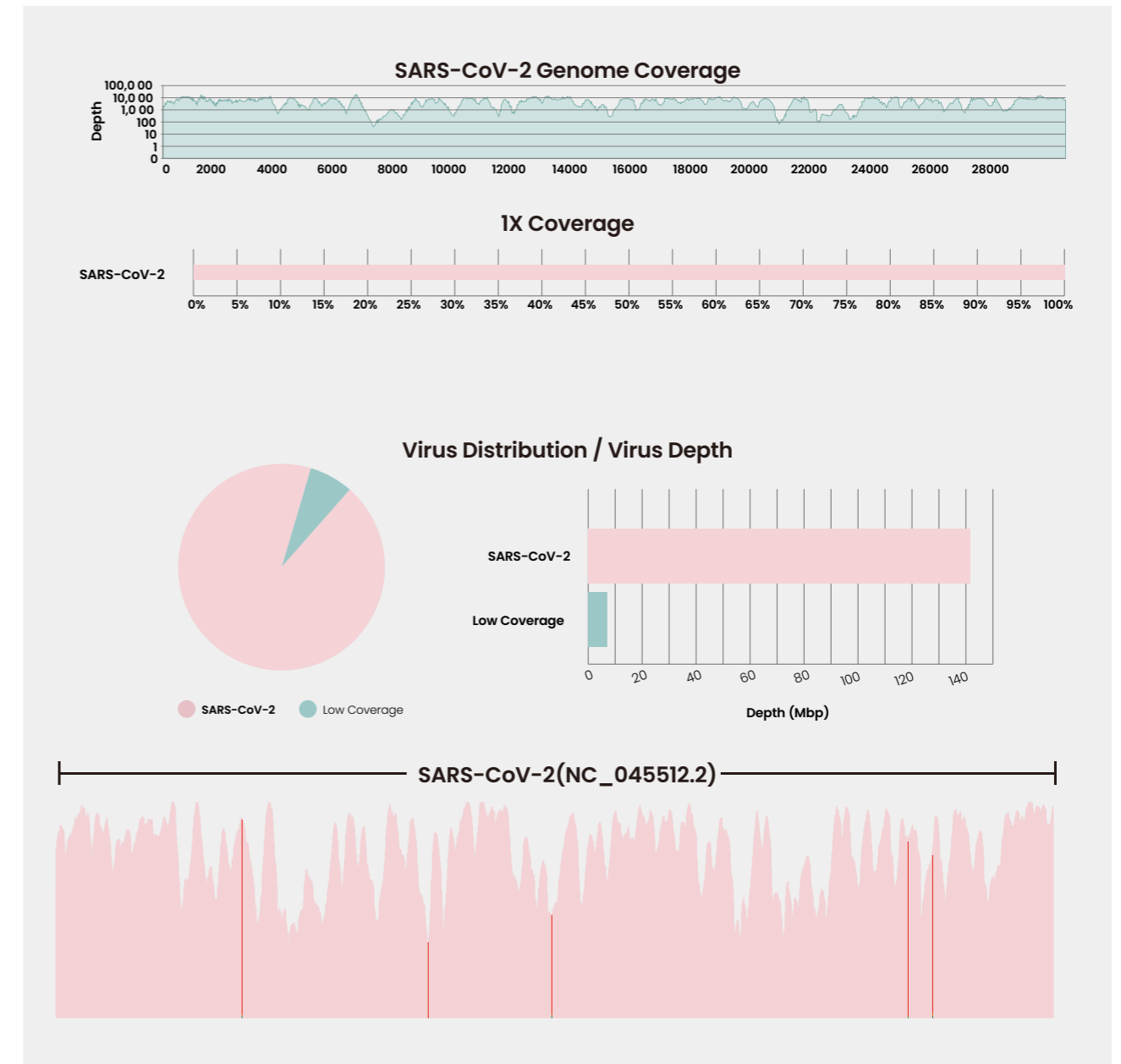
Example of viral strain identification in reference sample



- Human_Enterovirus_EV-D68
- Influenza_virus_A-H1_H1N1
- Influenza_virus_A-H3_H3N2
- Low Coverage
- Influenza_virus_B
- SARS-CoV-2
- Parainfluenza_virus_4A

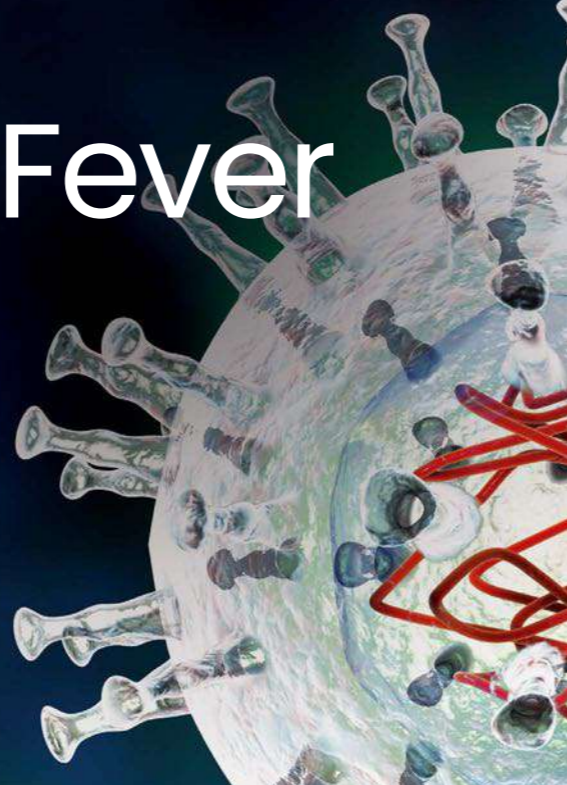
CRV PANEL RESULTS GENERATED THROUGH CELEMICS VIRUS VERIFIER (STAND-ALONE SOFTWARE)

Celemics provides stand-alone software for bioinformatics analysis, allowing customers to access the detailed data analysis information and ensuring the security of client sequence information.



African Swine Fever Virus Panel

Virus Research, Virus WGS Analysis



DESCRIPTION

The high morbidity and mortality of African swine fever (ASF) has a severe impact on the global swine industry. However, currently there is no effective treatments or vaccines commercially available. The ASFV panel is designed to identify 26 strains of genotype II virus in a single NGS run. The panel can be utilized for identifying the cause and infection route.

KEY FEATURES

1. Swine-specific blocking reagent	Provides swine-specific blocking reagent that effectively blocks repetitive sequences and allows for selectively retrieving the ASFV sequence
2. Comprehensive analysis of ASFV subtypes	Detect genotype II virus subtypes with specifically designed probes
3. Convenient testing	Highly accurate results from blood samples, often considered more challenging due to the lower viral load compared to concentrated culture supernatant or spleen tissue sample

SPECIFICATION

Target viruses*	ASFV 26 strains
Target size	192 kb
Mutation type	Virus detection, Virus genome assembly
Sample type (amount)	Swine blood (50 ng of fragmented DNA)
Platform	All sequencers from Illumina, Thermo Fisher, MGI, PacBio, and Oxford Nanopore
Bioinformatics pipeline	Celemics ASFV Pipeline (FASTQ to Result)

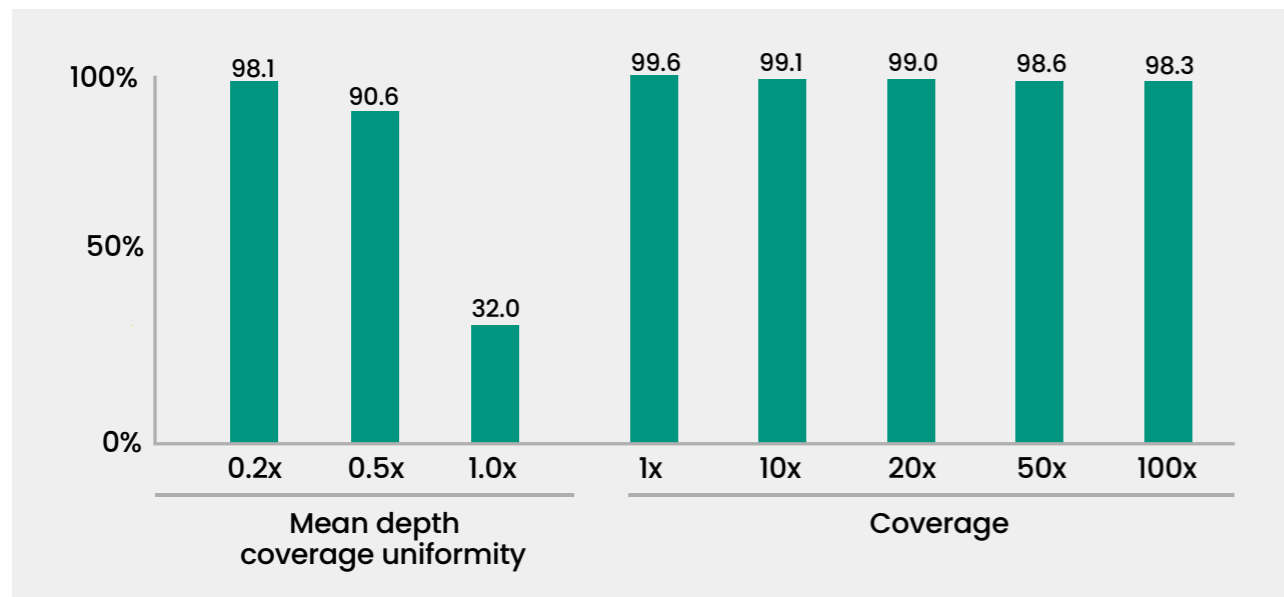
* Gene Add-On Service: Genes can be added by customer's request

ASFV DETECTION WORKFLOW

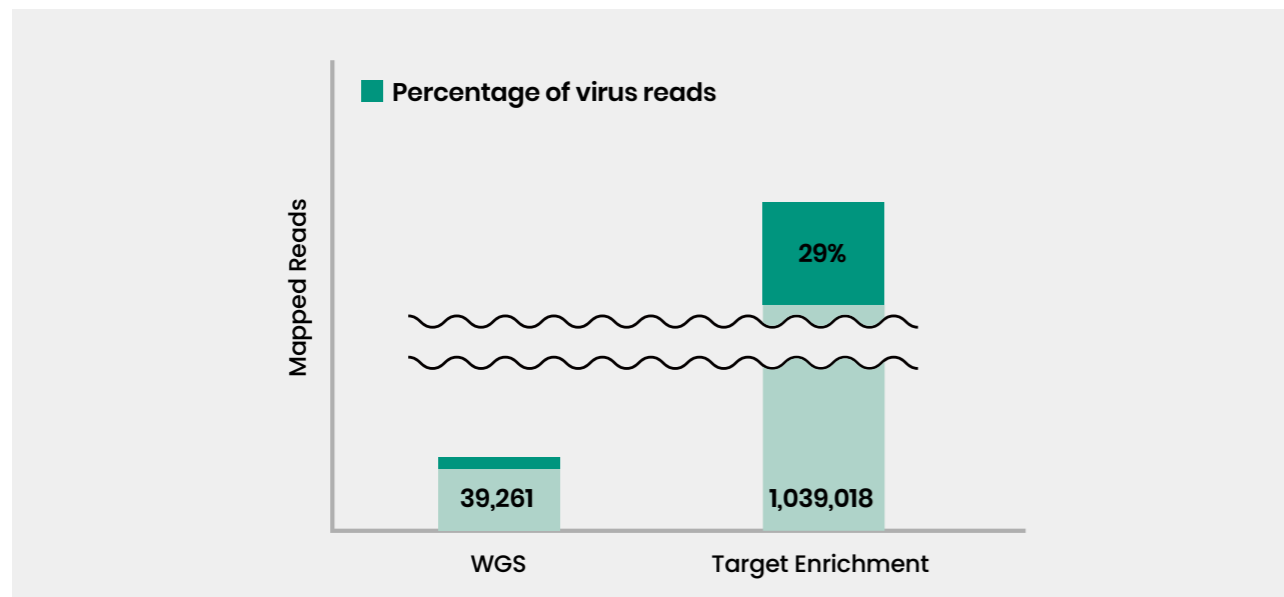


PERFORMANCE

Advanced target enrichment technology enabling exceptional capture performance with high coverage and uniformity



The panel validation result shows high uniformity and high coverage at all levels.



With the same sequencing amount, target enrichment NGS yielded 29% virus reads out of a total of 1,039,018 reads, while whole genome sequencing (WGS) yielded 0.5% virus reads (green) out of a total of 39,261 reads.

