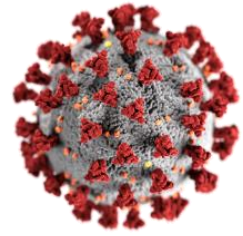


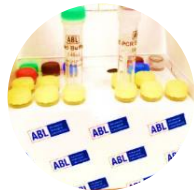
ABLAdvanced
Biological
Laboratories

DeepChek® Assay Whole Genome **SARS-CoV-2** Genotyping

REF 159A48 CE IVD



Flexible & Innovative End-to end Solution for SARS-CoV-2 Whole Genome Sequencing & Genotyping for Routine Diagnostic Settings

RNA
Extraction

RT-PCR

NGS
sequencing

Data analysis

Automation
(lab & IT)

- Next Generation Sequencing (NGS) Assay & Software
- **Compatible** with most NGS platforms (iSeq-100, MiSeq, MinIon...)
- Multiplex targeting SARS-CoV-2 **Whole Genome** (>99% genome covered)
- **Flexible** design - for small to large sequencing series (<24, 48 or 96)
- Sample to result in **2 – 3 days**
- **Pooling** of SARS-CoV-2 samples with other applications (HIV...)
- Downstream analysis **software** (variants & mutations detections, QC...)
- Ability to identify all VOC (**Omicron, Delta, Alpha...**) as well as well-characterized mutations (like E484K , D614G...)
- **Up-to-date** knowledge databases (viral infectivity, vaccine efficacy...) including **Pangolin & NextClade**
- Reporting capacity suited to routine diagnostics (PDF reports...), **consensus..**
- Automation capacity (lab robot & IT integrations - LIMS) – **LargeScale Module**
- **Secured** data hosting (healthcare-level compliance, local installations...)

Proprietary, ABL S.A. - January 2022

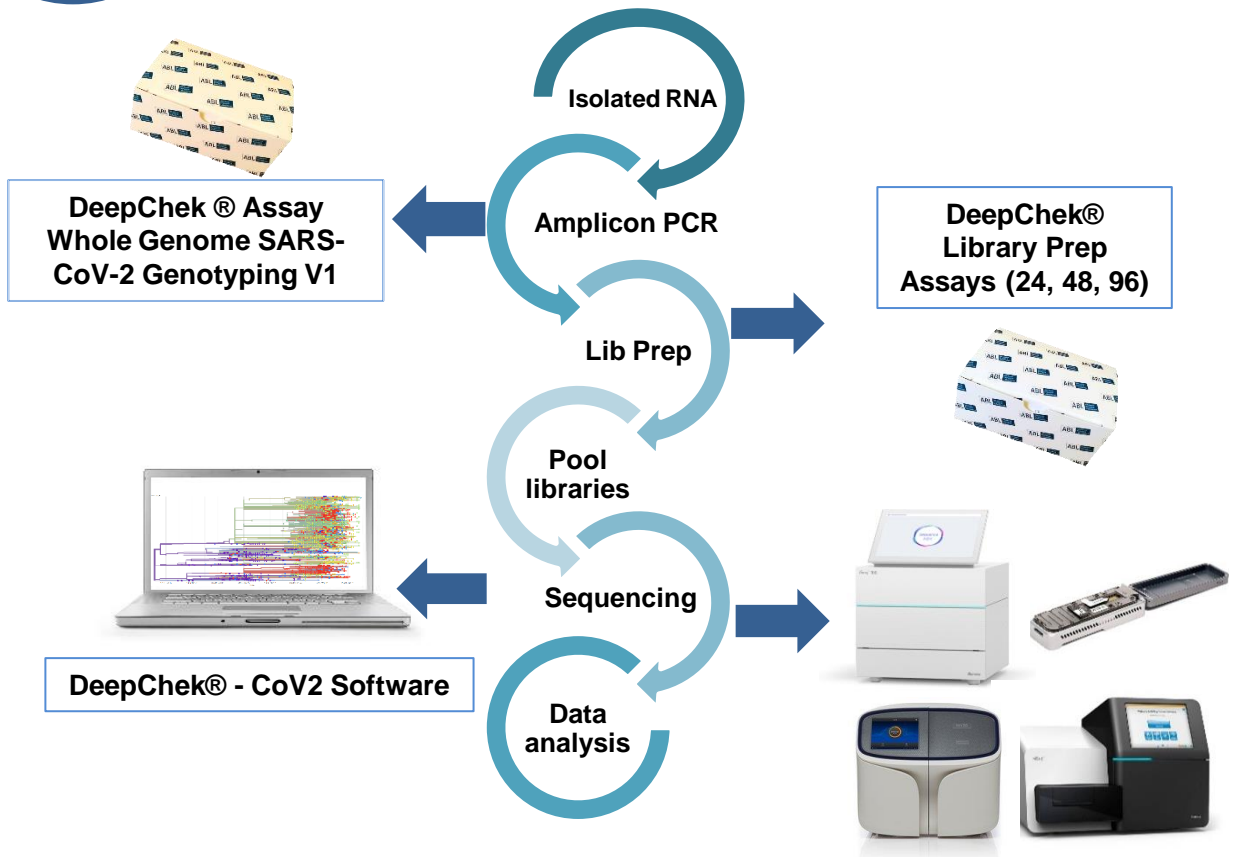
Please contact the ABL support team to request more information & registration status of the above mentioned products for your respective territories.

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contact@ablsa.com
<http://www.ablsa.com>



WORKFLOW



NUMBER OF SARS-CoV-2 SAMPLES PER RUN
 (can be **pooled** with other samples: HIV, HCV, 16s...)

NGS platform	Samples/run
iSeq-100	24
MiniSeq	24 – 96
MiSeq	24 – 96
NextSeq	24 – 96
Ion S5	24 – 96
MinIon	>24



REPORTING

DEEPCHEK® CoV-2 Software

READY-TO-USE GENOTYPING REPORT

Increased infectivity & transmissibility
 ⚡ K417N ⚡ S477N ⚡ N501Y ⚡ D614G ⚡ P681H ⚡ H69_V70del

The Omicron variant has been classified as a Variant Of Concern (VOC) due to the presence of several mutations that may have an impact on transmissibility, severity of infection and vaccine effectiveness and due to preliminary evidence of an increased risk of reinfection.

Sample assigned to the Omicron variant (lineage B.1.1.529, clade 21K, first detected in South Africa on November 2021).

⚡ G339D ⚡ S371L ⚡ K417N ⚡ N440K ⚡ G446S ⚡ S477N ⚡ T478K ⚡ E484A ⚡ Q493R ⚡ G496S ⚡ Q498R ⚡ N501Y ⚡ T547K ⚡ D614G ⚡ H655Y ⚡ A67V ⚡ N679K ⚡ P681H ⚡ N764K ⚡ D796Y ⚡ N856K ⚡ T95I ⚡ Q954H ⚡ N969K

Mutations characterizing the lineage were chosen according to the SARS-CoV-2 VOCs by ABL based on the SFM and Constellations (Version 5.3 26-11-2021)



REPORTING

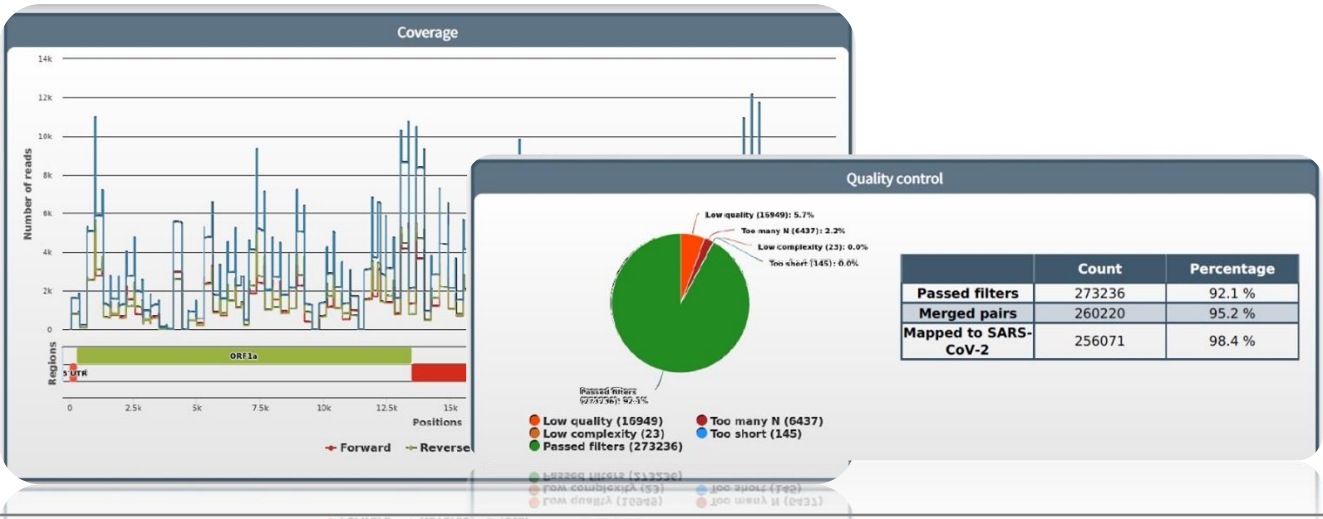
DEEPCHEK® CoV-2 Software

SARS-COV-2 MUTATIONS DETECTION

Mutation analysis			
Region	Mutation	Frequency	Comments
ORF1a	T265I	99.03 %	
	K1655N	98.95 %	
	N2596S	98.93 %	
	K3353R	97.94 %	
	A3456V	99.54 %	
ORF1b	S3675del3	99.36 %	
	P314L	99.41 %	
S	L18F	99.56 %	
	D80A	99.02 %	
	D215G	99.52 %	
	T240fs	98.73 %	
	L241del2	98.73 %	
	A243fs	98.73 %	
	K417N	98.76 %	
	E484K	98.52 %	Escape to some mAbs Escape to some convalescent sera
	N501Y	98.52 %	Fast growing lineage and sits in the Receptor Binding Motif (RBM) Has been described to increase binding affinity to hACE2 receptor
	D614G	98.93 %	Moderate effect on transmissibility (increase infectivity)
	A701V	99.44 %	
ORF3a	Q57H	99.09 %	
	S171L	100 %	
	P71L	99.09 %	
E	T205I	99.57 %	
N			

In red are the mutations of interest as defined in section DeepChekR® Whole genome SARS-CoV2 scientific references

INTEGRATED EXPERT SYSTEM FOR QUALITY CONTROL





ADVANCED DATA ANALYSES & FEATURES

DEEPCHEK® CoV-2 Software

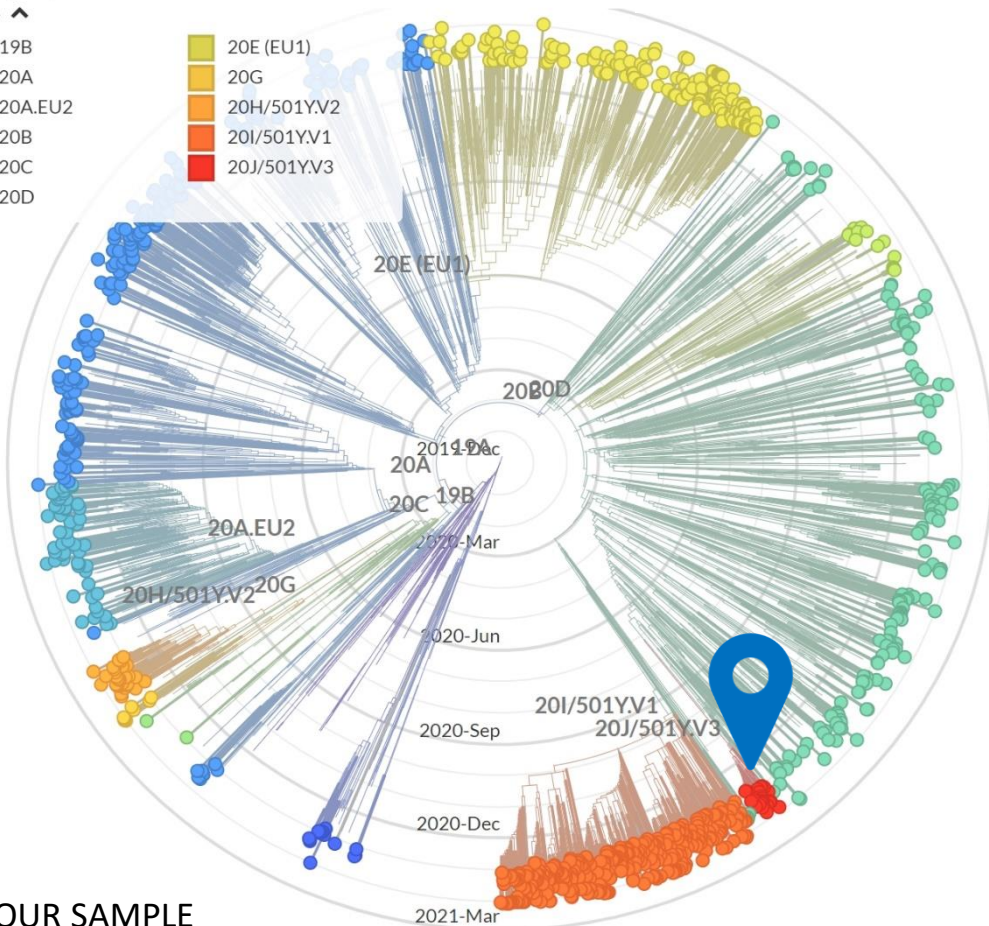
PHYLOGENETIC TREES THROUGH CONSENSUS SEQUENCES

Phylogeny

Clade ^

- 19B
- 20A
- 20A.EU2
- 20B
- 20C
- 20D

- 20E (EU1)
- 20G
- 20H/501Y.V2
- 20I/501Y.V1
- 20J/501Y.V3



YOUR SAMPLE



Product References



ASSAYS

- DeepChek Assay Whole Genome SARS-CoV-2 Genotyping V1 (48 tests) (CE IVD). 159A48 **CE IVD**
- DeepChek Assay Whole Genome SARS-CoV-2 Genotyping V2 (48 tests) (RUO). 159B48

SEQUENCING REAGENTS

- DeepChek® NGS LIB PREP (24 indexes). 116B24 + 124B24
- DeepChek® NGS LIB PREP (48 indexes). 116B48 + 124B48
- DeepChek® NGS LIB PREP (95 indexes). 116B96 + 124B96
- DeepChek® NGS LIB PREP (384 indexes). 116B384 + 124B384
- DeepChek® NGS Clean-up beads (60mL). N411-02

SOFTWARE

- DeepChek® CoV-2 Software. S-12-023 (CVL)
- DeepChek® - CoV2 LargeScale Premium Module. S-12-023 (CVS)



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