

## Hyris System (Interim Order- CE IVD): Monitoring update regarding SARS-CoV-2 novel variants

Mutations of SARS-CoV-2 have been observed globally. Some of them are innocuous, while others may give the virus a selective advantage. Based on a risk assessment by major authorities involved in the fight against the spread of COVID-19, such as WHO<sup>i</sup>, ECDC<sup>ii</sup>, CDC<sup>iii</sup>, these mutations are identified as Variants of Concern and monitored.

The updated list of the Variants of Concern emerged so far is:

- United Kingdom variant known as VOC 202012/01 iv
- South Africa variant known as 501Y.V2 <sup>v</sup>
- Brazil variant known as 484 K.V2 vi
- $\bullet$  Indian variant known as B.1.617  $^{\rm vii}$
- Californian variants known as B.1.429 and B.1.427 VIII

Hyris is monitoring the surveillance data and has performed routine in silico analysis of SARS-CoV-2 sequences (from GISAID database: https://www.gisaid.org/) in order to safeguard both public health and the quality of the product, by assessing their potential impact on inclusivity and performance characteristics.

All sequences investigated showed no variations from the reference sequence of SARS-CoV-2 in the oligonucleotides annealing sites. These include all the Variants of Concern mentioned above.

## Coverage of the Hyris System (bCUBE, bKIT, bAPP) is currently 100% based on in silico analysis. Accordingly, no variations on assay performances are expected.

Disclaimer: this Document has been developed by Hyris Ltd as a meaningful update to be provided to Hyris customers using the bKITs in the 'Hyris Virus Finder' family; more specifically:

- bKTE-SCV2.01 SARS-CoV-2 Environmental
- bKTH-SCV2.02 Virus Finder COVID-19

Please note that it is still your laboratory's or trained resources' responsibility to validate any test according to your country's existing laws.

Stefano Lo Priore CEO

## REFERENCES

GLOBAL DIAGNOSTICS

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<sup>i</sup>World Health Organization, accessed January 2021. <u>https://www.who.int/csr/don/31-december-2020-sars-cov2-variants/en/</u>

<sup>ii</sup> European Centre for Disease Prevention and Control, accessed January 2021 <u>https://www.ecdc.europa.eu/en/publications-data/covid-19-risk-assessment-spread-new-variants-concern-eueea-first-update</u>

<sup>III</sup> CDC, accessed January 2021 <u>https://www.cdc.gov/coronavirus/2019-ncov/transmission/variant.html</u>

<sup>iv</sup> Andrew Rambaut, Nick Loman, Oliver Pybus, Wendy Barclay, Jeff Barrett, Alesandro Carabelli, Tom Connor, Tom Peacock, David L Robertson, Erik Volz, on behalf of COVID-19 Genomics Consortium UK (CoG-UK)9. "Preliminary genomic characterisation of an emergent SARS-CoV-2 lineage in the UK defined by a novel set of spike mutations".

<sup>v</sup> Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) lineage with multiple spike mutations in South Africa. Houriiyah Tegally, Eduan Wilkinson, Marta Giovanetti, Arash Iranzadeh, Vagner Fonseca, Jennifer Giandhari, Deelan Doolabh, Sureshnee Pillay, Emmanuel James San, Nokukhanya Msomi, Koleka Mlisana, Anne von Gottberg, Sibongile Walaza, Mushal Allam, Arshad Ismail, Thabo Mohale, Allison J Glass, Susan Engelbrecht, Gert Van Zyl, Wolfgang Preiser, Francesco Petruccione, Alex Sigal, Diana Hardie, Gert Marais, Marvin Hsiao, Stephen Korsman, Mary-Ann Davies, Lynn Tyers, Innocent Mudau, Denis York, Caroline Maslo, Dominique Goedhals, Shareef Abrahams, Oluwakemi Laguda-Akingba, Arghavan Alisoltani-Dehkordi, Adam Godzik, Constantinos Kurt Wibmer, Bryan Trevor Sewell, Jose Lourenco, Luiz Carlos



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<sup>vi</sup> Paola Cristina Resende1\*, João Felipe Bezerra2, Romero Henrique Teixeira de Vasconcelos2, Ighor Arantes3, Luciana Appolinario1, Ana Carolina Mendonça1, Anna Carolina Paixao1, Ana Carolina Duarte Rodrigues1, Thauane Silva1, Alice Sampaio Rocha1, Alex Pauvolid-Corrêa1,4, Fernando Couto Motta1, Dalane Loudal Florentino Teixeira5, Thiago Franco de Oliveira Carneiro5, Francisco Paulo Freire Neto6, Isabel Diniz Herbster7, Anderson Brandao Leite8, Irina Nastassja Riediger9, Maria do Carmo Debur9, Felipe Gomes Naveca10, Walquiria Almeida11, Mirian Livorati12, Gonzalo Bello3A, Marilda M Sigueira1A. Spike E484K mutation in the first SARS-CoV-2 reinfection case confirmed in Brazil

<sup>VII</sup> Sarah Cherian1, #, Varsha Potdar1, #, Santosh Jadhav1, Pragya Yadav1, Nivedita Gupta2, Mousmi Das1, Partha Rakshit3, Sujeet Singh3, Priya Abraham1\*, Samiran Panda2 and NIC team@. Convergent evolution of SARS-CoV-2 spike mutations, L452R, E484Q and P681R, in the second wave of COVID-19 in Maharashtra, India

<sup>VII</sup> Xianding Deng1,2&, Miguel A Garcia-Knight3&, Mir M. Khalid4,5&, Venice Servellita1,2&, Candace Wang1,2&, Mary Kate Morris6&, Alicia Sotomayor-González1,2,Dustin R, Glasner1,2,KevinRReyes1,2,AmeliaS.Gliwa1,2,NikithaP.Reddy1,2, Claudia Sanchez, San Martin1,2, ScotFederman7, Jing Cheng4, Joanna Balcerek1, Jordan Taylor1, Jessica, A Streithorst1,Steve Miller1, G. Renuka Kumar4,5,Bharath Sreekumar4,5, Pei-Yi Chen4,5, Ursula Schulze-Gahmen4,5, Taha Y. Taha4,5, Jennifer Hayashi4,5, Camille R., Simoneau4,5, Sarah McMahon4,5, Peter V. Lidsky3, Yinghong Xiao3, Peera Hemarajata8, Nicole M. Green8, Alex Espinosa6, Chantha Kath6, Monica Haw6,John Bell6, Jill K., Hacker6, Carl Hanson6, Debra A. Wadford6, Carlos Anaya9, Donna Ferguson9, Liana F., Lareau10,11,PhillipA.Frankino11,HaridhaShivram11,StaciaK.Wyman11,Melanie, Ott4,5,11,RaulAndino3,Charles Y.Chiu1,2,4,11. Transmission, infectivity, and antibody neutralization of an emerging SARS-CoV-12 variant in California carrying a L452R spike protein mutation.