Gdansk, 1st February 2022

To whom it may concern,

The GeneMe considering the latest information on the mutation of the SARS-CoV-2 genome and its influence on the results of RT-PCR assays. We hereby present our Research and Development report the objective of which was to determine if the recently observed mutations in the SARS-CoV-2 affect the loss of specificity of the SAVD+ RT-PCR test. This research and development report summarizes our findings regarding the influence of ORF1aband N1 gene mutations in SARS-CoV-2 on SAVD+ primers hybridization. For this purpose, bioinformatic analysis of the mutated sequences of the coronavirus ORF1ab and the human N1 gene was performed to assess if the point mutation or deletions lay in the hybridization region of SAVD+ RT-PCR primers.

The SAVD+ by GeneMe SARS-CoV-2 Direct Rapid Detection Kit is designed for the *in vitro* identification of the new coronavirus SARS-CoV-2, in a single reaction. The presence of the innovative and patented *Taq* polymerase and specific primers and probes made it possible to create a highly specific and sensitive test. The individually designed primers are compatible with the SARS-CoV-2 genomic RNA sequence of the ORF1ab and N gene as deposited in the NCBI database and human RNase P gene. Amplification of the targeted nucleic acids is observed by an increase of fluorescence signal during the reaction.

We, signed below, can definitively state that SAVD+ RT-PCR assay's ability to detect SARS-CoV-2 remains at the highest level regardless of these new mutations.

The GeneMe constantly cooperates with diagnostic laboratories in Poland and abroad (UK, Norway, Uganda, Mexico), regularly validating the test on clinical trials - swabs and saliva samples to make sure that the SAVD+ test maintains its sensitivity and specificity to the current SARS-Co-2 virus strains.

Yours sincerely,

Dr Sabina Żołędowska,
CQO

Dr Eng. Marta Skwarecka,
Head of Research and Development Department

GeneMe Sp. z o.o. | Gdańsk, Poland | www.geneme.eu
Ul. Piotrkowska 41C, 80-180 Gdańsk | M: kontakt@geneme.eu | T: +48 517 169 126

GENEME

GENEME	**Research and Development**

NAME: ***Marta Skwarecka, Head of RnD GeneMe***

DATE: ***23.01.2022***

PROPOSED PRODUCT: ***SAVD+***

REVISION: ***1.0***

1.Title

Detection of different variants of SARS-CoV-2 virus by SAVD+ test.

2. Purpose and scope

The aim of the study is to check the universality of the SAVD+ test for the identification of known variants of the SARS-CoV-2 virus. The most popular variants of the mutant SARS-CoV-2 virus from Alfa to Omicron were analyzed in sillico. The most popular of them are B.1.1.7 United Kingdom, B.1.351 South Africa (also known as S.501Y.V2), B.1.1.28 Brazil P1, P2, B.1.617 India, B.1.429/ B.1.427 California variant (also known as epsilon variant), Vietnamese variant (Delta variant B.1.617.2 with additional mutations) and Omicron variant B.1.1.529.

3. Method

Date of the test:	--
Place of the test:	***GeneMe, ul. Kampinoska 25, 80-180 Gdansk, Poland***
Test conditions (temperature, humidity):	***Temp: 22°C*** ***Humidity: 36%***
The person performing the tests:	***Dr Eng. Marta Skwarecka***
LOT of reagents analyzed:	--
LOT of reference reagents and trade name:	--

Description of the tested method:

The study consisted of:

1. *Finding in the analyzed variants of the SARS-CoV-2 virus the resulting mutations in the ORF1ab gene relative to the native strain and locating them in the genomic RNA of the virus.*
2. *Assigning individual mutations to appropriate nucleotides.*

GeneMe Sp. z o.o. | Gdańsk, Poland | www.geneme.eu
Ul. Piotrkowska 41C, 80-180 Gdańsk | M: kontakt@geneme.eu | T: +48 517 169 126

GENEME

3. *Comparison of the location of the mutated nucleotides with the location of the ORF1ab gene fragment, which is the target of the SAVD+ test.*
4. *Confirmation or exclusion of the effect of the mutation on the SAVD+ test identification capabilities*

4. Tested samples

Sample number	Name	Supplier	Producer (as commercial material)	Concentration (as commercial material)
1.	*n/a*	*n/a*	*n/a*	*n/a*

5. Results

Table 1 and 2 shows the popular variants of the SARS-CoV-2 virus along with the changed nucleotides and compared with the target sequence of the SAVD+ test.

Table 1. Mutations in the ORF1ab gene of popular variants of the SARS-CoV-2 virus and their impact on the possibility of identification with the SAVD+ test.

Virus variant	Country of origin (emergence)	Amino-acid mutation	Nucleotide mutation	Location of mismatch (5'-3') in the SAVD+ test	Detection with the SAVD+ test
Reference Strain: Wuhan-Hu-1, nCoV	*China*	-	-	*absence*	*Yes*
B.1.617	*India*	*synonymous mutation*	*C3037T*	*absence*	*Yes*
		synonymous mutation	*C3457T*	*absence*	
		T1567I	*C4965T*	*absence*	
		synonymous mutation	*G8491A*	*absence*	
		T3646A	*A11201G*	*absence*	
		P4715L	*C14408T*	*absence*	

GeneMe Sp. z o.o. | Gdańsk, Poland | www.geneme.eu
Ul. Piotrkowska 41C, 80-180 Gdańsk | M: kontakt@geneme.eu | T: +48 517 169 126

		synonymous mutation	*G14772A*	*absence*	
		synonymous mutation	*C16134T*	*absence*	
		G5530C	*G16852T*	*absence*	
		M5753I	*G17523T*	*absence*	
		K6711R	*A20396G*	*absence*	
		S6713A	*T20401G*	*absence*	
B.1.1.28 P1, P2	*Brazil*	*synonymous mutation*	*T733C*	*absence*	*Yes*
		synonymous mutation	*C2749T*	*absence*	
		S1188L	*C3828T*	*absence*	
		L1795Q	*A5648C*	*absence*	
		synonymous mutation	*A6319G*	*absence*	
		synonymous mutation	*A6613G*	*absence*	
		synonymous mutation	*C12778T*	*absence*	
		synonymous mutation	*C13860T*	*absence*	
		E1264N	*G17259T*	*absence*	
		synonymous mutation	*C100T*	*absence*	
		L3468V	*T10667G*	*absence*	
		synonymous mutation	*C11824T*	*absence*	
		L3930F	*C12053T*	*absence*	
B.1.351 (S.501Y.V2)	*South Africa*	*Thr265I*	*C1059T*	*absence*	*Yes*
		L1655Asn	*G5230T*	*absence*	
		L3353R	*A10323AG*	*absence*	

GeneMe Sp. z o.o. | Gdańsk, Poland | www.geneme.eu
Ul. Piotrkowska 41C, 80-180 Gdańsk | M: kontakt@geneme.eu | T: +48 517 169 126

B.1.1.7	*UK*	*T1001I*	*C3267T*	*absence*	*Yes*
		A1708D	*C5388A*	*absence*	
		I2230T	*T6954C*	*absence*	
		SGF 3675-3677 deletion	*11288-11296 deletion*	*absence*	
B.1.617.2	*India*	*P4715L*	*14408-14410*	*absence*	*Yes*
		P5401L	*16466-16468*	*absence*	
		G5063S	*20515-20517*	*absence*	
B.1.617.2+ (Delta+)	*Vietnamese*	*synonymous mutation*	*C3037T*	*absence*	*Yes*
		synonymous mutation	*C3457T*	*absence*	
		T1567I	*C4965T*	*absence*	
		synonymous mutation	*G8491A*	*absence*	
		T3646A	*A11201G*	*absence*	
		P4715L	*C14408T*	*absence*	
		synonymous mutation	*G14772A*	*absence*	
		synonymous mutation	*C16134T*	*absence*	
		G5530C	*G16852T*	*absence*	
		M5753I	*G17523T*	*absence*	
		L6711R	*A20396G*	*absence*	
		S6713A	*T20401G*	*absence*	
		T1001I	*C3267T*	*absence*	
		A1708D	*C5388A*	*absence*	
		I2230T	*T6954C*	*absence*	

GeneMe Sp. z o.o. | Gdańsk, Poland | www.geneme.eu
Ul. Piotrkowska 41C, 80-180 Gdańsk | M: kontakt@geneme.eu | T: +48 517 169 126

		SGF 3675-3677 deletion	11287-11295 deletion	absence	
		P4715L	14407-14409	absence	
		P5401L	16465-16467	absence	
		G5063S	15451-15453	absence	
B.1.429, B.1.427	California (USA)	T265I	1057-1059	absence	Yes
		S3158T	9736-9738	absence	
		I4205V	12877-1279	absence	
		P314L	1204-1206	absence	
		P976L	3190-3192	absence	
		D1183T	3811-3813	absence	
B.1.1.529 BA.1	South Africa	K856R	2830-2832	absence	Yes
		SL2083-2084I	6511-6516	absence	
		A2710T	8392-8394	absence	
		T3255I	10027-10029	absence	
		P3395H	10447-10449	absence	
		3674-3676 deletion	33056-11292	absence	
		I3758V	11536-11538	absence	
		P4715L	14407-14409	absence	
		I5967V	18163-18165	absence	
B.1.1.529 BA.2	South Africa	-	-	absence	Yes
B.1.525	Worldwide	L4715F	14407-14409	absence	Yes
B.1.1.28.3, P3	Philippines	L3201P	9865-9867	absence	Yes
		D3681E	11305-11307	absence	

GeneMe Sp. z o.o. | Gdańsk, Poland | www.geneme.eu
Ul. Piotrkowska 41C, 80-180 Gdańsk | M: kontakt@geneme.eu | T: +48 517 169 126

		L3930F	*12052-12054*	*absence*	
		P4715L	*14407-14409*	*absence*	
B.1.526	*USA*	*del3675-3677*	*11287-11295*	*absence*	*Yes*
B.1.1.1.C37	*Peru*	-	-	*absence*	*Yes*

Table 2. Mutations in the N1 gene of popular variants of the SARS-CoV-2 virus and their impact on the possibility of identification with the SAVD+ test.

Virus variant	**Country of origin (emergence)**	**Amino-acid mutation**	**Nucleotide mutation**	**Location of mismatch (5'-3') in the SAVD+ test**	**Detection with the SAVD+ test**
Reference Strain: Wuhan-Hu-1, nCoV	*China*	-	-	*absence*	*Yes*
B.1.617	*India*	-	-	*absence*	*Yes*
B.1.1.28 P1, P2	*Brazil*	*P80R*	*28513-28515*	*absence*	*Yes*
		R203K	*28882-28884*	*absence*	
		G204R	*28885-28887*	*absence*	
B.1.351 (S.501Y.V2)	*South Africa*	*T205I*	*28978-28980*	*absence*	*Yes*
B.1.1.7	*UK*	*D3L*	*28282-28284*	*absence*	*Yes*
		S235F	*28978-28980*	*absence*	
B.1.617.2	*India*	*D63G*	*28462-28464*	*absence*	*Yes*

GeneMe Sp. z o.o. | Gdańsk, Poland | www.geneme.eu
Ul. Piotrkowska 41C, 80-180 Gdańsk | M: kontakt@geneme.eu | T: +48 517 169 126

		R203M	28882-28884	absence	
		D377Y	29404-29406	absence	
B.1.617.2+ (Delta+)	Vietnamese	D63G	28462-28464	absence	Yes
		R203M	28882-28884	absence	
		D377Y	29404-29406	absence	
B.1.429, B.1.427	California (USA)	T205I	28888-28890	absence	Yes
B.1.1.529 BA.1	South Africa	31-33del	28366-28374	absence	Yes
		R203K	28882-28884	absence	
		G204R	28885-28887	absence	
B.1.1.529 BA.2	South Africa	-	-	absence	Yes
B.1.525	Worldwide	L4715F	14407-14409	absence	Yes
B.1.1.28.3, P3	Philippines	R203K	28882-28884	absence	Yes
		G204R	28885-28887	absence	
B.1.526	USA	-	-	absence	Yes
B.1.1.1.C37	Peru	-	-	absence	Yes

Link to the data repository kept in the cloud: --

6. Conclusions

The presented analysis shows that none of the mutations occurring in the variants of the SARS-CoV-2 virus, i.e., Alpha(B.1.1.7), Beta (B.1.351, S.501Y.V2), Gamma (B.1.1.28.1, P1), Delta (B.1.617.2), Delta+ (B.1.617.2+), Omicron BA.1 (B.1.1.529), Omicron BA.2 (BA.2), Epsilon (B.1.429, B.1.427), Zeta (B.1.1.28.2, P2), Eta (B.1.525), Theta (B.1.1.28.3, P3), Iota (B.1.526), Kappa (B.1.617.1), Lambda (B.1.1.1.C37) did affect the effectiveness of the virus detection with the SAVD+ test. All analyzed variants are fully identifiable with the SAVD+ test.

GeneMe Sp. z o.o. | Gdańsk, Poland | www.geneme.eu
Ul. Piotrkowska 41C, 80-180 Gdańsk | M: kontakt@geneme.eu | T: +48 517 169 126

7. References

1. *Lopez-Rincon, C. A. Perez-Romero, A. Tonda, L. Mendoza-Maldonado, E. Claassen, J. Garssen, A. D. Kraneveld, Design of Specific Primer Sets for the Detection of B.1.1.7, B.1.351 and P.1 SARS-CoV-2 Variants using Deep Learning, bioRxiv January 21, 2021.*
2. *T. Tapp, First Cases of Brazilian And More Contagious South African Covid-19 Variants Detected in Los Angeles; U.K. Variant Surges, April 7, 2021*
3. *F. Naveca, V. Nascimento, V. Souza et al. Phylogenetic relationship of SARS-CoV-2 sequences from Amazonas with emerging Brazilian variants harboring mutations E484K and N501Y in the Spike protein, 9 Feb 2021*

A. *M. Voloch et al., Genomic characterization of a novel SARS-CoV-2 lineage from Rio de Janeiro, Brazil, J Virol, 1 March 2021*

4. *N. R. Faria, I. Morales Claro, D. Candido et al., Genomic characterisation of an emergent SARS-CoV-2 lineage in Manaus: preliminary findings, 12 January 2021*
5. *SARS-CoV-2 B.1.617 emergence and sensitivity to vaccine-elicited antibodies, bioRxiv 9 May 2021*
6. *Pragya Dhruv Yadav et al., SARS CoV-2 variant B.1.617.1 is highly pathogenic in hamsters than B.1 variant, bioRxiv 5 May 2021.*
7. *Markus Hoffmann et al., SARS-CoV-2 variant B.1.617 is resistant to Bamlanivimab and evades antibodies induced by infection and vaccination, bioRxiv 5 May 2021.*
8. *Vipul Kumar et al., Possible link between higher transmissibility of B.1.617 and B.1.1.7 variants of SARS-CoV-2 and increased structural stability of its spike protein and hACE2 affinity, bioRxiv 29 April 2021*
9. *Sarah Cherian et al., Convergent evolution of SARS-CoV-2 spike mutations, L452R, E484Q and P681R, in the second wave of COVID-19 in Maharashtra, India, bioRxiv 24 April 2021*
10. *Pragya Yadav et al. Neutralization of variant under investigation B.1.617 with sera of BBV152 vaccinees, bioRxiv 23 April 2021*
11. *https://outbreak.info/situation-reports?pango=B.1.617*
12. *https://www.cdc.gov/coronavirus/2019-ncov/science/science-briefs/scientific-brief-emerging-variants.html*
13. *Jamie Lopez Bernal et al., Effectiveness of COVID-19 vaccines against the B.1.617.2 variant, London 2021*
14. *https://www.france24.com/en/asia-pacific/20210603-who-rules-out-new-hybrid-covid-19-variant-in-vietnam*
15. *https://www.reuters.com/world/asia-pacific/vietnam-detects-hybrid-indian-uk-covid-19-variant-2021-05-29/?utm_medium=Social&utm_source=Twitter*
16. *https://indianexpress.com/article/explained/covid-delta-variant-coronavirus-cases-7344758/*
17. *https://www.republicworld.com/world-news/global-event-news/covid-19-know-about-delta-k417n-mutant-which-has-been-spotted-about-90-times-worldwide.html*
18. *https://outbreak.info/situation-reports?pango=B.1.617.2*
19. *https://outbreak.info/situation-reports?pango=B.1.617*
20. *https://outbreak.info/situation-reports?pango=B.1.1.7*
21. *https://cov-lineages.org/lineage.html?lineage=B.1.427*
22. *https://cov-lineages.org/lineage.html?lineage=B.1.429*
23. *https://viralzone.expasy.org/9556*
24. *Implications of the emergence and spread of the SARS-CoV-2 B.1.1. 529 variant of concern (Omicron) for the EU/EEA, THREAT ASSESSMENT BRIEF, 26.11.2021*
25. *https://cov-lineages.org/lineage.html?lineage=B.1.1.529*
26. *https://viralzone.expasy.org/9556*

Approved for external release by Sabina Żołędowska, CQO

Date of approval: 01.02.2022

Signature Sabina Żołędowska

GeneMe Sp. z o.o. | Gdańsk, Poland | www.geneme.eu
Ul. Piotrkowska 41C, 80-180 Gdańsk | M: kontakt@geneme.eu | T: +48 517 169 126

GENEME