EUROIMMUN
a PerkinElmer company
UNITED STATES OF AMERICA

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SARS-CoV-2 Variants of Concern (VOC) Alpha, Beta, Gamma and Delta

Dear Sir or Madam,

Recently different SARS-CoV-2 variants, Alpha, Beta, Gamma and Delta have been described to lead to an increased number of COVID-19 cases in several regions. These variants are mainly characterized by having several mutations in the S-gene, which encodes the spike protein and since there was a high increase of persons being infected with these variants in a short period of time, it was assumed that it is more infectious than other SARS-CoV-2 variants. However, comprehensive scientific evidence still has to be provided to confirm this hypothesis.

Although the discovered SARS-CoV-2 variants have mutations in the receptor-binding domain (RBD), which is an important component of the S1 domain of the spike protein used as an antigen in the Anti-SARS-CoV-2-ELISA (IgA/IgG; order no.: EI 2606-#### A/G) and Anti-SARS-CoV-2-QuantiVac-ELISA (IgG; order no.: EI 2606-####-10 G), it is not expected that these mutations affect the performance of these test systems. Usually, individual amino acid exchanges of an antigen do not essentially affect the binding properties of antibodies against the overall protein, because only a single epitope is affected. However, since proteins have a large number of epitopes, even the failure of a single binding point can be compensated. In addition, an individual amino acid exchange does not necessarily mean that antibodies against this variant cannot bind to the original variant. In many cases, no deterioration of the binding behavior is to be expected, since, for example, not every place within an epitope is a target of the antibody.

Based on comparisons of primer and probe sequences with the published sequences for these SARS-CoV-2 variants including detection of the variants Alpha, Beta, Gamma and Delta it is expected that all variants can be reliably detected with the EURORealTime SARS-CoV-2 and EURORealTime SARS-CoV-2/Influenza A/B test systems.

Kind regards,

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