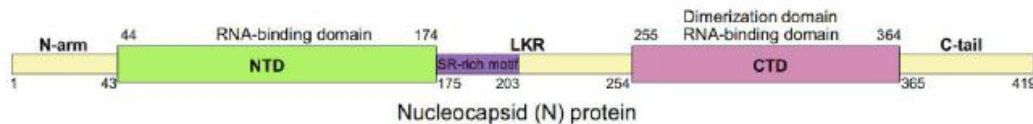


Using the mutated proteins to verify our COVID-19 antibodies pairs

1) The full-length structure of the COVID-19 N protein:



According to the full-length structure of the COVID-19 protein, the full-length N protein is divided into fragments of different regions for expression, including N-Arm, NTD, LKR-SR, LKR-R, CTD, C-Tai, as well as N-Arm-NTD, NTD-LKR-SR, LKR, LKR-R-CTD, CTD-C-Tail. And the approximate area of the antibody epitope was analyzed preliminarily.

The epitope of the coated antibody is 44-54, but the structure of the LKR-SR position will affect the binding of the antibody to the antigen. The labelled antibody epitope is a conformational epitope that is located at NTD. The core region is 149-178 which is affected by the amino acid at positions 104-149. By analyzing the presently popular mutant strains, the experiment successfully verify that the antibodies pairs can detect the mutations in the NTD position, while the other mutations are not in the NTD position.

Product Name	Description	Use
Anti-COVID -19 nucleocapsid Mab Cat. No. ZLA81120M	Mouse IgG Epitope: aa44-54	Coated Ab
Anti- COVID -19 nucleocapsid Mab Cat. No. ZLA81122H	Humanized IgG Conformational epitope, at NTD	Labelled Ab

2) The result of detection of variant strains:

Strains	Mutations	Repeat 1	Repeat 2
B.1.1.7 (Alpha)	D3L, R203K, G204R, S235F	+	+
B.1.351 (Beta)	T205I	+	+
B.1.2	P67S, P199L	+	+
P.1(Gamma)	P80R	+	+
P.2	A119S, M234I	+	+
B.1.617.2 (Delta)	R203M, D377Y	+	+
B.1.617.3	P67S, R203M, D377Y	+	+
C.37 (Lambda)	P13L, R203K, G204R, G214C	+	+

3) Result Analysis:

The antibodies pairs can recognize and react well with B.1.1.7, B.1.351, B.1.2, P1, P2, B.1.617.2, B.1.617.3, and C.37.