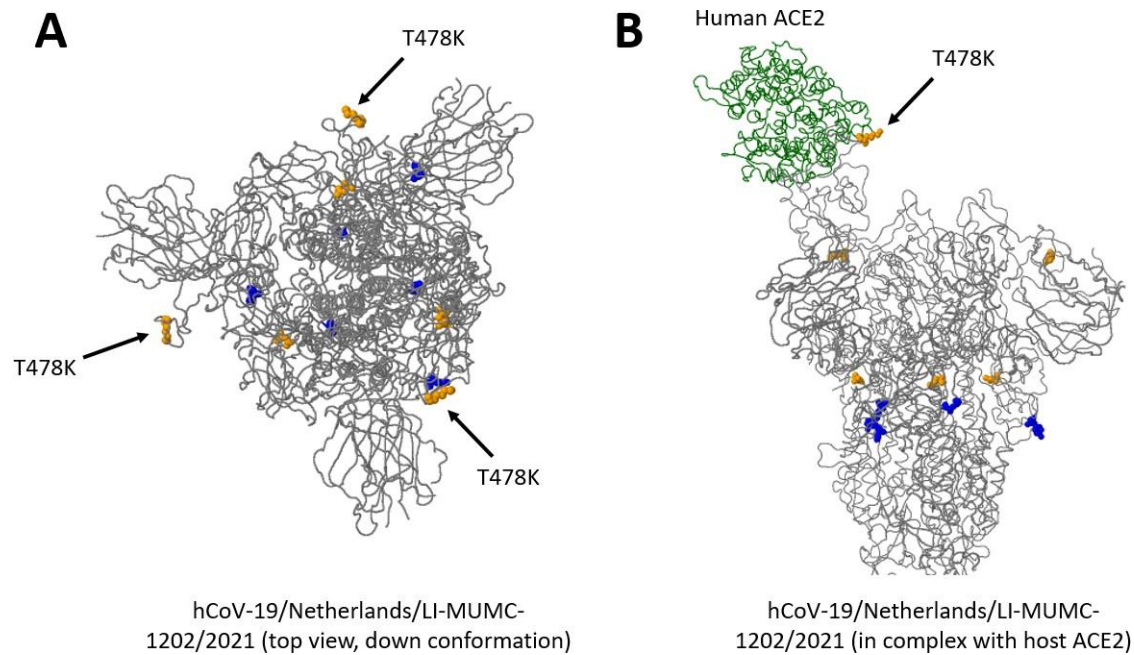


**Additional file 1**



**Figure S1.** Position of the T478K amino acid substitution in the 3D-model of the SARS-CoV-2 Spike protein of the B.1.1.519 variant in down conformation (**A**), or bound to the human Ace2 receptor (**B**)

**Table S1.** Oligonucleotides used in this study.

Target	Primer/Probe	5' mod	Seq 5' – 3'	3' mod	Tm (°C)	Notes
SARS-CoV-2 E gene	SARS-CoV-2-E_F	FAM	ACAGGTACGTTAATAGTTAATAGCGT	BHQ1	62.6	Sarbecovirus/ SARS-CoV broad
	SARS-CoV-2-E_R		ATATTGCAGCAGTACGCACACA		64.8	
	SARS-CoV-2-E_P		ACACTAGCCATCCTTACTGCGCTTCG		69.3	
SARS-CoV-2 N1 gene	SARS-CoV-2-N1_F	ABY*	GACCCCAAATCAGCGAAAT	QSY	61.1	SARS-CoV-2 specific
	SARS-CoV-2-N1_R		TCTGGTTACTGCCAGTTGAATCTG		64.5	
	SARS-CoV-2-N1_P		ACCCCGCATTACGTTTGGTGGACC		70.3	
mCMV-ie	mCMV-ie_F	Cy5	CAACATTGACCACGCACTAGATG	BHQ3	63.6	MUMC RNA internal control
	mCMV-ie_R		TTAAACTCCCCAGGCAATGAA		62.2	
	mCMV-ie_P		TCTTGGCCCATGCGGCACG		69.7	