1 Materials and methods

2 <u>Cell culture</u>

Vero E6 cells (ATCC-CRL-1586) were cultured without antibiotics in minimal in medium
(MEM, Gibco, USA) with 2 mM L-glutamine and 10% foetal bovine serum (FBS) at 37°C in
a 5% CO₂ incubator. Vero E6 cells were then prepared at a concentration of 5x10⁵ cells/mL in
ninety-six-well plates for the neutralization tests of SARS-CoV-2 in MEM growth medium
with glutamine and 4% FBS (M4 media).

8

9 <u>SARS-CoV-2 viral strains</u>

The ten SARS-CoV-2 strains used in this study were isolated in cells culture and stored at -10 80°C from patients's nasopharyngal swabs tested SARS-CoV-2 positive in our institute IHU-11 Méditerranée Infection during the pandemic [1,2]. The supernatant of each strains was then 12 harvested and was genotyped by whole genome next generation (NGS) as previously 13 14 described[3] (Supplementary table S2). For the neutralization tests, we inoculated the viral strains in 96-well Vero E6 cells plate at a concentration of 5×10^5 cells/mL. Forty-eight hours 15 post-viral infection, viral suspension was harvested and quantified by real-time reverse-16 transcription RT-PCR and TCID50. 17

18

19 <u>Monoclonal antibodies dilutions</u>

Bamlavinimab and etesevimab were first diluted at 1:10 then each mAbs was diluted in a 1:5
serial dilutions (from 3500 µg/mL to 0.0089 µg/mL). For the combination of the two mAbs,
we tested the mixture in the highest concentration for each mAbs alone with 2 times more
etesevimab than bamlavinimab.

Casirivimab and imdevimab were first diluted at 1:10 then each mAbs was diluted each in a 1:5 serial dilutions (from 12 000 μ g/mL to 0,00614 μ g/mL). For the combination of these two 26 mAbs, we tested the mixture in the highest concentration for each mAbs alone in the same27 proportion.

Tixagevimab and cilgavimab were first diluted at 1:10 then each mAbs was diluted each in a 1:5 serial dilutions (from 10 000 μ g/mL to 0,0512 μ g/mL). For the combination of these two mAbs, we tested the mixture in the highest concentration for each mAbs alone in the same proportion

32 <u>Micro-neutralization assay</u>

Each dilution of mAbs was mixed volume by volume with each viral strains with standardized 33 34 inoculum at 25 Ct as previously described[4]. The mixture of viral suspension and mAbs was incubated 1h at 37 ° C under 5% CO₂. Then, 100µl of medium in the 96-well plates was 35 removed and 100µL of the mixture for each dilution was added in guadruplate on the Vero E6 36 cells. Five days post-viral infection, cytopathic effect was determined with the inverted 37 optical microscope to determine the neutralization titer to obtain 50% of neutralization. Each 38 mAbs and combination of mAbs were tested three times against the 9 SARS-CoV-2 strains, 39 except for omicron variant that was tested four times. 40

41

42 **<u>References</u>**

47

53

[2] Jaafar R, Aherfi S, Wurtz N, Grimaldier C, Van Hoang T, Colson P, et al. Correlation
Between 3790 Quantitative Polymerase Chain Reaction-Positives Samples and Positive
Cell Cultures, Including 1941 Severe Acute Respiratory Syndrome Coronavirus 2
Isolates. Clin Infect Dis Off Publ Infect Dis Soc Am 2021;72:e921.
https://doi.org/10.1093/cid/ciaa1491.

[3] Colson P, Levasseur A, Delerce J, Pinault L, Dudouet P, Devaux C, et al. Spreading of a new SARS-CoV-2 N501Y spike variant in a new lineage. Clin Microbiol Infect Off Publ

^[1] La Scola B, Le Bideau M, Andreani J, Hoang VT, Grimaldier C, Colson P, et al. Viral
RNA load as determined by cell culture as a management tool for discharge of SARSCoV-2 patients from infectious disease wards. Eur J Clin Microbiol Infect Dis Off Publ
Eur Soc Clin Microbiol 2020;39:1059–61. https://doi.org/10.1007/s10096-020-03913-9.

56 57 58	Eur Soc Clin Microbiol Infect Dis 2021;27:1352.e1-1352.e5. https://doi.org/10.1016/j.cmi.2021.05.006.
59 60 61 62	[4] Jaafar R, Boschi C, Aherfi S, Bancod A, Le Bideau M, Edouard S, et al. High Individual Heterogeneity of Neutralizing Activities against the Original Strain and Nine Different Variants of SARS-CoV-2. Viruses 2021;13:2177. https://doi.org/10.3390/v13112177.
63	Supplementary data S1: Neutralization curves in Vero E6 cells for each strains tested
64	with each mAb : A, C, E, G, I, K, M, N, O, Q, S : bamlanivimab, etesevimab and mixture of
65	bamlanivimab and etesevimab – B, D, F, H, J, L, N, P, R, T : casirivimab, imdevimab and
66	REGN-CoV-2. Each experiment was done three times, except for Omicron variant four times.
67	Supplementary data S2 : Neutralization curves in Vero E6 cells for the three strains
68	tested with new mAb : A : $B.1.1 - B : AY.71 - C : B.1.1.529$ with tixagevimab, cilgavimab
69	and combination of both. Each experiment was done four times.
70	Supplementary table S3: Lineage of SARS-CoV-2 isolates and mutations in the spike
71	protein. In this table are indicated for the ten SARS-CoV-2 strains: genome sequence
72	submitted to GISAID databe (https://www.gisaid.org/), nexstrain clade, Pangolin lineage,

73 IHU name isolate (IHUMI) and the corresponding nucleotide substitutions, nucleotide74 deletions, amino acid substitutions and amino acid deletion

75