Methods S1: Expression and purification of cilgavimab and tixagevimab in *N. benthamiana* plants.

Variable region sequences for light chain (LC) and heavy chain (HC) of cilgavimab and tixagevimab from literature (Dong et al., 2021) were synthesized by GENEWIZ and were genetically fused to a human kappa constant sequence of the LC and a human gamma IgG1 constant sequence of HC (Lai et al., 2010). LC and HC genes were then cloned into a bean yellow dwarf virus (BeYDV)-based geminiviral vector and transiently expressed in *N. benthamiana* plants by agroinfiltration as described previously (Chen and Lai, 2014).

7D11 mAb were extracted and purified according to published protocols (Jugler et al., 2020). Briefly, mAb-expressing *N. benthamiana* leaves 7 days post infiltration were harvested and homogenized in extraction buffer (1X phosphate-buffered saline, pH 5.2 with 10 mg/mL Na-L-ascorbate, 2mM phenylmethylsulfonyl fluoride, and 1mM ethylenediaminetetraacetic acid). The pH of the homogenate was adjusted to 5.2 and then centrifuged several times. The supernatant was filtered through a 0.2-micron vacuum filter. The clarified protein extract was subsequently subjected to Protein A (MabSelect, Cytiva) chromatography according to the manufacture's protocol prior to further analysis.

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Variant	pTixagevimab(IC_{50})	pCilgavimab (IC_{50})
Omicron BA.4.6	90.65 μg/ml	568.30 μg/ml

Table S1. Half-maximal inhibitory concentrations (IC_{50}) of pTixagevimab and pCilgavimab against Omicron BA.4.6 pseudovirus.