

Theories of the origin of SARS-CoV-2 in the light of its continuing evolution

Florence Débarre^a and Zach Hensel^b

^a Institute of Ecology and Environmental Sciences, CNRS UMR 7618, Sorbonne Université, UPEC, IRD, INRAE, Paris, France

^b ITQB NOVA, Universidade NOVA de Lisboa, Av. da República, Oeiras, Lisbon 2780-157, Portugal

E-mails: florence.debarre@normalesup.org (F. Débarre), zach.hensel@itqb.unl.pt (Z. Hensel)

811 **Supplementary figures**

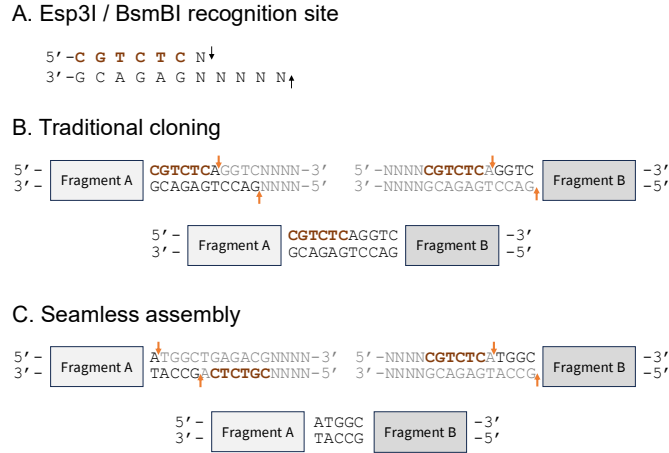


Figure S1. Traditional and seamless assembly. A. Cutting site of BsmBI and Esp3I restriction enzymes. B. Traditional cloning, leaves remnants of the restriction sites. C. Seamless assembly (also called “No See’m” technique) removes the restriction sites. Figure adapted from [48].



Figure S2. Evolution of SARS-CoV-2's sequence around the cleavage site for major variants. The black triangle locating the cleavage site is drawn only once but applies to all sequences.