*In vitro* selection of Remdesivir resistance suggests evolutionary predictability of SARS-CoV-2

Agnieszka M. Szemiel1¶, Andres Merits2, Richard J. Orton1, Oscar A. MacLean1, Rute Maria Pinto1, Arthur Wickenhagen1, Gauthier Lieber1#a, Matthew L. Turnbull1, Sainan Wang2, Wilhelm Furnon1, Nicolas M. Suarez1, Daniel Mair1, Ana da Silva Filipe1, Brian J. Willett1, Sam J. Wilson1, Arvind H. Patel1, Emma C. Thomson1, Massimo Palmarini1, Alain Kohl1, and Meredith E. Stewart1¶\*

**Affiliations**

1MRC-University of Glasgow Centre for Virus Research, Glasgow G61 1QH, UK.

2Institute of Technology, University of Tartu, 50411 Tartu, Estonia.

#aInstitut für Medizinische Virologie, Winterthurerstrasse 190, CH-8057 Zurich, Switzerland

\*Correspondence to: Meredith.Stewart@glasgow.ac.uk

We have included the data used to generate the figures and relevant statistic in their own file. Ie the data for Fig 3D is in a subfolder Fig3D&E within the folder Figure 3.

All supplementary figure data has been included. Found in a folder labeled supplementary data.

All datasets have also been included.