## Table S4. Model Assumptions

Assumption	Model	Implications	Mitigation strategy
There is a linear relationship between HCQ concentrations and effect on viral decline.	Clinical PK/PD model.	Extrapolation to much higher doses using a linear function may lead to overprediction of the drug effect.	Doses used in simulations were capped at 600mg BID. Simulations were repeated using preclinical Emax PKPD relationships to understand if higher doses might offer clinical benefit.
The viral kinetics were modelled with a first- order growth and a first-order death rate, and a saturable maximal viral load.	Translational and Clinical PK/PD models.	There is limited knowledge regarding the replication and death of SARS-Cov-2, especially in patients. Additionally, limited natural history data is publicly available.	A sensitivity analysis was performed to understand how various natural history population profiles might impact interpretation of HCQ efficacy at different dose levels.
HCQ pharmacokinetics are equivalent between (i) healthy or malaria infected patients and (ii) COVID-19 patients.	Clinical PK simulations Clinical PK/PD model.	There is no longitudinal PK data available from COVID- 19 patients to develop a robust PK model, so population PK parameters derived from a pool of both healthy and malaria infected patients was used for PK simulations.	The PK model we employed from healthy and malaria infected populations predicted the sparse PK data in patients with COID-19 well.
The concentration QTc prolonging effect of CQ is the same or greater than that of HQC and the effect is linear.	Clinical PK-QTc model	There are no models to describe the relationship between HCQ concentration and QTc prolongation. In order to explore how a higher HCQ dose might affect the QT interval we employed a model describing the relationship between CQ and QTc.	QTc prolongation must be studied carefully in this unique population group.
The viral kinetics of SARS-CoV-1 and SARS- CoV-2 are similar.	Translational PK/PD model	There is limited knowledge regarding the replication and death of SARS-Cov-2, especially in patients.	SARS-CoV-1 and SARS-CoV-2 share an estimated 79.6% sequence homology, and therefore, it is not unreasonable to concluded that they may also share similar replication kinetics. (35)