## Supplementary Material

**Supplementary Table 2.** Sequencing data of SARS-CoV-2 genome consensus sequences obtained at day 1 and day 164.

| Sequence ID          | Date of collection | Mean coverage | % of genome with ≥1-fold | % of genome with ≥10-fold | GiSAID accession |
|----------------------|--------------------|---------------|--------------------------|--------------------------|------------------|
| Portugal/PT1525a/2020| 2020-06-16 (day 1) | 3855x         | 99.8%                    | 99.7%                    | EPI_ISL_941339   |
| Portugal/PT1525b/2020| 2020-11-26 (day 164) | 2297x         | 99.6%                    | 97.7%                    | EPI_ISL_941340   |

* Regions with depth of coverage below 10-fold were automatically masked in INSaFLU pipeline by placing undefined bases “N” in the consensus sequence. One of these small regions (22986-23122) in the Portugal/PT1525b/2020 sequence falls within S gene (coverage between 2- and 9-fold). Due to its biological relevance, all reads were inspected, showing no differences for the reference genome (this region was then unmasked).