

**Supplementary table:**

| Variables                     | SARS-CoV-1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | SARS-CoV-2 (COVID-19)                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Original reservoir            | Bats [1]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Bats [2]                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| Main transmission mode        | Person-to-person through droplets [3]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Person-to-person through droplets [2]                                                                                                                                                                                                                                                                                                                                                                                                                           |
| Incubation time               | <i>Estimated from China [1]:</i><br>Mean: 4.6 days (3.8- 5.8)                                                                                                                                                                                                                                                                                                                                                                                                                                                             | <i>Estimated from China [4]</i><br>Mean: 4 days (2-7)<br><br><i>Estimated from Wuhan, China [5]</i><br>Mean: 5.2 days (4.1; 7.0)                                                                                                                                                                                                                                                                                                                                |
| Basic R <sub>0</sub>          | <i>Estimated from modelling [6]:</i><br>Range from 2.2 – 3.6<br><br><i>Estimated worldwide [7]:</i><br>Range 2 – 5                                                                                                                                                                                                                                                                                                                                                                                                        | <i>Estimated from cases in Wuhan [5]</i><br>2.2 (1.4 – 3.9)<br><br><i>Average and range reported in review [8]</i><br>3.28 (1.4- 6.49)<br><br><i>Estimated from modeling [9]:</i><br>2.68 (2.48 – 2.86)                                                                                                                                                                                                                                                         |
| Progression to severe disease | 8-20 days [7]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 8-20 days [7]                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| Case Fatality rate            | <i>Estimated from modelling [9]</i><br>Worldwide: 9.6%<br>Mainland China: 6.4%<br>Hong Kong: 17%<br><br><i>Estimated from hospital cases in Beijing [10]</i><br>< 20 years: 0.5%<br>20-64 years: 4.8%<br>> 65 years: 27.7%<br><br><i>Estimated from Hong Kong department of health database [11]</i><br>< 60 years: 6.8% (4.0; 9.6)<br>> 60 years: 55.5% (45.3; 64.7)<br><br><i>Estimated from CDC China [12]</i><br>Overall: 6.4%<br>20 -39 years: 2.4%<br>40-59 years: 8.9%<br>60-79 years: 25.5%<br>80-93 years: 17.7% | <i>Estimated from mainland China 1<sup>st</sup> week of epidemic [13]:</i> 0.15% (0.12- 0.18)<br><br><i>Estimated from Hubai province (not Wuhan) [13]:</i><br>1.41 % (1.38 – 1.45)<br><br><i>Estimated from Wuhan city [13]</i><br>5.25% (4.89 – 5.51)<br><br><i>Estimated from multiple sources [14]</i><br>Wuhan: 4.42%<br>Rest of Hubai: 3.09%<br>Hubei: 4.07%<br>Rest of China: 0.84%<br>China: 3.53%<br>International 46 countries: 1.83%<br>Total: 3.46% |
| Viral shedding                | Nasopharyngeal viral shedding from peak 6 – 11 days after onset of illness [15]                                                                                                                                                                                                                                                                                                                                                                                                                                           | High viral load in upper respiratory tract, day 2 to 6 after onset of illness (Zou 2020) [16]                                                                                                                                                                                                                                                                                                                                                                   |
| Genome                        | The conserved replicase domains of SARS-CoV-2 are 94.6% identical to SARS-CoV implying the two belong to the same species [14]                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Cell entry                    | Both viruses use the same cell entry receptor (ACE2). SARS-CoV-2 has 10-20 folds higher affinity with ACE2 than SARS-CoV resulting in higher infectiousness [14].                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |

## References supplementary table

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### **Box 1: Explanation of quanta and estimation assumed quanta for *Legionella pneumophila***

#### *Explanation parameter quanta*

A quantum is a hypothetical infectious dose estimated from epidemiological studies describing the outbreak of a pathogen with a known infectious dose (Fennelly et al. 2004; Riley et al. 1978; Sze To and Chao 2010; Wells 1955). One quantum presents the number of bacteria or viruses in an airborne particle that is required to infect 63.2% ( $1-e^{-1}$ ) of susceptible people per hour, also described as  $1.25 \times ID_{50}$  (infectious dose of 50%) (Fennelly et al. 2004).

#### *Formula for quanta estimation*

- Quantum =  $1.25 \times ID_{50}$
- Quanta number generation = number of CFU in one quantum divide by number of released CFU in the air
- Assumed upper and lower limit calculation =  $\pm 35\%$

#### *Input values from literature*

- $ID_{50}$  of *L. pneumophila* = 11.7 CFU (Armstrong and Haas 2007)
- CFU load *L. pneumophila* in the air per  $m^3$  per hour in a dental clinic = 112.5 CFU/ $m^3$ /h (Dutil et al. 2007)

#### *Calculations with *L. pneumophila**

- One quantum =  $1.25 \times 11.7 = 14.6$
- Quanta number generation =  $122.5/14.6 = 8.39$
- Upper limit quanta = 11.32
- Lower limit quanta = 5.45

### **Box 2: description of modelled scenarios.**

- A low-risk scenario in which the Dental Healthcare Worker (DHW) is exposed to an infectious source that generates the lowest quanta. The DHW is placed in low risk conditions wearing an FFP-2 mask and works in good indoor air quality (400-800 PPM  $CO_2$ ).
- An intermediate-risk scenario in which the DHW is exposed to an infectious source that generates the middle value quanta. The DHW wears a medical face mask and works in average indoor air quality (1100–1500 PPM  $CO_2$ ).
- A high-risk scenario in which the DHW is exposed to an infectious source that generates the highest value quanta. The DHW does not wear a medical face mask, nor covers the nose with the medical face mask and works in poor indoor air quality ( $>1500$  PPM  $CO_2$ ).