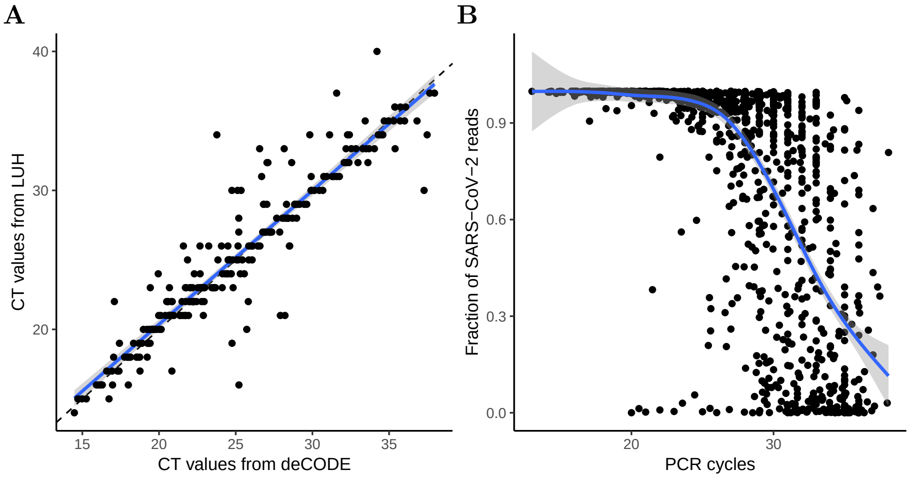
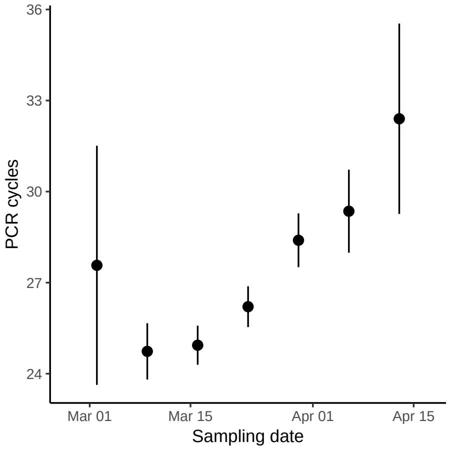
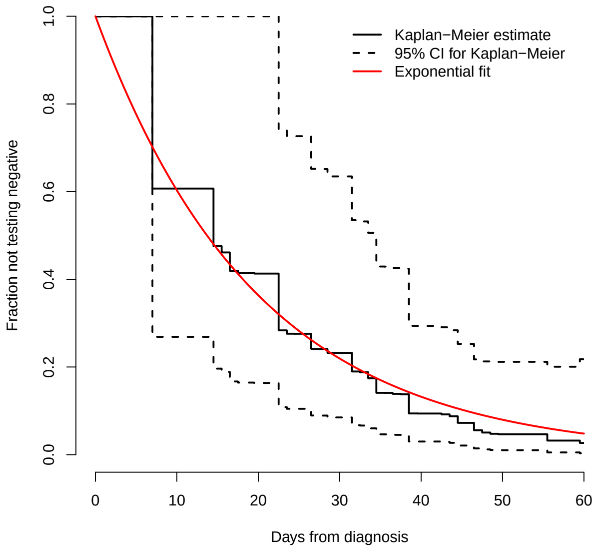
Supplementary Information



Supplementary Figure 1: Different measures of viral load.
A, CT values from LUH against CT values from deCODE. Subset of the samples (238) were measured both by LUH and deCODE. **B**, Fraction of reads mapping to SARS-CoV-2 against the aggregated CT values. The error bands are 95%-CIs and the centre in the bands are means from the regressions.

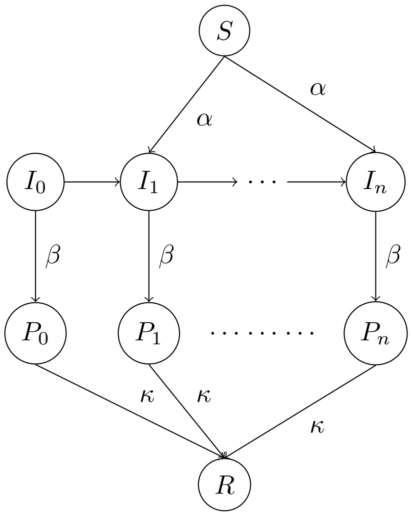


Supplementary Figure 2: qPCR-CT values as function of sampling date in the Australian data.
The centre values are means and the error bars are 95%-CIs. The number of samples in the bins are 7, 72, 252, 303, 194, 65 and 5 ordered by date.



Supplementary Figure 3: Molecular traces of SARS-CoV-2 recovery with indeterminable samples. The fraction of individuals that remained positive as a function of days from the initial positive test.

A



B

$$\begin{aligned} dS &= -\alpha S \sum_i I_i \\ dI_0 &= -\beta I_0 \\ dI_1 &= -\beta I_1 + \alpha S I_0 \\ &\vdots \\ dI_n &= -\beta I_n + \alpha S I_{n-1} \\ dP_0 &= -\kappa P_0 + \beta I_0 \\ &\vdots \\ dP_n &= -\kappa P_n + \beta I_n \\ dR &= +\kappa \sum_i P_i \end{aligned}$$

Supplementary Figure 4: Ordinary differential equations of the susceptible, infected, positive and recovered epidemiological model. **A**, schematic view of the flow of individuals in the epidemiological model. The susceptible individuals are infected by individuals in different infection generations ($I_0 \dots I_n$). These individuals then recover from the symptoms but test positive ($P_0 \dots P_n$). In the final stage, the positive individuals transition to the recovered and negative state. **B**, Ordinary differential equations. The infected and positive states are broken by the generation of the virus transmission to keep track of the viral generations

Supplementary Table 1: Example of a serial dilution of a positive sample

A synthetic RNA control (TaqPath control) is provided by the manufacturer at a concentration of 25 copies/µL. A serial dilution of the control shows that the detection limit in our assay setup is between approximately 1 and 6 copies of RNA. A serial dilution of a positive sample with a measured Ct value of 20.6, shows that this sample would still be determined positive after a 100,000X dilution (Ct = 35.8).

TaqPath qPCR assay			
Assay volume: 6.25 µL			
RNA input: 2.5 µL			
	Ct-value		
Sample 1	20.6		
10X dilution	23.7		
100X dilution	27.9		
1,000x dilution	31.6		
10,000X dilution	33.4		
100,000X dilution	35.8		
	Ct-value	Copies	
TaqPath-Control	30.7	62.5	
10X dilution	34.7	6.25	
100X dilution	Not determined	0.625	