

Supplementary Materials for  
**Viral genomes reveal patterns of the SARS-CoV-2 outbreak in  
Washington State**

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**This PDF file includes:**

- Fig. S1. Number of lineages through time for different local transmission clusters
- Fig. S2. Workplace mobility trends of different counties in Washington State compared to King county.
- Fig. S3.  $R_e$  estimates using the coalescent skygrowth model compared to Google mobility data.
- Fig. S4. Effective reproduction number and workplace mobility in Yakima County
- Fig. S5. Substitutions and success of a SARS-CoV-2 introduction.
- Fig. S6. Probability that a newly sampled case reveals a new introduction.
- Fig. S7. Histogram of primers used by UW Virology across time.
- Fig. S8. Comparison of cycle threshold (Ct) across SARS-CoV-2 Spike variant.
- Fig. S9. Symptom and cycle threshold (Ct) values across time.
- Fig. S10. Comparing cycle threshold (Ct) by viral clade.
- Fig. S11. Cycle threshold by number of substitutions
- Fig. S12. Age of infected individuals by 614D or 614G variant over time.
- Fig. S13 Dependence of the local outbreak clusters and the number of background sequences used.

Fig. S14. Principle of the multi-tree coalescent.

Fig. S15. Estimation of effective population sizes and rates of introductions from simulations.

Fig. S16. Estimation of the percentage of new cases due to introductions from simulations.

Table S1. GLM of Ct with N1, N2 primers in patients at UW affiliates

Table S2. GLM of Ct with ORF1ab primers in patients at UW affiliates

**Other Supplementary Material for this manuscript includes the following:**  
(available at [stm.sciencemag.org/cgi/content/full/scitranslmed.abf0202/DC1](http://stm.sciencemag.org/cgi/content/full/scitranslmed.abf0202/DC1))

Data file S1. GISAID acknowledgment table. (tsv)

Data file S2. Cycle threshold values for isolates. (tsv)