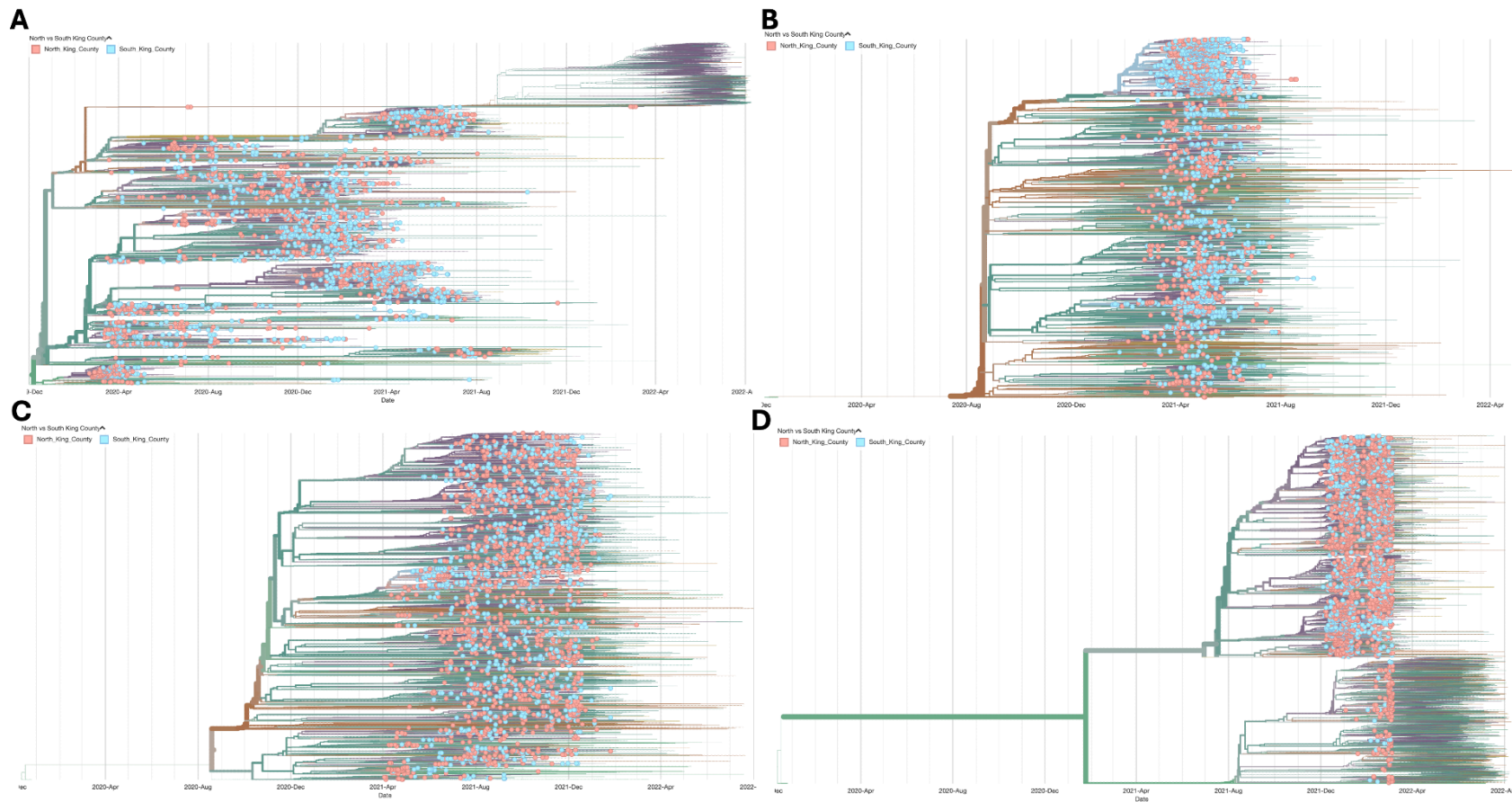
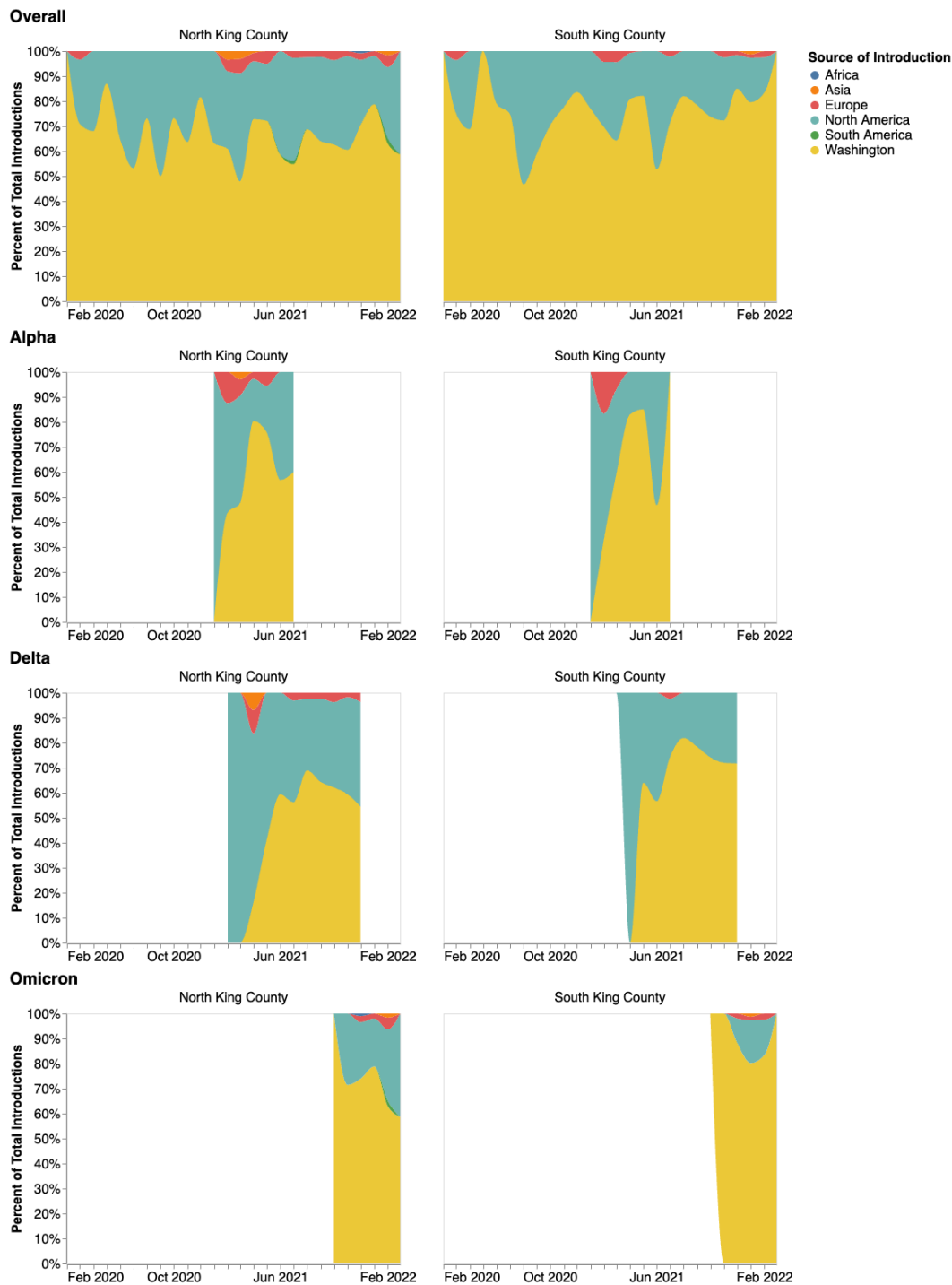


Supplementary Materials: a list of the supplementary materials, followed by the actual text of the Supplementary Materials.

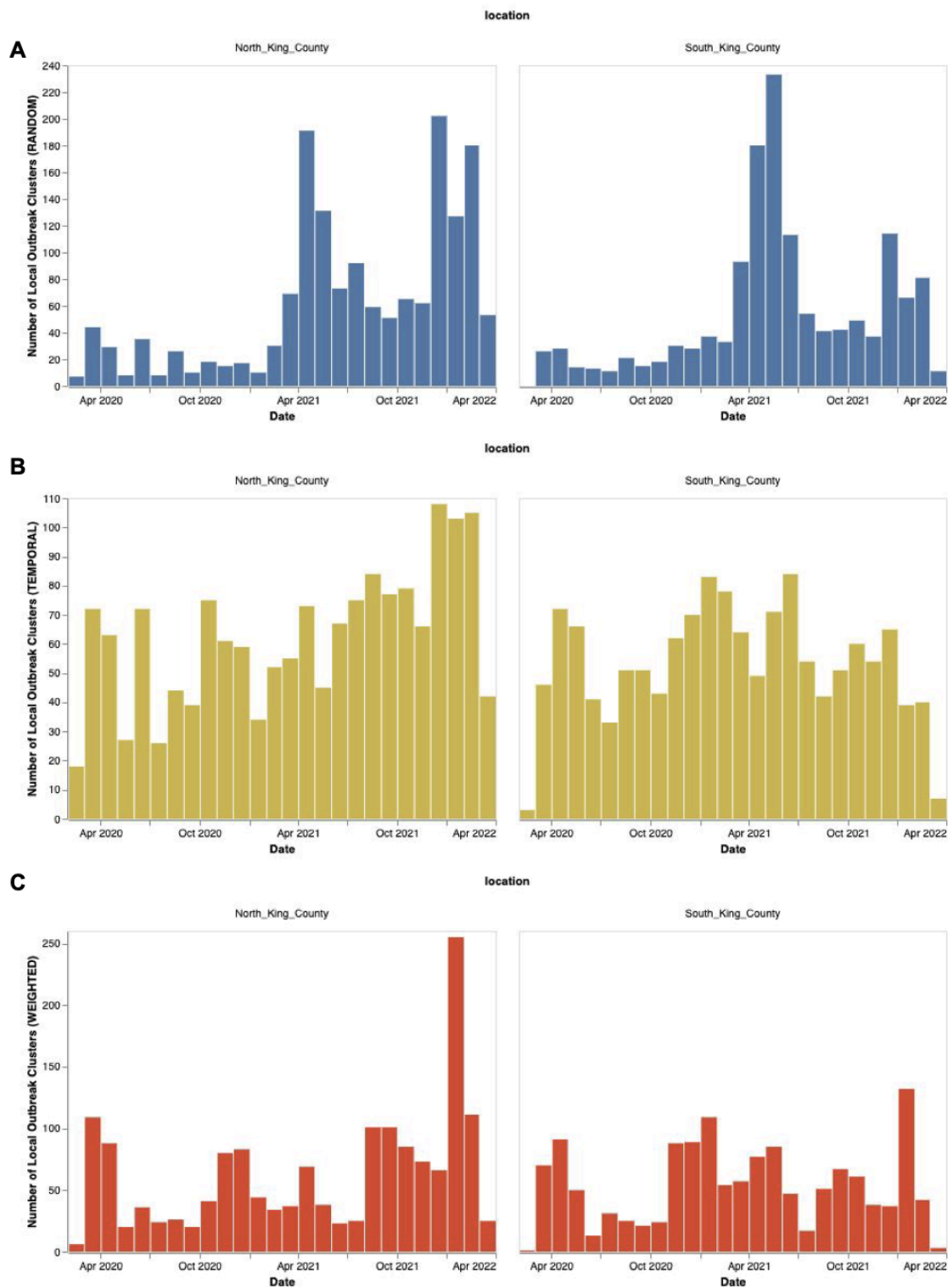
1. **Supp.Fig 1:** Time-resolved maximum likelihood phylogenies for King County, WA
2. **Supp.Fig 2:** Source of introduction for each identified King County cluster
3. **Supp.Fig 3:** Number of local outbreak clusters over time by subsampling scheme
4. **Supp.Fig 4:** R_t estimation using phylodynamic estimates
5. **Supp.Fig 5:** Phylodynamic estimates of SARS-CoV-2 transmission in King County with equal temporal subsampling.
6. **Supp.Fig 6:** Phylodynamic estimates of SARS-CoV-2 transmission in King County with subsampling weighted by hospitalizations.
7. **Supp. Table 1:** Geocoding for different geographical scales in King County, WA
8. **Supp.Table 2:** Sequence Accession IDs and acknowledgements table



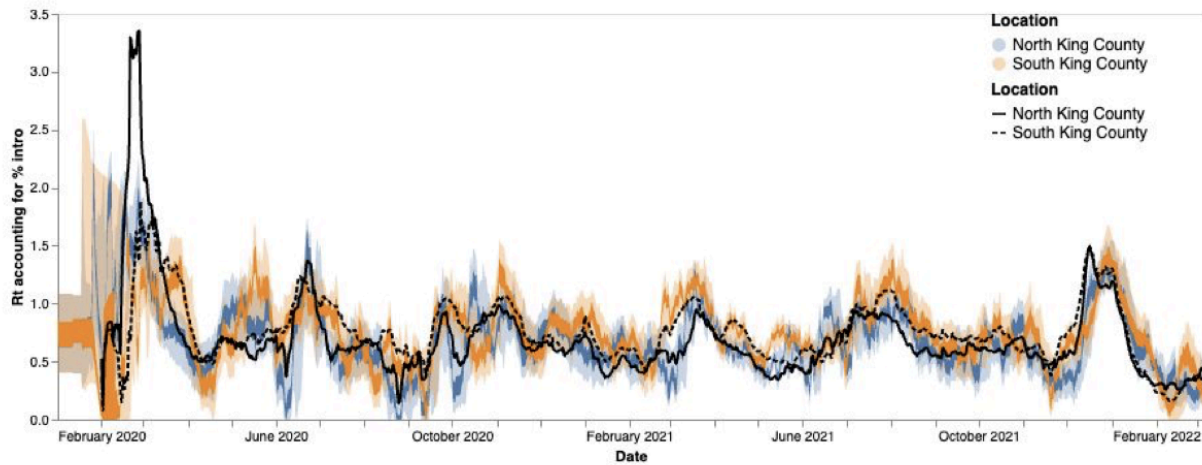
Supplementary Figure 1: Time-resolved maximum likelihood phylogenies for King County, WA by dominant variant wave with sample collection dates between February 1 2020 and March 6 2022. Trees are filtered to highlight genomes from King County among contextual sequences from around the globe. Tip color represents the region within King County, with pink corresponding to North King County and blue representing South King County. Branches are colored based on inferred ancestry. Panel A represents all variant clades excluding Alpha, Delta, and Omicron (the full tree can be explored interactively at <https://nextstrain.org/groups/blab/ncov-king-county/other>), the other panels represent Alpha (B, <https://nextstrain.org/groups/blab/ncov-king-county/alpha>), Delta (C, <https://nextstrain.org/groups/blab/ncov-king-county/delta>), and Omicron (D, <https://nextstrain.org/groups/blab/ncov-king-county/omicron>)



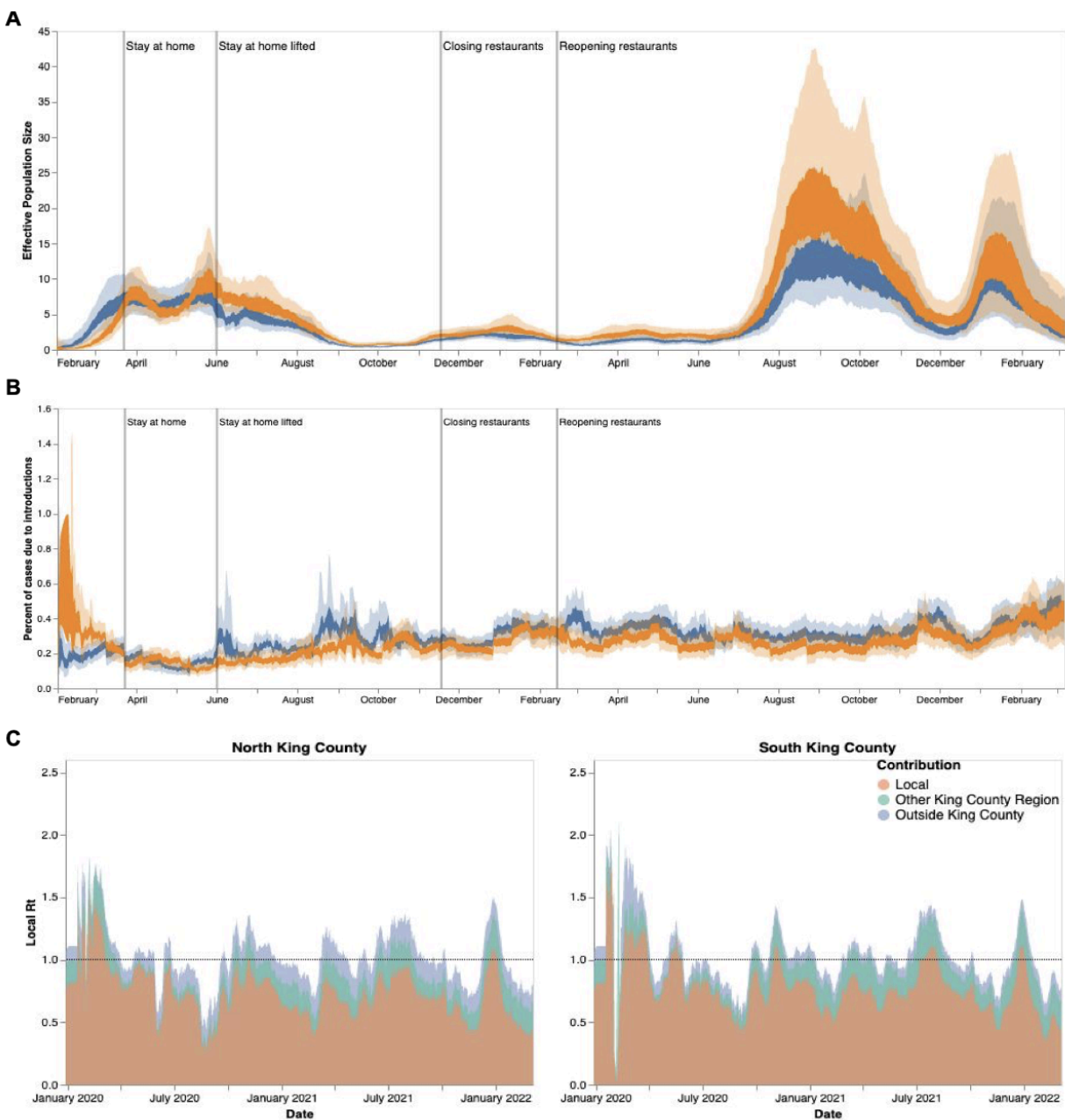
Supplementary Figure 2: Source of introduction for each identified King County cluster. The left column is introductions into North King County, the right into South King County. The panels show how the inferred geographical source of each introduction changes over time as a percentage of all introductions into the regions for that time period. The top row contains all the introductions among the four different time-resolved phylogenies. Each subsequent row represents a different variant studied and is labeled accordingly.



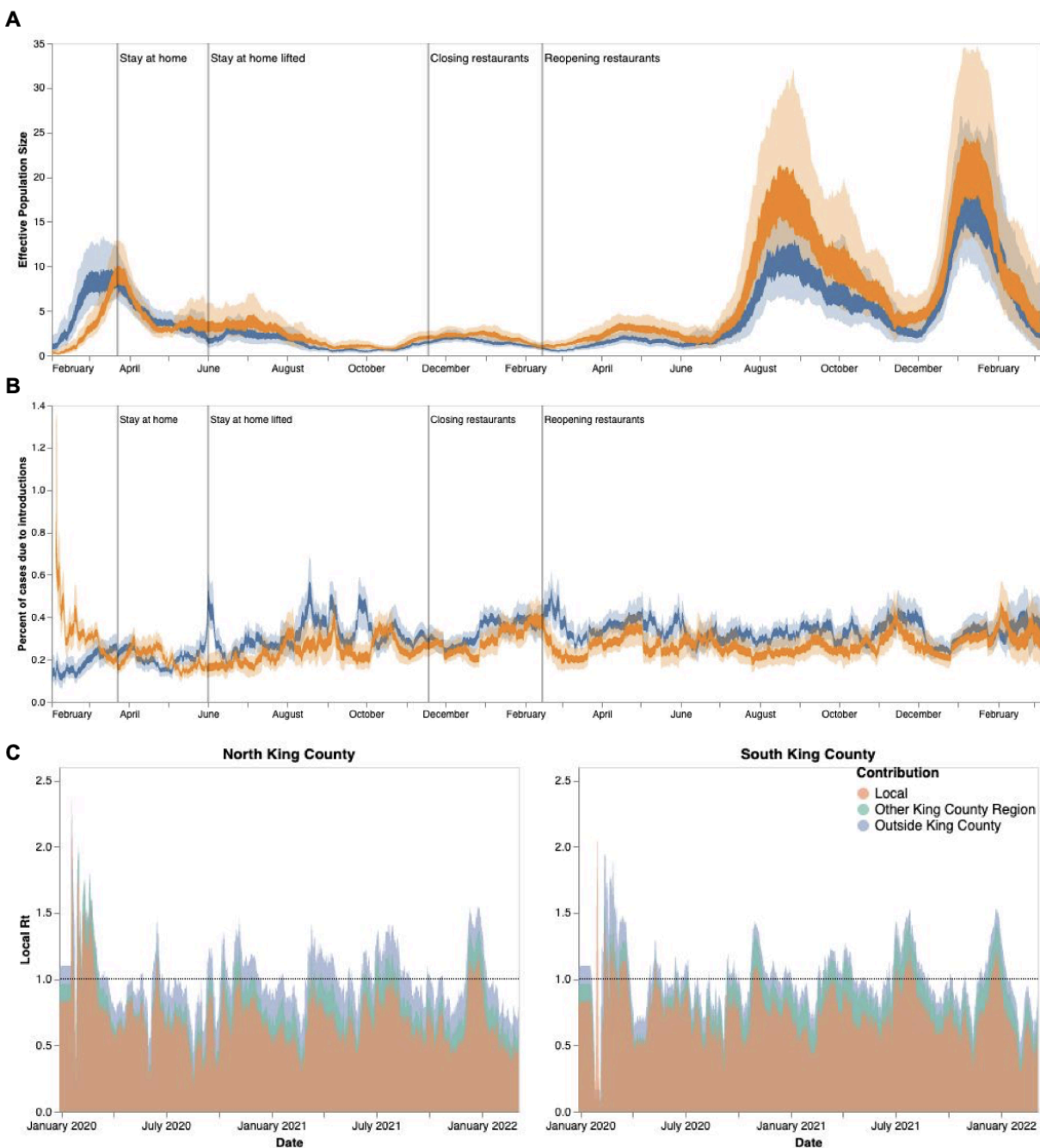
Supplementary Figure 3: Number of local outbreak clusters over time by subsampling scheme: random (A, Blue), equal temporal weighting by year-week (B, Gold), and subsampling weighted by daily hospitalizations calculated using a 14 day moving average (C, Red)



Supplementary Figure 4: R_t estimation using phylodynamic estimates (Blue North King County; Orange = South King County) and case data (Black lines, solid = North King County, dashed = South King County) The inner area denotes the 50% HPD interval and the outer area denotes the 95% HPD interval.



Supplementary Figure 5: Phylodynamic estimates of SARS-CoV-2 transmission in King County with equal temporal subsampling. Results presented above were inferred using 3000 sequences subsampled using equal temporal weighting by year-week. Analyses presented, as defined previously, are: effective population size over time (A), percent of cases due to introductions (B), and local R_t estimations divided by region and source of contribution (C). Orange denotes South King County; blue denotes North King County.



Supplementary Figure 6: Phylodynamic estimates of SARS-CoV-2 transmission in King County with subsampling weighted by hospitalizations. Results presented above were inferred using 3000 sequences subsampled using weighting by hospitalizations over time using a 14 day rolling average. Analyses presented, as defined previously, are: effective population size over time (A), percent of cases due to introductions (B), and local R_t estimations divided by region and source of contribution (C). Orange denotes South King County; blue denotes North King County.

Supplementary Table 1: Geocoding for different geographical scales in King County, WA

Region	PUMA	ZIPCODE
North King County	11601	98103
		98107
		98117
	11602	98105
		98115
		98125
		98195
	11603	98101
		98102
		98104
		98109
		98119
		98121
		98154
		98164
		98199
	11604	98112
		98118
		98122
		98144
	11605	98106
		98108
		98116
		98126
		98134
		98136
	11606	98133
98155		
98177		

		98011
		98028
	11607	98033
		98034
		98052
	11608	98004
		98005
		98006
		98007
		98008
		98039
	11609	98040
		98029
		98076
		98075
	11616	98045
		98065
		98014
		98077
		98053
98024		
98072		
98019		
South King County	11610	98055
		98057
		98056
		98178
	11611	98146
		98148
		98166
		98168

		98188
	11612	98003
		98023
		98198
		98070
	11613	98030
		98031
		98032
		98092
	11614	98001
		98002
		98047
	11615	98010
		98022
		98038
		98051
		98027
		98042
		98059
		98058