

1 Supplemental information for: Longitudinal lineage and variant detection of SARS-CoV-2 across
2 Southern California wastewater.

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4 Jason A. Rothman^{a*}, Andrew Saghir^a, Amity G. Zimmer-Faust^b, Kylie Langlois^b, Kayla
5 Raygoza^{ab}, Joshua A. Steele^b, John F. Griffith^b, Katrine L. Whiteson^{a*}

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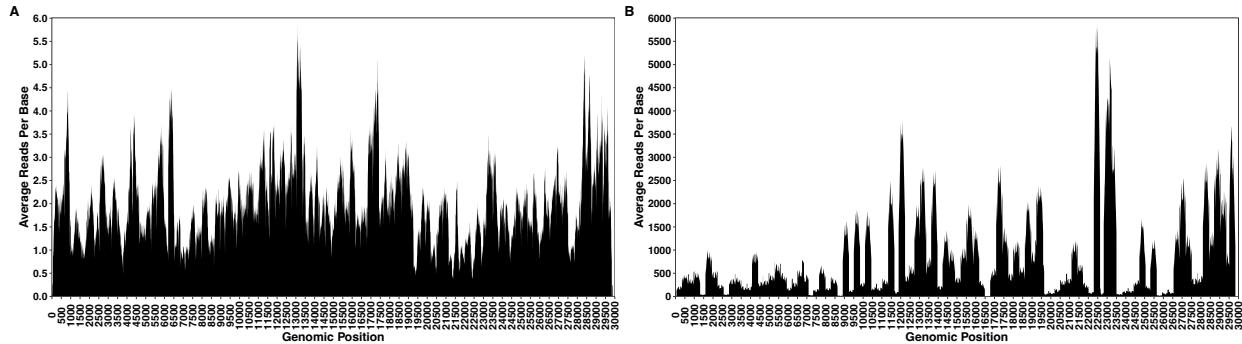
7 ^a Department of Molecular Biology and Biochemistry, University of California, Irvine, Irvine,
8 CA, USA.

9 ^b Southern California Coastal Water Research Project, Costa Mesa, CA, USA

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11 * Co-corresponding authors: Jason A. Rothman, University of California, Irvine, CA,
12 92697, (949) 824-3509, rothmanj@uci.edu. Katrine L. Whiteson, University of California,
13 Irvine, Irvine, CA, 92697, (949) 824-9032, katrine@uci.edu.

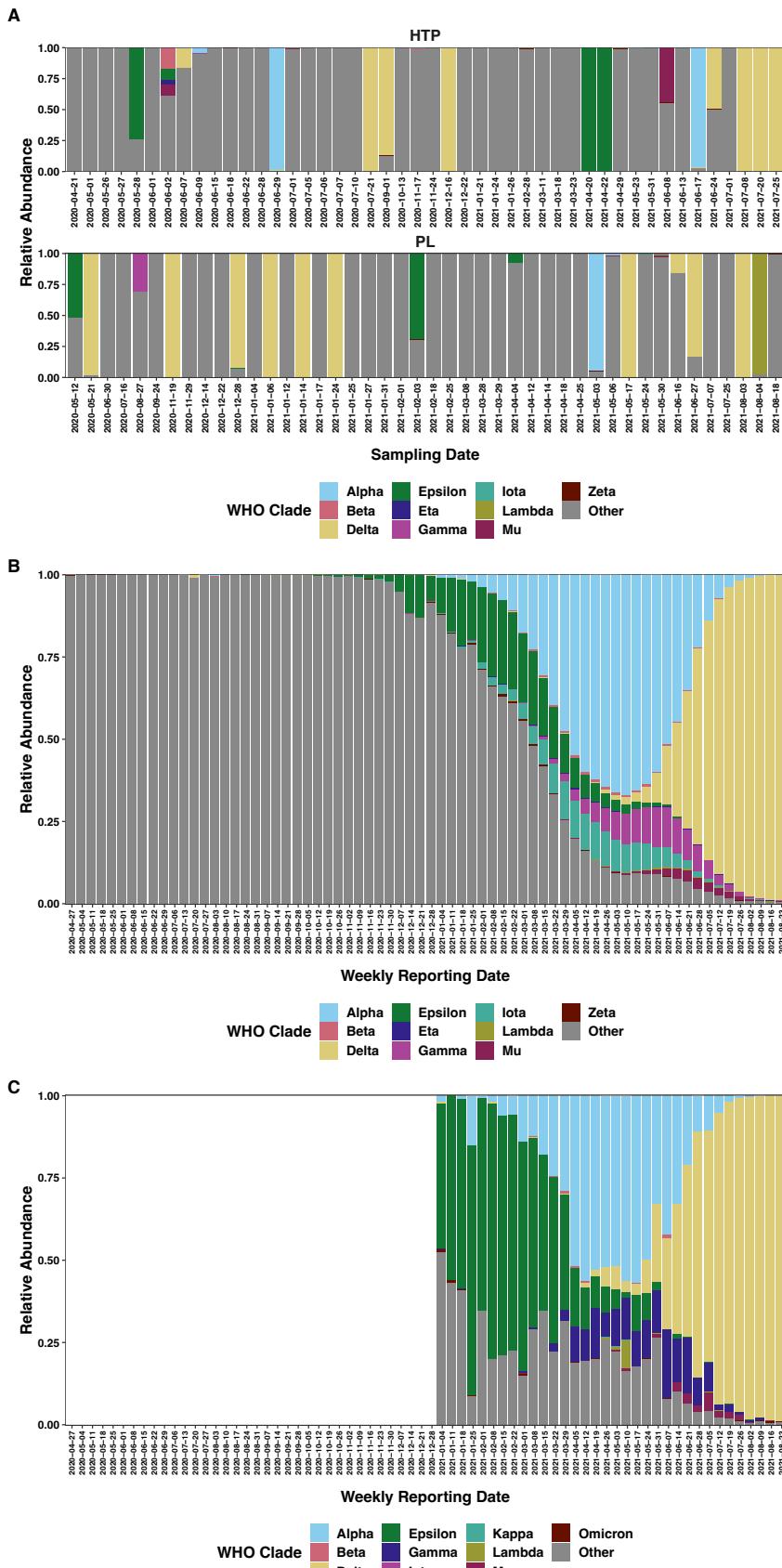
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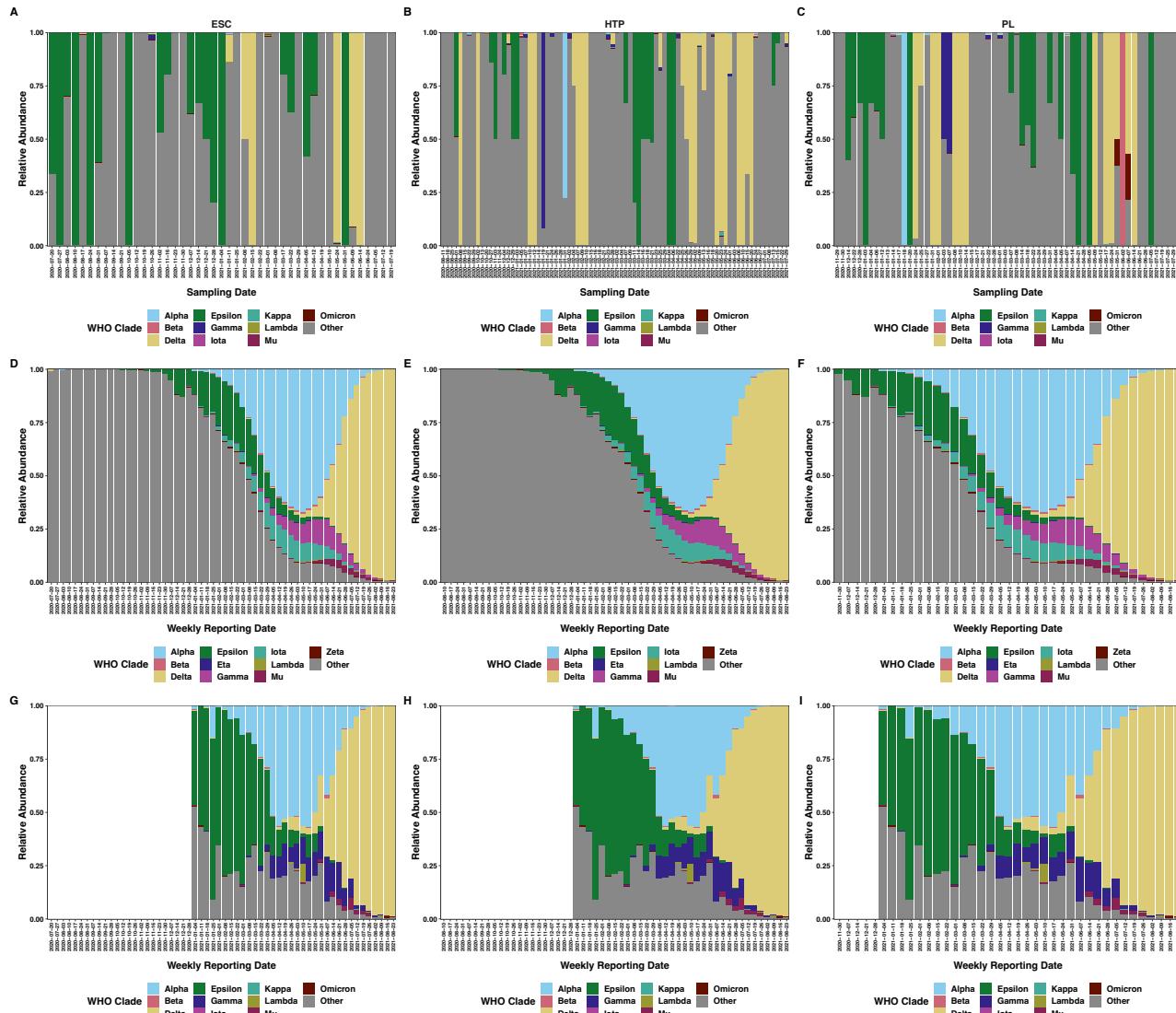
16 Figure S1: Area plot of the average reads per base mapped to the SARS-CoV-2 genome across
 17 all samples. Panel A represents libraries prepared with the Illumina Respiratory Virus
 18 Enrichment Panel (IRV) and Panel B represents libraries prepared for tiled amplicon sequencing.

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21 Figure S2: The relative proportional abundance of the ten most abundant SARS-CoV-2 lineages
22 plus others in A) tiled-amplicon libraries, B) weekly GISAID-reported data for clinical samples
23 from the United States, and C) California Health and Human Services (CalHHS)-reported
24 clinical data. Panel A is faceted by WTP and labeled with sampling date and panel B is labeled
25 by the aggregate of GISAID-reported data. Note that one sample date from the North City Water
26 Reclamation Plant is not shown, and variant data from CalHHS are not available before 1/1/21 so
27 those dates are left blank.

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30 Figure S3: The relative proportional abundance of the ten most abundant SARS-CoV-2 lineages
 31 plus others in Illumina Respiratory Virus Panel enriched libraries for A) Escondido, B)
 32 Hyperion, and C) Point Loma water treatment facilities. Panels D, E, and F are weekly GISAID-
 33 reported data for clinical samples from the United States corresponding to the approximate time
 34 periods of panels A, B, and C, respectively. Panels G, H, and I are CalHHS-reported clinical data
 35 corresponding to the approximate time periods of panels A, B, and C, respectively. Variant data
 36 from CalHHS are not available before 1/1/21 so those dates are left blank.

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38 Supplemental File SF1: This file contains several worksheets of information: A README sheet
39 with detailed information, sample metadata, single nucleotide variants for IRV and tiled
40 amplicon samples, and PANGO sublineages as output by Freyja for IRV and tiled amplicon
41 samples.