

**SUPPLEMENTARY INFORMATION:**

Detection of SARS-CoV-2 intra-host recombination during superinfection with Alpha and Epsilon variants in New York City

J. Wertheim et al.

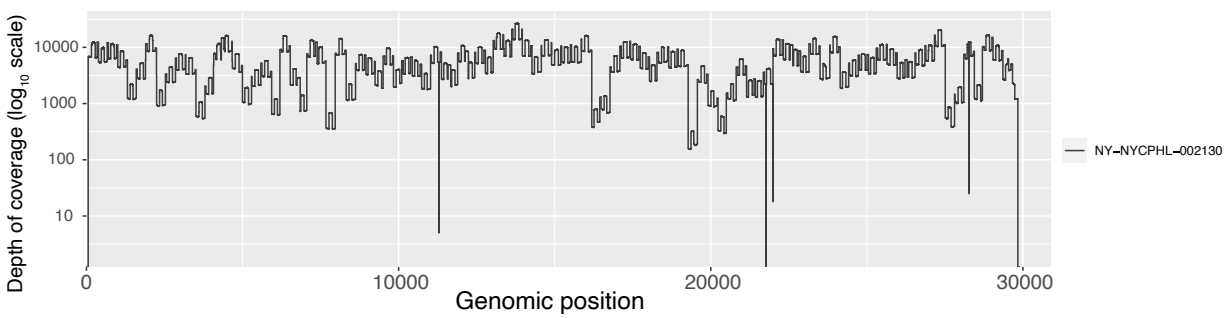
**Supplementary Table 1. Recombinant haplotype frequencies across separate extractions, reverse transcription, and PCR amplification in high-throughput sequencing for 947 nt S gene fragment, nucleotide positions 23604 and 23709.**

Haplotypes			Count (frequencies)			
Type	23604	23709	NYCPHL-002461-A	NYCPHL-002461-B	NYCPHL-002461-C	NYCPHL-002461-D
<b>MAJOR</b>	<b>A</b>	<b>T</b>	3633 (78.57%)	4095 (76.43%)	3778 (76.40%)	4745 (78.24%)
<b>MINOR</b>	<b>C</b>	<b>C</b>	634 (13.71%)	776 (14.48%)	762 (15.41%)	851 (14.03%)
<b>MIX</b>	<b>A</b>	<b>C</b>	162 (3.50%)	234 (4.37%)	191 (3.86%)	237 (3.91%)
<b>MIX</b>	<b>C</b>	<b>T</b>	195 (4.22%)	253 (4.72%)	214 (4.33%)	232 (3.83%)
<b>Depth</b>			4624 (100%)	5358 (100%)	4945 (100%)	6065 (100%)

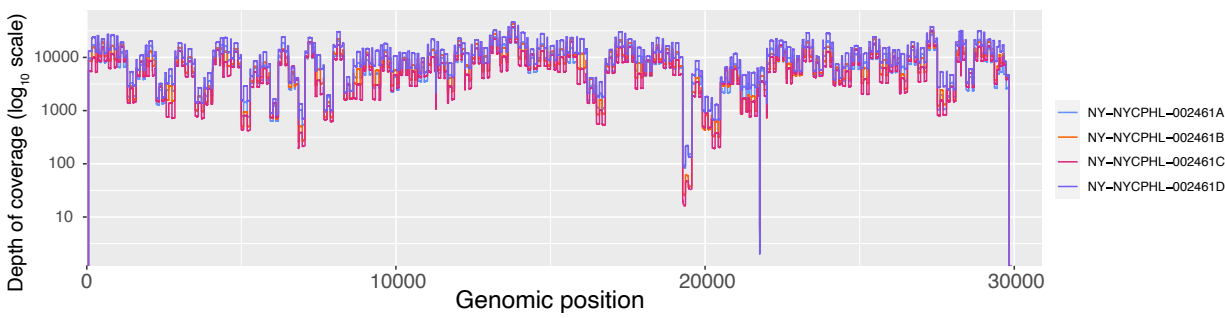
**Supplementary Table 2. Recombinant haplotype frequencies across separate extractions, reverse transcription, and PCR amplification in high-throughput sequencing for the 476 nt ORF8 fragment, nucleotide positions 27972, 28048, 28095, 28111.**

Haplotypes					Count (frequencies)			
Type	27972	28048	28095	28111	NYCPHL-002461-A	NYCPHL-002461-B	NYCPHL-002461-C	NYCPHL-002461-D
<b>MAJOR</b>	T	T	T	G	1382 (70.22%)	1164 (69.83%)	1110 (68.90%)	1873 (70.26%)
<b>MINOR</b>	C	G	A	A	381 (19.36%)	305 (18.30%)	347 (21.54%)	505 (18.94%)
<b>MIX</b>	T	G	A	A	57 (2.90%)	40 (2.40%)	31 (1.92%)	77 (2.89%)
<b>MIX</b>	C	T	T	G	50 (2.54%)	60 (3.60%)	55 (3.41%)	66 (2.48%)
<b>MIX</b>	T	T	A	A	40 (2.03%)	43 (2.58%)	28 (1.74%)	48 (1.80%)
<b>MIX</b>	C	G	T	G	34 (1.73%)	28 (1.68%)	18 (1.12%)	45 (1.69%)
<b>MIX</b>	T	T	T	A	8 (0.41%)	7 (0.42%)	6 (0.37%)	12 (0.45%)
<b>MIX</b>	C	G	A	G	4 (0.20%)	6 (0.36%)	4 (0.25%)	12 (0.45%)
<b>MIX</b>	T	G	T	G	6 (0.30%)	8 (0.48%)	7 (0.43%)	15 (0.56%)
<b>MIX</b>	C	T	A	A	1 (0.05%)	3 (0.18%)	3 (0.19%)	5 (0.19%)
<b>MIX</b>	C	G	T	A	1 (0.05%)	1 (0.06%)	NULL	NULL
<b>MIX</b>	T	T	A	G	1 (0.05%)	1 (0.06%)	2 (0.12%)	7 (0.26%)
<b>MIX</b>	C	T	A	G	1 (0.05%)	1 (0.06%)	NULL	NULL
<b>MIX</b>	T	G	T	A	1 (0.05%)	NULL	NULL	NULL
<b>MIX</b>	C	T	T	A	1 (0.05%)	NULL	NULL	1 (0.04%)
<b>Depth</b>					1968 (100%)	1667 (100%)	1611 (100%)	2666 (100%)

(A) Index case



(B) Named contact partner



**Supplementary Figure 1. Genomic sequencing depth in the (A) index case NY-NYCPHL-002130 and (B) named contact partner NY-NYCPHL-002461.**