



England/201061439/2020	3/4/2020	82	296	no	yes	no	no	no	no	no	no	1
USA/WA-UW-22859/2020	8/5/2020	85	1	no	no	no	no	no	no	no	yes	1
USA/WA-UW-12771/2020	6/29/2020	86	151	no	no	yes	yes	no	no	no	no	2
Wuhan/HBCDC-HB-04/2019	12/30/2019	87	1	no	no	no	yes	no	no	no	yes	2
USA/WA-UW-19260/2020	8/1/2020	91	1	no	no	no	no	no	no	no	yes	1
USA/TX-HMH-2673/2020	6/1/2020	93	5	no	yes	no	no	no	no	no	no	1
India/KA-InStem-NCBS-0080/2020	6/17/2020	94	1	yes	no	yes	no	yes	no	no	yes	4 <sup>b</sup>
England/MILK-99250B/2020	8/27/2020	94	4	yes	no	yes	yes	no	no	no	yes	4 <sup>b</sup>
England/MILK-99A9BC/2020	8/29/2020	96	1	no	no	no	no	no	no	no	yes	1
England/ALDP-9BDA83/2020	9/10/2020	99	264	no	no	yes	yes	no	yes	yes	yes	4 <sup>b</sup>

<sup>a</sup>Refers to 100 subsets of data randomly subsampled (without replacement) from n = 100,296 SARS-CoV-2 full genomes

<sup>b</sup>Recombination event indicated to be possibly due to another process other than recombination (this is annotated for those events supported by  $\geq 3$  methods)

\*SARS-CoV-2 sequence accession numbers available at [https://github.com/conte1/recombination\\_in\\_coronaviruses](https://github.com/conte1/recombination_in_coronaviruses)