S3 Table. Genome information used to calculate points in Fig.5. We have used a 14 days time window, i. e., every sequenced genome within an interval of 14 days were considered as infected ones, while the previous were considered to be recovered.

Point Number*	Infected Genomes	Recovered Genomes	Date Interval
#1	#03 → #19	#1 → #02	30 Dec 2019 → 12 Jan 2020
#2	#13 → #19	#1 → #12	01 Jan 2020 → 14 Jan 2020
#3	#14 → #19	#1 → #13	02 Jan 2019 → 15 Jan 2020
#4	#16 → #19	#1 → #15	03 Jan 2019 → 16 Jan 2020
#5	#17 → #27	#1 → #16	10 Jan 2019 → 23 Jan 2020
#6	#19 → #28	#1 → #18	11 Jan 2019 → 24 Jan 2020
#7	#20 → #45	#1 → #19	17 Jan 2019 → 30 Jan 2020
#8	#21 → #46	#1 → #20	20 Jan 2019 → 02 Feb 2020
#9	#22 → #46	#1 → #21	21 Jan 2019 → 03 Feb 2020
#10	#23 → #46	#1 → #22	22 Jan 2019 → 04 Feb 2020
#11	#28 → #48	#1 → #27	24 Jan 2019 → 06 Feb 2020
#12	#29 → #48	#1 → #28	25 Jan 2019 → 07 Feb 2020
#13	#32 → #48	#1 → #31	26 Jan 2019 → 08 Feb 2020
#14	#38 → #48	#1 → #37	27 Jan 2019 → 09 Feb 2020
#15	#40 → #48	#1 → #39	28 Jan 2019 → 10 Feb 2020
#16	#43 → #48	#1 → #42	29 Jan 2019 → 11 Feb 2020
#17	#46 → #48	#1 → #45	02 Feb 2019 → 15 Feb 2020
#18	#47 → #48	#1 → #46	05 Feb 2019 → 18 Feb 2020
#19**	#49 → #49	#1 → #48	
#20†	#50 → #55	#1 → #49	24 Mar 2019 → 06 Apr 2020

*In Fig.4 from the main text, points are numbered from left to right.
**Since there is only one genome in this time window, we cannot estimate a distance among the infected population, so genome #49 was not used.
† This point was not included in Fig.4 because it is lacking more than one month of genetic information between points #18 and #19, therefore the distance among the recovered population cannot be well inferred.