

Infectivity Table ID	Isolate	Resource environment	Phage Exposure	Days in Resource Environment	Days exposed to phage	calculated resistance			predicted mutations via <i>breseq</i>		
						average	against PL phage	against NL phage	Total	non- synonymous point mutations	synonymous point mutations
1	WH7803 ¹	PL	+Ph	0	0	0	0	0			
2	03N1S1 ²	NL	-Ph	134	9						
3	01N2S4 ¹	NL	+Ph	119	0	0.323	0.380	0.261	1	0	1
4	01N3S3 ¹	NL	+Ph	119	0	0.323	0.400	0.239	5	4	1
5	01N5S4 ¹	NL	+Ph	119	0	0.323	0.400	0.239	4	3	1
6	03N2S5 ¹	NL	+Ph	134	9	0.313	0.360	0.261	0	0	0
7	03N3S2 ¹	NL	+Ph	134	9	1.000	1.000	1.000	3	2	1
8	03N3S4 ¹	NL	+Ph	134	9	0.298	0.375	0.217	3	2	1
9	03N5S2 ²	NL	+Ph	134	9	0.287	0.375	0.196	6	4	2
10	05N2S5 ¹	NL	+Ph	148	23	1.000	1.000	1.000	0	0	0
11	05N3S3 ¹	NL	+Ph	148	23	1.000	1.000	1.000	5	4	1
12	16N5S4 ¹	NL	+Ph	225	100	1.000	1.000	1.000	4	2	2
13	19N3S4 ¹	NL	+Ph	254	129				4	3	1
14	21N2S3 ²	NL	+Ph	291	166	0.500	0.960	0.000	5	4	1
15	21N3S2 ²	NL	+Ph	291	166	0.000	0.000	0.000	5	4	1
16	01P3S1 ¹	PL	-Ph	119	0	0.340	0.396	0.283	5	3	0
17	03P3S5 ¹	PL	-Ph	134	0	0.362	0.354	0.370	3	2	1
18	05P3S1 ¹	PL	-Ph	148	0	0.292	0.300	0.283	6	5	1
19	12P3S4 ¹	PL	-Ph	197	0	1.000	1.000	1.000	7	5	2

20	16P3S2 ¹	PL	-Ph	225	0	1.000	1.000	1.000	2	1	1
21	19P3S4 ¹	PL	-Ph	254	0	1.000	1.000	1.000	3	2	0
22	21P3S4 ²	PL	-Ph	291	0	0.358	0.449	0.261	3	3	0
23	01P4S5 ¹	PL	+Ph	119	0	0.309	0.354	0.261	2	0	2
24	01P5S1 ¹	PL	+Ph	119	0	0.367	0.435	0.295	3	2	1
25	03P2S4 ²	PL	+Ph	134	9	0.316	0.367	0.261	4	3	1
26	03P5S3 ¹	PL	+Ph	134	9	0.415	0.479	0.348	3	2	1
27	05P2S1 ¹	PL	+Ph	148	23	0.990	1.000	0.978	3	1	2
28	05P2S2 ¹	PL	+Ph	148	23	1.000	1.000	1.000	0	0	0
29	05P4S4 ¹	PL	+Ph	148	23	1.000	1.000	1.000	5	4	1
30	05P5S4 ¹	PL	+Ph	148	23	0.354	0.400	0.304	0	0	0
31	12P2S5 ¹	PL	+Ph	197	72	1.000	1.000	1.000	0	0	0
32	12P4S2 ¹	PL	+Ph	197	72	1.000	1.000	1.000	0	0	0
33	16P5S2 ¹	PL	+Ph	225	100	1.000	1.000	1.000	0	0	0
34	19P5S2 ¹	PL	+Ph	254	129	1.000	1.000	1.000	3	1	2
35	21P2S4 ²	PL	+Ph	291	166				10	7	3
36	21P4S2 ²	PL	+Ph	291	166	1.000	1.000	1.000	32	17	15
37	21P5S1 ²	PL	+Ph	291	166	0.926	0.918	0.935	5	4	1

¹ 100 bp reads on Illumina HiSeq; ² 250 bp paired end reads on Illumina MiSeq