

Dataset 3: Manual curation of within-isolate polymorphisms. Position is the nucleotide position in the corresponding de novo consensus sequence, length is size of the mutation, freq. is the frequency of the mutation (count/coverage), F./R. is the ratio of reads mapping in the forward to reverse orientations, avg. score is the average Phred score, and manual curation gives the results of inspections of the read mappings.

Virus	Position	Class	Length	Reference	New	Count	Coverage	Freq.	F./R.	Avg. Score	Manual curation
BNG	10396	Deletion	1	T	-	221	3915	5.645	0.457	36.742	Artefact repeated T stretch
	10396	Insertion	1	-	T	135	3867	3.491	0.431	37.733	Artefact repeated T stretch
	14399	Insertion	1	-	T	1277	3392	37.647	0.487	37.288	Artefact repeated T stretch
	14399	Deletion	1	T	-	84	3503	2.398	0.447	36.702	Artefact repeated T stretch
	29118	Deletion	1	A	-	106	3447	3.075	0.433	36.434	Artefact repeated A stretch
	35000	SNV	1	C	A	155	3881	3.994	0.442	37.465	Authentic
	35202	SNV	1	C	T	1623	3455	46.975	0.500	37.212	Authentic
	40062	Deletion	1	A	-	173	2940	5.884	0.383	36.457	Artefact repeated A stretch
	41180	SNV	1	G	A	60	2910	2.062	0.478	36.967	Authentic
	45843	Deletion	3	TAG	-	92	3669	2.507	0.472	36.935	Artefact repeated T stretch
	54562	Insertion	1	-	A	792	3571	22.179	0.492	37.556	Artefact repeated A stretch
	54562	Deletion	1	A	-	123	3818	3.222	0.485	36.333	Artefact repeated A stretch
	68688	Deletion	2	AC	-	168	3577	4.697	0.451	37.015	Artefact repeat region
	94442	Deletion	1	T	-	245	4343	5.641	0.436	36.878	Artefact repeated T stretch
	97803	SNV	1	C	T	217	3219	6.741	0.271	37.230	Artefact repeat region
	97957	Deletion	3	TCG	-	364	1382	26.339	0.403	37.357	Artefact repeat region
	97961	Deletion	14	CCACGTTTCGATCAT	-	382	1354	28.213	0.413	37.370	Artefact repeat region
	97977	SNV	1	A	C	562	2375	23.663	0.379	37.527	Artefact repeat region
	97977	Deletion	2	AT	-	341	2427	14.050	0.482	37.388	Artefact repeat region
	97978	Deletion	1	T	-	1505	2427	62.011	0.387	36.747	Artefact repeat region
	97979	SNV	1	A	T	558	2467	22.619	0.376	37.427	Artefact repeat region
	104686	Insertion	1	-	A	133	4810	2.765	0.477	37.534	Artefact repeated A stretch
	110733	Deletion	1	T	-	313	4491	6.969	0.427	36.572	Artefact repeated T stretch
	110733	Insertion	1	-	T	98	4461	2.197	0.415	37.153	Artefact repeated T stretch
	111904	SNV	1	C	T	407	3822	10.649	0.493	37.314	Authentic
	112846	Insertion	1	-	T	230	3989	5.766	0.434	37.626	Artefact repeated T stretch
	112846	Deletion	1	T	-	105	4049	2.593	0.458	36.724	Artefact repeat region
116029	Deletion	3	GAT	-	89	4360	2.041	0.439	36.647	Artefact repeated GAT sequence	
TAX1	3227	Deletion	2	GT	-	386	4894	7.887	0.471	35.933	Artefact repeated region
	10393	Insertion	1	-	T	110	4637	2.372	0.459	37.436	Artefact repeated T stretch
	16680	Deletion	2	TA	-	451	4992	9.034	0.453	36.230	Artefact repeated region
	16680	Insertion	2	-	TA	263	4463	5.893	0.389	37.736	Artefact repeated region
	16680	Deletion	4	TATA	-	109	5245	2.078	0.393	36.770	Artefact repeated region
	26850	Deletion	1	T	-	238	5251	4.532	0.476	36.882	Artefact repeated T stretch
	26850	Insertion	1	-	T	106	5185	2.044	0.482	37.585	Artefact repeated T stretch
	29143	Deletion	1	A	-	151	4594	3.287	0.381	36.728	Artefact repeated A stretch
	45848	Deletion	3	TAG	-	153	5202	2.941	0.434	37.013	Artefact related to TAG repeats
	55296	Deletion	1	A	-	161	4978	3.234	0.495	37.366	Artefact repeated region
	68638	Deletion	2	AC	-	200	3684	5.429	0.424	36.700	Artefact repeated region
	91564	Deletion	3	GAC	-	89	4095	2.173	0.418	36.921	Artefact repeated region
	94483	Deletion	1	T	-	298	5559	5.361	0.422	36.990	Artefact repeated T stretch
	94483	Insertion	1	-	T	117	5491	2.131	0.452	37.179	Artefact repeated T stretch
	97943	Insertion	1	-	A	513	544	94.301	0.499	36.690	Artefact repeated region.
	97943	Insertion	1	-	C	27	544	4.963	0.444	37.333	Artefact repeated region
	97944	SNV	1	T	G	540	544	99.265	0.494	36.157	Artefact repeated region.
	98204	SNV	1	C	A	416	2995	13.890	0.436	35.007	Authentic
	113154	Insertion	1	-	T	1961	5016	39.095	0.436	37.303	Artefact repeated T stretch
	115768	Deletion	3	TAC	-	166	6201	2.677	0.476	37.404	Artefact related to TAC repeats
	119268	Deletion	2	CA	-	177	5444	3.251	0.492	36.836	Artefact repeated region
	120114	Deletion	1	T	-	177	6079	2.912	0.477	37.249	Artefact repeated T stretch