Supplementary material

Table S1: Primer set used for long fragment analysis of the PPRV genome

Fragment 1 (4050 bp) *PPRV-3F* CAAACAAAGTTGGGTAAGGA *PPRV-4053R* TTCTCCCATGAGCCGACTATGTA
Fragment 2 (3663 bp) *PPRV-3394F* TATTACAAAAAACTTAGGAGCAAGGG *PPRV-7057R* CAGCAGCATATTAATGTGACAAG
Fragment 3 (3816 bp) *PPR-6025F* CTTGCAAATAAGGAGACCATACT *PPRV-9841R* GGCATATATGGGACTGTTCTTT
Fragment 4 (3800 bp) *PPRV-9247F* CACAACCCAGCCAACAATGTTAT *PPRV-13066R* GCTAGCATCCAAGCTTCACTCCATGA
Fragment F5 (3335 bp) *PPR-12607F* CGCCTTTCCAATTATGATTA *PPRV-15942R* GAGACAAAGCTGGGAATAGA

Table S2: Pairwise Manhattan distances calculated based on the base frequencies and the consensus sequences (diagonal from top/left to bottom/right highlighted in bold), the base frequencies in the populations (above the diagonal), or the consensus sequences (below the diagonal), respectively

	WTcons	P47CHS1	P50	P58	P62	P65	P67	P69	P70	P75	Vaccin	P75C5	P75C10	P80	P85	P90	P99	P130	P149
WTcons	**0**	49.7	39.8	62.7	52.9	53.8	46.1	61.2	72.7	58.7	59.2	71.1	59.4	50.8	60.9	60.5	61.4	69.1	62.9
P47CHS1	28	**32.6**	36.4	43.8	41.9	39.3	35.3	48.4	53.5	34.9	40.9	54.4	43.9	49.8	38.1	52.2	48.6	48.9	48.8
P50	24	4	**16.1**	43.5	36.6	31.3	24.2	46.1	54.01	40.3	39.9	53.9	42.2	34.4	43.6	41.5	46.9	53.7	45.3
P58	32	12	8	**36.7**	34.4	31.4	32.6	29.3	44.7	25.7	26.2	47.3	37.6	48.1	38.3	54.5	38.9	49.3	44.2
P62	32	12	8	4	**25.5**	26.6	22.2	32.9	42.5	27.1	27.5	41.6	30.04	34.6	31.6	45.9	33.29	41.8	34.4
P65	32	12	8	4	0	**22.6**	17.2	32.3	44.7	29.9	30.3	43.7	32.1	33.3	32.7	43.1	36.1	42.2	34.8
P67	32	12	8	4	0	0	**14.3**	31.23	38.9	25.03	24.8	39.4	27.4	24.3	28.8	34.7	31.7	38.5	30.4
P69	32	12	8	4	0	0	0	**37.3**	35.1	25.1	26.7	47.7	36.7	44.8	39.1	51.6	34.4	49.7	43.2
P70	32	12	8	4	0	0	0	0	**44.9**	30.7	39.1	59.3	49.4	52.5	43.7	51.8	48.2	51.9	53.8
P75	32	12	8	4	0	0	0	0	0	**30.9**	17.2	38.6	28.5	40.3	23.4	38.7	29.8	34.9	35.9
Vaccin	32	12	8	4	0	0	0	0	0	0	**31.7**	36.8	23.7	33.9	28.4	47.3	31.003	42.5	36.3
P75C5	46	26	22	18	14	14	14	14	14	14	14	**38.2**	24.1	47.5	29.1	61.3	46.9	54.3	48.6
P75C10	42	22	18	14	10	10	10	10	10	10	10	4	**28.3**	30.7	22.8	51.1	36.1	43.7	37.01
P80	40	20	16	12	8	8	8	8	8	8	8	10	6	**23.6**	36.3	41.02	46.1	1	44.9
P85	38	18	14	10	6	6	6	6	6	6	6	8	4	2	**31.2**	44.3	38.8	36.3	37.5
P90	34	14	10	6	2	2	2	2	2	2	2	16	12	6	8	**34.7**	48.01	47.9	51.8
P99	38	18	14	10	6	6	6	6	6	6	6	20	16	14	12	8	**36.9**	41.1	32.4
P130	48	28	24	20	16	16	16	16	16	16	16	30	26	24	22	18	10	**40.45**	28.4
P149	44	24	20	16	12	12	12	12	12	12	12	26	22	20	18	14	6	4	**23.1**

P47CHS1: Passage 47 on Vero cells + one passage on CHS cells; P50: 50th passage on Vero cells (like other Ps… in these plots)

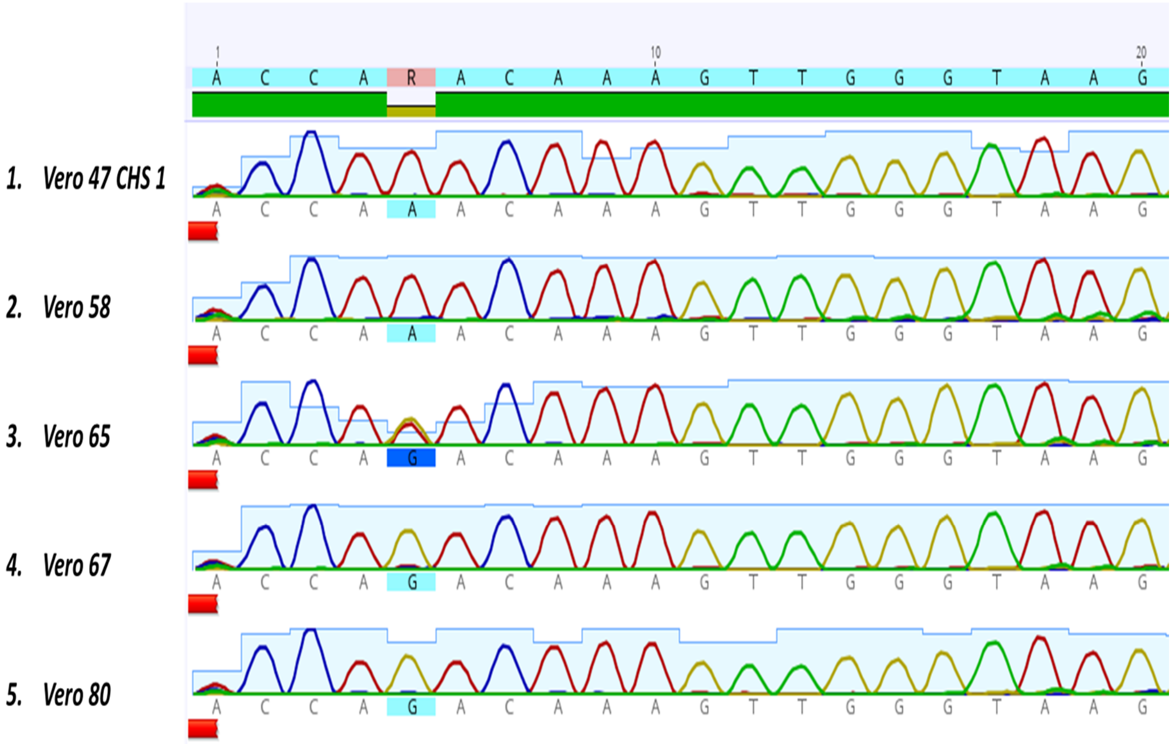

Figure S1: Chromatogram alignment of the RACE PCR Sequencing. As can be seen in the figure, we observed a double peak on the 5th position of the 65th passage on Vero cells.

Figure S2: Variants appeared and/or disappeared during cell passages. The number at the top of each histogram shows its position in the genome. Orange bars represent the alternative variant, blue bars represent the wild version.