Summary of unique recombination events identified by the Recombination Detection Program v.3.31 (RDP3)

RDP, GENECONV, Bootscan, Maxchi, Chimera, and SiScan, implemented in RDP3, were used for the automated scanning of SMV sequence alignments.

I. Results summary for P1 sequence alignment recombination analysis.

Isolates are identified by their respective Genebank accession numbers (please see Additional file 1 for the list of all analyzed isolates).

Event number	Breakpoint position in recombinant sequence		Recombinant Sequence(s)	Parental sequence(s)		Detection methods implemented in RDP3 (see RDP3 reference for details)					
	Begin	End		Minor	Major	RDP	GENECONV	Bootscan	Maxchi	Chimaera	SiSscan
1 (1)	23*	351	AJ628758	AJ628759 AJ628761 AJ628760	AJ628762	2.00E-07	4.11E-05	1.05E-04	8.38E-08	6.91E-09	1.24E-16
2 (2)	156	334	AF200538 AF200555 AF200544	AF200535	AJ639654 AJ639653 AJ639651 AJ639647 AJ558194 AF200567 AF200564 AF200561	NS	NS	NS	NS	NS	2.39E-05
3 (3)	547	727	AF200535 AF200541	AF200550	AF200567 AJ639653 AJ639647 AF200564	NS	NS	NS	NS	NS	1.44E-03

* = The actual breakpoint position is undetermined (it was most likely overprinted by a subsequent recombination event).

Minor Parent = Parent contributing the smaller fraction of sequence.

Major Parent = Parent contributing the larger fraction of sequence.

Unknown = Only one parent and a recombinant need be in the alignment for a recombination event to be detectable. The sequence listed as unknown was used to infer the existance of a missing parental sequence.

NS = No significant P-value was recorded for this event using this method.

II. Results summary for CP sequence alignment recombination analysis.

Isolates are identified by their respective Genebank accession numbers (please see Additional file 1 for the list of all analyzed isolates).

Event number	Breakpoint position in recombinant sequence		Recombinant Sequence(s)	Parental sequence(s)		Detection methods implemented in RDP3 (see RDP3 reference for details)					
	Begin	End		Minor	Major	RDP	GENECONV	Bootscan	Maxchi	Chimaera	SiSscan
1 (5)	2048	2603*	X96665	DQ517429 DQ517432 DQ517427 AY216485 AY216481 AF200584 AF200557 AF200552 AF200546 AF200540 AF200537	AY216483 X63771 DQ517431 DQ517430 DQ517428 AY216489 AY216487 AY216479 AB100448 AB100447 AB100445 AB100444 AB085900 AF200581 AF200578 AF200572 AF200563 AF200560 AF200554 AF200549 AF200543 D88615	4.08E-04	6.06E-03	1.76E-04	3.38E-05	5.17E-04	5.35E-09
2 (8)	101	414	AB206827	DQ517429	AB181493	NS	NS	NS	NS	NS	8.90E-04

			AB206829 AB206828 AB100446 D88616	AF200537	AB206834 AB206833 AB206832 AB206831 AB206830 AJ609298						
3 (9)	84	599	AF200566 AB206834 AB206833 AB206832 AB206831 AB206830 AB181493 AY799852 AJ609298 AF200569	AF200563 AY216487 AY216483	AY216481 AY216485 AF200584	NS	NS	NS	3.42E-05	2.56E-03	4.86E-04
4 (10)	541	795*	AB100444	AB181492	AB100447	NS	NS	NS	NS	9.73E-03	NS

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NS = No significant P-value was recorded for this event using this method.

III. Results summary for the recombination analysis of of full-length sequence alignment.
Isolates are identified by their names, as used throughout the manuscript (please see Additional file 1 for accession numbers and the list of all analyzed isolates).

Event number	Breakpoint position in recombinant sequence Begin	End	Recombinant Sequence(s)	Parental sequence(s) Minor	Major	ed in RDP3 (see RDP3 reference for details) RDP	GENECONV	Bootscan	Maxchi	Chimaera	SiSscan
1 (1)	6959	9335	HZ HH5	Unknown (CN18)	L G7H G2 G5 N L-RB	9.57E-42	5.34E-43	1.02E-47	9.79E-23	2.94E-21	1.61E-19
2 (2)	**4297 ('w', #**	**5484 ('x')**	**G5** HH5 HZ	G7d G7f Aa Aa15-M2 G7x	G7H G2 N HH5 HZ L L-RB	4.81E-33	6.90E-10	4.72E-32	5.25E-15	1.51E-16	2.93E-12
3 (3)	**5581* ('y')**	**6351 ('z', #)**	**G7H** HH5 HZ	CN18 G7f Aa Aa15-M2 G7d G7x HH5	G5 G2 N L L-RB	1.82E-25	4.35E-17	1.14E-24	1.58E-12	2.34E-12	3.63E-16
4 (4)	6972	9350	CN18	L G7H G2 G5 N L-RB	Aa G7f Aa15-M2 G7d G7x	7.21E-22	1.99E-09	1.19E-17	1.79E-13	3.49E-15	7.90E-18
5 (5)	3148	4290	CN18	Aa G7f	HH5	8.47E-14	1.09E-06	1.51E-13	5.21E-13	8.63E-10	6.68E-17

				Aa15-M2 G7d G7x							
6 (6)	0*	109	CN18	Unknown (G5) Unknown(G7H) Unknown(G2) Unknown(N) Unknown(Aa) Unknown(Aa15-M2) Unknown(HH5) Unknown(HZ) Unknown(L) Unknown(L-RB)	G7d G7f Aa Aa15-M2 G7x	4.49E-10	3.86E-13	2.23E-07	1.14E-03	1.02E-02	NS
7 (7)	47*	2681	Aa Aa15-M2	L G7H G2 G5 N HH5 HZ L-RB	G7d G7f G7x	1.46E-07	NS	NS	4.46E-10	7.31E-11	6.16E-21
8 (8)	4862	5468*	HH5 G5 G7f Aa Aa15-M2 G7d G7x HZ	CN18 G5 Aa15-M2	G7H G2 N L L-RB	1.30E-04	7.93E-05	1.53E-09	2.97E-09	7.77E-10	1.77E-10
9 (9)	5554*	6971*	CN18 HH5 HZ	G7d G7f Aa Aa15-M2 G7x	N G7H G2 L L-RB	6.32E-11	6.52E-07	8.99E-05	2.41E-08	7.48E-08	3.74E-10
10 (10)	163*	3147*	CN18	G7H	Unknown (L) Unknown(G2) Unknown(N) Unknown(L-RB)	NS	NS	2.78E-02	7.52E-10	1.17E-06	3.03E-09
11 (11)	**8852 ('e')**	**9021 ('f')**	**G7f**	N G2 L L-RB	G7x Aa Aa15-M2 G7d	NS	1.40E-06	1.26E-07	NS	NS	NS
12 (12)	4933*	4951*	G2	Unknown (CN18) Unknown(G7f) Unknown(Aa) Unknown(Aa15-M2) Unknown(G7d) Unknown(G7x)	L G7H N L-RB	NS	3.93E-07	NS	NS	NS	NS
13 (13)	9342*	25*	HH5 HZ	Unknown (Aa) Unknown(Aa15-M2)	N G2 G5 L L-RB	1.99E-02	NS	4.52E-04	5.16E-03	7.62E-03	NS
14 (14)	**5108* ('a')**	**5258 ('b')**	**G7f**	G2 G7H	G7x Aa	NS	4.75E-04	2.91E-03	3.40E-03	3.34E-03	NS

				N L L-RB	Aa15-M2 G7d						
15 (15)	**6024 ('c')**	**6147 ('d')**	**G7f**	N G2 L L-RB	G7x Aa Aa15-M2 G7d	NS	9.27E-03	1.44E-03	NS	NS	NS
16 (16)	4012	4097	G2	G7d G7f Aa Aa15-M2 G7x	N L	NS	3.41E-03	NS	NS	NS	NS
17 (17)	4296*	4481	G7H G2 N L L-RB	Unknown (CN18)	Aa15-M2 Aa	3.77E-02	NS	1.60E-02	NS	NS	2.86E-03

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Notes on manual verification of recombiantion events in full length sequences:
Manually verified recombination events are shown in bold font (events 2, 3, 11, 14, 15)
Notation, used in the manuscript, for the recombination sites identified manually is indicated within brackets for each recombination event.
= small disagreement between the location of recombination site found manually and by RDP3.
Analysis of specific sites supporting recombination events supported the recombinaiton event positions determined in manual analyses.

The RDP listed all potential parental and recombinant sequences (i.e. all sequences in which recombination signature was apparent). The most likely pattern of recombination, including the most likely parental isolates or isolate groups, was detected by manual recombination analysis. This analysis also took into consideration the histories of the isolates in determining the identities of parental sequences. For instance, the same informative sites supported G2 and N as the minor parent of G7f between its recombination sites. However, because sequencing of isolates G2 and G7f was reported at the same time and the isolates at some point may have come into contact, we proposed G2 as the minor parent of G7f. However, isolate N was also a possible parent. Conclusions about parental isolate identities thus often apply to the origin of the sequence fragments on the level of isolate groups. Precise identification of the parental isolate sequences requires additional information than what was available for our analysis and a controlled environment where only certain isolates are allowed to come into contact, which is not what usually occures in the field.