Appendix

Table A1: Detailed results of the SNP analysis

List of all validated SNPs found in the experiment. SNPs were called using LoFreq algorithm and further filtered: only the SNPs found in both technical replicates were considered reliable and are listed in the table. The p-values reported by LoFreq designate the probability of observed SNP arising as a sequencing error and are modelled using Poisson–binomial distribution, including site specific error rate and sequencing depth into the calculations.

LoFreq detected 116 SNPs in sample VP1 and 120 in sample VP2; 103 SNPs were common for both replicates. 154 SNPs were detected in sample sRNA1 and 198 in sample sRNA2; 121 SNPs were common for both sRNA replicates. 81 SNPs were common for both pools (VP and sRNA).

Position: position in PVY genome; *SNP*: observed SNP (consensus nt > variant nt); *gene*: corresponding gene or UTR, *consensus amino acid*; *variant amino acid* and *BLOSUM62*: score for corresponding amino acid change. Minus (-) designates that SNP was not found in the pool. NA: SNP is within UTR region and is thus without amino acid annotations. *%*: relative frequency in corresponding sample; *coverage*: coverage for the site in corresponding sample; *p-value (LoFreq)*: p-value from the LoFreq analysis.

						sRNA 1			**sRNA 2**			**VP 1**			**VP 2**		
position	**SNP**	**gene**	**consensus amino acid**	**variant amino acid**	**BLOSUM 62**	**%**	**coverage**	**p-value (Lofreq)**	**%**	**coverage**	**p-value (Lofreq)**	**%**	**coverage**	**p-value (Lofreq)**	**%**	**coverage**	**p-value (Lofreq)**
22	A>C	5UTR	NA	NA	NA	0.42	6209	3.3E-20	0.53	6262	1.0E-27	-	-	-	-	-	-
27	A>T	5UTR	NA	NA	NA	1.42	7459	1.1E-121	1.47	7429	7.8E-127	-	-	-	-	-	-
117	A>G	5UTR	NA	NA	NA	0.20	15703	1.5E-13	0.13	15342	2.0E-08	0.33	3374	6.8E-10	0.38	3450	1.1E-10
150	T>G	5UTR	NA	NA	NA	1.04	11845	1.4E-100	0.91	11688	9.2E-90	1.11	1885	3.0E-24	1.07	1954	1.9E-23
321	A>T	P1	Q	L	-2	10.90	9397	0.0E+00	10.44	8804	0.0E+00	12.02	4660	0.0E+00	12.05	4525	0.0E+00
342	G>T	P1	R	M	-1	24.46	13370	0.0E+00	25.44	13179	0.0E+00	7.52	8630	0.0E+00	7.45	8378	0.0E+00
403	T>A	P1	T	T	5	0.06	41496	1.4E-06	0.06	43300	8.2E-07	-	-	-	-	-	-
406	T>C	P1	D	D	6	-	-	-	-	-	-	0.12	17021	2.9E-08	0.19	16034	1.7E-17
481	A>G	P1	S	S	4	0.26	10257	6.2E-16	0.24	9818	1.8E-13	0.17	10582	2.6E-10	0.21	9844	1.1E-13

499	C>T	P1	I	I	4	0.17	18156	2.4E-09	0.22	18552	3.3E-19	0.21	12137	7.9E-14	0.21	11496	2.8E-14
635	A>G	P1	I	V	3	0.40	6537	7.7E-23	0.31	6492	1.1E-16	-	-	-	-	-	-
652	A>G	P1	Q	Q	5	1.38	3041	5.7E-48	1.31	2668	3.9E-40	0.51	2144	4.8E-10	0.56	2159	6.1E-10
815	C>T	P1	R	C	-3	0.14	20961	2.1E-12	0.10	21762	1.9E-07	0.16	16337	1.6E-11	0.15	15494	1.3E-09
844	G>A	P1	K	K	5	0.42	15354	7.6E-47	0.33	15539	2.9E-35	0.48	14490	4.4E-52	0.45	13765	4.0E-47
909	C>T	P1	T	I	-1	-	-	-	-	-	-	0.44	4567	2.9E-09	0.34	4647	2.0E-09
982	C>T	P1	I	I	4	0.37	8113	7.4E-24	0.28	7773	3.7E-18	-	-	-	-	-	-
1074	A>G	HC-Pro	N	S	1	0.61	3924	2.9E-20	0.82	3653	1.1E-28	1.06	10585	7.5E-128	0.73	9954	1.1E-72
1318	A>G	HC-Pro	K	K	5	0.89	11891	5.4E-48	0.97	11934	6.8E-58	-	-	-	-	-	-
1549	C>T	HC-Pro	I	I	4	3.64	9170	0.0E+00	2.92	9403	0.0E+00	2.92	6081	5.0E-239	2.74	6404	4.1E-227
1795	A>G	HC-Pro	V	V	4	3.16	5493	1.2E-217	3.02	5446	4.8E-202	2.32	7504	7.7E-217	2.24	7662	3.1E-197
1855	G>A	HC-Pro	G	G	6	1.84	2061	4.3E-34	1.58	1706	1.1E-19	1.16	3261	4.8E-39	1.32	2868	5.5E-41
1866	A>G	HC-Pro	K	R	2	0.41	5411	2.1E-17	0.45	5314	5.8E-20	0.80	7889	3.8E-58	0.75	7449	3.0E-57
1885	T>C	HC-Pro	D	D	6	0.62	17591	1.1E-81	0.62	18987	8.1E-83	1.30	20478	1.5E-292	1.20	20122	1.6E-256
1993	C>T	HC-Pro	G	G	6	11.34	6943	0.0E+00	11.34	6530	0.0E+00	5.21	5557	0.0E+00	5.96	5488	0.0E+00
2002	G>A	HC-Pro	K	K	5	0.54	10090	1.2E-52	0.51	9948	2.0E-48	0.54	7267	1.4E-36	0.47	7191	9.2E-24
2025	A>G	HC-Pro	N	S	1	0.17	10512	1.4E-08	0.23	10651	2.8E-14	0.19	14457	6.8E-16	0.19	15059	4.9E-18
2036	T>C	HC-Pro	L	L	4	0.88	6791	2.7E-60	0.65	6717	4.8E-39	0.65	8824	2.9E-51	0.88	9206	1.7E-80
2230	T>C	HC-Pro	H	H	8	4.33	14505	0.0E+00	4.56	14735	0.0E+00	2.95	6565	8.6E-261	3.32	6632	1.0E-298
2254	A>G	HC-Pro	L	L	4	0.74	24185	3.6E-152	0.78	25107	1.5E-176	1.03	23358	5.9E-268	1.01	22952	6.0E-240
2266	G>A	HC-Pro	E	E	5	32.26	20793	0.0E+00	32.27	21714	0.0E+00	24.08	19199	0.0E+00	24.65	18540	0.0E+00
2368	T>A	HC-Pro	D	E	2	0.53	6197	1.4E-15	0.88	6223	7.0E-39	0.99	8307	1.8E-77	0.80	8479	7.8E-65
2480	T>C	P3	S	P	-1	0.73	12798	1.8E-71	0.66	12803	1.4E-53	1.57	21284	0.0E+00	1.42	21304	6.4E-302
2485	A>G	P3	A	A	4	0.43	16087	5.6E-54	0.36	16003	6.7E-41	0.96	21853	1.2E-222	0.98	21975	8.3E-235
2593	G>A	P3	L	L	4	25.87	6038	0.0E+00	25.09	5970	0.0E+00	50.18	6056	0.0E+00	49.53	5874	0.0E+00
2666	A>G	P3	M	V	1	13.46	5732	0.0E+00	14.44	5407	0.0E+00	29.69	1073	0.0E+00	26.31	1041	0.0E+00
2695	C>T	P3	A	A	4	15.33	9599	0.0E+00	15.79	9668	0.0E+00	15.87	1215	0.0E+00	16.26	1117	7.6E-316
2751	C>T	P3	A	V	0	0.19	9888	4.5E-11	0.19	9422	5.3E-10	-	-	-	-	-	-
2845	A>G	P3	R	R	5	0.97	12104	1.2E-88	1.07	12346	2.6E-87	-	-	-	-	-	-
2861	A>T	P3	T	S	1	0.22	8583	6.4E-12	0.29	8907	8.0E-17	0.56	4092	4.9E-24	0.61	4100	1.4E-26

2899	C>T	P3	S	S	4	0.17	22282	4.6E-14	0.19	23365	4.3E-20	-	-	-	-	-	-
2903	G>A	P3	V	I	3	0.13	24259	9.1E-14	0.11	25353	8.9E-10	-	-	-	-	-	-
2915	G>A	P3	E	K	1	0.19	8006	6.3E-07	0.21	7970	9.8E-09	0.25	11749	9.6E-19	0.34	12160	2.6E-25
2977	A>T	P3	L	F	0	1.26	1984	1.4E-27	1.04	1728	5.5E-12	0.90	3539	1.2E-31	1.09	3497	1.9E-40
2991	A>T	P3	Y	F	3	0.30	13907	1.5E-24	0.32	14135	1.6E-26	-	-	-	-	-	-
3109	C>T	P3	V	V	4	0.92	3253	7.9E-32	0.89	3367	1.9E-30	1.31	3210	4.7E-38	0.95	3146	2.2E-28
3478	A>G	P3	E	E	5	0.79	6426	1.6E-44	0.86	6286	4.1E-52	1.69	5133	6.9E-108	1.96	5096	3.1E-124
3622	C>T	6K1	V	V	4	-	-	-	-	-	-	0.55	2558	4.6E-13	0.48	2273	2.8E-08
3664	C>T	CI	D	D	6	5.70	25620	0.0E+00	6.01	27601	0.0E+00	4.69	7697	0.0E+00	4.83	7902	0.0E+00
3835	A>G	CI	E	E	5	-	-	-	-	-	-	0.14	9779	1.1E-07	0.21	9683	1.5E-13
3850	C>T	CI	T	T	5	0.35	7675	2.0E-19	0.39	7124	1.4E-16	0.78	3602	2.2E-25	0.75	3474	2.4E-27
3895	C>T	CI	D	D	6	1.22	3372	3.7E-51	1.41	3109	2.9E-54	0.56	4304	3.7E-19	0.68	4395	3.9E-31
3940	G>A	CI	L	L	4	48.24	6466	0.0E+00	49.39	6382	0.0E+00	31.90	13463	0.0E+00	32.32	12930	0.0E+00
3943	T>C	CI	P	P	7	0.25	8245	3.9E-09	0.25	8115	2.4E-11	0.16	13986	1.2E-09	0.16	13470	6.1E-10
4036	C>T	CI	F	F	6	0.39	7257	4.4E-19	0.37	7032	8.8E-20	0.36	2805	3.5E-09	0.59	2720	9.2E-13
4042	G>A	CI	K	K	5	0.28	6664	2.6E-11	0.35	6370	1.9E-16	1.03	2039	1.4E-19	0.75	1997	1.5E-16
4093	C>T	CI	I	I	4	0.50	5651	6.9E-23	0.68	5753	1.8E-35	-	-	-	-	-	-
4118	C>T	CI	L	L	4	-	-	-	-	-	-	0.18	8802	2.8E-08	0.18	8673	1.1E-09
4220	C>T	CI	L	L	4	0.75	11392	5.6E-79	0.66	11151	1.1E-69	0.26	5391	1.0E-10	0.47	5294	2.4E-22
4318	A>G	CI	L	L	4	0.35	3959	4.9E-11	0.43	3497	8.2E-13	1.39	1649	6.8E-21	1.52	1637	4.0E-24
4489	T>C	CI	V	V	4	8.22	6567	0.0E+00	8.52	6510	0.0E+00	8.87	11157	0.0E+00	9.10	10974	0.0E+00
4501	A>G	CI	T	T	5	6.77	11506	0.0E+00	7.01	11915	0.0E+00	8.19	10242	0.0E+00	8.06	10116	0.0E+00
4597	G>A	CI	L	L	4	0.34	14254	2.0E-30	0.33	14543	1.0E-32	-	-	-	-	-	-
4685	G>A	CI	V	I	3	0.43	3460	1.4E-12	0.43	3288	4.0E-13	-	-	-	-	-	-
4777	T>C	CI	I	I	4	1.09	5738	1.1E-51	0.74	5677	2.2E-40	0.67	9519	4.6E-65	0.49	9989	8.5E-41
5134	C>T	CI	F	F	6	6.59	4601	0.0E+00	6.66	4564	0.0E+00	3.96	1336	5.2E-76	3.98	1280	1.3E-70
5434	A>T	CI	A	A	4	25.68	4502	0.0E+00	25.89	4024	0.0E+00	47.92	4118	0.0E+00	49.35	4219	0.0E+00
5479	A>G	CI	E	E	5	0.66	9649	5.5E-61	0.75	9639	8.7E-69	0.95	5785	2.0E-59	1.22	5755	5.1E-79
5542	G>A	CI	Q	Q	5	0.18	13088	1.1E-11	0.17	13471	3.1E-11	-	-	-	-	-	-
5619	T>C	6K2	V	A	0	35.63	8148	0.0E+00	36.64	8115	0.0E+00	46.75	5025	0.0E+00	45.85	4853	0.0E+00

5659	A>G	6K2	G	G	6	-	-	-	-	-	-	0.25	12550	1.4E-16	0.31	12113	6.0E-23
5908	A>G	VPg	G	G	6	0.74	7674	2.4E-51	0.56	7529	1.0E-37	-	-	-	-	-	-
6001	C>T	VPg	I	I	4	0.37	7550	1.6E-16	0.63	7405	3.3E-37	-	-	-	-	-	-
6046	T>C	VPg	D	D	6	0.29	7709	1.4E-16	0.36	8018	4.6E-21	0.50	12298	5.6E-45	0.59	12092	7.8E-51
6326	A>G	NIa	T	A	0	0.37	11923	4.0E-22	0.43	11352	2.0E-29	-	-	-	-	-	-
6351	T>C	NIa	V	A	0	1.25	21798	3.3E-264	1.37	22737	2.5E-301	0.82	13716	3.6E-107	0.77	14248	2.8E-104
6367	T>G	NIa	S	S	4	0.77	14339	7.5E-89	0.80	14685	4.1E-85	0.67	16169	4.8E-95	0.64	16322	1.6E-93
6484	G>A	NIa	L	L	4	39.80	6576	0.0E+00	40.82	6319	0.0E+00	32.24	5307	0.0E+00	34.08	5404	0.0E+00
6703	C>T	NIa	H	H	8	41.88	4581	0.0E+00	43.10	4379	0.0E+00	25.10	12630	0.0E+00	25.92	13178	0.0E+00
6733	A>G	NIa	G	G	6	0.31	9265	1.2E-20	0.34	9355	7.7E-19	0.13	14982	5.8E-10	0.15	15030	6.7E-12
6760	G>A	NIa	G	G	6	0.54	2985	2.0E-10	0.87	2528	7.3E-17	-	-	-	-	-	-
6767	G>A	NIa	V	I	3	-	-	-	-	-	-	0.56	5763	9.1E-32	0.62	5467	9.7E-31
6840	G>A	NIa	S	N	1	32.06	8451	0.0E+00	32.00	8462	0.0E+00	23.66	7779	0.0E+00	25.17	8291	0.0E+00
6862	G>A	NIa	E	E	5	0.33	12950	4.3E-24	0.18	12982	1.1E-09	0.89	11762	2.5E-99	0.89	12116	2.0E-98
6931	G>A	NIa	K	K	5	-	-	-	-	-	-	0.40	6766	1.2E-15	0.36	6421	1.7E-12
7052	T>C	NIb	L	L	4	0.31	5876	1.2E-06	0.44	5618	1.6E-12	-	-	-	-	-	-
7089	C>T	NIb	T	I	-1	0.63	10795	2.7E-60	0.61	10560	2.1E-56	0.85	11429	4.7E-97	0.80	10910	4.8E-87
7143	A>G	NIb	D	G	-1	0.36	13205	2.3E-18	0.33	12886	6.0E-13	-	-	-	-	-	-
7206	G>A	NIb	R	K	2	1.22	1381	2.2E-11	1.06	1216	2.9E-09	0.83	3730	1.5E-18	0.70	3707	5.9E-13
7255	T>C	NIb	V	V	4	1.16	11281	4.5E-145	1.09	11560	9.1E-133	1.86	16615	0.0E+00	1.67	16419	0.0E+00
7348	C>T	NIb	T	T	5	0.51	8994	2.7E-35	0.40	8828	3.8E-24	2.18	2479	1.9E-68	1.41	2409	3.0E-43
7353	A>G	NIb	E	G	-2	0.47	7678	6.8E-29	0.38	7273	4.2E-22	2.22	2569	9.4E-76	2.09	2536	3.3E-68
7452	A>G	NIb	K	R	2	-	-	-	-	-	-	0.51	7453	1.0E-32	0.62	7596	1.5E-45
7456	G>A	NIb	E	E	5	1.73	3515	7.0E-54	2.14	3407	1.6E-76	2.17	7413	1.2E-204	2.46	7507	1.8E-225
7558	A>G	NIb	A	A	4	16.39	2291	0.0E+00	17.48	2145	0.0E+00	10.62	5704	0.0E+00	11.61	5694	0.0E+00
7640	T>C	NIb	F	L	0	1.70	6617	2.9E-119	1.48	6474	1.4E-86	-	-	-	-	-	-
7657	T>C	NIb	I	I	4	0.28	11016	6.7E-20	0.38	10843	4.2E-30	-	-	-	-	-	-
7721	C>T	NIb	L	L	4	-	-	-	-	-	-	0.37	13765	8.0E-43	0.36	13892	4.0E-40
7894	A>G	NIb	S	S	4	2.01	5870	2.7E-140	2.42	5488	1.8E-154	1.74	4369	9.2E-93	1.92	4427	1.4E-101
7933	T>C	NIb	N	N	6	1.97	1967	1.6E-41	1.91	1831	1.5E-41	1.23	2115	5.5E-26	0.80	2134	6.5E-17

7954	C>T	NIb	T	T	5	9.90	7771	0.0E+00	8.88	7637	0.0E+00	29.59	4420	0.0E+00	28.95	4391	0.0E+00
8031	T>C	NIb	I	T	-1	0.15	19697	8.4E-14	0.14	19844	1.8E-11	-	-	-	-	-	-
8083	G>A	NIb	V	V	4	0.32	10334	3.7E-21	0.28	10242	1.1E-16	-	-	-	-	-	-
8101	T>A	NIb	S	R	-1	9.44	6285	0.0E+00	9.19	5888	0.0E+00	14.46	15004	0.0E+00	14.98	14845	0.0E+00
8128	C>T	NIb	F	F	6	2.33	9062	2.5E-221	2.64	9110	2.6E-258	0.70	7597	2.3E-43	0.61	7998	2.7E-42
8135	C>G	NIb	L	V	1	1.89	21253	0.0E+00	1.79	21664	0.0E+00	-	-	-	-	-	-
8458	G>A	NIb	K	K	5	-	-	-	-	-	-	0.19	12052	1.5E-13	0.25	11526	1.0E-19
8474	A>G	NIb	T	A	0	1.02	12929	4.4E-79	1.04	13639	3.1E-79	1.13	10121	4.0E-117	1.41	10053	3.0E-166
8477	G>A	NIb	V	I	3	0.22	9695	5.4E-15	0.19	10263	7.7E-10	0.33	10862	3.9E-23	0.39	10871	6.7E-31
8610	C>T	CP	A	V	0	1.57	6869	2.4E-133	1.53	7302	2.1E-138	0.36	9120	5.5E-26	0.50	9519	2.9E-41
8630	A>G	CP	I	V	3	-	-	-	-	-	-	0.29	4198	7.2E-08	0.48	4370	1.2E-16
8635	A>G	CP	Q	Q	5	0.26	5680	2.3E-11	0.27	5609	8.2E-07	0.51	4322	8.7E-21	0.50	4613	3.7E-22
8644	C>T	CP	L	L	4	-	-	-	-	-	-	0.25	7166	2.7E-07	0.29	7593	1.8E-08
8690	C>T	CP	H	Y	2	0.09	25849	1.3E-08	0.08	26032	1.1E-06	-	-	-	-	-	-
8716	C>T	CP	I	I	4	5.28	10694	0.0E+00	5.23	10783	0.0E+00	4.85	6688	0.0E+00	4.88	6289	0.0E+00
8987	G>A	CP	V	I	3	1.36	10286	2.9E-155	1.36	10487	6.7E-165	0.99	12482	9.7E-137	1.29	12274	1.9E-183
8989	C>T	CP	V	V	4	-	-	-	-	-	-	0.23	14791	4.5E-21	0.14	14728	3.9E-09
9008	A>G	CP	I	V	3	1.30	13274	2.1E-196	1.38	13371	1.4E-215	0.71	14407	1.6E-104	0.67	14642	3.9E-98
9100	A>G	CP	E	E	5	0.26	5763	1.9E-11	0.43	5634	2.2E-20	0.51	4290	5.7E-21	0.38	4173	8.7E-15
9202	G>A	CP	R	R	5	0.89	5587	4.4E-53	0.62	5819	2.7E-36	-	-	-	-	-	-
9377	G>A	3UTR	NA	NA	NA	0.61	19488	9.4E-105	0.53	20273	2.4E-89	0.38	50405	7.1E-136	0.41	47974	1.5E-147
9405	C>T	3UTR	NA	NA	NA	2.01	1339	1.6E-30	1.42	1261	5.1E-20	1.09	12741	3.9E-168	0.90	12381	7.5E-126
9474	C>T	3UTR	NA	NA	NA	1.32	1132	3.5E-17	2.21	991	6.8E-27	3.81	2203	1.9E-79	3.64	2092	4.5E-74
9508	T>C	3UTR	NA	NA	NA	-	-	-	-	-	-	0.11	43717	4.4E-18	0.11	43513	1.2E-21
9524	T>G	3UTR	NA	NA	NA	1.75	6736	1.0E-111	1.87	6780	1.3E-125	2.00	29056	0.0E+00	2.06	30192	0.0E+00
9541	A>G	3UTR	NA	NA	NA	0.37	4281	1.3E-14	0.32	4367	5.6E-12	-	-	-	-	-	-
9613	C>T	3UTR	NA	NA	NA	-	-	-	-	-	-	0.10	25245	1.2E-08	0.12	24123	2.2E-13