

Supplement 1 Table S1. SCAR markers of *Rpi*-genes in F1 progeny and parental lines

Genotypes	<i>Genes /SCAR markers</i>									
	<i>R1</i>	<i>R2=Rpi-blb3</i>		<i>R3a</i>		<i>R3b</i>	<i>Rpi-blb 1 = Rpi-sto1</i>		<i>Rpi-vnt1.3</i>	
	R1-1205	R2-1137	R2-686	Rpi-blb3-305	R3a-1380	R3b-378	RB-226	Blb-821	Rpi-sto1-890	Rpi-vnt1.3-616
13/11-09	0	0	0	0	0	1	1	1	1	1
Сударыня	0	1	1	0	1	1	1	1	1	0
952-1	0	0	0	0	0	0	0	0	0	0
952-2	0	0	0	0	1	1	1	1	1	0
952-3	0	0	0	0	0	1	1	1	1	0
952-4	0	0	0	0	1	1	1	1	1	0
952-5	0	0	0	0	0	1	1	1	1	1
952-6	0	0	1	0	0	1	0	0	0	0
952-7	0	0	0	0	0	1	0	0	0	1
952-8	0	0	1	0	0	1	1	1	1	1
952-9	0	0	0	0	1	1	1	1	1	0
952-10	0	0	0	0	0	1	1	0	0	0
952-12	0	0	0	0	0	1	1	1	1	0
952-13	0	0	0	0	0	0	0	0	0	0
952-14	0	0	0	0	0	1	0	0	0	1
925-15	0	0	0	0	0	1	0	0	0	0

Genotypes	<i>Genes /SCAR markers</i>									
	<i>R1</i>	<i>R2=Rpi-blb3</i>		<i>R3a</i>		<i>R3b</i>	<i>Rpi-blb 1 = Rpi-sto1</i>			<i>Rpi-vnt1.3</i>
	R1-1205	R2-1137	R2-686	Rpi-blb3-305	R3a-1380	R3b-378	RB-226	Blb-821	Rpi-sto1-890	Rpi-vnt1.3-616
952-16	0	0	0	0	0	1	1	1	1	0
952-17	0	0	1	0	0	0	1	0	0	1
952-18	0	0	0	0	0	0	0	0	0	0
952-19	0	1	1	0	1	1	1	1	1	0
952-20	0	0	0	0	0	0	1	1	1	1
952-21	0	0	1	0	1	1	1	1	1	0
952-22	0	0	0	0	0	1	1	1	1	0
952-23	0	0	0	0	1	1	1	1	1	0
952-24	0	0	0	0	1	1	1	1	1	0
952-25	0	0	0	0	0	1	0	0	0	1
952-26	0	1	1	0	0	1	1	1	1	1
952-27	0	0	0	0	0	0	1	1	1	0
952-28	0	0	1	0	0	0	0	0	0	0
952-29	0	0	1	0	0	1	1	1	1	0
952-30	0	0	0	0	1	1	1	1	1	0
952-31	0	0	0	0	1	1	1	1	1	0
952-32	0	0	0	0	0	1	1	1	1	0

Genotypes	<i>Genes /SCAR markers</i>									
	<i>R1</i>	<i>R2=Rpi-blb3</i>		<i>R3a</i>		<i>R3b</i>	<i>Rpi-blb 1 = Rpi-sto1</i>			<i>Rpi-vnt1.3</i>
	R1-1205	R2-1137	R2-686	Rpi-blb3-305	R3a-1380	R3b-378	RB-226	Blb-821	Rpi-sto1-890	Rpi-vnt1.3-616
952-33	0	1	0	0	1	1	1	1	1	0
952-35	0	0	1	0	1	1	1	0	1	1
952-36	0	1	0	0	1	1	1	1	1	0
952-37	0	1	1	0	0	0	1	1	1	0
952-38	0	0	0	0	0	0	1	1	1	0
952-39	0	1	0	0	1	1	0	0	0	0
952-40	0	0	1	0	1	1	0	0	0	0
952-41	0	1	1	0	0	1	1	1	1	0
952-42	0	0	0	0	0	1	1	1	1	0
952-43	0	1	1	0	0	1	1	1	1	0
952-44	0	0	0	0	0	1	1	1	1	0
952-45	0	1	0	0	0	1	1	1	1	0
952-46	0	0	0	0	1	1	0	0	0	0
952-47	0	0	0	0	0	0	1	1	1	0
952-49	0	0	0	0	0	1	0	0	0	1
952-50	0	0	0	0	1	1	0	0	0	0
952-51	0	0	0	0	1	1	0	0	0	0

Genotypes	<i>Genes /SCAR markers</i>									
	<i>R1</i>	<i>R2=Rpi-blb3</i>		<i>R3a</i>		<i>R3b</i>	<i>Rpi-blb 1 = Rpi-sto1</i>			<i>Rpi-vnt1.3</i>
	R1-1205	R2-1137	R2-686	Rpi-blb3-305	R3a-1380	R3b-378	RB-226	Blb-821	Rpi-sto1-890	Rpi-vnt1.3-616
952-52	0	1	1	0	1	1	0	0	0	0
952-54	0	0	0	0	1	1	1	1	1	0
952-55	0	0	0	0	0	1	1	0	0	1
952-56	0	0	0	0	0	0	1	1	1	0
952-57	0	1	1	0	1	1	1	1	1	1
952-58	0	1	1	0	0	0	1	1	0	0
952-59	0	0	0	0	1	1	1	1	1	0
952-60	0	0	0	0	0	1	1	1	1	0
952-61	0	0	0	0	1	1	0	1	0	0
952-62	0	0	1	0	1	1	1	1	1	0
952-63	0	0	0	0	1	1	1	1	1	0
952-64	0	1	1	0	0	0	1	1	1	1
952-65	0	1	1	0	1	1	1	1	1	0
952-66	0	0	0	0	1	1	1	1	1	0
952-67	0	1	1	0	0	1	0	0	0	1
952-69	0	0	1	0	0	1	1	1	1	0

Figure S1. Alignment of *Rpi-vnt1* homologs and predicted amino acid sequences of *Rpi-vnt1* protein homologs

		3		102
CP047560_59492023-59491423	(1)	TTCCTCATCCTCACATTTAGAAAAAGAAATTTAAAGAAATTTAAAGGATGATGGCTGAAATTTCTCTACAGCAGTCATCAATAAATCAATAGAAATAG		
GU338312_89-700	(3)	TTCCTCATCCTCACATTTAGAAAAAGAAATTTAAAGAAATTTAAAGGATGATGCTGATATTCTTCTACAGCAGTCATCAATAAATCAATAGAAATAG		
Hybrid_13/11	(1)	TTCCTCATCCTCACATTTAGAAAAAGAAATTTAAAGAAATTTAAAGGATGATGCTGATATTCTTCTACAGCAGTCATCAATAAATCAATAGAAATAG		
FJ423044_758-1367	(1)	TTCCTCATCCTCACATTTAGAAAAAGAAATTTAAAGAAATTTAAAGGATGATGGCTGAAATTTCTCTACAGCAGTCATCAATAAATCAATAGAAATAG		
FJ423046_91-700	(1)	TTCCTCATCCTCACATTTAGAAAAAGAAATTTAAAGAAATTTAAAGGATGATGGCTGAAATTTCTCTACAGCAGTCATCAATAAATCAATAGAAATAG		
MH297492_51-660	(1)	TTCCTCATCCTCACATTTAGAAAAAGAAATTTAAAGAAATTTAAAGGATGATGGCTGAAATTTCTCTACAGCAGTCATCAATAAATCAATAGAAATAG		
Consensus	(3)	TTCCTCATCCTCACATTTAGAAAAAGAAATTTAAAGAAATTTAAAGGATGATGGCTGAAATTTCTCTACAGCAGTCATCAATAAATCAATAGAAATAG		
		103		202
CP047560_59492023-59491423	(96)	CTGCAAAATCTACTCTTTCAAGAAGGTACCGCGTTTATATTGGTTGAAAGAGGACATCGATTGGCTCCAGAGAGAAATGAGACACATTCGATCATATGTAGA		
GU338312_89-700	(103)	CTGCAAAATCTACTCTTTCAAGAAGGTACCGCGTTTATATTGGTTGAAAGAGGACATCGATTGGCTCCAGAGAGAAATGAGACACATTCGATCATATGTAGA		
Hybrid_13/11	(101)	CTGCAAAATCTACTCTTTCAAGAAGGTACCGCGTTTATATTGGTTGAAAGAGGACATCGATTGGCTCCAGAGAGAAATGAGACACATTCGATCATATGTAGA		
FJ423044_758-1367	(103)	CTGCAAAATCTACTCTTTCAAGAAGGTACCGCGTTTATATTGGTTGAAAGAGGACATCGATTGGCTCCAGAGAGAAATGAGACACATTCGATCATATGTAGA		
FJ423046_91-700	(101)	CTGCAAAATCTACTCTTTCAAGAAGGTACCGCGTTTATATTGGTTGAAAGAGGACATCGATTGGCTCCAGAGAGAAATGAGACACATTCGATCATATGTAGA		
MH297492_51-660	(101)	CTGCAAAATCTACTCTTTCAAGAAGGTACCGCGTTTATATTGGTTGAAAGAGGACATCGATTGGCTCCAGAGAGAAATGAGACACATTCGATCATATGTAGA		
Consensus	(103)	CTGCAAAATCTACTCTTTCAAGAAGGTACCGCGTTTATATTGGTTGAAAGAGGACATCGATTGGCTCCAGAGAGAAATGAGACACATTCGATCATATGTAGA		
		203		302
CP047560_59492023-59491423	(196)	CAATGCAAGGCAAGGAAGTTGGAGGCGATTCAAGGGTAAAAAAGTTAT		TAAAAAGATATTCAACAACATGGCAGGTGATGTGGAGGATCTATTAGATGAG
GU338312_89-700	(203)	CAATGCAAGGCAAGGAAGTTGGAGGCGATTCAAGGGTAAAAAAGTTAT		TAAAAAGATATTCAACAACATGGCAGGTGATGTGGAGGATCTATTAGATGAG
Hybrid_13/11	(201)	CAATGCAAGGCAAGGAAGTTGGAGGCGATTCAAGGGTAAAAAAGTTAT		TAAAAAGATATTCAACAACATGGCAGGTGATGTGGAGGATCTATTAGATGAG
FJ423044_758-1367	(203)	CAATGCAAGGCAAGGAAGTTGGAGGCGATTCAAGGGTAAAAAAGTTAT		TAAAAAGATATTCAACAACATGGCAGGTGATGTGGAGGATCTATTAGATGAG
FJ423046_91-700	(201)	CAATGCAAGGCAAGGAAGTTGGAGGCGATTCAAGGGTAAAAAAGTTAT		TAAAAAGATATTCAACAACATGGCAGGTGATGTGGAGGATCTATTAGATGAG
MH297492_51-660	(201)	CAATGCAAGGCAAGGAAGTTGGAGGCGATTCAAGGGTAAAAAAGTTAT		TAAAAAGATATTCAACAACATGGCAGGTGATGTGGAGGATCTATTAGATGAG
Consensus	(203)	CAATGCAAGGCAAGGAAGTTGGAGGCGATTCAAGGGTAAAAAAGTTAT		TAAAAAGATATTCAACAACATGGCAGGTGATGTGGAGGATCTATTAGATGAG
		303		402
CP047560_59492023-59491423	(296)	TTTCTTCCAAAAATTCACAATCCAATAAGTTCATTGTTGTCCTTAAGAC		GGTTTCTTTTGCCGATGAGTTTGCTATGGAGATTGAGAAGATAAAAAGAA
GU338312_89-700	(303)	TTTCTTCCAAAAATTCACAATCCAATAAGTTCATTGTTGTCCTTAAGAC		GGTTTCTTTTGCCGATGAGTTTGCTATGGAGATTGAGAAGATAAAAAGAA
Hybrid_13/11	(301)	TTTCTTCCAAAAATTCACAATCCAATAAGTTCATTGTTGTCCTTAAGAC		GGTTTCTTTTGCCGATGAGTTTGCTATGGAGATTGAGAAGATAAAAAGAA
FJ423044_758-1367	(303)	TTTCTTCCAAAAATTCACAATCCAATAAGTTCATTGTTGTCCTTAAGAC		GGTTTCTTTTGCCGATGAGTTTGCTATGGAGATTGAGAAGATAAAAAGAA
FJ423046_91-700	(301)	TTTCTTCCAAAAATTCACAATCCAATAAGTTCATTGTTGTCCTTAAGAC		GGTTTCTTTTGCCGATGAGTTTGCTATGGAGATTGAGAAGATAAAAAGAA
MH297492_51-660	(301)	TTTCTTCCAAAAATTCACAATCCAATAAGTTCATTGTTGTCCTTAAGAC		GGTTTCTTTTGCCGATGAGTTTGCTATGGAGATTGAGAAGATAAAAAGAA
Consensus	(303)	TTTCTTCCAAAAATTCACAATCCAATAAGTTCATTGTTGTCCTTAAGAC		GGTTTCTTTTGCCGATGAGTTTGCTATGGAGATTGAGAAGATAAAAAGAA
		403		502
CP047560_59492023-59491423	(396)	GAGTTGCTGATATTGACCGGTGAAGGACAACCTTACAGATCAAGTACAAATAGTGATGATTGCATTCCATTGGACCGAGAGAAGATTGTT		
GU338312_89-700	(403)	GAGTTGCTGATATTGACCGGTGAAGGACAACCTTACAGATCAAGTACAAATAGTGATGATTGCATTCCATTGGACCGAGAGAAGATTGTT		
Hybrid_13/11	(401)	GAGTTGCTGATATTGACCGGTGAAGGACAACCTTACAGATCAAGTACAAATAGTGATGATTGCATTCCATTGGACCGAGAGAAGATTGTT		
FJ423044_758-1367	(403)	GAGTTGCTGATATTGACCGGTGAAGGACAACCTTACAGATCAAGTACAAATAGTGATGATTGCATTCCATTGGACCGAGAGAAGATTGTT		
FJ423046_91-700	(401)	GAGTTGCTGATATTGACCGGTGAAGGACAACCTTACAGATCAAGTACAAATAGTGATGATTGCATTCCATTGGACCGAGAGAAGATTGTT		
MH297492_51-660	(401)	GAGTTGCTGATATTGACCGGTGAAGGACAACCTTACAGATCAAGTACAAATAGTGATGATTGCATTCCATTGGACCGAGAGAAGATTGTT		
Consensus	(403)	GAGTTGCTGATATTGACCGGTGAAGGACAACCTTACAGATCAAGTACAAATAGTGATGATTGCATTCCATTGGACCGAGAGAAGATTGTT		
		503		601
CP047560_59492023-59491423	(496)	CCTTCATGCTGATGAAACAGAGGTATCGGTTGGGAAGTACTTCAATA		AGCTSCAAGCCAAATTAATTGATCAGATTGTCCTTATGGAGTTGTTTC
GU338312_89-700	(500)	CCTTCATGCTGATGAAACAGAGGTATCGGTTGGGAAGTACTTCAATA		ACTACAAGCCAAATTAATTGATCAGATTGTCCTTATGGAGTTGTTTC
Hybrid_13/11	(498)	CCTTCATGCTGATGAAACAGAGGTATCGGTTGGGAAGTACTTCAATA		ACTACAAGCCAAATTAATTGATCAGATTGTCCTTATGGAGTTGTTTC
FJ423044_758-1367	(500)	CCTTCATGCTGATGAAACAGAGGTATCGGTTGGGAAGTACTTCAATA		ACTACAAGCCAAATTAATTGATCAGATTGTCCTTATGGAGTTGTTTC
FJ423046_91-700	(498)	CCTTCATGCTGATGAAACAGAGGTATCGGTTGGGAAGTACTTCAATA		ACTACAAGCCAAATTAATTGATCAGATTGTCCTTATGGAGTTGTTTC
MH297492_51-660	(498)	CCTTCATGCTGATGAAACAGAGGTATCGGTTGGGAAGTACTTCAATA		ACTACAAGCCAAATTAATTGATCAGATTGTCCTTATGGAGTTGTTTC
Consensus	(503)	CCTTCATGCTGATGAAACAGAGGTATCGGTTGGGAAGTACTTCAATA		ACTACAAGCCAAATTAATTGATCAGATTGTCCTTATGGAGTTGTTTC
		110		204
ACJ66594_17-219	(110)	KFICCLKTVSFADEFAMEIEKIKRRVADIDRVRTTYSITDTSNNN-DDCIPLDRRLFLHADETEVIGLEDDFNLLQAKLLDHDLPYGVVSIVGM		
ACJ66596_31-233	(110)	KFICCLKTVSFADEFAMEIEKIKRRVADIDRVRTTYSITDTSNNN-DDCIPLDRRLFLHADETEVIGLEDDFNLLQAKLLDHDLPYGVVSIVGM		
Hybrid	(110)	KFICCLKTVSFADEFAMEIEKIKRRVADIDRVRTTYSITDTSNNN-DDCIPLDRRLFLHADETEVIGLEDDFNLLQAKLLDHDLPYGVVSIVGM		
S. pin	(102)	KFICCLKTVSFADEFAMEIEKIKRRVADIDRVRTTYSITDTSNNNSDDCIPLDRRLFLHADEXEVIGLXDDFNLLQAKLLDHDLPYGVVSIVGM		
QAY29223_17-219	(110)	KFICCLKTVSFADEFAMEIEKIKRRVADIDRVRTTYSITDTSNNN-DDCIPLDRRLFLHADETEVIGLEDDFNLLQAKLLDHDLPYGVVSIVGM		
Consensus	(110)	KFICCLKTVSFADEFAMEIEKIKRRVADIDRVRTTYSITDTSNNN-DDCIPLDRRLFLHADETEVIGLEDDFNLLQAKLLDHDLPYGVVSIVGM		

Supplemental Fig. 1A. Alignment of *Rpi-vnt1* homologs. Hybrid 13/11, amplicon sequence from clone 13/11-09; FJ423044, *S. venturii* *Rpi-vnt1.1* gene; FJ423046, *S. venturii* *Rpi-vnt1.3* gene; MH297492, *S. tuberosum* cv. Alouette *Rpi-vnt1.3* gene; GU338312, *S. microdontum* ssp. *gigantophyllum* isolate GIG362-4 *rpi-vnt1*-like protein pseudogene; CP047560_59492023-59491423, *S. pinnatisectum* cv. CGN17745 fragment from chromosome 9.

Supplemental Fig. S1B. Alignment of predicted amino acid sequences of *Rpi-vnt1* protein homologs. Hybrid 13/11; sequence corresponding to the amplicon from clone 13/11-09; ACJ66594, protein *Rpi-vnt1.1* from *S. venturii*; ACJ66596, protein *Rpi-vnt1.3* from *S. venturii*; QAY29223, protein *Rpi-vnt1.3* from *S. tuberosum* cv. Alouette; S.pin, predicted amino acid sequence of the *S. pinnatisectum* cv. CGN177459 chromosome 9 fragment (59492023 to 59491423 bp).