

Title: New powdery mildew resistance QTL found on chromosome 9 in *Solanum cheesmaniae*

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SUPPLEMENTARY INFORMATION

Table S1 list of the accessions used to screen tomato powdery mildew resistance

Whole name	Name on Fig. 2	Species
MarocFavet	Maroc	<i>S. lycopersicum</i> var. <i>lycopersicum</i>
Rose de Berne	RdB	<i>S. lycopersicum</i> var. <i>lycopersicum</i>
LA1033	LA1033	<i>S. habrochaites</i>
LA3863	LA3863	<i>S. habrochaites</i>
LA3864	LA3864	<i>S. habrochaites</i>
LA1777	LA1777	<i>S. habrochaites</i>
PI247087	PI24	<i>S. habrochaites</i>
PI308182	-	<i>S. habrochaites</i>
G1 1560	G1560	<i>S. habrochaites</i>
Mex-10	Mex-10	<i>S. lycopersicum</i> var. <i>cerasiforme</i>
Mex-121-A	Mex-121-A	<i>S. lycopersicum</i> var. <i>cerasiforme</i>
Matt's Wild Cherry	MWC	<i>S. lycopersicum</i> var. <i>cerasiforme</i>
LA2078	LA2078	<i>S. lycopersicum</i> var. <i>cerasiforme</i>
PI438556	PI438	<i>S. lycopersicum</i> var. <i>cerasiforme</i>
LA2254	LA2254	<i>S. lycopersicum</i> var. <i>cerasiforme</i>
LA1376	LA1376	<i>S. pennellii</i>
LA1297	LA1297	<i>S. pennellii</i>
LA0751	LA0751	<i>S. pennellii</i>
CGN 15820	CGN 15820	<i>S. cheesmaniae</i> x <i>S. lycopersicum</i>
LA0421	LA0421	<i>S. cheesmaniae</i>
LA0429	LA0429	<i>S. cheesmaniae</i>
LA0531	LA0531	<i>S. cheesmaniae</i>
LA0746	LA0746	<i>S. cheesmaniae</i>
LA0749	LA0749	<i>S. cheesmaniae</i>
LA1036	LA1036	<i>S. cheesmaniae</i>
LA1406	LA1406	<i>S. cheesmaniae</i>
LA1412	LA1412	<i>S. cheesmaniae</i>
LA1447	LA1447	<i>S. cheesmaniae</i>
LA1450	LA1450	<i>S. cheesmaniae</i>
LA1401	-	<i>S. galapagense</i>
LA1482	LA1482	<i>S. lycopersicum</i> var. <i>cerasiforme</i>

Table S2 Marker lists with their genetic positions and sequences

Marker name	Position	Sens	Sequence marker A1 (RdB)	Sequence marker A2 (LA0421)	Sequence marker commun
CH09_1353423_K535	1 353 423	REV	GACGAACCTGATCTGCTCCAAAAT	GACGAACCTGATCTGCTCCAAAAC	GGCATGTTTGAGACTAATTCCACAA
CH09_2632688_K536	2 632 688	REV	GTTTTGGCCTAAGCATTTCTCCGC	TTTTGGCCTAAGCATTTCTCCGT	AACATTGGTGCTCTGACTAATCTGG
CH09_2837551_K670	2 837 551	FOR	TAAAGTGAGCATCATTTCTCAG	GTCTTAAAGTGAGCATCATTTCTCAA	CACCGAACATCTAGCAATTCTTTTA
CH09_3298197_K671	3 298 197	REV	TGGTTTCGAATAATTGTTTTACCAA	TGGTTTCGAATAATTGTTTTACCAT	GTTAGGCAAGAAACCTTCATTTCTCA
CH09_4594188_K672	4 594 188	REV	CCAAAACCTCCTACAAGGATGAGC	CCAAAACCTCCTACAAGGATGAGT	CAGGCAGCCTATTGGTTTTCATC
CH09_5053284_K673	5 053 284	REV	AATCAGAAAATCCCGCCCTCATT	AATCAGAAAATCCCGCCCTCATC	AGAACATCTTTTGATGAGCAACCAG
CH09_5241203_K537	5 241 203	FOR	GACTTGCATAAGGTGGTTCAATACA	GACTTGCATAAGGTGGTTCAATACG	ATTAATGCCTCATGCCTGTCTAGG
CH09_5511353_K538	5 511 353	FOR	TACACCAACTCTTAAGGACACTAGA	TACACCAACTCTTAAGGACACTAGG	GAAATGACTCGGGAGTGCAACATTT
CH09_11409858_K539	11 409 858	FOR	CAAGGAAATACTTCCCTCGGT	CAACAAGGAAATACTTCCCTCGGC	TCTATCAGCCTCATCCAAAACCTACA
CH09_57011053_K689	57 011 053	FOR	GATAAGCAACAAGTAGATTTGTTTCATTA	AAGCAACAAGTAGATTTGTTTCATTG	GCCCTTCCTCTTCTACTTGGT
CH09_59761374_S002	59 761 374	REV	TGCTGCTCTCTGCTCCTATAGA	TGCTGCTCTCTGCTCCTATAGT	ACCTCAAAGTGCTTCATTTTGGT
CH09_59911474_K541	59 911 474	FOR	GAGCTGTGAGATGGTTTTCTGATG	CGAGCTGTGAGATGGTTTTCTGATA	AGCAGAGTACATATGGATCCAAGAAA
CH09_60197391_K542	60 197 391	REV	ACTTGCAGCCGTAGGAATTTGAT	CTTGCAGCCGTAGGAATTTGAC	GTTGCAGACTGATAGAGCTGTAATG
CH09_62355688_K660	62 355 688	REV	AACCGTTCGATGTATTCTTGTTTTT	AACCGTTCGATGTATTCTTGTTTTT	TTGTGTTAATTGGGAATTGCAGAGG
CH09_63583464_K545	63 583 464	REV	GAAATGATTCCGAAGCGATCTCAG	GAAATGATTCCGAAGCGATCTCAA	TACTCATACGTCTAACCGACGATGT
CH09_63883322_K543	63 883 322	REV	GTACGGATGGACTAACACACCCCAA	GTACGGATGGACTAACACACCCCAAG	ACTCTCATTTACCTGAAGGATCCAG
CH09_64906267_K661	64 906 267	REV	TCGATAAGAGTTTTATGGTGCTGTT	TCGATAAGAGTTTTATGGTGCTGTA	TCGATTGGACTGCTACATACTTCAA
CH09_65367830_K662	65 367 830	REV	CTATACCTGTCATTGGTGGGTGGC	CTATACCTGTCATTGGTGGGTGGT	TAGTCTAGCATGCAAACCAAGTGAA
CH09_66155620_K674	66 155 620	FOR	TGTGTTAGTGGTGAAGATTATGGTAA	TGTGTTAGTGGTGAAGATTATGGTAT	TTCATTAATGGTTGCACTTTCTCTCA
CH09_67483858_K665	67 483 858	FOR	GGTCCGGTTGACCCTATAAAATGC	GGTCCGGTTGACCCTATAAAATGT	CTGTTCCACCGGCGATTCCAG

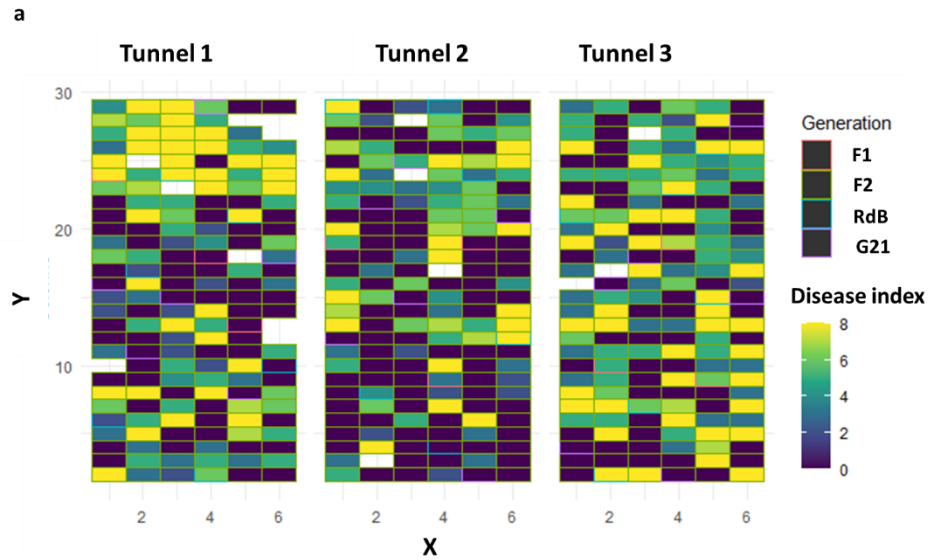
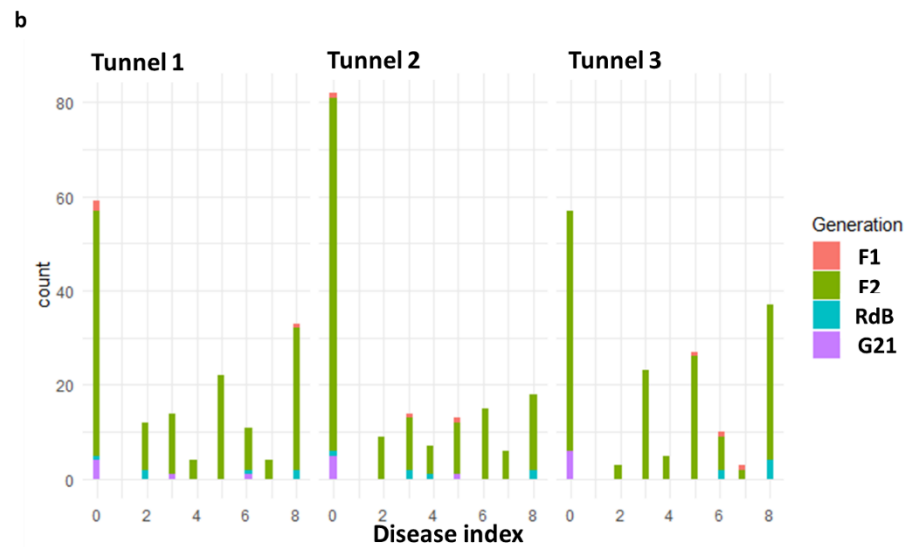


Fig. S1 Representation of total plant score. a) Disease index space in the three tunnels according to their X and Y positions. The color of the boxes corresponds to the values of the total score, ranging from black (total score =0) to yellow (total score =8). The color of the outline of the rectangles designates the nature of the plant: F_1 = orange, F_2 = green, RdB = blue and LA0421 = purple. b) Histogram of the total score of plants in the three tunnels. Scores on the abscissa and number of plants on the ordinate. The different colors represent the nature of the plant: F_1 = orange, F_2 = green, RdB = blue and LA0421 = purple



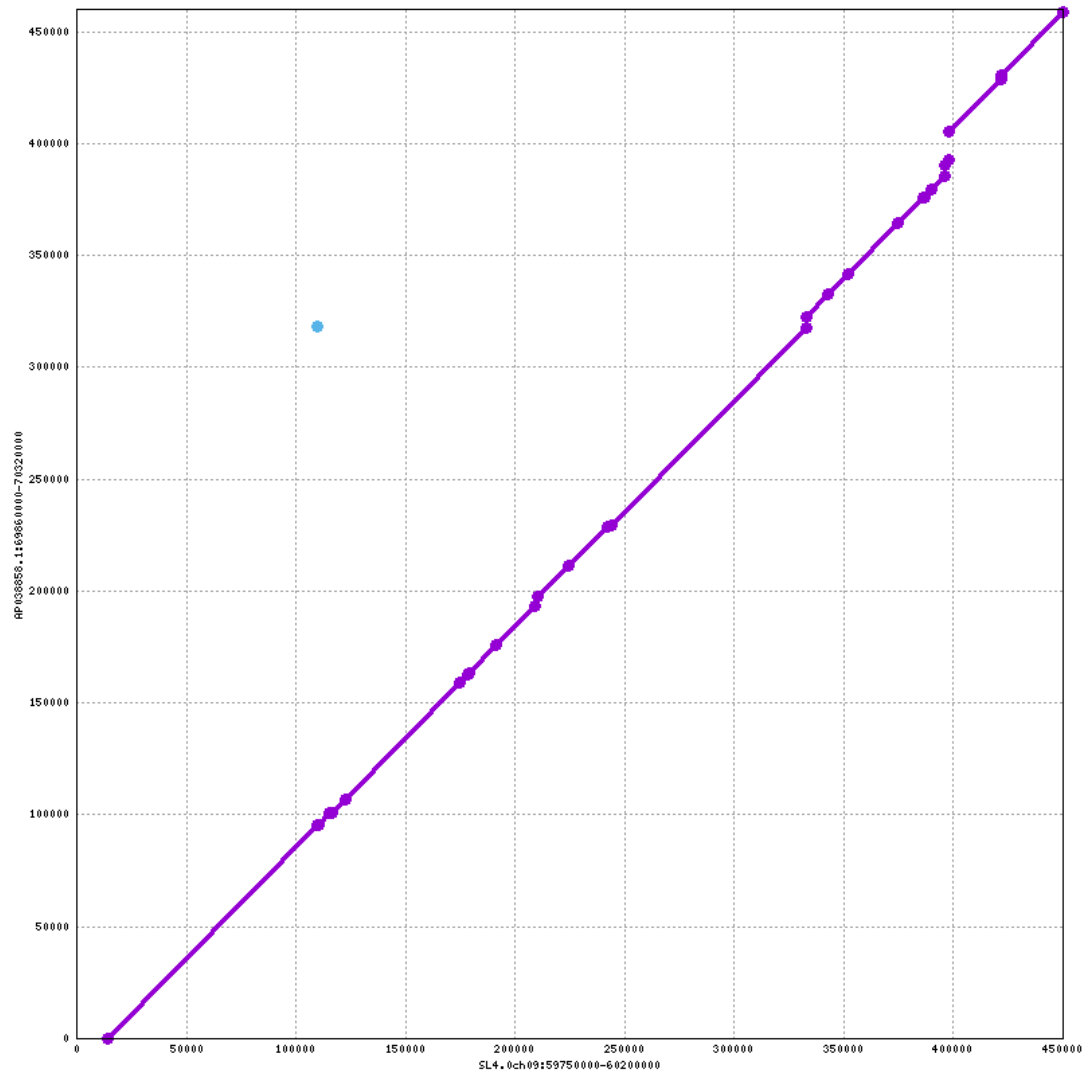


Fig. S2 Dot plot generated using MUMmer v4 to compare sequences of SL4.0 and SCH_r1.0 within the markers CH09_59761374_K660 and CH09_60197391_K542

Table S3 Genes annotated within markers CH09_59761374_K660and CH09_60197391_K542 on SL4.0 tomato reference genome

Name	Start	End	Strand	Functions
<i>Solyc09g065540.3.1</i>	59756389	59770639	+	Biotin-binding protein
<i>Solyc09g065550.4.1</i>	59780341	59789062	+	Kinase interacting
<i>Solyc09g065560.3.1</i>	59789136	59797686	-	Sulfate transporter
<i>Solyc09g065565.1.1</i>	59821112	59822220	+	NIMA-related kinase 2
<i>Solyc09g065570.5.1</i>	59824403	59826491	+	Serine/threonine-protein kinase Nek2
<i>Solyc09g065580.4.1</i>	59826831	59829907	+	2-oxoglutarate (2OG) and Fe (II)-dependent
<i>Solyc09g065590.3.1</i>	59844028	59848450	+	Auxin canalization protein
<i>Solyc09g065600.4.1</i>	59848293	59856267	-	GDP-mannose transporter GONST4
<i>Solyc09g065610.2.1</i>	59858294	59858470	-	Bax inhibitor-1 family protein
<i>Solyc12g049235.2.1</i>	59868633	59869577	+	Zinc finger BED domain-containing protein
<i>Solyc09g065620.3.1</i>	59880955	59882889	+	Chlorophyllase
<i>Solyc09g065630.3.1</i>	59893373	59898768	+	Tify domain-containing protein/CCT-2 domain-containing protein
<i>Solyc09g065640.3.1</i>	59908607	59915336	+	Ethylene overproducer-like 1
<i>Solyc09g065650.3.1</i>	59921685	59946294	-	Protein phosphatase 2C family protein
<i>Solyc09g150148.1.1</i>	59961196	59963018	+	Non-specific lipid-transfer protein
<i>Solyc09g065660.4.1</i>	59975274	59977539	+	Heat shock transcription
<i>Solyc09g065670.3.1</i>	59999711	60004939	+	Unknown protein
<i>Solyc09g065680.1.1</i>	60014180	60014472	-	Unknown protein
<i>Solyc09g065690.4.1</i>	60014836	60027427	-	2-oxoglutarate (2OG) and Fe (II)-dependent oxygenase superfamily protein
<i>Solyc09g065700.3.1</i>	60040900	60061994	+	BEACH domain
<i>Solyc09g065710.1.1</i>	60063791	60066607	+	Pentatricopeptide repeat-containing protein
<i>Solyc09g065720.4.1</i>	60106675	60114638	+	Peptidyl-prolyl cis-trans isomerase

(Continued)

Name	Start	End	Strand	Functions
<i>Solyc09g065730.3.1</i>	60114946	60117780	-	2-methyl-6-phytyl-1 _Note2=4-hydroquinone methyltransferase_Note3=chloroplastic
<i>Solyc09g065740.2.1</i>	60120672	60123783	+	Ammonium transporter
<i>Solyc09g065750.3.1</i>	60124430	60129781	-	Beta-carotene isomerase D27 _Note2=chloroplastic-like
<i>Solyc09g065755.1.1</i>	60130818	60135349	-	Histone H2A
<i>Solyc09g065760.4.1</i>	60140807	60143746	+	DUF506 domain-containing protein
<i>Solyc09g065770.1.1</i>	60155430	60156482	+	Protein ELC-like
<i>Solyc09g065780.3.1</i>	60156869	60158438	-	3-ketoacyl-CoA synthase
<i>Solyc09g065800.4.1</i>	60169347	60171149	-	3-ketoacyl-CoA synthase
<i>Solyc09g065810.3.1</i>	60179149	60191006	+	Guanylate-binding protein
<i>Solyc09g065820.4.1</i>	60194165	60198712	+	bHLH transcription factor 59

Table S4 Genes annotated within markers CH09_59761374_K660and CH09_60197391_K542 on SCH_r1.0 tomato reference genome

Name	Start	End	Strand	Functions
<i>SCH1.0ch09.g56340.1</i>	69852387	69864951	+	Methylcrotonoyl-CoA carboxylase subunit alpha _Note2=mitochondrial
<i>SCH1.0ch09.g56360.1</i>	69877103	69884697	+	Protein NETWORKED 1D
<i>SCH1.0ch09.g56370.1</i>	69885297	69893579	-	Sulfate transporter 3.1
<i>SCH1.0ch09.g56380.1</i>	69918084	69922275	+	Serine/threonine-protein kinase Nek2
<i>SCH1.0ch09.g56390.1</i>	69940163	69944265	+	VAN3-binding protein
<i>SCH1.0ch09.g56400.1</i>	69945009	69952242	-	GDP-fucose transporter 1
<i>SCH1.0ch09.g56410.1</i>	69954389	69957341	-	Protein LIFEGUARD 2
<i>SCH1.0ch09.g56420.1</i>	69976186	69977213	+	Chlorophyllase-1 _Note2=chloroplastic
<i>SCH1.0ch09.g56430.1</i>	69988104	69992683	+	Protein TIFY 4B
<i>SCH1.0ch09.g56440.1</i>	70003959	70009502	+	ETO1-like protein 1
<i>SCH1.0ch09.g56460.1</i>	70016855	70045562	-	Probable inactive protein kinase At3g63330
<i>SCH1.0ch09.g56470.1</i>	70072268	70074015	+	Heat stress transcription factor A-6b
<i>SCH1.0ch09.g56480.1</i>	70095245	70100090	+	Zinc finger protein MAGPIE
<i>SCH1.0ch09.g56500.1</i>	70115291	70122628	-	Lysine-specific demethylase JM31
<i>SCH1.0ch09.g56510.1</i>	70136175	70156738	+	Protein SPIRRIG
<i>SCH1.0ch09.g56520.1</i>	70159062	70161878	+	Pentatricopeptide repeat-containing protein At3g63370 _Note2=chloroplastic
<i>SCH1.0ch09.g56530.1</i>	70204099	70213852	+	Peptidyl-prolyl cis-trans isomerase CYP63
<i>SCH1.0ch09.g56540.1</i>	70214729	70217160	-	2-methyl-6-phytyl-1 _Note2=4-hydroquinone methyltransferase _Note3=chloroplastic
<i>SCH1.0ch09.g56550.1</i>	70220148	70223257	+	Ammonium transporter 2 member 5
<i>SCH1.0ch09.g56560.1</i>	70223903	70224762	-	Beta-carotene isomerase D27 _Note2=chloroplastic
<i>SCH1.0ch09.g56570.1</i>	70230639	70240157	-	Probable histone H2A variant 1
<i>SCH1.0ch09.g56590.1</i>	70272587	70273639	+	Protein ELC-like

(Continued)

Name	Start	End	Strand	Functions
<i>SCH1.0ch09.g56610.1</i>	70286764	70287996	-	3-ketoacyl-CoA synthase 11
<i>SCH1.0ch09.g56620.1</i>	70298198	70309504	+	Guanylate-binding protein 4
<i>SCH1.0ch09.g56630.1</i>	70313297	70317324	+	Transcription factor UNE12