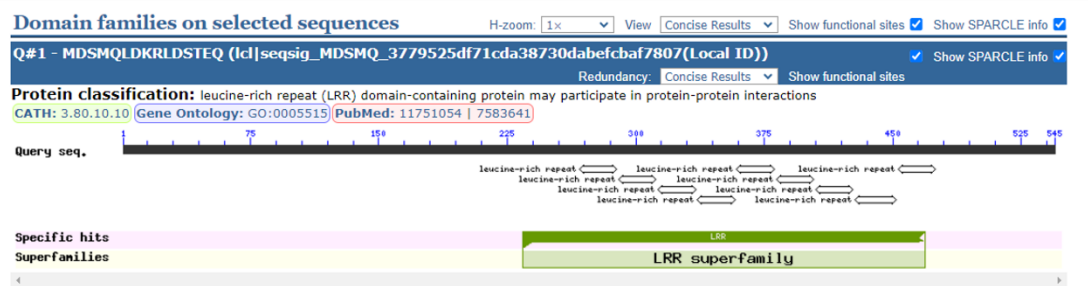
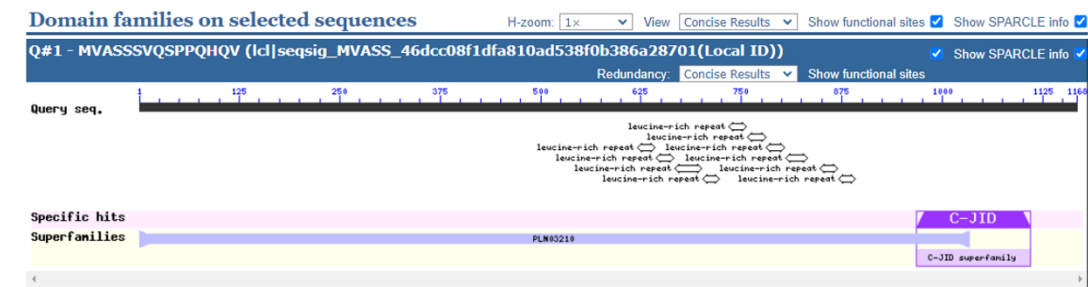


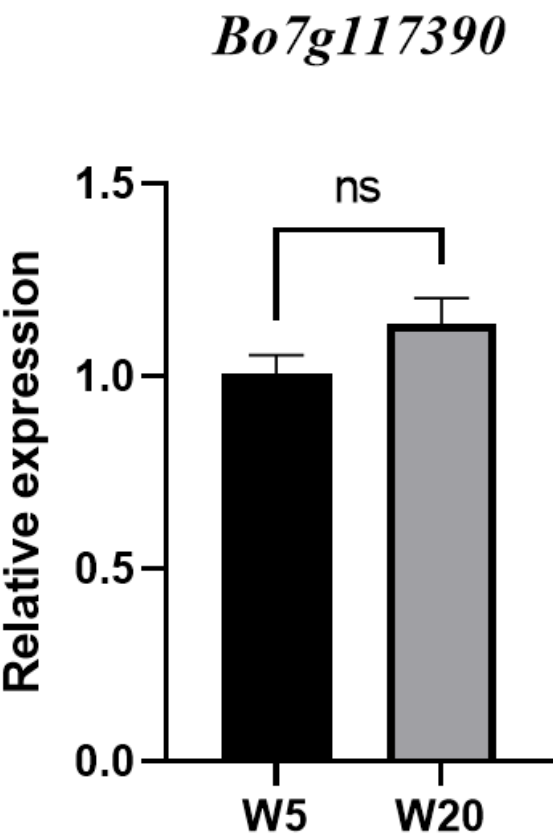
Bo7g117390



Bo7g117810



Supplement Figure 1. conserved domain of Bo7g117390 and Bo7g117810.



Supplement Figure 2. Gene expression of Bo7g117390 in R and S sister lines.



Supplement Figure 3. Analysis of 148 cabbage inbred lines using marker I1-3.

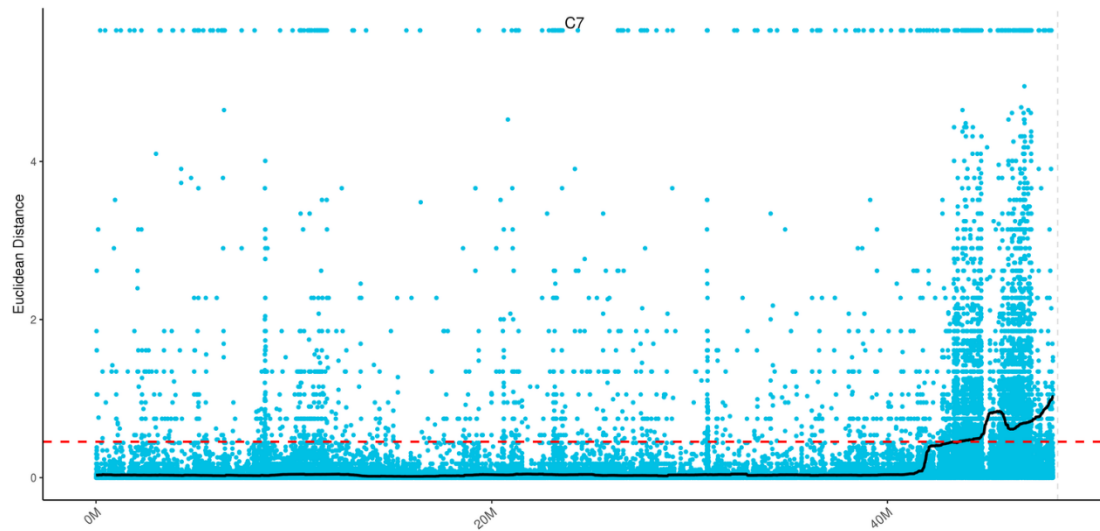


Fig. S4. The Euclidean Distance (ED) value peak of C7.

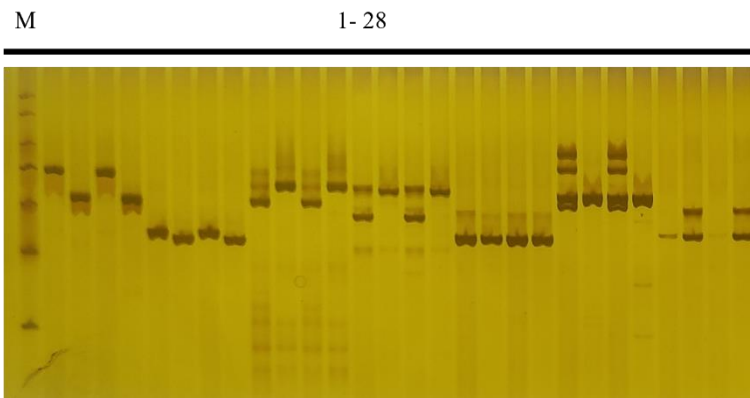


Fig. S5 Initial mapping primer screening. M represents the marker, lanes 1-28 represent the lanes. In lanes 1-4, lanes 1 and 3 represent the amplification of primer 1 in resistant individuals, and lanes 2 and 4 represent the amplification of primer 1 in susceptible individuals. Lanes 5 and 7 represent the amplification of primer 2 in resistant individuals, and lanes 6 and 8 represent the amplification of primer 2 in susceptible individuals, and so on.

$$ED = \sqrt{(A_{mut} - A_{wt})^2 + (C_{mut} - C_{wt})^2 + (G_{mut} - G_{wt})^2 + (T_{mut} - T_{wt})^2}$$

A_{mut} is the frequency of the A base in the mutated pool, and A_{wt} is the frequency of the A base in the wild-type pool. C_{mut} is the frequency of the C base in the mutated pool, and C_{wt} is the frequency of the C base in the wild-type pool. G_{mut} is the frequency of the G base in the mutated pool, and G_{wt} is the frequency of the G base in the wild-type pool. T_{mut} is the frequency of the T base in the mutated pool, and T_{wt} is the frequency of the T base in the wild-type pool.

Fig.S6 The Euclidean Distance (ED) calculation formula

Supplement Table 1. RT-qPCR primers used to monitor the expression of candidate genes

primer name	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')	gene
810-b1	TTTCTAGATTGTTGCGGATTATGC	ACTAAACACCTCACGTAATACTCAT	Bo7g117810
390-q1	AAGCTTCTTGATCTCGAACTGTT	ACTTCTCGGAGGAATACAAGTTTC	Bo7g117390

Supplement Table 2. Phenotypes displayed by sister lines in response to the downy mildew pathogen *Hyaloperonospora parasitica*.

Phenotypes Displayed by Sister Lines in Response to the Downy Mildew Pathogen <i>Hyaloperonospora parasitica</i> (Data Collected on December 3rd)									
sister line	total number	calss	calss	calss	calss	calss	calss	DI	resistance level
		0	1	2	3	4	5		
W4	43	0	10	6	12	13	2	55.81%	S
W5	43	0	1	1	9	20	12	79.07%	HS
W6	43	25	11	5	2	0	0	12.56%	R
W7	43	0	5	15	12	4	7	56.74%	S
W8	43	22	15	3	2	0	1	14.88%	R
W9	43	0	10	5	13	10	5	57.67%	S
W10	86	0	1	15	7	30	33	78.37%	HS
W11	43	11	20	6	5	1	0	23.72%	R
W12	86	23	38	12	11	1	1	24.19%	R
W13	43	13	21	3	5	1	0	21.40%	R
W14	43	0	7	7	8	10	11	65.12%	S
W15	43	0	3	13	10	10	7	62.33%	S
W16	86	18	40	7	11	10	0	29.53%	R
W17	43	0	8	9	10	10	6	58.60%	S
W18	86	0	3	15	20	40	8	68.14%	S
W19	43	41	2	0	0	0	0	0.93%	HR
W20	43	36	6	1	0	0	0	3.72%	HR
W21	43	0	14	5	4	10	10	58.60%	S
W22	43	0	5	14	7	10	7	60.00%	S
W23	86	37	34	12	3	0	0	15.58%	R
W24	43	0	3	15	4	11	10	64.65%	S

W25	43	0	0	15	5	13	10	68.37%	S
W26	43	0	0	15	8	15	5	64.65%	S
W27	43	0	5	9	8	13	8	64.65%	S
W28	86	66	19	1	0	0	0	4.88%	HR
W29	43	14	9	20	0	0	0	22.79%	R
W30	43	4	20	15	4	0	0	28.84%	R
W31	86	19	22	30	15	0	0	29.53%	R
W32	43	8	19	1	15	0	0	30.70%	R
W33	86	3	3	20	40	15	5	57.67%	S
W34	43	1	5	6	6	15	10	67.44%	S
W35	86	36	20	30	0	0	0	18.60%	R
W36	43	11	17	15	0	0	0	21.86%	R
W37	43	0	6	8	14	10	5	60.00%	S
W38	43	15	23	3	2	0	0	16.28%	R
W39	43	2	6	10	10	10	5	56.28%	S
W40	43	0	14	0	12	13	4	56.74%	S
W41	43	0	1	14	7	15	6	65.12%	S
W42	43	0	1	10	12	15	5	66.05%	S
W43	43	8	22	12	1	0	0	22.79%	R
W44	43	2	1	9	12	10	9	65.12%	S
W45	43	2	2	19	5	6	9	57.67%	S
W46	86	30	30	26	0	0	0	19.07%	R
W47	43	0	4	12	11	10	6	60.93%	S
W48	43	16	15	11	1	0	0	18.60%	R
Phenotypes Displayed by Sister Lines in Response to the Downy Mildew Pathogen <i>Hyaloperonospora parasitica</i> (Data Collected on December 15th)									
sister line	total number	calss	calss	calss	calss	calss	calss	DI	resistance level
		0	1	2	3	4	5		
W4	43	0	4	2	15	17	5	67.91%	S
W5	43	0	0	0	2	25	16	86.51%	HS
W6	43	3	25	15	0	0	0	25.58%	R
W7	43	0	1	5	18	10	9	69.77%	S
W8	43	6	18	13	0	5	1	32.09%	R
W9	43	0	1	4	15	15	8	71.63%	S
W10	86	0	0	5	10	31	40	84.65%	HS
W11	46	10	11	13	11	1	0	32.17%	R
W12	86	6	35	36	6	3	0	31.86%	R
W13	43	7	16	16	3	1	0	28.37%	R
W14	43	0	0	14	1	12	16	73.95%	S
W15	43	0	1	8	9	15	10	71.63%	S
W16	86	13	38	12	13	10	0	32.79%	R
W17	43	0	1	6	13	12	11	72.09%	S

W18	86	0	0	13	9	44	20	76.51%	S
W19	43	25	18	0	0	0	0	8.37%	HR
W20	43	29	13	1	0	0	0	6.98%	HR
W21	43	0	10	6	6	5	16	65.12%	S
W22	43	0	0	10	13	5	15	71.63%	S
W23	86	4	43	38	0	1	0	28.60%	R
W24	43	0	0	10	6	12	15	74.88%	S
W25	43	0	0	8	8	15	12	74.42%	S
W26	43	0	0	10	5	20	8	72.09%	S
W27	43	0	3	11	3	13	13	70.23%	S
W28	86	46	39	1	0	0	0	9.53%	HR
W29	43	9	14	10	10	0	0	29.77%	R
W30	44	0	27	13	4	0	0	29.55%	R
W31	86	10	28	31	17	0	0	32.79%	R
W32	43	0	10	18	10	5	0	44.65%	MR
W33	86	0	8	8	30	30	10	66.05%	S
W34	44	0	1	9	9	10	15	73.18%	S
W35	86	21	13	36	16	0	0	30.93%	R
W36	43	5	19	12	7	0	0	29.77%	R
W37	43	0	0	1	15	19	8	75.81%	S
W38	43	10	13	15	5	0	0	26.98%	R
W39	43	0	3	15	9	8	8	61.40%	S
W40	43	0	5	8	6	15	9	66.98%	S
W41	43	0	0	8	15	10	10	70.23%	S
W42	43	0	0	5	12	18	8	73.49%	S
W43	43	4	15	13	9	2	0	35.35%	MR
W44	43	0	0	6	15	13	9	71.63%	S
W45	43	0	0	13	15	4	11	66.05%	S
W46	86	20	25	31	10	0	0	27.21%	R
W47	43	0	2	3	23	5	10	68.37%	S
W48	43	10	10	17	6	0	0	28.84%	R

Supplement Table 3. Functional annotations of all genes in the candidate region

TO1000	TAIR	Function
Bo7g117230	AT2G17510	ribonuclease II family protein
Bo7g117240	AT4G35160	Encodes a cytosolic N-acetylserotonin O-methyltransferase that can convert N-acetylserotonin to melatonin and serotonin to 5-methoxytryptamine in the process of melatonin synthesis.
Bo7g117250	AT4G35160	Encodes a cytosolic N-acetylserotonin O-methyltransferase that can convert N-acetylserotonin to melatonin and

		serotonin to 5-methoxytryptamine in the process of melatonin synthesis.
Bo7g117260	AT4G35170	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
Bo7g117270	AT4G35180	LYS/HIS transporter 7
Bo7g117280	AT4G35200	hypothetical protein (DUF241)
Bo7g117290	AT4G35200	hypothetical protein (DUF241)
Bo7g117300	AT4G35270	Nitrate responsive transcriptional regulator involved in nitrate utilization
Bo7g117310	AT1G14800	Nucleic acid-binding, OB-fold-like protein
Bo7g117320	AT4G35280	Target promoter of the male germline-specific transcription factor DUO1
Bo7g117330	AT4G35310	calmodulin-domain protein kinase CDPK isoform 5
Bo7g117340	AT4G35320	hypothetical protein
Bo7g117350	no	
Bo7g117360	no	
Bo7g117370	AT4G35450	Involved in targeting of chloroplast outer membrane proteins to the chloroplast
Bo7g117380	AT4G35460	NADPH-dependent thioredoxin reductase 1
Bo7g117390	AT4G35470	Encodes PIRL4, a member of the Plant Intracellular Ras-group-related LRRs
Bo7g117400	AT4G35480	Encodes a putative RING-H2 finger protein RHA3b
Bo7g117410	AT4G35490	mitochondrial ribosomal protein L11
Bo7g117420	AT4G35490	mitochondrial ribosomal protein L11
Bo7g117430	AT4G35500	SRPK-family member protein
Bo7g117440	AT4G26340	F-box/RNI-like/FBD-like domains-containing protein
Bo7g117450	AT4G35510	PHD finger-like protein
Bo7g117460	AT4G35520	DNA mismatch repair protein similar to MutL. Required for normal levels of meiotic crossovers
Bo7g117470	AT4G35530	phosphatidylinositolglycan-like protein
Bo7g117480	AT4G35550	Encodes a WUSCHEL-related homeobox gene family member with 65 amino acids in its homeodomain
Bo7g117490	AT4G35560	Target promoter of the male germline-

		specific transcription factor DUO1
Bo7g117500	AT2G17560	Encodes a protein belonging to the subgroup of HMGB (high mobility group B) proteins that have a distinctive DNA-binding motif, the HMG-box domain
Bo7g117510	AT4G12735	Encodes a peroxisomal protein
Bo7g117520	AT4G35600	Encodes a receptor-like cytoplasmic kinase that acts as a spatial inhibitor of cell separation
Bo7g117530	AT4G35600	Encodes a receptor-like cytoplasmic kinase that acts as a spatial inhibitor of cell separation
Bo7g117540	AT4G35620	Cyclin B2
Bo7g117550	AT4G35660	selection/upkeep of intraepithelial T-cells protein, putative (DUF241)
Bo7g117560	AT4G35670	Pectin lyase-like superfamily protein
Bo7g117570	AT3G55120	Catalyzes the conversion of chalcones into flavanones
Bo7g117580	AT2G13770	nuclease
Bo7g117590	AT4G35690	hypothetical protein (DUF241)
Bo7g117600	AT4G35720	DUF241 domain protein
Bo7g117610	AT4G35725	transmembrane protein
Bo7g117620	AT4G35790	Encodes a protein with phospholipase D activity
Bo7g117630	AT4G35840	RING/U-box superfamily protein
Bo7g117640	AT4G35860	GTP-binding protein ATGB2
Bo7g117650	AT4G35890	Encodes a cytoplasmic LAM domain containing protein that is involved in leaf senescence
Bo7g117660	AT4G35900	bZIP protein required for positive regulation of flowering. Mutants are late flowering
Bo7g117670	AT4G35905	Trm112p-like protein
Bo7g117680	AT4G35920	Encodes an integral plasma membrane protein
Bo7g117690	AT4G35930	F-box family protein which is required to repress excessive divisions in stomatal development
Bo7g117700	AT4G35940	hypothetical protein
Bo7g117710	AT2G17800	A member of ROP GTPase family.

Bo7g117720	AT4G35985	Senescence/dehydration-associated protein-like protein
Bo7g117730	AT4G36020	Encodes a cold shock domain protein.
Bo7g117740	AT4G36030	Armadillo repeat protein
Bo7g117750	AT4G36040	DNA J protein
Bo7g117760	AT4G36060	Negative TF that regulates Fe homeosta
Bo7g117770	AT4G36070	member of Calcium Dependent Protein Kinase
Bo7g117780	AT4G36110	SAUR-like auxin-responsive protein family
Bo7g117790	AT4G36130	Ribosomal protein L2 family
Bo7g117800	AT4G36140	Intracellular immune receptor; in a head-to-head configuration with SADR1 similar to the sensor/executor TNL pair RRS1
Bo7g117810	AT4G36150	TIR domain containing intracellular immune receptor; required for defense signaling initiated by some transmembrane pattern recognition receptors and contributes to the unbridled spread of cell death in lesion simulating disease 1
Bo7g117820	AT4G36160	Encodes a NAC-domain transcription factor that is expressed in developing xylem
Bo7g117830	AT4G36195	Serine carboxypeptidase S28 family protein
Bo7g117840	AT4G36220	CYP84A1, CYTOCHROME P450 84A1, F5H, FAH1, FERULIC ACID 5-HYDROXYLASE 1

Supplement Table 4. Primer sequences required for cloning the genes Bo7g117810 and Bo7g117390

primer name	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')
390-1	CCGTCGCATTAAAAACCTAAAAGA	GCTTCTCTCCATCATTGCCTATAC
390-3	AGGAGGTTAGGATCAGCATTGTAT	TGACTCGAGTTTCAAACCAAAGAA
390-6	AAGTTAAGGAAAGCACTCTATGGC	GGTGGTAAAGATCTGTGAAGTCTC
810-1	AATTGCATTGCTTCCACCAAATC	TCACAAGTGCACTGTAATGAGAA
810-2.1	TACCATTGTTCAGTTTATCATCTC	CAGAAAACCATACTAAAAGAAGAAG
810-2.2	AGGTGGAAGGAAGACCGTTTACT	TACCAATACCAGGCATCCCGACA

810-2.3	AGGTGGAAGGAAGACCGTTTACT	GTGTTCTCGCACTGGAAATCTAA
810-3	CGTGACGTAATAAATCTCTTCTTC	GAAAGCTGTCACTGCCACTC
810-4	GAATGCGACTGGATCAAGAAAAG	TCGAACATTAGAGACAAATAGGT
810-5	TTGGTGCACTGAAGAAAAGAGC	ACAGTCATAAAAGCTAGGCAAC
810-6.1	TGTGTCTCTGCTTCACCCAT	TGTTCAAGATTGTTGCAGTTGG
810-6.2	CTGCTTCACCCATTATGATTTTGTC	ATCCTTTGCAACTTGTTCAAGATTG
810-7.1	ATCCTCCTCATTGCGTCGTCTA	CACCCCTTAACTCGAAACCCTA
810-7.2	CCTCCTCATTGCGTCGTCTAT	ACCCCTTAACTCGAAACCCTA
810-7.3	GACAACAGGCTTTCAACAATAGT	AAAATAAATTTCAAATTCCACCCC
810-7.4	GATCCACGTAAAGCTGAAGTTTC	GTTCTATTCTAGTGTATTTCTCGATCA
810-7.5	ACTCTAAGTTCATTTTACCAACTG	TCTATTCTAGTGTATTTCTCGATCA
810-7.6	GGAAATGTTTCAGAAGCTTTGCTC	TCAAAAATACAACCTTGTTTATGTG

Supplement Table 5. Summary of sequencing data for R and S pools

pool_ID	depth	Clean_Reads	Clean_Base	Q20(%)	Q30(%)	GC(%)
R pool	30×	64,260,336	19,222,565,408	97.33	92.77	37
S pool	30×	64,417,798	19,246,208,216	97.65	93.53	37.22