

## Supplementary Information

### Development of Molecular Marker linked with Bacterial Fruit Blotch resistance in Melon (*Cucumis melo* L.)

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**Table S1:** Details of 22 melon accessions used and their disease response, as determined by bioassay and PCR-based assay using polymorphic InDel marker MB157-2.

Sl.	Genotype	Taxonomy	Origin	Bioassay		Genotype (InDel marker MB157-2)
				Percent infected area per leaf	Phenotype	
1	PI 353814	<i>Cucumis melo</i> subsp. <i>melo</i>	Israel	0	Resistant (Control)	+
2	PI 614596	<i>Cucumis melo</i> subsp. <i>melo</i>	Madhya Pradesh, India	93	Susceptible (Control)	-
3	PI 140471	<i>Cucumis melo</i>	USA	3	Resistant	+
4	PI 420145	<i>Cucumis melo</i>	USA	5	Resistant	+
5	PI 614525	<i>Cucumis melo</i> subsp. <i>agrestis</i>	Madhya Pradesh, India	86	Susceptible	-
6	PI 482398	<i>Cucumis melo</i> subsp. <i>melo</i>	Zimbabwe	54	Susceptible	-
7	PI482399	<i>Cucumis melo</i> subsp. <i>melo</i>	USA	48	Susceptible	-
8	PI 536473	<i>Cucumis melo</i> subsp. <i>agrestis</i>	Maldives	39	Susceptible	-
9	PI 504558	<i>Cucumis ficifolius</i>	India	47	Susceptible	-
10	PI 343701	<i>Cucumis pustulatus</i> (Wild)	Nigeria	35	Susceptible	-
11	PI 614401	<i>Cucumis melo</i> subsp. <i>melo</i>	Rajasthan, India	24	Susceptible	-
12	PI 614601	<i>Cucumis melo</i> subsp. <i>melo</i>	Rajasthan, India	49	Susceptible	-
13	PI 147065	<i>Cucumis anguria</i> var. <i>longaculeatus</i> (Wild)	Amazonas, Brazil	28	Susceptible	-
14	PI 157076	<i>Cucumis melo</i> subsp. <i>melo</i>	China	44	Susceptible	-
15	PI 157082	<i>Cucumis melo</i> subsp. <i>melo</i>	Cornell University, USA	37	Susceptible	-
16	CornellIZPPM	<i>Cucumis melo</i>	Cornel University, USA	48	Susceptible	-
17	PI 357152	<i>Cucumis melo</i> subsp. <i>melo</i>	Peru, Tacna	36	Susceptible	-
18	PI 378171	<i>Cucumis melo</i> subsp. <i>melo</i>	Israel	55	Susceptible	-
19	PI 381763	<i>Cucumis melo</i> subsp. <i>melo</i>	India, Rajasthan	50	Susceptible	-
20	PI 422164	<i>Cucumis melo</i> subsp. <i>melo</i>	Czech Republic	72	Susceptible	-

21	PI 504531	<i>Cucumis melo</i> subsp. <i>melo</i>		Korea, South	39	Susceptible	-
22	PI 512417	<i>Cucumis melo</i> subsp. <i>melo</i>		Spain, Cordoba	31	Susceptible	-
23	PI 512568	<i>Cucumis melo</i>		Spain, Castellon de Plana	64	Susceptible	-
24	SCNU1154	<i>Cucumis melo</i>		SCNU, South Korea	48	Susceptible	-

Resistant (PI 353814) and susceptible parent (PI 614596) were included as control in both bioassay and PCR based assay. All landraces/inbred were collected from USDA, USA, except SCNU1154 which was collected from South Korea. '+' and '-' indicate resistant and susceptible bands for the InDel marker BM157-2.

**Table S2:** Comparison of *Acidovorax citrulli* bioassay results and InDel marker BM157-2 bands for the putative R-gene MELO3C022157 in a population of 491 F2 melon individuals raised from resistant and susceptible parental accessions PI 353814 and PI 614596, respectively. “+”, “и” and “-” indicate resistant, heterozygous and susceptible bands for the InDel marker BM157-2.

Sl.	PIA/L	P	G																
1	46	S	-	45	97	S	-	89	45	S	-	133	8	R	и	177	0	R	и
2	0	R	+	46	10	R	+	90	5	R	и	134	0	R	+	178	42	S	-
3	2	R	и	47	5	R	+	91	3	R	+	135	0	R	и	179	77	S	-
4	39	S	-	48	0	R	+	92	9	R	+	136	3	R	и	180	0	R	и
5	31	S	-	49	100	S	-	93	6	R	и	137	4	R	и	181	38	S	-
6	53	S	-	50	2	R	+	94	14	R	и	138	0	R	+	182	7	R	и
7	1	R	и	51	8	R	и	95	5	R	и	139	44	S	и	183	41	S	-
8	3	R	и	52	29	S	и	96	4	R	и	140	0	R	и	184	3	R	+
9	6	R	+	53	4	R	и	97	11	R	и	141	6	R	+	185	5	R	и
10	4	R	+	54	16	R	и	98	74	S	-	142	0	R	и	186	0	R	+
11	9	R	+	55	43	S	-	99	7	R	и	143	3	R	+	187	0	R	и
12	44	S	-	56	5	R	и	100	38	S	-	144	32	S	и	188	53	S	-
13	17	R	и	57	12	R	+	101	45	S	-	145	2	R	и	189	3	R	и
14	5	R	и	58	24	S	-	102	0	R	и	146	0	R	и	190	64	S	и
15	7	R	+	59	5	R	+	103	33	S	-	147	5	R	+	191	6	R	и
16	3	R	+	60	9	R	и	104	2	R	и	148	7	R	и	192	3	R	и
17	11	R	и	61	4	R	и	105	0	R	+	149	4	R	+	193	0	R	+
18	29	S	-	62	0	R	и	106	27	S	-	150	9	R	+	194	0	R	и
19	5	R	и	63	27	S	-	107	4	R	и	151	0	R	и	195	56	S	-
20	14	R	и	64	3	R	и	108	3	R	+	152	10	R	и	196	28	S	-
21	33	S	-	65	5	R	и	109	15	R	+	153	13	R	и	197	23	S	-
22	3	R	и	66	59	S	-	110	61	S	-	154	18	R	и	198	41	S	-
23	2	R	+	67	15	R	+	111	25	S	-	155	4	R	и	199	50	S	-
24	6	R	и	68	7	R	и	112	0	R	и	156	0	R	+	200	0	R	и
25	10	R	и	69	12	R	и	113	2	R	и	157	6	R	и	201	4	R	+
26	52	S	-	70	6	R	и	114	46	S	-	158	30	S	-	202	22	S	-
27	0	R	+	71	11	R	и	115	7	R	+	159	0	R	и	203	29	S	-
28	4	R	и	72	38	S	-	116	23	S	-	160	73	S	-	204	33	S	-
29	71	S	-	73	52	S	-	117	9	R	и	161	0	R	и	205	46	S	-
30	5	R	и	74	32	S	-	118	3	R	+	162	0	R	и	206	5	R	+
31	3	R	и	75	0	R	и	119	0	R	+	163	5	R	и	207	26	S	-
32	49	S	+	76	6	R	и	120	4	R	и	164	0	R	+	208	4	R	и
33	10	R	+	77	2	R	+	121	75	S	-	165	2	R	и	209	3	R	+
34	3	R	+	78	5	R	+	122	5	R	+	166	4	R	+	210	12	R	и
35	5	R	+	79	9	R	+	123	83	S	-	167	0	R	и	211	5	R	и
36	13	R	+	80	4	R	+	124	0	R	+	168	3	R	и	212	30	S	-
37	2	R	+	81	30	S	-	125	0	R	и	169	0	R	и	213	0	R	и
38	0	R	и	82	7	R	и	126	8	R	и	170	4	R	+	214	24	S	-
39	7	R	и	83	3	R	и	127	2	R	+	171	62	S	-	215	6	R	и
40	53	S	-	84	0	R	+	128	3	R	и	172	43	S	-	216	10	R	и
41	64	S	-	85	13	R	и	129	0	R	+	173	8	R	и	217	8	R	+
42	76	S	-	86	98	S	-	130	6	R	+	174	34	S	-	218	5	R	и
43	3	R	и	87	39	S	-	131	8	R	и	175	47	S	-	219	27	S	-
44	61	S	-	88	9	R	+	132	0	R	+	176	3	R	и	220	3	R	и

SL.	PIA/L	P	G
221	6	R	и
222	0	R	+
223	5	R	+
224	9	R	+
225	5	R	и
226	6	R	+
227	3	R	и
228	4	R	+
229	0	R	+
230	13	R	+
231	4	R	и
232	0	R	+
233	33	S	и
234	0	R	и
235	7	R	+
236	9	R	+
237	10	R	и
238	0	R	и
239	11	R	+
240	14	S	-
241	8	R	и
242	5	R	+
243	9	R	и
244	5	R	+
245	2	R	+
246	14	R	и
247	0	R	+
248	8	R	и
249	12	R	и
250	5	R	и
251	0	R	+
252	34	S	+
253	3	R	и
254	6	R	+
255	0	R	+
256	4	R	и
257	3	R	и
258	4	R	и
259	24	R	и
260	0	R	+
261	24	S	-
262	51	S	-
263	62	S	-
264	43	S	-
265	6	R	+
266	22	S	-
267	25	S	-
268	30	S	-
269	43	S	-
270	7	R	+
271	11	R	и
272	28	S	-
273	10	R	и
274	0	R	+
275	4	R	и
276	0	R	и
277	0	R	+
278	9	R	+
279	36	S	-
280	6	R	и
281	4	R	+
282	12	R	и
283	84	S	-
284	0	R	+
285	5	R	и
286	0	R	+
287	31	S	-
288	24	S	-
289	5	R	и
290	8	R	+
291	3	R	и
292	0	R	+
293	6	R	и
294	78	S	-
295	4	R	и
296	0	R	+
297	24	S	-
298	73	S	-
299	0	R	и
300	6	R	и
301	35	S	-
302	5	R	и
303	57	S	-
304	10	R	и
305	46	S	-
306	74	S	-
307	0	R	и
308	0	R	+
309	0	R	и
310	62	S	-
311	6	R	+
312	0	R	и
313	31	S	-
314	0	R	и
315	48	S	-
316	8	R	+
317	26	S	-
318	39	S	-
319	22	S	-
320	15	R	+
321	36	S	-
322	82	S	-
323	12	R	и
324	10	R	и
325	3	R	+
326	5	R	+
327	34	S	-
328	0	R	и
329	3	R	+
330	7	R	и
331	9	R	и
332	32	S	-
333	5	R	и
334	51	R	+
335	25	S	-
336	3	R	и
337	65	S	-
338	77	S	-
339	27	S	-
340	6	R	+
341	3	R	и
342	34	S	-
343	0	R	и
344	23	S	-
345	35	S	-
346	2	R	и
347	25	S	-
348	0	R	и
349	23	S	-
350	0	R	и
351	5	R	+
352	7	R	и
353	0	R	+
354	9	R	и
355	39	S	+
356	0	R	+
357	0	R	и
358	4	R	+
359	6	H	+
360	2	R	и
361	0	R	+
362	10	R	и
363	5	R	и
364	13	R	и
365	4	R	+
366	37	S	+
367	0	R	и
368	6	R	и
369	0	R	+
370	7	R	+
371	5	R	и
372	6	R	+
373	7	R	и
374	5	R	+
375	0	R	и
376	9	R	+
377	0	R	+
378	0	R	и
379	4	R	+
380	0	R	и
381	4	R	+
382	0	R	+
383	6	R	и
384	3	R	и
385	8	R	+
386	0	R	и
387	0	R	+
388	5	R	и
389	5	R	и
390	0	R	и
391	0	R	+
392	0	R	и
393	0	R	и
394	6	R	+
395	37	S	+
396	4	R	+
397	0	R	и
398	0	R	и
399	4	R	и
400	0	R	+
401	0	R	и
402	0	R	и
403	0	R	и
404	0	R	+
405	5	R	+
406	7	R	и
407	0	R	и
408	11	R	и
409	5	R	+
410	0	R	и
411	0	R	и
412	5	R	и
413	3	R	и
414	0	R	и
415	47	S	-
416	0	R	и
417	3	R	и
418	0	R	и
419	4	R	+
420	0	R	и
421	0	R	и
422	5	R	и
423	40	S	-
424	0	R	-
425	35	S	-
426	30	S	-
427	7	R	и
428	6	R	+
429	0	R	и
430	8	R	и
431	4	R	и
432	31	S	-
433	35	S	-
434	3	R	и
435	6	R	и
436	0	R	и
437	9	R	и
438	0	R	+
439	2	R	и
440	0	R	и
441	0	R	и
442	0	R	+
443	4	R	+
444	5	R	и
445	2	R	и
446	29	S	-
447	50	S	-
448	27	S	-
449	53	S	-
450	0	R	и
451	4	R	и
452	0	R	+
453	0	R	и
454	24	S	-
455	66	S	-
456	4	R	и
457	38	S	-
458	31	S	-
459	0	R	и
460	35	S	-
461	24	S	-
462	0	R	и
463	0	R	и
464	36	S	-
465	56	S	-
466	2	R	+
467	24	S	-
468	47	S	-
469	0	R	и
470	5	R	и
471	0	R	и
472	0	R	и
473	0	R	+
474	0	R	и
475	0	R	и
476	3	R	и
477	0	R	и
478	5	R	+
479	8	R	+
480	69	S	-
481	0	R	и
482	72	S	-
483	0	R	+
484	3	R	+
485	0	R	+
486	0	R	+
487	0	R	+
488	33	S	-
489	5	R	+
490	8	R	и
491	54	S	-

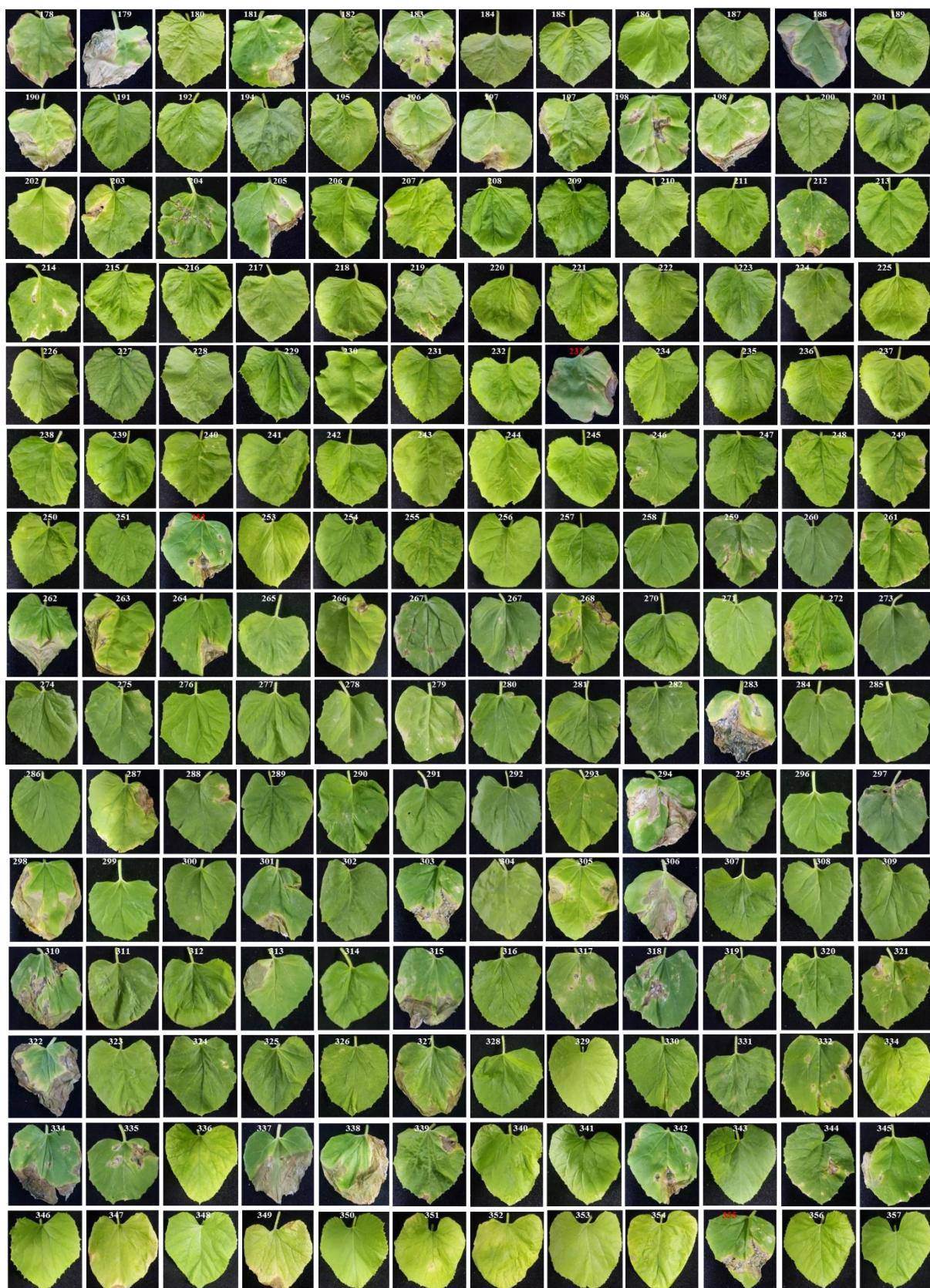
PIA/L. Percent infected Area per leaf, P. phenotype and G. Genotype. Red text indicate mismatch between bioassay phenotype and marker assisted genotype.



**Figure S1:** Disease scores used to assess the severity of bacterial fruit blotch (BFB) caused by *A. citrulli* at 12 days after inoculation. Scores range from 1 to 6, with 1 representing leaves with no damage and 6 representing maximum damage. All leaves were detached just before photographs were taken.



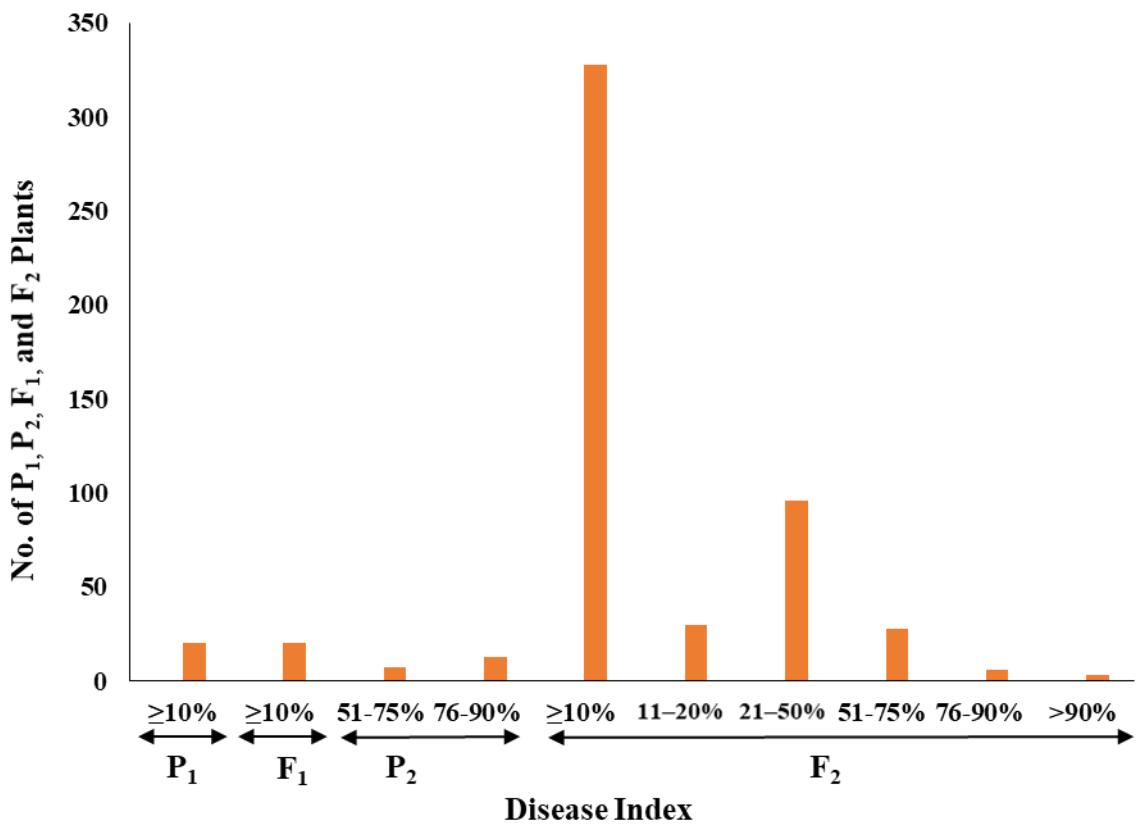
Fig. S1. Continued



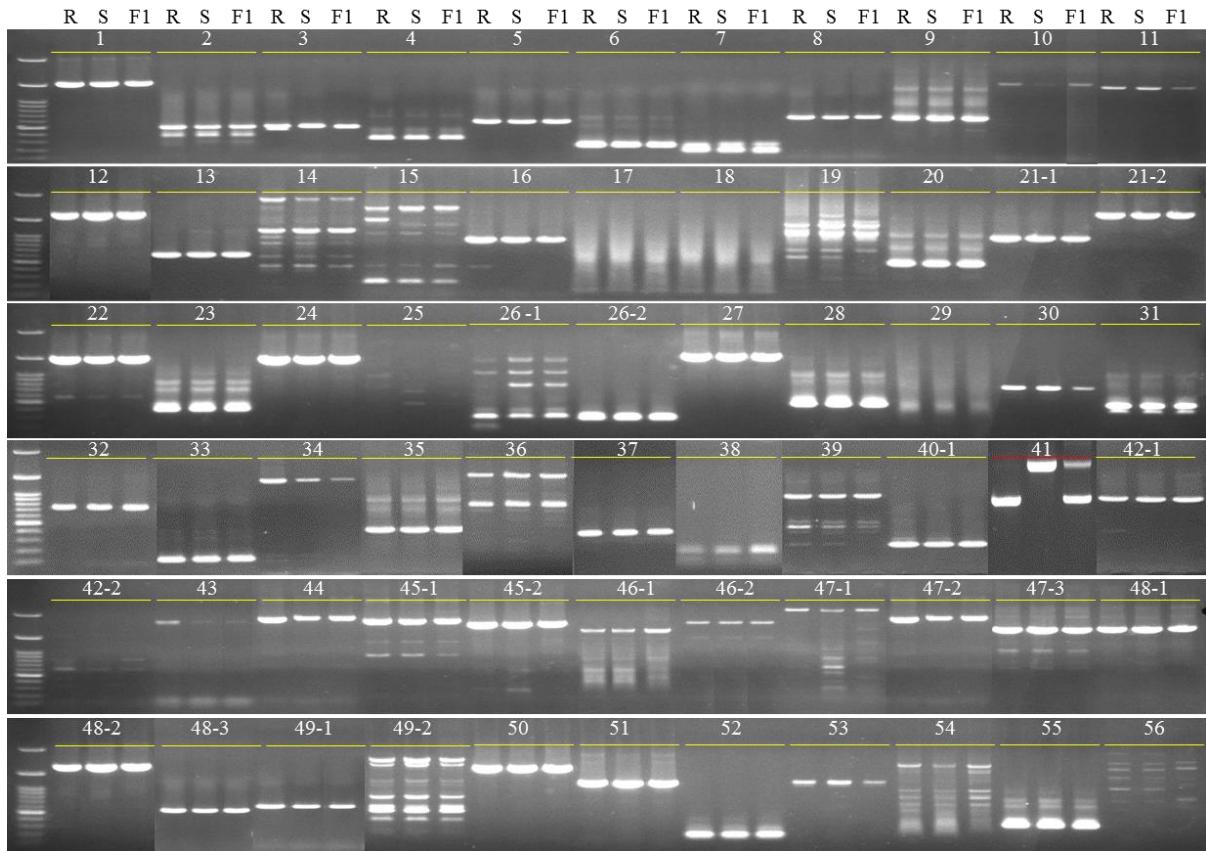
**Fig S1. Continued**



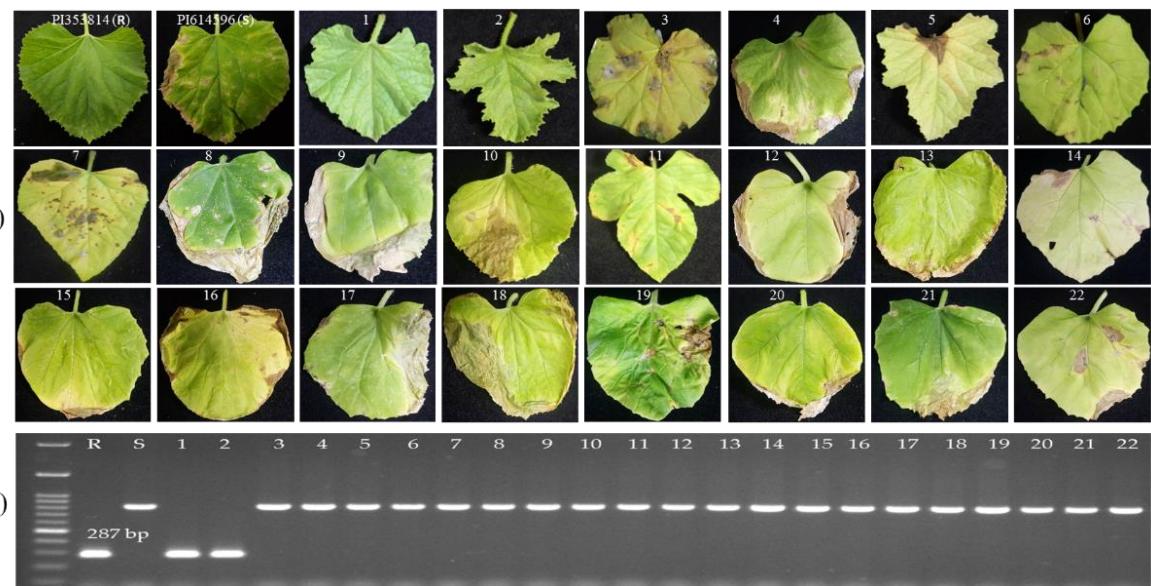
**Figure S2:** Disease symptoms on resistant (R) and susceptible (S) melon parental accessions PI 353814 and PI 614596, respectively, their F1 hybrid and 491 individuals of the F2 population at 12 days after inoculation with *A. citrulli*. All leaves were detached just before photographs were taken.



**Figure S3:** Frequency distribution of BFB scores in melon P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub> and F<sub>2</sub> populations.



**Figure S4:** Detection of length polymorphism in 57 putative disease resistance genes containing NBS, LRR, CC and TIR domains by PCR-based assay. Details of the genes and corresponding primer specifications are presented in Table 1. Genes 40-2 and 57 were not amplified. Gene 41 (red underline) showed conspicuous length polymorphism. R—resistant parent PI 353814, S—susceptible parent PI 614596 and F1—hybrid (PI 614596 × PI 353814).



**Figure S5:** (a) Bacterial fruit blotch (BFB) disease symptoms on 22 melon accessions at 12 days after inoculation with *A. citrulli*. Details of these 22 melon accessions are shown in Supplementary Table S1. All leaves were detached just before photographs were taken. (b) Validation of resistance status to BFB using InDel marker MB157-2 in the 22 melon accessions. R—resistant (PI 353814) and S—susceptible (PI 614596) used as control.

**a. Genomic DNA (gDNA) sequence (with intron)**

>MELO3C022157Ref

ATGGAAGCAATTGAGGAATCAAGAACAGCTATTGGGTTTATCACAAAACATTCTACTTCAGATGGTGT  
TGAGAGAATTGGAGAAGATTATGGAATCCATGGACGGACAAATCGAGTTCTCCTGTGTTTACCATGT  
AGATCCTCTCATGTCATCAATCTGGACCTTTGAGAGAAGCTTGTGAATATGAAAATAATGGACAAG  
ACTCACAAGAGCAGGTTCATCGTGGAGGGATGCTTCGCTAGAGTTGCCATCTGCAGGGTCGTAGTAAA  
CAAAAACAGGTAGGGCTCACTCTCATTATCATTCTTTTATATATAATTATTCGTATG  
GTTAGATGTTAGGAACAACAGACCTCCAATATCTCACAATAATATGATATTATCCACTTAAACATACAT  
CCTCATGGTTTCTTCTTCACTCAAAAAACTATCTCATATATACCGTTGAACCAAAATCCATGGTCA  
TCCCCCTAGTCTTATTAACCGAAATGTGAAACTTGTGATCGCTTCTCACTCGCATTAGACAAAATTGGGTG  
ACTCTAATACCATTGAAACCTAATAGTCTTGTGAGTTGTGCGTCTGATACTATACGTTAGTGATAAACAT  
CCTATTATCTCAAAAACCAATTGACTAATGATCAGGAAGCTAGAGGGAGTACTAGGTCAATTGTTATCTT  
CAAACATGCATTTATGAGGTCTGAACTCCTTGTGTTTCAATGTAGCACACAACTAGCTAACACACTT  
TATTTTTAGCATTCAAGTACATAAAATAATGCAAGTAGAAGAAGTTAGAGATTCTAAATTAAATAGCCTA  
ATAAAATAGTACTTAAAAAAATAATATTACACATAATTGTTCTTACATATTCTAGAATCTGTTGTTCTA  
AAAAGTCTCATGGAATATAGAAGGAGCCGACTAATTGAAGAATTAGATAACACAAACTTTTAAATTGAA  
GGAAAATAACTCTTCAATTGATGGTGTGATTATAGTGGGATTCTGTTAATAGTCGTTCAATTGTTACTA  
TAGGAAGAAAAGCGAATCCAAGCACACCATAAATTGATAAGTGCAGACACTATGTTGACATAC  
TGAAGTGGACAGTATCAACCGAATACCAATCAAATATTGATAAGTGCAGACACTATGTTAATAGGCC  
AATCAATTGAATTACTGGTGTGATTGAAAGTGAAGTAAGCTAAGGGATATCAATAACCTACTTGACTTGAATCAG  
ATGAAGTACGATTAGGAATAGTGGATGGGTGATTGGTAAACAAACTATTGCAAAGTAACTTACACGA  
CAGTATTGCATTACATTATTGGTAAAATTCTGCTTGTCACTATGTCTGGCGTGATATCGTCACGGTCC  
AATGTCTACTACTCTCGACTCTTGAACAGGGAGAATATTAAACATTAGAAAAGAATGAAGGAGC  
CATGATTAAGATTGTTGAGTAGGAGAAGGTTGATTATTGATGGGTGAATGATAGAGAGGAA  
GGATACATAGCCGAAGTTGATTGGTGGAGGAAGTCGAGTCATCATTACCACTAGAAAATAAATG  
TTTTCTCACCCAAATCATGAACAAGTTCAACTCTACAATGTGAAACCACTTGATTACAACACTTCA  
CTTTTGGAAAGCATGCATTGATCAACAAAGTGGGGTCAAGTGAACAAACAATTACACAACTTAGTCAGA  
ATATAGTGGAAAAGGTGAAAGGAAATCCACAAGCATTGAAACAAATTGGATCATTGCTGGTAAAGATA  
TTAATGTATGGAAAAGAATTGAAGAGCCTGTTAGTGTGATAATGAACGTCTTCAAAATATTAAAGAT  
AAAGTTTGTCAATTAGGGACAAAAGGCCAACAGCTTTCTGTTGATTTGGCATGTTCTCAATGGAAAAGT  
ACAGGCAAATTGAAACTTGCAGGTTAGAATACAATTCCCCAGCGAAGTACTAAAGTTGTTG  
ATAGATATCTTATTGAAATTAGAGATGGAGACACAGTATGTATGCCAATTGATACAAGAAATGGTC  
AATAGAACGAAAAAACGTCAAAGAACAGGATTGGCTTAGAAGAGATGCTTCGACATATTGATGAACA  
ACATGTAAGTCTATATGTTACATTATATTGTACATTATTCCATGTTATTAAATTATTAACGTT  
ACTTGGCAGGGAGTAAAGACATAAAAGGTGTTGAGGACAGAGAGACACAGAACCAACTAAAGT  
GAAGGCTAAACAATTACAAGATATGAGCCGTTAAAATATTAGAGATTGACAATGTCAGCTGAGTCCAAG  
AAATCAAATGATCTCAAATCAGCTCGATTGCTCCACTGGGATGGCTTCCCTCAGACACTTGC  
ATTTCGAAGCACCATAATTGAAACTTCTCGCTTAATGCACAAACCACTCATTTGAAAGAAACTAAAG  
GTAGACATATTGCAAATACTTAAACCTGCGCTATATATATATGTTGTTGATTTGCTATTGCAATA  
ATTTCACAAATTCTTCATAACATATAAACATGTTGTTATTGTAACAGGGATTTAGAAATTAA  
AGGTAAATCGATGTTAGCAATTCCAAACTTGGAGACACCGAATTGAGTGTGCTTCAAATCTAGAAAAG  
ATTGATTCTATGTAATTGACAAGATTGAAAGAAAATTGATAATTCAATTACAAATTGAGACTTCTAGTTT  
TAGACCTCACAGGCTGTGTTGCCCTCGAAACATCCGAGTGCATCGATATCTGAAGAGTCGCCAACAGTAGA  
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 GGCTAGTTCTACAGTGCCTAACATTGAAAGGTATTGTTATTGCTAAATTTCACTTCTTTTAA  
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 ACTCACAAGAGCAGGTCATCGTGGAGGGATGCTTCGCTAGAGTTGGCATCTGCAGGGTCGTAGTAAA  
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 GTTAGATGTTAGGAACAACAGACCTCCAAATATCTTACAATAATATGATATTATCCACTTTAACATACAT  
 CCTTCATGGTTTCCGTTCACTCCAAATTAAAGTGGCATCTGCAGGTCTCTCATATTCTTCTTATAT  
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 AAAAACCAATTGACTAATGATCAGGAAGCTAGAGGGAGTACTAGGTCTATGTATCTTAAACATGCATT  
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 AGCGAATCCAAGCACACCATAAATTGGGATTCTGACATACTACTCTTGGCCATGCAGCCCTGAAGTGGACAGTA  
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 GTGCCAATCATTGAAAGGTATTGTTATTCGTAAATTTCACTTCTTTAAATTCAAGGATCATTG  
 TGAA

**b. CLUSTALW multiple sequence alignment of gDNA sequence (with intron)**

CLUSTAL 2.1 multiple sequence alignment

MELO3C022157Ref	ATGGAAGAACATTGAGGAATCAAGAACAGCTATTGGTTTATCACAAACTATTCTACT	60
PI353814_R	ATGGAAGAACATTGAGGAATCAAGAACAGCTATTGGTTTATCACAAACTATTCTACT	60
PI614596_S	ATGGAAGAACATTGAGGAATCAAGAACAGCTATTGGTTTATCACAAACTATTCTACT	60
*****	*****	*****
MELO3C022157Ref	TCAAGATGGTGCCTTGAGAGATTGGAGAAGATTGGAAATCCATGGACGACGGAACAAAT	120
PI353814_R	TCAAGATGGTGCCTTGAGAGATTGGAGAAGATTGGAAATCCATGGACGACGGAACAAAT	120
PI614596_S	TCAAGATGGTGCCTTGAGAGATTGGAGAAGATTGGAAATCCATGGACGACGGAACAAAT	120
*****	*****	*****
MELO3C022157Ref	CGAGTTCTCCTGTGTTTACCATGTAGATCCTCTCATGTTGTCATCACTGGACCT	180
PI353814_R	CGAGTTCTCCTGTGTTTACCATGTAGATCCTCTCATGTTGTCATCACTGGACCT	180
PI614596_S	CGAGTTCTCCTGTGTTTACCATGTAGATCCTCTCATGTTGTCATCACTGGACCT	180
*****	*****	*****
MELO3C022157Ref	TTTGAGAGAACGTTGTAATGAAAATAATGGACAAGACTCACAAGAGCAGGTTCAT	240
PI353814_R	TTTGAGAGAACGTTGTAATGAAAATAATGGACAAGACTCACAAGAGCAGGTTCAT	240
PI614596_S	TTTGAGAGAACGTTGTAATGAAAATAATGGACAAGACTCACAAGAGCAGGTTCAT	240
*****	*****	*****
MELO3C022157Ref	CGGTGGAGGGATGCTTCGCTAGAGTTGGCCATCTGCAGGGGCGTAGTAAACAAAAC	300
PI353814_R	CGGTGGAGGGATGCTTCGCTAGAGTTGGCCATCTGCAGGGGCGTAGTAAACAAAAC	300
PI614596_S	CGGTGGAGGGATGCTTCGCTAGAGTTGGCCATCTGCAGGGGCGTAGTAAACAAAAC	300
*****	*****	*****
MELO3C022157Ref	AGGTAGGGCTCACTCTCATTATCATTTCCTTTTTTTATATATAATTATT	360
PI353814_R	AGGTAGGGCTCACTCTCATTATCATTTCCTTTTTTTATATATAATTATT	360
PI614596_S	AGGTAGGGCTCACTCTCATTATCATTTCCTTTTTTTATATATAATTATT	360
*****	*****	*****
MELO3C022157Ref	CTTCGTATGGTAGATGTTAGGAACACAGACCTCAAATATCTCACAATAATATGAT	420
PI353814_R	CTTCGTATGGTAGATGTTAGGAACACAGACCTCAAATATCTCACAATAATATGAT	420
PI614596_S	CTTCGTATGGTAGATGTTAGGAACACAGACCTCAAATATCTCACAATAATATGAT	420
*****	*****	*****
MELO3C022157Ref	ATTATCCATTAAACATACATCCTCATGGTTTC-----	457
PI353814_R	ATTATCCATTAAACATACATCCTCATGGTTTC-----	457
PI614596_S	ATTATCCATTAAACATACATCCTCATGGTTTCGTTCACTCCAAATTAAAGGAAACCAAAACAA	480
*****	*****	*****
MELO3C022157Ref	-----	457
PI353814_R	-----	457
PI614596_S	CATCTTGCAGGTCTTCATTATCATTCTTATATATAATAAAACAAACCAAAACAA	540
MELO3C022157Ref	-----	457
PI353814_R	-----	457
PI614596_S	CCAAAACCTTCGCAGAGTTGAACCTTCGCAGAGTTGCATCTGCAGGGCGTAGTA	600
MELO3C022157Ref	-----	457
PI353814_R	-----	457
PI614596_S	AACAAACAACCAAAACCTTCGCAGAGTTGCATCTGCAGGGCGTAGTA	660
MELO3C022157Ref	-----	457
PI353814_R	-----	457
PI614596_S	-----	457

PI614596_S	<b>TCGCAGAGTTGGCATCTTGCAGGTCTCATTATCATTCTCTTCTTCTTCTCAGGCTCACTCG</b>	720
MEL03C022157Ref	-----	457
PI353814_R	-----	457
PI614596_S	<b>CAGAGTTGGCATCTTGCAGGTCTCATTATTTATATAATTATTCGTATGGT</b>	780
MEL03C022157Ref	-----	457
PI353814_R	-----	457
PI614596_S	<b>AGATTGTTCACTCCAAAACAACCAACCTTGCAGAGTTGGCATCTTGCAGGGTCGT</b>	840
MEL03C022157Ref	-----	457
PI353814_R	-----	457
PI614596_S	<b>GTTAGGGAACAACAGAGGTCGTAGTAACACAAAAACGGTAGGGTCTCACCTCAAATATCT</b>	900
MEL03C022157Ref	-----	457
PI353814_R	-----	457
PI614596_S	<b>TCACAAGTAGGGTCTCATATAATGATATTATCCACTTAAACACATACATCCTTCATGGTC</b>	960
MEL03C022157Ref	-TTTGTCTTCACTAAAAACTATCTCATATAT <b>ACCGTTGAACCAAAATCCATGGTC</b>	516
PI353814_R	-TTTGTCTTCACTAAAAACTATCTCATATAT <b>ACCGTTGAACCAAAATCCATGGTC</b>	516
PI614596_S	<b>CTTTGTCTTCACTAAAAACTATCTCATATAT<b>ACCGTTGAACCAAAATCCATGGTC</b></b>	1020
MEL03C022157Ref	*****	
PI353814_R	ATCCCCTAGTCTTATTAACGAAATGTGAAACTTGTGATCGTTCTCACCTCGCATT	576
PI614596_S	ATCCCCTAGTCTTATTAACGAAATGTGAAACTTGTGATCGTTCTCACCTCGCATT	576
	ATCCCCTAGTCTTATTAACGAAATGTGAAACTTGTGATCGTTCTCACCTCGCATT	1080
MEL03C022157Ref	*****	
PI353814_R	GACAAAATTGGGTGTACTCTAATACCATTGGTGAACCTAATAGTCTTGTG	636
PI614596_S	GACAAAATTGGGTGTACTCTAATACCATTGGTGAACCTAATAGTCTTGTG	636
	GACAAAATTGGGTGTACTCTAATACCATTGGTGAACCTAATAGTCTTGTG	1140
MEL03C022157Ref	*****	
PI353814_R	GTTCTGATACTATACGTTAGTGTATAAACATCCTATTATCTCAAAAACCAATTGACT	696
PI614596_S	GTTCTGATACTATACGTTAGTGTATAAACATCCTATTATCTCAAAAACCAATTGACT	696
	GTTCTGATACTATACGTTAGTGTATAAACATCCTATTATCTCAAAAACCAATTGACT	1200
MEL03C022157Ref	*****	
PI353814_R	ATGATCAGGAAGCTAGAGGGAGT <b>ACTAGGT</b> CATTGTATCTTACAAACATGCATTATGA	756
PI614596_S	ATGATCAGGAAGCTAGAGGGAGT <b>----</b> GTCTTACAAACATGCATTATGA	751
	ATGATCAGGAAGCTAGAGGGAGT <b>ACTAGGT</b> CATTGTATCTTACAAACATGCATTATGA	1260
MEL03C022157Ref	*****	
PI353814_R	GGTCTGAACCTCTTGTCTTCCAATGTAGCACACAACTAGCTCAACACACTTTAT	816
PI614596_S	GGTCTGAACCTCTTGTCTTCCAATGTAGCACACAACTAGCTCAACACACTTTAT	811
	GGTCTGAACCTCTTGTCTTCCAATGTAGCACACAACTAGCTCAACACACTTTAT	1320
MEL03C022157Ref	*****	
PI353814_R	TTTTAGCATTCAAGTACATAAAATAATATGCAATAGAAGAAGTTAGAGATTCTCAAAT	876
PI614596_S	TTTTAGCATTCAAGTACATAAAATAATATGCAATAGAAGAAGTTAGAGATTCTCAAAT	871
	TTTTAGCATTCAAGTACATAAAATAATATGCAATAGAAGAAGTTAGAGATTCTCAAAT	1380
MEL03C022157Ref	*****	
PI353814_R	TAATAGCCTAATAAAATAGTCTTAAAAAAATAATTACACATAATTGTTCTTACAT	936
PI614596_S	TAATAGCCTAATAAAATAGTCTTAAAAAAATAATTACACATAATTGTTCTTACAT	931
	TAATAGCCTAATAAAATAGTCTTAAAAAAATAATTACACATAATTGTTCTTACAT	1440
MEL03C022157Ref	*****	
PI353814_R	ATTCCTAGAATCTCTGTTGTTCTAAAAGTCTCATGGAATATATAGAAAGGCCGAC	996
PI614596_S	ATTCCTAGAATCTCTGTTGTTCTAAAAGTCTCATGGAATATATAGAAAGGCCGAC	991
	ATTCCTAGAATCTCTGTTGTTCTAAAAGTCTCATGGAATATATAGAAAGGCCGAC	1500
MEL03C022157Ref	*****	
PI353814_R	TAATTGAAGAATTAGATACACAAACTTTTGAAGATTAGGAAATAACTCTTCTATTGA	1056
PI614596_S	TAATTGAAGAATTAGATACACAAACTTTTGAAGATTAGGAAATAACTCTTCTATTGA	1051
	TAATTGAAGAATTAGATACACAAACTTTTGAAGATTAGGAAATAACTCTTCTATTGA	1560
MEL03C022157Ref	*****	
PI353814_R	TGGTGTGGATTATAGTGGGATTCTGTTAATAGTCGTCATTGTATACTATAGGAAGA	1116
PI614596_S	TGGTGTGGATTATAGTGGGATTCTGTTAATAGTCGTCATTGTATACTATAGGAAGA	1111
	TGGTGTGGATTATAGTGGGATTCTGTTAATAGTCGTCATTGTATACTATAGGAAGA	1620
MEL03C022157Ref	*****	
PI353814_R	AAGAAAGCGAATCCAAGCACACCATAAATT <b>TT</b> TTTGACATACTACTCTTGGCCATGC	1176
PI614596_S	AAGAAAGCGAATCCAAGCACACCATAAATT <b>TT</b> TTTGACATACTACTCTTGGCCATGC	1171
	AAGAAAGCGAATCCAAGCACACCATAAATT <b>TT</b> TTTGACATACTACTCTTGGCCATGC	1680
MEL03C022157Ref	*****	
PI353814_R	AGCCCTGAAGTGGACAGTATCAACCGAATCACCACCAATATTGATAAGTTGCGAAGA	1236
PI614596_S	AGCCCTGAAGTGGACAGTATCAACCGAATCACCACCAATATTGATAAGTTGCGAAGA	1231
	AGCCCTGAAGTGGACAGTATCAACCGAATCACCACCAATATTGATAAGTTGCGAAGA	1740
MEL03C022157Ref	*****	
PI353814_R	CCTATGTTAATAGGCCCTAATCAATTGAAATTACTGGTTGATATGCGAAGTAAGCTAAGG	1296
PI614596_S	CCTATGTTAATAGGCCCTAATCAATTGAAATTACTGGTTGATATGCGAAGTAAGCTAAGG	1291
	CCTATGTTAATAGGCCCTAATCAATTGAAATTACTGGTTGATATGCGAAGTAAGCTAAGG	1800

MELO3C022157Ref	GATATCAATAACCTACTTGACTTTGAATCAGATGAAGTACGATTATAGGAATAGTTGGA	1356
PI353814_R	GATATCAATAACCTACTTGACTTTGAATCAGATGAAGTACGATTATAGGAATAGTTGGA	1351
PI614596_S	GATATCAATAACCTACTTGACTTTGAATCAGATGAAGTACGATTATAGGAATAGTTGGA	1860
MELO3C022157Ref	ATGGGTGGTATTGGTAAAACAACATTGCAAAAGTTTACACGACAGTATTGCATTACA	1416
PI353814_R	ATGAGTGGTATTGGTAAAACAACATTGCAAAAGTTTACACGACAGTATTGCATTACA	1411
PI614596_S	ATGGGTGGTATTGGTAAAACAACATTGCAAAAGTTTACACGACAGTATTGCATTACA	1920
MELO3C022157Ref	TTATTTGGTAAAATTCTTGCTTTGCACTATGCTCTGGCGTGATATCGCACGGTCAA	1476
PI353814_R	TTATTTGGTAAAATTCTTGCTTTGCACTATGCTCTGGCGTGATATCGCACGGTCAA	1471
PI614596_S	TTATTTGGTAAAATTCTTGCTTTGCACTATGCTCTGGCGTGATATCGCACGGTCAA	1980
*****SNP at 2035 <sup>th</sup> on susceptible parent		
MELO3C022157Ref	TGTCTACTACTCTCTCGACTTCTTGAACTAGGGAGAATATTAACATTTAGAAAAGAAT	1536
PI353814_R	TGTCTACTACTCTCTCGACTTCTTGAACTAGGGAGAATATTAACATTTAGAAAGAAT	1531
PI614596_S	TGTCTACTACTCTCTCGACTTCTTGAACTAGGGAGAATATTAACATTTAGAAAGAAT	2040
MELO3C022157Ref	GAAGGAGCAACATGATTAAGATTGTTGAGTAGGAGAAAGGTTTGATTATTTGAT	1596
PI353814_R	GAAGGAGCAACATGATTAAGATTGTTGAGTAGGAGAAAGGTTTGATTATTTGAT	1596
PI614596_S	GAAGGAGCAACATGATTAAGATTGTTGAGTAGGAGAAAGGTTTGATTATTTGAT	2100
MELO3C022157Ref	GGGGTGAATGATAGAGAGGAATTAGGATACATAGCCGAAGTTTGATTGGTTGGTCGA	1656
PI353814_R	GGGGTGAATGATAGAGAGGAATTAGGATACATAGCCGAAGTTTGATTGGTTGGTCGA	1651
PI614596_S	GGGGTGAATGATAGAGAGGAATTAGGATACATAGCCGAAGTTTGATTGGTTGGTCGA	2160
MELO3C022157Ref	GGAAGTCGAGTCATCATTACACTAGAAATAAAATGTTTCTCACCCCAATCATGAA	1716
PI353814_R	GGAAGTCGAGTCATCATTACACTAGAAATAAAATGTTTCTCACCCCAATCATGAA	1711
PI614596_S	GGAAGTCGAGTCATCATTACACTAGAAATAAAATGTTTCTCACCCCAATCATGAA	2220
MELO3C022157Ref	CAAGTTCAACTCTACAATGTGAAACCACTTGAATTACAACACTTCACTTTTTGG	1776
PI353814_R	CAAGTTCAACTCTACAATGTGAAACCACTTGAATTACAACACTTCACTTTTTGG	1771
PI614596_S	CAAGTTCAACTCTACAATGTGAAACCACTTGAATTACAACACTTCACTTTTTGG	2280
MELO3C022157Ref	AAGCATGCATTGATCAACAAAGTGGGGTCCAAGTGAACAAACATTACAACTTAGT	1836
PI353814_R	AAGCATGCATTGATCAACAAAGTGGGGTCCAAGTGAACAAACATTACAACTTAGT	1831
PI614596_S	AAGCATGCATTGATCAACAAAGTGGGGTCCAAGTGAACAAACATTACAACTTAGT	2340
MELO3C022157Ref	CAGAATATAGTGGAAAAGGTCGAAGGAAATCCACAAGCATTGGAACAAATTGGATCATTT	1896
PI353814_R	CAGAATATAGTGGAAAAGGTCGAAGGAAATCCACAAGCATTGGAACAAATTGGATCATTT	1891
PI614596_S	CAGAATATAGTGGAAAAGGTCGAAGGAAATCCACAAGCATTGGAACAAATTGGATCATTT	2400
MELO3C022157Ref	TTGCGTGGTAAAGATATTAATGTATGGAAAGAAGATTGAAGAGCCTGTTAGTTGAT	1956
PI353814_R	TTGCGTGGTAAAGATATTAATGTATGGAAAGAAGATTGAAGAGCCTGTTAGTTGAT	1951
PI614596_S	TTGCGTGGTAAAGATATTAATGTATGGAAAGAAGATTGAAGAGCCTGTTAGTTGAT	2460
MELO3C022157Ref	AATGAACGCTCTTCAAAATATAAAGATAAGTTGATCAATTAGGGACAAAAGGCCAA	2016
PI353814_R	AATGAACGCTCTTCAAAATATAAAGATAAGTTGATCAATTAGGGACAAAAGGCCAA	2011
PI614596_S	AATGAACGCTCTTCAAAATATAAAGATAAGTTGATCAATTAGGGACAAAAGGCCAA	2516
MELO3C022157Ref	CAAGCTTTCTTGATTGGCATGTTCTTCAATGGAAAAAGTACAGGCAAATTATTGAA	2076
PI353814_R	CAAGCTTTCTTGATTGGCATGTTCTTCAATGGAAAAAGTACAGGCAAATTATTGAA	2071
PI614596_S	CAAGCTTTCTTGATTGGCATGTTCTTCAATGGAAAAAGTACAGGCAAATTATTGAA	2576
MELO3C022157Ref	ATACTTGCAGTTAGAATACAATTCCCCCAGCGAAGTACTAAAGTTGTTGTGATAGA	2136
PI353814_R	ATACTTGCAGTTAGAATACAATTCCCCCAGCGAAGTACTAAAGTTGTTGTGATAGA	2131
PI614596_S	ATACTTGCAGTTAGAATACAATTCCCCCAGCGAAGTACTAAAGTTGTTGTGATAGA	2636
MELO3C022157Ref	TATCTTATTGAAATTAGAGATGGAGACACAGTATGTATGCCAATTGATACAAGAAATG	2196
PI353814_R	TATCTTATTGAAATTAGAGATGGAGACACAGTATGTATGCCAATTGATACAAGAAATG	2191
PI614596_S	TATCTTATTGAAATTAGAGATGGAGACACAGTATGTATGCCAATTGATACAAGAAATG	2696
MELO3C022157Ref	GGTCGAGAAATAGAACCAACGGTCAAAGAACGAGCAGGATTGGCTTAGAAGAGATGCT	2256
PI353814_R	GGTCGAGAAATAGAACCAACGGTCAAAGAACGAGCAGGATTGGCTTAGAAGAGATGCT	2251
PI614596_S	GGTCGAGAAATAGAACCAACGGTCAAAGAACGAGCAGGATTGGCTTAGAAGAGATGCT	2756
MELO3C022157Ref	TTCGACATATTGATGAACACATGTAAGTCTATATGTTACATTATATTGTACAT	2316
PI353814_R	TTCGACATATTGATGAACACATGTAAGTCTATATGTTACATTATATTGTACAT	2311
PI614596_S	TTCGACATATTGATGAACACATGTAAGTCTATATGTTACATTATATTGTACAT	2816
MELO3C022157Ref	TATTTCCATGTTATTAAATTATTAACTGATTACTTGGCAGGGAGTAAAGACATA	2376
PI353814_R	TATTTCCATGTTATTAAATTATTAACTGATTACTTGGCAGGGAGTAAAGACATA	2371
PI614596_S	TATTTCCATGTTATTAAATTATTAACTGATTACTTGGCAGGGAGTAAAGACATA	2876

MELO3C022157Ref	AAAGGTGTTGTTGGACAAGAGAGACACAGAACAAACTTAAAGTGAGGCTAAACAA	2436
PI353814_R	AAAGGTGTTGTTGGACAAGAGAGACACAGAACAAACTTAAAGTGAGGCTAAACAA	2431
PI614596_S	AAAGGTGTTGTTGGACAAGAGAGACACAGAACAAACTTAAAGTGAGGCTAAACAA	2936
MELO3C022157Ref	TTACAAGATATGAGCGTTTA <sub>AA</sub> ATATTAGAGATTGACAATGTGCAGCTGAGTCAGA	2496
PI353814_R	TTACAAGATATGAGCGTTTA <sub>AA</sub> ATATTAGAGATTGACAATGTGCAGCTGAGTCAGA	2491
PI614596_S	TTACAAGATATGAGCGTTTA <sub>AA</sub> ATATTAGAGATTGACAATGTGCAGCTGAGTCAGA	2996
MELO3C022157Ref	AATCAAATGATCTCTCAAATCAGCTCGATTGCTCCACTGGGATGGCTTCCAGAC	2556
PI353814_R	AATCAAATGATCTCTCAAATCAGCTCGATTGCTCCACTGGGATGGCTTCCAGAC	2551
PI614596_S	AATCAAATGATCTCTCAAATCAGCTCGATTGCTCCACTGGGATGGCTTCCAGAC	3056
MELO3C022157Ref	ACTTTGCCACTAAATTGCAAGCACCATATTGAACTTCTCTGCCTAATGCACAA	2616
PI353814_R	ACTTTGCCACTAAATTGCAAGCACCATATTGAACTTCTCTGCCTAATGCACAA	2611
PI614596_S	ACTTTGCCACTAAATTGCAAGCACCATATTGAACTTCTCTGCCTAATGCACAA	3116
MELO3C022157Ref	ACCACTCATCTTGGAAAGAACATAAGGTTAGACATATTTGCAAAACTTAAACCTGC	2676
PI353814_R	ACCACTCATCTTGGAAAGAACATAAGGTTAGACATATTTGCAAAACTTAAACCTGC	2671
PI614596_S	ACCACTCATCTTGGAAAGAACATAAGGTTAGACATATTTGCAAAACTTAAACCTGC	3176
MELO3C022157Ref	GCTATATATATATATGTTGATTGCTATTGCAATAATTTCAAATTTCCTTC	2736
PI353814_R	GCTATATATATATATGTTGATTGCTATTGCAATAATTTCAAATTTCCTTC	2731
PI614596_S	GCTATATATATATATGTTGATTGCTATTGCAATAATTTCAAATTTCCTTC	3236
MELO3C022157Ref	ATAACATATAAACATGTTGTTATTGGAACAGGGATTTAAGAAATTAAAGGT	2996
PI353814_R	ATAACATATAAACATGTTGTTATTGGAACAGGGATTTAAGAAATTAAAGGT	2991
PI614596_S	ATAACATATAAACATGTTGTTATTGGAACAGGGATTTAAGAAATTAAAGGT	3296
MELO3C022157Ref	ATCGATGTTAGCAATTCCAAACTTGGTGGAGACACCGAATTGAGTGCTGTTCCAAAT	2856
PI353814_R	ATCGATGTTAGCAATTCCAAACTTGGTGGAGACACCGAATTGAGTGCTGTTCCAAAT	2851
PI614596_S	ATCGATGTTAGCAATTCCAAACTTGGTGGAGACACCGAATTGAGTGCTGTTCCAAAT	3356
MELO3C022157Ref	CTAGAAAGATTGATTCTATGTAATTGACAAGATTGATAATTCAATTACA	2916
PI353814_R	CTAGAAAGATTGATTCTATGTAATTGACAAGATTGATAATTCAATTACA	2911
PI614596_S	CTAGAAAGATTGATTCTATGTAATTGACAAGATTGAGAAATTGATAATTCAATTACA	3416
MELO3C022157Ref	AAATTGAGACTCTAGTTTAGTAGACCTCACAGGCTGTGTCGCTCGAACACATCCGAG	2976
PI353814_R	AAATTGAGACTCTAGTTTAGTAGACCTCACAGGCTGTGTCGCTCGAACACATCCGAG	2971
PI614596_S	AAATTGAGACTCTAGTTTAGTAGACCTCACAGGCTGTGTCGCTCGAACACATCCGAG	3476
MELO3C022157Ref	TGCATCGATATCTTGAAGAGTCGCCAACAGTAGAACCTCGTGGCTAGTCTACAGTGT	3036
PI353814_R	TGCATCGATATCTTGAAGAGTCGCCAACAGTAGAACCTCGTGGCTAGTCTACAGTGT	3031
PI614596_S	TGCATCGATATCTTGAAGAGTCGCCAACAGTAGAACCTCGTGGCTAGTCTACAGTGT	3536
MELO3C022157Ref	CGCCAATCATGAAAGGTATTGTTATTCGTAATTGTTCACTTCTTTAAAATT	3096
PI353814_R	CGCCAATCATGAAAGGTATTGTTATTCGTAATTGTTCACTTCTTTAAAATT	3091
PI614596_S	CGCCAATCATGAAAGGTATTGTTATTCGTAATTGTTCACTTCTTTAAAATT	3596
MELO3C022157Ref	CAGGATCATTTGTGTA <sub>AA</sub> 3114	
PI353814_R	CAGGATCATTTGTGTA <sub>AA</sub> 3109	
PI614596_S	CAGGATCATTTGTGTA <sub>AA</sub> 3614	

### (c)InterProScan (protein)

#### Reference (MELO3C022157)

5'3' Frame 1  
**ME**AIEE~~SRTAIVVLSQNYS~~TSRWCL~~RELEKIM~~**E**MS~~MDDGTN~~RVL~~PVFYHVDPSHVRHQSGPFERSFVEYENNQDSQE~~QVHRWRDA~~FARVGHLAGVVVNKN~~SPEVDS~~SINRITNQI~~FDKLRRP~~MLIGPNQNL~~YLD~~RSKLRD~~INNNLDFESDE VR~~FIGIVG~~**G**GGIGKTTIAKVLHSIAFTL~~FGENS~~CFV~~TMSGRD~~I~~VTVQ~~LLSRL~~LGT~~TRN~~NILE~~NEGAN~~MIKDC~~LSRKV~~LI~~1~~FDGVND~~REELG~~YIAGSF~~DFWGR~~GSRV~~I~~ITTR~~KNVFSHPNHEQVQLNVP~~KPLD~~YN~~TSFL~~WKA~~H~~ DQ~~QSGGP~~SEQQFIQLS~~QNI~~VE~~KVE~~GN~~PALE~~Q~~IGS~~FLRG~~KD~~IN~~W~~KEEL~~KS~~L~~V~~L~~V~~D~~N~~ER~~LF~~K~~IL~~1~~SDQ~~LG~~TK~~Q~~QA~~FL~~DL~~AC~~FNG~~K~~STG~~R~~II~~EL~~IAS~~LY~~N~~SP~~E~~V~~L~~K~~L~~CD~~R~~Y~~L~~IE~~1~~RD~~D~~T~~V~~C~~M~~N~~L~~IQ~~E~~RE~~ER~~K~~R~~Q~~S~~R~~I~~WL RRDAD~~F~~IF~~D~~E~~H~~G~~V~~K~~D~~I~~K~~G~~V~~LL~~K~~R~~D~~T~~E~~P~~N~~L~~K~~A~~Q~~L~~Q~~D~~M~~S~~R~~K~~L~~I~~E~~D~~N~~V~~O~~L~~S~~PR~~Q~~N~~D~~L~~S~~N~~Q~~L~~R~~L~~H~~WD~~G~~F~~P~~S~~D~~T~~L~~PN~~F~~E~~A~~Y~~L~~FE~~LL~~LP~~NA~~Q~~T~~TH~~W~~K~~E~~L~~K~~G~~F~~K~~KK~~L~~V~~ID~~V~~S~~N~~S~~Q~~L~~T~~V~~E~~T~~P~~N~~L~~S~~A~~V~~N~~L~~E~~R~~L~~I~~L~~C~~N~~C~~T~~R~~L~~K~~I~~NS~~I~~ TKL~~R~~L~~L~~V~~D~~L~~T~~GC~~V~~R~~L~~E~~T~~SEC~~I~~D~~L~~K~~S~~R~~P~~T~~V~~EL~~R~~GL~~V~~L~~Q~~C~~R~~SL~~K~~G~~C~~Y~~I~~R~~K~~FFF~~K~~I~~Q~~D~~H~~V-

#### Resistant Parent

5'3' Frame 1  
**ME**AIEE~~SRTAIVVLSQNYS~~TSRWCL~~RELEKIM~~**E**MS~~MDDGTN~~RVL~~PVFYHVDPSHVRHQSGPFERSFVEYENNQDSQE~~QVHRWRDA~~FARVGHLAGVVVNKN~~SPEVDS~~SINRITNQI~~FDKLRRP~~MLIGPNQNL~~YLD~~RSKLRD~~INNNLDFESDE VR~~FIGIVG~~**G**GGIGKTTIAKVLHSIAFTL~~FGENS~~CFV~~TMSGRD~~I~~VTVQ~~LLSRL~~LGT~~TRN~~NILE~~NEGAN~~MIKDC~~LSRKV~~LI~~1~~FDGVND~~REELG~~YIAGSF~~DFWGR~~GSRV~~I~~ITTR~~KNVFSHPNHEQVQLNVP~~KPLD~~YN~~TSFL~~WKA~~H~~ DQ~~QSGGP~~SEQQFIQLS~~QNI~~VE~~KVE~~GN~~PALE~~Q~~IGS~~FLRG~~KD~~IN~~W~~KEEL~~KS~~L~~V~~L~~V~~D~~N~~ER~~LF~~K~~IL~~1~~SDQ~~LG~~TK~~Q~~QA~~FL~~DL~~AC~~FNG~~K~~STG~~R~~II~~EL~~IAS~~LY~~N~~SP~~E~~V~~L~~K~~L~~CD~~R~~Y~~L~~IE~~1~~RD~~D~~T~~V~~C~~M~~N~~L~~IQ~~E~~RE~~ER~~K~~R~~Q~~S~~R~~I~~WL RRDAD~~F~~IF~~D~~E~~H~~G~~V~~K~~D~~I~~K~~G~~V~~LL~~K~~R~~D~~T~~E~~P~~N~~L~~K~~A~~Q~~L~~Q~~D~~M~~S~~R~~K~~L~~I~~E~~D~~N~~V~~O~~L~~S~~PR~~Q~~N~~D~~L~~S~~N~~Q~~L~~R~~L~~H~~WD~~G~~F~~P~~S~~D~~T~~L~~PN~~F~~E~~A~~Y~~L~~FE~~LL~~LP~~NA~~Q~~T~~TH~~W~~K~~E~~L~~K~~G~~F~~K~~KK~~L~~V~~ID~~V~~S~~N~~S~~Q~~L~~T~~V~~E~~T~~P~~N~~L~~S~~A~~V~~N~~L~~E~~R~~L~~I~~L~~C~~N~~C~~T~~R~~L~~K~~I~~NS~~I~~ TKL~~R~~L~~L~~V~~D~~L~~T~~GC~~V~~R~~L~~E~~T~~SEC~~I~~D~~L~~K~~S~~R~~P~~T~~V~~EL~~R~~GL~~V~~L~~Q~~C~~R~~SL~~K~~G~~C~~Y~~I~~R~~K~~FFF~~K~~I~~Q~~D~~H~~V-

#### Susceptible Parent

5'3' Frame 1  
**ME**AIEE~~SRTAIVVLSQNYS~~TSRWCL~~RELEKIM~~**E**MS~~MDDGTN~~RVL~~PVFYHVDPSHVRHQSGPFERSFVEYENNQDSQE~~QVHRWRDA~~FARVGHLAGVVVNKN~~SPEVDS~~SINRITNQI~~FDKLRRP~~MLIGPNQNL~~YLD~~RSKLRD~~INNNLDFESDE VR~~FIGIVG~~**G**GGIGKTTIAKVLHSIAFTL~~FGENS~~CFV~~TMSGRD~~I~~VTVQ~~LLSRL~~LGT~~TRN~~NILE~~NEGAN~~MIKDC~~LSRKV~~LI~~1~~FDGVND~~REELG~~YIAGSF~~DFWGR~~GSRV~~I~~ITTR~~KNVFSHPNHEQVQLNVP~~KPLD~~YN~~TSFL~~WKA~~H~~ DQ~~QSGGP~~SEQQFIQLS~~QNI~~VE~~KVE~~GN~~PALE~~Q~~IGS~~FLRG~~KD~~IN~~W~~KEEL~~KS~~L~~V~~L~~V~~D~~N~~ER~~LF~~K~~IL~~1~~SDQ~~LG~~TK~~Q~~QA~~FL~~DL~~AC~~FNG~~K~~STG~~R~~II~~EL~~IAS~~LY~~N~~SP~~E~~V~~L~~K~~L~~CD~~R~~Y~~L~~IE~~1~~RD~~D~~T~~V~~C~~M~~N~~L~~IQ~~E~~RE~~ER~~K~~R~~Q~~S~~R~~I~~WL RRDAD~~F~~IF~~D~~E~~H~~G~~V~~K~~D~~I~~K~~G~~V~~LL~~K~~R~~D~~T~~E~~P~~N~~L~~K~~A~~Q~~L~~Q~~D~~M~~S~~R~~K~~L~~I~~E~~D~~N~~V~~O~~L~~S~~PR~~Q~~N~~D~~L~~S~~N~~Q~~L~~R~~L~~H~~WD~~G~~F~~P~~S~~D~~T~~L~~PN~~F~~E~~A~~Y~~L~~FE~~LL~~LP~~NA~~Q~~T~~TH~~W~~K~~E~~L~~K~~G~~F~~K~~KK~~L~~V~~ID~~V~~S~~N~~S~~Q~~L~~T~~V~~E~~T~~P~~N~~L~~S~~A~~V~~N~~L~~E~~R~~L~~I~~L~~C~~N~~C~~T~~R~~L~~K~~I~~NS~~I~~ TKL~~R~~L~~L~~V~~D~~L~~T~~GC~~V~~R~~L~~E~~T~~SEC~~I~~D~~L~~K~~S~~R~~P~~T~~V~~EL~~R~~GL~~V~~L~~Q~~C~~R~~SL~~K~~G~~C~~Y~~I~~R~~K~~FFF~~K~~I~~Q~~D~~H~~V-

**Figure S6:** Sequences and alignments of cloned and sequenced TIR-NBS-LRR gene MELO3C022157 from resistant (PI353814) and susceptible (PI614596) melon accessions. (a) Genomic sequences of reference, resistant and susceptible accessions. (b) Their alignment with reference sequences retrieved from the Cucurbit Genomics database (<http://cucurbitgenomics.org>) considering DHL92 as the reference genome. In the sequence alignment, asterisks (\*) indicate sequence similarity and absence of asterisks indicates sequence dissimilarity; em-dash (—) and green color designate insertion/deletion of nucleotides. In the gDNA sequences, grey highlights illustrate the position of exons, yellow highlights indicate InDel primer (MB157-2-F and MB157-2-R) sequences and light blue indicates the primer name and InDel position. (c) Translated protein sequences of reference gene, resistant and susceptible parent sequences determined using the “Translate Tool-ExPASy” (<https://web.expasy.org/translate/>) web-based database and showing amino acid alterations and truncated protein in the susceptible parent.