

S1 Table. DNA markers displaying polymorphisms between the resistant line TY172 and the susceptible counterpart M-82, on tomato chromosome 4. Markers are displayed according to their approximate distance in Kb from *Nac1*.

Marker	Distance from <i>Nac1</i> (Kb)	Forward (F) and Reverse (R) primers	Restriction enzyme
<i>Nac1</i>	0	F- TGCCTGGTTTCTGCTGTCA R- TAAAGCTGAAGAAGGACTTACCCT	<i>TaqI</i>
31	6	F- TTCCATTGACACTTGTCTGAG R- CCGTTTGTATAACGATAAGGGC	<i>HinfI</i>
22	6.7	F- CCCTTATCGTTATACAAACGGC R- TTTGTGCGAGAATTGATGAGAG	<i>HinfI</i>
41	7.6	F- ATCTAATTCCATCCGGTGGTC R- TCCATAAGCTTCCTTGTGTTG	<i>PmlI</i>
34	8.7	F- CAGTTGCTCGTGTGTTTTGTTC R- GCGCTCTATAGCTACGGTTTTG	<i>AclI</i>
25	18.5	F- ATTGCTTCTAAAGTCTGGCAGG R- TTTAGCTTTAAGGGGTCGTTTG	<i>TspRI</i>
1.8	33.2	F- CCTTGACAATCAACAATGCTTC R- TCACGTGTGTGATTTATGCTTG	<i>AluI</i>
<i>RP5</i>	184.3	F- ATTCCTCTTCAATAGGTCCACG R- GTCTCATCTGTTCCGAGTCC	<i>AluI</i>
<i>RP3</i>	186.5	F- CAAACTCTCCCATGCTTCTTTC R- TCATTCCGGGAAATTAACCTACG	<i>BglII</i>
7.4	218.7	F- GTGAATTATCATGGCACCATTC R- TATGAAGCTACGATATCCGGG	<i>EarI</i>
<i>DJ</i>	220.7	F- ATAGTTCAAGAAAAGTCGAACC R- CGAATTAATAATCATGAAACAATG	PCR
<i>Ring</i>	231.7	F- GTTCATGATGGAGTAGAAGAAGAAG R- CTTAGTCAACCCTCTTTAGGTTGC	<i>MnlI</i>
4.4	249.9	F- AAAATTTAAGGAATCCCATAGCG R- TTTGAAATATCTTATGTTTGTTCGG	<i>AflIII</i>
<i>Pelo</i>	268.2	F- AAATTTGTTTCATTCAATATGAAGATTGT R- CGTTTTCTTCATCTGGGGT	McSNP
4.8	270.7	F- GGTTCTTTTGAGCTATAACTCTGC R- ATATTGGGCCAACCATAACTTC	<i>RsaI</i>
9.4	271.6	F- AATTAATGTGAGACGGAGCCAG R- CCAAGTCACATGGTAAATGCAG	<i>AseI</i>
5.4	273.9	F- CAAATATGTCAATGGATGGTGG R- AAGGTGCGGTGGATTATTAAG	<i>HphI</i>
3.1	291.6	F- GTAAATAAAGCACAAATGCCCC R- AATTGTTGTGCCACCACTAGAC	<i>CviKI</i>
9.8	301.3	F- TAACGAACACCAACTGTTTCGAC R- ATCATTTCCTTACCATTAC	<i>NlaIV</i>
0.1	316.2	F- CTAGCCTCTGTGTAAGATCGGG R- TCAAAACATCTCAAACGACCTC	<i>BsaAI</i>
0.3	333.3	F- CCAGTGATAATGATGGATGTGG R- ATGGAAAAATGATGGGACTACG	<i>BceI</i>
0.4	340.8	F- TGCTATTGACTTTTCCACTTGC R- TTGAATTTACGTCATTGGC	<i>HinfI/ClaI</i>
0.5	348.9	F- TTCATATTGATCACTTGCGGTC R- ATTTGGCTAATGGAATCTCCTG	<i>AvaII</i>
5.8	351	F- CTTGTAAACCCATGTGGTAGGG R- AACGTGTGAGTGAAGCAAAAAG	<i>BglII</i>
3.8	579.3	F- TTTTACCTCGGGAGCTAGGAG R- GCCGAGATAACATTAGTGGTGAC	<i>HphI</i>
4.9	693	F- AGTGCCACGTAAGCTAAAAAGG R- AAGTTGATCCAATTCAAGCTGC	<i>BstUI</i>
<i>C2_At5g37360</i>	43,552	F- AGCTCATGAATGCTTATTGTGAC R- ACCATATTAAGAGTAAACTTTTACAAATG	<i>TaqI</i>