

Table S1. MFA Segregation of fruit mature abscission for F₃ families

Population	Total number	None-MFA	MFA	Exception ratio	χ^2 Chi-square
F ₃ -83	150	114	36	3:1	0.46 ^a
F ₃ -57	142	102	40	3:1	0.33 ^b
F ₃ -42	130	61	59	3:1	15.51
F ₃ -97	128	81	37	3:1	1.11
F ₃ -109	122	121	1	3:1	32.07

$X^2_{(0.05,1)}=3.84$

a: F₃-83 family was controlled by a single gene with *AL3*, it was used to mapped another candidate gene (Sheng et al., 2022)

b: F₃-57 was another single gene segregation population

Table S2. Candidate gene qRT-PCR primer and Subcellular localization primer information

Gene ID	Forward sequence	Reverse sequence	Enzyme
MELO3C012405	CTTGTTCTGGGCTCAGATGGA	GTCAACAGGTGGTGGACCTT	
MELO3C012406	GCTGAGCCGATGACGATTCT	TACAAAGCGACCACAGCACA	
MELO3C012407	CAACTTGCCAATGTGTCGCT	TATTTACTGCCGCTGGTGCT	
MELO3C012408	GACGTTGCCATGGTCGTAGA	TGGCTCTACATCGTGCTCCT	
MELO3C012409	ACTTTGATGTATGCGGGGGT	ATGCCAAGACCCACAAGCAA	
MELO3C012410	AGGCTATTGCAGATGCGGAG	GCTAATCCGGCTCGAACAAC	
AB033599	GGTGATGAAGCTCAGTCCAA	TGTAGAAGGTGTGATGCCAAA	
CmARM14	ATCCTCGAGCTGCAGGAGCTCATGGGTCCATCGGAGAAAGATATGG	CCCTTGCTCACCATCACTAGTCCTAGATTAGGTGATGGTCTATCAAAACG	SacI, SpeI
GFP-FCX	TTGTGGCCGTTTACGTCGCC		
CmARM14R1	CTCGAGATCACTAACTCATG		
CmARM14R2	GACAATGGTTCTTTTGTTAC		

Note: CmARM14 primer is the cloning primer. GFP-FCX, CmARM14R1 and CmARM14R2 are the sequencing primers.

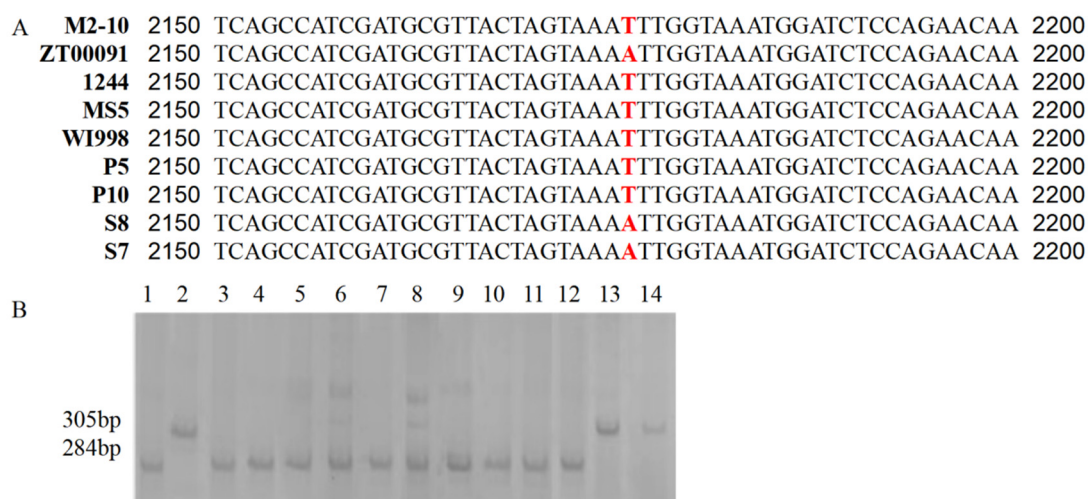


Figure S1 Natural population sequence analysis and electropherograms. A. Sequence analysis of the candidate gene *CmARM14* in different varieties (2150-2200 bp). In 7 natural populations, S8 and S7 are MFA varieties. The other varieties are None MFA. B. Electrophoretic maps of the markers screened for detection in 7 natural populations. No.1,3 and 4 are M2-10. No.2 is ZT00091. No.5-14 are 1244, MS5, WI998, P5, P10, S8 and S7.

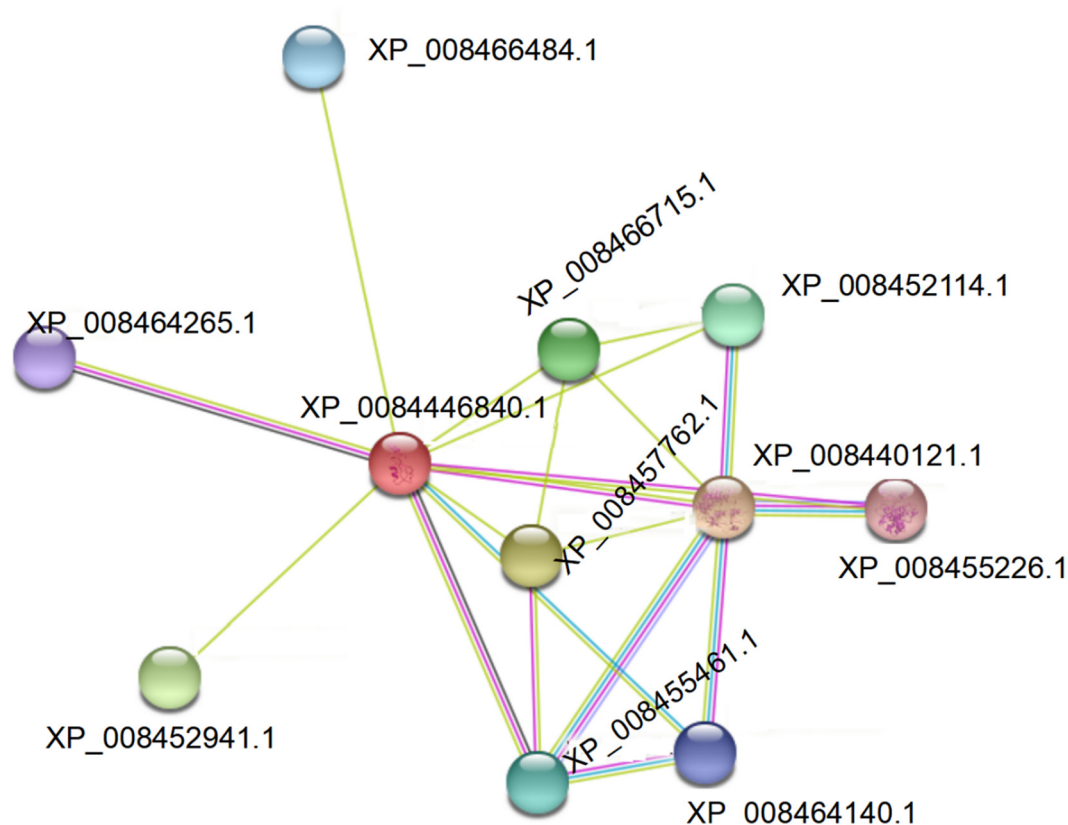


Figure S2. Prediction The interaction Protein with *CmARM14*. Using <https://cn.string-db.org/cgi> (accessed on 2 June 2022) web to predict interacted protein with *CmARM14*.