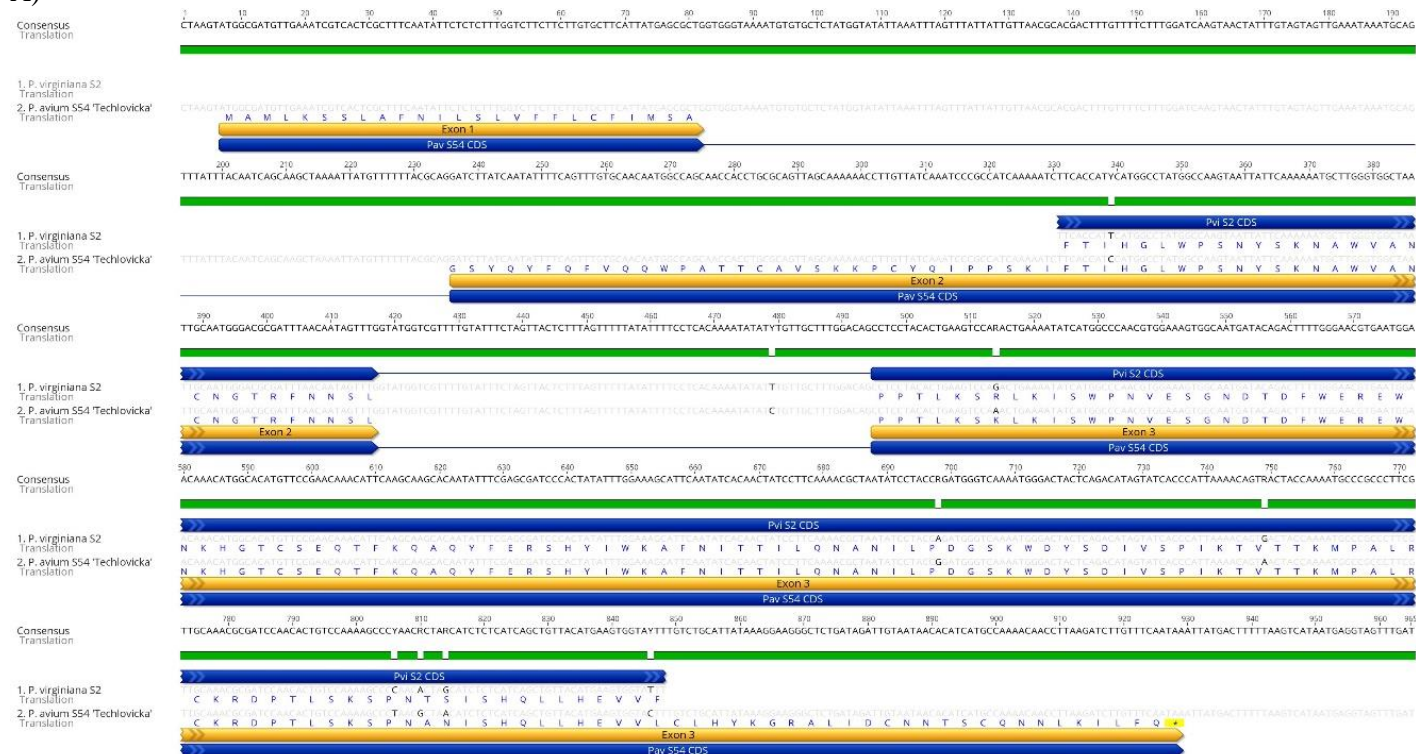


Supplementary material

Figure S1. The *P. avium* S54 allele from the ‘Techlovicka’ cultivar sequence analysis. A) genomic DNA alignment [OQ555802 for *P. avium* S54; JQ627790 for *P. virginiana* S2]; B) protein alignment [OQ555802 translation for *P. avium* S54; AFJ20682 for *P. virginiana* S2].

A)



B)

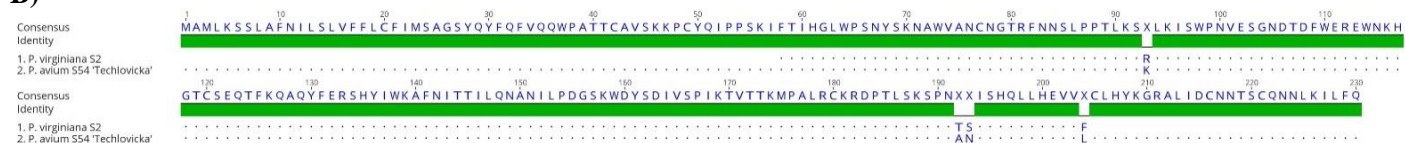


Figure S2. The *P. avium* S54 allele from the ‘Techlovicka’ cultivar phylogenetic tree. The S54 protein sequence was compared with BLAST records and the phylogenetic tree was constructed using Geneious Prime software. Branches are denoted by GenBank numbers.

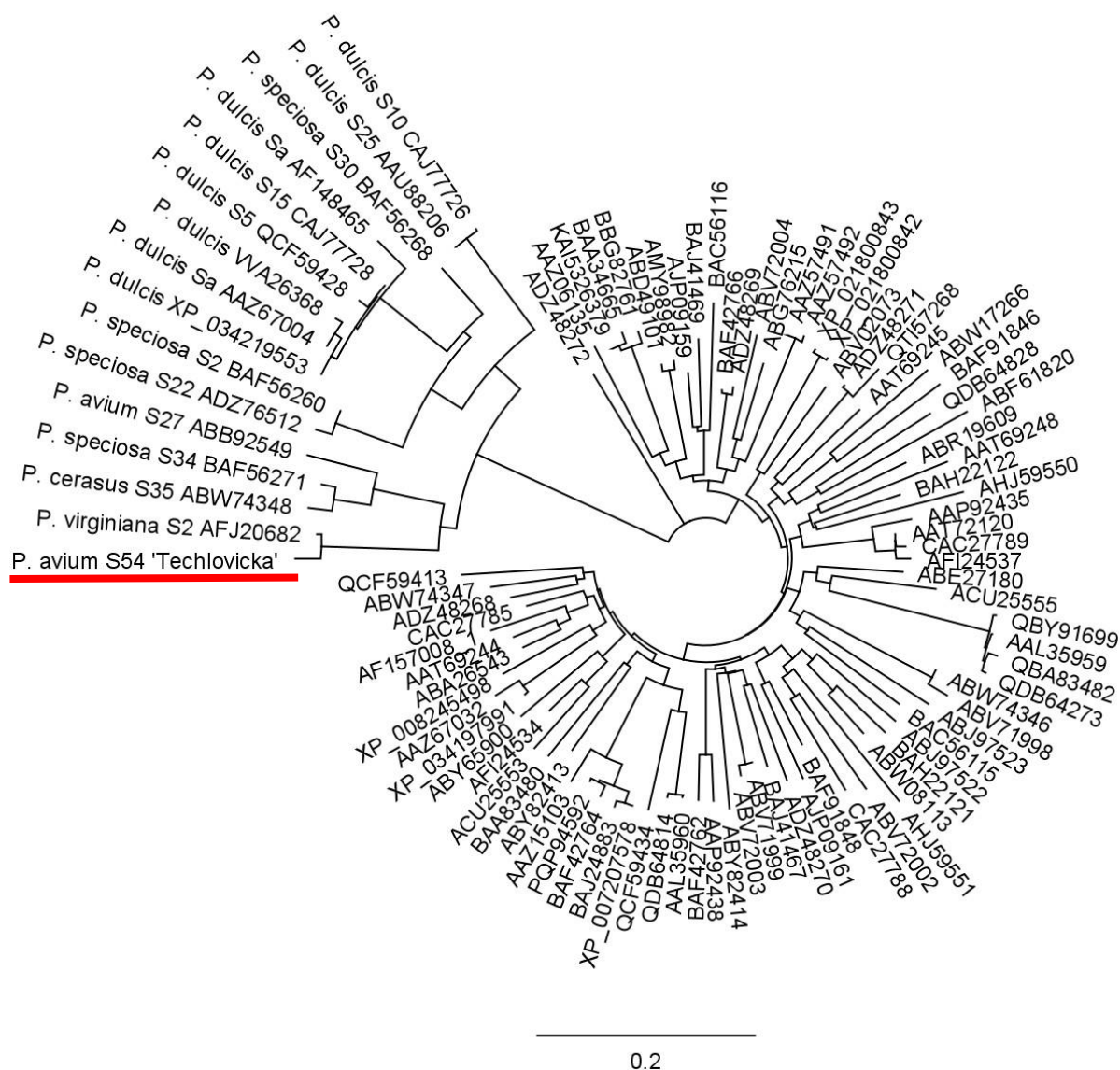


Figure S3. The S-RNase-Ex3-R primer binding site sequence analysis in selected S-alleles. The mismatched nucleotide is shown in bold red, and the region of the primer in the pink frame.

S-RNase-Ex3-R		
CGTGGAAAGTGGCAATGATAC		
S-RNase S1, Early Rivers, AJ635281	AAGAGATCTTGGCCCGAC CGTGGAAAGTGGCAATGATAC AAGATTTTGGGAAGGCGAATGG	597
S-RNase S2, Early Rivers, AJ635283	AAGAGATCTTGGCCCGACGTGGAAAGTGGCAATGATAC AAGATTTTGGGAAGGCGAATGG	1933
S-RNase S6, Colney, AJ635291	CAGACATCTTGGCCCGACGTGGAAAGTGGCAATGATAC AAAGTTTGGGAAGGCGAATGG	306
S-RNase S7, Charger, AJ635268	AAGATACTTGGCCAGACGTGGAAAGTGGCAATGATAC AAATTTTGGGAAGGCGAATGG	1985
S-RNase S9, Inge, AJ635270	AAGAGATCTTGGCCCGACGTGGAAAGTGGCAATGATAC AAGTTTGGGAAGGCGAATGG	527
S-RNase S12, Schneiders Spaete Knorp., AJ635274	AAGAAATCTTGGCCCGACGTGGAAAGTGGCAATGATAC AAATTTTGGGAAGGCGAATGG	1496
S-RNase S13, Noble, AJ635276	AAAAGATCTTGGCCCGACGTGGAA CTGGCAATGATAC AAATTTTGGGAAGGCGAATGG	597
S-RNase S22, Kiechelsberger Kracher, DQ336138	AAGAAATCTTGGCCCGACGTGGAAAGTGGCAATGATAC AAATTTTGGGAAGGCGAATGG	332
S-RNase S24, Pico Colorado, CDS AY259112	CAGACATCTTGGCCCGACGTGGAAAGTGGCAATGATAC AAAGTTTGGGAAGGCGAATGG	92

Figure S4. Sequence analysis of MGST alleles. MGSTins: ‘Cristobalina’; MGSTdel: ‘Kronio’; MGSTwt: ‘Satonishiki’

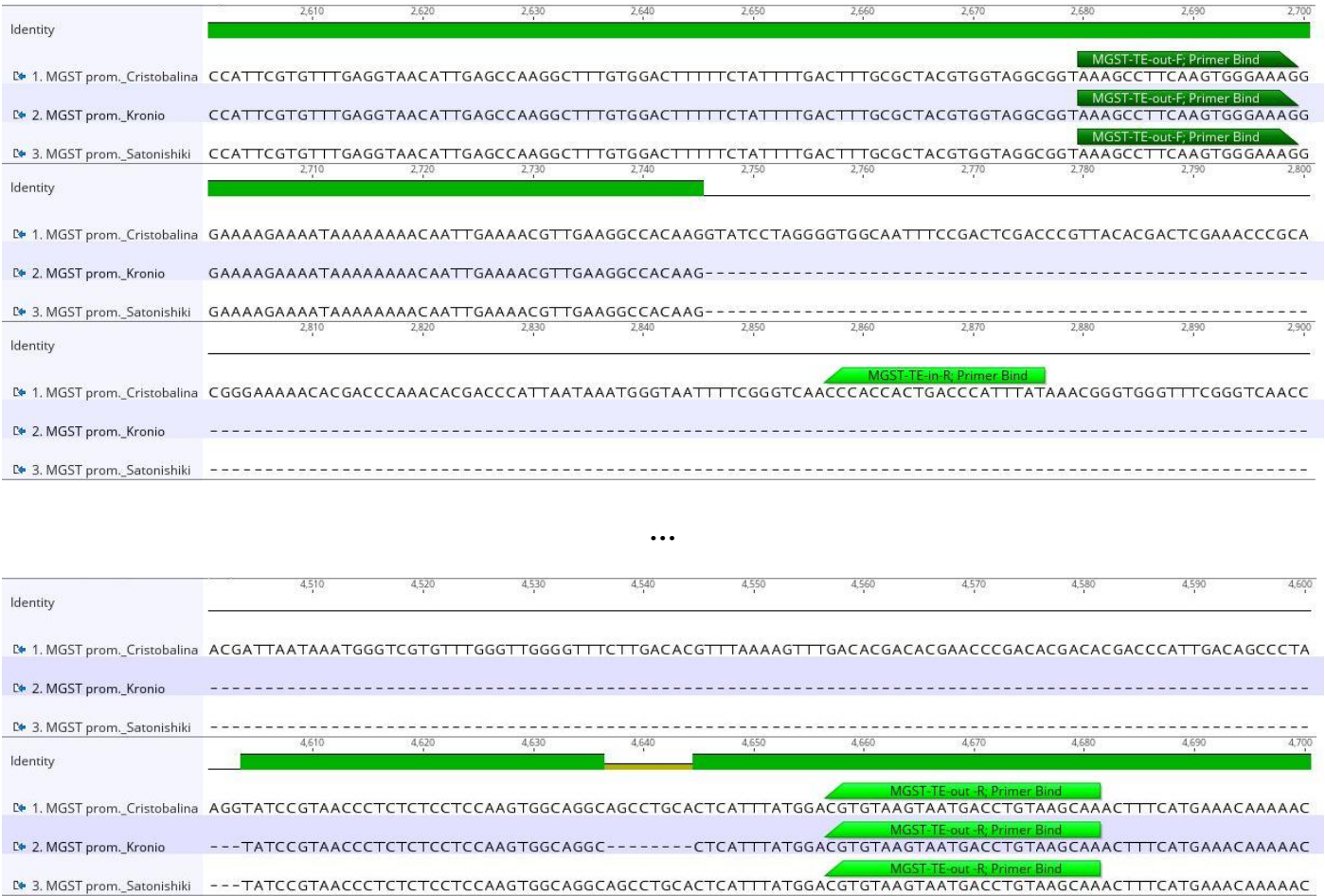
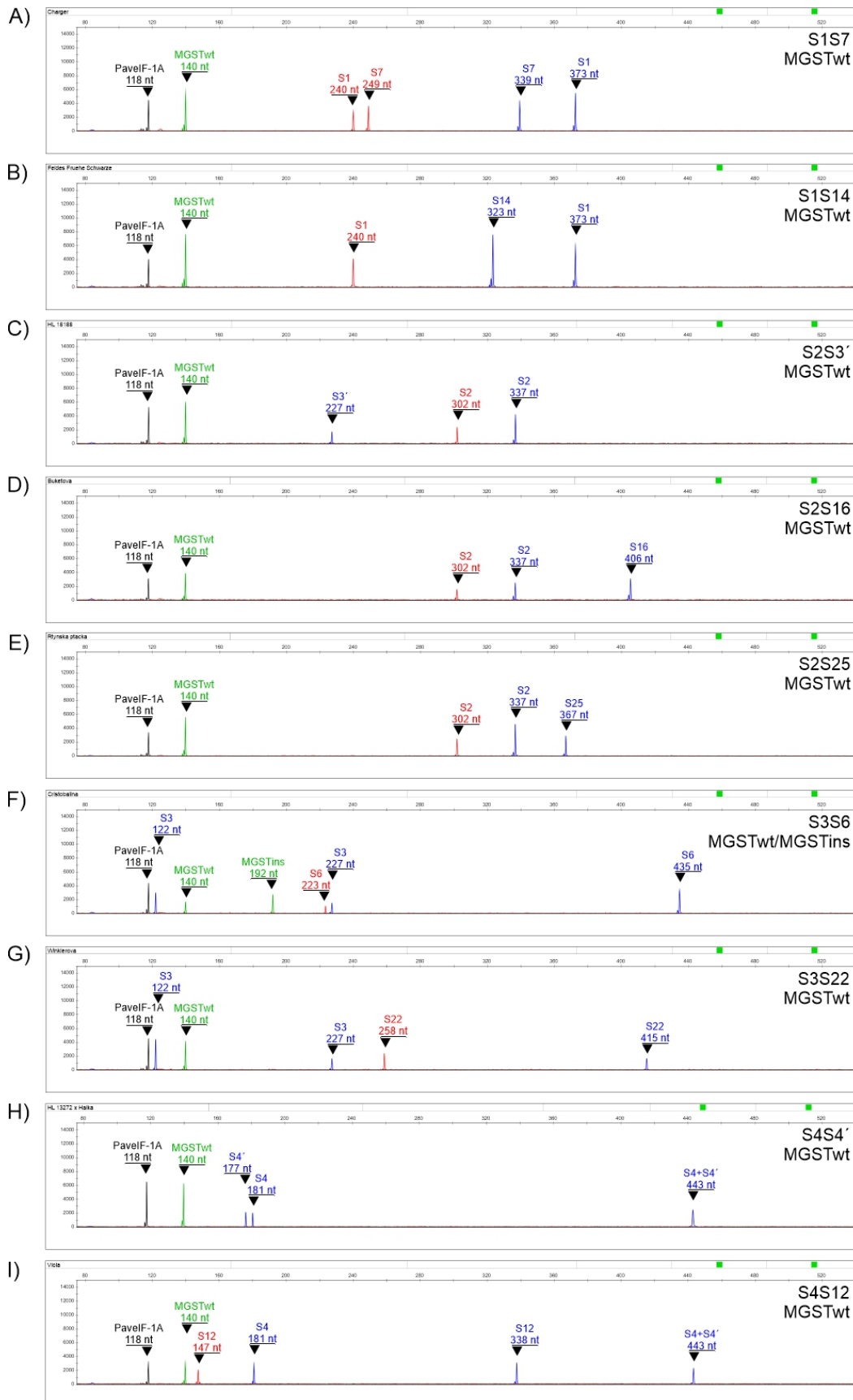


Figure S5. Outputs of fragment analyses of all tested S-alleles and MGST alleles. A) 'Charger' (S1S7 MGSTwt); B) 'Feldes Fruehe Schwarze' (S1S14 MGSTwt); C) HL18188 (S2S3' MGSTwt); D) 'Buketova' (S2S16 MGSTwt); E) Rtyńska ptacka (S2S25 MGSTwt); F) 'Cristobalina' (S3S6 MGSTwt/MGSTins); G) 'Winklerova' (S3S22 MGSTwt); H) HL 13272 x 'Halka' (S4S4' MGSTwt); I) 'Viola' (S4S12 MGSTwt); J) 'Techlovicka' (S4S54 MGSTwt); K) 'Felicita' (S4'S9 MGSTwt); L) 1:1 mixed sample of 'Kronio' (S5'S6 MGSTwt/MGSTdel) + 'Uriase de Bystrita' (S5S12 MGSTwt); M) 'Uriase de Bystrita' (S5S12 MGSTwt); N) 'Rita' (S5S22 MGSTwt); O) 'Kronio' (S5'S6 MGSTwt/MGSTdel); P) 437 NDR (S7S9 MGSTwt); Q) Italia 2 (S13S14 MGSTwt); R) P-HL-A (S13S25 MGSTwt).



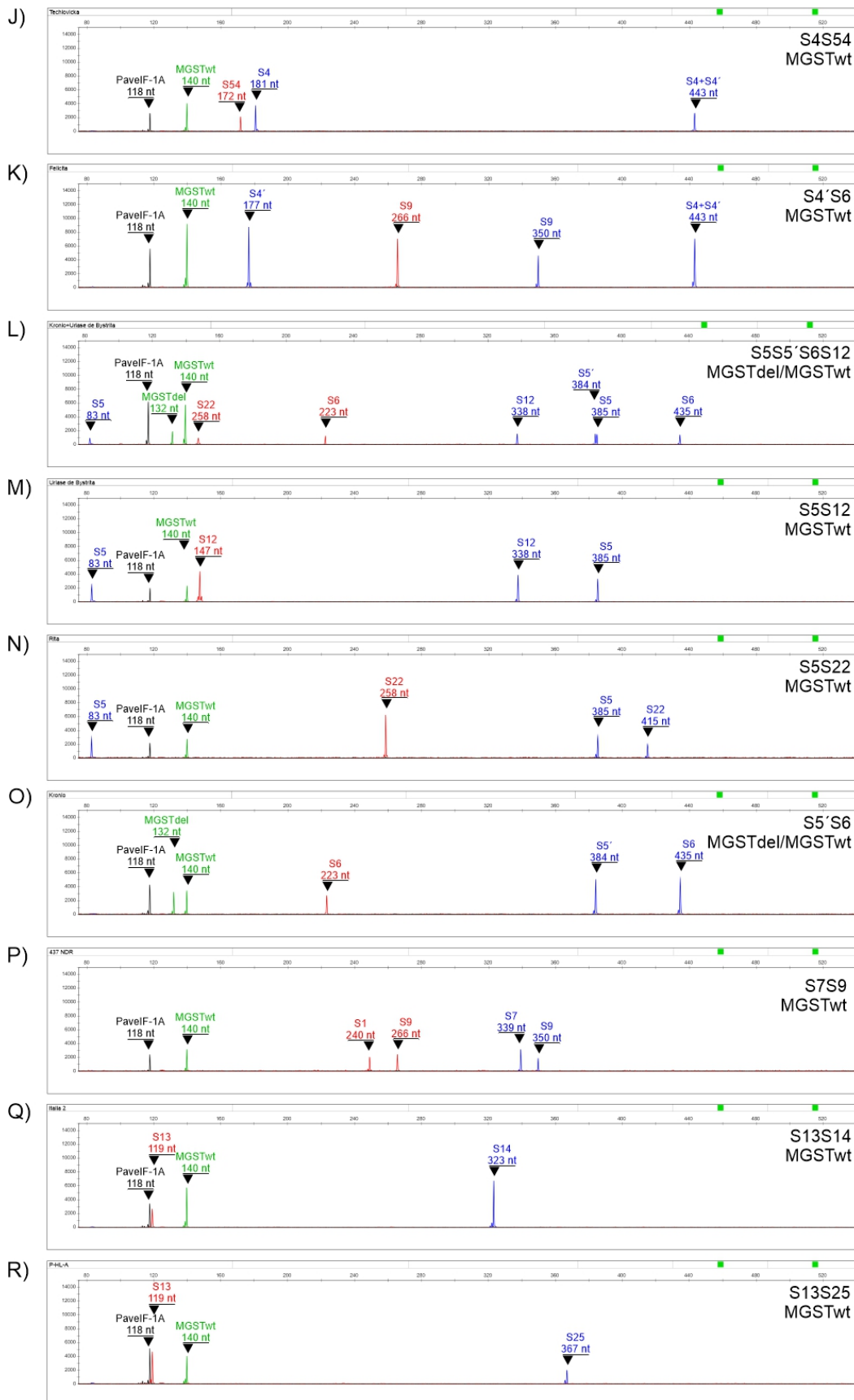


Figure S6: Outputs of fragment analyses in two cultivars using three different PCR reagents: Phusion Flash High-Fidelity PCR Master Mix (ThermoFisher Scientific), PCR Master Mix (2X) (ThermoFisher Scientific) and qPCR 2x Blue Master Mix (Top-Bio). A) 'Felicita'; B) 'Feldes Frühe Schwarze'.

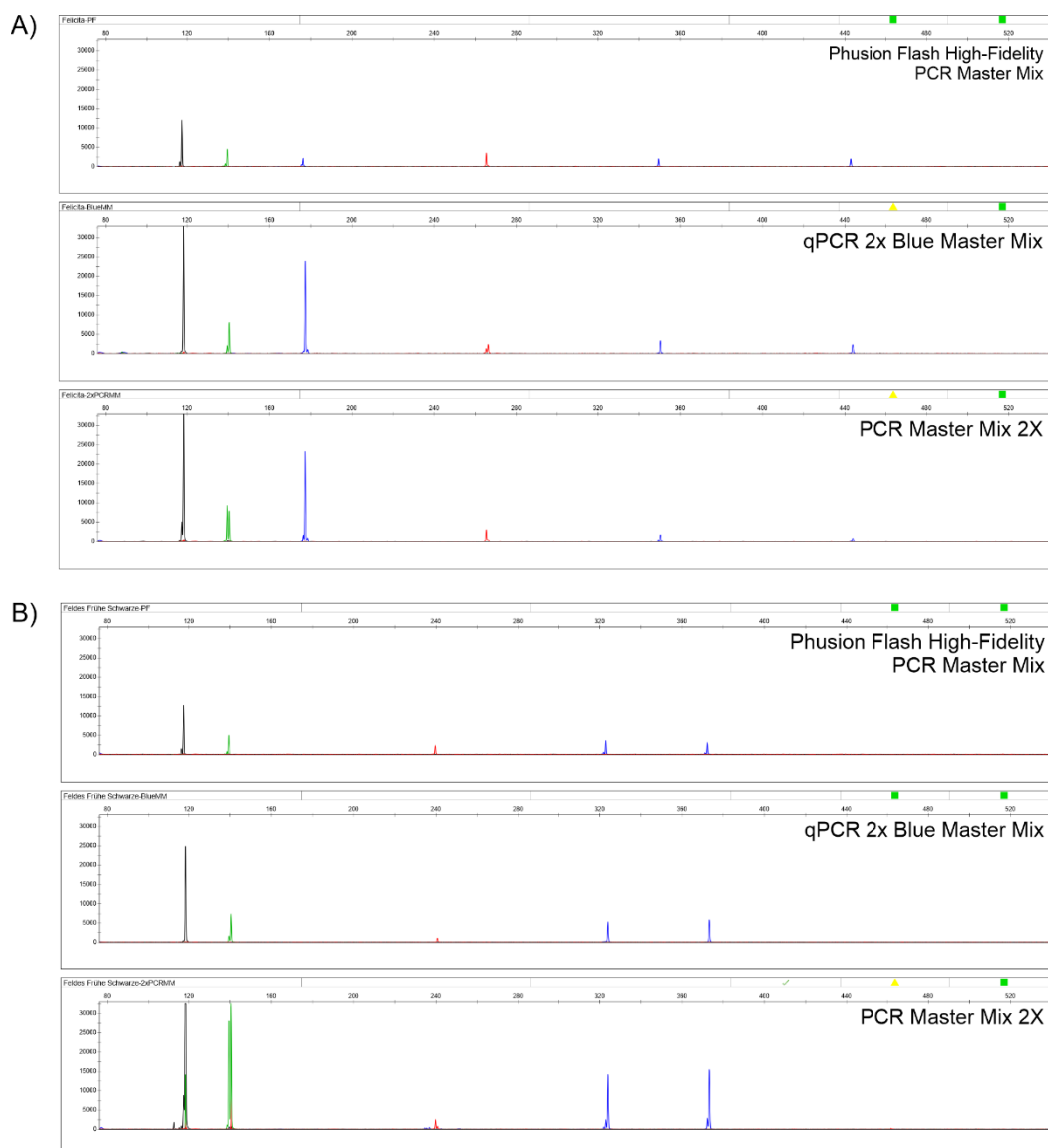


Table S1. The list of sweet cherry varieties used in the study.
Provided as a separate Excel file.

Table S2. Sequences used in the study. Reference sequences retrieved from the GenBank ([National Center for Biotechnology Information \(nih.gov\)](https://www.ncbi.nlm.nih.gov/)) or [GDR \(rosaceae.org\)](https://www.rosaceae.org/).

	S-RNase*	SFB	MGST*	PaveIF-1A
S1	AJ635282; AJ635281	AB111518		
S2	AJ635284; AJ635283	AB111519		
S3	AY571663	AY571665		
S3'				
S4	AB028154.1	AB111521		
S4'		AY649873		
S5	AJ635290; AJ635289	AB111520		
S5'	EU077235	EU077237		
S6	AY571664; AJ635291	AY805051		
S7	EU035974; AJ635268	EU035976		
S9	AJ635271; AJ635270	DQ422809		
S10	JQ280519	AY805053		
S12	AY259115; AJ635274	AY805054.1		
S13	DQ385842; AJ635276	DQ385844		
S14	AJ635278; AJ635277			
S16	AJ635280; AJ635279	AY805056.1		
S17	JQ280528			
S18	JQ280533			
S19	DQ336139			
S20	AJ862659			
S21	AJ863119			
S22	EF429142; DQ336138			
S23	AY259114			
S24	AY259112			
S25	AY259113			
S27	DQ266439			
S28	DQ266440			
S29	DQ266441			
S30	DQ266442			
S31	DQ266443			
S32	DQ266444			
S34	JQ280525			
S37	JQ280522			
S38	JQ280516			
S54	OQ555802; this study			
MGSTwt			LG_3: 18395575 – 15400614**	
MGSTdel				
MGSTins			LC371380	
PaveIF-1A				LG_3: 15263431 – 15262737**

* In case sequences or their parts necessary for alignments were missing, sequences were generated in this study. See the text for more details.

** Retrieved from Sweet cherry Genome v1.0.