

Table S1. SNP information of candidate gene between *F. vesca* 10-41 and 18-86.

Accession number	Gene name	SNP loci	SNP differential base	
			10-41	18-86
XP_004302175.1	<i>FvARI8</i>	435	T	C
XP_004306305.1	<i>FvCAL</i>	406	G	A
		426	T	G
		57	C	R
		174	G	T
		192	C	A
		345	G	T
		390	C	T
		447	T	G
		558	C	T
		654	T	C
		657	A	G
XP_011467948.1	<i>FvKHDP-2</i>	849	G	A
		879	G	C
		885	C	T
		894	A	T
		1023	C	T
		1041	G	A
		1080	T	C
		1299	C	A
		1437	C	T
		1477	G	A
		69	T	C
		278	G	A
		336	G	A
		374	C	A
		402	A	G
		409	G	A
		510	T	C
		513	A	G
XP_004289907.1	<i>FvDRIP2</i>	525	A	T
		549	G	T
		577	A	C
		780	G	A
		792	C	T
		807	C	T
		815	T	C
		902	A	G
		1108	A	G
XP_004293392.1	<i>FvBRO1</i>	142	G	A
		678	T	C
		268	G	T
XP_004298676.1	<i>FvLTP3</i>	308	C	G
		329	G	T
		314	A	T
XP_004290481.1	<i>FvTAR4</i>	354	T	C
		454	G	A

654	A	G
807	T	C
933	A	T
948	A	G
1014	G	C
1083	G	A
1105	C	T
1324	A	C

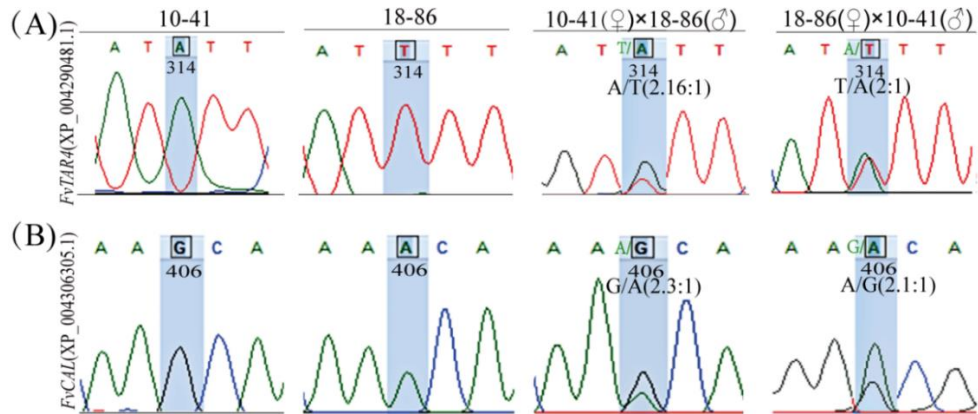


Figure S1. *FvTAR4* and *FvCAL* are biallelic expressions in the endosperms of the hybrid of two *Fragaria vesca* ecotypes. Sequencing of (A) *FvTAR4* and (B) *FvCAL* was used to confirm imprinting status in 10-41 × 18-86 and 18-86 × 10-41. At least ten colonies were sequenced for each amplicon. SNP sites are shaded in blue. *FvTAR4* and *FvCAL* showing a biallelic expression, and their variation ratio of SNPs is close to the 2:1 expected ratio in reciprocal cross.

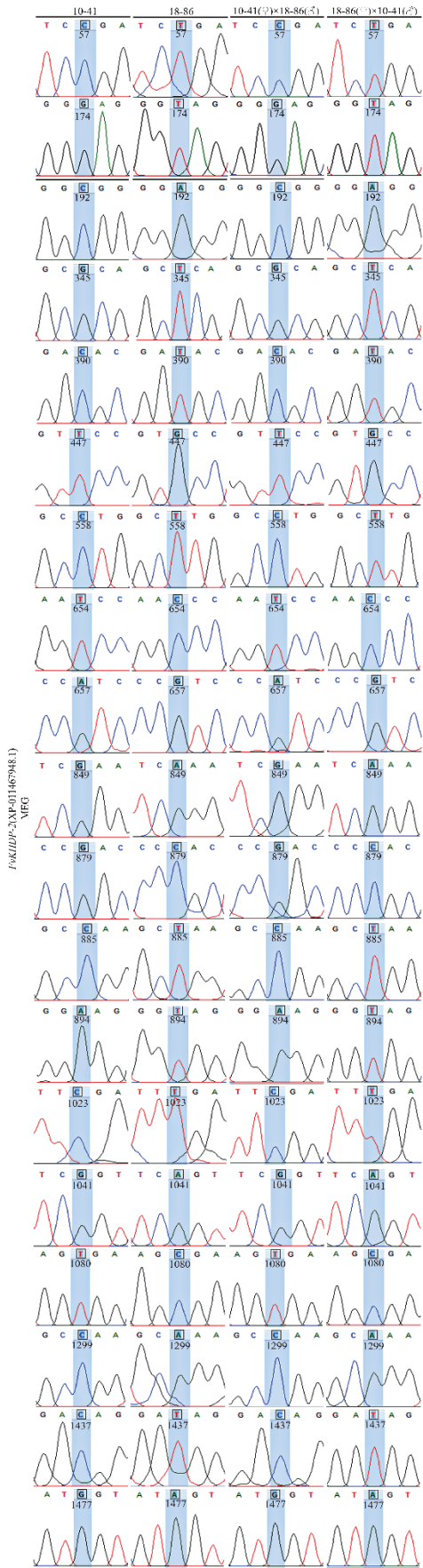


Figure S2. Monallelic expression of *FvKHDP-2* in reciprocal cross endosperm of two *Fragaria vesca* strains.

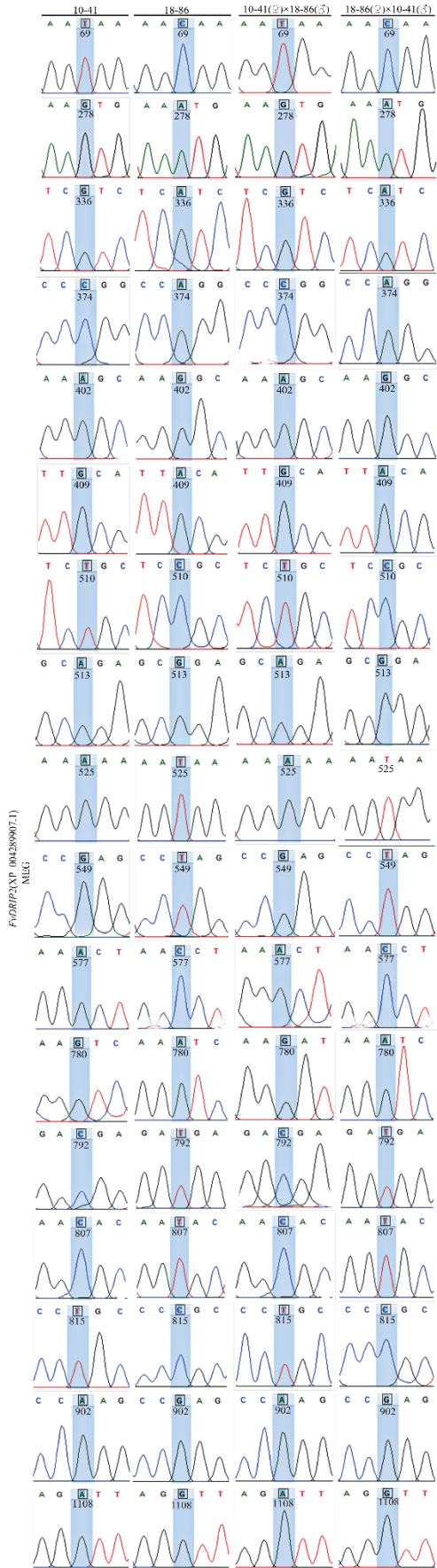


Figure S3. Monolallelic expression of *FvDRIP2* in reciprocal cross endosperm of two *Fragaria vesca* strains.

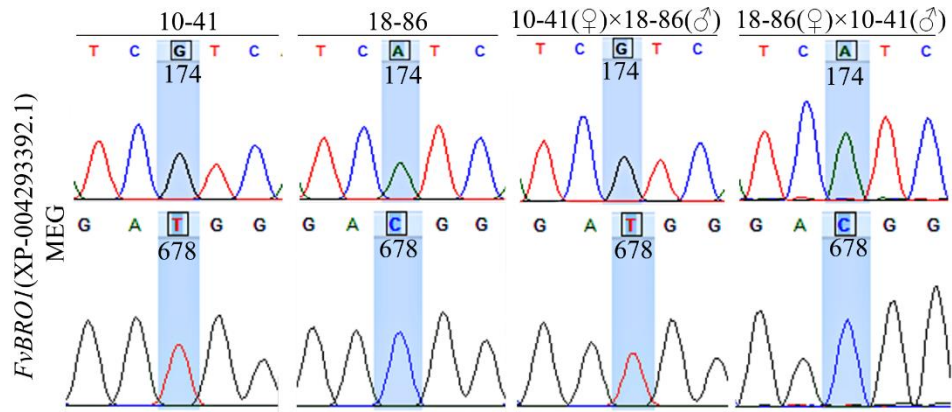


Figure S4. Monallelic expression of *FvBRO1* in reciprocal cross endosperm of two *Fragaria vesca* strains.

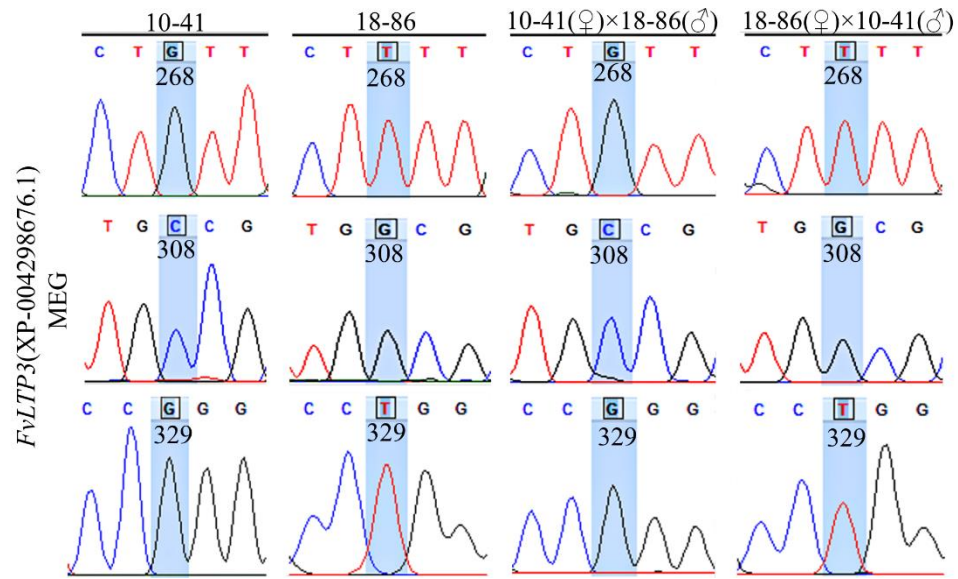


Figure S5. Monallelic expression of *FvLTP3* in reciprocal cross endosperm of two *Fragaria vesca* strains.

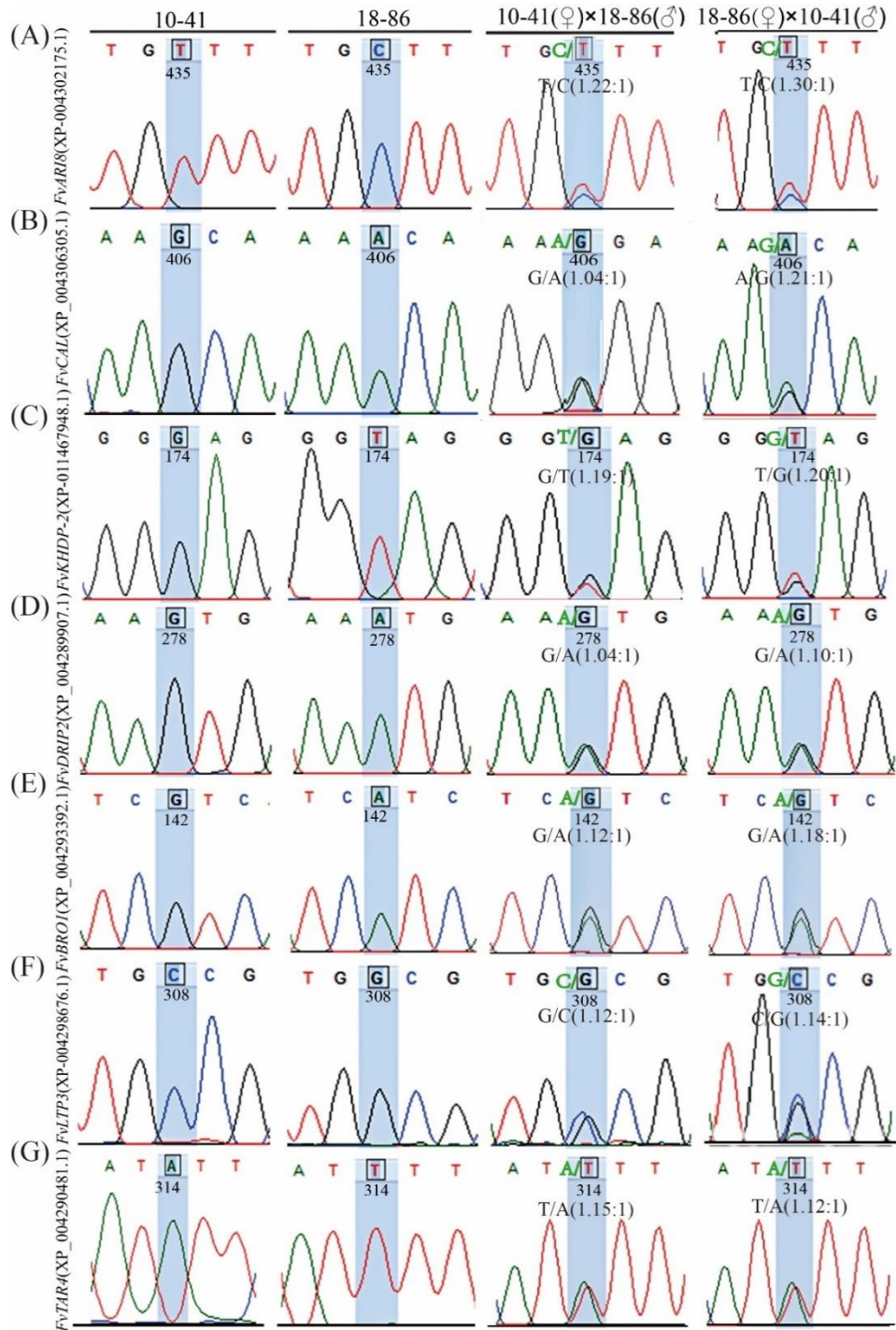


Figure S6. Biallelic expression of seven candidate genes in reciprocal cross embryo of two *Fragaria vesca* ecotypes. (A–G) Seven candidate genes with SNPs were cloned in reciprocal cross embryos, and sequencing showed that their variation ratio of SNPs is close to the 1:1 expected ratio. We only show part of the biallelic expression of SNPs, because there is enough to confirm that these candidate genes are not imprinted genes.