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

Accession number Gene name SNP loci 10-41 18-86		Gene name	SNP loci	SNP differential	
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$\begin{array}{c ccccccccccccccccccccccccccccccccccc$			807	C	T
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_	XP_004290481.1	FvTAR4	314	A	T
454 G A			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	С

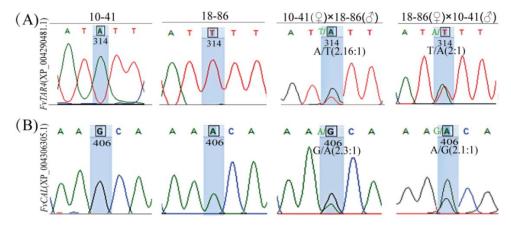
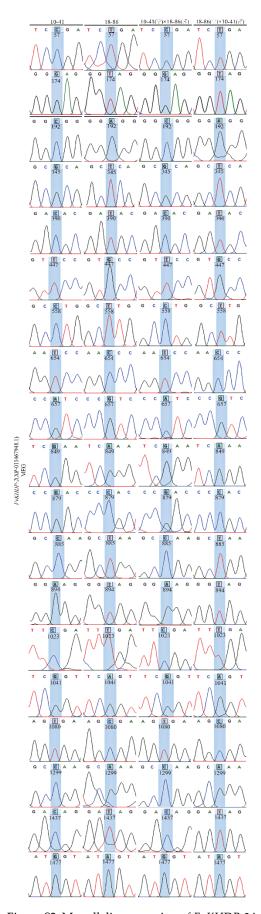
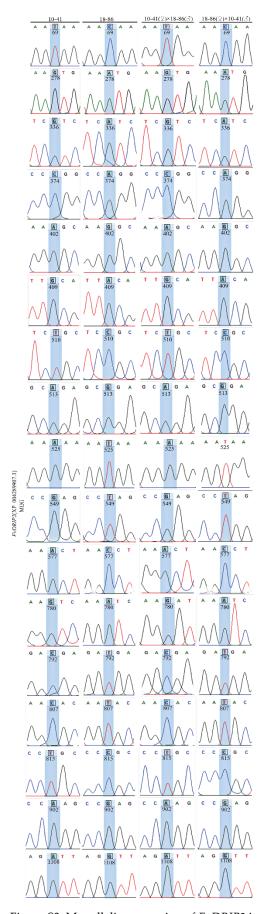


Figure S1. FvTAR4 and FvCAL are biallellic expressions in the endosperms of the hybrid of two $Fragaria\ vesca$ ecotypes. Sequencing of (A) FvTAR4 and (B) FvCAL was used to confirm imprinting status in $10-41\times18-86$ and $18-86\times10-41$. At least ten colonies were sequenced for each amplicon. SNP sites are shaded in blue. FvTAR4 and FvCAL showing a biallellic expression, and their variation ratio of SNPs is close to the 2:1 expected ratio in reciprocal cross.



 $Figure \ S2.\ Monollelic\ expression\ of\ \textit{FvKHDP-2}\ in\ reciprocal\ cross\ endosperm\ of\ two\ Fragaria\ vesca\ strains.$



 $Figure \ S3. \ Monollelic \ expression \ of \ \textit{FvDRIP2} \ in \ reciprocal \ cross \ endosperm \ of \ two \ Fragaria \ vesca \ strains.$

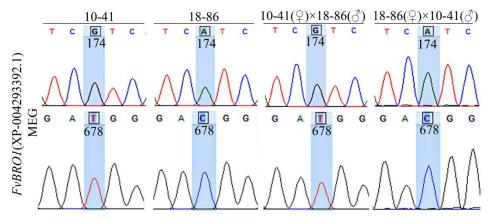


Figure S4. Monollelic expression of FvBRO1 in reciprocal cross endosperm of two Fragaria vesca strains.

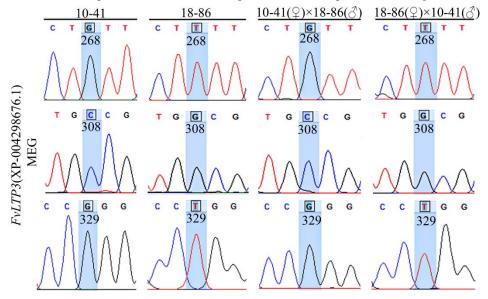


Figure S5. Monollelic expression of FvLTP3 in reciprocal cross endosperm of two Fragaria vesca strains.

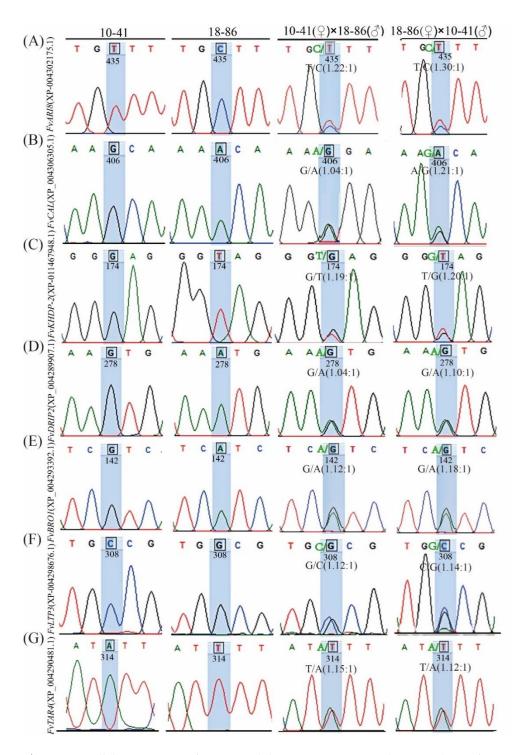


Figure S6. Biallelic expression of seven candidate genes in reciprocal cross embryo of two *Fragaria vesca* ecotypes. (A–G) Seven candidate genes with SNPs were cloned in reciprocal cross embryos, and sequencing showed that their variation ratio of SNPs is close to the 1:1 expected ratio. We only show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