

Supplemental material

Manuscript title

A bHLH transcription factor, *DvIVS*, is involved in regulation of anthocyanin synthesis in dahlia (*Dahlia variabilis*)

Authors

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Supplemental figures

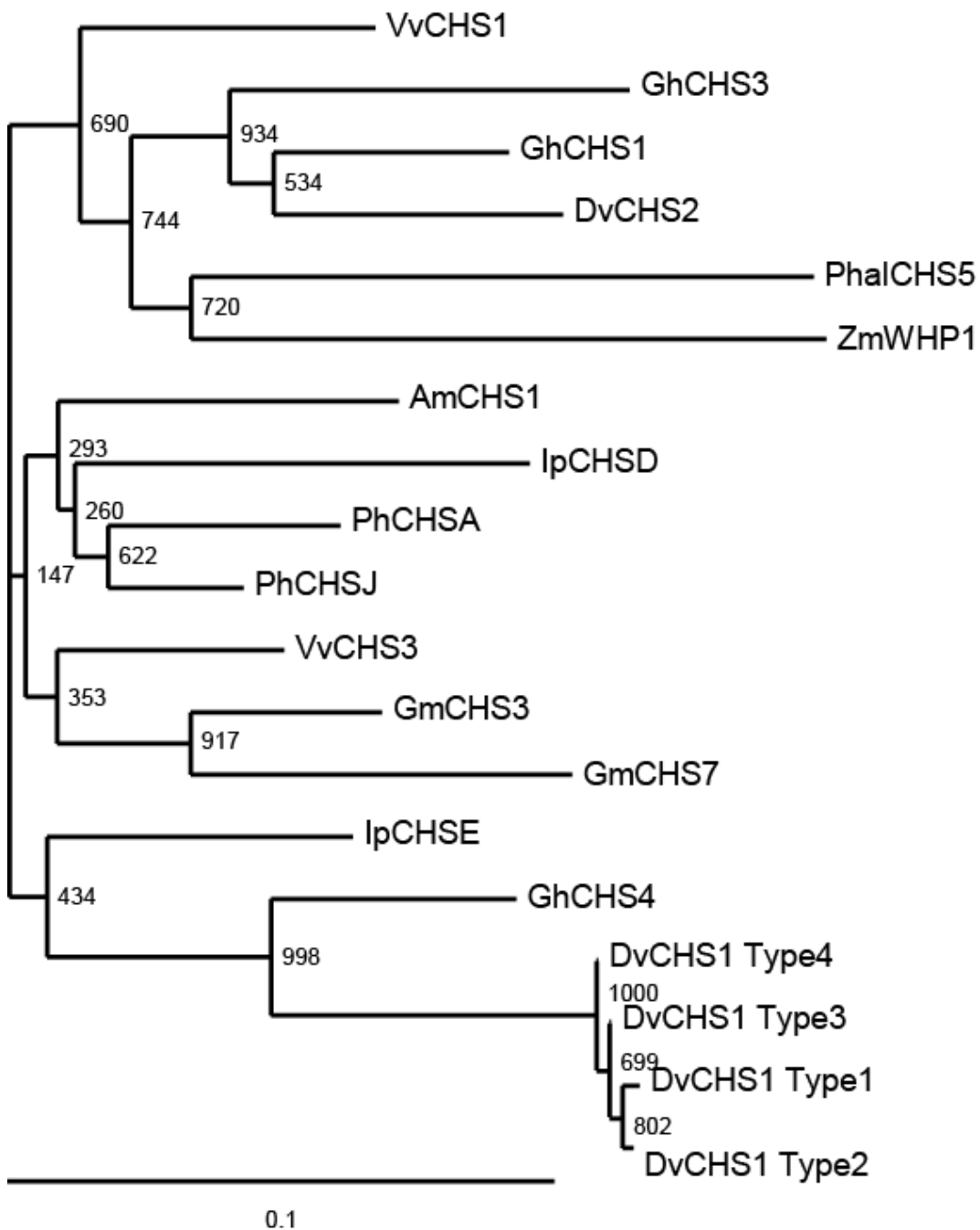


Fig. S1. Phylogenetic tree for CHS associated with flavonoid synthesis. The entire amino acid sequences were aligned using ClustalW, and the tree was constructed by the neighbor-joining method. The bootstrap values of 1000 retrials are indicated on each branch, and the scale shows 0.1 amino acid substitutions per site. DvCHS1 were classified into 4 types on the basis of each deduced amino acid sequence. The abbreviation shown in front of each protein indicates plant species: Dv, *Dahlia*

variabilis; Am, *Antirrhinum majus*; Gh, *Gerbera hybrida*; Gm, *Glycine max*; Ip, *Ipomoea purpurea*; Ph, *Petunia hybrida*; Phal, *Phalaenopsis* hybrid cultivar; Vv, *Vitis vinifera*; Zm, *Zea mays*. Accession numbers of each protein: DvCHS1 Type1 (BAJ14515), DvCHS1 Type2 (BAJ14516), DvCHS1 Type3 (BAJ14517), DvCHS1 Type4 (BAJ14518), DvCHS2 (BAJ14519), AmCHS1 (X03710), GhCHS1 (Z38096), GhCHS3 (Z38098), GhCHS4 (CAP20328), GmCHS3 (AAQ62589), GmCHS7 (AAA33950), IpCHSD (AB001818), IpCHSE (AB001819), PhCHSA (X14591), PhCHSJ (X14597), PhalCHS5 (AAY83389), VvCHS1 (ABM67586), VvCHS3 (BAB84111), and ZmWHP1 (CAA42763).

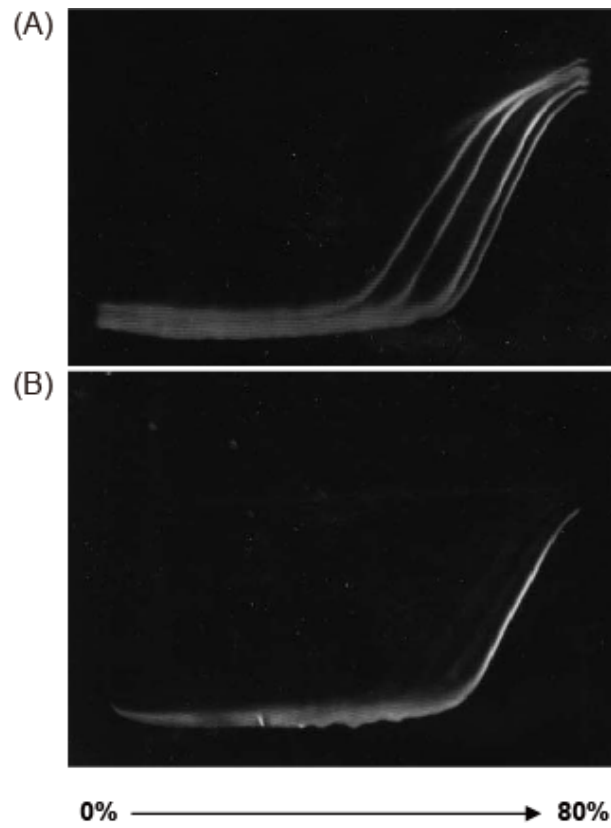


Fig. S2. DGGE analysis of *DvCHS1* cDNA from MJOr (A) and MJY (B). The percentages below the figure indicate the concentration gradient of denaturation. Primers used detected SNPs between 1024 and 1237, as shown in Table S7.

Supplemental tables

Table S1. Degenerate primers used for isolating the cDNA fragment

Genes	Forward Primer	Reverse Primer	Used sequences for designing primers
<i>DvCHS1</i>	GTGTGCTCCGAGATYACKGC	ACGCTTTTGGAGDAGATGAAA	DQ521272 (<i>Chrysanthemum x morifolium</i>) Z67988 (<i>Callistephus chinensis</i>) Z38096 (<i>Gerbera hybrid</i>)
<i>DvCHI</i>	TKICCI GTIARI GGIARDAT	AARTTYACIGBIATHGGIGT	EF094933 (<i>Chrysanthemum x morifolium</i>) Z67980 (<i>Callistephus chinensis</i>) AF509335 (<i>Saussurea medusa</i>) AB080768 (<i>Ipomoea batatas</i>) AB234907 (<i>Verbena x hybrida</i>) prf: 1807331B (<i>Petunia x hybrida</i>) AB213651 (<i>Nicotiana tabacum</i>) DQ120521 (<i>Camellia sinensis</i>)
<i>DvF3H</i>	CATCGTTTCTAGCCATCTTC	TTCASCACTACYTTTTGGTC	U86837 (<i>Chrysanthemum x morifolium</i>) X72593 (<i>Callistephus chinensis</i>)
<i>DvDFR</i>	GACACAAGAAGGAAGCTTTG	GATRAAYGGACCAACTACYA	Z67981 (<i>Callistephus chinensis</i>) Z17221 (<i>Gerbera hybrid</i>)
<i>DvANS</i>	TACCCAAAATGCCCTCAACC	CAACTTGTGTTCCATATG	AF015885 (<i>Callistephus chinensis</i>) AY997840 (<i>Gerbera hybrid</i> cultivar Tacora) AY997841 (<i>Gerbera hybrid</i> cultivar Ansofie) AY997842 (<i>Gerbera hybrid</i> cultivar Fame) AY547342 (<i>Saussurea medusa</i>)
<i>DvDEL</i>	GGTACTAYAATGGMGAYATHAARA	AATACGGAAARCAYACWACWGTCT	M84913 (<i>Antirrhinum majus</i>) AF020545 (<i>Petunia x hybrida</i>) AB024050 (<i>Perilla frutescens</i>) AB232774 (<i>Ipomoea nil</i>) AJ007709 (<i>Gerbera hybrid</i> cv. 'Terra Regina')
<i>DvIVS</i>	ATGGRTAYTAYAACGGYGCRATAAA	ATCACTCTCKATRATIGAHACYTCYA	AB154369 (<i>Ipomoea purpurea</i>) AB154370 (<i>Ipomoea tricolor</i>) AB103172 (<i>Perilla frutescens</i>) AJ277509 (<i>Arabidopsis thaliana</i>) AF260919 (<i>Petunia x hybrida</i>)
<i>DvActin</i>	GCCAAYAGAGARAAGATGAC	ACCAGARTCCARCACAATAC	AY064043 (<i>Arabidopsis thaliana</i>) AB047313 (<i>Oryza sativa</i>) AY372368 (<i>Trifolium pratense</i>) AY305724 (<i>Gossypium hirsutum</i>) AF548026 (<i>Stevia rebaudiana</i>)

Table S2. Primers used for RACE

Genes		First PCR Primers	Nested PCR Primers
<i>DvCHS1</i>	5'RACE 3'RACE	CGCGCCTCCACTATCCGGTAGAATA GGTGACGGTGACGCCGCGATCAT	
<i>DvCHS2</i>	5'RACE 3'RACE	GGCGGGGTTGCAGTGCCGATGGCAA TGGCTCCGTCTTTGGACGCCCGTCA	GCTCGGTAAAGATGCGGCTGTCAAA
<i>DvCHI</i>	5'RACE 3'RACE	GGGACCAGTAACGATGTCCCTAAA GGCAAACCGCCACGAGTTGAC	TGGGTCAACTCGTGGGCGGTTTT GGACATCGTTACTGGTCCCTTTGA
<i>DvF3H</i>	5'RACE 3'RACE	AGGGCCTCTTTTTCAAGGCCATT TGGGCGGTTCAAGAACGCGGATCA	AGAGCTTGCAGGCCAGGCCATTAA ACGCGGATCACCAAGCCGTGGTCAA
<i>DvDFR</i>	5'RACE 3'RACE	GTGACTCGTCATAGACCGGAAGTT ACTTCCTCTGCCGGAACGGTAAA	
<i>DvANS</i>	5'RACE 3'RACE	CCTTAGAAACCGTCTCCGGGAGCGGTT CCCAAAATGCCCTCAACCGGAGCTA	CCGGGAGCGGTTTCAGGATGATCTT CCGGAGCTAGCACTCGGTGTTGAA
<i>DvMYB1</i>	5'RACE 3'RACE	CAGATAGTGTGGGTGACGGGACTA GCGGGGAGAATACCAGGAAGAACT	GGGTGACGGGACTAACCCTTGGGAAATA1 TTCGACCCCGTCCCAAACCACAAA
<i>DvMYB2</i>	5'RACE 3'RACE	TGGTGGTGGTGGCGGGGACGGTTGT CCGCCCTGACCTCAAATGTGGCAACT	CCACTTGTACCAAGAAGGCTATGGA GTGGCAACTTCTCCGAAGAAGAAGA
<i>DvDEL</i>	5'RACE 3'RACE	CCTTCTCTGGTACGCCGAACTCAA CCACGAAGGCCTCTGGCTGCATTGT	GGTACGCCGAACTCAACTATACCTT CCTCTGGCTGCATTGTCCCCTGAAGAT
<i>DvIVS</i>	5'RACE 3'RACE	CCAAGGATCGACGCCTTGTCATT TCCATCGCCTCTCGCCTCGGCAAAA	GTCACCAACGGCACCAACGTTCTAA GCGCGAACCACGTCCTAGCGGAA
<i>DvWDR1</i>	5'RACE 3'RACE	AAGCCGACCACTGCACCTGGTTAAT CCGTTAGGGTTTTCGACCTTCGCGATA	GGAGCCCAAGCAATCGCATTGACACT TCGACCTTCGCGATAAGGAACACT
<i>DvWDR2</i>	5'RACE 3'RACE	TGCGAATCATCCCGACCGTACAT GGATAGTGCGAAGGTTGTGGTGCTT	GCAATCGCGTTCACACTCGACTGAT CGTTTCCCGACGTTACCTGTTGT
<i>DvActin</i>	3'RACE	TATGTTGCTATCCAGGCCGT	TCTCTTTATGCCAGTGGTCG

Table S3. Primers used for semi-quantitative RT-PCR

Genes	Forward Primers	Reverse Primers
<i>DvCHS1</i>	AATCCCGGTTTCAAGTGATTA	ATGCAATGTAAGTGACAACATA
<i>DvCHS2</i>	TCTTATTACTGCTCGCAATATCTT	AGTTAGGGCGAAATCGGCATGGTA
<i>DvCHI</i>	ATGGCTGGTCTKGAGGTCGAA	GGGCTGAGCTTATTTATTAC
<i>DvF3H</i>	CATCTTTGAAATGGGACGAGACTTC	GATTACTCAAACACTTCATTATTT
<i>DvDFR</i>	ATCGGCTCCTGGTTAGTTAT	CCATTAATAATATGAACTTTATTAA
<i>DvANS</i>	TACCTTCCATCCATCATGGTCACTT	GTTCTTAGAATGACCCAAACAACAA
<i>DvMYB1</i>	CACAAACATTTTCAATAGAAAATTG	TAAGAAAGTTATACTCCGTTACATC
<i>DvMYB2</i>	ACAAAAAGATATCAAAAAGAACAA	AAATCCAAATGAGAATTCATTTTTCAT
<i>DvDEL</i>	ATCTCCTCCAATTCATCAAGATTTT	CCTTTTCTACAGATCAATCAAACAT
<i>DvIVS</i>	TTTGACGTAATTTTGGACCTAATTT	CATCCATTTTTAAATTGTTTGTGGT
<i>DvWDR1</i>	TTTCTACTTTTCCAATAATATCACA	AGATTCTGTAAAACCTTAATATGACT
<i>DvWDR2</i>	GATACAGATTATCCCAATTCCAAA	GTATTCCCAAACCTATATAGGCTAA
<i>DvActin</i>	TGCTTATGTTGGTGATGAAG	CCCTGTTAGCCTTAGGATTT

Table S4. Primers used for real-time RT-PCR

Genes	Forward Primers	Reverse Primers
<i>DvCHS1</i>	CATGTGCTAAGCGAATACGG	CCTCTCCGGTGGTATTGAAC
<i>DvCHS2</i>	TGTCCCAACTACCATGCCGATTT	TTACACATTAAAATGACACAGTGA
<i>DvIVS</i>	GCATATGCAAAGCAGCAAGATCT	TGAAGAAAAGTTTCACATGTTGA
<i>DvActin</i>	TGCTTATGTTGGTGATGAAG	CCCTGTTAGCCTTAGGATTT

Table S5. Primers used for analyzing the *DvIVS* genomic region and *Tdv1*

Genes		Primers
<i>DvIVS</i>	IVS-Full-F	TTTGACGTAATTTTGGACCTAATTT
	35S-IVS-F	ATGGCTGCCGCTGGTTCGGTAAACG
	IVS-474F	CGGTGAGCAACAGGTGGCGGAGAA
	IVS-611R	CCGACACCAGGAGGAAATGAGAAA
	IVS-625F	GCATATGCAAAGCAGCAAGATCTAT
	IVS-725F	CGGTGATATGCATCCCTGTACTAAA
	IVS-826R	TGAAGAAAAGTTTCACATGTTGAAT
	IVS-1082F	TGCCTCACAATAATAAAGATTCAAT
	IVS-1316F	CAGAAGAATTTGCACCGGAGTTTA
	IVS-1614R	GAGCTCTTCGTGCGACGTCGTTTT
	IVS-G1163F	TCCCAGCTCACGGTTCAGTTTTAAA
	IVS-G2241F	AAGTGCTGAGCCAGTAAGACTGTTT
	IVS-G2633F	TTGAATAAACAAAGTTGATAGTAAT
	IVS-G2844F	GATTAGGGATCCTTTTCAACAACAT
	IVS-G2869R	AATGTTGTTGAAAAGGATCCCTAAT
	IVS-G3415F	ATATCTGATCGTAATTTAACAAATT
	IVS-GR3012R	CTTGGGTACATTTTCATATGTAATTT
	IVS-GR3637R	GATTCACGTGTGACGTATTATTGTT
	IVS-GR4193R	AGTACTTTTATGACTTTTATGAGAAA
	IVS-Full-R	CATCCATTTTTAAATTGTTTGTGGT
<i>Tdv1</i>	IVS-TP1F	TAGCGGCGACAATTGTCGCCGCT
	IVS-TP2F	CGAAATATAAACAAACAAAGTTAAA
	IVS-TP3F	ATATTCAACTTTTAGTTTATTCAA
	IVS-TP4F	ACATATTAGCATTTTAAACTTGT
	IVS-TP1R	CACTACAAGAAATATAGTCAATA
	IVS-TP2R	GAGCATTTATACATTTGATAAAT
	IVS-TP3R	CATAAGTAAATGGTGGGCCTCATA
	IVS-TP4R	TGTCAAACATGTCAGTCAAACAT
	IVS-TP5R	CGTGTGCAAAATGTCAGAATACT
	IVS-TP6R	TAATGAGAGTCGGTGGGTCGATA
	IVS-TP7R	ACTCCTTCAATACGTGTAACAAA
	IVS-TP8R	AATGTTTGCATAATTAGGCATTT
	IVS-TP9R	CATTAACGTATTAGCGGCGACACTA

Table S6. Primers used for confirming the sequence

Genes	5' direction Primers	3' direction Primers
<i>DvCHS1</i>	TGTTGTTCTCGGCCAAGTCT	GTCGGGCTAACGTTTCATCT
<i>DvF3H</i>	GTGAATTATTACCCAAAGTGTCCAC	TTGGTCCATATCAACACAAGCTTTT
<i>DvDFR</i>	TCCAATGTGACTCGTCATAGA	TGGGATCGATGAGGATTTATC

Table S7. SNPs of *DvCHS1* cDNA in MJOr and MJY

Line	Deduced AA Type	Number of clones	Number of bases																														
			27	45	47	197	203	287	377	446	491	602	611	614	623	641	644	657	719	761	764	773	809	942	953	1024	1025	1154	1178	1184	1237	1345	1348
MJOr	1	3	C	C	G	G	T	C	A	A	T	G	T	T	G	A	C	A	C	T	G	C	T	T	T	A	A	G	G	G	T	T	C
		1	C	C	G	G	T	C	A	A	T	G	T	T	G	A	C	A	C	T	G	C	T	T	T	A	A	G	G	G	T	T	C
		15	G	A	A	A	C	A	C	G	T	G	C	T	G	G	C	A	A	C	T	C	G	C	C	A	G	G	C	G	T	A	T
	2	1	G	A	A	A	C	A	C	G	T	G	C	T	G	G	C	A	A	C	T	C	G	C	C	A	G	G	C	G	T	A	T
		1	G	A	A	A	C	A	C	G	T	G	C	T	G	G	C	A	A	C	T	C	G	C	C	A	G	G	C	G	T	A	T
		1	C	C	G	A	C	A	C	G	T	G	C	T	G	G	C	A	A	C	T	C	G	C	C	A	G	G	C	G	T	A	T
		1	C	C	G	A	C	A	C	G	T	G	C	T	G	G	C	A	A	C	T	C	G	C	C	A	G	G	C	G	T	A	T
	3	1	C	C	G	A	C	A	C	G	C	C	A	C	C	G	T	G	C	C	G	T	G	C	C	A	G	C	C	G	T	A	T
		12	C	C	G	A	C	A	C	G	C	C	A	C	C	G	T	G	C	C	G	T	G	C	C	A	G	C	G	A	C	A	C
	4	1	C	C	G	A	C	A	C	G	C	C	A	C	C	G	T	G	C	C	G	T	G	C	C	A	G	C	G	A	C	A	C
		1	G	A	A	A	C	A	C	G	C	C	A	C	C	G	T	G	C	C	G	T	G	C	C	A	G	C	G	A	C	A	C
	MJY	4	11	C	C	G	A	C	A	C	G	C	C	A	C	C	G	T	G	C	C	G	T	G	C	C	A	G	C	G	A	C	A

The same number of Deduced AA Type indicates the same deduced amino acid sequence.

ORF (51–1220 bases).

SNPs of 287, 657, 764, and 1024 bases cause amino acid substitution.

SNPs observed in only 1 clone are omitted.

Table S8. SNPs of *DvCHI* cDNA in MJOr and MJY

Line	Deduced AA type	Number of clones	Number of bases													
			12	62	78	114	197	225	266	300	396	464	486	655	713	
MJOr	1	11	T	C	A	C	C	C	G	G	T	T	G	T	T	
		1	T	C	A	C	C	C	G	G	T	T	G	C	T	
		9	G	C	A	C	C	C	G	G	T	T	G	T	T	
		1	G	C	C	C	C	C	G	G	T	T	G	T	T	
	2	2	T	C	C	A	C	G	C	A	A	C	A	C	T	
		1	G	C	C	A	C	G	C	A	A	C	A	C	T	
		1	G	C	C	A	C	G	C	A	A	C	A	T	T	
	3	3	G	C	C	C	G	G	C	G	A	C	A	T	A	
		2	T	C	C	C	G	G	C	G	A	C	A	T	A	
		1	G	C	C	C	G	G	C	G	A	C	A	T	T	
		1	T	C	C	C	G	G	C	G	A	C	A	T	T	
	4	1	T	T	C	C	C	C	G	G	T	T	G	T	T	
		1	G	T	C	C	C	C	G	G	T	T	G	T	T	
	5	2	T	T	C	C	C	C	G	G	A	C	A	C	T	
		1	G	T	C	C	C	C	G	G	A	C	A	C	T	
	6	1	G	T	C	C	G	G	C	G	A	C	A	T	A	
	MJY	1	12	T	C	A	C	C	C	G	G	T	T	G	T	T
			1	T	C	A	C	C	C	G	G	T	T	G	T	A
1			T	C	C	C	C	C	G	G	T	T	G	T	T	
4			G	C	A	C	C	C	G	G	T	T	G	T	T	
1			G	C	C	C	C	C	G	G	T	T	G	T	T	
1			T	C	A	C	C	C	G	G	T	T	G	C	T	
2		6	T	C	C	A	C	G	C	A	A	C	A	C	T	
		1	G	C	C	A	C	G	C	A	A	C	A	C	T	
3		2	T	C	C	C	G	G	C	G	A	C	A	T	A	
		1	G	C	C	C	G	G	C	G	A	C	A	T	A	
		1	T	C	A	C	G	G	C	G	A	C	A	T	A	
4		1	G	T	C	C	C	C	G	G	T	T	G	T	T	
5		2	G	T	C	C	C	C	G	G	A	C	A	C	T	
7		1	G	C	A	C	C	C	G	G	A	C	A	C	T	
		2	T	C	C	C	C	C	G	G	A	C	A	C	T	

The same number of Deduced AA Type indicates the same deduced amino acid sequence.

ORF (1–675 bases).

SNPs of 62, 197, 225, 266, and 464 bases cause amino acid substitution.

SNPs observed in only 1 clone are omitted.

Table S9. SNPs of *DvF3H* cDNA in MJOr and MJY

Line	Deduced AA type	Number of clones	Number of bases																			
			36	118	228	259	270	282	314	380	467	617	635	705	728	797	890	905	1018	1073	1102	1133
MJOr	1	26	G	T	C	A	T	T	G	C	G	A	A	G	G	C	G	A	C	T	G	T
		1	G	T	C	A	T	T	G	C	G	G	A	G	G	C	A	A	C	C	T	T
		1	G	T	C	A	T	T	G	C	G	A	A	G	G	C	G	A	C	T	G	-
	2	2	A	A	C	T	C	C	C	T	G	G	G	A	A	T	A	A	C	C	G	T
		4	A	A	C	T	C	C	C	T	G	G	G	A	A	T	A	A	C	C	T	T
	3	2	G	A	T	T	C	T	C	C	C	G	A	G	G	C	G	G	C	T	G	T
		1	G	A	T	T	C	T	C	T	C	A	A	G	G	C	G	G	C	T	G	-
	4	1	G	T	C	A	T	T	G	C	G	A	A	G	G	C	G	A	T	T	G	T
	5	1	G	T	C	T	C	C	C	T	G	G	A	G	G	C	G	A	C	C	T	T
	MJY	1	20	G	T	C	A	T	T	G	C	G	A	A	G	G	C	G	A	C	T	G
2			G	T	C	A	T	T	G	C	G	A	A	G	G	C	G	A	C	T	T	T
2		5	A	A	C	T	C	C	C	T	G	G	G	A	A	T	A	A	C	C	G	T
		1	A	A	C	T	C	C	C	T	G	G	G	A	A	T	A	A	C	T	G	T
3		1	G	A	T	T	C	T	C	C	C	G	A	G	G	C	G	G	C	T	G	T
		1	G	A	T	T	C	T	C	C	C	G	A	G	G	C	G	G	C	T	T	T
6		1	G	T	C	A	T	T	G	C	C	G	A	G	G	C	G	G	C	T	G	T
7		1	G	A	C	A	T	C	C	C	G	A	A	G	G	C	G	A	C	T	G	T
8		1	G	A	T	T	C	C	C	C	G	A	A	G	G	C	G	A	C	T	G	T
9		1	G	A	C	T	C	C	C	T	G	G	G	A	A	T	A	A	C	C	G	T
10		1	A	A	C	T	C	C	C	T	G	A	A	G	G	C	G	A	C	T	G	T
11	1	A	A	C	T	C	C	C	T	G	G	G	A	A	T	A	A	T	T	G	T	

The same number of Deduced AA Type indicates the same deduced amino acid sequence.

ORF (-10 to 1076 bases).

SNPs of 36, 118, 228, 259, 270, 282, 467, 705, and 1018 bases cause amino acid substitution.

SNPs observed in only 1 clone are omitted.

Table S10. SNPs of *DvDFR* cDNA in MJOr and MJY

Line	Deduced AA type	Number of clones	Number of bases																		
			43	219	241	258	285	353	486	490	589	601	628	738	834	922	940	942	986	1131	1134
MJOr	1	13	A	T	A	A	T	C	G	G	A	G	T	A	G	C	G	C	C	G	T
	2	7	A	T	T	G	A	C	G	G	A	G	T	A	G	C	G	C	C	G	T
	3	2	C	T	A	G	A	T	G	G	G	A	T	A	G	C	G	C	T	G	T
	4	5	A	T	A	A	T	C	G	G	A	G	T	A	G	C	G	C	T	G	T
		2	A	T	A	G	A	C	G	G	A	G	T	A	G	C	G	C	T	G	T
	5	3	A	T	A	G	A	T	A	A	A	G	G	G	A	T	A	T	T	C	—
	6	1	A	T	A	G	A	T	G	G	G	A	T	A	G	C	G	C	C	G	T
	7	1	A	T	A	A	T	C	G	G	G	A	T	A	G	C	G	C	C	G	T
8	1	C	T	A	G	A	T	A	A	A	G	G	G	A	T	A	T	T	C	—	
MJY	1	9	A	T	A	A	T	C	G	G	A	G	T	A	G	C	G	C	C	G	T
		1	A	A	A	A	T	C	G	G	A	G	T	A	G	C	G	C	C	G	T
	2	5	A	T	T	G	A	C	G	G	A	G	T	A	G	C	G	C	C	G	T
	3	8	C	T	A	G	A	T	G	G	G	A	T	A	G	C	G	C	T	G	T
		1	C	C	A	G	A	T	G	G	G	A	T	A	G	C	G	C	T	G	T
	4	4	A	T	A	G	A	C	G	G	A	G	T	A	G	C	G	C	T	G	T
	9	1	C	T	T	G	A	C	G	G	A	G	T	A	G	C	G	C	C	G	T
	10	1	C	T	A	G	A	C	G	G	A	G	T	A	G	C	G	C	C	G	T

The same number of Deduced AA Type indicates the same deduced amino acid sequence.

ORF (18–1028 bases).

SNPs of 43, 241, 353, 490, 589, 601, 628, 940, and 986 bases cause amino acid substitution.

SNPs observed in only 1 clone are omitted.

Table S11. SNPs in the exon of the *DvCHS1* genomic region in MJOr, MJY, and MJW

Line	Deduced AA type	Number of clones	Number of bases																																			
			27	45	47	197	203	287	377	446	491	802	811	814	823	841	844	857	719	781	784	773	809	842	853	1024	1025	1154	1178	1184	1237	1345	1348					
MJOr	1	6	C	C	G	G	T	C	A	A	T	G	T	T	G	A	C	A	C	T	G	C	T	T	T	A	A	G	G	G	T	T	C					
	2	1	C	C	G	A	C	A	C	G	T	G	C	T	G	G	C	A	A	C	T	C	T	T	T	A	A	G	G	G	T	T	C					
	9	--	--	--	A	C	A	C	G	T	G	C	T	G	G	C	A	A	C	T	C	G	C	C	A	G	G	C	G	T	A	T						
	4	9	C	C	G	A	C	A	C	G	C	C	A	C	C	G	T	G	C	C	G	T	G	C	C	G	G	C	G	A	C	A	C					
MJY	1	5	C	C	G	G	T	C	A	A	T	G	T	T	G	A	C	A	C	T	G	C	T	T	T	A	A	G	G	G	T	T	C					
	1	1	C	C	G	A	C	C	A	A	T	G	T	T	G	A	C	A	C	T	G	C	T	T	T	A	A	G	G	G	T	T	C					
	1	1	G	A	A	G	T	C	A	A	T	G	T	T	G	A	C	A	A	C	T	C	G	T	T	A	A	G	G	G	T	T	C					
	4	9	C	C	G	A	C	A	C	G	C	C	A	C	C	G	T	G	C	C	G	T	G	C	C	G	G	C	G	A	C	A	C					
MJW	1	7	C	C	G	G	T	C	A	A	T	G	T	T	G	A	C	A	C	T	G	C	T	T	T	A	A	G	G	G	T	T	C					
	2	3	--	--	--	A	C	A	C	G	T	G	C	T	G	G	C	A	A	C	T	C	G	C	C	A	G	G	C	G	T	A	T					
	4	6	C	C	G	A	C	A	C	G	C	C	A	C	C	G	T	G	C	C	G	T	G	C	C	G	G	C	G	A	C	A	C					

The same number of Deduced AA Type indicates the same deduced amino acid sequence.

ORF (51–1220 bases).

We could not determine a part of type 2 sequence from 1 to 54.

SNPs observed in only 1 clone are omitted.

Table S12. SNPs in the intron of the *DvCHS1* genomic region in MJOr, MJY, and MJW

Line	Deduced AA type	Number of clones	Number of bases																																															
			17-21	121	123	171	221	222	243	260	284	285	298	341	343	396	411	412	429	481	484	512-626	641	658	700	730	731	732	740	741	771	780	781																	
MJOr	1	5	—	T	—	C	G	C	T	—	G	G	T	T	T	T	A	A	A	A	T	—	G	T	T	T	A	C	—	—	T	A	A																	
	2	9	○	A	T	C	G	T	T	A	C	A	C	T	G	T	A	A	G	G	A	—	G	C	A	A	G	T	T	—	C	C	C																	
	4	8	○	A	A	T	A	C	G	—	G	G	T	A	T	A	G	C	A	A	A	○	A	C	A	T	G	T	T	T	C	A	A																	
	1	1	○	A	T	C	G	T	T	A	C	A	C	T	G	—	—	—	—	A	A	○	A	C	A	T	G	T	T	—	C	A	A																	
1	1	○	A	A	T	A	C	G	—	G	G	T	A	T	A	G	C	A	A	A	○	A	C	A	T	G	T	T	—	C	A	A																		
MJY	1	6	—	T	—	C	G	C	T	—	G	G	T	T	T	T	A	A	A	A	T	—	G	T	T	T	A	C	—	—	T	A	A																	
	2	1	○	A	T	C	G	T	T	A	C	A	C	T	G	T	A	A	G	G	A	—	G	C	A	A	G	T	T	—	C	C	C																	
	4	9	○	A	A	T	A	C	G	—	G	G	T	A	T	A	G	C	A	A	A	○	A	C	A	T	G	T	T	—	C	A	A																	
	1	1	○	A	T	C	G	T	T	A	G	G	T	T	T	T	A	A	A	A	T	—	G	T	T	T	A	C	—	—	T	A	A																	
MJW	1	7	—	T	—	C	G	C	T	—	G	G	T	T	T	T	A	A	A	A	T	—	G	T	T	T	A	C	—	—	T	A	A																	
	2	3	○	A	T	C	G	T	T	A	C	A	C	T	G	T	A	A	G	G	A	—	G	C	A	A	G	T	T	—	C	C	C																	
	4	6	○	A	A	T	A	C	G	—	G	G	T	A	T	A	G	C	A	A	A	○	A	C	A	T	G	T	T	—	C	A	A																	

The number of Deduced AA Type indicates the deduced amino acid sequence coded by the exon.

SNPs observed in only 1 clone are omitted.