

Table 1 Suppl. Gene numbers.

Gene	Number
<i>AlF3'H</i>	487632
<i>AtF3'H</i>	AT5G07990.1
<i>BdF3'H1</i>	Bradi1g17180.1
<i>BdF3'H2</i>	Bradi3g04750.1
<i>BrF3'H</i>	Brara.J02462.1
<i>CcF3'H2</i>	Ciclev10019637m
<i>CpF3'H</i>	evm.model.supercontig_94.31
<i>CrF3'H</i>	Carubv10000754m
<i>CsF3'H</i>	Cucsa.198180.1
<i>EgF3'H1</i>	Eucgr.B00580.1
<i>EgF3'H2</i>	Eucgr.B00580.2
<i>EgF3'H3</i>	Eucgr.B00582.1
<i>EgF3'H4</i>	Eucgr.B00578.1
<i>GmF3'H1</i>	Glyma17g08550.1
<i>GmF3'H2</i>	Glyma06g21920
<i>LuF3'H</i>	Lus10021158
<i>MdF3'H1</i>	MDP0000286933
<i>MdF3'H2</i>	MDP0000190489
<i>MeF3'H</i>	cassava4.1_005702m
<i>MeF3'H2</i>	cassava4.1_005668m
<i>MgF3'H</i>	Migut.D01697.1
<i>MtF3'H</i>	Medtr3g025230.1
<i>OsF3'H1</i>	LOC_Os10g16974.1
<i>OsF3'H2</i>	LOC_Os10g17260.1
<i>PpF3'H</i>	Phpat.027G019400.1
<i>PtF3'H</i>	Potri.013G073300.1
<i>PvF3'H</i>	Phvul.009G192400.1
<i>RcF3'H</i>	30138.m003983
<i>SbF3'H1</i>	Sobic.004G200800.1
<i>SbF3'H2</i>	Sobic.004G201100.1
<i>SbF3'H3</i>	Sobic.004G200900.1
<i>SiF3'H</i>	Si035224m
<i>ThF3'H</i>	Thhalv10013289m
<i>VvF3'H</i>	GSVIVT01007878001
<i>ZmF3'H1</i>	GRMZM2G313750_T01
<i>ZmF3'H2</i>	GRMZM2G025832_T01
<i>BdF3'5'H</i>	Bradi1g61577.1
<i>CcF3'5'H</i>	Ciclev10018289m
<i>CpF3'5'H</i>	evm.model.supercontig_157.54
<i>CsF3'5'H</i>	orange1.1g047593m
<i>CsF3'5'H</i>	orange1.1g047593m

<i>GmF3'5'H</i>	Glyma13g04210
<i>MtF3'5'H</i>	CU651565_9.1
<i>OsF3'5'H</i>	LOC_Os10g17260.1
<i>SbF3'5'H1</i>	Sobic.001G360700.1
<i>SbF3'5'H2</i>	Sobic.001G360800.1
<i>SiF3'5'H</i>	Si035183m
<i>VvF3'5'H</i>	GSVIVT01033633001
<i>VvF3'5'H</i>	GSVIVT01033633001
<i>ZmF3'5'H</i>	GRMZM2G119067_T01

Fig. 1 Suppl. The multi-alignment of CHS.

Ma CHS	20	40	60	80	75
Rs CHS	20	40	60	80	129
Cs CHS	20	40	60	80	129
Nn CHS	20	40	60	80	129
AmCHS	20	40	60	80	129
Gh CHS	20	40	60	80	129
Hs CHS	20	40	60	80	129
Ma CHS	100	120	140	160	161
Rs CHS	100	120	140	160	215
Cs CHS	100	120	140	160	215
Nn CHS	100	120	140	160	215
AmCHS	100	120	140	160	215
Gh CHS	100	120	140	160	215
Hs CHS	100	120	140	160	215
Motif I					
Ma CHS	180	200	220	240	2
Rs CHS	180	200	220	240	247
Cs CHS	180	200	220	240	301
Nn CHS	180	200	220	240	301
AmCHS	180	200	220	240	301
Gh CHS	180	200	220	240	301
Hs CHS	180	200	220	240	301
Motif II					
Ma CHS	60	280	300	320	287
Rs CHS	60	280	300	320	344
Cs CHS	60	280	300	320	344
Nn CHS	60	280	300	320	344
AmCHS	60	280	300	320	344
Gh CHS	60	280	300	320	344
Hs CHS	60	280	300	320	344
Motif III					

Online resource 3 Multi-alignment of CHS. The amino acid sequences were obtained from NCBI with the accession numbers as below: RsCHS(CAC88858.1); CsCHS(AFE56210.1); NnCHS(ADD74168.1); AmCHS(ACE60221.1); GhCHS(ABS52573.1); HsCHS(AFU52909.1).

Fig. 2 suppl. The multi-alignment of F3H.

		20	40	60						
Ma F3H :	-----	LEVLSEAMGLEKEALT	KACVDMQKVVINYYPKCPQ	PDLTLGLKRHTDPGTITL	: 54					
Ca F3H :	PHGWI	AVTEKYSEKLMELACKL	LEVLSEAMGLEKEALT	KACVDMQKVVNFYKCPQ	PDLTLGLKRHTDPGTITL : 77					
AmF3H :	PEGWRS	VTVEYSDKLMGLACKL	LEVLSEAMGLEKEALT	KACVDMQKVI	VNYYPKCPQ	PDLTLGLKRHTDPGTITL : 226				
Pa F3H :	PEGWRS	VTVEYSDKLMGLACKL	LEVLSEAMGLEKEALT	KACVDMQKVI	VNYYPKCPQ	PDLTLGLKRHTDPGTITL : 223				
Dc F3H :	PEGWRS	ATGEYSEKLMGLGCKL	LEVLSEAMGLDKEAIT	KACVDMQKVVVNYYPKCPQ	PDLTLGLKRHTDPGTITL : 224					
Cj F3H :	PEEWRA	VTKEYSSLMELACKL	LEVLSEAMGLEKEALT	NACVDMQKVVVNYYPKCPQ	PDLTLGLKRHTDPGTITL : 114					
Jn F3H :	PEGWRS	VTVEYSDKLMGLACKL	LEVLSEAMGLEKEALT	KACVDMQKVVVNYYPKCPQ	PDLTLGLKRHTDPGTITL : 203					
Pl F3H :	PEGWRS	VTVEYSEKLMGLACKL	LEVLSEAMGLEKEALT	NACVDMQKVVVNYYPKCPQ	PDLTLGLKRHTDPGTITL : 226					
Cn F3H :	PEGWRS	ATVEYSEKLMGLACKL	LEVLSEAMGLEKEALT	KACVDMQKVVINFYKCPQ	PDLTLGLKRHTDPGTITL : 226					
Ps F3H :	PEGWRS	VTVEYSEKLMGLAC L	LEVLSEAMGLEKEALT	KACVDMQKVVVNYYPKCPQ	PDLTLGLKRHTDPGTITL : 226					
		Motif III								
		80	100	120	140					
Ma F3H :	LLQDQV	GGLQATRDG	GN	TWITVQ	PVEGAFV	VNLGDHGHYLSNGR	FKNADHQAVVNSNY	SRLSIATFQNP	-----	: 123
Ca F3H :	LLQDQV	GGLQATKDNG	K	TWITV	KPIEGAF	VVNLGDHGHYLSNGR	FKNADHQAVVNSNS	SRLSIATFQNP	PEAIVY	: 153
AmF3H :	LLQDQV	GGLQATRDG	GK	TWITVQ	PVEGAFV	VNLGDHGHYLSNGR	FKNADHQAVVNSNS	SRMSIATFQNP	PAPNATVY	: 302
Pa F3H :	LLQDQV	GGLQATRDG	GK	TWITVQ	PVEGAFV	VNLGDHGHYLSNGR	FKNADHQAVVNSNS	SRMSIATFQNP	PAPNATVY	: 299
Dc F3H :	LLQDQV	GGLQATRDG	GK	TWITVQ	PVEGAFV	VNLGDHGHYLSNGR	FKNADHQAVVNSNY	SRLSIATFQNP	PAPNATVY	: 300
Cj F3H :	LLQDQV	GGLQATRDG	GK	TWITVQ	PVEGAFV	VNLGDHGHYLSNGR	FKNADHQAVVNSNS	SRLSIATFQNP	PEAIVY	: 190
Jn F3H :	LLQDQV	GGLQATRDG	GK	TWITVQ	PVEGAFV	VNLGDHGHYLSNGR	FKNADHQAVVNSNY	SRLSIATFQNP	-----	: 272
Pl F3H :	LLQDQV	GGLQATRDG	GK	TWITVQ	PVEGAFV	VNLGDHGHYLSNGR	FKNADHQAVVNSNY	SRLSIATFQNP	PEAIVY	: 302
Cn F3H :	LLQDQV	GGLQATRDG	GK	TWITVQ	PVEGAFV	VNLGDHGHYLSNGR	FKNADHQAVVNSNC	SRLSIATFQNP	PEAIVY	: 302
Ps F3H :	LLQDQV	GGLQATRDG	GK	TWITVQ	PVEGAFV	VNLGDHGHYLSNGR	FKNADHQAVVNSNY	SRLSIATFQNP	PEAIVY	: 302
		Motif IV				Motif V				

Online resource 4 Multi-alignment of F3H. The amino acid sequences were obtained from NCBI with the accession numbers as below: CaF3H(ACN60402.1); AmF3H(AAX21539.1); PaF3H(AAX21535.1); DcF3H(AAD56577.1); CjF3H(BA166080.1); JnF3H(ACR47976.1); PlF3H(AFI71897.1); CnF3H(ADZ28514.1); PsF3H(AEN71544.1).

Fig. 3 Suppl. The multi-alignment of two MaF3'H from mulberry.

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      *           20           *           40
MoF3'H1 : MASITITILLSILLAVLVYRLVNNLIRSR----RKIPPGPRQWPVIG
MoF3'H2 : MPSIFTILGILLSILLAVLLFCLENQLRSRRSVPGRRIPPGPRWPPIIG

      *           60           *           80           *
MoF3'H1 : NLPHLGPAPHQTMAALARKHGPLMHLRLGQVDVVVAASASVAAQFL
MoF3'H2 : NLPQLGPAPHQTIAALARKHGPLMHLRFGLVDVVVAASASVAAQFL

      100           *           120           *           1
MoF3'H1 : KTHDANFSSRPPNSGAKHIAINYQDLVFRPYGQRWRLLRKITSVHL
MoF3'H2 : KAHD TNFLSRPPSSAAKHVGYNYHDLVLAPYGPWRRLMRKIASVHL

      40           *           160           *           180
MoF3'H1 : FSGKALEDFRHVRQEEVAVLISALANTGSTAVNLGQLLNVCTVNAL
MoF3'H2 : LSGKALEDFRYVRQEEAAVLIRGLANAGPTAINLAQLLHLCTTNTL

      *           200           *           220           *
MoF3'H1 : GRTMLGYRVFGDGSGKSEPRADEFKSMVVEVMVLAVGFNIGDFVPA
MoF3'H2 : GRAMLGYRVFGDGSGKSDPRADEFKSMVVEALAVAGVFNIGDFVPA

      240           *           260           *
MoF3'H1 : LDWLDLQGVAAARMKKLHNRFDAFLTITIEEHKANVGKGKHTDLLST
MoF3'H2 : LEWLDLQGVVARMKKVHKRFDAFLTRIIEEHKANAGNGKHTDMLTT

      280           *           300           *           320
MoF3'H1 : LLSLKDDAEGEDE-KLTDTEIKALLNMFTAGTDTTSSTVEWAIAE
MoF3'H2 : LLSVKEDADGHEGGKLTETEIKALLNIFIAGTDTTSSTVEWAIAE

      *           340           *           360
MoF3'H1 : LIRHPKILAKVQEELDRVVGDRDLVSELDLAQLTYLQAVMKETFRL
MoF3'H2 : LIRHPKILAQVQEELDRVVGDRDLVSELDLPLQTYLKALVKETFRL

      *           380           *           400           *
MoF3'H1 : HPSTPMSVPRMANESCEINGYHIPKGTLLNVNVAIARDPAEWTDP
MoF3'H2 : HPSTPLSLPRIAENCDINGYHIPKGTLLNVNVAIARDPAEWTDP

      420           *           440           *           460
MoF3'H1 : LEFRPERFLPGGEKAQVDIRGNDFEVIPFGAGRRICAGMSLGVRMV
MoF3'H2 : LLFRPERFLPGGEKAEVDVRGNDFEVIPFGSGRRMCVGMRLGLRTV

      *           480           *           500
MoF3'H1 : QLLTATLVQAFNLGLPNGLVPEKLNMD EAYGLTLQRAAPLMVHPQP
MoF3'H2 : QLLTASLVHAFNFGLANGLVPEKLNMD EAYGLTLQRASPLMVHPWP

      *
MoF3'H1 : RLDQHLY----
MoF3'H2 : RLSEHVYEAKI

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Fig. 4 Suppl. The multi-alignment of DFR.

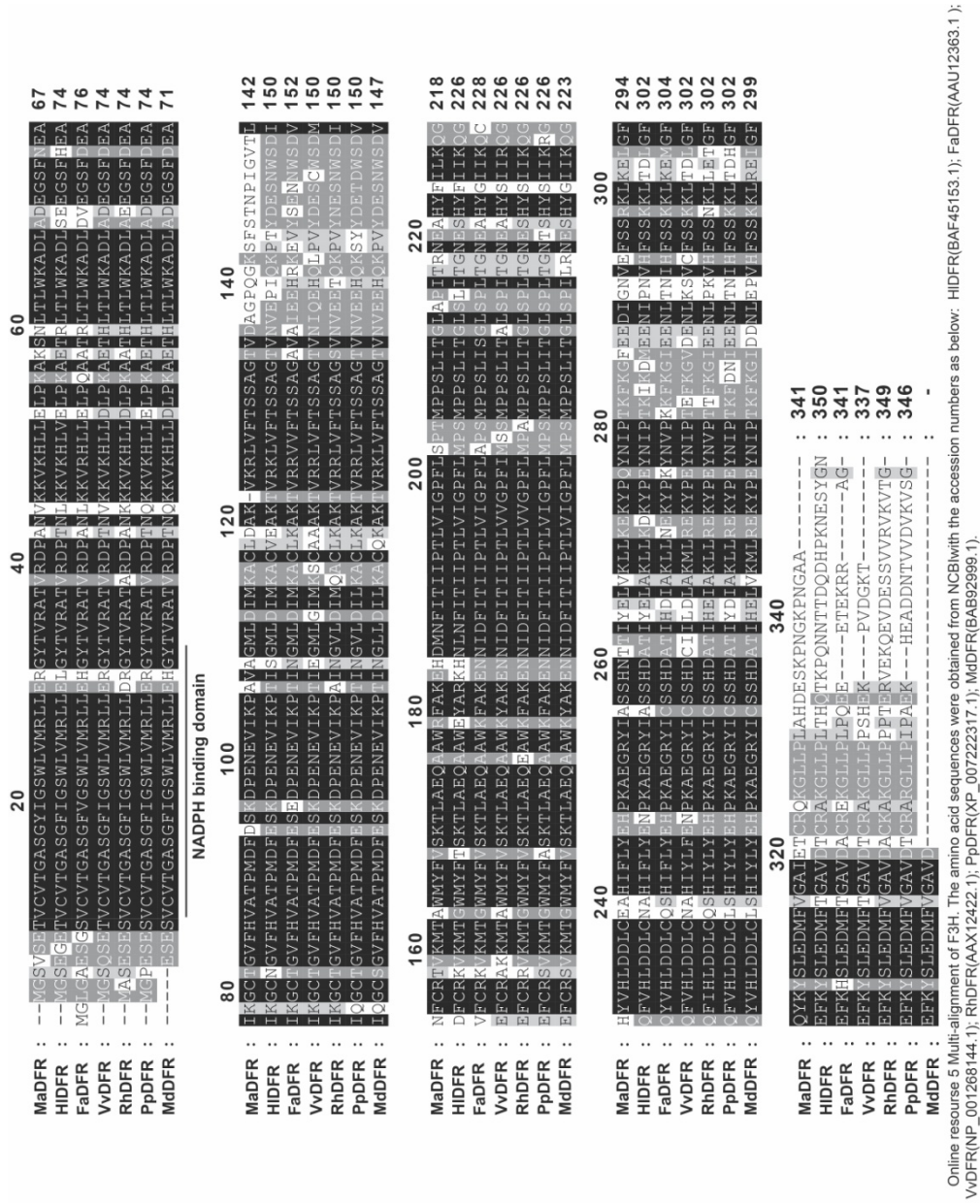
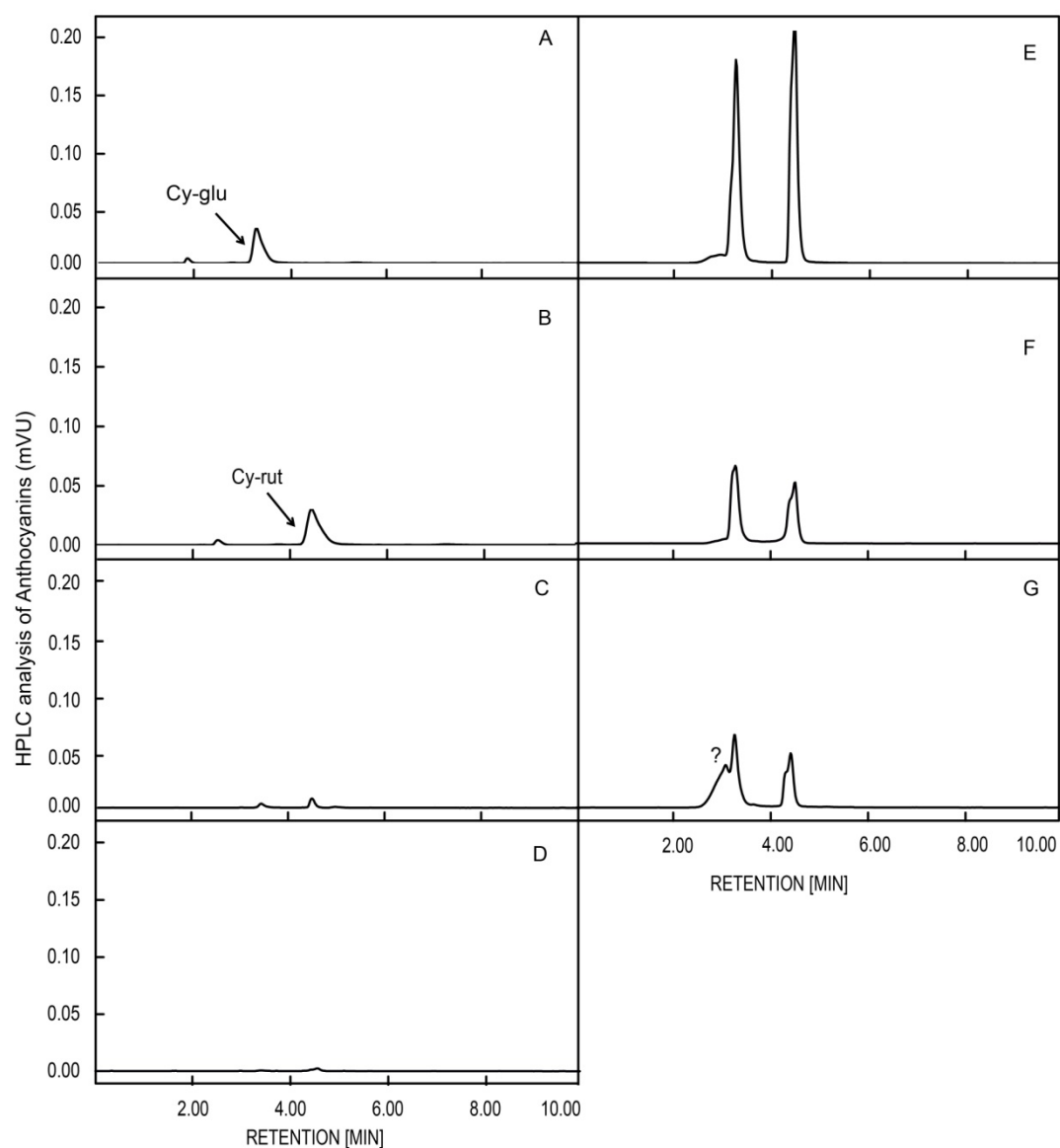


Fig. 5 Suppl. HPLC for the anthocyanins from mulberry fruits.



The content of anthocyanins and total favonoids in the female flowers and fruit from white and purple fruit cultivars. (A and B) Authentic standards of cyanidin 3-O-glucoside (Cy-glu) and cyanidin 3-O-rutinoside (Cy-rut). (C – F) Anthocyanin profiles of BYW (C), ZZB (D), JL30 (E) and DS (F). Peaks identified are as follows: Cy-glu, cyanidin 3-O-glucoside; Cy-rut, cyanidin 3-O-rutinoside. (G) Anthocyanin profiles in female flowers of ZZB.

Fig. 6 Suppl. The proposed pathway of anthocyanins synthesis in mulberry.

