Identification and characterization of flavonoid biosynthetic enzyme genes in *Salvia miltiorrhiza*

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Concentra	Accession number	ORF	AA	MW	a I
Gene name		(bp)	Len	(Da)	PI
AtCHS	AT5G13930	1188	395aa	43115.72	6.08
AtCHI	AT3G55120	741	246aa	26595.61	5.43
AtF3H	AT3G51240	1077	358aa	40275.72	5.29
AtFLS1	AT5G08640	1011	336aa	38281.77	5.63
AtFLS2	AT5G63580	753	250aa	28482.41	4.77
AtFLS3	AT5G63590	927	308aa	35451.53	5.13
AtFLS4	AT5G63595	840	279aa	31900.58	6.56
AtFLS5	AT5G63600	981	326aa	37092.85	4.66
AtFLS6	AT5G43935	882	293aa	33456.13	5.67
AtF3'H	AT5G07990	1542	513aa	56786.57	7.83
AtDFR	AT5G42800	1149	382aa	42774.96	5.43
AtANS	AT4G22880	1071	356aa	40396.42	5.23
CsF3′5′H	ABA40923.1	1533	510aa	57041.53	8.82
GmF3'5'H	AAM51564.1	1527	508aa	57185.75	9.11

Table S1. Sequence features of flavonoid metabolism pathway genes in *Arabidopsis thaliana* and other plants.

 Table S2. Primers used for full-length coding region cloning.

Gene name	Primer name	Sequence (5' to 3')
SmCHS1	CHS1-F	AACAAGAATGGTGACCGTGGA
	CHS1-R	TCAATTGATGTTGACGCTGTGCAG
SmCHS2	CHS2-F	CCAATGTGCAAGAATCCAATTTAGAG
	CHS2 -R	GTTGCACACCATGTTAAATATAGC
SmCHS3	CHS3 -F	ATGGCAAGCGTGGAGGAGATC
	CHS3 -R	TTATAAATCAATCGGCATGCTG
SmCHS4	CHS4 -F	ATGGCGACCGTGGAGGAGATC
	CHS4 -R	TTAATTAATCGGCATACTACGTAGC
SmCHS5	CHS5 -F	ATGGCAAGCGTGGAGGAGATC
	CHS5 -R	TTATAATTCAATCGGAATGCTGCGC
SmCHS6	CHS6 -F	TGTAATGTCGACAAAGCAGCAG
	CHS6 -R	GATAGTTAATGGAGGAGGCTTCGC
SmCHS7	CHS7-F	CAAACCCCGCCTAACAACAACG
	CHS7-R	CGTTATATTTAAATCGGCATGCTGTG
SmCHS8	CHS8-F	CAAACCCCGCCTAACAACAACG
	CHS8-R	GAACACAGACTAGAGGCCCGAGAC
SmCHI1	CHI1-F	CCACCTTCATCTTCATCTTCACC
	CHI1 -R	CATGTTTCTTGATTCATTGTGCCTC

Sm CHI2	СНІЗ Е	
SmCH12	CHI2-F CHI2-R	CATGTTTCTTGATTCATTGTGCCTC
SmCH13	CHI3-F	GAGGCTGTGATGGTGGATGAAGTTC
	CHI3-R	TTATTTGGATAACTCGGCGGAGAGAG
SmCHI4	CHI4-F	CCATTGTTAACCACCTTCATCTTCAC
	CHI4 -R	CATGTTTCTTGATTCATTGTGCCTCA
SmF3H1	F3H1-F	CATGGCTGAAATGAAAATATCTCC
	F3H1-R	TGGTGGAATCAACCTTAATTTAGAA
SmF3H2	F3H2-F	ATGGCTGCACAAATGAAAATCTG
	F3H2-R	TAATAAAGGGTTGTTTTGGCTGGC
SmF3′5′H	F3′5′H-F	CAACATATAGTAGGCATGCAAGGTG
	F3′5′H-R	ACCTAGCTAGCTGCATAACAATGTG
SmF3'H1	F3′H1-F	ATATATTCACGTTGGCATGCA
	F3′H1-R	GCAAACACTTAAGCATGGTAAAC
SmF3′H2	F3′H 2-F	ACACACACATCACATATATGCAATG
	F3′H 2-R	TCAGATTTGGGCTTGATAAACATGG
SmF3′H3	F3′H 3-F	ATGCAGAGCTTCCACGAATTTCTAT
	F3′H 3-R	GCAACGGTACATTCATTCATCAAC
SmF3'H4	F3′H 4-F	CCTTGTCAATTAGTTTCGCTTCAG
	F3'H 4-R	CCAGTCATCACTCATACAAACTAGG
SmF3'H5	F3′H 5-F	CCTCTCAAACACAACTCTCATCG
	F3′H 5-R	CAAACCGAGGCATAAAATTCACATAG
SmF3′H6	F3′H 6-F	CTCTCTCCAAATTTAATTAGCAATGG
	F3′H 6-R	GCAGAGCCATAAATTCACATAG
SmFLS1	FLS1-F	CTATACCACCACCATGTAAGATCAC
	FLS1-R	CTCAAATCAGGGACAGTGGTTAT
SmFLS2	FLS2-F	AAATGGAGGTTGAGAGAGTGC
	FLS2-R	TATTTGTTTGGTGGGTAGAGTGA
SmFNS II	FLS II -F	GCGAGTTGTACTGATATGGAGCTAG
	FLS II -R	ACAGTAGCTAAACCGAATCAGGC
SmDFR	DFR-F	AATGCCGCTAGAAACCACCCCTC
	DFR-R	TCAATCACATTTGCCATTCTCGCCT
SmANS	ANS-F	CCATGCATTTCCACCCTAACATAC
	ANS-R	TACAACTCACACAATCAACTCGA

Table S2. Cont.

SmUBQ10 UBQ10-RT-F AGATGGGCGGACACTTGCTGATTA UBQ10-RT-R ACTCTCCACCTCCAAAGTGATGGT SmCHS1 CHS1-RT-F CAAGCGCATGTGTGAAAAGTCGA CHS1-RT-R TGCAGAAGACGAGGTGGGTGA	Gene name	Primer name	Sequence (5' to 3')
UBQ10-RT-RACTCTCCACCTCCAAAGTGATGGTSmCHS1CHS1-RT-FCAAGCGCATGTGTGAAAAGTCGACHS1-RT-RTGCAGAAGACGAGGTGGGTGA	SmUBQ ₁₀	UBQ10-RT-F	AGATGGGCGGACACTTGCTGATTA
SmCHS1CHS1-RT-FCAAGCGCATGTGTGAAAAGTCGACHS1-RT-RTGCAGAAGACGAGGTGGGTGA		UBQ10-RT-R	ACTCTCCACCTCCAAAGTGATGGT
CHS1-RT-R TGCAGAAGACGAGGTGGGTGA	SmCHS1	CHS1-RT-F	CAAGCGCATGTGTGAAAAGTCGA
		CHS1-RT-R	TGCAGAAGACGAGGTGGGTGA
SmCHS2 CHS2-RT-F ATGGGAATCGGTGAATTGTGTAA	SmCHS2	CHS2-RT-F	ATGGGAATCGGTGAATTGTGTAA
CHS2-RT-R GCAAAGTCGGACAAGCTTCTG		CHS2-RT-R	GCAAAGTCGGACAAGCTTCTG
SmCHS3 CHS3 – RT-F GGCTTCTTATCGATCTCGTCAGA	SmCHS3	CHS3-RT-F	GGCTTCTTATCGATCTCGTCAGA
CHS3 – RT-R CCAACCTTCGCCTCCACCTGAT		CHS3-RT-R	CCAACCTTCGCCTCCACCTGAT
SmCHS4 CHS4 – RT-F CATTTAAGCGCATGTGAGAGC	SmCHS4	CHS4 –RT-F	CATTTAAGCGCATGTGTGAGAGC
CHS4 – RT-R CATGTGGATGCTGCCGTTGGT		CHS4-RT-R	CATGTGGATGCTGCCGTTGGT
SmCHS5 CHS5 – RT-F GTCTGCTGCGAGTCCACC	SmCHS5	CHS5-RT-F	GTCTGCTGCGAGTCCACC
CHS5 – RT-R GATACCTTTTGCGAGATCTATGAGA		CHS5-RT-R	GATACCTTTTGCGAGATCTATGAGA
SmCHS6 CHS6 – RT-F ATGTCGACAAAGCAGCAGCGC	SmCHS6	CHS6-RT-F	ATGTCGACAAAGCAGCAGCGC
CHS6 – RT-R TCGTCGTTTTGCAGAGGCGTTG		CHS6-RT-R	TCGTCGTTTTGCAGAGGCGTTG
SmCHS7 CHS7-RT-F CAAGCATCGCCGACTACGA	SmCHS7	CHS7-RT-F	CAAGCATCGCCGACTACGA
CHS7-RT-R CAAGTCGGCGGAAGTGGT		CHS7-RT-R	CAAGTCGGCGGAAGTGGT
SmCHS8 CHS8-RT-F CGTTTCCTGATTACTACTTCCGTGT	SmCHS8	CHS8-RT-F	CGTTTCCTGATTACTACTTCCGTGT
CHS8-RT-R CGGGATGTTGGGTTTTCTTTGA		CHS8-RT-R	CGGGATGTTGGGTTTTCTTTGA
SmCHI1 CHI1-RT-F TGCCGATGAACTGGCCGATTCCA	SmCHI1	CHI1-RT-F	TGCCGATGAACTGGCCGATTCCA
CHI1-RT-R CCGTTAGTGGCAGAATCATAGTC		CHI1-RT-R	CCGTTAGTGGCAGAATCATAGTC
SmCHI2 CHI2-RT-F AGTCTTCAAGGATGAAAGCTTCTC	SmCHI2	CHI2-RT-F	AGTCTTCAAGGATGAAAGCTTCTC
CHI2-RT-R CCAAGCTCTGCCTCGTGGTA		CHI2-RT-R	CCAAGCTCTGCCTCGTGGTA
SmCH13 CH13-RT-F GCTCCTACCGTCCAGATTGTATT	SmCHI3	CHI3-RT-F	GCTCCTACCGTCCAGATTGTATT
CHI3-RT-R TTATTTGGATAACTCGGCGGA		CHI3-RT-R	TTATTTGGATAACTCGGCGGA
SmCHI4 CHI4-RT-F TTCCCACCACAGCGAAGCCACG	SmCHI4	CHI4-RT-F	TTCCCACCACAGCGAAGCCACG
CHI4-RT-R AATGAAGTCGGCGGAATCGG		CHI4-RT-R	AATGAAGTCGGCGGAATCGG
SmF3H1 F3H1-RT-F CAATGGGAGGTTCAAGAATGCAG	SmF3H1	F3H1-RT-F	CAATGGGAGGTTCAAGAATGCAG
F3H1-RT-R GAAAAGAGGTTTGTTTTGGTTGGCG		F3H1-RT-R	GAAAAGAGGTTTGTTTTGGTTGGCG
SmF3H2 F3H2-RT-F GACCCGGGATGACGGCAACACAT	SmF3H2	F3H2-K1-F F3H2-RT-R	
IJII2-KI-K GAACETCCCATGCTIACAIAAT		10112-111-1	GAACEICCCATIGETIACAIAAI
<i>SmF3'5'H</i> F3'5'H-RT-F ACTGAACTTGTTTACTGCAGGGAC	SmF3′5′H	F3′5′H-RT-F	ACTGAACTTGTTTACTGCAGGGAC
F3'5'H-RT-R GGTATGCTAGTTTCGGAATGTCG		F3′5′H-RT-R	GGTATGCTAGTTTCGGAATGTCG
SmE3'H1 E3'H1-RT-F TTAGACACCACCAACCCCCATT	SmF3'H1	F3'H1-RT-F	TTAGACAGGAGGAAGCGGGATT
F3'H1-RT-R ACTCCTCCGCCTTCTCGTCTCCA		F3'H1-RT-R	ACTCCTCCGCCTTCTCGTCTCCA

Table S3. Primers used for qRT-PCR.

Table S3. Cont.

SmF3'H2	F3'H 2-RT-F	TCCGCCATGTTAGAGAGGAAGAAGT
	F3'H 2-RT-R	TCCACCATCGCCTTCAACTCTT
SmF3′H3	F3'H 3-RT-F	CCTTGGCTTAGTTTCCTCGATTTG
	F3′H 3-RT-R	TCAGTACCACCAGTTAGCAAGTCCT
SmF3'H4	F3'H 4-RT-F	CATGGATATGGTAGTAGGAGGAACG
	F3'H 4-RT-R	GCAGTTTGTTGATGTGGGATTCTT
SmF3'H5	F3'H 5-RT-F	AGACTGTAAGGTGGATGGGTATGA
	F3'H 5-RT-R	TCGAAATCTTGTCCCTTCACAT
SmF3'H6	F3'H 6-RT-F	ACATGACTGTAAGGTGGATGGGT
	F3'H 6-RT-R	TCGAAATCCTGTCCCTTCACAT
SmFLS1	FLS1-RT-F	CCTGATTATAGGGAGGTTACTGAAG
	FLS1-RT-R	ACCCCAAGAACCAAGTCCGG
SmFLS2	FLS2-RT-F	GGCGACCAAATTGAGATACTAAG
	FLS2-RT-R	TCACAAGCTTTGGAATTGGC
SmFNS II	FNS II -RT-F	ATTCTGGATTTTTTTACCGCCG
	FNS II -RT-R	CTCTCTGATCCCACCACTTTTGC
SmDFR	DFR-RT-F	GATGATCCCGAGAATGAAGTGATC
	DFR-RT-R	AGACACAAAGTACATCCATCCAGTC
SmANS	ANS-RT-F	CTGATTATATACCGGCTACATG
	ANS-RT-R	AATCCGCCGACTTCTTTCTC

Protein name	Plant Species	Accession number
OsCHS1	Oryza sativa	A2ZEX7.1
OsCHS2	Oryza sativa	BAA19186.2
ZmCHS(C2)	Zea mays	CAA42764.1
ZmCHS(Whp)	Zea mays	CAA42763.1
ZmCHSL	Zea mays	NP_001149508.1
GhyCHS1	Gerbera hybrida	CAA86218.1
GhyCHS3	Gerbera hybrida	CAA86220.1
GhyCHS4	Gerbera hybrida	CAP20328.1
AtCHS	Arabidopsis thaliana	NP_196897.1
AtPKS-B	Arabidopsis thaliana	Q8LDM2.1
AtPKS-A	Arabidopsis thaliana	O23674.1
VvCHS1	Vitis vinifera	BAA31259.1
VvCHS2	Vitis vinifera	BAB84112.1
PcCHS	Petroselinum crispum	P16107.1
RgCHS1	Ruta graveolens	Q9FSB9.1
RgCHS2	Ruta graveolens	Q9FSB8.1
RgCHS3	Ruta graveolens	Q9FSB7.1
SvCHS	Scutellaria viscidula	ACC68839.1
SbaCHS1	Scutellaria baicalensis	AMW91735.1
SbaCHS2	Scutellaria baicalensis	AMW91736.1
AmCHS	Antirrhinum majus	CAA27338.1
ArCHS	Agastache rugosa	AFL72079.1
SsCHS	Solenostemon scutellarioides	ABP57071.1
PfCHS	Perilla frutescens	BAA19548.1
IpCHSA	Ipomoea purpurea	AAB02620.1
IpCHSB	Ipomoea purpurea	AAC49030.1
IpCHSC	Ipomoea purpurea	AAC49031.1
IpCHSD	Ipomoea purpurea	ABW69675.1
IpCHSE	Ipomoea purpurea	BAA87337.1
IpCHSFL1	Ipomoea purpurea	AAB41103.1
PhCHSA	Petunia hybrida	CAA32731.1
PhCHSB	Petunia hybrida	CAA32732.1
PhCHSD	Petunia hybrida	CAA32733.1
PhCHSF	Petunia hybrida	CAA32734.1
PhCHSG	Petunia hybrida	CAA32735.1
PhCHSH	Petunia hybrida	CAA32736.1
PhCHSJ	Petunia hybrida	CAA32737.1
SICHS1	Solanum lycopersicum	CAA38980.1
SICHS2	Solanum lycopersicum	CAA38981.1
MdCHS1	Malus domestica	AAY45748.1
MdCHS2	Malus domestica	AGE84303.1

Supplementary Table S4. The proteins used in the phylogenetic tree of CHS.

Table S4. Cont.

MdCHS3	Malus domestica	ACJ54531
NnCHS	Nelumbo nucifera	ADD74168.1
GmCHS1	Glycine max	NP_001337038.1
GmCHS2	Glycine max	CAA46590.1
GmCHS3	Glycine max	NP_001276296.1
GmCHS4	Glycine max	CAA36317.1
GmCHS5	Glycine max	AAB01004.1
GmCHS6	Glycine max	AAA33951.1
GmCHS7	Glycine max	AAA33950.1
GmCHS8	Glycine max	NP_001304585.2
GmCHS9	Glycine max	ABQ63059.1
MsCHS1	Medicago sativa	AAA02823.1
MsCHS2	Medicago sativa	AAA02824.1
MsCHS3	Medicago sativa	CAA48226.1
MsCHS4	Medicago sativa	AAA02825.1
MsCHS8	Medicago sativa	AAA02826.1
MsCHS9	Medicago sativa	AAA02827.1
PnCHS	Psilotum nudum	BAA87922.1
EaCHS	Equisetum arvense	BAA89501.1
GbCHS	Ginkgo biloba	AAY52458.1
PstCHS	Pinus strobus	CAA06077.1
PsyCHS	Pinus sylvestris	CAA43166.1
PrCHS	Pinus radiata	AGY80771.1
PrCHSL	Pinus radiata	AAB80804.1
PhaCHS	Phalaenopsis hybrida	AAV70116.1
PpaCHS	Physcomitrella patens	ABB84527.1
NsCHSL	Nicotiana sylvestris	CAA74847.1

Protein name	Plant Species	Accession number
AtCHI	Arabidopsis thaliana	At3g55120
AtCHIL	Arabidopsis thaliana	AT5g05270
AtFAP1	Arabidopsis thaliana	At3g63170
AtFAP2	Arabidopsis thaliana	At2g26310
AtFAP3	Arabidopsis thaliana	At1g53520
LjCHI1	Lotus japonicus	BAC53983.1
LjCHI2	Lotus japonicus	BAC53984.1
LjCHI3	Lotus japonicus	BAC54038.1
LjCHI4	Lotus japonicus	BAC53984.1
AhCHI I	Arachis hypogaea	AFP33452.1
AhCHI II	Arachis hypogaea	AJF45950.1
GmCHI1A	Glycine max	Glyma.20G241500.1
GmCHI1B1	Glycine max	Glyma.20G241600.1
GmCHI1B2	Glycine max	Glyma.10G292200.1
GmCHI2	Glycine max	Glyma.20G241700.1
GmCHI3A1	Glycine max	Glyma.13G262500.1
GmCHI3A2	Glycine max	Glyma.15G242900.1
GmCHI3B1	Glycine max	Glyma.03G154600.1
GmCHI3B2	Glycine max	Glyma.19G156900.1
GmCHI3C1	Glycine max	Glyma.14G098100.1
GmCHI3C2	Glycine max	Glyma.17G226600.1
GmCHI4A	Glycine max	Glyma.06G143000.1
GmCHI4B	Glycine max	Glyma.04G222400.1
VvCHI1	Vitis vinifera	P51117.1
VvCHI2	Vitis vinifera	A5ANT9.1
PfCHI	Perilla frutescens	BAG14301.1
SbaCHI	Scutellaria baicalensis	ADQ13184.1
ArCHI	Agastache rugosa	AFL72080.1
InCHIL	Ipomoea nil	BAO58578.1
GhCHI	Gossypium hirsutum	ABM64798.1
SmeCHI	Saussurea medusa	AAM48130.1
CsCHI	Camellia sinensis	AAZ17563.2
DcCHI	Dianthus caryophyllus	CAA91931.1
PcCHI	Pyrus communis	ABQ08639.1
ІрСНІ	Ipomoea purpurea	ABW69677.1
PhCHIA	Petunia hybrida	AAF60296.1
PhCHIB	Petunia hybrida	P11651.1
RsCHI	Raphanus sativus	O22651.1
NtCHI	Nicotiana tabacum	Q33DL3.1
ZmCHI	Zea mays	Q08704.1
HvCHI	Hordeum vulgare	AAM13449.1

Table S5. The proteins used in the phylogenetic tree of CHI

Table S5. Cont.	
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OsCHI	Oryza sativa	AAM13448.1
SICHI1	Solanum lycopersicum	Solyc05g010320.2.1
SICHI2	Solanum lycopersicum	Solyc05g010310.2.1
SICHI3	Solanum lycopersicum	Solyc05g052240.2.1
SICHI4	Solanum lycopersicum	Solyc07g062030.2.1
SICH15	Solanum lycopersicum	Solyc08g061480.2.1
SICHI6	Solanum lycopersicum	Solyc02g067870.2.1
SICHI7	Solanum lycopersicum	Solyc06g084260.2.2
MsCHI	Medicago sativa	P28012.1
PvCHI	Phaseolus vulgaris	P14298.2
PICHI	Pueraria lobata	Q43056.1
LaCHIL1	Lupinus angustifolius	CCM80407.1
LaCHIL2	Lupinus angustifolius	CCM80406.1

Protoin name	Plant Spacios	A according membran
r rotein name	r fant Species	Accession number
PtFNSII	Perilla frutescens	ВАВ59004.1
SbaFNSII-1	Scutellaria baicalensis	AMW91728.1
SbaFNSII-2	Scutellaria baicalensis	AMW91729.1
ThFNSII	Torenia hybrida	BAA84072
AmFNSII	Antirrhinum majus	BAA84071.1
GtFNSII	Gentiana triflora	BAD91809.1
GmFNSII	Glycine max	ACV65037.1
LeFNSII	Lobelia erinus	BAF49323.1
CcFNSII	Callistephus chinensis	AAF04115.1
PoFNSII	Pilosella officinarum	ACB56919.1
GhyFNSII	Gerbera hybrida	AAD39549.1
CsFNSII	Camellia sinensis	ACH99109.1
GeFNSII	Glycyrrhiza echinata	P93149.2
MtFNSII	Medicago truncatula	ABC86159.1
SbFNSII	Sorghum bicolor	XP_002461286.1
OsFNSII	Oryza sativa	BAG94859.1
ZmFNSII	Zea mays	XP_008663013.1
GmF3'H	Glycine max	BAD97828.1
MtF3'H	Medicago truncatula	XP_003598945.1
MdF3'H	Malus domestica	ACR14867.1
GhF3'H	Gossypium hirsutum	ADP24159.1
BnF3'H	Brassica napus	ABC58722.1
AtF3'H	Arabidopsis thaliana	Q9SD85.1
ThF3'H	Torenia hybrida	BAB87838.1
AmF3'H	Antirrhinum majus	ABB53383.1
PfF3'H	Perilla frutescens	BAB59005.1
GtF3'H	Gentiana triflora	BAD91808
IbF3'H	Ipomoea batatas	AEH42499.1
InF3'H	Ipomoea nil	BAD00190
IpF3'H	Ipomoea purpurea	AAR00229.1
SlF3'H	Solanum lycopersicum	NP_001289844.1
PhF3'H (Ht1)	Petunia hybrida	Q9SBQ9.1
LeF3'H	Lobelia erinus	BAF49324.1
VvF3'H1	Vitis vinifera	BAE47003.1
VvF3'H2	Vitis vinifera	BAE47003.2
VvF3'H3	Vitis vinifera	BAE47003.3
VvF3'H4	Vitis vinifera	BAE47003.4
CsF3'H1	Camellia sinensis	AKJ86992
CsF3'H2	Camellia sinensis	AKM12329.1
CsF3'H3	Camellia sinensis	AKM12330.1

Table S6. The proteins used in the phylogenetic tree of FNSII, F3'5'H and F3'H

Table S6. Cont.

CnF3'H	Camellia nitidissima	ADZ28515.1
OhF3'H	Osteospermum hybrida	ABB29899.1
GhyF3'H	Gerbera hybrida	ABA64468
EsF3'H	Epimedium sagittatum	ADE80941.1
SbF3'H1	Sorghum bicolor	ABG54319.1
SbF3'H2	Sorghum bicolor	ABG54320.1
SbF3'H3	Sorghum bicolor	ABG54321.1
ZmF3'H	Zea mays	AEF33624.1
GbF3'H-like	Ginkgo biloba	AJO67233.1
SiF3'H-like	Sesamum indicum	XP_011095827.1
PhyF3'5'H	Phalaenopsis hybrida	AAZ79451.1
DgF3'5'H	Delphinium grandiflorum	AAX51796.1
LeF3'5'H	Lobelia erinus	BAF49321.1
CmF3'5'H	Campanula medium	O04773
EsF3'5'H	Epimedium sagittatum	ADE80942.1
GhiF3'5'H	Gossypium hirsutum	AAP31058
VvF3'5'H	Vitis vinifera	ABH06585
CpF3'5'H	Cyclamen persicum	ACX37698.1
CsF3'5'H	Camellia sinensis	ABA40923.1
CtF3'5'H	Clitoria ternatea	BAE72870
GmF3'5'H	Glycine max	AAM51564.1
VwF3'5'H	Viola wittrockiana	BAF93855.1
EeF3'5'H	Eustoma exaltatum	Q96418
GtF3'5'H	Gentiana triflora	BAA12735
VmF3'5'H	Vinca major	BAC97831.1
CrF3'5'H	Catharanthus roseus	CAA09850
PhF3'5'H (Hf1)	Petunia hybrida	CAA80266.1
PhF3'5'H1 (Hf2)	Petunia hybrida	CAA80265.1
StF3'5'H	Solanum tuberosum	AAV85470.1
SIF3'5'H	Solanum lycopersicum	ADC80513.1
SmeF3'5'H	Solanum melongena	P37120
ThF3'5'H	Torenia hybrida	BAB20076
AkF3'5'H	Antirrhinum kelloggii	BAJ16329.1
GlhF3'5'H	Glandularia hybrida	AAT34974.1

Protein name	Plant Species	Accession number
GbF3H	Ginkgo biloba	AAU93347.1
ZmANS	Zea mays	NP_001106074.1
SbANS	Sorghum bicolor	XP_002451336.1
OsANS	Oryza sativa	CAA69252.1
TaANS	Triticum aestivum	BAE98276.1
AcANS1	Allium cepa	ABR24157.1
AcANS2	Allium cepa	ABM66367.1
SsANS	Solenostemon scutellarioides	ABP57079.1
PfANS	Perilla frutescens	BAA20143.1
AtANS	Arabidopsis thaliana	NP_194019.1
NtANS1	Nicotiana tabacum	AFM52334.1
NtANS2	Nicotiana tabacum	AFM52335.1
PhANS	Petunia hybrida	P51092.1
StANS1	Solanum tuberosum	NP_001274859.1
StANS2	Solanum tuberosum	AEJ90548.1
MtANS	Medicago truncatula	ABU40983.1
GmANS	Glycine max	AAR26525.1
EgANS	Eustoma grandiflorum	BAJ08929.2
TcANS	Theobroma cacao	ADD51355.1
VvANS	Vitis vinifera	NP_001268147.1
CsANS	Citrus sinensis	NP_001275784.1
FaANS	Fragaria ananassa	AAU12369.1
PpANS	Prunus persica	ABX89943.1
MdANS	Malus domestica	AAD26205.1
PcANS	Pyrus communis	ABB70119.1
GmF3H1	Glycine max	NP_001236797.1
GmF3H2	Glycine max	AAU06218.1
VvF3H	Vitis vinifera	CAA53579.1
AtF3H	Arabidopsis thaliana	NP_190692.1
MtF3H	Medicago truncatula	ACR15123.1
StF3H	Solanum tuberosum	NP_001274930.1
PhF3H	Petunia hybrida	AAC49929.1
CsF3H	Citrus sinensis	BAA36553.1
FaF3H	Fragaria ananassa	BAE17126.1
PpF3H	Prunus persica	AQX36284.1
PcF3H	Pyrus communis	AGL81347.1
MdF3H	Malus domestica	BAB92997.1
EgF3H	Eustoma grandiflorum	BAD34459
PcrF3H	Petroselinum crispum	AAP57394.1
AcF3H	Allium cepa	AAO63022.1
NtF3H	Nicotiana tabacum	AAC15414.1

Table S7. The proteins used in the phylogenetic tree of F3H, FLS and ANS

Table S7. Cont.

AmF3H	Antirrhinum majus	BAX37181.1
SsF3H	Solenostemon scutellarioides	ABP57073.1
PfF3H	Perilla frutescens	BAA19657.1
OsF3H	Oryza sativa	NP_001054157.1
TaF3H	Triticum aestivum	ABR13013.1
SbF3H	Sorghum bicolor	ADB66755.1
ZmF3H1	Zea mays	NP_001130275.1
ZmF3H2	Zea mays	AAA91227.1
TcF3H	Theobroma cacao	EOX90852.1
GbF3H	Ginkgo biloba	AAU93347.1
MdFLS	Malus domestica	AAX89401.1
PpFLS	Prunus persica	AJO70134.1
PcFLS	Pyrus communis	ABB70118.1
FaFLS	Fragaria ananassa	ABH07784.1
MtFLS1	Medicago truncatula	AES97739.1
MtFLS2	Medicago truncatula	AES71332.1
GmFLS	Glycine max	NP_001237419.1
VvFLS	Vitis vinifera	BAE75807.1
AmFLS	Antirrhinum majus	ABB53382.1
EgFLS	Eustoma grandiflorum	BAD34463.1
PcrFLS	Petroselinum crispum	AAP57395.1
StFLS	Solanum tuberosum	CAA63092.1
PhFLS	Petunia hybrida	CAA80264.1
NtFLS	Nicotiana tabacum	ABE28017.1
AcFLS	Allium cepa	AQR58516.1
TcFLS	Theobroma cacao	EOY09743.1
CsFLS1	Citrus sinensis	XP_006485472.1
CsFLS2	Citrus sinensis	XP_006466183.1
AtFLS1	Arabidopsis thaliana	NP_196481.1
AtFLS2	Arabidopsis thaliana	NP_201163.1
AtFLS3	Arabidopsis thaliana	NP_201164.1
AtFLS4	Arabidopsis thaliana	NP_680463.1
AtFLS5	Arabidopsis thaliana	NP_001032131.1
AtFLS6	Arabidopsis thaliana	NP_680388.1
OsFLS	Oryza sativa	BAD17324.1
TaFLS	Triticum aestivum	AHW49495.1
ZmFLS	Zea mays	NP_001140915.1
SbFLS	Sorghum bicolor	EES07584.1
GbFLS	Ginkgo biloba	ACY00393.1

Protein name	Plant Species	Accession number
FhDFR1	Freesia hybrida	APG32498.1
FhDFR2	Freesia hybrida	APG32494.1
FhDFR3	Freesia hybrida	APG32495.1
IhDFR	Iris hollandica	BAF93856.1
ApDFR	Agapanthus praecox	BAE78769.1
BfDFR	Bromheadia finlaysoniana	AAB62873.1
LhDFR	Lilium hybrida	BAB40789.1
ZmDFR	Zea mays	NP_001152467.2
OsDFR	Oryza sativa	BAA36182.1
HvDFR	Hordeum vulgare	P51106.1
TaDFR1	Triticum aestivum	AAO60213.1
TaDFR2	Triticum aestivum	AAQ77347.1
AtrDFR	Amborella trichopoda	XP_006878526.1
GbDFR	Ginkgo biloba	AGR34043.1
LjDFR1	Lotus japonicus	BAE19948.1
LjDFR2	Lotus japonicus	BAE19949.1
LjDFR3	Lotus japonicus	BAE19950.1
LjDFR4a	Lotus japonicus	BAE19951.1
LjDFR4b	Lotus japonicus	BAE19952.1
LjDFR5	Lotus japonicus	BAE19953.1
MtDFR1	Medicago truncatula	AAR27014.1
MtDFR2	Medicago truncatula	AAR27015.1
GmDFR1	Glycine max	NP_001238612.2
GmDFR2	Glycine max	ABM64803.1
RhDFR	Rosa hybrida	BAA12723.1
FaDFR	Fragaria ananassa	AAC25960.1
MdDFR	Malus domestica	AAO39816.1
VvDFR	Vitis vinifera	NP_001268144.1
AtDFR	Arabidopsis thaliana	BAA85261.1
DcDFR	Dianthus caryophyllus	CAA91924.1
GhDFR1	Gossypium hirsutum	AHG97389.1
GhDFR2	Gossypium hirsutum	ACV72642.1
PtDFR1	Populus trichocarpa	XP_002300759.1
PtDFR2	Populus trichocarpa	XP_002307667.2
PhDFR	Petunia hybrida	AAF60298.1
NtDFR	Nicotiana tabacum	ABN80437.1
SIDFR	Solanum lycopersicum	NP_001234408.1
InDFR	Ipomoea nil	BAA22072.1
IpDFR	Ipomoea purpurea	BAA74700.1
CsDFR	Camellia sinensis	BAA84940.1
VmDFR	Vaccinium macrocarpon	AAL89714.1

Table S8. The proteins used in the phylogenetic tree of DFR

Table S8. Cont.

GjDFR	Gerbera jamesonii	AHF58605.1	
GhyDFR	Gerbera hybrid cultivar	CAA78930.1	
AmDFR	Antirrhinum majus	CAA33543.1	
AaDFR	Angelonia angustifolia	AHM27144.1	
PbDFR	Penstemon barbatus	AIY51701.1	
PfDFR	Perilla frutescens	BAA19658.1	
SsDFR	Solenostemon scutellarioides	ABP57077.1	



Figure S1. Exon/intron Structures of flavonoid biosynthesis related genes. Thick yellow lines represent exons. Thin gray lines represent introns. Unknown sequences in introns of *SmCHS4* and *SmANS* are indicated by '//'.



Figure S2. Cont.



Figure S2. Conserved domains in flavonoid biosynthesis related proteins in *S. miltiorrhiza*. Conserved domains were predicated by searching Pfam and shown in blue boxes. Names of conserved domains are indicated below the boxes.

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Sachas	AtCHS SmCHS1	MVMAGASSLU 	EIRCAORADG EIRRAORAEG	PAGILAIGT/ PATVLAIGT/	ANPENHVLQAE ATPLNCVDOSI	YPDYYFRI	NSEHMTDLK NSEHKTELK	KFKRMCDKSTI KFKRMCEKSMI	RKRHMHL KKRYMHL
Sec.33	SmCHS3	<mark>Masv</mark> e	EISRARRAEG	PATVLAIGT	TPPNCVEQSS	FPDYYFRV	IN <mark>SEH</mark> K <mark>TEL</mark> K	KFMRICENSMI	KKRYMHL
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SmcH33 GPH PSVI (BTUMCOR GCY GG AAAB RAXED AXBMARNINA AA RUVUVCE IT RAITOPE GPS AAH PS AND UT GALGA AL RAYED AXBAN AAAR AXDUVVCE STRUITOPE GPS AAH PS AND UT GALGA AL RAYED AXBAN AAAR AXDUVVCE STRUITOPE GPS AAH PS AND UT GALGA AL RAYED AXBAN AAAR AXDUVVCE STRUITOPE GPS AAH PSU GALGA GALGA AL RAYED AXBAN AAAR AXDUVVCE STRUITOPE GPS AAH PSU GALGA GALGA AL RAYED AXBAN AAAR AXDUVVCE STRUITOPE GPS AAH PSU GALGA GALGA AL RAYED AXBAN AAAR AXDUVVCE STRUITOPE GPS AAH PSU GALGA GALGA AL RAYED AXBAN AAAR AXDUVVCE STRUITOPE GPS AAH PSU GALGA GALGA AL RAYED AXBAN AAAR AXDUVVCE STRUITOPE GPS AAH PSU GALGA GALGA AL RAYED AXBAN AAAR AXDUVVCE STRUITOPE GPS AAH PSU GALGA GALGA AL RAYED AXBAN AAAR AXDUVVCE STRUITOPE GPS AAH PSU GALGA GALGA AL RAYED AAAN DI AXBAN AAAR AXDUVVCE STRUITOPE GAS GALGA AL RAYED AAAN DI AXBAN AAAR AXDUVVCE STRUITOPE GAS GALGA AL RAYED AAAN DI AXBAN AGALYAVE AA TER GAS AAAH PSU GALGA AAAN TA GALGA ANA TA TER GAS AAAA TA TER GAS AAAAA TA TER GAS AAAAA TA TER GAS AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	SmCHS1	GLRPSVARL GLRPSVARL	MYQQGCFAGG	T <mark>VLRM</mark> AK <mark>DL</mark>	AENNAG <mark>A</mark> RVL	VCSEITAV	FRGPSDIHLI	SLVGQALF SDG	AAALIVG AAAVIVG
SmCH35 CH SS VITE IN SOLFCOCCASE ATERANO VASIMA ARVIVUC CENT ICREGES AND ANALIVE SmCH35 CH PYVIRI MICONCOCCCC GALLERANO LARMN ARAVIVUC CENT ICREGES AND POLVCOLFOD AAALVUC SmCH36 CH PYVIRI MICONCOCCCC GALLERANO LARMN ARAVIVUC CENT ICREGES AND POLVCOLFOD AAALVUC SmCH36 CH PYVIRI MICONCOCCCC GALLERANO LARMN ARAVIVUC CENT ICREGES AND POLVCOLFOD AAALVUC SmCH36 ADADTOON UNIVELCOV COVALERAND LARMN ARAVIVUC CENT ICREGES AND POLVCOLFOD AAALVUC SmCH36 ADADTOON UNIVELCOV COVALERAND IARNN POSINULLAI SETTII GREPPINK SRPVDLVCAALFGOLAAAVVUC ALEAND VARVULVELCOV COVALERAND IARNN POSINULLAI SETTII GREPPINK SRPVDLVCAALFGOLAAAVVUC SmCH36 ADADTOON UNIVELCOV COVALERAND IARNN POSINULLAI SETTII GREPPINK SRPVDLVCAALFGOLAAAVVUC SmCH36 ADADTOON UNIVELCOV COVALERAND I ADAD SECAL DELEMAND OF THE KUVE KINS NITK KALDEAPKEN LETSDWN SmCH37 ADDVCMC REDEFENSAATII LODSCAAL DELEMAND OF THE KUVE KINS NITK KALDEAPKEN LETSDWN SmCH33 ADD .VVCMC REDEFENSAATII LODSCAAL DELEMAND OF THE KUVE KINS NITK KALDEAPKEN LETSDWN SmCH37 ADDAAAR EDFOLWSAATII LODSCAAL DELEMAND OF THE KUVE KINS NITK KALDEAPKEN LETSDWN SmCH37 ADDAAAR EDFOLWSAATII LODSCAAL DELEMAND OLINE ARAVENUE KINS NITK KALDEAPKEN LETSDWN SmCH37 ADDAAAR EDFOLWSAATII LODSCAAL DELEMAND OLINE ARAVENUE KINS NITK KALDEAPKEN LETSDWN SmCH37 ADDAAAR EDFOLWSAATII LODSCAAL DELEMAND OLINE ARAVENUE KINS NITK KALDEAPKEN MOT SDWN SmCH32 ADDAAAR EDFOLWSAATII LODSCAAL DELEMAND OLINE ARAVENUE KINS NITK KALDEAPKEN MOT SDWN SmCH33 ADDAAAR EDFOLWSAATII LODSCAAL DELEMAND OLINE ARAVENUE KINS NITK KALDEAPKEN MOT SDWN SmCH35 ADDAAAR EDFOLWSAATII LODSCAAL DELEMAND OLINE ARAVENUE KINS NITK KALDEAPKEN MOT SDWN SmCH35 ADDAAAR EDFOLWSAATII LODSCAAL DELEMAND OLINE ARAVENUE KINS NITK KALDEAPKEN MOT SDWN SmCH35 STEVEN ADD CONTANTO VATA KIN THE KEKNNA REHVISSEY CONSES ACVUF VUDENKK KST MOT SDWN SmCH35 STEVEN ADD KINS KINK KALDEAPKEN KINS KENNE KINS KEVEN DELEMAND OLINE KINS KENNE KINS KEVEN DELEMAND OLINE KINS KEVEN DELEMAND OLINE KI	SmCHS3 SmCHS4	GLEP TVKRSM	MCOHGCYGGA	AALRLAKEM	AENNAA <mark>A</mark> RVLV	VCCEITAI VSSETTII	FRGPSEAHVO FRGPSGAHPF	GDLVGQALFADG	AAAVIVG AAALIVG
SmcH36 GENPYU RINKLOOCGYGG GAALALAND LAANNAAAWUVYC BLIN I CHRGJSENH YED WYCOALAGAAAWUY SmcH32 GENPYU RINKLOOCGYGG GAALALAND LAANNAAWUVYC BLIN I CHRGJSENH YED WYCOALAGAAAWUY GENPYU RINKLOONGYGYG YG GAALALAND LAANNA RIVUYC BITTI CHRGJSENH YD DYGOALAGGAA AA IYG SmcH36 AFRANVAR RIVER CYGGYT GHAVARD I AANNA FG SWULLA TSTTII CHRGJSENH YD DYGOALAGGAA AA IYG ARRANVAR YM YN YN LEGYG YT GHAVARD I AANNA FG SWULLA TSTTII CHRGJSENH YD DYGOALAGGAA AA IYG SmcH36 AFRANVAR YN HYN HYN HYN HYN HYN HYN HYN HYN HYN	SmCHS5	GLCSSVTRTM	MSQHGCCGGA	S <mark>alrlakdv</mark> i	AENNAAARVL	VCCESTVI	FRGPNEARIC	GD <mark>LVGQAI</mark> F <mark>GD</mark> A	A <mark>A</mark> ALIVG
SINCH SZ. GLARPDICE WOLVENS GOG GOG VACUE WAAD I AENN POS RVILLATSE TILLOTE PANA DRAPYD U GOAL GOG AA ALGO ALRNDVAR WLYP GOG GOG VICUNAND I AENN POS RVILLATSE TILLOTE PANK SR PYD U GAAL GOG AA AVVVC 230 240 250 260 270 280 290 MeCH SZ. SDD. VEPTE KPTE MVVTAOT I AED SE CALD GHLREAGT THE UKDVP GIVSK NT TKALVEAFEF L GISDYN Atchs SDD. TSV GOR PIE MVVAAO TILD DSDCAD CHLREAGT THE UKDVP GIVSK NT TKALVEAFEF L GISDYN MECH SZ. SDD. VEPTE KPTE MVVTAOT I AED SE CALD GHLREAGT THE UKDVP GIVSK NT TKALVEAFEF L GISDYN MECH SZ. SDD. VEPTE KPTE MVVAAO TILD DSDCAD CHLREVSIT THE UKDVP GIVSK NT TKALVEAFEF L GISDYN MECH SZ. SDD. VEPTE KPTE MVVAAO TILD DSDCAD CHLREVSIT THE UKDVP GIVSK NT TKALVEAFEF L GISDYN MECH SZ. SDD. VEPTE KPTE MVSAAO TILD DSDCAD CHLREVSIT THE UKDVP GIVSK NT TKALVEAFEF L GISDYN MECH SZ. SDD. VEPTE KPTE MVSAAO TILD DSDCAD CHLREVSIT THE UKDVP GIVSK NT TKALVEAFEF L GISDYN MECH SZ. SDD. VEPTE KPTE MVSAAO TILD DSDCAD CHLREVSIT THE UKDVP GIVSK NT TKALVEAFEF WGISSWN SmCH SZ. AD 2. AAAS PIE DIMSAAO TILD SDD. CHCREW CLIPH KUDVP DIN SDD. GAS LEEAFFF WGISSWN SmCH SZ. AD 2. AAAS PIE DIMSAAO TILD GENE GENREAG LUDU KACUP GUSS NT GESLERAFCF WGISSWN SmCH SZ. AD 2. AAAS PIE DIMSAAO TILD SDD. CHCREW GARAFAG LUDU KACUP GUSS NT GESLERAFCF WGISSWN SmCH SZ. AD 2. AAAS PIE DIMSAAO TILD SDD. CHCREW GARAFAG LUDU KACUP GUSS NT GESLERAFCF WGISSWN SmCH SZ. AD 2. AAAS PIE DIMSAAO TILD SDD. CHCREW GARAFAG LUDU KACUP GUSS NT GESLERAFCF WGISSWN SmCH SZ. AD 2. VP CYT AFMELNYAAO FILO CHT FE GISSR NT WING SDO. VIE FILDEMAK SS CHCLITTGE CLEW GUL S SmCH SZ. SIN I AFM GOPAL LDOVE I KLG MER KALL DE GRIFE GOT SFR VIE DI DEMKK SS CHCLITTGE CLEW GUL S SmCH SZ. SIN I AFM GOPAL LDOVE I KLG MER KALL DE GRIFE SGUN SS OVER VIE DI DEMKK SS CHCLITTGE CLEW GUL S SmCH SZ. SIN I AFM GOPAL LDOVE KLG MER KALL DE GRIFE SGUN SS OVER VIE DI DEMKK SS CHCLITTGE CLEW GUL S SmCH SZ. SIN I AFM GOPAL LDOVE KLG MER KALL SK KALMEN SK GN SS OVER VIE DEMKK SS CHCLITTGE CLEW GUL S SmCH SZ. SIN I AFM GOPAL LDOVE KLG	SmCHS7 SmCHS8	GLRPTVIRTM GLRPSVIRTM	ILCQQGCYGGG ILCOHGCYGGG	AALRLAKDL AALRLAKDL	AENNAAARVLV AENNAEARVLV	VCCELNTI VCCELTAI	CFRGPSEDHVE CFRGPSEAHPW	DLVGQALFGDA DLVGOGIFADG	AAAVIVG AAAAIVG
SMCH30 ADDALADY RVED 11 DEBUG GUT 1 DEBUG GUT 1 DEBUG ADDALATO DI LI LO LO LO LA DALADO VICE 230 240 250 260 270 280 290 MSCH32 SDD VPETE VIETE VIETE MUNTAGITI DISDGAD GHLRENGLITHED LKDVPGUSSKITTKALVERFERT	SmCHS2	GLRPDTQRVM	ILYFSGCSCGV	AGLRVAKDI	AENNPG <mark>SRVL</mark>	ATSETTII	YRPPNADRPY	DLVGVALFGDG	A <mark>GAAII</mark> G
30 240 250 260 270 280 290 MSCH32 SDT. VP PERKPTF MYWIN OT THE DERGAD GHLREAGLITH HILK VVECTUSK NITKAL VEAFEP LGISDYN SmCH31 SDP. VVGVERUFFLVSAAOT ILED BGAD GHLREVGLITH LKVVECTUSK NITKAL VEAFEP LGISDYN SmCH31 SDP. VVGVERUFFLVSAAOT ILED BGAD GHLREVGLITH LKVVECTUSK NITKAL VEAFEP LGISDYN SmCH32 SDP. VAGVELDFLVSAAOT ILED BGAD GHLREVGLITH LKVVECTUSK NITKAL VEAFEP CISDYN SmCH35 SDP. VAGVELDFLVSAAOT ILED BGAD REGRINP AGLIV LVGVENKINTKAL VEAFEP CISDYN SmCH35 ADP. VAGVELDFG VISAAO TIEPEBGA BDER GENREPAGLIV LVGVENKINTK SLKAPCP CISDYN SmCH35 ADP. VAGVELDFG VISAAO TIEPEBGA RGRINP AGLIVD PKD IF CLISEN IGENLERAFCP CISDYN SmCH35 ADP. AAAF RVFO INSAAO TIEPEBEGA RGRINP AGLIVD PKD IF CLISEN IGENLERAFCP CISDYN SmCH35 ADP. AAAF RVFO INSAAO TIEPEBEGA RGRINP AGLIVD PKD IF CLISEN IGENLERAFCP CISDYN SmCH35 ADP. AAAF RVFO INSAAO TIEPEBEGA RGRINP AGLIVD PKD IF CLISEN IGENLERAFCP CISDYN SmCH35 ADP. AAAF RVFO INSAAO TIEPEBEGA RGRINP AGLIVD PKD IF CLISEN IGENLERAFCP CISDWN SmCH35 ADP. AAAF RVFO INSAAO TIEPEBEGA RGRINP AGLIVD PKD IF CLISEN IGENLEAFED CISCHDVN SmCH35 SIGNIA GAUSTANAO TIEPEBEGA RGRINP AGLIVD PKD INSAO TIEPEBEGA RGRINP AGLIVD PKD INGE CLISEN CLISEN INGENCONCECLISEN CUNTSTICK INGENCONCECLISEN CUNTSTICKONCECLISEN CUNTSTICKONCE	SMCHS6	ARNDVARVE	TIFICCICC	IGLEVARDI	AENNPGSKVL		FRPPNKSRP		AAAVVVG
300 240 250 260 270 280 290 MSCHS2 SDD JVS UP DESKPTTE MAYWING TITED SEGA DIGHTRE ACTIFTE LKDUPC USKNITT KALL SAFEP 1.1 STSUYN MSCHS1 SDD JVS UP DESKPTTE MAYWING TITED SEGA DIGHTRE METHELKDUPC USKNITT KALL SAFEP 1.1 STSUYN MSCHS3 ADD P.PAAR RD LFOLWSAAG TITED SDGA DIGHTRE METHELKDUPC USKNITT KALL SAFEP 1.1 STSUYN SmCH35 ADD P.PAAR RD LFOLWSAAG ATTEG SDD REARGAN BAGLUD VRD LFD UVS NIGAS LEARFOP 1.1 STSUN SmCH35 ADD P.PAAR RD LFOLWSAAG ATTEG SDD REARGAN BAGLUD VRD LFD UVS NIGAS LEARFOP 1.1 STSUN SmCH35 ADD P.AAR RD LFOLMSAAG ATTEG SDD CHARMENAGLUD VRD LFD USKNIGAS LEARFOP 1.1 STSUN SmCH35 ADD P.AAR RD LFOLMSAAG ATTEG SDD CHARMENAGLUD FRO LFL SUN NIGAS LEARFOP 1.1 STSUN SmCH35 ADD P.AAR RD LFOLMSAAG ATTEG SDD SCHARGAN REAGLUD HAR UVR LVS NIGAS LEARFOP 1.0 STSUN SmCH35 ADD P.AAR RD LFOLMSAAG ATTEG SDD SCHARGAN REAGLUD HAR UVR LVS NIGAS LEARFOP 1.0 STSUN SmCH35 ADD P.AAR RD LFOLMSAAG ATTEG SDD SCHARGAN REAGLUD HAR UVR LVS NIGAS LEARFOP 1.0 STSUN SmCH35 STEMTARGAN REVEOUNSAAG ATTEG SDD SCHARGAN REAGLUD HAR UVR LVS LVS NIGAS LEVEN LVS NIGAS LEARFOP 1.0 STSUN SmCH35 STEMTARGAN REVEOUNSAAG ATTEG SDS STEME ASSUN 1.0 STSUN 1.0 STSUN <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th></th>									
MSCH22 DD . VPETE VPETE VIEW VTAC TIAD DEECA DGHLR CALTPET LKDVPGLTSKNTTKATVEREP I GISDYN AtCHS SDP DTSVGE VPIFENVSAC TILD SDGA DGHLR VSLTPH LKDVPGLTSKNTTKATVEREP I GISDYN SmCH33 DD . VVGVG PPFELVSAAC TILD SDGA DGHLR VSLTPH LKDVPGLTSKNTVKSLDEARKP I GISDYN SmCH34 SmCH31 DDP . VVGVG PPFELVSAAC TILD SDGA DGHLR VSLTPH LKDVPGLTSKNTVKSLDEARKPC I GISDYN SmCH34 DD . VVGVG PPFELVSAAC TILD SDGA DGHLR VSLTPH LKDVPGLTSKNTVKSLDEARKPGP I GISDYN SmCH35 SmCH34 DDP . AAAR PPFO IMSAAC AT TEGDDE RGRNRBACLL DI TVVVS DI GASLEARFGP KISDYN SmCH35 DD . AAAR PPFO IMSAAC AT TEGDDE RGRNRBACL LUD TKDIPC VS DI GGLEE AFFGP KISDYN SmCH35 SmCH35 ADP . AAAR PPFO IMSAAC AT TEGDDE CHC RNRBACL LUD FKDIPC IS ELEARFGP KISDYN SmCH35 ADP . AAAR PPFO IMSAAC AT TEGDDE KIR BGLRBACL LUD FKDIPC IS ELEARFGP KISDYN SmCH36 SmCH35 ADP . AAAR PPFO IMSAAC AT TEGDDE KIR BGRIRBACL LUD FKDIPC IS ELEARFGP		230	240	250	260	270	280	29	0
AtCHS SDEDTSVGERETEEMVSAAGTILDEDSDGALDGELREVSLITFHELKDVEGLISKNITVKSLDEAFRELGIEDW SmCHS1 SDE.VVGVERELEFEVSAAGTILGSDGALDGELREVSLITFHELKDVEGLISKNITVKSLDEAFRELGIEDW SmCHS3 ADEP.PAABRELGINSAAGATIGSDGATGGURREAGLIDDVKRDVEGLISKNITVKSLDEAFREVGIESW SmCHS5 ADE VAGVERELEFOVSAAGATIGSDGTRGRUREAGLIDDVKRDVEGLISKNITVKSLDEAFREVGIESW SmCHS5 ADEAASLELGOINSAAGATIGSDGTRGRUREAGLIDDVKRTAGTAGLVSDNIGGSLDEAFGEVGIESW SmCHS5 ADEAASLEVGOINSAAGATIGSDGTRGRUREAGLIDDVKRTAGTAGLVSDNIEGSLDEAFGEVGIESW SmCHS5 ADEAASLEVGOINSAAGATUGSDGTRGRUREAGLIDDVKRTAGTAGLVSDNIEGSLDEAFGEVGIESW SmCHS5 ADEAASLEVGOINSAAGATUGSDGTRGRUREAGLIDDVKRTAGTAGLVSDNIEGSLDEAFGEVGIESW SmCHS6 ADEAASLEVGOINSAAGATUGSTGTGTGTRGRUREAGLIDDVKRTAGTAGUSSDNIEGSLDEAFGEVGIESW SmCHS6 ADEAASLEVGOINSAAGATUGSTGTGTGTGTGTGTGTGTGUSSTGTGTGTUSSGGTVFKUGGUSSDNIEGSLDEAFGEVGIESW SmCHS6 ADEAASLEVGOINSAAGATUGSTGTGTGTGTGTGTGTGUSSGTGTGTGTGTGTGTGTG	MsCHS2	SDP.VPEIEK	PIFEMVWTAQ	TI AP D SE GA	D <mark>GHLREAGL</mark> I	FH <mark>L</mark> L KDVP (G IVS K <mark>NI</mark> TKAI	VE <mark>AFEP</mark>	L <mark>GISDYN</mark>
SmcH33 App P PAR R LFQ INSAA TID CSDRT RGRMRPACILID UNDER LVSDNIGASLERAFGP WGISEWN SmcH35 Spc VACVE LSFQ UVSAAA TID CSDDC R CRMRPACILID LAKGIA GLVSDNIGASLERAFGP WGISEWN SmcH35 App P. AAAB LP LFQ INSAAA TID CSDDC RCRMRPACILID LAKGIA GLVSDNIGASLERAFGP WGISDWN SmcH37 App P. AAAB LP LFQ INSAAA TID CSDDC RCRMRPACILUD LAKGIA GLVSDNIGASLERAFGP WGISDWN SmcH36 App P. AAAB LP LFQ INSAAA TID CSDDC RCRMRPACILUD LAKGIA GLVSDNIGASLERAFGP WGISDWN SmcH36 App P. STGTE PELENSSTQ RFLDDTEKI I DGRIEBEGI SFRUDRELFQITEDNVQGFCDELC EGKMDYN SmCH36 App P. STGTE PELENSSTQ RFLDDTEKI I DGRIEBEGI SFRUDRELFQITEDNVQGFCDELC EGKMDYN SmCH36 App P. VPCVETAFMELNTAAQ OF LCTSHV ID GRIEBEGI YFRU GRULFQITEDNVQGFCDELC EGKMDYN SmCH36 App P. VPCVETAFMELNTAAQ OF LCTSHV ID GRIEBEGI YFRU GRULFQITEDNVQGFCDELC EGKMDYN SmCH36 App P. VPCVETAFMELNTAAQ OF LCTSHV ID GRIEBEGI YFRU GRULFQUTEDNVQGFCDELC EGKMDYN SmCH36 Aso 350 360 370 MSCH32 SIF WITHPGGPAILDQVE KLALKPEKMATREVUESEVGNMSG ACVLF IDDEMRRKST ONG LKTTGEGLEWGVLF SmCH35 SIF WITHPGGPAILDQVE KLALKPEKMATREVUESEVGNMSG ACVLF UDEMRRKST NG LKTTGEGLEWGVLF SmCH35 SIF WITHPGGPAILDQVE KLGLEREKKRSTRHVUESEVGNMSG ACVLF VDEMRRKST EGG STTGEGLEWGVLF SmCH35 SIF WITHPGGPAILDQVE KLGLEREKKRSTRHVUESEVGNMSG PSVLFVLDEMRRKST EGG STTGEGLEWGVLF SmCH35 SIF WITHPGGPAILDQVE AKGLKPEKLRSRRVUESEVGNMSG PSVLFVLDEMRRKST EGG STTGEG LWGVLF SmCH35 SIF WITHPGGPAILDQVE AKGLKPEKLRSRRVUESEVGNMSG PSVLFUDEMRRKASA EGG STTGEG LWGVLF SmCH36 SIF WITHPGGPAILDQVE AKGLKPEKLRSRRVUESEVGNMSG PSVLFUDEMRRKASA EGG STTGEG LWGVLF SmCH36 SIF WITHPGGPAILDQVE AKGLKPEKLRSRRVUESEVGNMSG PSVLFUDEMRRKASA EGG STTGEG LW	AtCHS SmCHS1	SDPDTSVGER SDP.VVGVER	PIFEMVSAAO PLFELVSAAO	TILPD SD GA TI LP D SD GA	DGHLREVSL DGHLREVGL	FHLLKDVP	G LIS KNIVKSI G LIS KNIEKSI	DEAFKP	LGISDWN LGITDWN
Smithst Sole VALUE DIC V VALUE CIVERAUALE INSUENCE VIEW VIEWER UNDER VIEWER UNDER VIEWER UNDER VALUE VIEWER VIEWER UNDER VIEWER vi	SmCHS3	ADPP.PAAEF	PLF DIMSAAO	AT <mark>IP</mark> G SD DR	R <mark>GRMREAGL</mark> I	ID <mark>L</mark> V <mark>RDLP</mark> I	LVSDNIGASI	ERAFGP	WGISEWN
SmcH83 ADP ADP <t< th=""><th>SmCHS4 SmCHS5</th><th>ADPAAAEI</th><th>PLFQIMSAVO</th><th>ATIPG<mark>SD</mark>DC</th><th>R CRMREAGL</th><th>IDLAKGIA</th><th>LVSDNIEESI</th><th>ERAFGP</th><th>WGISDWN</th></t<>	SmCHS4 SmCHS5	ADPAAAEI	PLFQIMSAVO	ATIPG <mark>SD</mark> DC	R CRMREAGL	IDLAKGIA	LVS DNIEESI	ERAFGP	WGISDWN
SmCHS2 TND.SIGNT PLEELHSSLORFLPDTEKINDGRLTEEGISFRUDRELPOTIEDNVGGFCDELCEGKMDYN SmCHS2 ADD.VPGWTAFMELNTAAQOFLPGTSHVIDGRLSEEGIYFKUGRDLPOKIEENIEEFCRRUMGGAAGLGEGGYDYN SmCHS2 SIFWIAHPGGPAILDQVEOKLALKPEKNNATREVLSEYGNMSSACVLFILDENRKKSTONGLKTTGEGLEWGVLF Atchs SIFWIAHPGGPAILDQVEOKLALKPEKNNATREVLSEYGNMSSACVLFILDENRKKSTONGLKTTGEGLEWGVLF SmCHS3 SIFWIAHPGGPAILDQVEOKLALKPEKNNATREVLSEYGNMSSACVLFILDENRKSTONGLKTTGEGLEWGVLF SmCHS3 SIFWIAHPGGPAILDQVEXCKLEWGVLSKRUVSEYGNMSSACVLFILDENRKSTCOGVATTGEGLEWGVLF SmCHS3 SIFWIAHPGGPAILDQVEXCKLEWEKIRSTRHVLSEYGNMSSACVLFILDEMRKASSAEGGISTTGEGLEWGVLF SmCHS3 SIFWIAHPGGPAILDQVEXCKLEWEKIRSTRHVLSEYGNMSSACVLFILDEMRKASSAEGGISTTGEGLEWGVLF SmCHS3 SIFWIAHPGGPAILDQVEXCLEWEKIRSTRHVLSEYGNMSSACVLFUDEMRKASSAEGGISTTGEGLEWGVLF SmCHS3 SIFWIAHPGGPAILDQVEAKGGIKPEKIRKSRHVLSEYGNNSSF SVLFVLDEMRKASSAEGGISTTGEGLEWGVLF SmCHS3 SIFWIAHPGGPAILDQVEAKGGIKPEKIRKSRHVLSEYGNNSSF SVLFVLDEMRKASSADEGRSTTGEGLEWGVLF SmCHS3 SIFWIAHPGGPAILDQVEAKGGIKPEKIRKSRHVLSEYGNNSSF SVLFVLDEMRKASADEGRSTTGEGLEWGVLF SmCHS5 SIFWIAHPGGPAILNEVEAKLGIKPEKIRKSRHVLSEYGNNSSF SVLFVLDEMRKASADEGRSTTGEGLEWGVLF SmCHS5 SIFWIAHPGGPAILNEVEXKININ SmCHS5 SIFWIAHPGGPAILNEWEKKLAILPEKLAASRALADYGNSF SVLFVLDEMRKASADEGRSTTGEGLEWGVLF SmCHS5 SIFWIAHPGGPAILNEWEKKK	SmCHS7	ADPAAAEF	PVFQIMSAAQ	AT <mark>VP</mark> G TD GR VTLPE SE GS	RGRAREAGLI	VDLFKDIP(GLLSENIGENI GLVSDNIGECI	ERAFGP	WGISDWN
SmCHS6 AD2. VPCMETAPMEINTAA00FLECTSHVHDGRLSEEGTYPRMGRDLPORTBENTBEPCRRLMGGAAGLGEGGYDYN 300 H 310 320 330 N 340 350 360 370 MsCHS2 STEW TAHPGGPAILDOVE (KLALKPEKNATREVLSEVONMSSA CVLFILDEMRRKSTONGLKTTGECLEWGVLF AtCHS SLEW TAHPGGPAILDOVE (KLALKPEKNATREVLSEVONMSSA CVLFILDEMRRKSTONGLKTTGECLEWGVLF StruthPGGPAILDOVE (KLALKPEKNATREVLSEVONMSSA CVLFILDEMRRKSTONGLKTTGEGLEWGVLF SmCHS3 SIFWJHPGGPAILDOVE (KLALKPEKNATREVLSEVONMSSA CVLFILDEMRRKSTONGLKTTGEGLEWGVLF SmCHS3 SIFWJHPGGPAILDOVE SKLGLEBAEKIRSTRUVISEVONMSSA CVLFILDEMRRASSADEGRSTTGEGLEWGVLF SmCHS3 SIFWJHPGGPAILDOVE AKUGLKPEKIRKSRUVISEVONWSS ATVLLIDEMRRASSADEGRSTTGEGLEWGVLF SmCHS4 SIFWJHPGGPAILDOVE AKUGLKPEKIRKSRUVISEVONWSS ATVLLIDEMRRASADEGRSTTGEGLEWGVLF SmCHS5 SIFWJHPGGPAILDOVE AKUGLKPEKIRWSRUVISEVONWSS SVLFVLDEMRRASADEGRSTTGEGLEWGVLF SmCHS5 SIFWJAHPGGPAILDOVE AKUGLKPEKIRWSRUVISEVONWSS SVLFVLDEMRRASADEGRSTTGEGLEWGVLF SmCHS5 SIFWJAHPGGPAILDOVE AKUGLKPEKIRWSRUVISEVONWSS SVLFVLDEMRRASADEGRSTTGEGLEWGVLF SmCHS5 SIFWJAHPGGPAILNNYKAKIT.LPEKLANSRHVLSEVONWSS SVLFVLDEMRRASADEGRSTTGEGLEWGVLF SmCHS5 SIFWJAHPGGPAILNNYKAKIT.LPEKLANSRHVLSEVONWSS SVLFVLDEMRRASADEGRSTTGEGLEWGVLF SmCHS5 SIFWJAHPGGPAILNNYKAKIT.LPEKLANSRHVLSEVONWSS SN	SmCHS2	T <mark>NP</mark> .SIG <mark>TE</mark> I	PLFELHSSLQ	RF <mark>lp</mark> d te ki	D <mark>GRLTEEGI</mark> S	FRLDRELP	IIE D NV QGF	DELC	EGKMDYN
300 H 310 320 330 340 350 360 370 MsCHS2 SIFWIAHPGGPAILDQVEOKLALKPEKMNATREVISEVONMSSACVLFILDEMRRKSTONGLKTTGEGLEWGVLF AtCHS SIFWIAHPGGPAILDQVEIKLGLKBEKMRATRHVISEVONMSSACVLFILDEMRRKSAKOGVATTGEGLEWGVLF SmCHS3 SIFWIAHPGGPAILDQVEXKLGLEBAEKIRSTRHVISEVONMSSACVLFILDEMRRKSSKOGVATTGEGLEWGVLF SmCHS3 SIFWIAHPGGPAILDQVEXKLGLEBAEKIRSTRHVISEVONMSSACVLFILDEMRRKSSEGCITTGEGLEWGVLF SmCHS3 SIFWIAHPGGPAILDQVEXKLGLEBAEKIRSTRHVISEVONMSSACVLFILDEMRRKSSEGCITTGEGLEWGVLF SmCHS3 SIFWIAHPGGPAILDQVEXKLGLEBAEKIRSTRHVISEVONMSSACVLFILDEMRRKSSEGCITTGEGLEWGVLF SmCHS5 SIFWAVHSGGPAILDQVEAKLGLEPEKIRSTRHVISEVONSSATVLLILDEMRRKSSDEGRSTTGEGLEWGVLF SmCHS5 SIFWAVHSGGPAILDQVEAKLGLEPEKIRSTRHVISEVONSSATVLLILDEMRRKSADEGRSTTGEGVENGVLI SmCHS5 SIFWAVHSGGPAILDQVEAKLGLEPEKIRSTRHVISEVONSSFSVLFVLDEMRKASADEGRSTTGEGVENGVLI SmCHS5 SIFWAVHSGGPAILDQVEAKLGLEPEKIRSTRHVISEVONSSFSVLFVLDEMRKASADEGRSTTGEGLEWGVLF SmCHS5 SIFWAVHSGGPAILDQVEAKLGLEPEKIRSTRHVISEVONSSFSVLFVLDEMRKASADEGRSTTGEGLEWGVLF SmCHS6 SIFWAVHSGGPAILDQVEAKLGLEPEKIRSTRHVISEVONSSFSVLFVLDEMRKASADEGRSTTGEGLEWGVLF SmCHS6 SIFWAVHSGGPAILDQVEAKLGLEPEKIRSTRHVISEVONSSFSVLFILDDMRKASADEGRSTTGEGLEWGVLF SmCHS6 SIFWAVHSGFAILDZVEAKLSTLDEGKLECSRKALMDYGNVSSNTIVYVLEYVLEEKKRLEFGGDEEKGEOMGUIL SmCHS6 SIFWAVHSGFAILNENNIN SmCHS6 SIFWAVHSGFAILSNNIN SmCHS6 SIFWAVHSGFAILSNNIN SmCHS6 SIFWAVHSGFAILSNNIN SmCHS6 SIFWAVHSGFAILNENNIN SmCHS6 SIFWAVHSGFAILSNNIN SmCHS6 SIFWAVHSGFAILNENNIN SmCHS6 SIFWAVHSGFAILNENNIN SmCHS6 SIFWAVHSGFAILNENNIN SmCHS6 SIFWAVHSGFAILNENNIN SmCHS6 SIFWAVHSGFAILNENNIN SmCHS6 SIFWAVHSGFAILNENNIN SmCHS6 SIFWAVHSGFAILNENNIN SmCHS6	SmCHS6	ADP.VPG <mark>VD</mark> I	AFMELNTAAO	QF LP G TS HV	DGRLSEEGI	FKIGRDLP	Q <mark>kie</mark> e ni eef(CRK lmgg aaglg	EGGYDYN
300 H 310 320 330 N 340 350 360 370 MSCH52 SIFWIAHPGOPAILDOVDOKLALKPEKNATREVISEYONMSSACVLFILDEMRRKSTORGLKTTGEGLEWGVLF AtCH5 SIFWIAHPGOPAILDOVDOKLALKPEKNATREVISEYONMSSACVLFILDEMRRKSTORGLKTTGEGLEWGVLF SmCH51 SIFWIAHPGOPAILDOVDOKLALKPEKNATREVISEYONMSSACVLFILDEMRRKSTCOVATTGEGLEWGVLF SmCH52 SIFWIAHPGOPAILDOVDOKLGUPEKLRSRRVISEYONMSSACVLFILDEMRRKSTEGGSTTGEGLEWGVLF SmCH53 SIFWIAHPGOPAILDOVDOKKGUPEKLRSRRVISEYONMSSACVLFILDEMRRKSTEGGSTTGEGLEWGVLF SmCH55 SIFWIAHPGOPAILDOVDOKAKGUKPEKLRSRRVISEYONMSSACVLFILDEMRRKSTEGGSTTGEGLEWGVLF SmCH55 SIFWIAHPGOPAILDOVDOKAKGUKPEKLRSRRVISEYONMSSACVLLUDEMRRKSAEGGSTTGEGLEWGVLF SmCH55 SIFWIAHPGOPAILDOVDOKAKGUKPEKLRSRRVISEYONMSSACVLLUDEMRRKSAEGGSTTGEGLEWGVLF SmCH56 SIFWIAHPGOPAILDOVDOKAKGUKPEKLRMSRHVISEYONSSFSVLLUDEMRRKSACEGGSTTGEGUEWGVLF SmCH56 SIFWIAHPGOPAILDOVDARSGUKPEKLRMSRHVISEYONSSFSVLFVLDEMRRKSACEGGSTTGEGUEWGVLF SmCH56 SIFWIAHPGOPAILDOVSARSGUKPEKLRMSRHVISEYONSSFSVLFILDEMRRKSACEGGSTGEGUEWGULF SmCH56 SIFWIAHPGOPAILDOVSARSGUKPEKLRMSRHVISEYONSSFSVLFILDEMRRKSACEGGSTGEGUEWGULF SmCH56 SIFWIAHPGOPAILDOVSARSGUKPEKLRMSRHVISEYONSSFSVLFILDEMRRKSACLGKKGDKGEGUHGLI SmCH56 SIFWIAHPGOPAILDOVSARSGUKPEKLRMSRHVISEYONSSFSVLFILDEMRRASACLGKKGDKGEGUHGLI SmCH56 SIFWIAHPGOPAILDOVSARSGUKPEKLRMSRHVISEYONSSFSVLFILDEMRRASACLGKKGDKGEGUHGLI SmCH56 SIFWIAHPGOPAILDOVSARSGUKPEKLRMSRHVISEYONSFSVFIFYVMEYMREELGKKGDKGEGUHGLI SmCH56 SIFWIAHPGOPAILDOVSARSGUKPEKLRSKUSSEN SMCH56 SIFWIAHPGOPAILDOVSARSGUKPEKLNSKUSSEN SMCH56 SIFWIAHPGOPAILDOVSARSGUKPEKLSKUSSEN SMC									
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ALCHS SLEWIAHPGCPAILDOVSIKLGIKEEKNRATRHVLSEVONMSSA OVLFILDEMRRKASKOGVATTEGLEWGVLF SMCHSI SIFWAHPGCPAILDOVSKLGLEAEKLRSTRHVLSEVONMSSA OVLFVLDEMRKASKOGVATTEGLEWGVLF SMCHS3 SIFWVLHPGCPAILDOVSKLGLEAEKLRSTRHVLSEVONMSSA OVLFVLDEMRKASEGGRSTTGEGLEWGVLF SMCHS4 SIFWIAHPGCPAILDOVSKLGLEAEKLRSTRHVLSEVONVSSATVLLIDEMRRASAEGGSTTGEGLEWGVLF SMCHS5 SIFWIAHPGCPAILDOVEAKGIKPEKLRUSRVLSEVONVSSATVLLIDEMRRASAEGGSTTGEGLEWGVL SMCHS5 SIFWIAHPGCPAILDOVEAKGIKPEKLRUSRVLSEVONVSSFVLFVLDEMRKASAEGGSTTGEGVEWGVL SMCHS5 SIFWIAHPGCPAILDOVEAKGIKPEKLRMSRHVLSEVONVSSFVLFVDEMRKASAEGGSTTGEGVEWGVL SMCHS5 SIFWIAHPGCPAILDOVEAKGIKPEKLRMSRHVLSEVONVSSFVLFVDEMRKASAEGGSTTGEGLEWGVLF SMCHS5 SIFWIAHPGCPAILDOVEAKGIKPEKLRMSRHVLSEVONVSSFVLFVDEMRKASAEGGSTTGEGLEWGVLF SMCHS6 SIFWIAHPGCPAILDOVEAKGIKPEKLRMSRHVLSEVONVSSFVLFUDEMRKASAEGGSTTGEGLEWGVLF SMCHS6 SIFWIAHPGCPAILDOVEAKGIKPEKLRMSRHVLSEVONVSSFVLFUDEMRKASAEGGSTTGEGLEWGVLF SMCHS6 SIFWIAHPGCPAILDOVEAKGIKPEKLRMSRHVLSEVONVSSFVLFIDOMRKASAEGGSTGEGLEWGULF SMCHS6 SIFWAHPGCPAILDOVEAKSGIKPEKLRMSRHVLSEVONVSSFVLFIDUMRKASAEGGSTGEGLEWGULF SMCHS6 SIFWAHPGCPAILDOVEAKSGIKPEKLRMSRHVLSEVONVSSFVLFIDUMRKASAEGGSTGEGLEWGULF SMCHS6 SIFWAHPGCPAILDOVEAKSGIKPEKLRMSRHVLSEVONMSSF SMCHS6 SIFWAHPGCPAILDOVEAKSGIKPEKLRMSRHVLSEVONMSSF SMCHS6 SIFWAHPGCPAILDOVEAKSGIKPEKLRMSRHVLSEVONMSSF SMCHS6 SIFWAHPGCPAILDOVEAKSGIKPEKLRMSRHVLSEVONMSSF SMCHS6 SIFWAHPGCPAILDOVEAKSGIKPEKLRMSRHVLSEVONMSSF SMCHS6 SIFWAHPGCPAILDOVEAKSGIKPEKLRMSRHVLSEVONMSSF SMCHS6 SIFWAHPGCPAILDOVEAKSGIKPEKLRMSRHVLSEVONMSSF SMCHS6 SIFWAHPGCPAILDOVEAKSGIKPEKLRMSRHVLSEVONMSSF SMCHS6 SIFWAHPGCPAILDOVEAKSGIKPEKLRMSRHVLSEVONMSSF SMCHS6 SIFWAHPGCPAILDOVEKSF SMCHS6 SIFWAHPGCPAILDOVEKSF SMCHS6 SIFWAHPGCF SMCHS6 SIFWAHF SMCHS6 SIFWAHPGCF SMCHS6 SIFWAHPGCF SMCHS6 SIFWAHF SMCHS6 SIFWAHF SMCHS6 SIFWAHF SMCHS6 SIFWAHF SMCHS6 SIFWAHF SMCHS6 SIFWAHF SMCHS6 SIFWAHF SMCHS6 SIFWAHF SMCHS6 SIFWAHF SMCHS6 SIFWAHF	MsCHS2	SIFWIAHPGO	PAILDOVEOK	LALKPEKMN	TREVISEYGN	MSSACVLFI	LDEMRKKST.	. QNGLKTTGEG	LEWGVLF
SICHS SIEWLARP GEPAILDOVEAKUG LKPELLRSRRVLSEVGNWUS SOLVLEVDEMRRESA. DEG RSTTEEGLENGVLE SmCHS3 SIEWLAPP GEPAILDOVEAKUG LKPELLRSRRVLSEVGNVSS AVVLLIDEMRRESA. DEG RSTTEEGLENGVLF SmCHS5 SIEWLAPP GEPAILDOVEAKUG LKPELLRSRRVLSEVGNVSS SVLLIDEMRRASA. DEG RSTTEEGLENGVLF SmCHS5 SIEWLAPP GEPAILDOVEAKUG LKPELLRSRRVLSEVGNVSS SVLLIDEMRRASA. DEG RSTTEEGVENGVLF SmCHS5 SIEWLAPP GEPAILDOVEAKUG LKPELLRMSRIVLSEVGNVSS SVLLIDEMRRASA. A. DEG RSTTEEGLENGVLF SmCHS5 SIEWLAPP GEPAILDOVEAKUG LKPELLRMSRIVLSEVGNVSS SVLLIDEMRRASA. A. DEG RSTTEEGVENGVLF SmCHS5 SIEWLAPP GEPAILDOVEAKUG LKPELLRMSRIVLSEVGNVSS SVLLIDEMRRASA. A. DEG RSTTEEGLENGVLF SmCHS5 SIEWLAPP GEPAILDOVEAKUG LKPELLRMSRIVLSEVGNVSS SVLLIDEMRRASA. A. DEG RSTTEEGLENGVLF SmCHS5 SIEWLAPP GEPAILDOVEAKUG LKPELLRMSRIVLSEVGNVSS SVLIEVULEEK LEG STEEGLENGVLF SmCHS6 SIEWLAPP GEPAILDOVEAKUG LKPELLRMSRIVLSEVGNVSS SVIEVIDE VLEEK KRLER GG DEEK GE OWGLID SmCHS6 SIEWLAPP GEPAILDOVEAKUG LKPELL SRRALMDVGNVSSNTIFYVMEYMREE, LGKKGD. KGEEWGLAI G372FGPG 380 MSCHS2 GF GF G TVETVVLRSVEI SmCHS6 GF GF G TVETVVLRSVEIN. SmCHS6 GF GF G TVETVVLRSVEIN. SmCHS6 GF GF G TVETVVLRSMFIN. SmCHS6 GF GF G TVETVVLRSMFIN. SmCHS6 FF GF G TVETVVLRSMFIN. SmCHS6 FF G G TVETVVLRSMFIN.	AtCHS	SLFWIAHPGG	PAILDOVEIK	LG <mark>LKEEKMR</mark>	ATRHVLSEYGN	MSSACVLFI	LDEMRRKSA.	K <mark>dg</mark> va <mark>ttge</mark> g	LEWGVLF
SmcH54 SIFWIAHPGOPKILDRIETGLGIKPEKIRLSRWUSEYONVSSRWULLIDEMRRASAEEGLSTTEEGUDWQUL SmcH55 SIFWIAHPGOPAILDQVBAKAGIKPEKIRVSRWULSEYONVSSRVULLIDEMRRASADEGRSTTEEGVEWQVL SmcH58 SIFWIAHPGOPAILDQVBAKAGIKPEKIRWSRWUSEYONVSSPVULLIDEMRRAAAEEGRSTTEEGVEWQVL SmcH58 SIFWIAHPGOPAILDQVBAKAGIKPEKIRWSRWUSEYONVSSPVULLIDEMRRAAAEEGRSTTEEGIEWQVL SmcH58 SIFWIAHPGOPAILDQVBAKAGIKPEKIRWSRWUSEYONWSSPVULLIDEMRRAAAEEGRSTTEEGIEWQVL SmcH56 SIFWAVHPGOPAILDVEAKAGIKPEKIRWSRWUSEYONWSSPVULIDEMRRAAAEEGRSTTEEGIEWQVL SmcH56 SIFWAVHPGOPAILWRESKLAILPEKIAASRALADYONASSNTIVYVLEYVLEPUEEKRRIERGGDEEKGEOWGLI SmcH56 SIFWAVHPGOPAILWRESALRIDEGKLECSRKAIMDYONVSSNTIFYVMEYMEELGKKGDKGEEWGLAI SmcH56 SIFWAVHPGOPAILWRESALRIDEGKLECSRKAIMDYONVSSNTIFYVMEYMEELGKKGDKGEEWGLAI SmcH56 SIFWAVHPGOPAILWRESALRIDEGKLECSRKAIMDYONVSSNTIFYVMEYMEELGKKGDKGEEWGLAI SmcH56 SIFWAVHPGOPAILWRESALRIDEGKLECSRKAIMDYONVSSNTIFYVMEYMEELGKKGDKGEEWGLAI SmcH56 SIFWAVHPGOPAILWRESALRIDEGKLECSRKAIMDYONVSSNTIFYVMEYMEE SmcH56 SIFWAVHPGOPAILWRESALRIDEGKLECSRKAIMDYONVSSNTIFYVMEYMEE SmcH56 SIFWAVHPGOPAILWRESALRIDEGKLECSRKAIMDYONVSSNTIFYVMEYMEE SmcH56 SIFWAVHFYVIRSVII SmcH56 SIFWAVHFYVIRSVII SmcH56 SIFWAVHFYVIRSVII SmcH56 SIFFOGITYETVVIRSVII SmcH56 SIFFOGITYETVVIRSVII	SmCHS1 SmCHS3	SIFWIAHPGG	PAILDQVESK	VG <mark>L</mark> KPEKLR	SRRVLSEIGN SRRVLSEYGN	MWSPSVLFV	LDEMRKASS.		LEWGVLF LEWGVLF
SmCHS7 SIFWIAHPGGPAILDQVEAKAGLKPEKLRMSRHVLSEYGNVSSPSVLFILDDMRKAAAEEGRSTTGEGLEWGVLF SmCHS8 SIFWIAHPGGPAILDQVEARSGLKPEKLRMSRHVLSEYGNVSSPSVLFILDDMRKAAAEEGRSTTGEGLEWGVLF SmCHS6 SLFWAVHPGGPAILNRMEKKLAALDPEKLAASRRALADYCNASSPSVLFILDDMRKABAAEGRSTTGEGLEWGVLF SmCHS6 SLFWAVHPGGPAILNRMEKKLALDPEKLAASRRALADYCNASSNTIFYVWEYMRBELGKKCDKGEEWGLAL G372FGPG 380 MsCHS2 GFGFGGTTETVVLRSVAT AtCHS GFGFGGTVETVVLRSVPL SmCHS1 GFGFGGTVETVVLRSVPL SmCHS3 GFGFGGTVETVVLRSVPIL SmCHS5 GFGFGGTVETVVLRSVPIL SmCHS5 GFGFGGTVETVVLRSVPIL SmCHS6 SLFWAVHPGGPAILPRELASMEIN SmCHS5 GFGFGGTVETVVLRSVPIL SmCHS6 SFGFGGTVETVVLRSVPIL SmCHS6 SFGFGGTVETVVLRSVFIL SmCHS6 SFGFGGTVETVVLRSVFIL SmCHS6 SFGFGTVETVVLRSVFIL SmCHS6 SFGFGTVETVVLRSVFIL	SmCHS4	SIFWIAHPGG SIFWAVHSGG	PATLNOVEAR	LG <mark>L</mark> KPEKLRI	LSRRVLSEYGN /SRHVLSEYGN	VSSATVLLI VSSPSVLFV	LDEMRRASA.	DEGRSTTGEG	LDWGVLF
SmCH58 SIFWITHPGCPAILDQVBARSGMKPEKLRMSRHVDSEVCMMSSFSVLFILDQMRRASAAEGRSTTGEGLEGVLF SmCH52 KLFWAVHPGCPAILMRMEKKLALPEKLASRRALADVCNASSNTIFVVLEVULEEVKRLERGCDEKGEOWGLIL SmCH56 SLFWAVHPGCPAILMRESALRLDEGKLECSRKALMDYCNVSSNTIFVVMEYMREELGKKCDKGEEWGLAL G372FGPG 380 MsCH52 GFGFGCTVETVVLRSVAI SmCH51 GFGFGCTVETVVLRSVPL SmCH51 GFGFGCTVETVVLRSVPL SmCH53 GFGFGCTVETVVLRSMFIDL SmCH54 GFGFGCTVETVVLRSMFID. SmCH55 GFGFGCTVETVVLRSMFIL SmCH55 GFGFGCTVETVVLRSMFI SmCH55 GFGFGCTVETVVLRSMFI SmCH55 GFGFGCTVETVVLRSMFI SmCH55 GFGFGCTVETVVLRSMFI SmCH55 GFGFGCTVETVVLRSMFI SmCH55 GFGFGCTVETVVLRSMFI SmCH55 GFGFGCTVETVVLRSMFI SmCH55 GFGFGCTVETVVLRSMFI	SmCHS7	SIFWIAHPGG	PAILDQVEAK	AGLKPEKLR	ISRHVLSEYGN	VSSPSVLLI	LDEMRKAAAA.	E <mark>EG</mark> RS <mark>TTGE</mark> G	LEWGVLF
SmCHS6 SLEWAVHPGGPAILNRLESALRLDEGKLECSRKALMDYGNVSSNTIFYVMEYMRPELGKKGDKGEEWGLAL G372FGPG MscHs2 AtCHS SmCHS1 GFGPGGTVETVVLRSVAL SmCHS3 GFGPGGTVETVVLRSMFID. SmCHS4 GFGPGGTVETVVLRSMFID. SmCHS5 GFGPGGTVETVVLRSMFID. SmCHS5 GFGPGGTVETVVLRSMFI SmCHS5 GFGPGGTVETVVLRSMFI SmCHS5 SmC	SmCHS8 SmCHS2	SIFWIAHPGG KLFWAVHPGG	PAILDQVEAR PAILNRMEKK	SGLKPEKLRI LALLPEKLAI	ISRHVLSEYGN Srraladygn	MSSPSVLF1 ASSNTIVY	LDQMRKASA. /LEYVLEEEKE	AEGRSTTGEG Rrierggdeekg	LEWGVLF EOWGLIL
G372FGPG 380 MscHs2 GFGPG TTETVVLRSVAT AtcHs GFGPG TVETVVLHSVPL SmcHs1 GFGPG TVETVVLHSVNIN. SmcHs4 GFGPG TVETVVLRSMPID. SmcHs4 GFGPG TVETVVLRSMPID. SmcHs5 GFGPG TVETVVLRSMPIT SmcHs5 GFGPG TVETVVLRSMPI SmcHs6 GFGPG TVETVVLRSMPI SmcHs6 BFGPG TVETVVLRSMPI SmcHs6 BFGPG TVETVVLRSMPI	SmCHS6	SLFWAVHPGG	PAILNRLESA	LR <mark>L</mark> DEG KL E	SRKALMDYGN	VSSNTIFY	MEYMREE	L <mark>GK</mark> KG <mark>DK</mark> G	EEWGLAL
G372FGPG 380 MscHs2 GFGPG TTETVVLRSVAI AtcHs GFGPG TVETVVLHSVPL SmcHs1 GFGPG TVETVVLHSVNIN. SmcHs3 GFGPG TVETVVLRSM FID.L SmcHs4 GFGPG TVETVVLRSM FID SmcHs5 GFGPG TVETVVLRSM FI SmcHs5 GFGPG TVETVVLRSM FI SmcHs6 GFGPG TVETVVLRSM FI SmcHs6 BFGPG TVETVVLRSM FI SmcHs6 BFGPG TVETVVLRSM FI		_							
MSCHS2 GFGFG TIETVVLRSVAI AtcHs GFGFG TVETVVLRSVAI SmCHS1 GFGFG TVETVVLRSVFIN. SmCHS3 GFGFG TVETVVLRSMFID. SmCHS4 GFGFG TVETVVLRSMFID. SmCHS5 GFGFG TVETVVLRSMFII SmCHS5 GFGFG TVETVVLRSMFI SmCHS5 GFGFG TVETVVLRSMFI SmCHS6 AFGFC TTEGILARNITV		705000							
MacHs2 GFGFGGHIETVVLRSVAI AtcHs GFGFGGVVETVVLHSVDL SmcHs1 GFGFGGVVETVVLHSVDIN. SmcHs4 GFGFGGVVETVVLRSMFID. SmcHs4 GFGFGGVVETVVLRSMFID. SmcHs5 GFGFGGVVETVVLRSTFIEL SmcHs6 GFGFGGVVETVVLRSMFI SmcHs6 GFGFGGTVETVVLRSMFI SmcHs6 AFGFGTTFEGILARNITV	G3	72FGPG 380							
SmCHS1 GFGPG GFVETVVLHSVNIN. SmCHS3 GFGPG GFVETVVLRSMPIDL SmCHS4 GFGPG GFVETVVLRSMPID. SmCHS5 GFGPG GFVETVVLRSMPIL. SmCHS7 GFGPG GFVETVVLRSMPI SmCHS2 AFGPG GFVETVVLRSMPI SmCHS2 AFGPG GFUETVULRSMPI SmCHS2 AFGPG GFUETVULRSMPI	MsCHS2 AtCHS	GFGPGLTIE GFGPGLTVE	TVVLRSVAI TVVLHSVPL						
SmCH33 GFGFGTVETVVLRSMFIDL SmCH35 GFGFGTVETVVLRSMFIN. SmCH35 GFGFGTVETVVLRSIFIEL SmCH36 GFGFGTVETVVLRSIFIEL SmCH38 GFGFGTVETVVLRSMFI SmCH32 AFGFGTTFEGTLARNITV	SmCHS1	GFGPGLTVE	TVVLHSVNIN.						
SmCHS5 GFGFGGTVETVVLRSIPTEL SmCHS7 GFGFGTVETVVLRSIPT SmCHS8 GFGFGTVETVVLRSMPT SmCHS2 AFGFGTTEGTLARNITV SmCHS2 AFGFGTTEGTLARNITV	SmCHS3 SmCHS4	GFGPGLTVE	TVVLRSMPIDI TVVLRSMPIN.						
SmCHS8 (GFCPCTVETVVLHSMCH SmCHS2 AFCPCTTVETVVLSMCH SmCHS2 AFCPCTTPECTLARNITV	SmCHS5	GEGEGETVE	TVVLRSIPIEL						
	SmCHS7 SmCHS8	GF GP GLTVE	TVVLRSMPI						
	SmCHS2 SmCHS6	AFGPGITEE AFGPGITEE	GILARNLTV						

Figure S3. Amino acid sequence alignment of SmCHS1 –SmCHS8 against *Medicago sativa* MsCHS2, and *Arabidopsis thaliana* AtCHS. Identical sites were shown in white letters on a red background, conserved sites were shown in black letters on a yellow background and others were shown in white background. The catalytic triad C164-H303-N336 and the gatekeeper F215 were boxed and marked in blue letters. The highly conserved CHS signature sequence, G372FGPG were boxed and marked in green letters. The figure was produced using the ESPript server (http://espript.ibcp.fr/ESPript/).



Figure S4. Amino acid sequence alignment of SmCHI1–SmCHI4 against *Medicago sativa* MsCHI, *Arabidopsis thaliana* AtCHI and AtCHIL. Residue numbering refers to the MsCHI sequence. Identical sites were shown in white letters on a red background, conserved sites are shown in black letters on a yellow background and others are shown in white background. Critical catalytic residue of *bona fide* CHI are boxed and indicated in blue letters. Among them, T190 are legume specific whereas S190 are much more conserved in other non-legume plant species. The figure was produced using the ESPript server (http://espript.ibcp.fr/ESPript/)

					Proline-ri	ich hinge	region			
CharENGII				20	30.		PTTCHT	50 HULCRI T	60.	
GMFNSII GMFNSII	MUSESL.	LVVFLIVF SETTLEL	ISASLLK IFTTALL	LLCLPIK LLFVREN	KPKAHLKI	NPPSPPAI PPPSPFT	PIIGHL	HLLGPLI HLLGPLI	HHSFRDL HOSFHRL	SIRIGSLI SLRYGPLL STLYGPLI
LjFNSII-2.1 LmFNSII-1.1	MWIFDLTI MLIFDLTI	SFTT LLFL SFTT LLFL	IFTTALL IFTTA	LLLKVFK LLLKVFK	KNHKLR.E KNHKLQ.E	PPPSPFTI PPPSPFTI	PIIGHL	HLLGPLI HLLGPLI	HQSFHRL HQSFHRL	STLYGPLI STLYGPLI
AmFNSII SbaFNSII-1	MDL <mark>V</mark> EV	LVYS <mark>TL</mark> F <mark>I</mark> FLYA <mark>AL</mark> F <mark>L</mark>	LSTL <mark>L</mark> LT LSAAFLL	LLTRTRR LIFAGD.	KTRPP	G <mark>P</mark> LA <mark>I</mark> G <mark>P</mark> FP <mark>I</mark>	PLIGHL PIIGHL	HLLGPK <mark>L</mark> HLLGPKL	HH <mark>TFH</mark> QF HQ SFH G <mark>L</mark>	<mark>SQ</mark> R <mark>YGPLI SQ</mark> RH <mark>GPLM</mark>
SbaFNSII-2 SmFNSII		FLNV AL L <mark>L</mark> GAYA AL F L	LSAA <mark>V</mark> CL VSAALSR	MVFTGKR SILRSKL	RRRLPN RRHAP	.PPG <mark>P</mark> FP <mark>I</mark> G <mark>P</mark> FP <mark>I</mark>	PLIGNL PIIGHL	NLVSPRL HLLG <mark>P</mark> RL	HH TFH ML HQ SFH EL	AQR <mark>YGPIM</mark> SQR <mark>YGPLM</mark>
	70	80	90	1	٥o	110	1	20	130	140
GhyFNSII GmFNSII	HLRLGSVP SLRIGSVK	CVVVSTPD FIV <mark>AST</mark> PS	LA <mark>KDF</mark> LK LA <mark>QEF</mark> LK	TNELAFS TNELTYS	SR <mark>KHS</mark> LAI SR <mark>KMN</mark> MAI	DHITYG. N <mark>mv</mark> tyhn	. V <mark>afaf</mark> a Ia tfaf a	P <mark>YGT</mark> YWK P <mark>YDT</mark> YWK	FIKKLFT FMKKLST	VELLGTQN Tellgn <mark>kt</mark>
LjFNSII-1.1 LjFNSII-2.1	QLKIGYIP QLKIGYIP	CVVASTPE CVVASTPE	LAKEFLK LA <mark>KEF</mark> LK	THELAFS THELAFS	SRKHSAAI	KLLTYD. KLLTYD.	VSFAFS VSFAFS	PYGPYWK Pygpywk	FIKKTCT	FELLGTRN FELLGTRN
AmFNSII-1.1 AmFNSII SbaFNSII-1		VVASTPE VVASTPE	LAREFLK LAREFLK LAKEFLK	THELDES	SRKHSAAJ	DIVIYD.	SFAFA SFAFA SFAFS	PIGPIWK PYGPYWK Pygpywk	FIKKLCT	YELLGARN YELLGARN
SbaFNSII-2 SmFNSII	KFRLGSIP QLRLGSIK	CLVVSTPE CVVASSPE	LA <mark>KDI</mark> LK LA <mark>KEF</mark> LK	THELIFS THDLVFS	SR <mark>VKS</mark> TAI SR <mark>KHS</mark> TAI	DIVTYG. DIVTYD.	V SFAF S S SFAF S	P <mark>YGP</mark> YWK P <mark>lgp</mark> ywk	YIKKLCT FIKKLCT	YELLGSRM YELLGARN
	1	50	160	170	1	L 8 0	190	2	0 0	210
GhyFNSII GmFNSII	LSHFLPIR LGHFLPIR	HEIRELL REVHDII	RT LM VKS OFLFHKS	RAKERVN KAOESVN	LTEELLKI LTEALLSI	TNNVISC	MMMMSIR	C <mark>SGTN</mark> SE S SGTD SO	ADEAKNL AEOARTL	VREV <mark>TKI</mark> F VREVTOIF
LjFNSII-1.1 LjFNSII-2.1	MNHFLPIR MNHFLPIR	INEIRRFL INEIRRFL	QV <mark>ML</mark> E <mark>K</mark> A QV <mark>ML</mark> EKA	KAŜEGV <mark>N</mark> Kasegvn	VTE <mark>ELIK</mark> I VTE <mark>ELIK</mark> I	L <mark>TN</mark> NVIS <mark>C</mark> LTNNVISC	MMFSTR MMFSTR	S <mark>SGTE</mark> G <mark>E</mark> S SGTE G <mark>E</mark>	AEEMRTL AEEMRTL	<mark>v</mark> rev <mark>tõi</mark> f vrevtõif
LmFNSII-1.1 AmFNSII	MNHFLPIR LSHFQPIR	INEIRRFL ALEVNSFL	QV MLEK A RI <mark>LYEK</mark> T	KASEGVN EQKQSVN	VTEELIKI VTEELVKI	LTNNVISC LTSNVISN	MMFSTR MMLGIR	SSGTEGE CSGTEGE	AEEVRTL AEVARTV	VREVTQIF IREVTQIF
SbaFNSII-1 SbaFNSII-2 SmFNSII	LNHFEPLR	LEVREFL LEVREFL	KDVMAMG	KAGKSEN	VTEELMKI LTEELVKI			AAESEEQ CSGTEGE	AEVARTL AEVARTL	IREVIEIF IREV <mark>SQL</mark> F VREVTOIF
	220	23	0	240	250		260		270	280
GhyFNSII	GOF NVSDF	WFCKNID	LQGFKKR	YEGTHRR	YDALLERI	IMGRE.E	NRRRGK	IKDG.	EG <mark>KDF</mark> DEKV KDE	LDMLLDVL
LjFNSII-1.1 LjFNSII-2.1	GEFNVSDF GEFNVSDF	KLCKNID	IGGF <mark>K</mark> KR IGGFKKR	SKDIQKR SEDIQKR	YDALLEKI YDALLEKI	ISERE SE	RARRGK RARRGK	NRETLG.	EEGG <mark>KDF</mark> EEGG <mark>KDF</mark>	LDMMLDTM LDMMLDTM
LmFNSII-1.1 AmFNSII	GEFNVSDF: GEFDVSEI	KL <mark>CKN</mark> ID WF <mark>CKN</mark> LD	<mark>I</mark> GGF <mark>K</mark> KR LQGI <mark>R</mark> KR	SEDIQKR SEDIRRR	YDALLE <mark>K</mark>] YDALLE <mark>K</mark>]	I <mark>ISE</mark> RESE I <mark>ISDRE</mark> RI	E <mark>R</mark> ARRGK LRGGG	NRETLG. GGG	EEGG <mark>KDF</mark> GGEV <mark>KDF</mark>	LD <mark>M</mark> MLDT <mark>M LDM</mark> LLDVM
SbaFNSII-1 SbaFNSII-2	GEFDAADI GEFDFGDM	WFCKNFD WFCKSFD	LQGIRKR FQGI <mark>K</mark> KR	SEDIQRR SKDIKVR	YDALLEKI YDALLEKI	LTDREKI LTDRENV	ARSHRG	G V	EAKDF EPKDM	LDIFLDIM LDMFLDIM
300 0311	GETUVADI		L Q G I KKK	SUDIARK	IDALLEN	I I DKENT	ROAAA	A	· · · · · · · · · · · · · · · · · · ·	
	2	20	Oxyge	n binding	pocket	220	220	2	4.0	350
GhyFNSII	EDGKAEIK	TRDHIKA	LILDFLT	AGTDTTA	IAIEWAL	ELINNP	IALEKAR	QEIDQVI	GDE <mark>RLV</mark> Q	ESDTPNLP
GMFNSII-1.1 LjFNSII-1.1	EDGKECEVE	TRDHIKA		AATDTTA AATDTTA AATDTTA	I AVEWTLZ I AVEWTLZ	AELISNPE AELISNPE	VERKAQ VEDKAR	EEVDRVI EEIDKVV	GNTQLVC GKH RLV T GKH RLV T	ELDTPNLP ELDTPNLP
LmFNSII-1.1 AmFNSII	EDGKCEVE ESEKSEVEI	TRDHIKA	LVLDFLT	AATDTTA AGTDTTA	IAVEWTLZ ITTEWALZ	AELISNPE AELISNPN	VFDKAR	EEIDKVV EEMDKVI	GKHRLVT GSORLLO	ELDTPNLP ESDAPNLP
SbaFNSII-1 SbaFNSII-2	DSGNSEVKI EGGKTDVEI	SREHLKA Trehlka	LILDFFT VILDFLT	AGTDTTA AGTDTTA	IST <mark>EWA<mark>I</mark> ITVEWVLI</mark>	A <mark>ELMNN</mark> PB A <mark>ELMNS</mark> PB	(<mark>V</mark> LK <mark>KA</mark> Q (<mark>A</mark> MK <mark>KA</mark> Q	EEIQKVV DEMDRVV	GSC <mark>RLM</mark> D GRE <mark>RMM</mark> A	ESDAP <mark>NLP</mark> ESDAP <mark>N</mark> LP
SmFNSII	ESGKAEVTI	TRDHLKA	LILDEFT	AGTDTTA	IVSEWAIS	ELINNPS	S <mark>V</mark> lk <mark>ka</mark> Q	DEIAKVV	GSERVLH	ESDGPKLP
	ExxF	motif	24-1)		36256236.00			0,002000	PERF m	otif
GhyFNSII	360 YIQ <mark>AIIKE</mark>	37 AL <mark>RLHPPI</mark>	0 P <mark>mlirks</mark>	380 Tenvivo	390 GYDIPAG	4 TLLFV <mark>N</mark> IW	IOO IS <mark>IGRNP</mark>	410 QC <mark>WETPL</mark>	4 EFK <mark>PHRF</mark>	20 <mark>LD</mark> GGDL
GmFNSII LjFNSII-1.1	YIHAIIKE Y <mark>I</mark> HAIIKE	TMRLHPPI SFRLHPPI	P <mark>MIM</mark> RKG PLLIRKS	IEDCVVN VQDCTVG	GNMIPKG GYHISAN	SIVCVNIW TILFVNIW	AMGRDP A <mark>IGRNP</mark>	NI <mark>WKN</mark> PL KY <mark>WESPM</mark>	EFKPERF KFWPERF	LEGEG LESNGPGP
LJFNSII-2.1 LmFNSII-1.1 AmFNSII	YIHAIIKE YIHAIIKE	SFRLHPPI SFRLHPPI	PLLIRKS PLVIRKS		GYHISAN GYHISAN GYTTDAK	CILFUNIW CILFINIW CLLEWNIW	AIGRNP AIGRNP ISMCRNP	KYWESPM KY <mark>WESPM</mark> NYWEND	KFWPERF KFWPERF FFFFFFFF	LESNGPGP LESNEPGS
SbaFNSII-1 SbaFNSII-2	YLEAIIKE	FRLHPPI FRLHPPI	PMLARKS PLIIRRS	VSDCVID	GYNIPAS GYHIPAD	LLFVNIW LAFINVW	IS IGRNP	ECWDSPF KYWDSPI	SFF PERF	EKDN
SmFNSII	YLQAVIKE	FFRLHPPI	PMLARKS	ISDCVVD	GYTIPSN	LLFVNLW	SMGRDP	KI <mark>WDCP</mark> E	VFFPERF	LEKAN





Figure S5. Comparison of SmFNSII proteins with other plant FNSII proteins. The amino acid sequences of SmFNSII was aligned with the amino acid sequences from *Gerbera hybrid* GhyFNSII, *Glycine max* GmFNSII, *Lonicera japonica* LjFNSII-1.1 and LjFNSII-2.1, *Lonicera macranthoides* LmFNSII-1.1, *Antirrhinum majus* AmFNSII and *Scutellaria baicalensis* SbaFNSII-1, SbaFNSII-2. Identical sites were shown in white letters on a red background, conserved sites are shown in black letters on a yellow background and others are shown in white background. P450s have conserved motifs including proline rich hinge region, oxygen binding pocket, E-R-R triade consisting of the E and R from the ExxR in the K-helix and the R from the "PERF" consensus sequence, and heme-binding pocket are boxed in blue. They are universal motifs among P450s. Among them, the E-R-R triad and the cysteine in the heme-binding domain are highly conserved in all primary amino acid sequence of plant P450s. The figure was produced using the ESPript server (http://espript.ibcp.fr/ESPript/).

			Proline-ricl	n hinge region	
AtF3H PhF3H SmF3H1 SmF3H2 SmF3H3 SmF3H4 SmF3H4 SmF3H5 SmF3H6	1 	10 2 1 2 1 2 1 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2	30 FSH <mark>RR</mark> NRSHNNRI P SSFF R KRYPL. PLP FQK R PEK. LP FQK R R LP VIF KR PSQR K LP ULLV K KSNRNP LP CLLQ NK KLNP P ULQ <u>NK</u> KLNP P	40 GPNPWPIIGNLPH GPKPWPIGNUVH GPRPWPIVGNLPO GPRPWPIVGNLPO GPRPWPIGNLNL GPRGUPIGNLNL GPKPWPVIGNLNL GPKPWPVIGNLNL	G C C C C C C C C C C C C C
	VVVAA	S			
AtF3'H PhF3'H SmF3'H1 SmF3'H2 SmF3'H3 SmF3'H4 SmF3'H5 SmF3'H6	70 80 TTYCPILHIRLGFVDVVVAA QTYCPLMYLKMCFVDVVVAA QVYCPLMHLKMCFVHVVVAA QKYCPLMLLKKGKFVHVVVAA QKYCPLMLLKFGKFPVLVVGS QKYCPIMLLKFCSAPVVVGS QKYCPIMLLKFCSAPVVVGS	90 XSVAQFLKIHDAN ASVAQFLKIHDAN AAVAQFLKHDAN AGVAEQFLRVHDIN HMAKQFLKVHDAN PHAKQFLKVHDAN PELAKQVLKDODIT VAAKIFLKIMDLT VAAKIFLKIMDLT	100 ASRPPNSGALHMAYN SRPPNSGALHWAYN SRPPNAGAKYYAYN LSRPPNAGAKYYAYN ATRPSLAAGKYTAYN ATRPSLAAGKTTAYN ARRDVPVVCREARYG ASRPKTSAGKITTYN ASRPKTSAGKITTYN	120 YQDLVFAPYGPRWI YQDLVFAPYGPRWI YQDLVFAPYGPRWI YQDLVFAPYGPRWI SVDIVWTPYGPRWI SVDITWSPYGPWI YSDITWSPYGPWI YSDITWSPYGPWI	130 LIRKISSVHLFS MURKICSVHLFS RURKICALHLFS CARKIFLSEVFN MURKVCVREMLG CARKMCLMELFS CARKMCLMELFS
	140 150 16	50 170	180 19	0	200
AtF3'H PhF3'H SmF3'H1 SmF3'H2 SmF3'H3 SmF3'H4 SmF3'H5 SmF3'H6	AKALEDEKHVROEEVGTLTRE TKALDERHVRODEVKTLTRA AKALDERHVROEEAGILCG AKALDERHVREEEVGILCG AKALDERHVREEEVGILVR AKALEFEEIRVEERRIFVS NATLESYEYIRAEEMSSLLKE ARRESYEYIRAEEMSSLKE ARRESYEYIRAEEMSSLKE	TVRVGT <mark>KPV</mark> NLGQLV TASAGO KPV KLGQLI TASAGO MPV KLGQLI TASAG OMPV KLGQNI TADAGHKPVRISET THSLS GKPV VLTPHI THSKAGTAVDVGEQ THSCAGTAVDVGEQ TFGESG RP FLLKDCI TFGLSG RP FMVKDCI	MCVVNALGREMIGR NVCTTNALARVNLGR NVCATNAISRVNLGR HVCATNAISRVNLGR SNYALSNISRMVLSN FVTVLNVITGMLWGG STVSLSVISRMVLGR STLSLNVISRMVLGR	RLFGAD RVFADGSGD RVVGHGGGG RVLGHGHGGG KYFSETADDHHRN TVKGEERAG RYLDGDEN RYLDGGDS	ADHKADEFRS VDPQAAEFKS GDEKAEEFKA SACGDTTAEELKA SIFKLHELOG LGAEFKE AVVSPEEFKK AVVSPEEFKK
	21.0			2.62	0.7.0
AtF3 ['] H PhF3 ['] H SmF3 ['] H1 SmF3 ['] H2 SmF3 ['] H3 SmF3 ['] H4 SmF3 ['] H5 SmF3 ['] H6	VICHMALACVENIGDEVESI MVVEMMVVACVENIGDEIPO MVVELMVVACVENIGDEIPO MVELMVIACVENIGDEIPE MVECHNSIACVENIGDEIPE MUECHLACVINIGDUEPE VVGEMTALIGAPNISDEFPAI MUELFELNGVINIGDLIEV MUELFLINGVINIGDLIEV	DWIDLOGVAGKWERI NWIDLOGVAAKWERI EGFDLOGVVAKWERI SFIDLOGVVAKWERI ERIDLOGYVKRMERI NFIDLOGYVKRMERI NFIDLOGYVKRMERI NFIDLOGYVKRMERI	HKRFDAFISSILKEH HARFDAFISSILKEH HKRFDFITDILEH HKRFDFITNIVADH HKKIDKFIEFVIDDH AKRFDRIFEMIEOR SKKFDRFLEHVIDEH SKKFDRFLEHVIDEH	LEMNGQDQKH KGKIFGEM KGKIFGEM KIDGPSRGH KINGSDDT.AGH QGRRAADKGFPPI LKMSGDHGSI EARRRTTE.YVSI EARRRTTD.YASI	TDMISTIISIKGT (DLISTIISIKND 7DLISTIISIKND 7DLISTIISIKBG (DVUDMIIVMAEK (DVVDMIIVMAEK (DFLQIILOMKET RDMVDVILELAED RDMVDVILELAED
	Oxyge	n binding pocket mo	tif		
AtF3'H PhF3'H SmF3'H1 SmF3'H2 SmF3'H3 SmF3'H4 SmF3'H5 SmF3'H6	280, 290, 3 DLDGDGGGKITDTEIKALLIN DADNDGGKITDTEIKALLIN D.DTQGGKITDTEIKALLIN D.NGEGGKITDIEIKALLID PNEVKLTRDCVKALQD PTLEVKLERHGVKAFTQD P.ALEVKLQRHGVKAFTQD	00 310 AGTDTSASTVDWA FVAGTDTSSSTVEWA FAGTDTTSSTVEWA ETAGTDTTSSTVEWA LTGGTDTSNAVTIEWA LAGGTESSAVTVEWA LAGGTESSAVTVEWA	320 33 TAPLIRHPDIMVKAQ AIABLIRHPKILAQAQ IIAPLIRHPEILRAQ IIAPLIRHPEILAQAQ IIAPLIRHPGVAEKAF VARIMARPEIMAKVQ AISELLKKPEIFKAAT IISEMMKKPEIFDKAF	340 EDIVVCRDRPV 21DKVVCRDRPV QELDSVVCRDRLV QELDSVCRDRLV QEDSVCRDRLV QEDSVCRDRLV QEDSVCRDRLV QEDSVCRDRLV QEDSVCRDRV QEDSVCRDVCRNV QEDSVCRDNV QEDRVCRDNV QEDRVCRDNV QEDRVCRDNV	350 NBSDIAQLPYLQA SELDIAQLYLQA ISDDPELVYLQA KESDIGQITFLQA ESDJSELPYISA ESSIIKLPYLSA KEKDIPSLPYVEA KEDDMPTLPYLQA
	ExxR motif			PERF motif	GEK VDVKG
AtF3'H PhF3'H SmF3'H1 SmF3'H2 SmF3'H3 SmF3'H4 SmF3'H5 SmF3'H6	360 370 VIKENERLHPETESIPHIAS IVKEDERLHPSTPISLPRIAS VIKENERLHPSTPISLPRIAS IVKENERLHPSTPISLPRIAS IVKENERLHPSTPILLPHCAN VMKEARLHPSLPILVPHCPS IVKETMRLHPVAPMLVPRLAE IVKETMRLHPVAPMLAPRIA	380 390 ESCEINGYHIPKGSI ESCEINGYHIPKGSI ESCEINGYHIPKGSI ESCEINGYHIPKGSI ESCENGYHIPKGSI ATSVVAGYDIKKGT EDCKVAGYDIKKGT CHDCKVDGYDIKKGT	400 ILLINIWAIARDPDOW ILLINUWAIARDPNAW ILLVNUWAIARDPNW VLINUWAIARDPNW VLINUWAIARDPNW VVINUWAIARDPSIW VVIVNIWAIARDPSIW VVIVNIWTIORDPSIW	410. S DPLAF * PERFLF A DPLEF RPERFLF TOPLEF PORFLA ADPLEF PORFLF DAPOF IPERFL ENPLEF PERFL ENPLF PERFL ENPLF PERFL ENPLF PERFL ENPLF PERFL ENPLF	GEK 5 GVDVKGSD GEK 5 GVDVKGD GEK PKVDVRGND GER NADVRGND GER NADVRGND GER NDVRGND GER NDVRGND GER NIDVKGQD GK. NIDVKGQD
	Heme-binding domain				
Atf3'H Phf3'H SmF3'H1 SmF3'H2 SmF3'H3 SmF3'H4 SmF3'H5 SmF3'H6	440 450 FELIPFGAGRRIGAG LSLGL FUIPFGAGRRIGAG MLGI FOLIPFGAGRRIGAG MSLGI FELMPFGAGRRIGAG MSLGI FSFLPFGSGRROPG VKLGL INYFPFGSGRROP VKLGL INYFPFGSGRROP VALGL FELLPFGSGRRM GYALGL FELLPFGSGRRM GYALGL	460 RTIQF LTATLVQGFD RMVQLITATLTHAFN RMVQLLTATLVHAFN RMVQLLTATLVHAFN KVIQTLANLHGFE RMFMYSLASLLHSFD KVIQSSLANLHGFN KVIQSSL <mark>SNLH</mark> GFN	470 480 WelagGVTPekinne FollangISPoninnd FelgngISPoninnd FelgngISPoninne KivegngISPoninne WSVPAGeridie WRLPDKMKPAElnne WKLPNEMKPOElnne	490 SYGLTLORAVPLY SAYGLTLORADPLY SAYGLTLORADPLY SAYGLTLORADPLY SUCLTVHPKDSU SUCLTVHPKDSU SUCLTVHFKDSU SIFGLSTPKFPLY SIFGLSTPKFPLY	500 VHPKPRLA.PNV VHPRPRLA.PHV VHPNPRLA.PHV VYPPRLA.SHV LIMEPKLA.PHL AVPTPRLSHPSL AVAEPRLP.LNC VLAHPRLP.QNL
	510				

	510
AtF3'H	GLGSG
PhF3'H	IG
SmF3'H1	HA
SmF3'H2	QAQI
SmF3'H3	QALIVDE
SmF3'H4	Ε
SmF3'H5	NSM
SmF3'H6	NSM

Figure S6. Amino acid sequence alignment of SmF3'H1–SmF3'H6 against *Arabidopsis thaliana* AtF3'H from and Petunia hybrid PhF3'H. Identical sites were shown in white letters on a red background, conserved sites are shown in black letters on a yellow background and others are shown in white background. The P450-featured conserved motif, including the proline-rich "hinge" region (P/I)PGPx(G/P)xP, oxygen binding pocket motif, E-R-R triade consisting of the EXXR and PERF motif and heme binding domain are boxed and indicated in blue letters. Three F3'H-specific conserved motifs "VVVAAS", "GGEK" and "VDVKG" have similarity counterparts at the corresponding sites of SmF3'H1 and SmF3'H2. They are boxed and indicated in green. The figure was produced using the ESPript server (http://espript.ibcp.fr/ESPript/).

					Proline-rich hi	nge region		
GmF35H PhF35H_Hf1_ PhF35H_Hf2_ S1F35H VvF35H SmF35H SmF35H	1 MDSLL1 MM1 MV1 MAIDTSL1 MQGEECILL:	10 LLKETATSILL LLTELGAATSI LLSELAAATLI RINELFVAAII LL.ELAAATLI IARGVIVAALI	20 IFLITRISIQT IFLIAHIIIST IFLITHIFIST LYIVHIIISK LFFITRFFIRS LYALIRLISR	30 FLKSYRQK. LISKTTGR. LSITNGR. LITTVRERG LLKSSRK. SSTTIDRHR	40 LPPGPK HLPPGPR LPPGPR RRLPLPPGPK LPPGPR	GWPVVGALP GWPVIGALP GWPVIGALP GWPVIGALP GWPVIGALP GWPLVGALP GFPVVGSLP	LIGSMPHVT LIGAMPHVS LIGSMPHVS LIGSMPHVA LIGNMPHVA SLIGDMPHVA	50 LAKMAK LAKMAK LAKMAK LAKMAK LAKMAK
GmF3'5'H PhF3'5'H_Hf1 PhF3'5'H_Hf2 S1F3'5'H V∀F3'5'H SmF3'5'H	70 KYGPIMYIK KYGAIMYIK KYGPIMYIK RYGPIMYIK RYGPIMYIK IYGPIMYIK	80 MGTINIMVVAS1 VGTCGMAVAS1 VGTCGMVVAS1 VGTCGMVVAS1 MGTINSMVVAS1 MGTLGMVVAS1	90 TPAAARAFIKT TPDAAKAFIKT TPDAAKAFIKT TPNAAKAFIKT TPGAARAFIKT TPDSARAFIKA	100 LDQNFSNRP LDINFSNRP LDLNFSNRP LDINFSNRP LDINFSNRP QDTNFSNRP	110 SNAGATHLAY PNAGATHLAY PNAGATHLAY PNAGATLLAY PNAGATILAY	120 DARDMVFA NAQDMVFA GAQDMVFA NAQDMVFA HAQDMVFA NRODMVFA NRODMVFA	130 (GSRWKLLR (GPRWKLLR) (GPRWKLLR) (GPRWKLLR) (GPKWRLLR)	KLS <mark>N</mark> LH KLSNLH KLSNLH KLSNLH KLSNLH KLS <mark>S</mark> LH
GmF3'5'H PhF3'5'H_Hf1 PhF3'5'H_Hf2_ S1F3'5'H VyF3'5'H SmF3'5'H	140 MLGGKALDD MLGGKALEN MLGGKALEN MLGGKALED MLGSKALEG	150 WAQIRDEEMGH WANVRANELG WANVRANELG WANVRANELG WADVRAVELG WADVRSTEVGH	160 IMLGAMYDCNK IMLKSMSDMSR IMLKSMFDMSR IMLKSMFDASQ IMLRAMLELSQ IMLRAMLELSR	170 RDEAVVVAE EGORVVVAE EGERVVVAE DGECVVIAD RAEPVVVPE RGEA <mark>VAL</mark> PE	180 MIIF AMANMI MITFAMANMI VITFAMANMI MITFSMANMI MITSMANMI	190 GQVTLSRRVI GQVMLSKRVI GQVTLSRRVI GQVTLSRRVI GQVILSRRVI	200 FETKGSESNI VDKGVEVNI VDKGVEVNI VEKGVEVNI FETKGSESNI VSKGKEVNI	EF <mark>KD</mark> MV EFKDMV EFKDMV EF <mark>KN</mark> MV EF <mark>RD</mark> MV EF <mark>RE</mark> MV
2 GmF3'5'H PhF3'5'H_Hf1_ PhF3'5'H_Hf2_ S1F3'5'H VvF3'5'H SmF3'5'H	10 2: VELMTVAGYI VELMTTAGYI VELMTTAGYI VELMTVAGYI VELMTSAGYI	20 2: FNIGDFIPFIA FNIGDFIPCIA FNIGDFIPCIA FNIGDFIPKIA FNIGDFIPWIA	30 24 WMDLQGIERG WMDLQGIEKG WMDLQGIEKG WMDIQGIEKG WLDIQGIERG	0 2 MKKIHKKFD MKRIHKKFD MKRIHKKFD MKNIHKKFD MKHIHRKFD MKKIHSKMD	25022 ALLTSMIEEH ALLTSMFDEH ALLTKMFDEH DILTKMFDEH RILTKMMEEH KIIGNMINEH	60 VASSHKRKG KATTYERKG KATSYERKG EATSNERKE TASAHERKG LKSTHVRKAH	270 (PDFLDMVM (PDFLDVVM (PDFLDVVM (PDFLDVVM (PDFLDVIM (PDFLDVSLL)	280 AHHS.E ENG.D ENR.D ANR.D ANR.D ANQ.E ANRDGD
		Oxvgen	binding pocket n	notif				
GmF35H PhF35H_Hf1_ PhF35H_Hf2_ S1F35H STF35H SmF35H SmF35H	290 NSDGELSL NSEGERLST NSEGERLST NSEGERLST NSTGEKLTI HEEEIKLST	300 TNIKALLINE TNIKALLINE TNIKALLINE TNIKALLINE TNIKALLINE TDIKALLINE	310 TAGTDTSSSI TAGTDTSSSA TAGTDTSSSA TAGTDTSSSV TAGTDTSSSE	320 IEWSLAEMI IEWALAEMM IEWALAEMM IEWALAEMI IEWSLAEML VEWALAEMM	330 KKPSIMKKAH KNPAILKKAQ KNPAILKKAQ KNPKIFKKAQ KNPSILKRAH KNPSIQKRAH	340 EEMDQVIGRI AEMDQVIGRI GEMDQVIGRI QEMDQVIGRI EEMDQVIGRI EEMDQVIGRI	RRLKESDI RRLLESDI RRLLESDI RRLLESDI RRLLESDI RRLVESDI RRLLESDI	50 NLPYF NLPYL NLPYL KLPYL KLPYL
GmF3'5'H PhF3'5'H_Hf1 PhF3'5'H_Hf2_ SlF3'5'H VvF3'5'H SmF3'5'H	ExxR mo 360 CAICKETTR RAICKETFR RAICKETFR AICKETFR AICKESFR AICKEATR	tif 370 KHPSTPINLPF KHPSTPINLPF KHPSTPINLPF KHPSTPINLPF KHPSTPINLPF	380 ISSEPCOVNG ISSEPCIVDG USSEPCTVDG VSSEPCTVDG VSSEACVVDG ISSEACVVDG	390 <u>YYIPENTRI</u> YYIPKNTRI YYIPKNTRI YYIPKNTRI YYIPKNTRI YHIPKDTRI	400 NVNIWAIGRD SVNIWAIGRD SVNIWAIGRD SVNIWAIGRD SVNIWAIGRD	410 PDVWNNPLE PQVWENPLE PEVWENPLE PDVWENPLE PDVWESPEE PDVWEDPLH	PERF motif 4 2 0 MPERFISC NPERFISC TPERFISC TPERFISC NPDRFMSC	KNAKID RNSKID RNSKII KNAKIE RNEKID KNAGIE
GmF35H PhF35H_Hf1 PhF35H_Hf2 S1F35H VvF35H SmF35H SmF35H	H 430 PRGNDFELII PRGNDFELII PRGNDFELII PRGNDFELII PRGNDFELII PAGNHFELII	eme-binding don 440 FGAGRRICAO FGAGRRICAO FGAGRRICAO FGAGRRICAO FGAGRRICAO	450 TRMGIVIVHY TRMGIVMVEY TRMGIVMVEY TRMGIVVVEY SRMGIVIVEY	460 ILGTLVHSF ILGTLVHSF ILGTLVHSF ILGTLVHSF ILGTLVHSF ILGSLVHAF	470 DWKLPNGVRE DWKLPSEVIE DWKLPSEVIE DWKLPNNVID DWKMPDGV.E RWELPPGTAE	480 IDMEESFGLI INMEEAFGLI INMEEAFGLI INMEESFGLI INMDEAFGLI MDMEETFGLI	490 ALQKKVPLA ALQKAVPLE ALQKAVPLE ALQKAVPLE ALQKAVPLA	500 ALVTPR AMVTPR AMVTPR AMVTPR AMVTPR ATLTPR
GmF3'5'H PhF3'5'H_Hf1_ PhF3'5'H_Hf2_ S1F3'5'H VvF3'5'H SmF3'5'H	LNPSAYIS. LQLDVYVP. LPIDVYAPI LSLDVYRC. LHQSAYAV. LPSHCYAAS							

Figure S7. Amino acid sequence alignment of SmF3'5'H against Glycine max GmF3'5'H, Petunia hybrid PhF3'5'H (Hf1) and PhF3'5'H (Hf2), Solanum lycopersicum SlF3'5'H, Vitis vinifera VvF3'5'H. The P450-featured conserved motif, including the proline-rich "hinge" region, oxygen binding pocket motif, E-R-R triade consisting of the EXXR and PERF motif and heme binding domain are boxed and indicated in blue letters. The figure produced using the ESPript was server (http://espript.ibcp.fr/ESPript/ESPript/).



Figure S8. Amino acid sequence alignment of SmF3H1 and SmF3H2 against other plant F3Hs. The amino acid sequences of F3H from *S. miltiorrhiza* was aligned with the amino acid sequences from *Malus domestica* MdF3H, *Vitis vinifera* F3H, and *Petunia hybrid* PhF3H. The amino acid residues involved in ferrus iron binding and 2-oxoglutarate binding are indicated in blue and green box. Seven highly conserved residues with critical roles in determing the activity of F3H are indicated in pink box. The figure was produced using the ESPript server (http://espript.ibcp.fr/ESPript/ESPript/).



Figure S9. Amino acid sequence alignment of SmFLS1 and SmFLS2 against other plant FLSs. The amino acid sequences of FLS from *S. miltiorrhiza* was aligned with the amino acid sequences from *Malus domestica* MdFLS, *Vitis vinifera* FLS, *Petunia hybrid* PhFLS and *Solanum tuberosum* StFLS. The amino acid residues involved in ferrus iron binding and 2-oxoglutarate binding are indicated in blue and green box, respectively. Five potential substrate binding residues are indicated in pink box. The figure was produced using the ESPript server (http://espript.ibcp.fr/ESPript/).



Figure S10. Amino acid sequence alignment of SmANS against other plant ANSs. The amino acid sequences of ANS from *S. miltiorrhiza* was aligned with the amino acid sequences from *Malus domestica* MdANS, Pyrus communis PcANS, *Vitis vinifera* VvANS and *Prunus persica* PpANS. The amino acid residues involved in ferrus iron binding and 2-oxoglutarate binding are indicated in blue and green box, respectively. Five potential substrate binding residues are indicated in pink box. The figure was produced using the ESPript server (http://espript.ibcp.fr/ESPript/).



Figure S11. Amino acid sequence alignment of SmDFR against other plant DFRs. The amino acid sequences of DFR from *S. miltiorrhiza* was aligned with the amino acid sequences from *Gerbera hybrid* GhyDFR, *Petunia hybrida* PhDFR, *Arabidopsis thaliana* AtDFR, *Vitis vinifera* VvDFR and *Malus domestica* DFR. The conserved catalytic triad site, S129, Y164 and K168 are boxed in dark blue and indicated in blue stars. NADPH-binding motif is boxed in light blue. The substrate binding region is indicated in green box. The amino acid residue at the 134th position is particularly important for the substrate specificity. It has been indicated in pink box. The figure was produced using the ESPript server (http://espript.ibcp.fr/ESPript/).