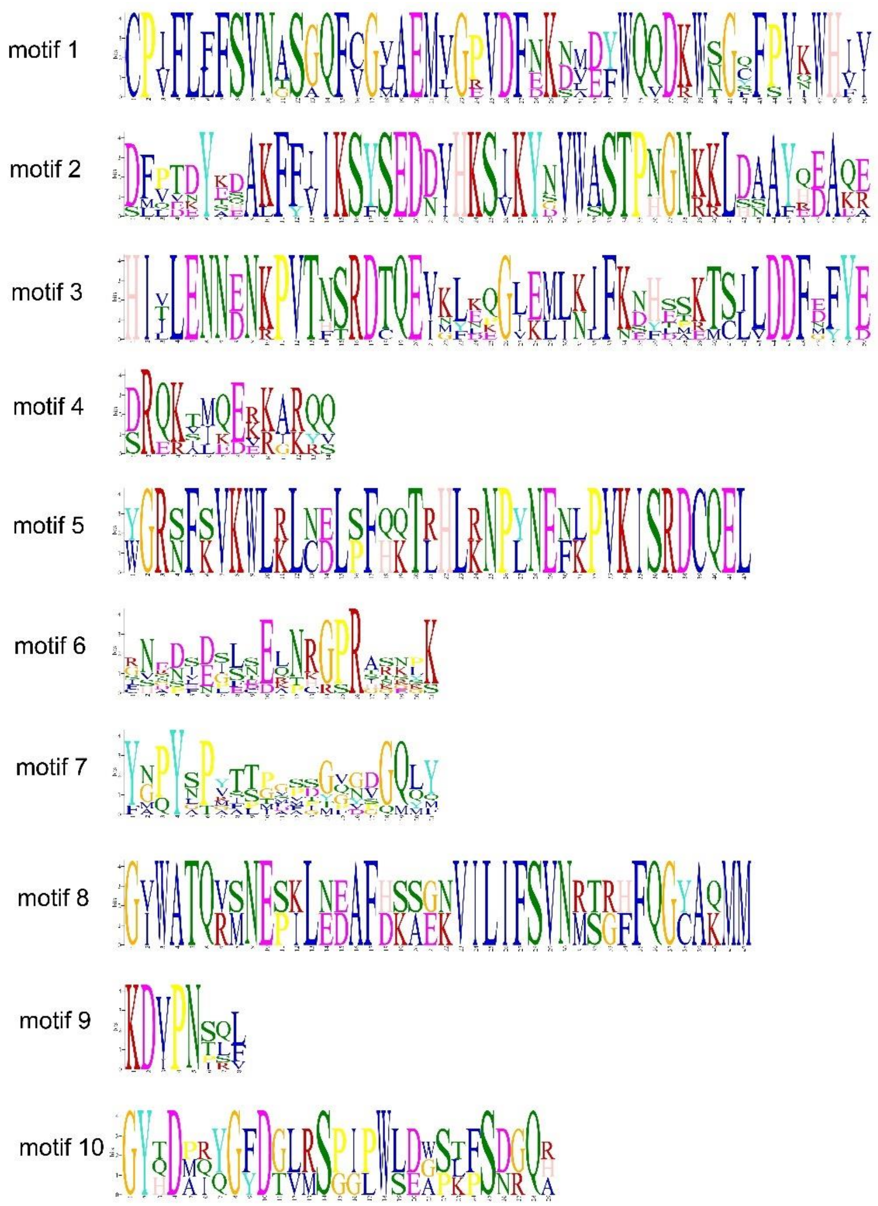
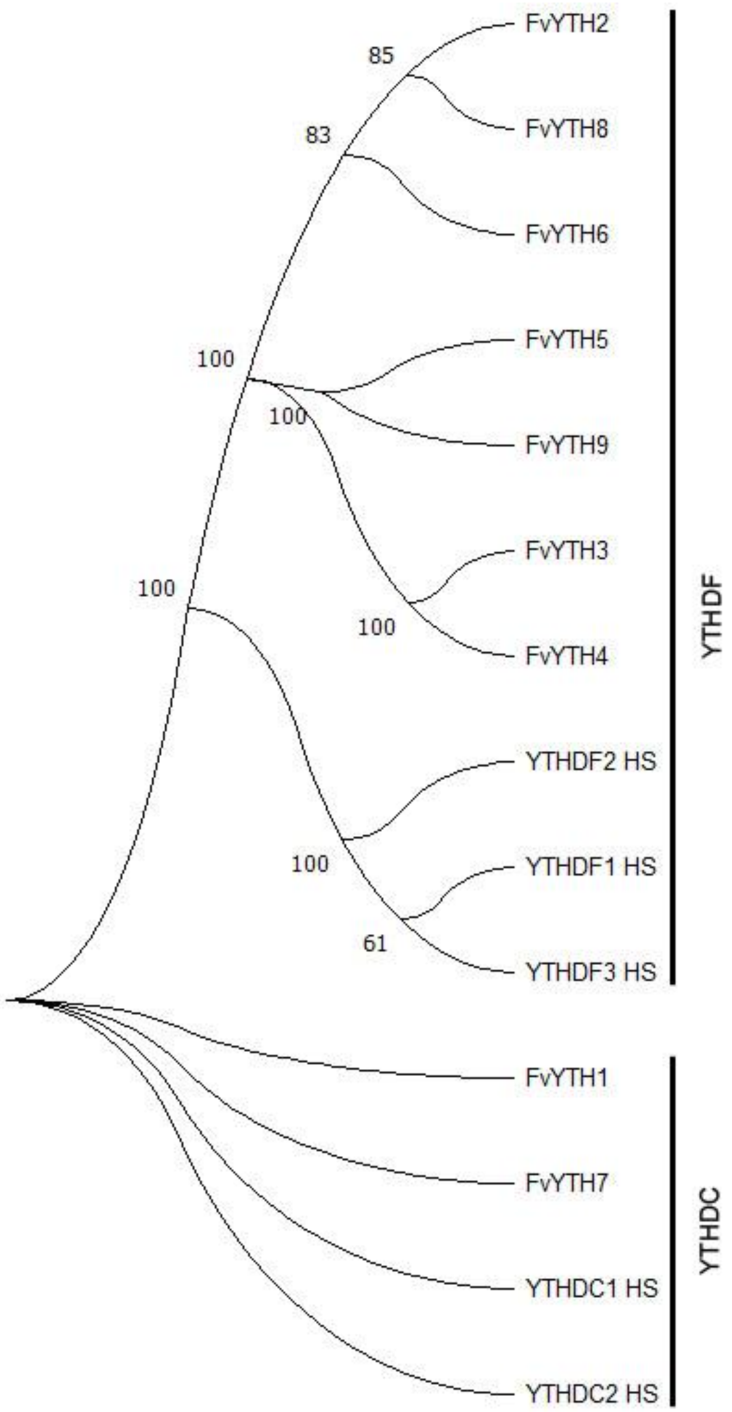
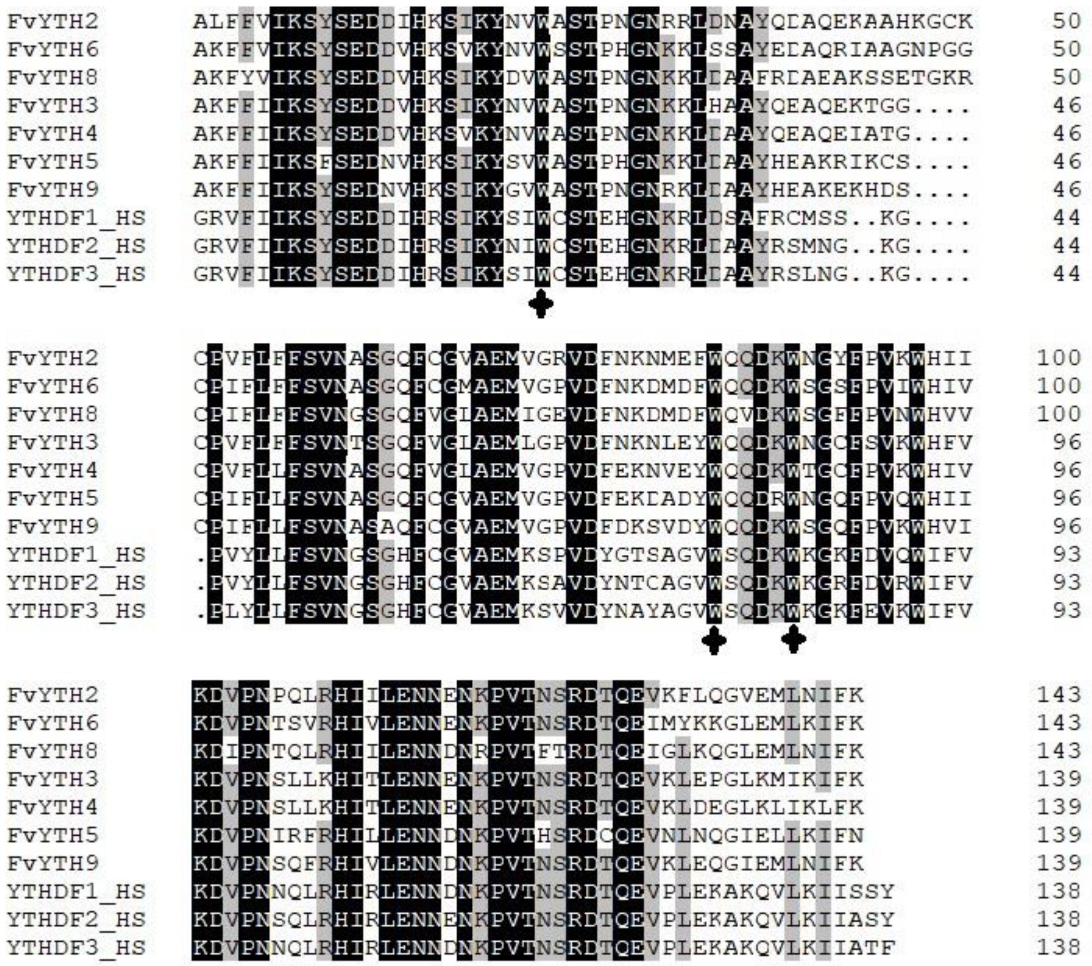
Supplementary Informations



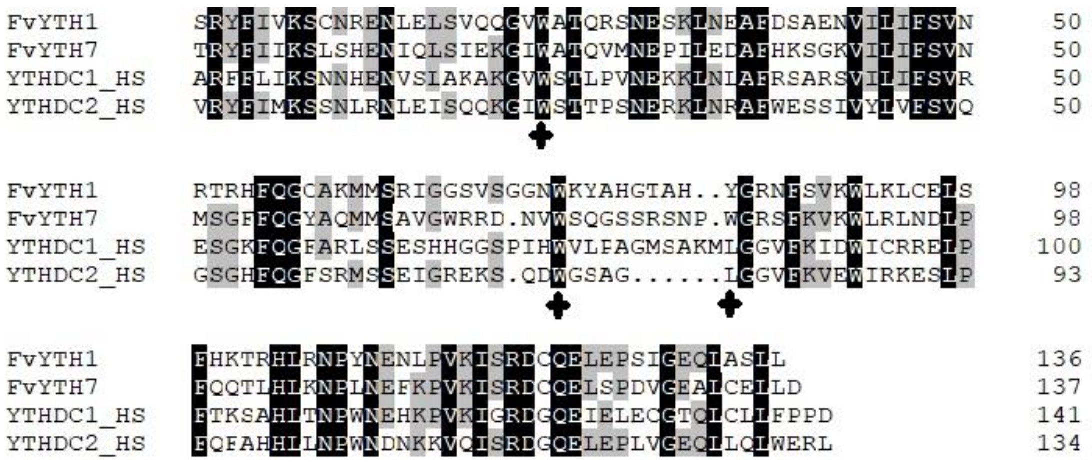
Supplementary Figure S1. Showing the logos of ten motifs in FvYTH proteins. The X axis of sequence logos refers to the amino acid with the highest frequency and the Y axis represents the relative frequency of the corresponding amino acid.



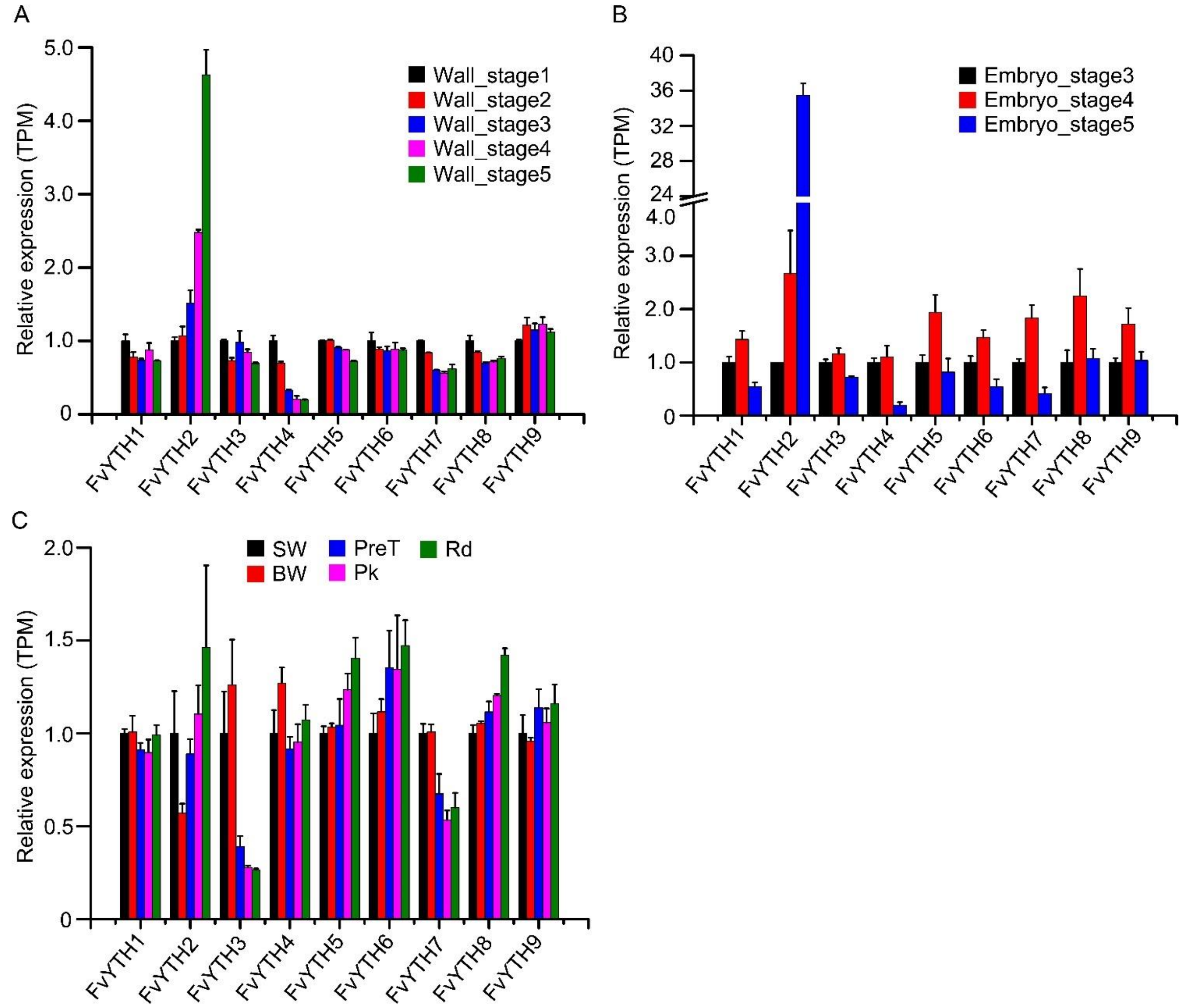
Supplementary Figure S2. Phylogenetic analysis of YTHs in strawberry and humans. The sequences of YTH proteins from strawberry and humans were used to constructed phylogenetic tree by NJ method, with 1000 bootstrap replications. HS represents humans.



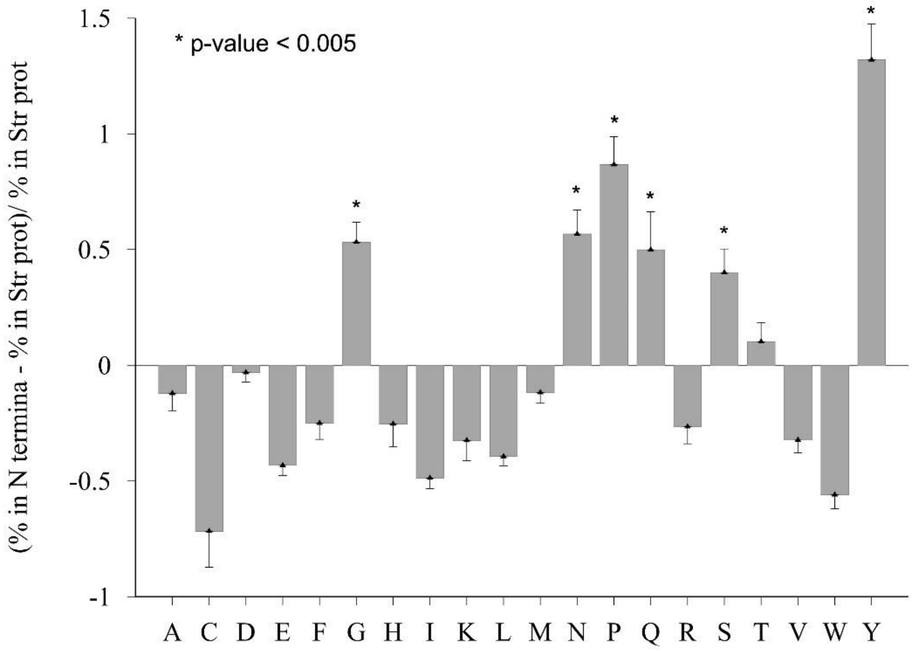
Supplementary Figure S3. Sequence alignments YTHDFs in strawberry and humans. The conserved amino acids involved in cage formation are indicated with asterisks.



Supplementary Figure S4. Sequence alignments YTHDCs in strawberry and humans. The conserved amino acids involved in cage formation are indicated with asterisks.



Supplementary Figure S5. The expression trends of *FvYTH* genes in different development stages. The expression trends of *FvYTH* genes in different development stages of carpel wall (A), embryo (B), and fruit (C). The TPM value of the selected first stage was normalized as 1. SW: small white stage; BW: big white stage; PreT: pre-turning stage; Pk: pink stage; Rd: red stage.



Supplementary Figure S6. The bias in composition of the N terminal of YTH proteins compared with all strawberry proteins. The y axis represents the proportion of each amino acid in the N-terminal region compared with a data base of all Strawberry proteins. The richer amino acids are statistically (P<0.005) overrepresented in this region. Statistical significance associated with a specific enrichment or depletion is estimated using the two-sample t test including a Bonferroni correction according to the Composition Profiler website (http://www.cprofiler.org (accessed on 22/2/2023)).

Supplementary Table S1. The identification of *FvYTH* genes in strawberry.

Target	Query Name	Accession	E-value	score
FvH4_3g09980	YTH	PF04146.15	5.10E-47	161.7
FvH4_3g13840	YTH	PF04146.15	4.70E-39	135.8
FvH4_3g45840	YTH	PF04146.15	1.90E-39	137.1
FvH4_3g45841	YTH	PF04146.15	8.40E-41	141.5
FvH4_4g00190	YTH	PF04146.15	2.50E-40	140
FvH4_4g21030	YTH	PF04146.15	9.60E-40	138
FvH4_5g01140	YTH	PF04146.15	8.90E-50	170.7
FvH4_5g30420	YTH	PF04146.15	2.80E-37	130
FvH4_6g36470	YTH	PF04146.15	4.20E-40	139.2

Supplementary Table S2. The properties of YTH proteins.

Gene Name	Gene ID	LOCALIZER	Plant-mPLoc	Instability Index	Grand Average of Hydropathicity（GRAVY)
FvYTH1	FvH4_3g09980	Y (RRSRHGEGKKKRRDS)	Nucleus	56.69	-0.964
FvYTH2	FvH4_3g13840	Y (KRIR)	Nucleus	40.8	-0.733
FvYTH3	FvH4_3g45840	-	Nucleus	34.12	-0.741
FvYTH4	FvH4_3g45841	Y (AKRQIRKKK)	Nucleus	35.51	-0.732
FvYTH5	FvH4_4g00190	Y (KKLDAAYHEAKRIKC)	Nucleus	49.96	-0.672
FvYTH6	FvH4_4g21030	-	Nucleus	32.59	-0.593
FvYTH7	FvH4_5g01140	Y (FKVK)	Nucleus	59.27	-0.853
FvYTH8	FvH4_5g30420	-	Nucleus	31.99	-0.696
FvYTH9	FvH4_6g36470	-	Nucleus	41.52	-0.685

Supplementary Table S3. The synteny relationships between forest strawberry and *Arabidopsis*.

chromosome	geneid		chromosome	gene name
At--Chr1	AT1G55500	==	Str--Fvb3	FvYTH3
At--Chr1	AT1G30460	==	Str--Fvb3	FvYTH1
At--Chr1	AT1G79270	==	Str--Fvb3	FvYTH2
At--Chr1	AT1G48110	==	Str--Fvb4	FvYTH6
At--Chr3	AT3G13460	==	Str--Fvb3	FvYTH3
At--Chr3	AT3G17330	==	Str--Fvb4	FvYTH6
At--Chr3	AT3G13060	==	Str--Fvb6	FvYTH9
At--Chr4	AT4G11970	==	Str--Fvb5	FvYTH7

Supplementary Table S4. The sequences of YTH domain from strawberry, rice, *Arabidopsis.*

Name	Sequences
AtECT1	AKFFVIKSYSEDDVHNCIKYGAWSSTPTGNKKLNAAYYEAKENSQECPVYLLFSVNASGQFVGLAEMVGPVDFNKTMEYWQQDK WIGCFPVKWHIIKDIPNSLLRHITLANNENKPVTNSRDTQEVNLEHGTKIIKIFK
AtECT2	AMFFIIKSYSEDDVHKSIKYNVWASTPNGNKKLAAAYQEAQQKAGGCPIFLFFSVNASGQFVGLAEMTGPVDFNTNVEYWQQDKW TGSFPLKWHIVKDVPNSLLKHITLENNENKPVTNSRDTQEVKLEQGLKIVKIFK
AtECT3	AKFYVIKSYSEDDIHKSIKYSVWSSTPNGNKKLDASYNEAKQKSDGCPVFLLFSVNTSGQFVGLAEMVGPVDFNKTVEYWQQDKW IGCFPVKWHFVKDIPNSSLRHITLENNENKPVTNSRDTQEVKLEQGIKVIKIFK
AtECT4	AKFFIIKSYSEDDVHKSIKYNVWASTPNGNKKLDAAYQEAQQKSSGCPVFLFFSVNASGQFIGLAEMKGPVDFNKNIEYWQQDKW TGSFPLKWHILKDVPNSLLKHITLEYNENKPVTNSRDTQEVKLEQGLKVVKIFK
AtECT5	AKLFIIKSYSEDNVHKSIKYNVWASTPNGNKKLDAAYREAKDEKEPCPLFLLFSVNASSQFCGVAEMVGPVDFEKSVDYWQQDKW SGQFPVKWHIIKDVPNSQFRHIILENNDNKPVTNSRDTQEVKLEQGIEMLKIFK
AtECT6	ARFFVIKSYSEDDVHKSIKYGVWSSTLNGNKKLQSVYEDAQRIATEKSRECPIFLFFSVNSSGLFCGVAEMTGPVSFDRDMDFWQ QDKWSGSFPVKWHIIKDVPNSYFRHIILHNNENKPVTNSRDTQEIILKQGLEVLKLFK
AtECT7	AKFFVIKSYSEDDVHKSIKYNVWSSTLHGNKKLQSAYEDAQRIATEKSCECPIFLFFSVNASGLFCGMAEMTGPVSFDKDMDFWQ QDKWSGSFPVKWHIIKDVPNSYFRHIILQNNENKPVTNSRDTQEIMLKQGLEVLKIFK
AtECT8	AIFFVIKSYSEDDIHKSIKYNVWSSTLNGNKKLDSAYQESQKKAADKSGKCPVFLFFSVNASGQFCGVAEMIGRVDYEKSMEFWQ QDKWTGYFPVKWHIIKDVPNPQLRHIILENNENKPVTNSRDTQEVRLPQGNEVLNIFK
AtECT9	AKFFVIKSYSEDNVHKSIKHCVWASTKNGNKKLDAAYREAKKKDVACPVFLLFSVNASSQFCGVAEMVGPVDFNTSVEYWQQDR WSGHFPVQWLIVKDVPNSLFRHIIIESNDNKPVTNSRDTQEVGLEKGIEMLDIFISCEMRSSILDDFNFYEERQIAIQDRKARQRAV
AtECT10	AKFFIVKSFSEDNVHRSIKYNVWASTPHGNKKLDTAYRDAEKMGGKCPIFLFFSVNASGQFCGVSEMVGPVDFEKDAGYWQQD RWSGQFPVKWHIVKDIPNNRFCHILLQNNDNKPVTHSRDSQEVKLRQGIEMLRIFK
AtECT11	AKFFVIKSYSEDDVHKSIKYSVWSSTINGNKKLDAAFRDAETKTLEDGKKRPIFLFFSVNASRQFVGLAEMVGYVDFNKDLDFWQ VDKWSGFFPVEWHVVKDIPNWELRHIILDNNEDKPVTHTRDTHEIKLKEGLQMLSIFK
AtECT12	TRYFIIKSLNYDNIQVSVEKGIWATQVMNEPILEGAFHKSGRVILIFSVNMSGFFQGYAEMLSPVGWRRDQIWSQGGGKNNPWG RSFKVKWLRLSELPFQKTLHLKNPLNDYKPVKISRDCQELPEDIGEALCELLD
AtCPSF30	RYFVVKSNNRENFELSVQQGVWATQRSNEAKLNEAFDSVENVILIFSVNRTRHFQGCAKMTSRIGGYIGGGNWKHEHGTAQYGR NFSVKWLKLCELSFHKTRNLRNPYNENLPVKISRDCQELEPSVGEQLAS LL
OsECT1	ARFFIIKSYSEDNVHKSIKYGVWASTTNGNKKLDSAYREAKEKEEHCPIFLLFSVNASAQFCGVAEMIGPVDFEKSVDYWQQDKW TGQFPVKWHIVKDVPNNLFRHIILENNDNKPVTNSRDTQEVKLEQGMEMLKIFK
OsECT2	RYFIVKSCNRENLEISVQQGIWATQRSNEAKLNEAFESIENVILIFSINRTRNFQGCAKMTSRIGGYIGGGNWKSAHGTAHYGRNF SIQWLKLCELSFQKTHHLRNPYNDNLPVKISRDCQELEPFIGEQLASLL
OsECT3	AKFFVIKSYTEDHVHRSIKYNVWASTASGNRKLDSAYRLAKEKEDYCPIFLFFSVNGSGQFCGVAEMIGPVDFDKSVDYWQQDK

	WSGQFPVKWHIIKDVPNNLLRHIILENNDNKPVTNSRDTQEVKLEHGLQMLTIFK
OsECT4	AKFFVIKSYTEDHVHRSIKYNVWASTASGNRKLDSAYRLAKEKEDYCPIFLFFSVNGSGQFCGVAEMIGPVDFDKSVDYWQQDK WSGQFPVKWHIIKDVPNNLLRHIILENNDNKPVTNSRDTQEVKLEHGLQMLTIFK
OsECT5	AKFFMIKSYSEDDIHKGIKYNVWASTPHGNNKLDAAFREAQILIKEKGKKCPVFLFFSVNSSGQFVGLAEILGPVDFKKTMDFWKL DRWNGFFPVTWHIIKDIPNRLFKHITLENNDNRIVTFSRDTQEIGLLQGLKMLKIFK
OsECT6	AKFFMIKSYSEDDVHKGIKYNVWASTPNGNNKLDAAFHEAQILMKEQGKRCPIFLFFSVNTSGQFVGLAEMLGPVDFKKTMDFW QQDKWNGFFPVMWHIIKDIPNRFFKHITLENNEGKVVTFSRDTQEIGLPQGLEMLKIFK VMWHIIKDIPNRFFKHITLENNEGKVVTFSRDTQEIGLPQGLEMLKIFK
OsECT7	AKFFIIKSYSEDDVHKSIKYNVWASTSNGNKKLDAAYQEAKEKSSDSSVFLLFSVNASGQFVGLAEMVGRVDFNKTLEHWQQDK WTGCFPVKWHIVKDVPNSLLKHIILENNENKPVTNCRDTHEVKLEPGLQVLKIFK
OsECT8	AKFFVIKSYSEDDVHKSIKYNVWSSTPNGNKRLDAAYSDVQGRAVGKCPIFLFFSVNASGQFCGVAEMVGPVDFHKDMDFWQQ DKWSGSFPVKWHLVKDVPNSTFRHIILENNENKPVTNSRDTQEIPFKSGTNMLKLFK
OsECT9	SNDLRVDYPFAKFFVIKSIGEDDVHKSIKYGVWSSSSSGNSKLDIAFKDANRIAKRNSTKCPVFLFFSVNGSGLFCGMAEMVGPV DFHKDMDFWCQDKWTGSFPNNENKPVTHSRDTQEIPYVPGISMLKILK
OsECT10	AKFFVIKSYSEDDIHKSIKYNVWASTTNGNKKLDAAYQEAQAKSSKCPIFLFFSVNTSGQFVGVAEMTGAVDFEKTLEYWQQDK WNGSLSLKWHIVKDVPNNILKHIILENNENKPVTNSRDTQEVNLDQGIQMLKIFK
OsECT11	ALFFVIKSYSEDDIHKSIKYNVWASTPNGNKRLDNAFKLAQERVAEKGTKCPMFLFFSVNASGQFCGVAEMVGPVDFNRNMNF WQQDKWNGFFPVKWHIIKDVPNPQFRHIILENNENKPVTNSRDTQEVKFPQGSEMLNIFK
OsECT12	AKFFVIKSYSEDDVHKSIKYNVWASTPNGNKKLDAGYREAQEKSSECPVFLFFSVNTSGQFVGVAEMVGPVDFEKTVDYWQQ DKWNGCFPIKWHVVKDVPNNILKHITLDNNDNKPVTNSRDTQEVKLEQGLEMLKIFK
OsECT13	ARFFIIKSYSEDNVHKSIKYGVWASTTNGNKKLDSAYREAKEKEEHCPIFLLFSVNASAQFCGVAEMIGPVDFEKSVDYWQQDKW TGQFPVKWHIVKDVPNNLFRHIILENNDNKPVTNSRDTQEVKLEQGMEMLKIFK
FvYTH1	SRYFIVKSCNRENLELSVQQGVWATQRSNESKLNEAFDSAENVILIFSVNRTRHFQGCAKMMSRIGGSVSGGNWKYAHGTAHY GRNFSVKWLKLCELSFHKTRHLRNPYNENLPVKISRDCQELEPSIGEQLASLL
FvYTH2	ALFFVIKSYSEDDIHKSIKYNVWASTPNGNRRLDNAYQDAQEKAAHKGCKCPVFLFFSVNASGQFCGVAEMVGRVDFNKNMEF WQQDKWNGYFPVKWHIIKDVPNPQLRHIILENNENKPVTNSRDTQEVKFLQGVEMLNIFK
FvYTH3	AKFFIIKSYSEDDVHKSIKYNVWASTPNGNKKLHAAYQEAQEKTGGCPVFLFFSVNTSGQFVGLAEMLGPVDFNKNLEYWQQD KWNGCFSVKWHFVKDVPNSLLKHITLENNENKPVTNSRDTQEVKLEPGLKMIKIFK
FvYTH4	AKFFIIKSYSEDDVHKSVKYNVWASTPNGNKKLDAAYQEAQEIATGCPVFLLFSVNASGQFVGLAEMVGPVDFEKNVEYWQQD KWTGCFPVKWHIVKDVPNSLLKHITLENNENKPVTNSRDTQEVKLDEGLKLIKLFK
FvYTH5	AKFFIIKSFSEDNVHKSIKYSVWASTPHGNKKLDAAYHEAKRIKCSCPIFLLFSVNASGQFCGVAEMVGPVDFEKDADYWQQDR WNGQFPVQWHIIKDVPNIRFRHILLENNDNKPVTHSRDCQEVNLNQGIELLKIFN
FvYTH6	AKFFVIKSYSEDDVHKSVKYNVWSSTPHGNKKLSSAYEDAQRIAAGNPGGCPIFLFFSVNASGQFCGMAEMVGPVDFNKDMDF

	WQQDKWSGSFPVIWHIVKDVPNTSVRHIVLENNENKPVTNSRDTQEIMYKKGLEMLKIFK
FvYTH7	TRYFIIKSLSHENIQLSIEKGIWATQVMNEPILEDAFHKSGKVILIFSVNMSGFFQGYAQMMSAVGWRRDNVWSQGSSRSNPWG RSFKVKWLRLNDLPFQQTLHLKNPLNEFKPVKISRDCQELSPDVGEALCELLD
FvYTH8	AKFYVIKSYSEDDVHKSIKYDVWASTPNGNKKLDAAFRDAEAKSSETGKRCPIFLFFSVNGSGQFVGLAEMIGEVDFNKDMDFW QVDKWSGFFPVNWHVVKDIPNTQLRHIILENNDNRPVTFTRDTQEIGLKQGLEMLNIFK
FvYTH9	AKFFIIKSYSEDNVHKSIKYGVWASTPNGNRKLDAAYHEAKEKHDSCPIFLLFSVNASAQFCGVAEMVGPVDFDKSVDYWQQDK WSGQFPVKWHVIKDVPNSQFRHIVLENNDNKPVTNSRDTQEVKLEQGIEMLNIFK

Note: At:*Arabidopsis*; Os: Oryza sativa L.; Fv: *Fragaria vesca L*.

Supplementary Table S5. The identification of *cis*-elements in the promoters of *FvYTH* genes.

Response Types	Responses involved	Cis-elements	FvYTH 1	FvYTH 2	FvYTH 3	FvYTH 4	FvYTH 5	FvYTH 6	FvYTH 7	FvYTH 8	FvYTH 9
hormone	auxin-responsive element	AuxRR-core/ TGA-element	0	0	0	0	1	2	1	0	0
	salicylic acid responsiveness	TCA element	1	2	0	0	0	1	4	0	2
	MeJA-responsiveness	TGACG-motif	1	0	2	0	0	2	1	8	2
	abscisic acid responsiveness	ABRE	2	2	3	5	0	3	4	4	3
	gibberellin-responsiveness	P-box/TATC-box	0	3	1	1	0	2	1	0	1
	ethylene-responsive element	ERE	0	0	1	1	1	0	2	0	0
	total		4	7	7	7	2	10	13	12	8
stress response	low-temperature responsiveness	LTR	0	0	0	2	2	1	0	1	0
	anaerobic induction	ARE	2	5	3	0	2	0	3	2	4
	activation by heat shock, osmotic stress, low pH, nutrient starvation	STRE	3	2	0	6	1	2	5	2	3
	wound-responsive element	WUN-motif	1	0	2	1	0	0	2	2	0
	dehydration- responsive element	DRE	2	0	0	0	1	0	0	2	0
	wound inducibility	WRE3	1	0	0	0	1	0	0	1	0
	wounding and pathogen responsievness	W box	2	0	1	2	0	1	2	0	1
	defense and stress responsiveness	TC-rich repeats	0	1	0	0	1	0	1	0	1
	stress-inducible	TCA	0	0	1	1	2	1	0	0	0
	total		11	8	7	12	10	5	13	10	9
development	meristem expression	CAT-box	2	0	1	0	2	1	1	0	0
	endosperm expression	GCN4_motif	1	0	0	0	0	0	0	0	0
	circadian control	circadian	0	2	0	0	0	0	0	0	0
	zein metabolism regulation	O2-site	0	2	1	0	0	0	0	0	0
	meristem specific activation	CCGTCC-box	0	1	0	0	1	0	0	1	0

	seed-specific regulation	RY-element	0	0	1	0	0	0	0	0	0
	palisade mesophyll cells	HD-Zip 1	0	0	0	0	1	0	0	0	0
	total		3	5	3	0	4	1	1	1	0
transcription factors binding site	Myc-binding site	MYC	4	1	3	4	1	2	4	0	6
	Myb-binding site	MYB	2	7	4	5	6	3	3	2	3
	ATBP-1 binding site	AT-rich element	0	0	1	1	1	0	0	0	0
	MYB binding site involved in drought-inducibility	MBS	1	0	0	1	0	0	0	1	1
	MYB binding site involved in light responsiveness	MRE	1	0	0	0	1	0	0	2	0
	MYB binding site involved in flavonoid biosynthetic genes regulation	MBSI	0	0	0	0	0	1	0	0	0
	total		8	8	8	11	9	6	7	5	10
light	light responsiveness		6	10	9	5	3	9	11	13	12

Supplementary Table S6. The CDS sequences of *FvYTH* genes.

Gene ID	Gene Name	Sequences
FvH4_3g09980	FvYTH1	ATGGAGGACCCCGACGGAGTCCTCAACTTCGACTTCGAGGGCGGCCTCGACTCCGCCGCCGTCTCCGCGC CCACCCACACCGGCCTGGCCTCCAGCGCCCCGATCCAGTCCGACTCGTTCGCCTCCCAGCCCAAAAACCA GGCCGCCCCGGCGCCGCAGCCCGACCCAAATGTCAACCCGTCGGGGCGGAAGAGCTTCCGGCAAACGGTG TGTCGTCACTGGCTCCGGAGCCTCTGTATGAAAGGCGAGGCCTGCGGGTTCCTTCATCAATACGACAAGT CGCGGATGCCGGTGTGCCGGTTCTTCCGTATGTACGGCGAGTGTAGGGAGCAGGATTGCGTGTATAAGCA TACCAACGAGGACATCAAGGAGTGTAATATGTACAAGTTAGGTTTTTGTCCAAATGGTCCTGATTGCCGG TATAGACATGCAAAGCTTCCTGGACCTCCACCCCCTGTGGAAGAAGTCCTTCAGAAGATCCAGCATTTGA ATTCGTACAATTACAACAACTCAAATAAGTTCTCCCAACCACGGAATGGTGGTTTTCCCCAACAACATGA TAGATCTCAGCCCGCACAAGTCACCAATTCATTCAATCAAGTGGTTGTAAGACCTTCAGCAGCAGAGTCT GCTAATGTCCAGCAGCCACAGCAATTTCAGCAAACCCAACAACCGGTTGCCCAGACTCAGGCACAAAGTG TTCCCAATGGCCTGGCTAGTCAGGCAAATAGAGCCGCACTGCCCTTGCCTCAAGGAATATCTAGGTATTT TATTGTTAAAAGTTGCAACCGTGAAAATTTGGAATTATCCGTACAACAAGGAGTTTGGGCAACTCAAAGG AGCAATGAATCCAAACTCAATGAAGCTTTCGACTCTGCAGAAAATGTCATATTAATTTTCTCAGTCAACC GGACTCGACATTTTCAGGGTTGTGCAAAGATGATGTCCAGAATTGGTGGGTCTGTTAGTGGAGGGAACTG GAAATATGCACATGGAACTGCACATTATGGCCGTAATTTCTCTGTCAAATGGTTAAAGCTATGTGAACTT TCCTTCCACAAAACTCGTCACTTGAGGAACCCATACAATGAGAACTTACCAGTGAAGATAAGTAGAGATT GTCAAGAGCTAGAGCCCTCCATCGGTGAGCAGTTGGCATCCTTGCTTTATCTTGAACCAGATAGTGAACT AATGGCAATCTCCATTGCAGCAGAGTCAAAACGAGAAGAAGAAAAAGCAAAGGGAGTCAATCCAGAGAAT GGTGGTGAGAACCCAGACATTGTCCCATTTGAGGACAATGAAGAAGAGGAAGAGGAAGAAAGTGACGACG AGGAAGACTATCAAGTTCCTGGTGGAGCAATTGAGAACAGAGGAAGGGGTAGAGTCATGTGGCCCCCTCA TATGCCACTAGGAGGAAGGGGTGGCAGACCTATGCCTGGGATGCAGGGGTTCCCTGGAATGATGGGTCCT GATGCAATGCCGTATGGACCAGTTACACCTGATGGATTTGTTATGCCCAATCCTTTTGGTATGGGCGGCC CTCGGGGTTTCAATCCATATGGTCCTAGGTTTTCCGGTGATTTTGGTGGGCCCAATCCTGGCATGATGTT TCGTGGGCGGCCTCCACAACCTGGTGGTATGTTTCCACCTGGTCCTTATGGGATGATGATGGGTCCTGGA CGTGGACCATTTATGGGAGGGATGGGGGTTGGAGGTAATAATCCAGCCCGAGGTGGTCGTCCAGGTGGTA TGCCACCAATGTTTCCCCCACACCCACCATCTCAAAACAATAACCGGTTGCAGAAGAGAGATCCAAGGGG ATCGGGCAATGATCGGAATGAGAGGTATAGTGCAGGATCAGGTCATGGCAAAGAAATGCAGGCTGGTGGA CCAGATGATGAGAACCATTATCAGCATTCATCAAAATCGTACCAGGAAGATTATGGTGCTGGGAACAATG GTAGGAATGATGACAGTGAAAGTGAAGACGAAGCACCGAGGCGGTCAAGGCATGGAGAGGGAAAGAAGAA ACGGCGAGACTCGGAAGGAGATGCTACCTCTGAGCACTAG
FvH4_3g13840	FvYTH2	ATGGCTGCTCCTCAATTTGAACAACACAATCCTCATCCTCATCAGACAACTCCCAAACAAGAAGAAGGGA AAGAAAAGGAAGCAAAACCAGATATTCAATCCACAGAGTCCTTCCAATCCAATCTGGCTCTTAGCAAGGA TGGAAGCTCATCTGATGCAGCATCATGTATATCAACTGCAGGAGATACAACTGCTAGTGTGAAAAAAGGT GATGCAGATGTAGATGCAGATTATGAATCCATGGCTTCCTATCCAACCACCGCCTATTATGGATACAGCT ATCCAGGTAGTTATGATATGGAAAACCAAGGATACTATGTCGGTGGAAATACTGGGATGGAAGCTCAATA CCCTGTCATGCAAGCAGATAATGGCTCTTTTGTCTACTTGATGCCAGGATTTCAGCCTGGCTATGATCCT

TACATGCAGTACCTGCCCATGACTACAATCAGTAGTGATGGACAATATGTTGGTCAACAGATGTATTCAT
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FvH4_3g45840 FvYTH3

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