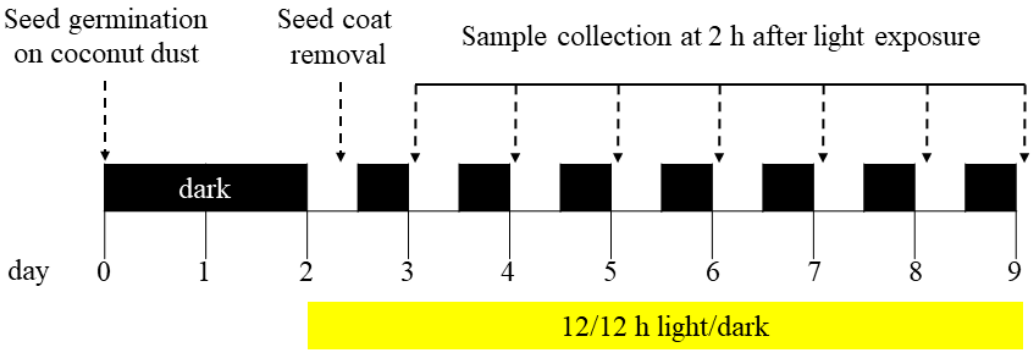
Supplementary Material

A



B

Supplementary FIGURE S1 | Sunflower sprouts used in this study. Schematic diagram of sampling in this study **(A)** and the representative sunflower sprouts were imaged at different timepoints (day 3 to day 9, from left to right respectively) during their germination period **(B)**.

```
SlHQT         -MG--SEKMMKINIKESTLVKPSKPTPT--KRIWSSNLDLIVGRIHLLTVYFYKPNGSSN   55
CcsHQT1       ---------MELTVKESLMVKPSKPTPN--QRLWNSNLDLVVGRIHILTVYFYRPNGSSN   49
CcsHQT2       -MGSDQKMMMNIDIMKSSIVPPSELIADCPKQLWTSNLDLVVGRIHILTVYFYRPNGSSK   59
CcsHQT3       ---------MNININKHSSFVQPSQPTPS--STIWTSNLDLVVGRIHILTVYFYRPNGASN   49
CcsHCT1       ---------MKIEVRESTMVRPAEETPR--INLWNSNVDLVVPNFHTPSVYFYRPNGAAN   49
CcsHCT2       ---------MKIAVRESTMVRPAEETPM--IKLWNSNVDLVVPNFHTPSVYFYRPTGAGN   49
CiHQT1        MTNGAGSEKMKVTVKESVIVKPSKTTPI--QRLWNSNIDLLVGRIHLLTIYFYRPNGSSD   58
CiHQT2        -MRSDQKMMMNINLKKSSIIPPSETIAECPKQLWTSNLDLVVGRIHILTVYFYRPNGSAN   59
CiHQT3        -MGSD-HKTMKININKQSSLVQPSKPTIPSNKKLWTSNLDLVVGRIHILTVYFYRPNGCSN   58
CiHCT1        ---------MKIEVRESTMVRPAEETPK--INLWNSNVDLVVPNFHTPSVYFYRPNGATN   49
CiHCT2        ---------MKIAIRESTMVRPAEETPR--IKLWNSNVDLVVPNFHTPSVYFYRPTGATN   49
HaHQT1        ---------MNLTVKQSLTIKPSKTTPC--HTIWCSNLDLIVGRIHIQTVYFYRPNGSSN   49
HaHQT2        -MKTDQTKPMNITITKSSIVPPSETINGSSNHIWTSNLDLVVGRIHILTVYFYRPNGSNN   59
HaHQT3        -MGTV-QKTLNININKQTTFVQPSKPTQASTKQLWTSNLDLVVGRIHILTVYFYRPIVCSN   58
HaHCT1        ---------MKIEVRESTMVKPAEETPK--INLWNSNVDLVVPNFHTPSVYFYRPNGAPD   49
HaHCT2        ---------MKITVTNSSMVRPAEETPR--IKLWNSNVDLVVPNFHTPSVYFYRPNGGSN   49
                      ::: : .:  : *::        :* **:**:* .:*  ::***:*    .

SlHQT         FFDNKVIKEALSNVLVSFYPMAGRLGRDEQGRIEVNCNGEGVLFVEAESDSCVDDFGDFT   115
CcsHQT1       FFDSGVLKKALADVLVSFFPMAGRLGNDGDGRVEINCNGEGVLFVEAEADCSIDDFGEIT   109
CcsHQT2       FFDPNVMKKALADVLVSFYPMAGRLGRDETDRIVINCNNEGVLFVEAESDSTLDDFGELK   119
CcsHQT3       FFDADVMKKALADVLVSFYPMAGRISRDRNGRLEINCNGEGVLFVEAELDSTLDDFGEFT   109
CcsHCT1       FFDPKVMKDALSRALVPFYPMGGRLKRDEDGRIEIDCQGQGVLFVEAESDGVIDDFGDFA   109
CcsHCT2       FFDPTVMKDALSRVLVPFYPMGGRLSRDEDGRIEIDCRGQGVLFVEAESDGMIDDFGDFA   109
CiHQT1        FFDSGVLKKALSDVLVSFFPMAGRLGKDGDGRVEINCNAEGVLFVEAEADCRIDDFGEIT   118
CiHQT2        FFDPNVMKKALADVLVSFYPMAGRLDRDESGRIVINCNGEGVLFVEAESDSTLDDFGEFT   119
CiHQT3        FFDPVVMKKALADVIVSFYPFAGRLSRDQNGRLEINCNGEGVLFVEAESDSTLDDFGEFT   118
CiHCT1        FFDPKVMKDALSKALVPFYPMGGRLKRDEDGRIEIDCQGQGVLFVEAESDGMVDDFGDFA   109
CiHCT2        FFDAKVMKDALSRALVPFYPMGGRLKRDEDGRIEIDCQGQGVLFVEAESDGVIDDYGDFA   109
HaHQT1        FFDSEVLKAALADVLVSFYPMSGRLGKDGDGRIEIVCNGEGVLFVEAEADCCIDDFGEIT   109
HaHQT2        YFDPNVMKQALADVLVPFYPMAGRLGRDESGRIVINCNGEGALFVEAESDSCLDDFGEFT   119
HaHQT3        FFDPLVMKKALADVLVTFYPMAGRMGKDQNGKVVINCNDEGVLFVEAESDSTLDDFGEFT   118
HaHCT1        FFDPKVMKDALSRALVPFYPMGGRLKRDEDGRIEIDCRGQGVLFVEAESDGVVDDFGDFA   109
HaHCT2        FFDPKVMIKALSKALVPFYPMGGRLTRDEDGRIEIDCQGQGVLFVEAESDGVIDDFGDFA   109
              :**  *:  **: .:* *:*:.**: .*  .:: : *. :*.****** *  :**:*::

SlHQT         PSLELRKLIPSVETSGDISTFPLVIF------QITRFKCGGVALGGGVFHTLSDGLSSIH   169
CcsHQT1       PSPELRKLAPTVDYSDQVSSYPLCIT------QVTRFNCGGVSLGCGLHHTLSDGLSSLH   163
CcsHQT2       PSPVFRQLTPSVDYSGDISSYPLLFA------QVTHFKCGGVALGCGVHHTLSDGLSLLH   173
CcsHQT3       PSPELRRLTPTVDYSGDISSYPLFFA------QVTHFKCGGVALGCGVFHALADGLSSIH   163
CcsHCT1       PTLELRKLIPAVDYTLGIESYSLLVL------QVTYFKCGGVSLGVGMQHHAADGASGLH   163
CcsHCT2       PTLELRKLIPAVDYSLGIESYSLLVL------QVTYFKCGGVSLGVGMQHHAADGASGLH   163
CiHQT1        PSPELRRLAPTVDYSGDISSYPLFIT------QVTRFKCGGVSLGCGLHHTLSDGFSSLH   172
CiHQT2        PSPEFRRLTPTVDYSGDISSYPLFFA------QVTHFKCGGVALGCGVFHTLSDGLSSLH   173
CiHQT3        PSPELRSLTPTVDYSGDISSYPLFFA------QVTHFKCGGVGLGCGVFHTLADGLSSIH   172
CiHCT1        PTLELRKLIPAVDYSQGIESYPLLVL------QVTYFKCGGVSLGVGMQHHAADGASGLH   163
CiHCT2        PTLELRKLIPAVDYSLGIESYSLLVL------QVTYFKCGGVSLGVGMQHHAADGASGLH   163
HaHQT1        PSPELGRLAPTVDYSGDISSYPLFVT------QVTRFKCGGVSLGSALHHTLADGLSALH   163
HaHQT2        PSPEFRSLTPTVDYSGDISSFPLFFA------QVTHFKCGGVALGCGVFHTLSDGLSSLH   173
HaHQT3        PSPELRRLTPTVDYSGDISSYPLFFAQVYWFDQVTHFKCGGVGLGCGVFHTLADGLSSLH   178
HaHCT1        PTLELRKLIPAVDYSQGIESYPLLVL------QVFNKFCGGVSLGVGMQHHAADGASGLH   163
HaHCT2        PTLELRKLIPVVDYTLGIGSYPLLVL------QVTYFKCGGVSLGVGMQHHAADGASGLH   163
              *:  :  * * *: :  : :: * .       *:    ****.** .: *  :** * :*
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Supplementary FIGURE S2 | Multiple sequence alignment of HQTs and HCTs from sunflower (HaHQTs and HaHCTs) and other representative species. Amino acid sequences of HaHQTs and HaHCTs are shown and aligned with those from other representative species including tomato (SlHQT; NP_001234850.2), globe artichoke (CcsHQT1; ABK79689.1, CcsHQT2; ADL62854.1, CcsHQT3; ADL62855.1, CcsHCT1; AAZ80046.1, and CcsHCT2; KVH99042.1), and chicory (CiHQT1; ANN12610.1, CiHQT2; ANN12611.1, CiHQT3; ANN12612.1, CiHCT1; ANN12608.1, and CiHCT2; ANN12609.1).

```
SlHQT        FINTWSDIARGLSVAVPPFIDRTLLRARDPPTSSFEHVEYHPPPTLNSSKNR--------   221
CcsHQT1      FINTWSDKARGLSVAIPPFIDRSLLRARDPPTAMFEHLEYHSPPSLIAPSQNQNF-TSHP   222
CcsHQT2      FINTWSDMARGLSVAIPPFIERTLLRAREPPTPTYDHVEYHSPPSMNTTAQKPGS-GSL-   231
CcsHQT3      FINTWSDMARGLSIAIPPFIDRTLLRAREPPTPTFDHIEYHAPPSMKTISQNPES-S---   219
CcsHCT1      FINTWSDLARGLDLAVPPFIDRTLLRSRDPPQPAFDHIEYQPAPPMKTAPTPTPTDDESV   223
CcsHCT2      FINAWSDMARGLDLTLPPFIDRTLLQARDPPVPVFEHVEYQPAPPMKLAPKSA------S   217
CiHQT1       FINTWSDVARGLSVAIPPFNDRTLLRARDPPTPMFDHVEYHPPPSLITPPENHK------   226
CiHQT2       FINTWSDMARGLSVAIPPFIERTLLRAREPPTPTHDHVEYHEPPSMSPTTQKSGS-GS--   230
CiHQT3       FINTWSDMTRGLSIAVPPFTDRTLLRARETPTPTFDHVEYHLPPTMNTTSQNPKS-S---   228
CiHCT1       FINTWSDMARGLDLTIPPFIDRTLLRARDPPQPAFEHVEYQPAPQMKTTS--KSTDEQPV   221
CiHCT2       FINTWSDMARGLDVSLPPFIDRTLLRAQDPPRPVFEHVEYQPAPPMKSTSEST------S   217
HaHQT1       FINTWSDKARGLTVAVPPFVDRTLLRARDPPTPMFDHVEYHQPPSMIAPLENQKS-TSDP   222
HaHQT2       FINTWSDVARGLSVAIPPFIDRTLLRARVPPTPTHDHVEYHPPPTMITTQ---KT-GSL-   228
HaHQT3       FINTWSDMARGLSIAIPPFIDRTLLRAREPPTPTFDHVEYHPPPSMKPDSQKPES-S---   234
HaHCT1       FINTWSDMARGLDITIPPFIDRTLLRARDPPQPVFDHIEYQPAPPMKNAP--TTTNDQPV   221
HaHCT2       FINAWSDMARGLDITLLPFIDRTLLKARDPPQPVFEHVEYQPAPPMKSLPEVE------S   217
             ***:*** :*** ::: ** :*:**:::  *   .:*:**:  * :

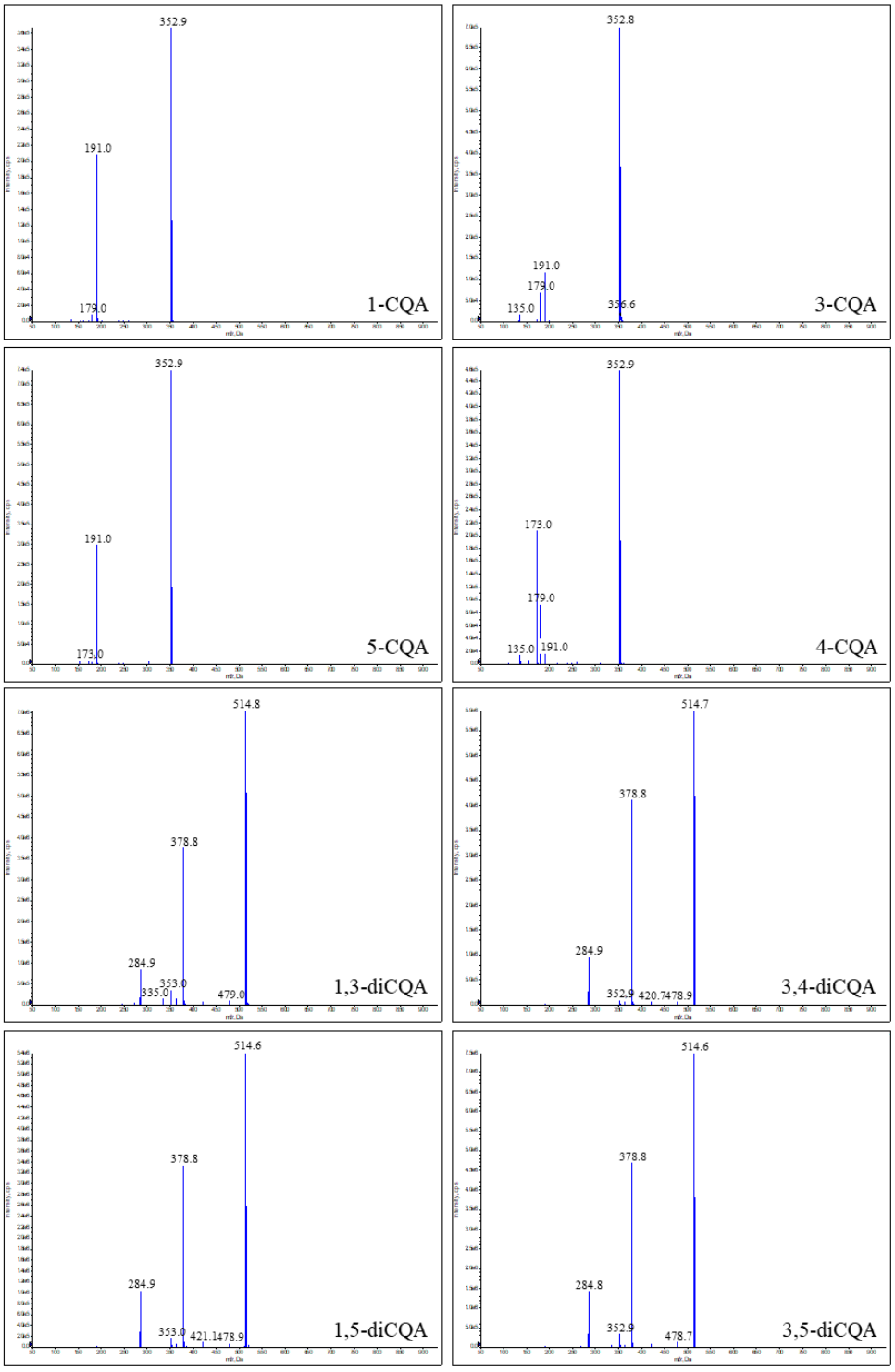
SlHQT        ESSTTTMLKFSSEQLGLLKSKSKNEG-----STYEILAAHIWRCTCKARGLPEDQLTKLH   276
CcsHQT1      KLASTAMLRLTLDQINGLKSKAKGDGS-VYHSTYEILAAHLWRCACEARGLSDDQPTKLY   281
CcsHQT2      SKSSTTMLKLTLDQLNSLKAKAKSESG-STHSTYEILAAHIWRCACKARGLPDDQLSKLY   290
CcsHQT3      RKPSTTVLKLTLDQLNVLKASTKNDGSNTTYSTYEILAAHLWRCACKARGLPDDQLTKLY   279
CcsHCT1      PETTVSIFKLTRDQVNALKGKSKEDGNTVNYSSYEMLSGHVWRCVCKARGLPDDQDTKLY   283
CcsHCT2      DETVVSMFKLTRDQLNGLKAKSKEDGNTINYSSYEMLSGHVWRSVCKARGLKDDQDTKLY   277
CiHQT1       PPATTTILRLTLDQINDLKSKGKGDGS-VYHSTFVIIAAHLWRSACKARGLSDDQPTKLY   285
CiHQT2       ---STTMLKLTLDQLNTLKVKAKIESG-QTHSTYEILAAHIWRCACKARGLPDDQLTKLY   286
CiHQT3       RKPSTNMLKLTIDQLNALKTAAKNDGGNTAYSTYEILAAHLWRCACKARGLPNDQQTKLY   288
CiHCT1       PETAVAIFKLTRDQLNALKAKSKENGNTINYSSYEMLSGHVWRCVCKARNLPADQDTKLY   281
CiHCT2       DETVVSMFKLTRDQLNVLKSKSKEAGNTINYSSYEMLSGHVWRSVCKARGLPEDQDSKLY   277
HaHQT1       KSASTMMLRLTLDQINDLKSKAKGDGS-AYHSTYEILAAHIWRCACKARGLSDDQPTKLY   281
HaHQT2       SKSSTTMLKLTLDQLNTLKAKAKSEGG-ASYSTYETLAAHIWRCACKARGLPDDQLTKLY   287
HaHQT3       RKPSTTILKLTLDQLNALKAAAKNDGGNTNYSTYEILAAHLWRCACKARGLPDDQLTKLY   294
HaHCT1       PETAVSIFKLTRDQLNALKAKSKEAGNTISYSSYEMLSGHVWRCVCKARGLPDDQDTKLY   281
HaHCT2       DETVVSIFKLTRDQLNALKSKSKEDGNAINYSSYEMLSGHVWRSVCKARGLTNDHDTKLY   277
                 . ::::: :*:. **   *  .     *::  ::.*:**..*:**.*  *: :**:

SlHQT        VATDGRSRLCPPLPPGYLGNVVFTATPIAKSCELQSEPLTNSVKRIHNELIKMDD-NYLR   335
CcsHQT1      VATDGRSRLNPPLPPGYLGNVVFTATPIAKSGEFKSESLADTARRIHSELAKMDD-QYLR   340
CcsHQT2      VATDGRSRLSPRLPPGYLGNVVFTATPVAKSGDLTSKSLSNTAKLIHTTLTKMDD-DYLR   349
CcsHQT3      VATDGRSRLSPQLPPGYLGNVVFTTTPVAKSGDLTTQSLSNAASLIRTTLTKMDN-NYLR   338
CcsHCT1      IATDGRARLRPSLPRGYFGNVIFTTTPIAVAGDLQSKPTWYAASKIHDALARMDD-DYLK   342
CcsHCT2      IATDGRARLQPALPAGYFGNVIFTTTPIAVAGELQSKPTWYAASKIHDALAKMNN-DYLK   336
CiHQT1       VATDGRSRLIPPLPCGYLGNVLFTTTPMAKSGEFKSESLADTARRIHTELARMDN-QYMR   344
CiHQT2       VATDGRSRLSPRLPPGYLGNVVFTATPVAKSGDLTSGSLSNTAKLIHTTLTKMDD-DYLR   345
CiHQT3       VATDGRSRLSPQLPPGYLGNVVFTATPMAKSGELTTQPLSNSASLIRSTLSKMDN-EYLR   347
CiHCT1       IATDGRARLRPSLPPGYFGNVIFTTTPIAVAGELMSNPTWYAAGKIHDGLAKMDN-DYLK   340
CiHCT2       IATDGRARLQPALPPGYFGNVIFTTTPIAAAGDLQSKPTWYAASKIHDALVKMDN-DYLK   336
HaHQT1       VATDGRSRLNPPLPRGYLGNVIFTATPIMKVGEFKSESLGDTARRIHNELGRMNXXXYLR   341
HaHQT2       VATDGRSRLSPHLPRGYLGNVVFTATPVAKSGTLTSDSLVNAAKLIHTTLKKMDD-DYLR   346
HaHQT3       VATDGRSRLSPQLPPGYLGNVVFTATPIAKSADLTTQPLANAASLIRTTLSKMDN-DYLR   353
HaHCT1       IATDGRARLRPSLPPGYFGNVIFTTTPIAVAGDLQSKPTWYAAGKIHDALARMDN-DYLR   340
HaHCT2       IATDGRARLQPALPSGYFGNVIFTTTPVAVAGELQSKPTWYAASKIHEALAKMNN-DYLK   336
             :*****:** * ** **:***:**:**:     : :     :.  *:  * :*:   *::
```

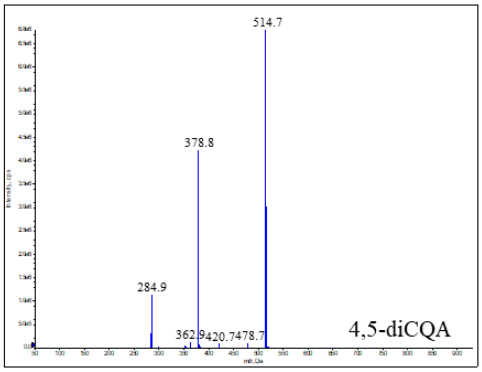
Supplementary FIGURE S2 | Multiple sequence alignment of HQTs and HCTs from sunflower (HaHQTs and HaHCTs) and other representative species. Amino acid sequences of HaHQTs and HaHCTs are shown and aligned with those from other representative species including tomato (SlHQT; NP_001234850.2), globe artichoke (CcsHQT1; ABK79689.1, CcsHQT2; ADL62854.1, CcsHQT3; ADL62855.1, CcsHCT1; AAZ80046.1, and CcsHCT2; KVH99042.1), and chicory (CiHQT1; ANN12610.1, CiHQT2; ANN12611.1, CiHQT3; ANN12612.1, CiHCT1; ANN12608.1, and CiHCT2; ANN12609.1). (continue)

```
SlHQT        SALDYLELQPDLSTLIRGPAYFASPNLNINSWTRLPVHECDFGWGRPIHMGPACILYEGT   395
CcsHQT1      SAIDYLELQPDLTALVRGPTYFASPNLNINSWTRLPIYESDFGWGRPIFMGPASILYEGT   400
CcsHQT2      SAIDYLESQPDLSALIRGPSYFASPNLNINAWTRLPVYDADLGWGRPIFMGPACILYEGT   409
CcsHQT3      SAIDYPEVQPDLSALIRGPSYFASPNLNINTWTRLPVHDADFGWGRPVFMGPACILYEGT   398
CcsHCT1      SALDYLELQPDLKALVRGAHTFKCPNLGITSWARLPIHDADFGWGRPIFMGPGGIAYEGL   402
CcsHCT2      SALDYLELQPDLKALVRGAHTFKCPNLGITSWARLPIHDADFGWGRPIFMGPGGIAFEGL   396
CiHQT1       SAIDYLELQLDLSALVRGPTYFASPNLNVNSWTRLPLYESDFGWGRPIFMGPANILYEGT   404
CiHQT2       SAIDYLESQKDLSALIRGPSYFASPNLNINAWTRLPVHDADFGYGRPIFMGPAQILYEGT   405
CiHQT3       SAIDYLEVQPDLSALIRGPSYFASPNLNINTWTRLPVHDADFGWGRPVFMGPAVILYEGT   407
CiHCT1       SALDYLELQPDLKALVRGAHSFRCPNLGITSWARLPIHDADFGWGRPIFMGPGGIAYEGL   400
CiHCT2       SALDYLELQPDLKALVRGAHTFKCPNLGITSWARLPIHDADFGWGRPIFMGPGGIAFEGL   396
HaHQT1       SAIDYLESITDLSTLVRGPSYFASPNLNVNSWTRLPIYDSDFGWGRPIFMGPASILYEGT   401
HaHQT2       SAIDYLETQPDISALIRGPSYFASPNLNINAWTRLPVHDADFGWGRPIFMGPATILYEGT   406
HaHQT3       SAIDYLEVQPDLSALIRGPSYFASPNLNINTWTRLPVHDADFGWGRPVFMGPACILYEGT   413
HaHCT1       SALDYLELQPDLKALVRGAHTFKCPNLGITSWARLPIHDADFGWGRPIFMGPGGIAYEGL   400
HaHCT2       SALDYLELQSDLKALVRGAHTFKCPNLGITSWARLPIHDADFGWGRPIFMGPGGIAYEGL   396
             **:** *   *:.:*:**   * .***.:.:*:***::::.*:*:***:.***. * :**
SlHQT        IYIIPSPNSKDRNLRLAVCLDAGHMSLFEKYLYEL   430
CcsHQT1      IYIIPSPSG-DRSVSLAVCLDPDHMSLFRKCLYDF   434
CcsHQT2      IYVLPSPNN-DRSVSLAVCLDANEQPLFEKFLYEF   443
CcsHQT3      IYVLPSPNN-DRSMSLAVCLDADEQPLFEKFLYDF   432
CcsHCT1      SFVLPSPIN-DGSLSIVISLQAEHMKLFSKFLYDI   436
CcsHCT2      SFVLPSPIN-DGSLSIAISLQSEHMKLFSKFLYDI   430
CiHQT1       IYIIPSPTD-DRSLKLAVCLDSDHMSLFQKYLYDF   438
CiHQT2       VYVLPSPNN-DRSVSLAVCLDANEQPLFEKFLYEM   439
CiHQT3       IYVLPSPNN-DRSMSLAVCLDADEQPLFEKFLYEF   441
CiHCT1       SFVLPSPIN-DGSLSIAISLQAEHMKVFSKFLYDI   434
CiHCT2       SFVLPSPVN-DGSLWIAISLLGEHMKLFSKFLYDI   430
HaHQT1       IYILPGPGG-DRSVALAVCLDPDHMALFKERLYDF   435
HaHQT2       VYVLPSPNN-DRSVSLAVCLDAKEQPLFEKYLYEL   440
HaHQT3       IYVLPSPNN-DRSMSLAVCLDADEQPLFEKFLYDF   447
HaHCT1       SFVLPSPDN-DGSLSIAISLQAEHMKLFSNLLYDI   434
HaHCT2       SFVLPSPIN-DGSLSIAISLQAQHMKLFSNYLYDI   430
              :::*.* . * .: :.:.*   .  :* : **::
```

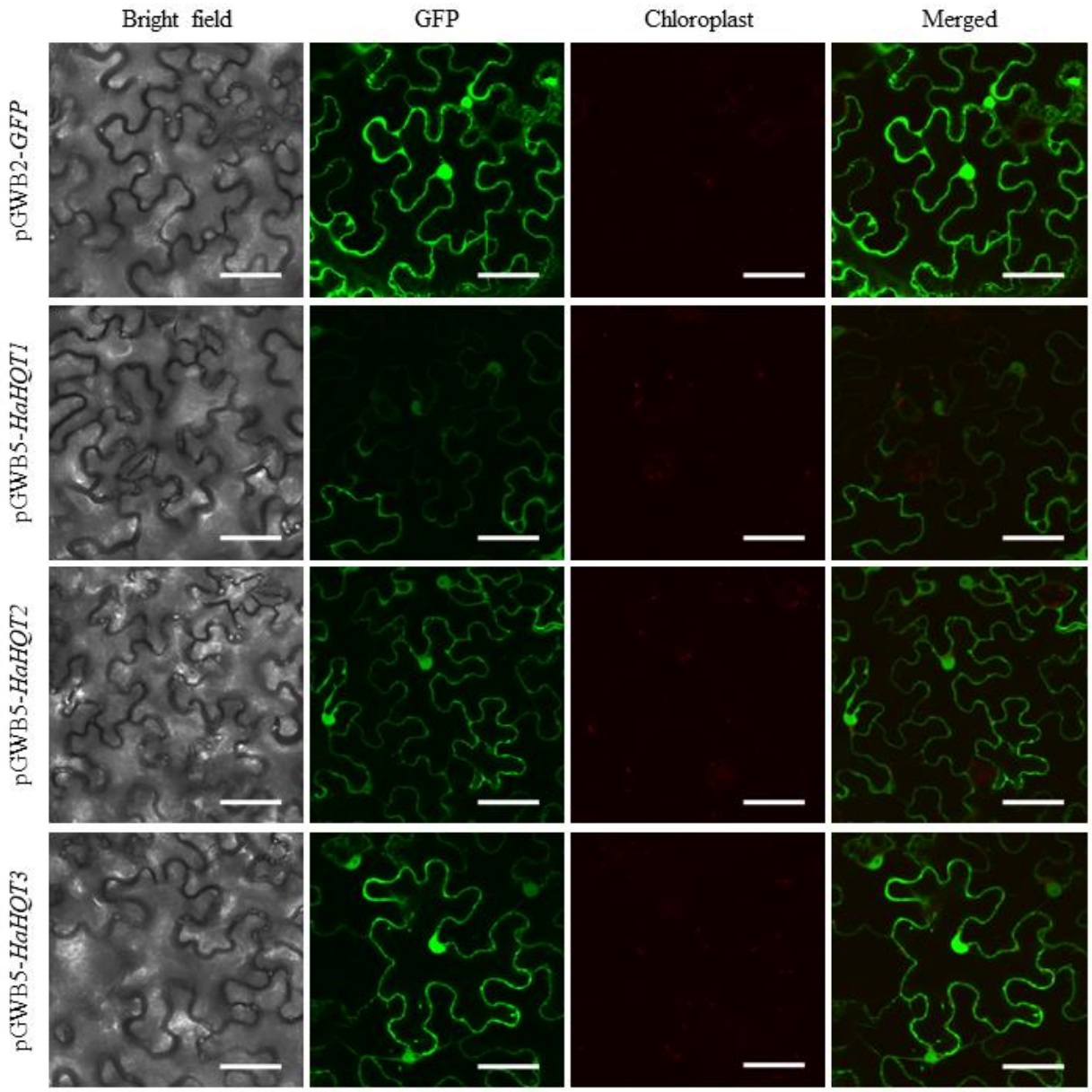
Supplementary FIGURE S2 | Multiple sequence alignment of HQTs and HCTs from sunflower (HaHQTs and HaHCTs) and other representative species. Amino acid sequences of HaHQTs and HaHCTs are shown and aligned with those from other representative species including tomato (SlHQT; NP_001234850.2), globe artichoke (CcsHQT1; ABK79689.1, CcsHQT2; ADL62854.1, CcsHQT3; ADL62855.1, CcsHCT1; AAZ80046.1, and CcsHCT2; KVH99042.1), and chicory (CiHQT1; ANN12610.1, CiHQT2; ANN12611.1, CiHQT3; ANN12612.1, CiHCT1; ANN12608.1, and CiHCT2; ANN12609.1). (continue)



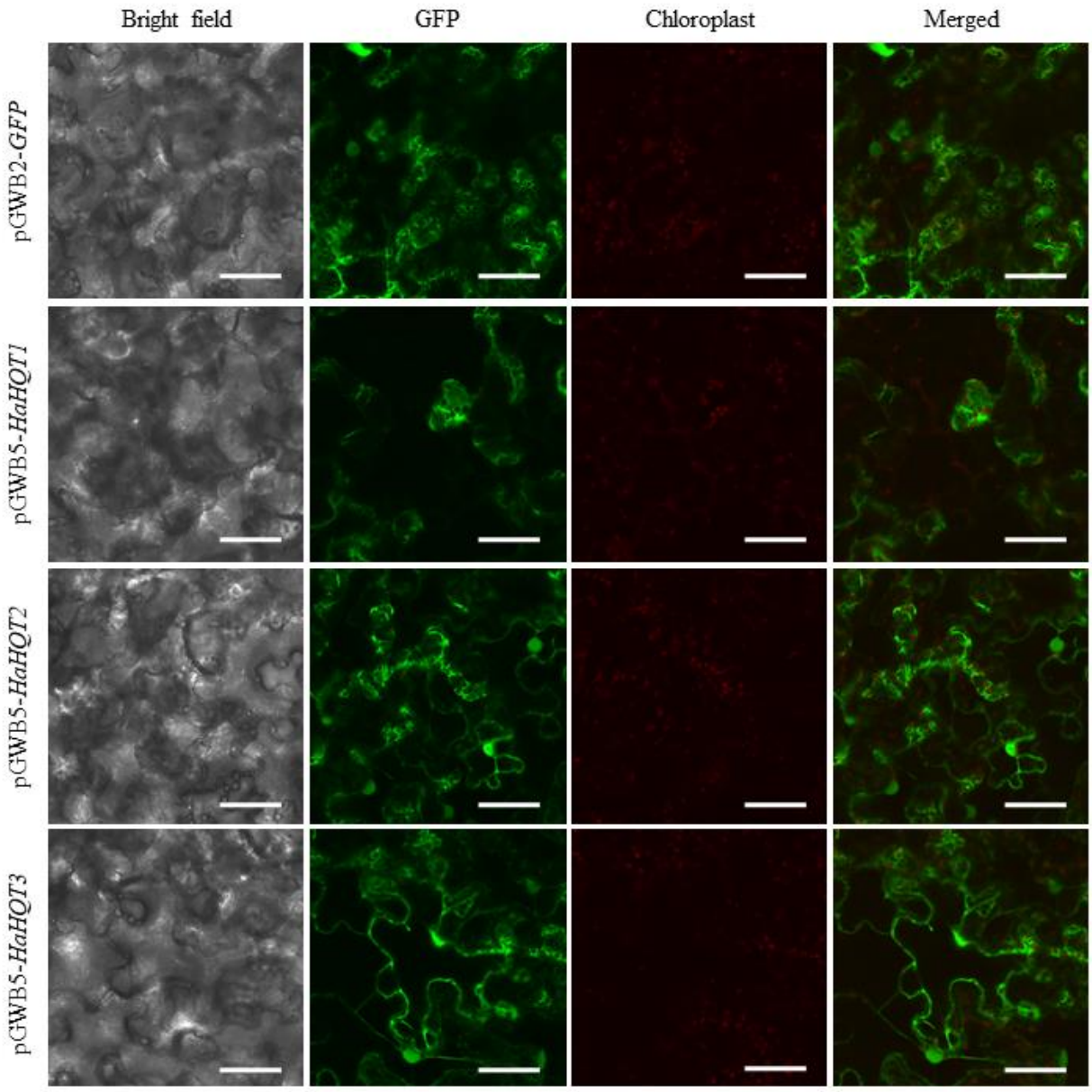
Supplementary FIGURE S3 | Negative ion MS^2 spectra of monocaffeoylquinic acids and dicaffeoylquinic acids. Enhanced Product Ion (EPI) profile of caffeoylquinic acid derivatives from authentic standards, including monnocaffeoylquinic acids such as 1-, 3-, 4- and 5-CQA, and diaffeoylquinic acids such as 1,3-, 1,5-, 3,4-, 3,5- and 4,5-diCQA.



Supplementary FIGURE S3 | Negative ion MS^2 spectra of monocaffeoylquinic acids and dicaffeoylquinic acids. Enhanced Product Ion (EPI) profile of caffeoylquinic acid derivatives from authentic standards, including monnocaffeoylquinic acids such as 1-, 3-, 4- and 5-CQA, and diaffeoylquinic acids such as 1,3-, 1,5-, 3,4-, 3,5- and 4,5-diCQA. (continued)



Supplementary FIGURE S4 | Subcellular localization of GFP-tagged HaHQTs in the epidermis of *Nicotiana benthamiana* leaves. Confocal microscopy image of epidermal cells from *N. benthamiana* leaves infiltrated with pGWB2-*GFP* (control), pGWB5-*HaHQT1*, pGWB5-*HaHQT2*, or pGWB5-*HaHQT3*. Bars=50 μm



Supplementary FIGURE S5 | Subcellular localization of GFP-tagged HaHQTs in the mesophyll of *Nicotiana benthamiana* leaves. Confocal microscopy image of epidermal cells from *N. benthamiana* leaves infiltrated with pGWB2-*GFP* (control), pGWB5-*HaHQT1*, pGWB5-*HaHQT2*, or pGWB5-*HaHQT3*. Bars=50 μm

Supplementary Table S1 | All primers used in this study.

Experiment	Gene	Accession number	Primer Sequence (5'→3')		Product size (bp)
			Forward	Reverse	
Cloning	*HaHQT1*	MK598073	ATGAACCTAACAGTAAAACAATCACTAA	CTAGAAATCATACAAACGTTCCTTAAA	1,305
	HaHQT2	MK598074	ATGAAAACCGATCAAACCAAA	TTACAATTCATACAAGTACTTCTCAAAAA	1,323
	HaHQT3	MK598075	ATGGGGACTGTTCAAAAGACA	TTAGAAGTCGTATAAGAACTTCTCAAACA	1,326
Subcellular localization	*HaHQT1*	MK598073	ATGAACCTAACAGTAAAACAATCACTAA	GAAATCATACAAACGTTCCTTAAA	1,302
	HaHQT2	MK598074	ATGAAAACCGATCAAACCAAA	CAATTCATACAAGTACTTCTCAAAAA	1,320
	HaHQT3	MK598075	ATGGGGACTGTTCAAAAGACA	GAAGTCGTATAAGAACTTCTCAAACA	1,323
qRT-PCR /ddPCR	*ETIF5*	XM_022156448.1	TTGTGCCCTCGTCCCATAAC	AAATCTGCTCCTCCCCCATC	231
	EFI2	XM_022137686.1	TTGACCGCTAAGCCACGTTT	AGGCACCAGAAAACCCGAAT	199
	ACT7	XM_022154554.1	TTGGAATGGAAGCTGCTGGT	CTGGAGGAGCAACCACCTTG	201
	HaHQT1	MK598073	ACCGCAAGGAGAATCCACAA	CGTCCCCATCCAAAGTCAGA	194
	HaHQT2	MK598074	TGGTAAACGCTGCGAAACTG	GTCGCGGGTCCCATAAAAAT	223
	HaHQT3	MK598075	CCCCGATGACCAACTAACCA	GCTGATAGATCGGGCTGCAC	246
	HaHCT1	MK598076	GAGCTGCAGCCCGATCTAAA	CCGGGCTTGGTAACACAAAA	184
	HaHCT2	MK598077	CGGCGCTTGATTACTTGGAG	CACCAGGCCCCATGAATATG	159

Supplementary Table S2 | List of regulatory elements found in the promoter regions of *HaHQT2* and *HaHQT3*.

IUPAC family	Number of elements found		Function
	***HaHQT2* promoter**	***HaHQT3* promoter**	
P$FAM002	3	12	light responsiveness, auxin/ salicylic acid/ abscisic acid/ jasmonate responsiveness, stress regulation, dehydration responsiveness
P$FAM003	5	3	phenylpropanoid biosynthesis, phytochrome regulation, MYB
P$FAM008	1	1	water stress responsiveness, MYB
P$FAM010	8	4	elicitor responsiveness, defense response regulation, salicylic acid responsiveness, sucrose responsiveness
P$FAM012	3	7	light responsiveness, light regulation, MYB
P$FAM013	1	3	abscisic acid responsiveness, dehydration responsiveness, low temperature responsiveness
P$FAM014	4	8	phytochrome regulation, sugar repression, MYB
P$FAM015	0	2	sugar repression
P$FAM022	3	1	storage protein
P$FAM024	3	4	storage protein
P$FAM025	1	0	sugar repression
P$FAM026	1	0	light responsiveness
P$FAM027	2	1	light regulation, circadian rhythms
P$FAM061	1	1	pathogen, ethylene, and jasmonate responsiveness
P$FAM069	1	2	auxin responsiveness, sulfur responsiveness
P$FAM085	0	1	light responsiveness
P$FAM098	0	2	auxin responsiveness
P$FAM099	1	0	phytochrome responsiveness
P$FAM107	1	1	sugar starvation
P$FAM116	1	0	abscisic acid and drought responsiveness
P$FAM124	1	0	ethylene responsiveness
P$FAM162	2	1	low temperature responsive element
P$FAM170	1	1	gibberellin responsiveness, MYB
P$FAM171	1	5	MYB
P$FAM172	4	2	dehydration responsiveness
P$FAM205	0	2	gibberellin responsiveness and sugar repression, Dof
P$FAM227	2	0	storage protein
P$FAM234	0	1	storage protein
P$FAM243	2	6	storage protein
P$FAM244	2	0	storage protein
P$FAM245	0	2	storage protein
P$FAM251	1	0	light responsiveness
P$FAM261	2	2	low temperature responsiveness

Supplementary Table S2 | List of regulatory elements found in the promoter regions of *HaHQT2* and *HaHQT3*. (continue)

IUPAC family	Number of elements found		Function
	***HaHQT2* promoter**	***HaHQT3* promoter**	
P$FAM262	1	0	light responsiveness and circadian expression
P$FAM263	5	3	abscisic acid responsiveness
P$FAM266	6	2	dehydration responsiveness, MYB
P$FAM267	10	17	auxin responsiveness, Dof
P$FAM273	1	1	gibberellin responsiveness, sugar starvation
P$FAM290	7	4	pathogen- and salt-induced
P$FAM302	2	3	light responsiveness, axillary bud outgrowth
P$FAM310	2	1	cytokinin
P$FAM311	1	1	low CO_2, MYB
P$FAM315	0	1	light responsiveness
P$FAM324	0	2	calmodulin
P$FAM325	3	0	cell cycle, MYB
P$FAM329	0	1	wood formation