

## TITLE PAGE

Down regulation of *p-coumarate 3-hydroxylase* in petunia uniquely alters the profile of emitted floral volatiles

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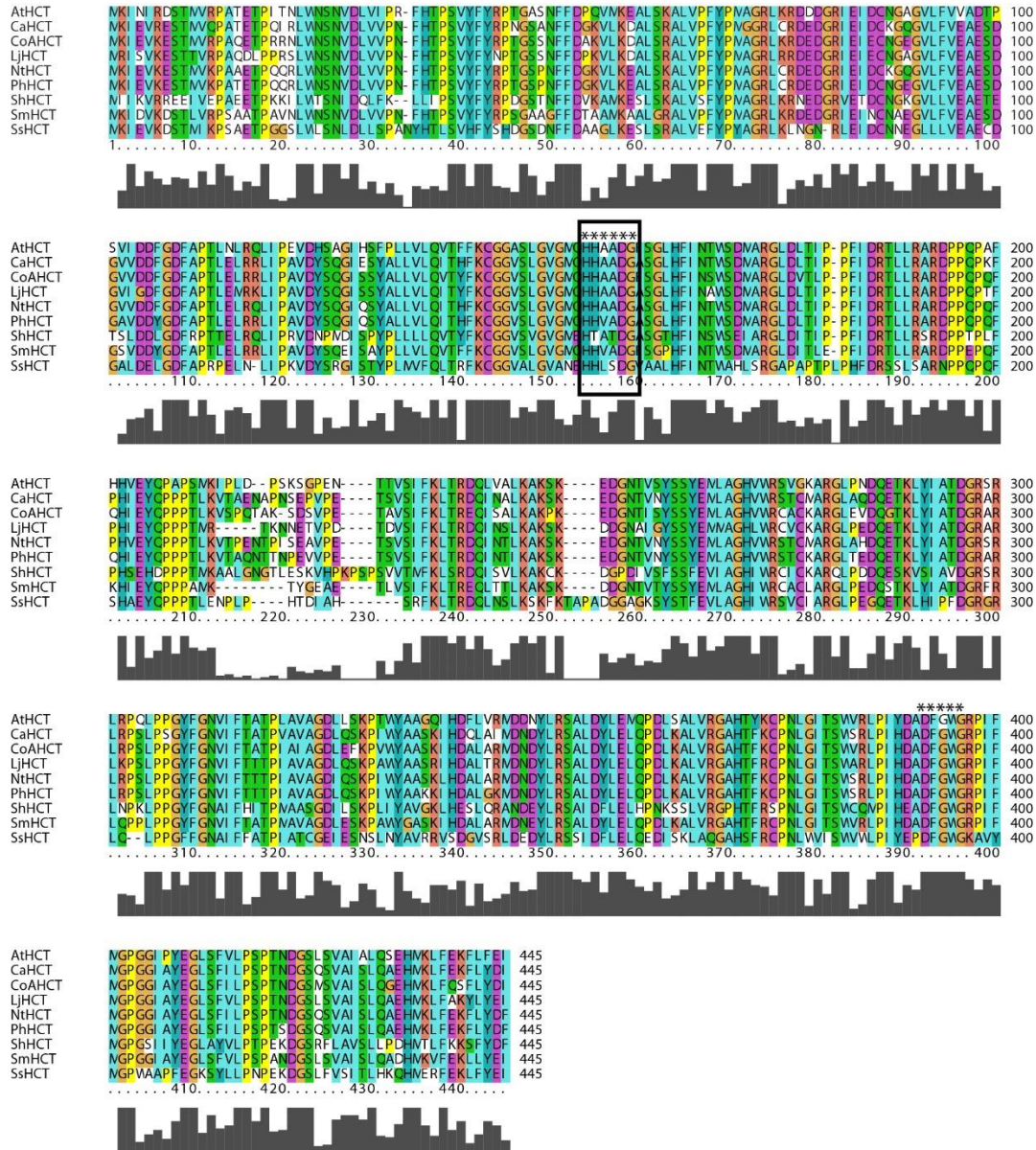


Figure S1. Predicted amino acid sequence alignment for HCT from various plants. The multiple alignment (ClustalX 2.0) was used to align the sequences. The predicted amino acids of *PhHCT* contain HHXXXD and DFGWG motifs for BAHD family.

AtHCT, *Arabidopsis thaliana* HCT (NP\_199704); CaHCT, *Capsicum annuum* HCT (NP\_001311756); CoAHCT, *Coffea arabica* HCT (CAJ40778); LjHCT, *Lonicera japonica* HCT (AFS68800); NtHCT, *Nicotiana tabacum* HCT (NP\_001312552); PhHCT, *Petunia x hybrida* HCT; ShHCT, *Sinopodophyllum hexandrum* HCT (ADB44897); SmHCT, *Salvia miltiorrhiza* HCT (ADG46003); SsHCT, *Solenostemon scutellarioides* HCT (CAK55166).

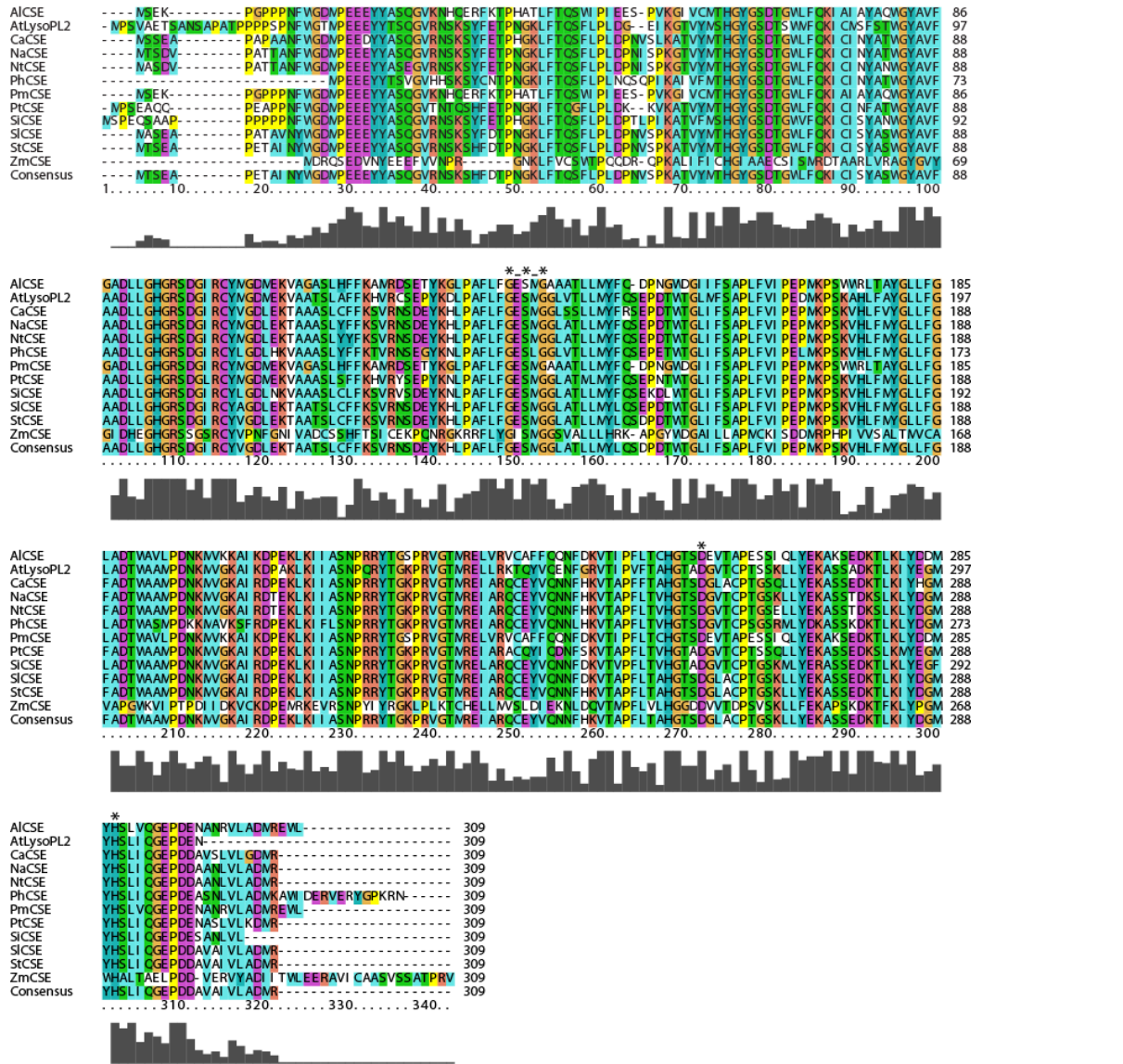


Figure S2. Predicted amino acid sequence alignment CSE from various plants. The multiple alignment (ClustalX 2.0) was used to align the sequences. The predicted amino acids of *PhCSE* contain nucleophile (GX-Nuc-XG)-acid-histidine catalytic triad which is conserved motif among members of  $\alpha/\beta$ -hydrolase family.

AICSE, *Arabidopsis lyrata* subsp. *lyrata* CSE (XP\_020891585); AtLysoPL2, *Arabidopsis thaliana* LysoPL2 (OAP14317); CaCSE, *Capsicum annuum* CSE (XP\_016562751); NaCSE, *Nicotiana attenuata* CSE (XP\_019241751); NtCSE, *Nicotiana tabacum* CSE (XP\_016470669); PmCSE, *Pinus massoniana* CSE (AKD43981); PtCSE, *Populus tomentosa* CSE (ALM55679); SiCSE, *Solanum lycopersicum* CSE (XP\_004235722); StCSE, *Solanum tuberosum* CSE (XP\_006341666); SiCSE, *Sesamum indicum* CSE (XP\_011072262); ZmCSE, *Zea mays* CSE (XP\_008674851).

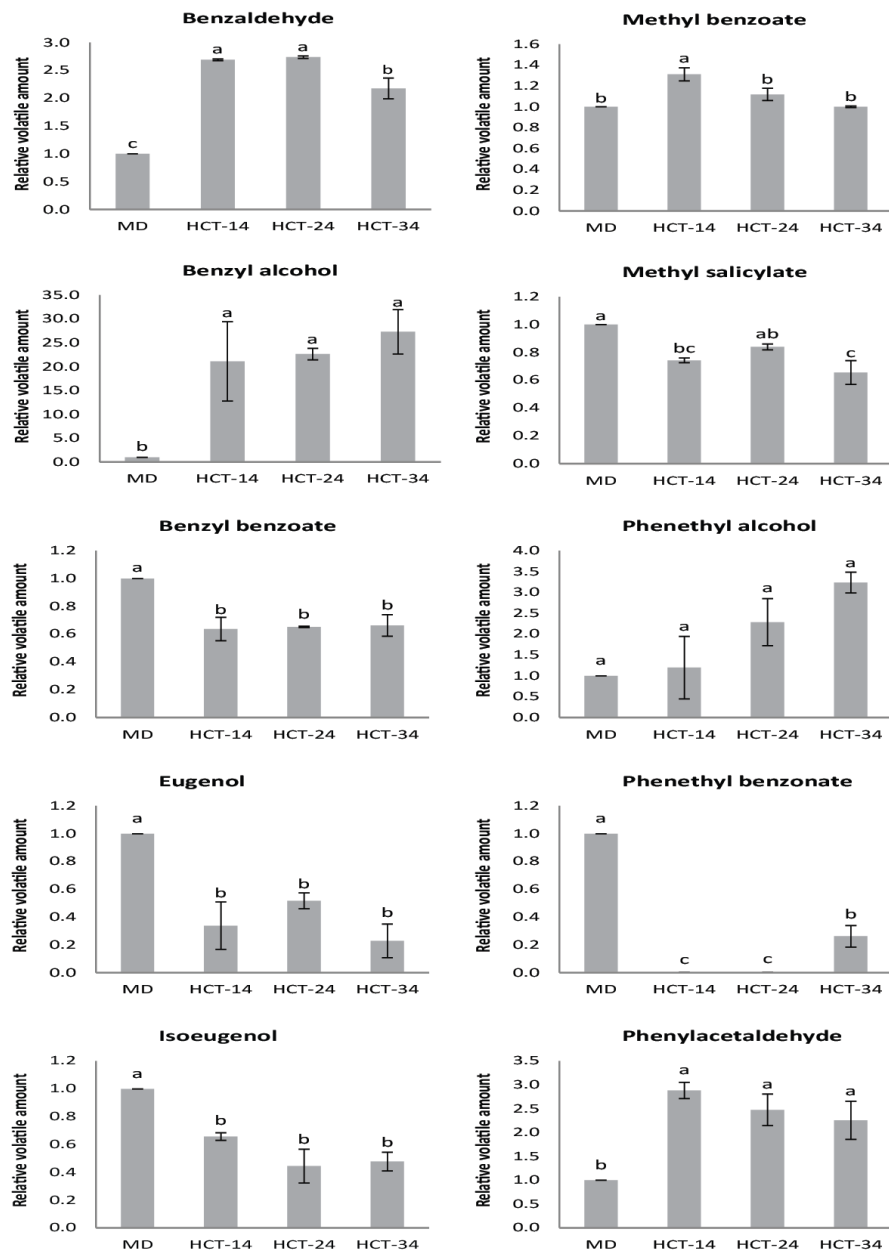


Figure S3. Effects of down-regulation of *PhHCT* on petunia floral volatiles. The open flowers (developmental stage 8) were used to collect volatiles at 18.0 h for 1hr and the calculated emission was compared to MD plants. Error bars represent standard error and means separation was analyzed by Duncan's multiple range test (one-way ANOVA,  $p < 0.05$ ).

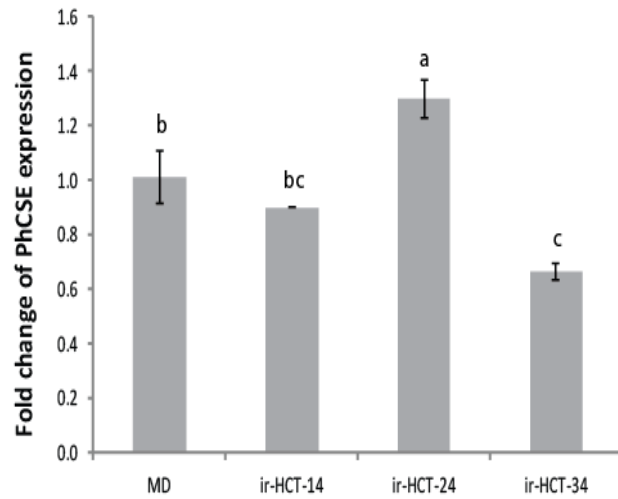


Figure S4. Transcript accumulation analysis of *phCSE* gene in *ir-PhHCT* plants. The open flowers (developmental stage 8) were used and relative quantities of the transcript of *PhCSE* gene were compared to MD plants. (q)RT-PCR was done with three biological replicates with *PhFBP1* as an internal reference. Error bars represent standard error and means separation was analyzed by Tukey test (one-way ANOVA,  $p < 0.05$ ).

Table S1. Primer sequences used in this research.

Name	Forward	Reverse
PhC3H-full	5'-ACATGGGGAAACCCAAAAA-3'	5'-TGTTTGCTCCTGGGTAATCC-3'
PhHCT-full	5'-AGCTGTTGGAAAATCAAGAATC-3'	5'-GGTTTCTTTCAAAGTCATACAAGA-3'
PhCSE-full	5'-GGACCTAATTCTGGGGTGAC-3'	5'-ATGCCAAAGACCAAGATGATCA-3'
PhC3H-RNAi	5'-TTACCCGAGCCATTATGGAG-3'	5'-GTATGGGAGGTTGGGGAAGT-3'
PhHCT-RNAi	5'-GGAGCTTCAGGTCTTCACTT-3'	5'-AGGTAACAAGCCCAGGGTTC-3'
		5'-TTGCAAGTGGATCGCCAT-3'
		5'-TTAAGCCTTCATAAGCAATA-3'
PhBPBT-qPCR	5'-AGTGATGCACCCGGTCTTGT-3'	5'-CAATTCTCGGCACCACACTG-3'
PhBSMT-qPCR	5'-TTTTCAGTGGAGTGCCTGGTT-3'	5'-GGCACCTGAGATAGCCACATG-3'
PhC3H-qPCR	5'-CGTCTCCGTTACAAGCTTCC-3'	5'-AGCAGCCGATCTACTCCTATG-3'
PhC4H1-qPCR	5'-AGCAGGTGTAACAACTGCAA-3'	5'-AAACTGGGACAGGGATAGGA-3'
PhC4H2-qPCR	5'-AACTGTCCAAACAAAATGGA-3'	5'-TGGCAATTTAAAACGTTTGCT-3'
PhCCR1-qPCR	5'-CTGAGGCATCTGGTCGGTAT-3'	5'-TGGTTTTACCCTTGGCTTG-3'
PhCCR2-qPCR	5'-TCCACACAGCTTCACCTGTTAC-3'	5'-CACATCGTTGGAAAGAATTGG-3'
PhCFAT-qPCR	5'-AGGCAACTCGCAATGGAAGT-3'	5'-AGGCGCTGAAACACTCCAAT-3'
PhCSE-qPCR	5'-ATTTGGGAATCACTTGGTG-3'	5'-CCTTGGATGGCTTCATTAGC-3'
PhFBP1-qPCR	5'-TGCGCCAATTGAGATAGCA-3'	5'-TGCTGAAACACTTCGCCAATT-3'
PhHCT-qPCR	5'-GACTATGGTGAAGCCAGCAA-3'	5'-ACATAGCCTCCCAGCCATAG-3'
PhIGS1-qPCR	5'-AGGAAGATGTCGCAGCCTACA-3'	5'-GTTTGCTGCCCTTGATCAT-3'
PhMYB4-qPCR	5'-ACAATTTCTTTTGCTGCTGGAA-3'	5'-TTCATCGTCCTTGATTTGTTCAA-3'
PhMYBA-qPCR	5'-CCCCATATATGTGAGTTAAGTGG-3'	5'-CCATAGGCACCTCCATGCAT-3'
PhODO1-qPCR	5'-TGCTTCAACCATGTCGAATTG-3'	5'-TCCGTGCCTGTTCTCTACGTT-3'
PhPAAS-qPCR	5'-CCAACCCGAACCAATTGAGA-3'	5'-CCTGGGAAAATATCGCTTCGA-3'
PhPAL1-qPCR	5'-GCTAGGCGGTGAGACGCTAA-3'	5'-CTCGGACAGCTGCACTGTCA-3'
PhPAL2-qPCR	5'-ACTGGCAGGCCTAATCCAA-3'	5'-GCGAAACGCTTCTTCAGCAT-3'
PhPAL3-qPCR	5'-ATGGCGAAAATGAGAAGAATG-3'	5'-GGCCACTAACTCATCCTCAAA-3'
PhPAR-qPCR	5'-AAGCCATTTCCGCCAAAGTACC-3'	5'-GTACAGAAGCACGTTACAA-3'
PhUbiq-qPCR	5'-GTCGATGGTCTTTGTTAGTGTGT-3'	5'-CAGAAACAGGAGCCAATTAAGCACT-3'