

Figure S1. Phylogenetic clustering of HD-Zip proteins from *F. vesca*, *Arabidopsis*, grape, and peach. All of these HD-Zip proteins are well separated into four major subfamilies (I-IV). This unrooted phylogenetic tree was constructed by the Neighbor-Joining (NJ) method with 1500 bootstrap replicates in MEGA10. Bootstrap values > 60 are shown.

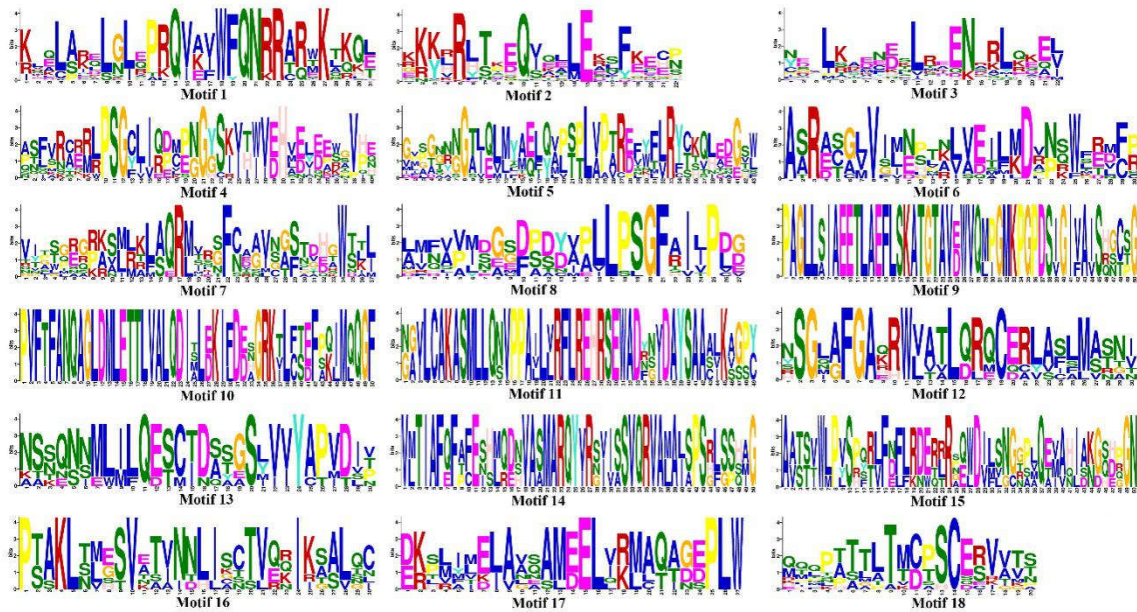


Figure S2. The sequence logos of each motif for *FveHDZ* proteins

FveHDZ25	MFQPGMFDSSHMSMLDMSTHKSSSESDMGRSRDDDFETKSGTETTDAPSGDELDPSPQPRPKRKYHRRHTQRQIQEMEAFKCEPHFDDKQRKLSRELGLE	100
FvH4_3g22020	0
Consensus Homeobox domain	
FveHDZ25	PLQVRFWFQNKRTQMKACQHERHENSILKNENDKLAENNRYKEALSNATCPNCGGPAALGEMSFDEQHLRIENARLREEIDRISALAAYVGRKMSSSSS	200
FvH4_3g22020	6
Consensus HALZ motif HALZ motif m s s s	
FveHDZ25	HLSSSQGPSRSILDVSSFGAPQSGYVGEMYSGDLIRSVVPIDADKPIVVELVWSAMBEIIRMPCGQGPITVVFADHNSSTTHHILN.....	289
FvH4_3g22020	QIEIDMRIPQEATTSQQVNMGSNVQVASNISRASDLIMAVISSAEVNMKISSELSAMBEVITKIDAPQEPPIWQCNIENSTERLSDEYLRFGHISASL	106
Consensus dll v i ela are l a a plw di	
FveHDZ25 EDEYMRITFPRLGKPKLGLRSEASRESALVIMNHVNLVEILMDVNQKSTIVFCGIVSRAMTLDILSTG.VAGNYNG	363
FvH4_3g22020	IEIIRMEVVGDSQSELPINNSEFLDESYRFVLAINQPKPEVYS..SESSFAIEYVWZARNLVQILMDLEQLLVFPNIVSRKLVGLSTRVGCNYG	204
Consensus e ey kp se sr v m nlv lnd gw vf ivsra ls v gny g	
FveHDZ25	ALQVMSAEFQVESPLMPTREMYFVRVYKCHTIGTRAVVVSDDSTIRENSISRRRRPSCGLIQEPNGYSKVIWVEHVEVDIRAVHNIYRPLVNSGLAFG	463
FvH4_3g22020	TLQVMTAEFHRETPIHPRASYFARYSKCLDSGMVVVDASIERIFQLSINVRKQPSGCLIQEPNGGSKVIWVEHVEVDNRVHNMFRPLVNSGLAFS	304
Consensus	lqvm aef p pl p r yf ry kq g w vvd sl l rr psgcliqe png skviwveh evd r vhn plv sglaf	
FveHDZ25	ARRWVVTILRQCEFLASSMANNHAGDLGVITSTHGRKSKYKIAQRMVISECTGVGASTAHMTITLSATGSDIVRMTRKSMITHRRPPEIVLSAATSEW	563
FvH4_3g22020	ARRWVSTINRQCEFLATINSTSHETSRLNFSQAGKSLKILTERMRSHVADISASTENRRKPTLEVGAEDVPVTTITNLNTHRRPPEITLSAATSEH	403
Consensus	a r w v t l r q c e l a p d v s g r k s l k l r m s f a s t w t l g d v v t d g p p g l s a t s	
FveHDZ25	LFVFPKRVFDRLEENSRSEWDILSNGGLVQBMIAIANGRTPGKCVSLLRVNSANSSQSNMLILQESCTDSGYSYVYARVDIVAMNVVSGGIDIVAT	663
FvH4_3g22020	LFVFRITQIYNLRGGSRYMNDMMSEKDTREHMIATGDPGRVSLIIVENGATKEIEIFYLQESYTDSSGYSYVYARVDIVAMNVVSGGIDIVAT	503
Consensus	lpvp lrd sr wd s e a ia g pgn vs v l qes tds gayv yap d am l g pd a	
FveHDZ25	LFSGEAILPDGEFFGGA.GGILDVSGSGSLTVAFQILVDSVPTAKLSLGSVATVNNLIKCTVERIRARVICTDN	737
FvH4_3g22020	LASGSILPDREVNDESGLTILALHITEEGATEDFIPPTVQNIINIIAGIVQITDVLSSNNGENSVEFEQ.	577
Consensus	l sgf ilpd p a gg l a tv	

Figure S3. The protein sequence alignment of *FveHDZ25* and *FvH4_3g22020*. The core domain regions of these 2 proteins were marked by colored lines.

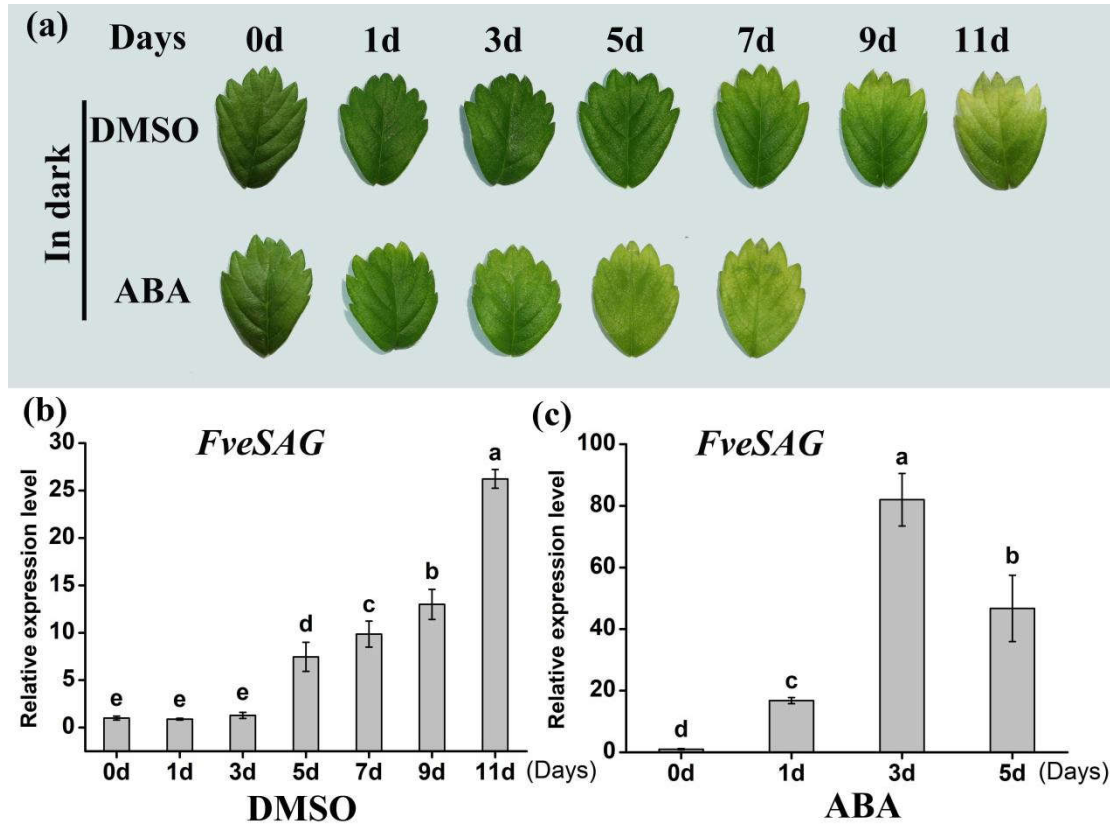


Figure S4. *F. vesca* leaves with different treatment days (a) and relative expression of the senescence-associated gene (*FveSAG*, FvH4_5g06770) in leaf by dark treatment with DMSO (b) or ABA (c). DMSO was the solvent of ABA. The expression of *FveSAG* at 0d was used as control and was normalized as “1”. Data was shown as mean \pm standard deviation derived from three biological replicates. The values with different letters were significant based on Duncan's multiple range tests ($P < 0.05$, $n = 3$).

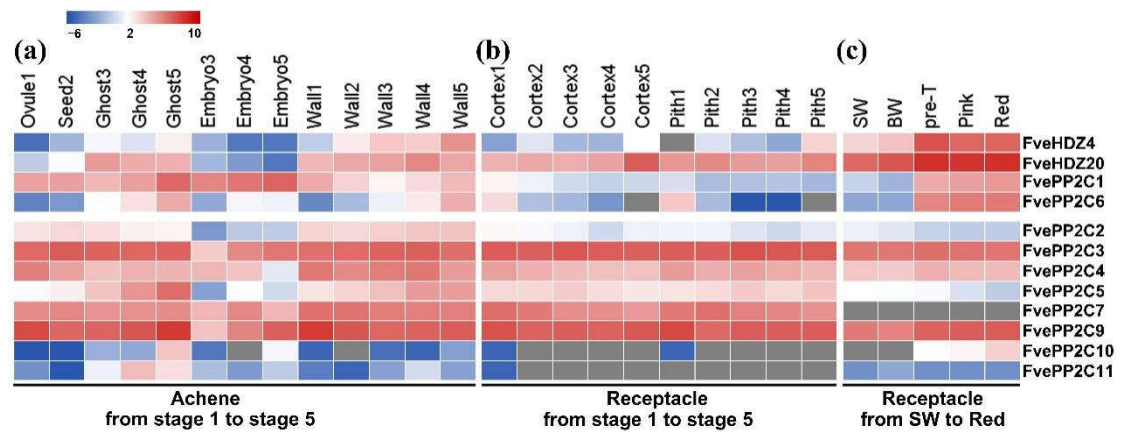


Figure S5. Expression profiles of the 10 *FvePP2Cs* and 2 *FveHDZs* in achene development (a) and receptacle development (b) and ripening (c). (a,b) Achenes included the ovule, seed, embryo, ghost and wall tissues, and receptacles included the cortex and pith tissues. Numbers after the tissues indicated different fruit development stages. Data from Kang et al. [43] and Hollender et al. [44]. (c) SW, small white; BW, big white; and Pre-T, pre-turning. Data from Gu et al. [45]. The heat map showed \log_2 “relative RPKM values” of individual *FveHDZ* genes. Gray boxes indicated undetectable expression of the genes.

>FvePP2C6-F1 (158bp)
GATGGATCTGTAAACCCTAATCTCTTAATTAATGACTAATGTAAGATTTTTTGC GGTTCC
ATTTTATCAAACATAAACCTTCACCAACTCAACCACAATCATTGAAAACCTGCCTAGTTT
ACAAATTTATACTCCAAAGCTTCCAAAGAAGAGAAGAG

>FvePP2C6-F2 (425bp)
CAGGAATTCTCTACGAGAGTAATATATTATGCGAGACATAATATGTTTGTATGCATATTA
CCCCCTCTATTTCTACCTTATACAAATGTGTCTGTACGATTTTTTTTTTAAGTGAGAAA
TATAACACAACCTCACGAGTTAAAGTGCATTCAACCATCAATCACTTCAATGTTTTGCT
AAGTTATTACCTTTGTCATAAATTCGATAATTACTTGCTTATATTGGATATACTAATGAT
TTACGATGATCTTTACCACTACCTCTTATAATTGAAAGATTAATATAACAATCTTGACTTA
ACGACTCGAGCAAATAATGTATTACTATTGTATTTTATTATTACTTGTCTTTTTGAGTAAA
TACTTAATTTTATAAATTTATTTATAGCCATAAGAGGCGTACATCAAATGTTGTCTTGAA
CCT

>FvePP2C1-F1 (298bp)
CAGTCTCATCAAATGCATGATAAAATGTGTACATTCTAATATATTTATTACCGATTAAGT
TTCAATGAACCTTGGATAAGATATGAATTATTGAATATATATCTCACATATATCTCTT
AACGTACATAGTACGTAGTGTTTACCTATTGAGTACTGATCAAGAGATTATTATGGTC
AATCACCTTTAAATGTAAATTTAATGATAAAAAATATTATTTAAATTAATTTATTTT
TAATCTTTAAATTTAAATTTAACGGTAATTAATCACATGACTGTCTCTTAACATA

Figure S6. The sequence of two fragments (FvePP2C6-F1 and FvePP2C6-F2) from *FvePP2C6* promoter and one fragment (FvePP2C1-F1) from *FvePP2C1* promoter, which were used for yeast one-hybrid assays.

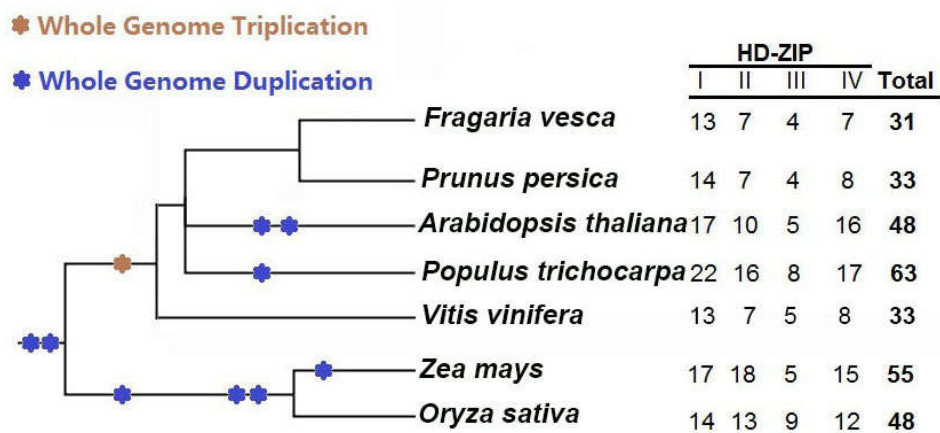


Figure S7. The Taxonomy Common Tree of the 7 species and the number of HD-Zip family genes in each species investigated. The information of HD-Zip family genes in different species (except *Fragaria vesca*) were obtained from previous studies [6, 7, 48, 49, 51]. The tree was constructed online by the Taxonomy Browser in NCBI (<http://www.ncbi.nlm.nih.gov/Taxonomy/CommonTree/wwwcmt.cgi> (accessed on 2 April 2022)).