

Fig. S1. Carotenoids (A) and capsaicinoids (B) biosynthetic pathways. A. Geranylgeranyl diphosphate that is synthesized from the prenyl lipid biosynthesis pathway is catalyzed by phytoene synthase to produce phytoene, which represents the first step in the carotenoid pathway. Then, after synthesizing lycopene, this pathway is divided into two different branches: α -carotene is finally developed into lutein, and β -carotene is ultimately formed into capsanthin or capsorubin as a function of capsanthin/capsorubin synthase (CCS). The ellipsis indicates intermediate steps. B. The two distinct pathways, the phenylalanine and chain fatty acid biosynthesis pathways, come together to produce capsaicin at the end of the catalysis of capsaicin synthase (CS). ZDS, ζ -carotene desaturase; CRTISO, carotenoids isomerase; LCYE, lycopene ϵ -cyclase; CrtZ-2, β -carotene hydroxylase-2; PAL, phenylalanine ammonia-lyase; C4H, cinnamate 4-hydroxylase; 4CL, 4-coumaroyl-CoA ligase; HCT, hydroxycinnamoyl transferase; C3H, p-coumaroyl shikimate/quinate 3-hydroxylase; COMT, caffeoyl-CoA 3-O-methyltransferase; HCHL, hydroxycinnamoyl-CoA hydratase lyase; AMT, aminotransferase; BCAT, branched-chain amino acid aminotransferase; Kas, ketoacyl-ACP synthase; ACL, acyl carrier protein; and FatA, acyl-ACP thioesterase.

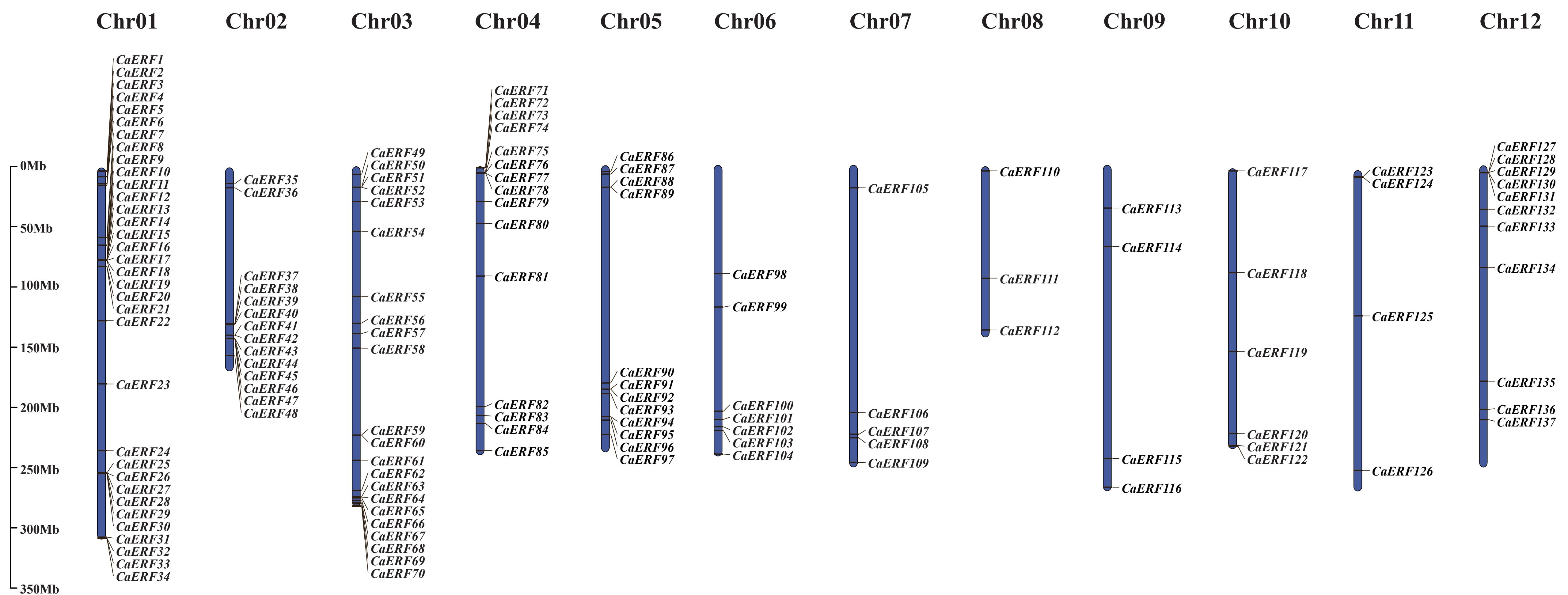


Fig. S2. Physical distribution of all candidate *CaERFs* among chromosomes (Chrs). The chromosome distribution of each pepper *ERF* was obtained from the genome annotation information, and then used the Map Gene 2 Chromosome v 2 (MG2C; http://mg2c.iask.in/mg2c_v2.0/) to make the linkage visualization.

A

DREB Subfamily

	10	20	30	40	50	60
CaERF84	LYRG VRQR - HWG KWWAE I RLPK -	- NRTRLWLGTFTDAEAAALAYDKAAYMLRG -	- DFARLNFS			
CaERF31	LYRG VRQR - HWG KWWAE I RL PQ -	- NRTRWLGTFTDAEAAALAYDKAAYMLRG -	- EYARLNFP			
CaERF1	LYRG VRQR - HWG KWWAE I RL PQ -	- NRTRWLGTFTDAEAAALAYDKAAYMLRG -	- EYARLNFP			
CaERF49	LFRG VRQR - HWG KWWAE I RL P R -	- NRTRWLGTFTDAEAAAFAYDTAAAYLLRG -	- DYAHLNFP			
CaERF107	LYRG VRQR - HWG KWWAE I RL P K -	- NRTRLWLGTFTDAEADAMAYDREAYKL RG -	- DNAKLNFP			
CaERF114	TYRG VRQR - TWG KWWAE I RLP C -	- KTRRLWLGTFTDAEAAARYDEAAKAMYG -	- HDAI LNFP			
CaERF97	TYRG VRQR - TWG KWWAE I RLP H -	- RGSRWLGTFTATAEAAALYDEAAKAMYG -	- PCARLNLP			
CaERF134	TYRG VRQR - TWG KWWAE I RLP N -	- RGARWLGTFTNTLEAARAYDDAARRLYG -	- ADAKLNL S			
CaERF122	TYRG VRQR - TWG KWWAE I RLP K -	- KTRRLWLGSFTAEEAAAMAYDEAAARRLYG -	- PDAYLNLP			
CaERF85	KYKG VRQR - TWG KWWAE I RLP N -	- RGARWLGTFTD NS YDAVAYDAAL KLYG -	- AEAKLNLP			
CaERF119	TYRG VRQR - TWG KWWAE I RLP N -	- RGACWLGTFTD NS YDAVAYDAAL KLYG -	- SNAI LNFP			
CaERF105	KYKG VRQR - TWG KWWAE I RLP N -	- RGARWLGTFTD NS YDAVAYDAAL KLYG -	- DKAOLNLP			
CaERF54	KFRG VRQR - SWG KWWAE I RLP R -	- KTRRWLGTFTATAEADARAYBRAA I LYG -	- SRAOLNLQ			
CaERF135	RYRG VRQR - HWG KWWAE I RLP C -	- KTRRLWLGTFTD S AEEAAI AYDVEAFLRK R -	- NKCAAA -			
CaERF16	MYRG VRKR - KWG KWWSE I RL P N -	- S RERI WLGSYDTPKAARAF DAAL FCLRG -	- SNANFNP			
CaERF80	KYKG VRMR - SWG KWWSE I RL P N -	- KQTRI WLGSYSTPEAAARAYDDAARRLYG -	- SNAI LNFP			
CaERF41	PYKG I RMR - KWG KWWAE I RLP N -	- KRSR I WLGSYSTPVAAAAYDTAVYLLRG -	- PSARLNFP			
CaERF142	PYRG I RMR - KWG KWWAE I RLP N -	- KRSR I WLGSYSTPVAAAAYDTAVYLLRG -	- PSARLNFP			
CaERF139	RYRG VRQR - NSG KWCCE VREP N -	- KKSRI WLGTFTPEAAARAHVAAL ALRG -	- RSACLNFA			
CaERF32	IYRG VRRR - NNNKWCCE LREP S -	- EOKRI WLGTFTPEAAARAHVAAL ALRG -	- NLATLNFP			
CaERF5	VYRG VRWR - HS EKWS E VRP VP -	- KKSRI WLGTFTPEAAARAHVAAL ALRG -	- HVALLNFP			
CaERF34	IYRG VRRR - NNNKWCCE I REP S -	- EOKRI WLGTFTPEAAARAHVAAL ALRG -	- NLATLNFE			
CaERF33	IYRG VRRR - NNNKWCCE I REP S -	- EOKRI WLGTFTPEAAARAHVAAL ALRG -	- NLAI LNFE			
CaERF12	IYRG VRMR - SWG KWWSE I RLP R -	- KKSRI WLGTFTPEAAARAHVAAL ALRG -	- NLAI LNFP			
CaERF90	TYRG VRKR - NWG KWWSE I RQP R -	- KKSRI WLGTFTPEAAARAHVAAL ALRG -	- NSAVLNFP			
CaERF4	LYHG VRKR - SWG KWWSE I RLP R -	- KKSRI WLGTFTPEAAARAHVAAL ALRG -	- HLA LNFP			
CaERF81	AYRG VRKR - KWG KWWSE I REP G -	- KKTRI WLGSFTPEAAEAAAAYDS AAL HE RG -	- HAAKLNFP			
CaERF23	LYRG VRRR - NRDKWCE I REP N -	- KKSRI WLGTFTPEAAEAAAAYDS AAL HE RG -	- TKA LNFP			
CaERF111	VF RG VRMR - NWG KWWSE I REP R -	- KKSRI WLGTFTPEAAEAAAAYDS AAL HE RG -	- TKA LNFP			
CaERF26	VYRG VRWR - HS EKWS E VRP VP -	- KKSRI WLGTFTPEAAEAAAAYDS AAL HE RG -	- TKA LNFP			
CaERF69	IYRG VRMR - SWG KWWSE I REP R -	- KKSRI WLGTFTPEAAEAAAAYDS AAL HE RG -	- NTAI LNFP			
CaERF30	TYRG VRKR - NWG KWWSE I RQP R -	- KKSRI WLGTFTPEAAEAAAAYDS AAL HE RG -	- NSAVLNFP			
CaERF136	IYRG VRRR - NNDKWCE VREP S -	- EOKRI WLGSYLTAEAAARAHVAAL ALRG -	- QLATLNFA			
CaERF120	VYKG I RKRKS SG KWWSE I REP R -	- SPNR I WLGTFTPEAAVAYDVAAL ALKG -	- RGAE LNFP			
CaERF60	AYRG VRQS - NSG KWCCKVRPEN -	- KKSRI WLGTFTPEAAVAYDVAAL ALKG -	- RSACI INF A			
CaERF3	VFRG I RCR - SG KWWSE I REP R -	- KTRRI WLGTFTPEAAVAYDVAAMAL KG -	- SDAI INF P			
CaERF98	NFG I RMR - NG KWWSE I REP R -	- KTTRI WLGTFTPEAAVAYDVAAL ALKG -	- PDAQLNFP			

B

ERF Subfamily

	10	20	30	40	50	60
CaERF87	RYRG VRQR - PWG KWA E I RD P YKA -	- TRVWLGTFTDTAEADARAYDEAAL K F RG SK -	- AKLNFP			
CaERF82	RYRG VRQR - PWG KWA E I RD P YKA -	- ARVWLGTFTDTAEAAARAYDEAAL K F RG NR -	- AKLNFP			
CaERF138	NYRG VRQR - PWG KWA E I RD P RKA -	- ARVWLGTFTNTAEADARAYDRAAIE F RG PR -	- AKLNFS			
CaERF66	KYRG VRQR - PWG KWA E I RD P KKA -	- ARVWLGTFTETAEAAALAYDEAAL T F KG NK -	- AKLNFP			
CaERF133	HYRG VRQR - PWG KWA E I RD P YKA -	- TRVWLGTFTDTAEAAASAYDEAAL R F RG SK -	- AKLNFP			
CaERF135	HYRG VRQR - PWG KWA E I RD P KKA -	- ARVWLGTFTDTAEAAALVYDEAAL R F RG NK -	- AKLNFP			
CaERF36	HYRG VRQR - PWG KWA E I RD P KKA -	- ARVWLGTFTDTAEAAALVYDEAAL R F RG SK -	- AKLNFP			
CaERF141	OYRG VRQR - PWG KWA E I RD P KKA -	- ARVWLGTFTHTAEADAAVAYDEAAL K F KG NK -	- AKLNFP			
CaERF118	NYRG VRQR - PWG KWA E I RD P RKA -	- ARVWLGTFTTAEDTARAYDRAAIE F RG PR -	- AKLNFS			
CaERF39	EFRG VRQR - PWG KWA E I RD P YKA -	- QRLWLGTFTATAEADARAYDKKAEF RG EK -	- AKTNFP			
CaERF40	EFRG VRKR - PWG KWA E I RD P YKA -	- QRVNLGTFTITAEDAARAYDKKAEF RG EK -	- AKTNFP			
CaERF104	KFRG VRQR - PWG KWA E I RD P YKA -	- RVWLGTFTPEAAK VYD KAA VV KLK -	- AVTNFP			
CaERF112	KFRG VRQR - PWG KWA E I RD P YKA -	- RIVWLGTFTETAEAAAMVDO AAI K I R -	- ALTNF I			
CaERF61	KFRG VRQR - PWG KWA E I RD P RRV -	- RLWLGTFTD EEE AMVYDNAA I KLR -	- ALTNF I			
CaERF99	KFRG VRQR - PWG KWA E I RD P RRV -	- ARVWLGTFTD EEE AMVYDNAA I KLR -	- ALTNF I			
CaERF2	KFRG VRQR - PWG KWA E I RD P RRV -	- RLWLGTFTD EEE AMVYDNAA I KLR -	- ALTNFA			
CaERF123	KYRG VRQR - KWG KWA E I RD P F KC -	- RRWLG TYSTAEE AS QAY E M K R L E F D -	- AMAKSLSSN			
CaERF67	KYRG VRQR - KWG KWA E I RD P F KC -	- KR I WLGTFTETVEAAS QAY E M K R L E F D -	- AMAKSLSSA			
CaERF22	KYRG I QRQ - TWG KWA E I RD P RKG -	- RVWLGTFTNTAEAAARAYDE AAK R I RG DK -	- AKLNFP			
CaERF53	LYRG I QRQ - PWG KWA E I RD P RKG -	- RVWLGTFTNTAEAAARAYDE AAK R I RG EK -	- AKVNFP			
CaERF70	LYRG I QRQ - PWG KWA E I RD P RKG -	- RVWLGTFTNTAEAAARAYDE AAK R I RG NK -	- AKVNFP			
CaERF137	QYRG I QRQ - PWG KWA E I RD P RKG -	- RVWLGTFTSTAEAAARAYDE AARR I RG NK -	- AKVNFP			
CaERF35	QYRG I QRQ - PWG KWA E I RD P RKG -	- RVWLGTFTSTAEAAARAYDV E ARR I RG NK -	- AKVNFP			
CaERF101	QYRG I QRQ - PWG KWA E I RD P RKG -	- IRWLG TFTNS AEE AA RAYDV E ARR I RG KK -	- AKVNFP			
CaERF48	QYRG I QRQ - PWG KWA E I RD P RKG -	- IRWLG TFTNS AEE AA RAYDV E ARR I RG KK -	- AKVNFP			
CaERF52	KYRG I QRQ - PWG KWA E I RD P RKG -	- RVWLGTFTNTAEAAARAYDE AAK R I RG DK -	- AKLNFP			
CaERF27	KYRG I QRQ - PWG KWA E I RD P RKG -	- RKRWLGTFTETAEADALYDQAAF KM RG SK -	- ARLNFP			
CaERF71	KYRG I QRQ - PWG KWA E I RD P RKG -	- RKRWLGTFTETAEADALYDQAAF KM RG NL -	- AILNFP			
CaERF38	KYRG I QRQ - PWG KWA E I RD P RKG -	- RKRWLGTFTETAEADALYDQAAF KM RG AK -	- ALNFP			
CaERF131	HYIG VRKR - I RD S R N G -	- T R R V L S R N G -	- T C L N F S			
CaERF127	HYIG VRKR - I RD S R N G -	- R R V W L T F T D E E A A L T Y D Q A A F C M R G P S -	- T C L N F S			
CaERF12	HYIG VRKR - I RD S R N G -	- R R V W L T F T D E E A A L T Y D Q A A F C M R G P S -	- T C L N F S			
CaERF132	S Y R G V R R R - PWG K Y A E I R D S R N S -	- R V R W L G T F T D E E A A L A Y D Q A A Y A A L H G T M -	- A V L N Y P			
CaERF56	S Y R G V R R R - PWG K Y A E I R D S R N S -	- R V R W L G T F T D E E A A L A Y D Q A A F A A M R G S M -	- A I L N F P			
CaERF128	QYIG VRKR - PWG K Y A E I R D S R N S -	- I R V W L G T F T D E E A A L A Y D Q A A F M R G P S -	- T Y L N F P			
CaERF37	HYRG VRKR - PWG K Y A E I R D S R N G -	- I R V W L G T F T D E E A A M A Y D K A A L R I RG PK -	- A N L N F P			
CaERF57	HYRG VRKR - PWG K Y A E I R D S R N G -	- I R V W L G T F T D E E A A M A Y D K A A L R I RG PK -	- A N L N F P			
CaERF55	HYRG VRKR - PWG K Y A E I R D S R N G -	- GTRVWLGTFTDVAADAKAYDRAAFLKLRGSK -	- A I L N F P			
CaERF51	HYRG VRKR - PWG K Y A E I R D S R N G -	- S R Q W L G T F T D E E A A A R A N D K A A F A N L K G H I -	- A I L N F P			
CaERF50	S Y R G V R R R - PWG K Y A E I R D S R N S -	- R V R W L G T F T D E E A A L A Y D Q A A F M R G S M -	- A I L N F P			
CaERF72	S Y R G V R R R - PWG K Y A E I R D S R N S -	- I R V W L G T F T D E E A A L A Y D Q A A F M R G T R -	- A I L N F S			
CaERF86	HYIG VRKR - PWG K Y A E I R D S R N G -	- I R V W L G T F T D E E A A L A Y D Q A A F M R G P L -	- A L N F P			
CaERF96	HYRG VRKR - PWG K Y A E I R D P K N G -	- ARVWLGTFTETAEQEEAIAYDQAAF C M R G P S -	- A L N F P			
CaERF93	KYRG VRRR - PWG K Y A E I R D P R K -	- G A R L W L G T E S P K D A A L A Y D R A A F K L R G T R -	- A L N F P			
CaERF78	KYRG VRRR - PWG K Y A E I R D P R K -	- G A R L W L G T E S P K D A A L A Y D R A A F K L R G T R -	- A L N F P			
CaERF25	KYRG VRRR - PWG K Y A E I R D P T K S -	- G A R L W L G T E S P K D A A L A Y D Q A A Y A A L H G T M -	- A V L N P			
CaERF58	KYRG VRRR - PWG K Y A E I R D P T K S -	- G R V W L G T F T D E E A A A L A Y D Q A A F M R G S M -	- A I L N F P			
CaERF129	HYIG VRKR - PWG K Y A E I R D P T K S -	- I R V W L G T F T D E E A A A L A Y D Q A A F M R G P S -	- T Y L N F P			
CaERF29	HYIG VRKR - PWG K Y A E I R D P T K S -	- I R V W L G T F T D E E A A A L A Y D Q A A F M R G P S -	- T Y L N F			

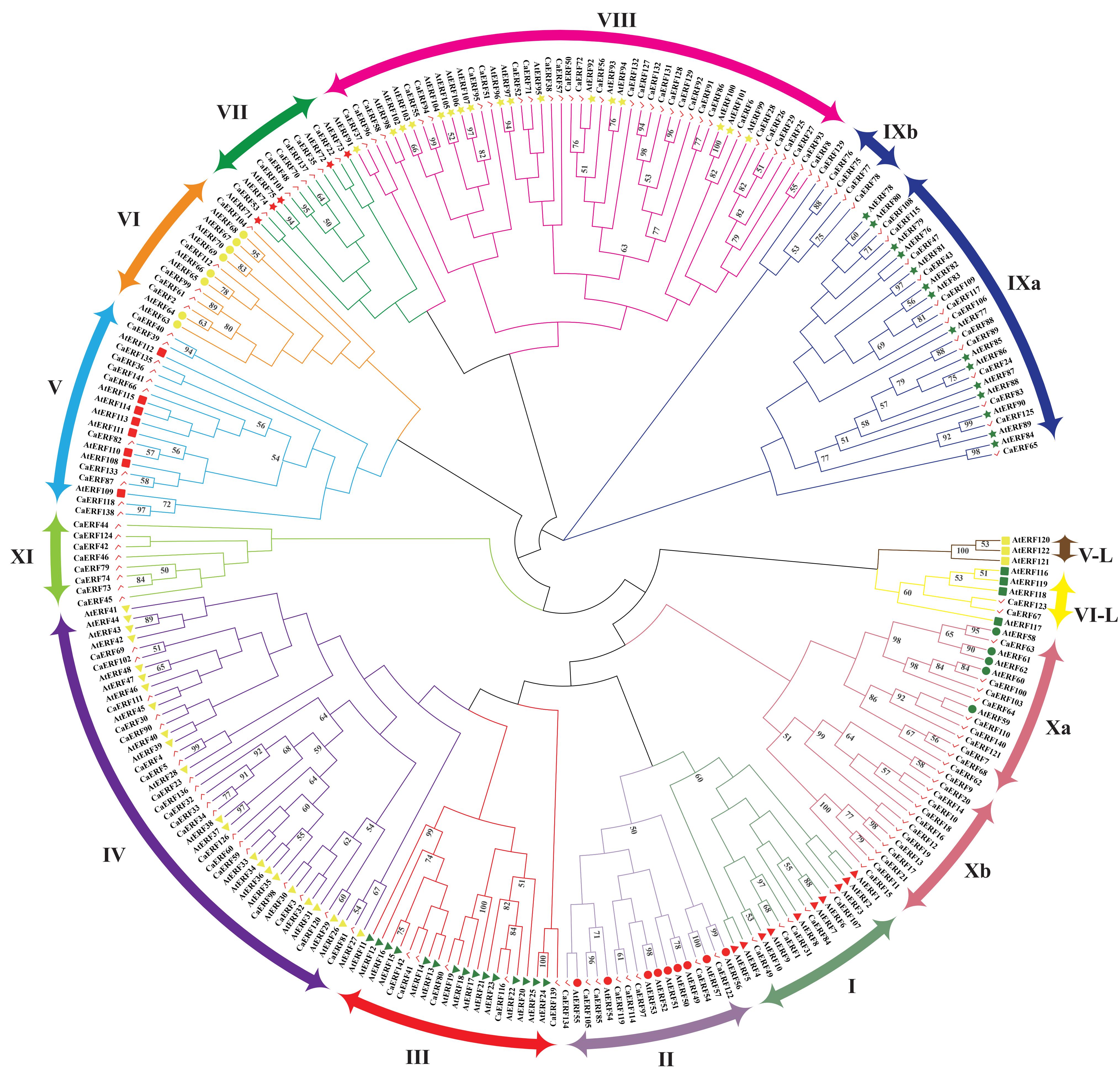


Fig. S4. Phylogenetic tree of the pepper ERF family in relation to *Arabidopsis*. The different-colored branch indicate different groups of ERF proteins. Red check represented ERF proteins in pepper, other different olor shapes indicated different groups in phylogeny of *Arabidopsis* (Nakano et al., 2006).

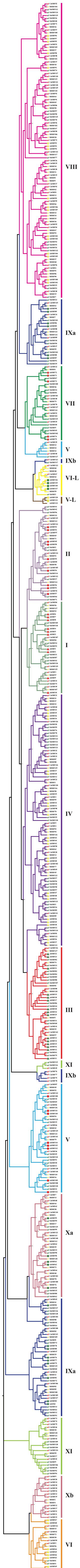


Fig. S5. Phylogenetic tree of the pepper ERF family in relation to tomato (137), rice (138) and *Arabidopsis* (122). The different-colored branch indicate different groups of ERF proteins. Red, yellow and green check represented ERF proteins in pepper, tomato and rice, respectively. Other different olor shapes indicated different groups in phylogeny of *Arabidopsis* (Nakano et al., 2006).

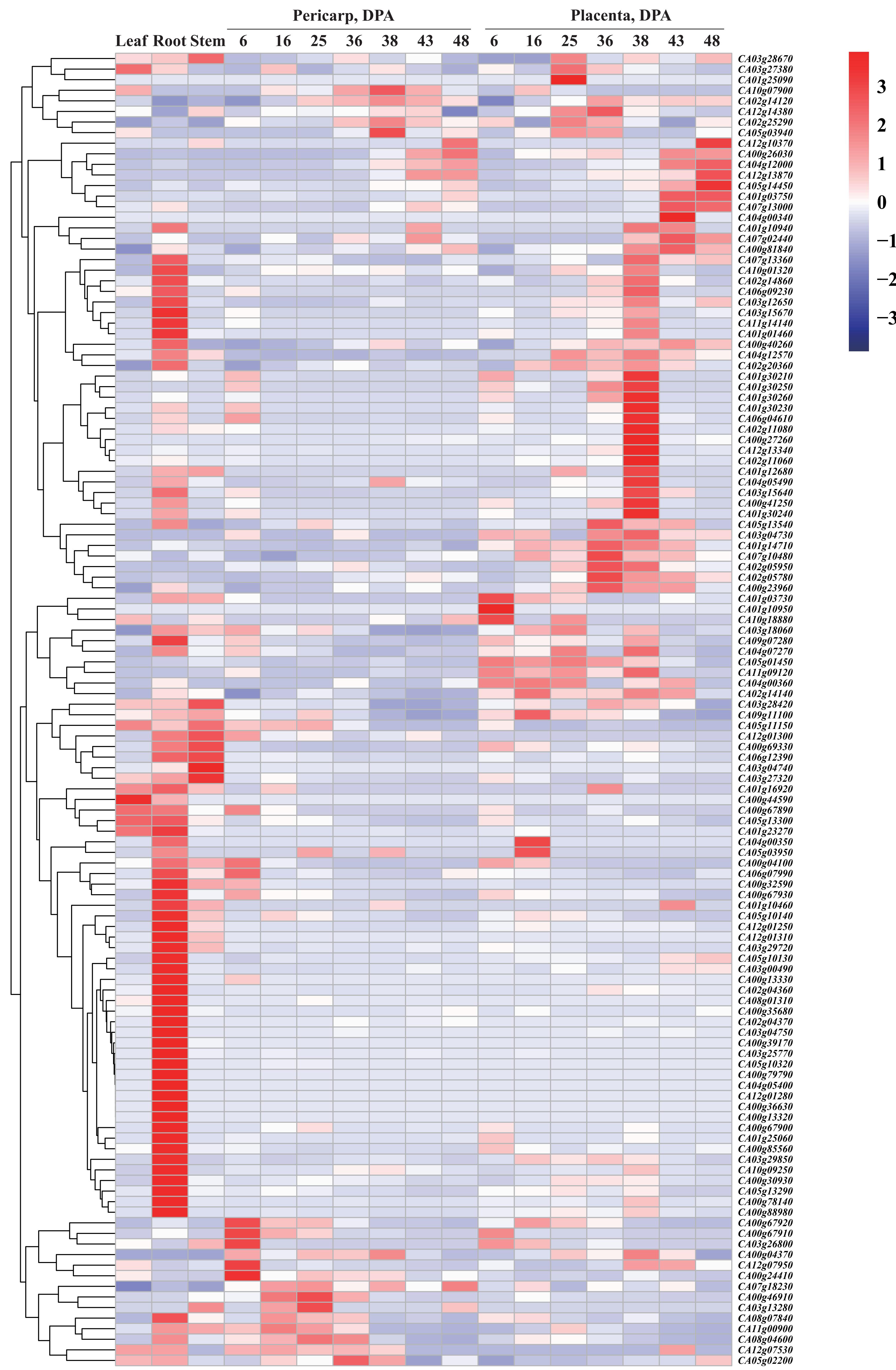


Fig. S6. The expression patterns of *CaERF* genes in different tissues . The heat map was directly constructed by using the RPKM value. The RPKM value was mapped to the *Capsicum annuum* genome of version 1.5 performed by Kim et al (2014).