Table S1 The primers of *OeCBF* genes for RT-qPCR analysis

Primer name	Sequence5'-3'
β-actin-F[1]	GGAATCTGCAGGAATCCACG
β-actin-R[1]	GAACCACCACTGAGGACGAT
tubulin-F[2]	AGATGATGATGACGAGTATG
tubulin-R[2]	GACGATGTATCCGTCTATCA
OeCBF1-DL-F	AATGGGTGTGTGAAGTGC
OeCBF1-DL-R	AAGCAGCTTGAAGAGCAG
OeCBF2-DL-F	TTCCATCCTTGAAGGGAC
OeCBF2-DL-R	ACCTCTGAATGCCAATGC
OeCBF3-DL-F	ATGGCTAGGAACTCATCC
OeCBF3-DL-R	GTTGTGTCCGATGTTGTC
OeCBF4-DL-F	GCTTCGAGTAAGTCCAAG
OeCBF4-DL-R	ACATCACTGGAGATTGGC

Note: [1] Mei, K.K.; Pu X.; Zhu Q.P.; Xie Q.D.; Chen H.P.; Yang Z.S.; Huang, Q.M. Identification and Characterization of the HMGR Multigene Family Involved in Terpenoids Biosynthesis in *Olea europaea*. *Genomics and Applied Biology* **2018**, 37(5), 2003-2012. DOI: 10.13417/j.gab.037.002003 (Chinese)

[2] Wang, L.J.; Wang, Y.; Lu B.; Luo M.; Xu, L.W.; Yuan, X.L.; Li, X.Z. Identification and expression analysis ofAP2/ERF transcription factor under water stress in *Olea europaea*. *Guihaia* **2022**, 42(12):2032-2043. DOI:10.11931/guihaia.gxzw202103044 (Chinese)

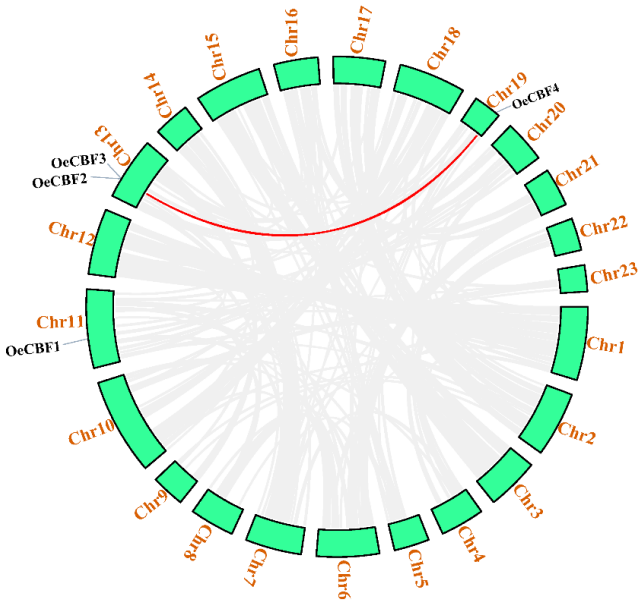


Figure S1 The gene collinearity of the *CBF* gene family in the *Olea europaea* genome. Chr1-Chr23 represent the 23 chromosomes of *Olea europaea*.

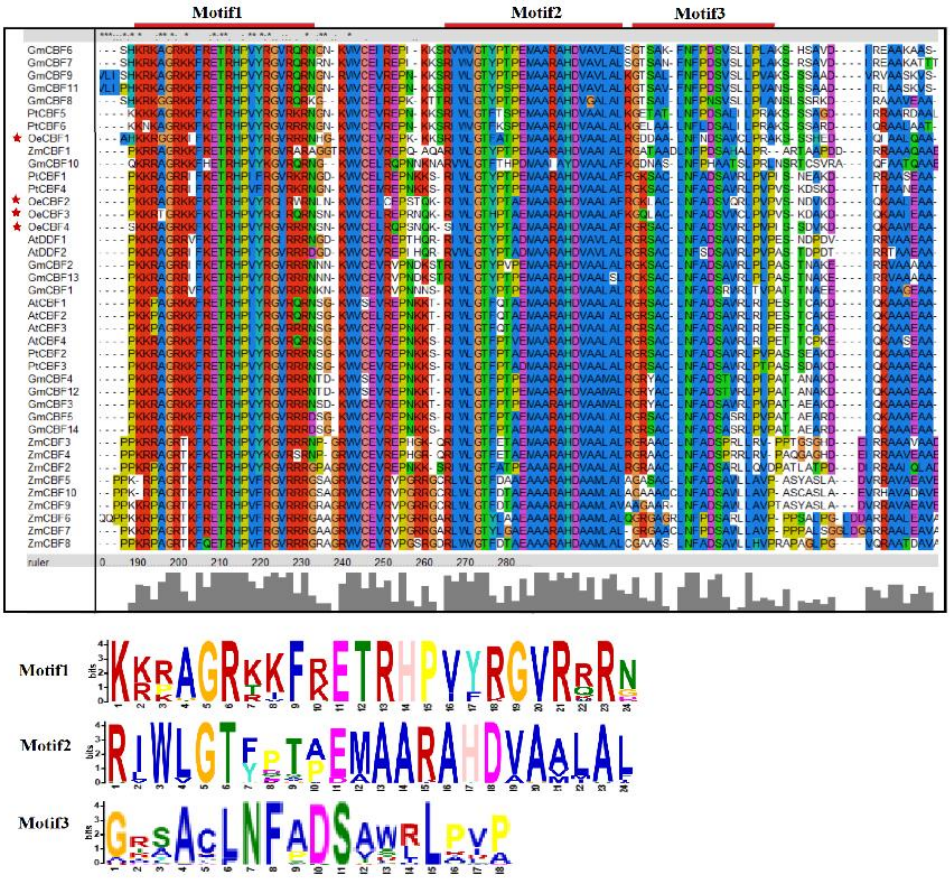


Figure S2 a. Multiple sequences alignment of CBFs of *Olea europaea, Zea mays, Glycine max, Populus trichocarpa, Arabidopsis thaliana*. b. The amino acid sequence of the motif1, motif2, and motif3.

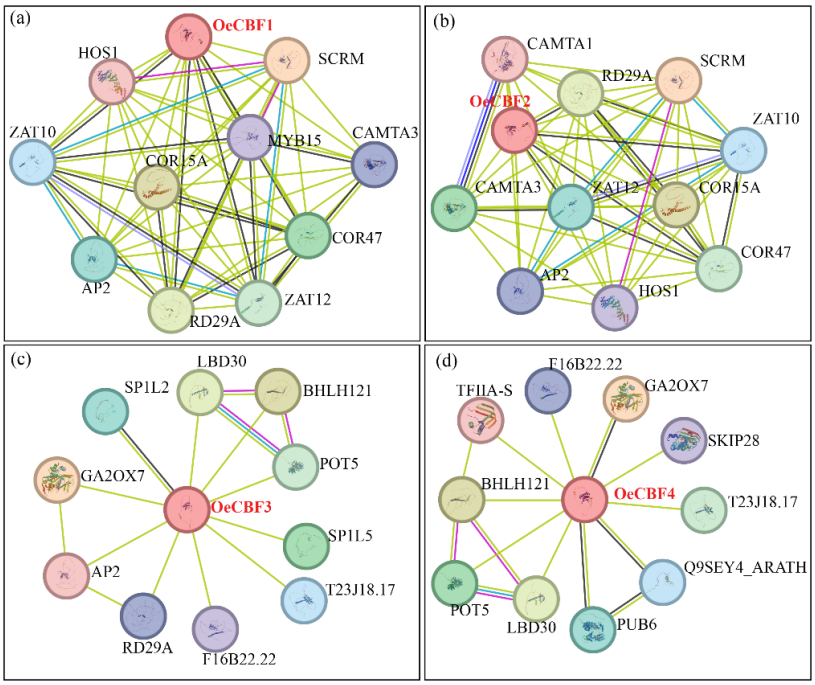


Figure S3 Predicted interactions of OeCBFs proteins based on the Arabidopsis reference genome.

a. OeCBF1. b. OeCBF2. c. OeCBF3. d. OeCBF4.