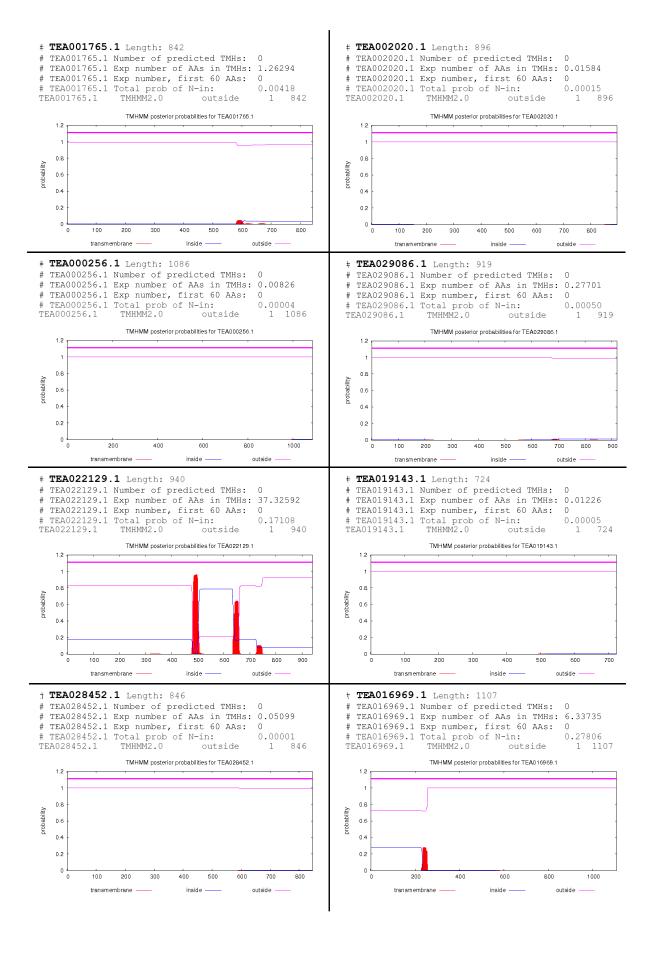
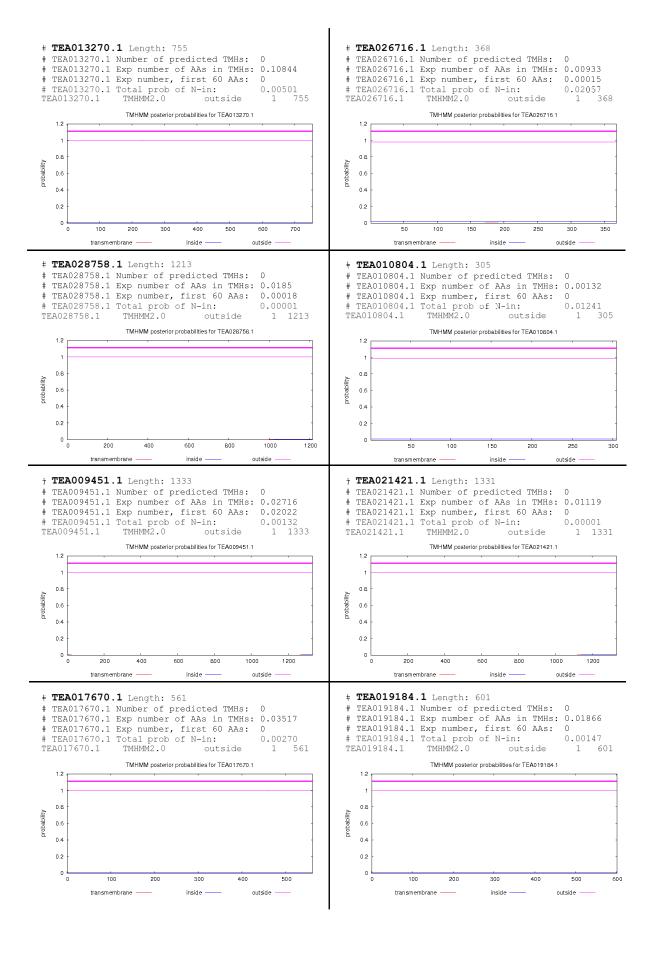
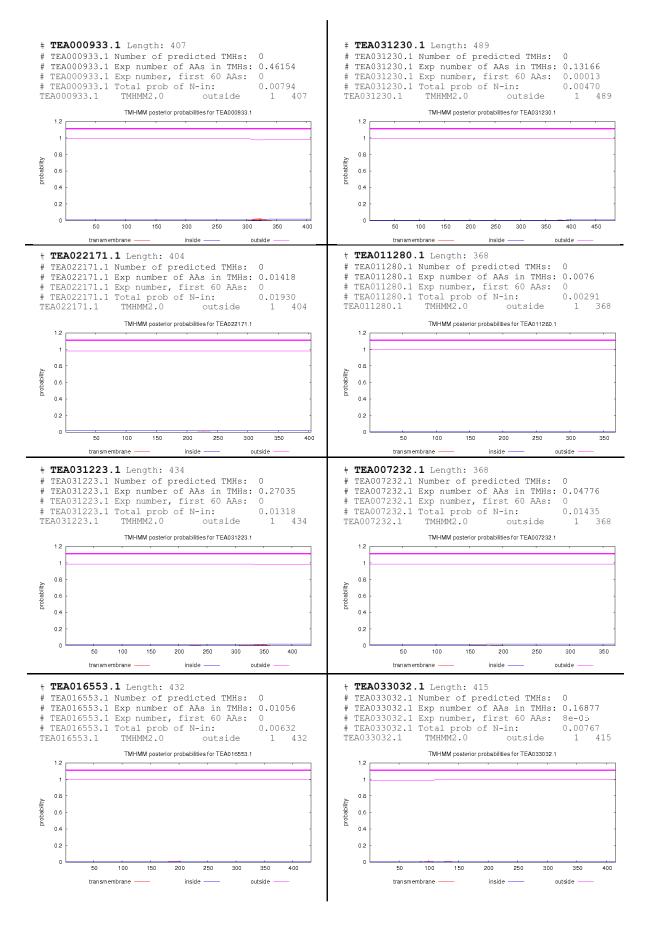
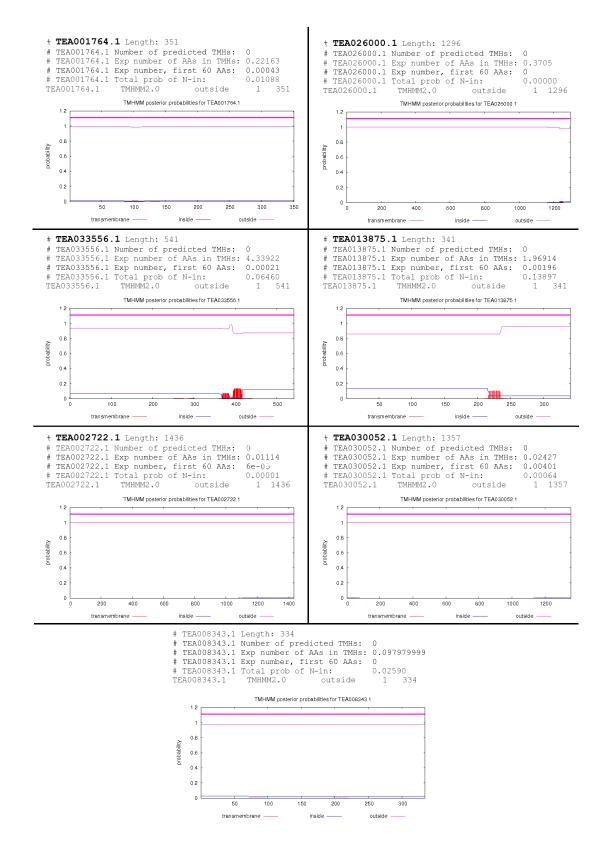


Supplementary Figure S1: Transmembrane helices of MAPKKKs of MEKK subfamily in *C. sinensis*. TMHMM Server, v.2.0 (http://www.cbs.dtu.dk/services/TMHMM/), was used to generate the transmembrane helices.

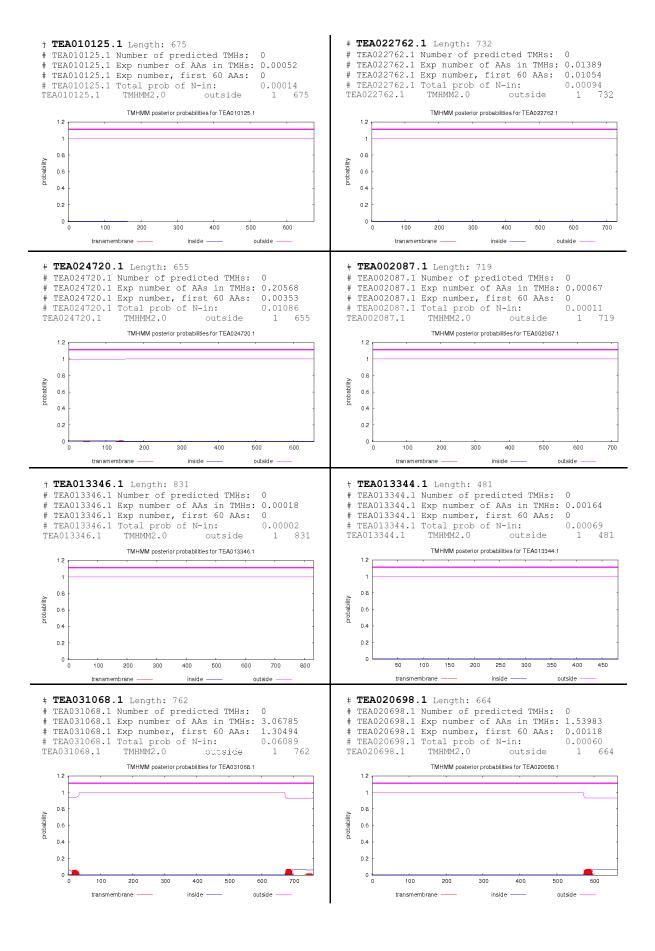


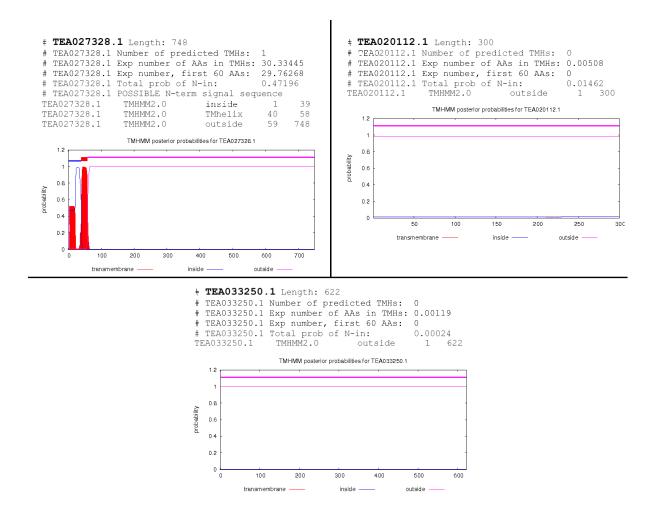




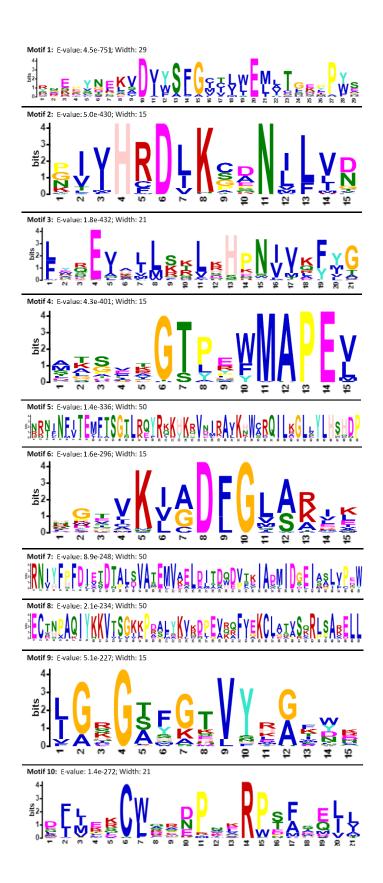


Supplementary Figure S2: Transmembrane helices of MAPKKKs of Raf subfamily in *C. sinensis*. TMHMM Server, v.2.0 (http://www.cbs.dtu.dk/services/TMHMM/), was used to generate the transmembrane helices.

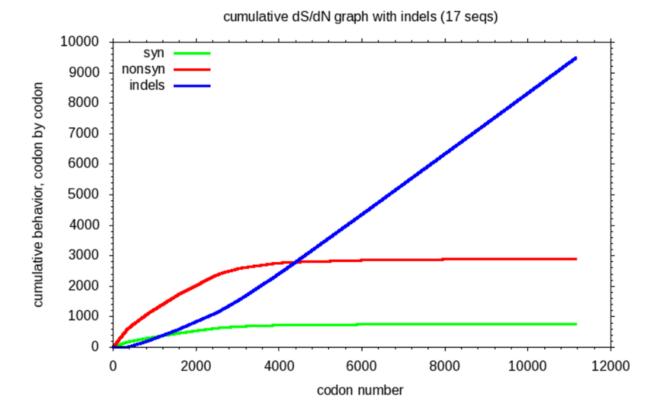




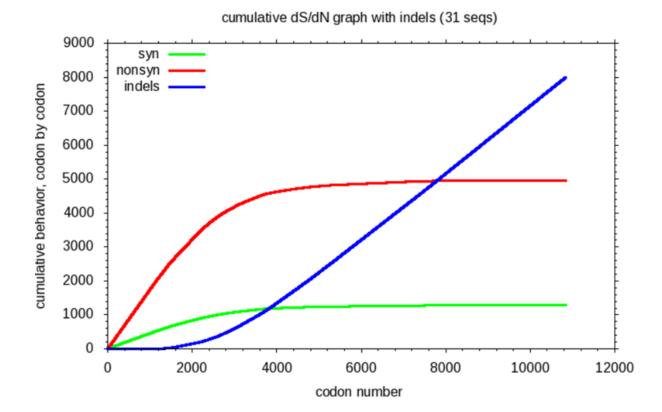
Supplementary Figure S3: Transmembrane helices of MAPKKKs of ZIK subfamily in *C. sinensis*. TMHMM Server, v.2.0 (http://www.cbs.dtu.dk/services/TMHMM/), was used to generate the transmembrane helices.



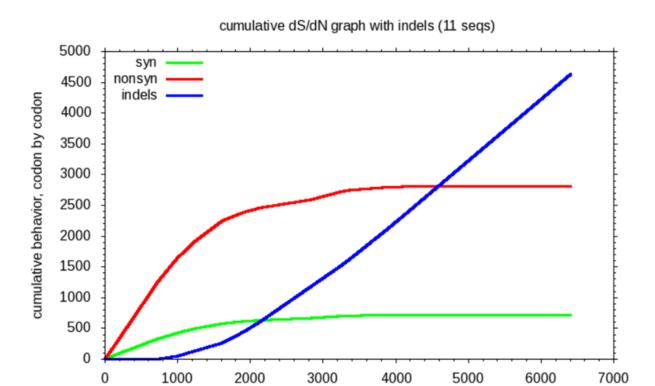
Supplementary Figure S4: Motif logos of the 10 identified motifs in 59 MAPKKKs of *C. sinensis*. The motif logos were generated by MEME suite.



Supplementary Figure S5: The ds/dn cumulative graph of MAPKKKs of MEKK subfamily in *C. sinensis*. SNAP server (https://www.hiv.lanl.gov/content/sequence/SNAP/SNAP.html) has been used to generate the graph.

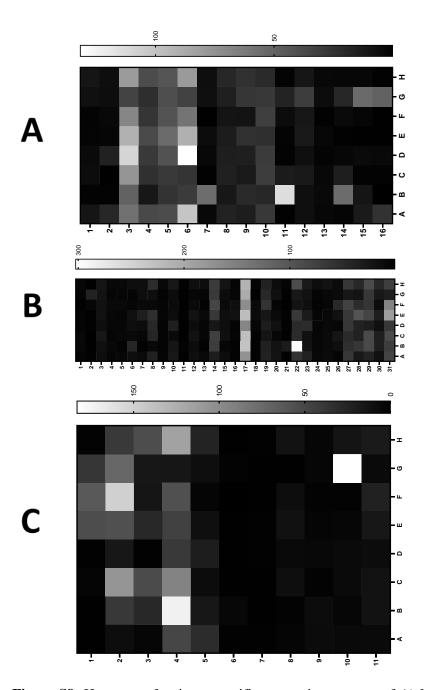


Supplementary Figure S6: The ds/dn cumulative graph of MAPKKKs of Raf subfamily in *C. sinensis*. SNAP server (https://www.hiv.lanl.gov/content/sequence/SNAP/SNAP.html) has been used to generate the graph.

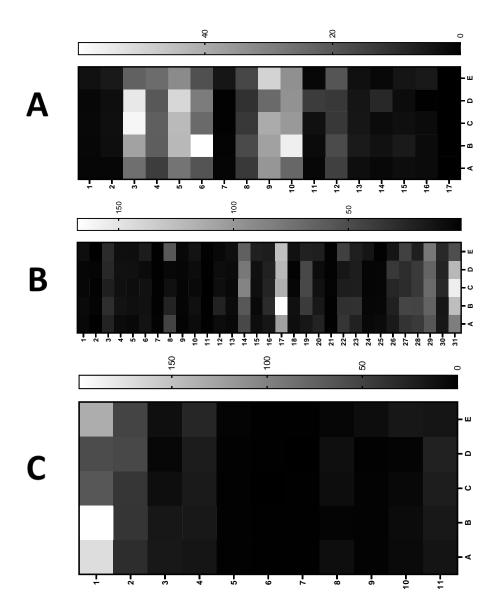


Supplementary Figure S7: The ds/dn cumulative graph of MAPKKKs of ZIK subfamily in *C. sinensis*. SNAP server (https://www.hiv.lanl.gov/content/sequence/SNAP/SNAP.html) has been used to generate the graph.

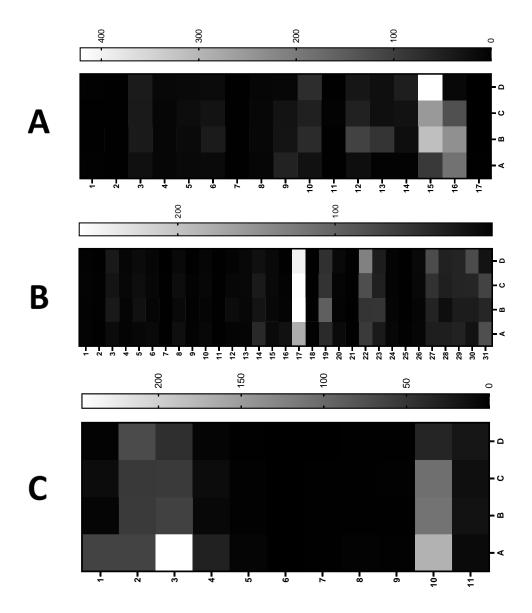
codon number



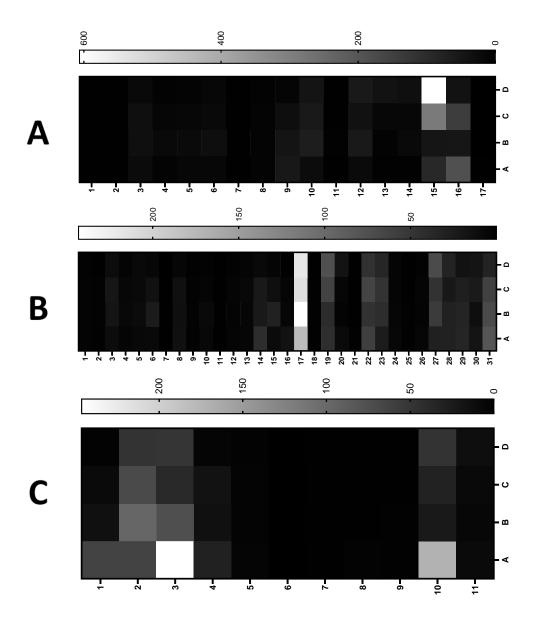
Supplementary Figure S8: Heat maps for tissue-specific expression patterns of A) MEKK; B) Raf and; C) ZIK genes in *C. sinensis*. The relative expression of these genes was analysed in different developmental stages, by using GraphPad Prism 8 software. The level of expression was in transcript per million (TPM). The numbers below represent the tea MAPKKK genes and the alphabets on the right represent the 8 different tissues.



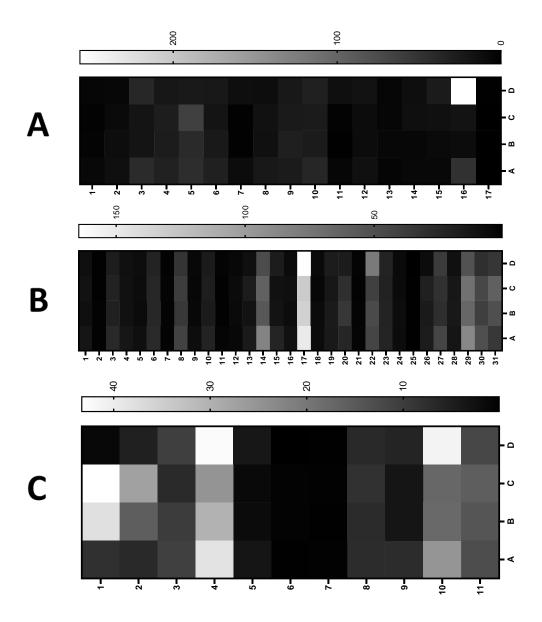
Supplementary Figure S9: Heat maps for cold stress expression patterns of A) MEKK; B) Raf and; C) ZIK genes in C. sinensis. The relative expression of these genes was analysed in different developmental stages, by using GraphPad Prism 8 software. The level of expression was in transcript per million (TPM). The numbers below represent the tea MAPKKK genes and the alphabets on the right represent the parameters of study.



Supplementary Figure S10: Heat maps for drought stress expression patterns of A) MEKK; B) Raf and; C) ZIK genes in *C. sinensis*. The relative expression of these genes was analysed in different developmental stages, by using GraphPad Prism 8 software. The level of expression was in transcript per million (TPM). The numbers below represent the tea MAPKKK genes and the alphabets on the right represent the parameters of study.



Supplementary Figure S11: Heat maps for salt stress expression patterns of (A) MEKK (B) Raf and (C) ZIK genes in *C. sinensis*. The relative expression of these genes was analysed in different developmental stages, by using GraphPad Prism 8 software. The level of expression was in transcript per million (TPM). The numbers below represent the tea MAPKKK genes and the alphabets on the right represent the parameters of study.



Supplementary Figure S12: Heat maps for MeJA treatment expression patterns of (A) MEKK (B) Raf and (C) ZIK genes in *C. sinensis*. The relative expression of these genes was analysed in different developmental stages, by using GraphPad Prism 8 software. The level of expression was in transcript per million (TPM). The numbers below represent the tea MAPKKK genes and the alphabets on the right represent the parameters of study.