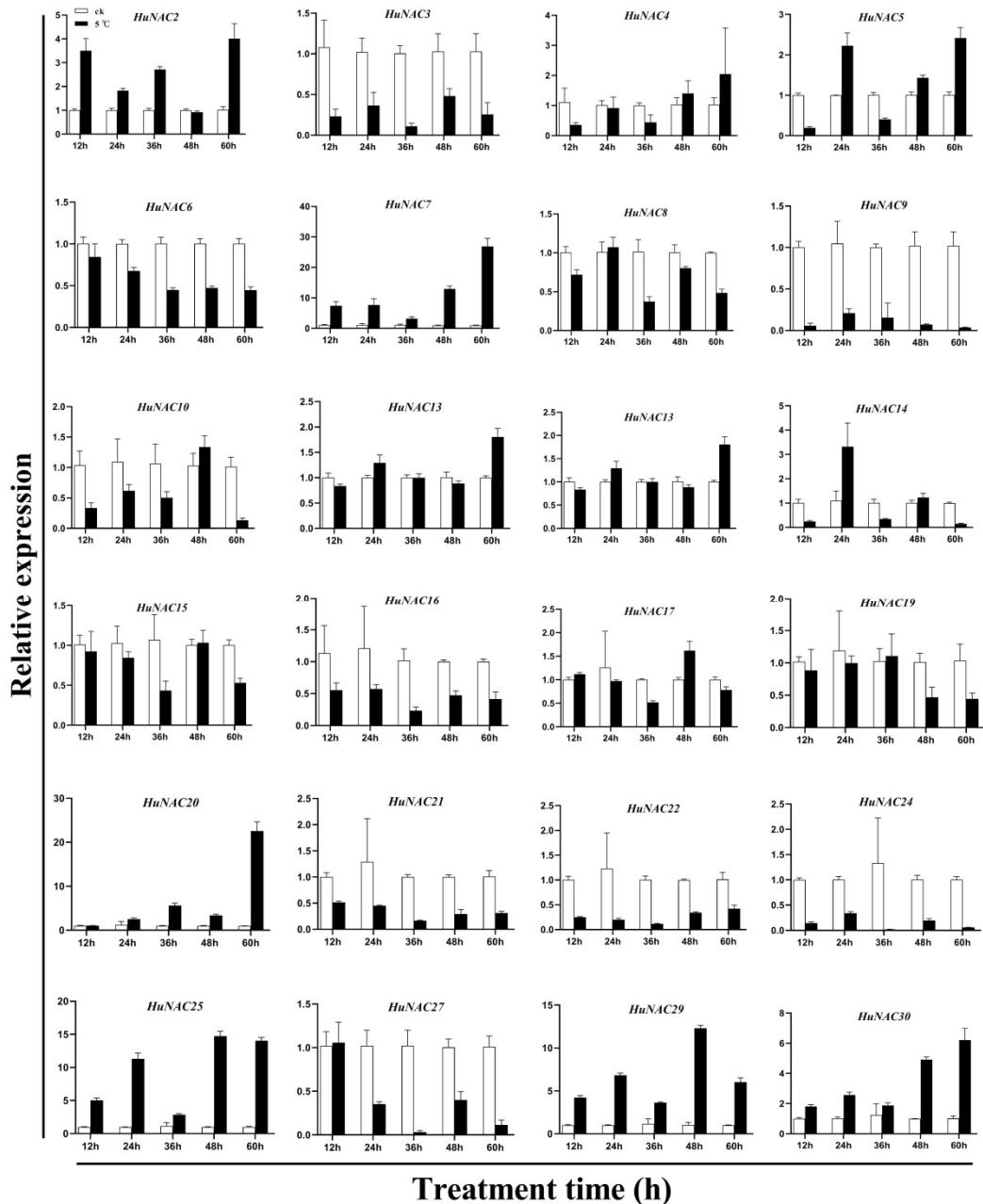




Figure S1. Multilevel consensus sequence and their logo of HuNAC proteins predicted by MEME web server.



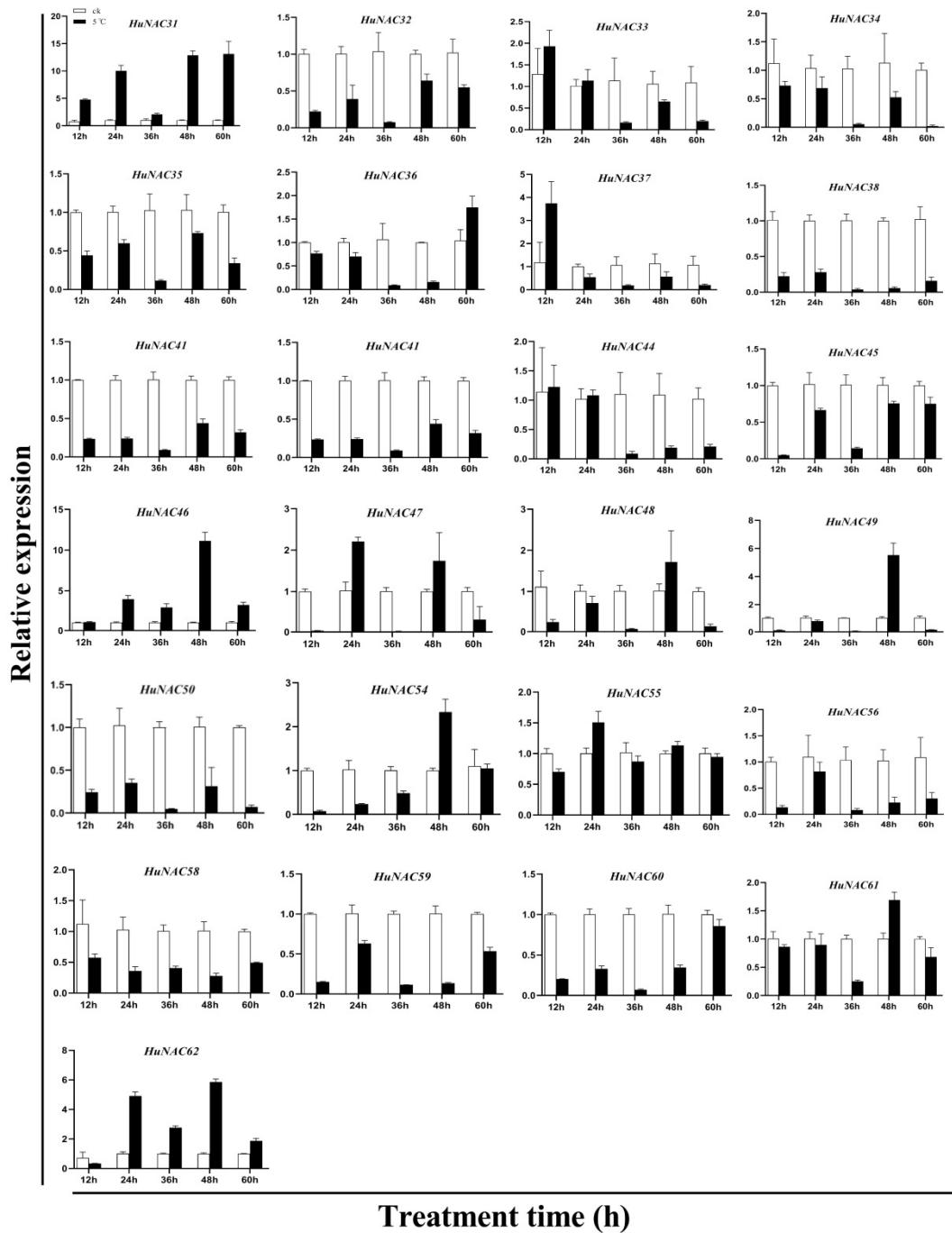


Figure S2. Expression patterns of 64 *HuNAC* genes under cold stress treatments. Three biological replicates were used and bars represent the relative expression of different genes under cold stress.

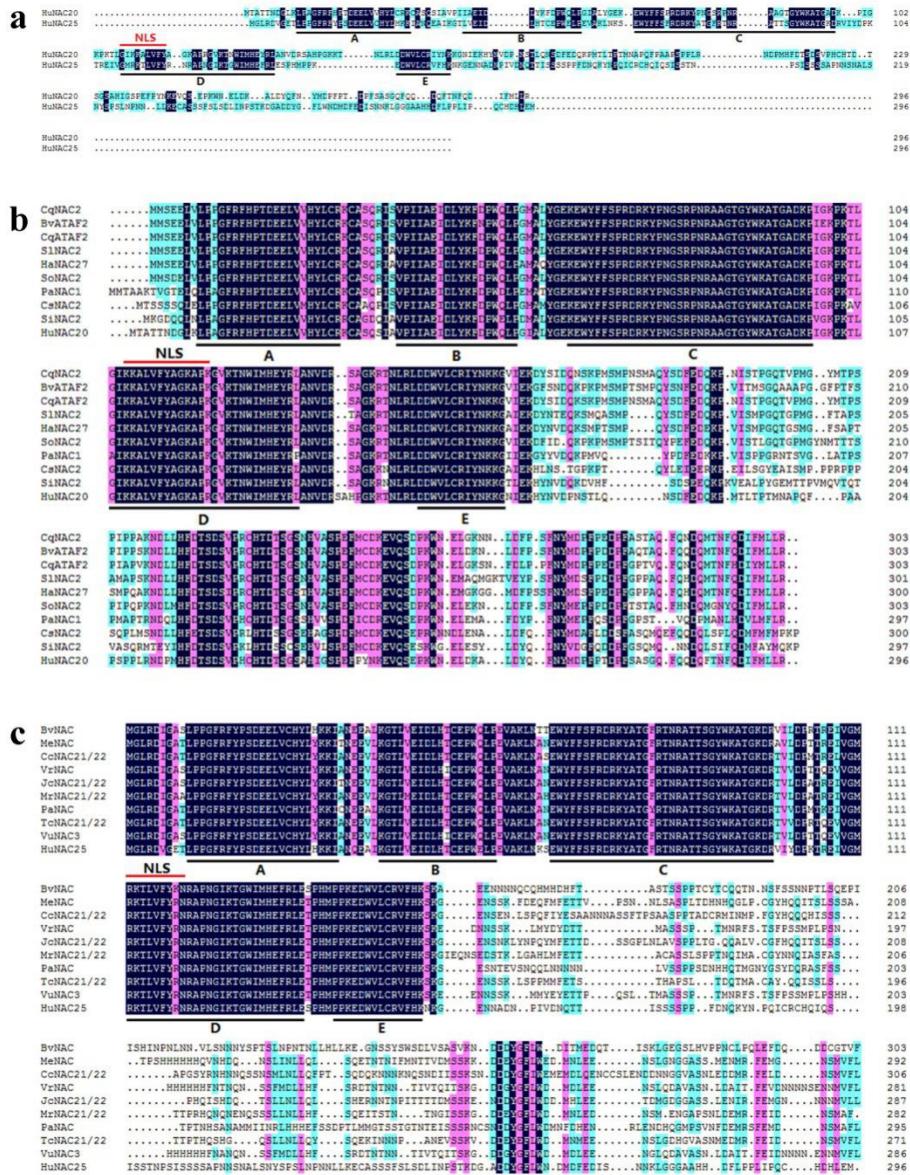


Figure S3. Multiple alignments of HuNAC20 and HuNAC25 proteins and other plant NAC proteins. The accession numbers are as follows: CqNAC2 (*Chenopodium quinoa*, XP_021772603.1), BvATAF2 (*Beta vulgaris*, QGZ00533.1), CqATAF2 (*Chenopodium quinoa*, XP_021734633.1), S1NAC2 (*Suaeda liaotungensis*, AGZ15313.1), HaNAC27 (*Haloxylon ammodendron*, AOC59210.1), SoNAC2 (*Spinacia oleracea*, XP_021863783.1), PaNAC1 (*Phytolacca acinosa*, ADQ00628.1), CsNAC2 (*Camellia sinensis*, XP_028092030.1), SiNAC2 (*Sesamum indicum*, XP_011099683.1), BvNAC (*Beta vulgaris*, XP_010679326.1), MeNAC (*Manihot esculenta*, XP_021630142.1), CcNAC21/22 (*Citrus clementine*, XP_006443820.1), VrNAC (*Vigna radiate var. radiate*, XP_014495173.1), JcNAC21/22 (*Jatropha curcas*, XP_012085297.1), MrNAC21/22 (*Morella rubra*, KAB1223758.1), PaNAC (*Parasponia andersonii*, PON62646.1), TcNAC21/22 (*Theobroma*

cacao, XP_007050267.1), VuNAC3 (*Vigna unguiculata*, XP_027920779.1)