

Figure S2 A



Figure S2 B

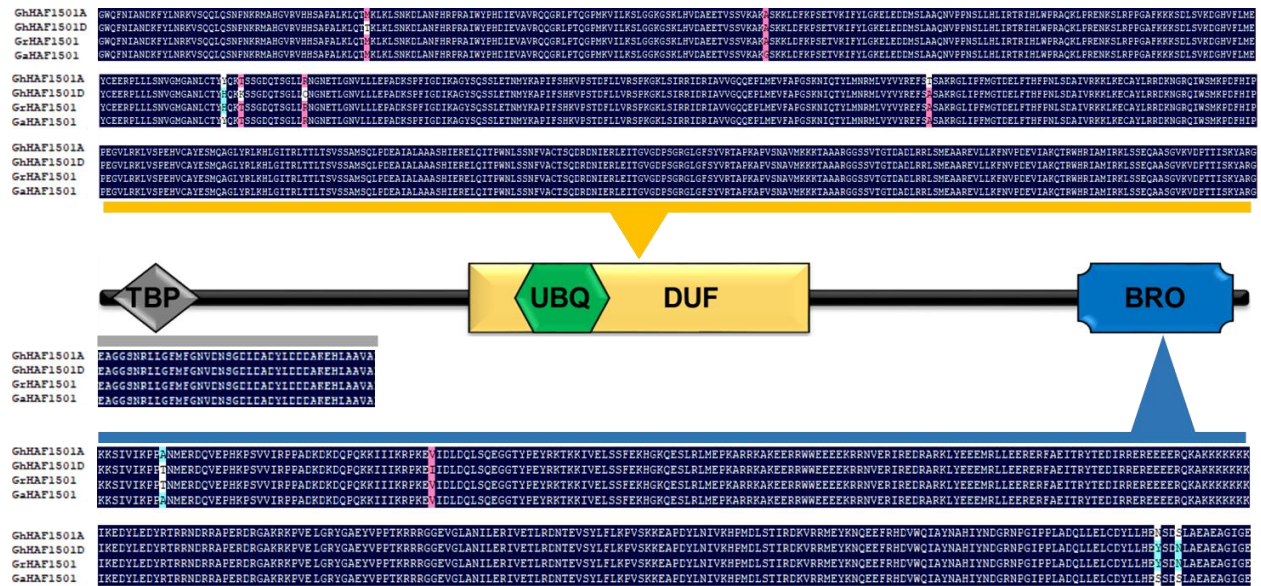


Figure S2 C

Figure S2 The amino acid sequence alignment of CBP (2A), GNAT (2B) and TAFii250 (2C) subgroups from *G. hirsutum*, *G. raimondii*, and *G. arboreum*. The conserved residues are highlighted in different colors.