Figure S1. Phylogenetic relationships of the CNGC family members in the diploid species of cotton. The amino acid sequences of cyclic nucleotide-gated channels (CNGCs) were aligned with ClustalW, and a consensus tree was generated by the Neighbor-Joining (NJ) method with 1000 bootstraps using MEGA X software (Kumar et al. *Mol Biol Evol*. 2018, 35:1547-1549). The cotton CNGCs were clustered into four groups (I, II, III, IV) and two subgroups (IV-A and IV-B), conforming to the classification of CNGCs in *Arabidopsis thaliana* (Talke et al. *Trends Plant Sci*. 2003, 8:286-293). *G. herbaceum*, GheCNGC1-20; *G. arboreum*, GaCNGC1-20; *G. raimondii*, GrCNGC1-20; *A. thaliana*, AtCNGC1-20.
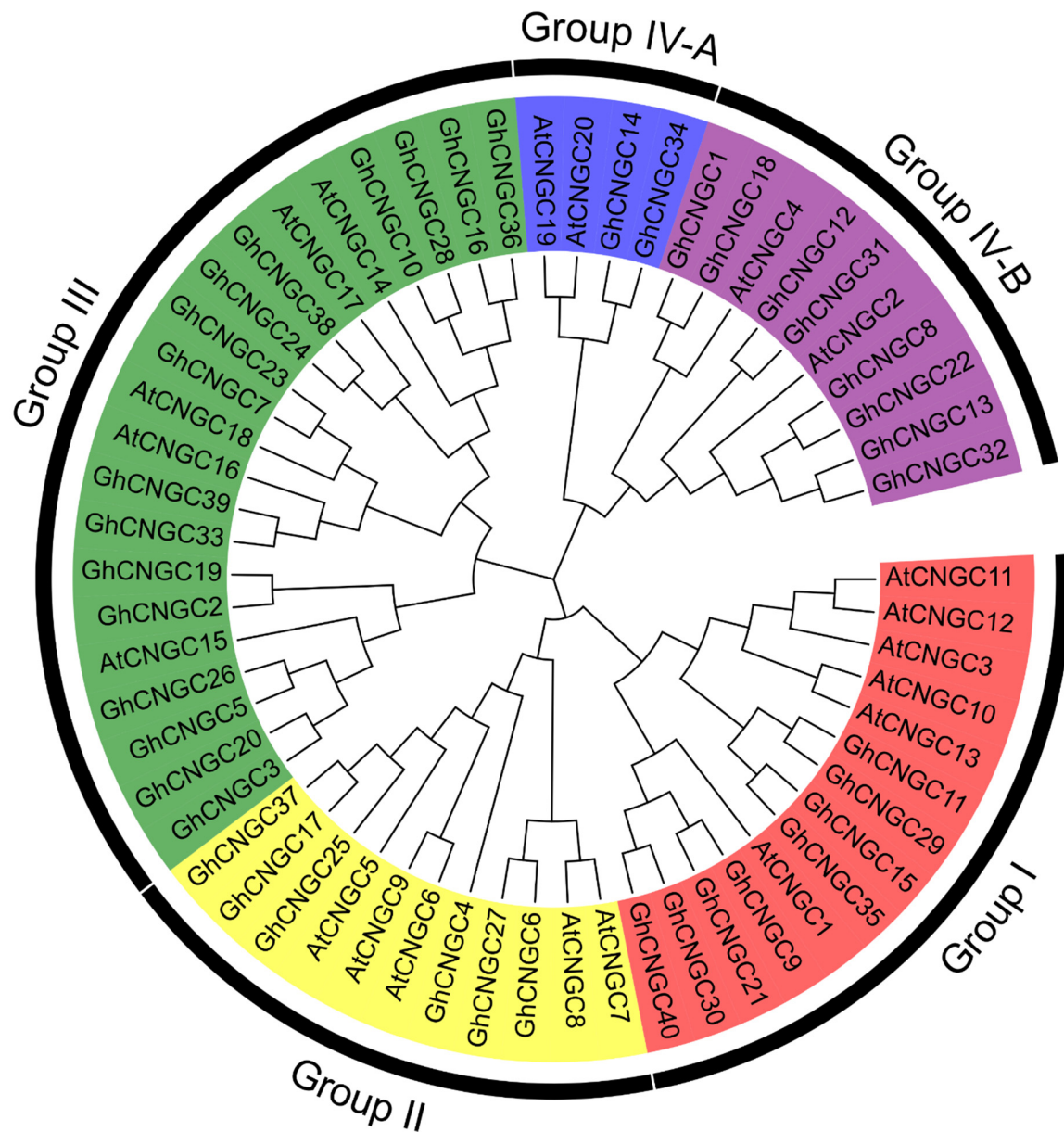
Figure S2. Phylogenetic relationships of the CNGC family members in the tetraploid species *Gossypium hirsutum*. The amino acid sequences of cyclic nucleotide-gated channels (CNGCs) were aligned with ClustalW, and a consensus tree was generated by the Neighbor-Joining (NJ) method with 1000 bootstraps using MEGA X software (Kumar et al. *Mol Biol Evol*. 2018, 35:1547-1549). The CNGCs in *G. hirsutum* were clustered into four groups (I, II, III, IV) and two subgroups (IV-A and IV-B), conforming to the classification of CNGCs in *Arabidopsis thaliana* (Talke et al. *Trends Plant Sci*. 2003, 8:286-293). *G. hirsutum*, GhCNGC1-40; *A. thaliana*, AtCNGC1-20.
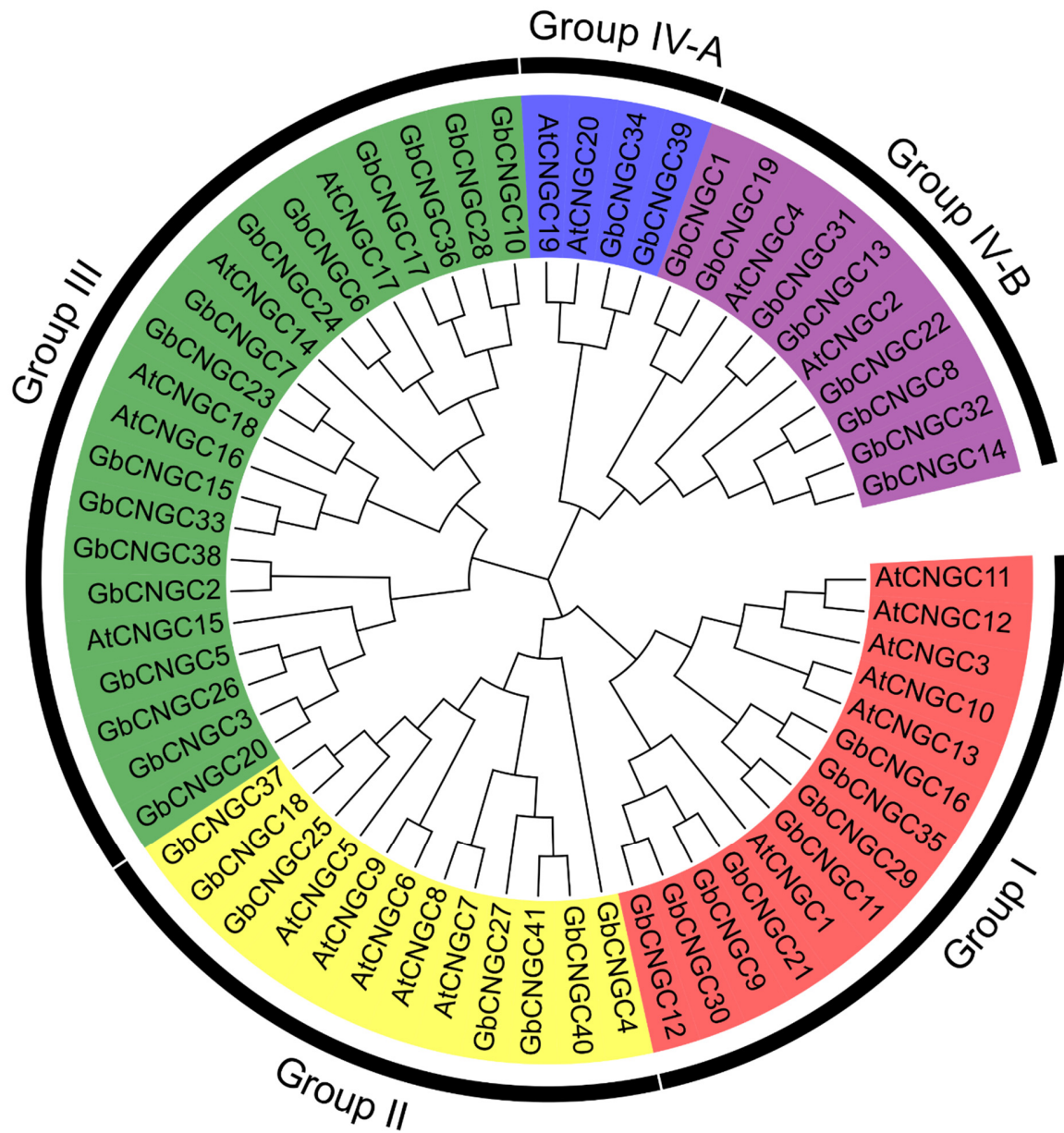
Figure S3. Phylogenetic relationships of the CNGC family members in the tetraploid species *Gossypium barbadense*. The amino acid sequences of cyclic nucleotide-gated channels (CNGCs) were aligned with ClustalW, and a consensus tree was generated by the Neighbor-Joining (NJ) method with 1000 bootstraps using MEGA X software (Kumar et al. *Mol Biol Evol*. 2018, 35:1547-1549). The CNGCs in *G. barbadense* were clustered into four groups (I, II, III, IV) and two subgroups (IV-A and IV-B), conforming to the classification of CNGCs in *Arabidopsis thaliana* (Talke et al. *Trends Plant Sci*. 2003, 8:286-293). *G. barbadense*, GbCNGC1-41; *A. thaliana*, AtCNGC1-20.

Figure S4. Phylogenetic relationships of the CNGC family members in the tetraploid species of cotton. The amino acid sequences of cyclic nucleotide-gated channels (CNGCs) were aligned with ClustalW, and a consensus tree was generated by the Neighbor-Joining (NJ) method with 1000 bootstraps using MEGA X software (Kumar et al. *Mol Biol Evol*. 2018, 35:1547-1549). The cotton CNGCs were clustered into four groups (I, II, III, IV) and two subgroups (IV-A and IV-B), conforming to the classification of CNGCs in *Arabidopsis thaliana* (Talke et al. *Trends Plant Sci*. 2003, 8:286-293). *G. hirsutum*, GhCNGC1-40; *G. barbadense*, GbCNGC1-41; *A. thaliana*, AtCNGC1-20.