

Genome-wide identification of *GhAAI* genes reveals that *GhAAI66* triggers a phase transition to induce early flowering

Ghulam Qanmber^{1,*}, Lili Lu^{1,*}, Zhao Liu^{1*}, Daoqian Yu¹, Kehai Zhou¹, Peng Huo¹, Fuguang Li^{1,2,†} and Zuoren Yang^{1,2,†}

1 State Key Laboratory of Cotton Biology, Key Laboratory of Biological and Genetic Breeding of Cotton, Institute of Cotton Research, Chinese Academy of Agricultural Sciences, Anyang, 455000, Henan, China

2 Zhengzhou Research Base, State Key Laboratory of Cotton Biology, Zhengzhou University, Zhengzhou, 4550001, Henan, China;

* These authors contributed equally to this work.

† Corresponding authors

Zuoren Yang: yangzuoren4012@163.com

Fuguang Li: aylifug@163.com

Author's information:

Ghulam Qanmber: gqkhan12@gmail.com

Lili Lu: biolll@126.com

Zhao Liu: liuzhaocaas@163.com

Daoqian Yu: yudaoqian88@163.com

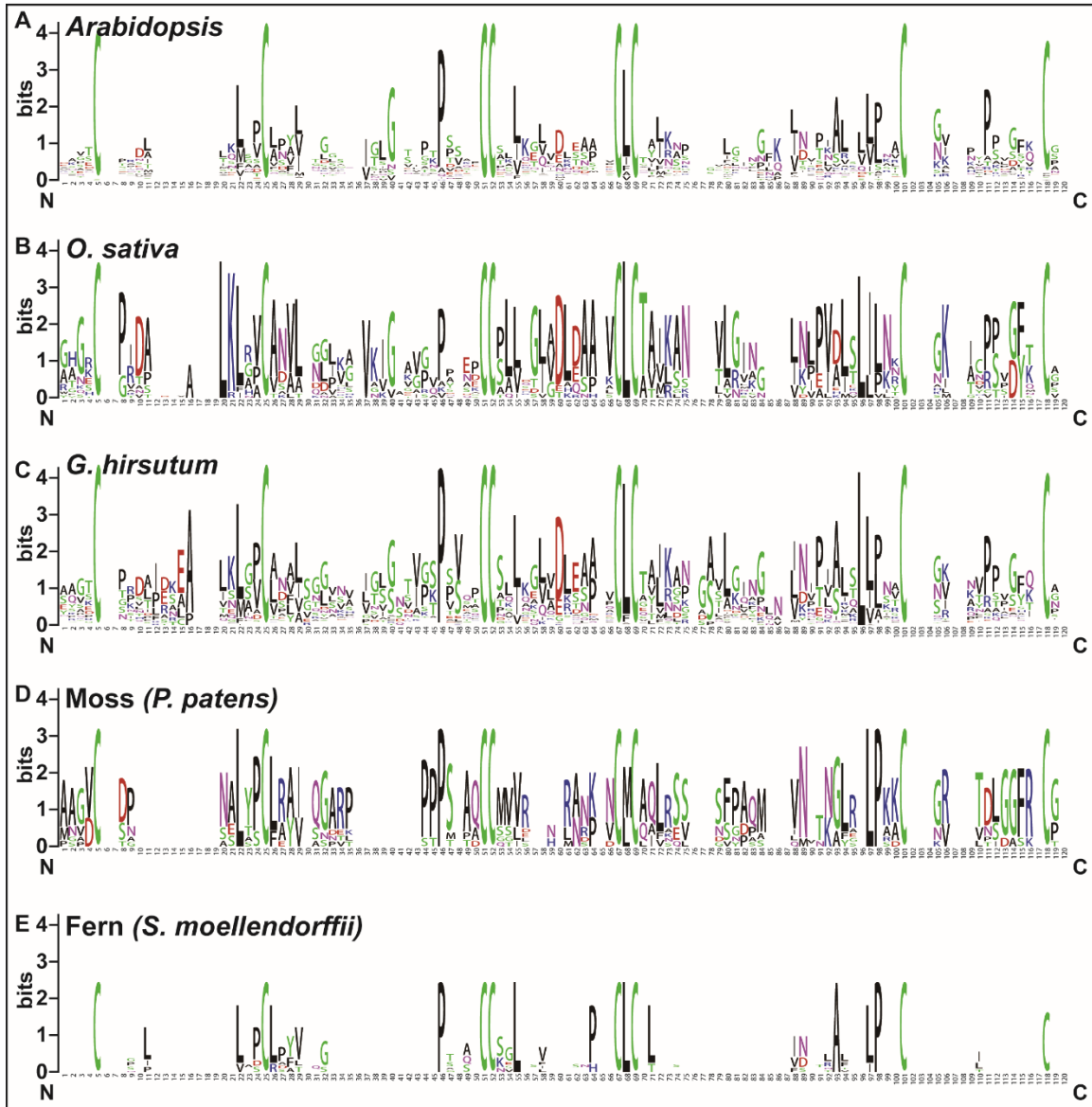
Kehai Zhou: zkhly@163.com

Peng Huo: hp20080224@126.com

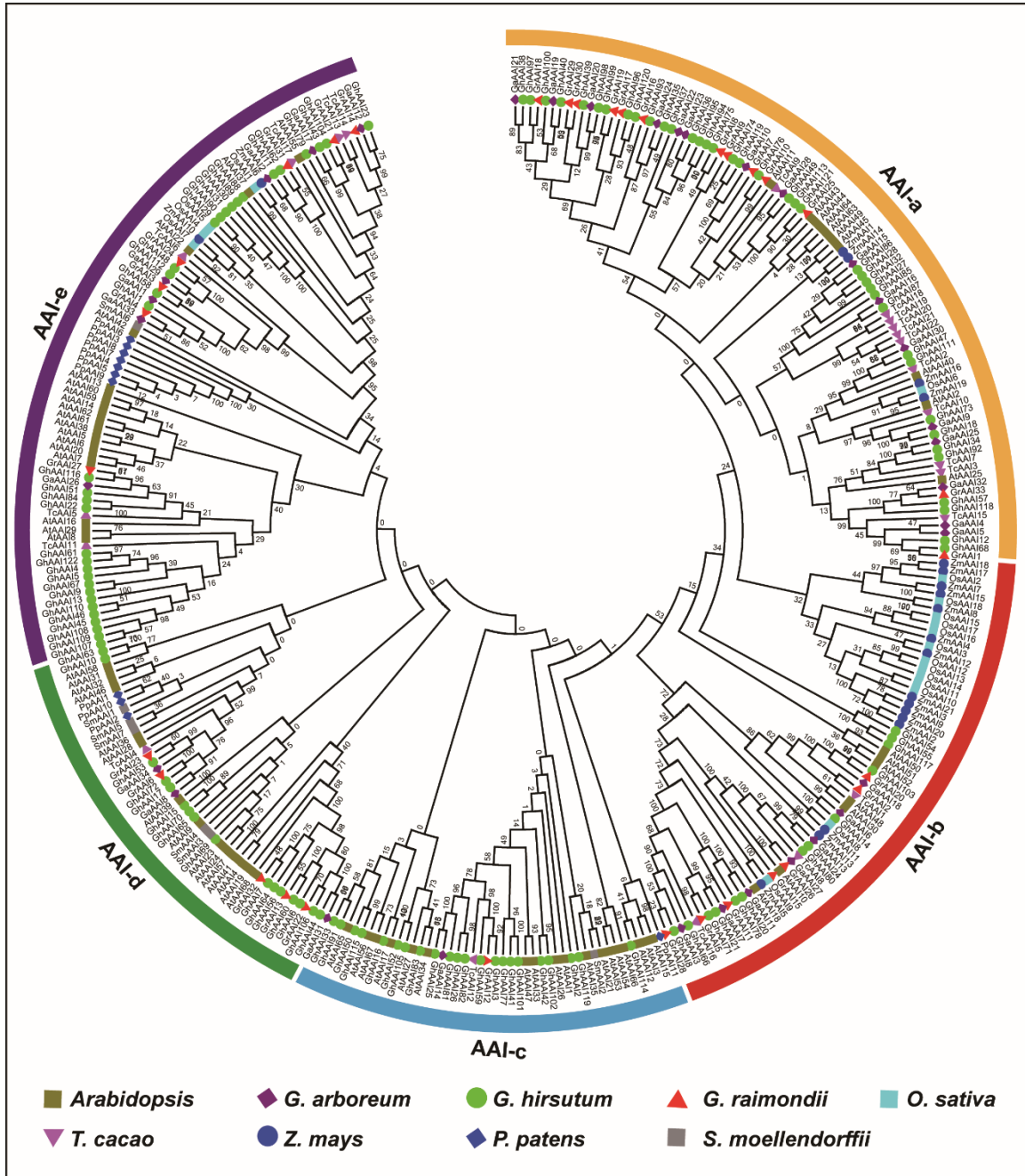
Fuguang Li: aylifug@163.com

Zuoren Yang: yangzuoren4012@163.com

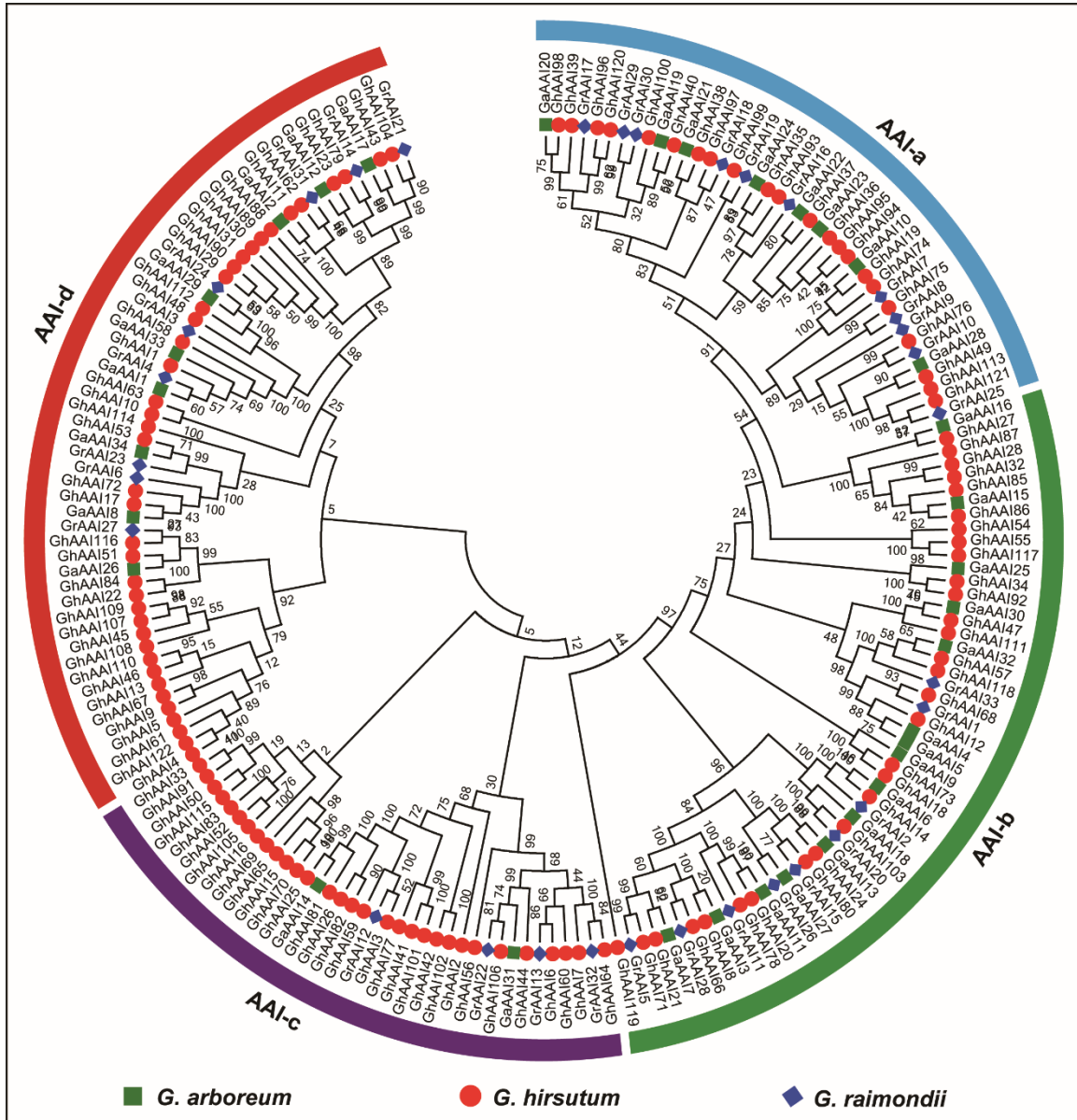
Supplementary Fig. S1. Conserved amino acid residue analysis among (A) *Arabidopsis*, (B) *O. sativa*, (C) *G. hirsutum*, (D) moss, and (E) fern *AAI* genes.



Supplementary Fig. S2. Phylogenetic tree constructed using ME. The phylogenetic tree divided all AAI genes from monocots, dicots, moss, and ferns into five major groups from AAI-a to AAI-e. The prefixes At, Ga, Gh, Gr, Tc, Os, Zm, Pp, and Sm were used before the names of *A. thaliana*, *G. arboreum*, *G. hirsutum*, *G. raimondii*, *T. cacao*, *O. sativa*, *Z. mays*, *P. patens* and *S. moellendorffii* AAI genes, respectively. Bootstrap values are noted near nodes of each branch.

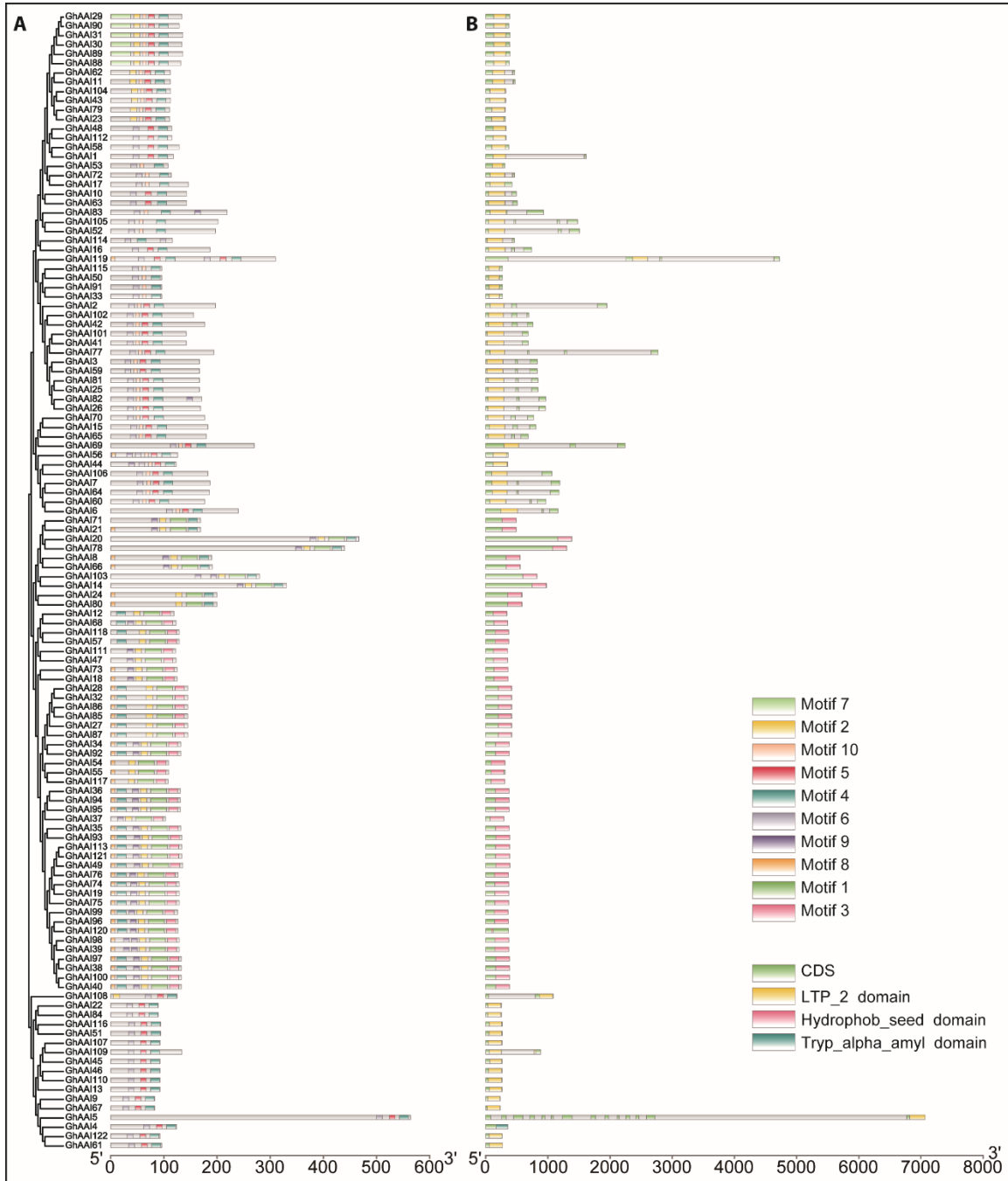


Supplementary Fig. S3. The phylogenetic tree was generated using the NJ method for cotton including *G. arboreum*, *G. hirsutum*, and *G. raimondii* AAI genes in order to estimate common ancestor hypothesis. Tree divided all cotton AAI genes into four groups represented by different colors. Bootstrap values are noted near nodes of each branch.

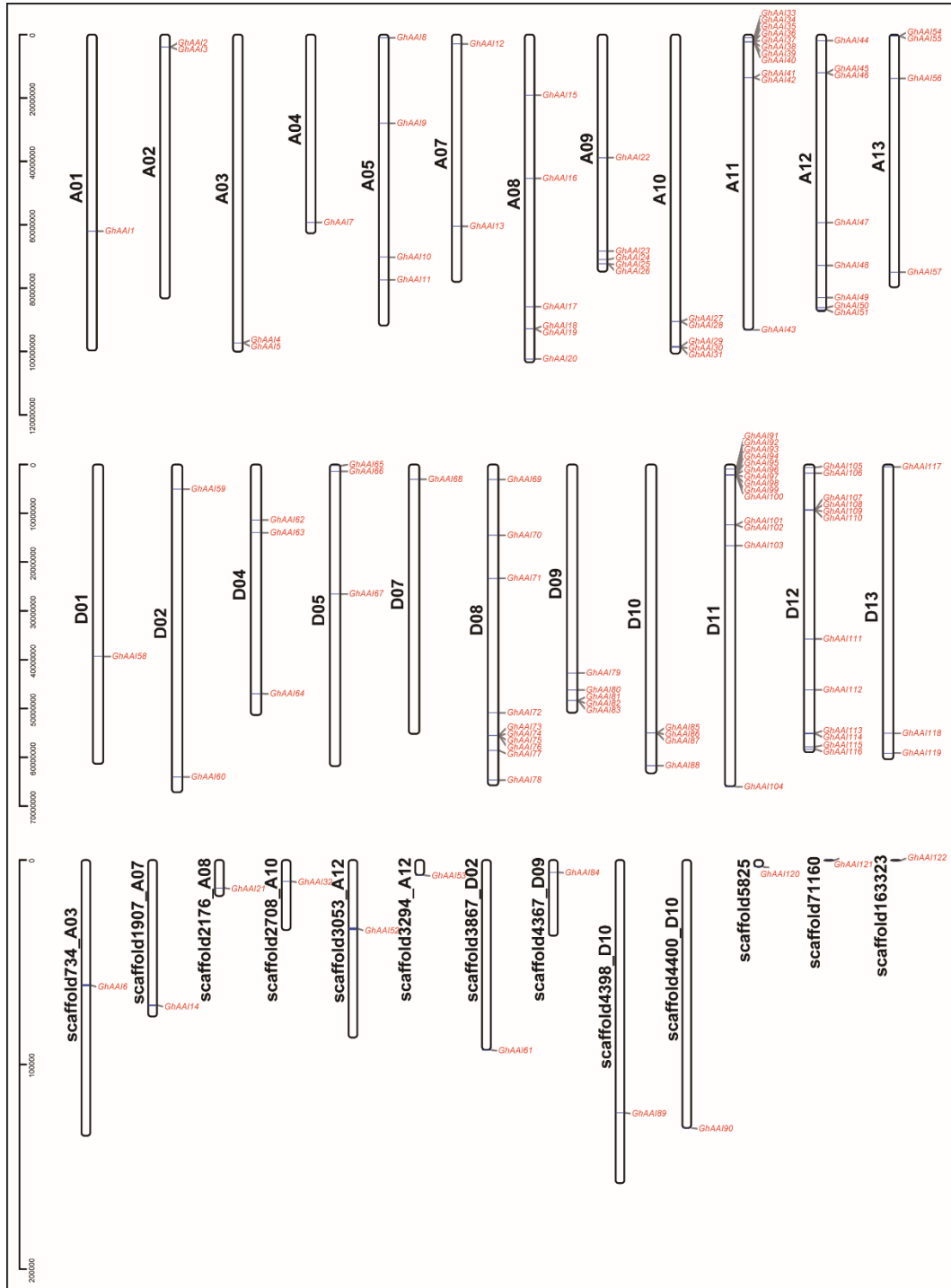


Supplementary Fig. S4. Protein motif distribution and gene structure (exon/intron) analysis of *GhAAI* genes along with phylogenetic tree inferred using the NJ method.

(A) Protein motif distribution in *GhAAI* genes. (B) Gene structure (exon/intron) and encoded protein prediction.



Supplementary Fig. S5. Chromosomal location of *GhAAI* genes on different chromosomes. A01 to A13 and D01 to D13 represent At and Dt sub-genomes of *G. hirsutum* chromosomes, respectively. Some *GhAAI* genes' locations were allotted on scaffolds. Chromosomal sizes were calculated from published genome data.



Supplementary Fig. S6. Expression pattern of *GhAAI* genes in different cotton tissues.

Heat map of 122 *GhAAI* genes in 22 different tissues. Data was obtained from publicly available transcriptomic data and color bar (down) represents expression level.

