

Figure S1. Changes in root, shoot biomass and shoot/root ratio at 12 (A) and 20 (B) d after MC treatment.

Values are the means ± SD (n = 3). Asterisks (\*) indicate a significant difference (P < 0.05) compared with the corresponding control.



Figure S2. The effect of MC on IAA distribution in LRI priming region of cotton root at 3 d after MC treatment.

(A) to (F) Immunolocalization of IAA from the region of 0.3-0.7, 0.7-1.1, 1.1-1.5 cm behind the root tip in the control (A, C, E) and MC-treated (B, D, F) cotton seedlings.

Fluorescent images are labeled FITC, bright field (BF) and the corresponding overlay images (overlay). Bar = 200 µm.



Figure S3.The expression of IAA amidohydrolase genes in the cotton seedlings.

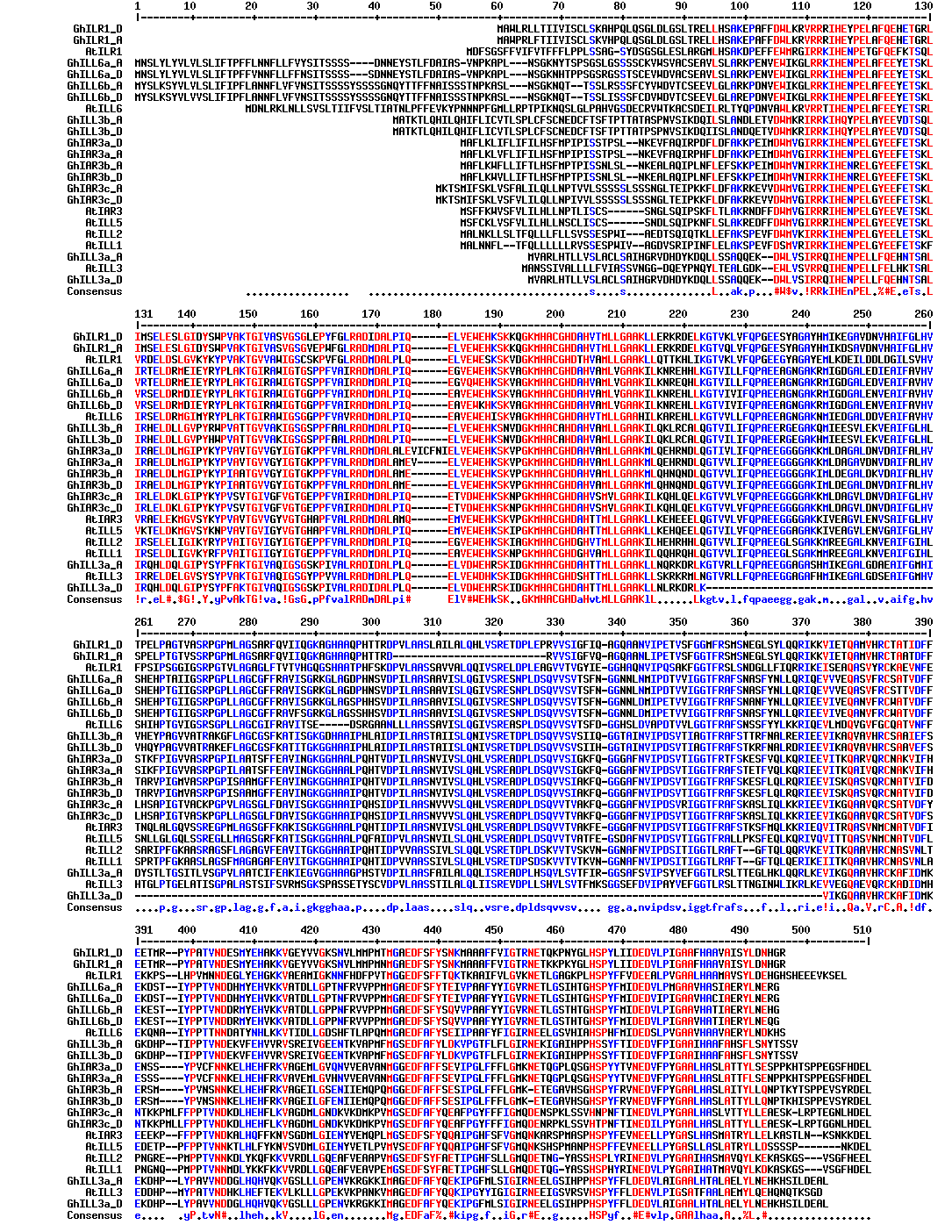


Figure S4. Amino acid sequence alignment of IAHs in cotton (*Gh*) and Arabidopsis (*At*). Alignment was performed using the Multalin website (http://multalin.toulouse.inra.fr/multalin/) with a hierarchical clustering approach.

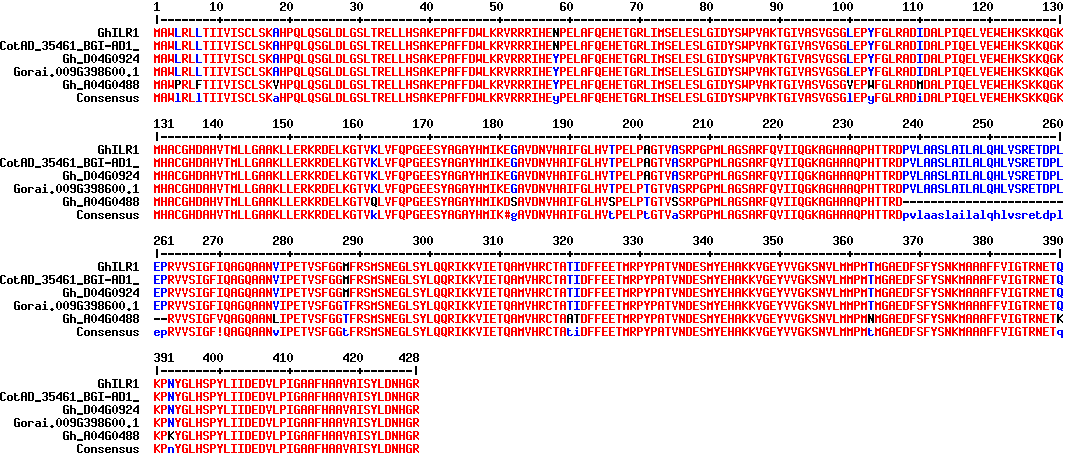
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Figure S5. Amino acid sequences alignment of ILR1 in *Gossypium hirsutum* (CGP-BGI Assembly: CotAD\_; NAU-NBI Assembly: Gh\_A/Gh\_D; Ncbi: XP\_.) and *Gossypium* *raimondii* (JGI assembly: Gorai. ). Alignment was performed using the Multalin website (http://multalin.toulouse.inra.fr/multalin/) with a hierarchical clustering approach. The green box indicated N-terminal signal sequence.

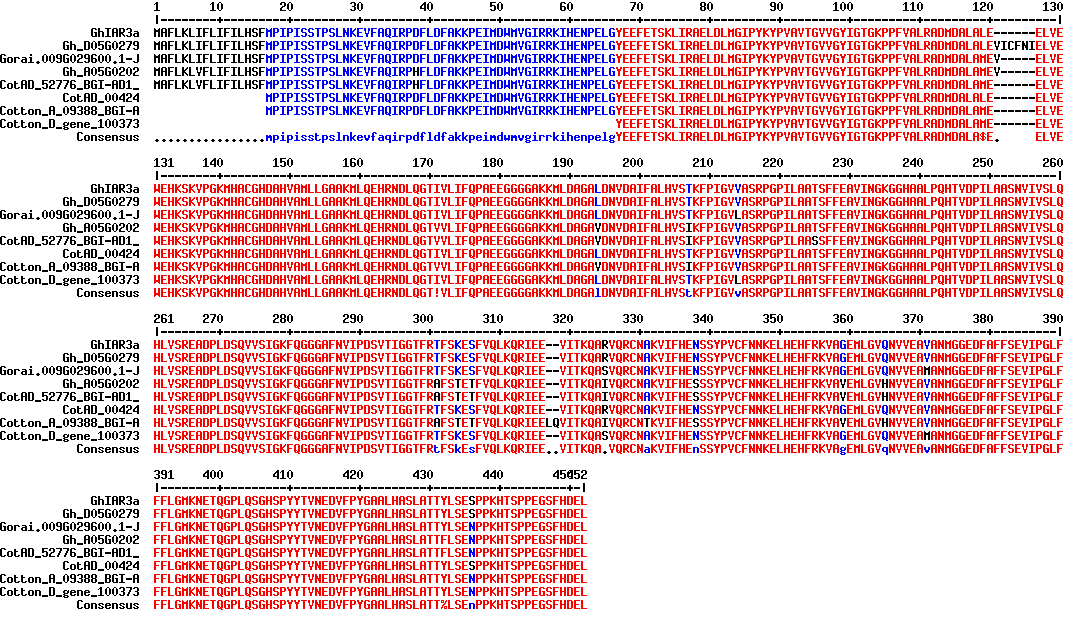


Figure S6. Amino acid sequences alignment of IAR3a in *Gossypium hirsutum*, *Gossypium arboretum* (BGI Assembly: Cotton\_A) and *Gossypium* *raimondii* (BGI-CGP v1.0 Assembly: Cotton\_D). Alignment was performed using the Multalin website (http://multalin.toulouse.inra.fr/multalin/) with a hierarchical clustering approach. The green box indicated N-terminal signal sequence.

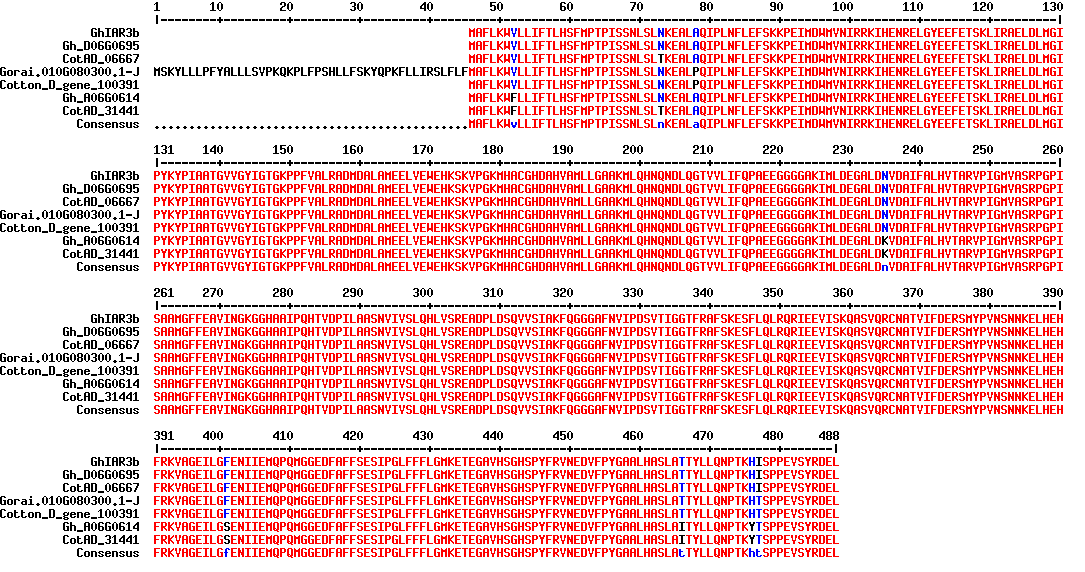


Figure S7. Amino acid sequences alignment of IAR3b in *Gossypium hirsutum*, *Gossypium arboretum* and *Gossypium* *raimondii*. Alignment was performed using the Multalin website (http://multalin.toulouse.inra.fr/multalin/) with a hierarchical clustering approach. The green box indicated N-terminal signal sequence.



Figure S8. Purified fusion protein GST-IAR3a, GST- IAR3b and His-ILR1 used in activity assays (A) and GhIAR3a was separated as the antigen (B).



Figure S9. Cross-Reactivity of mAb 3D11 and Rabbit Antisera against to GhIAR3a with GST (A), GhILR1 (B) and GhIAR3b (C).