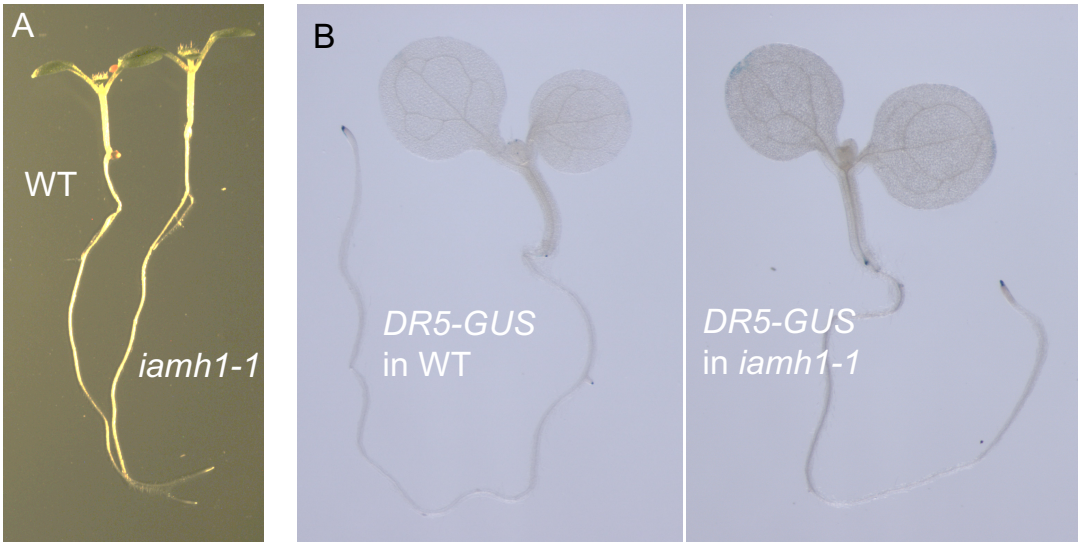
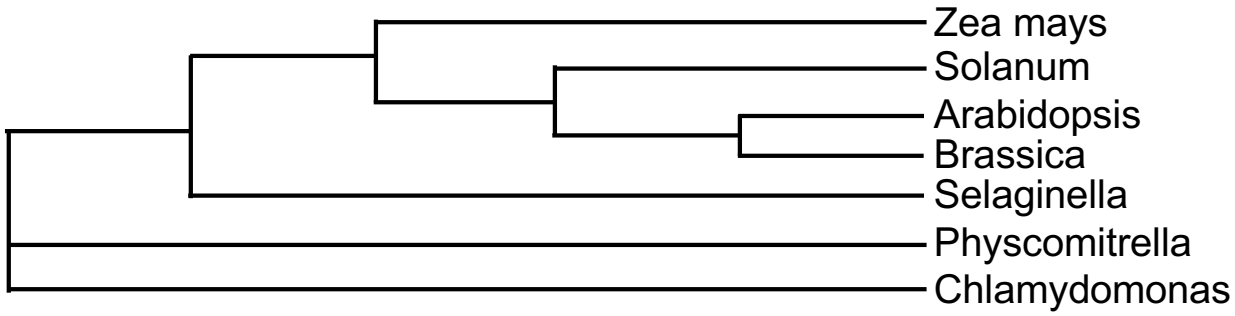
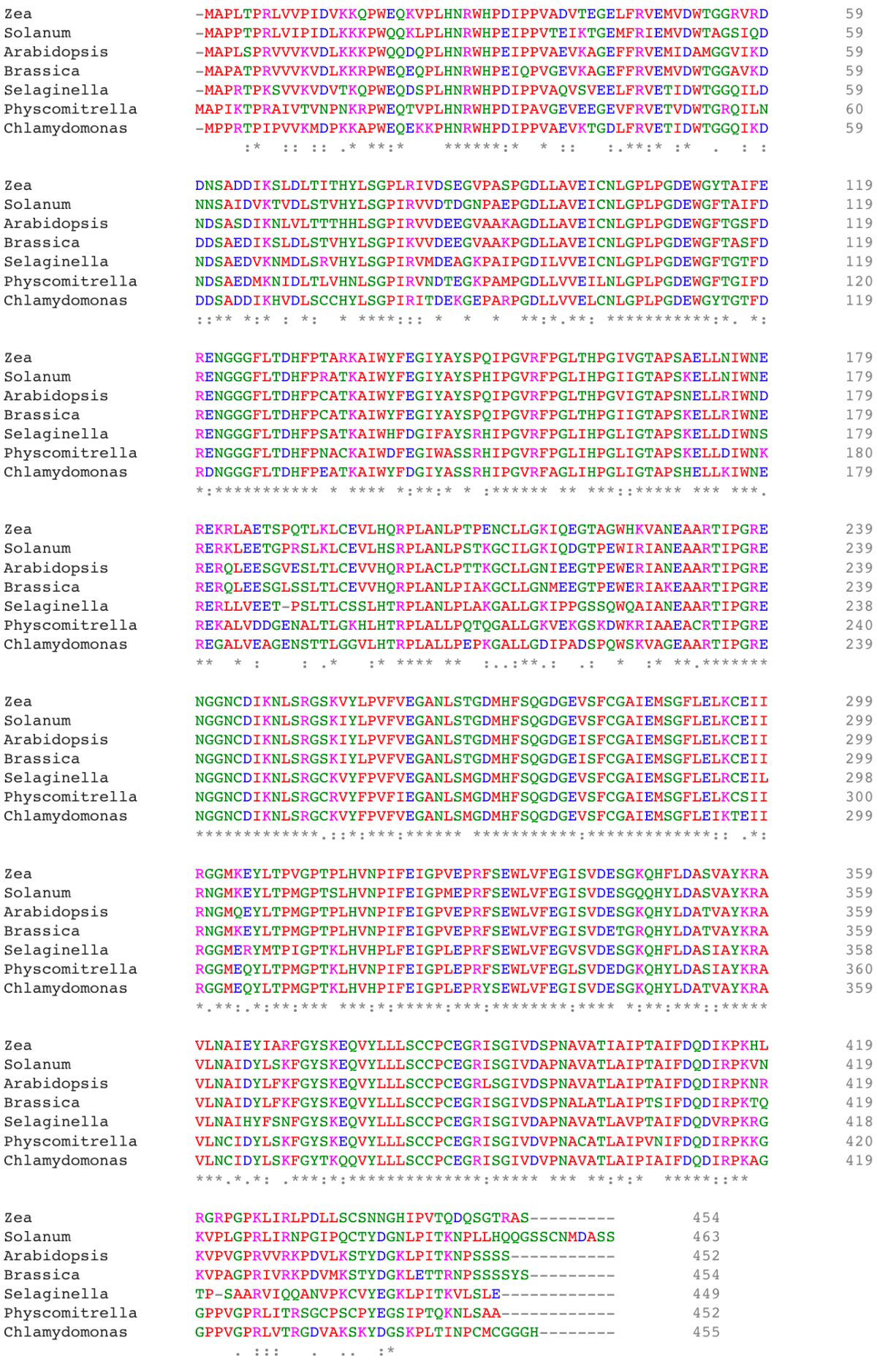


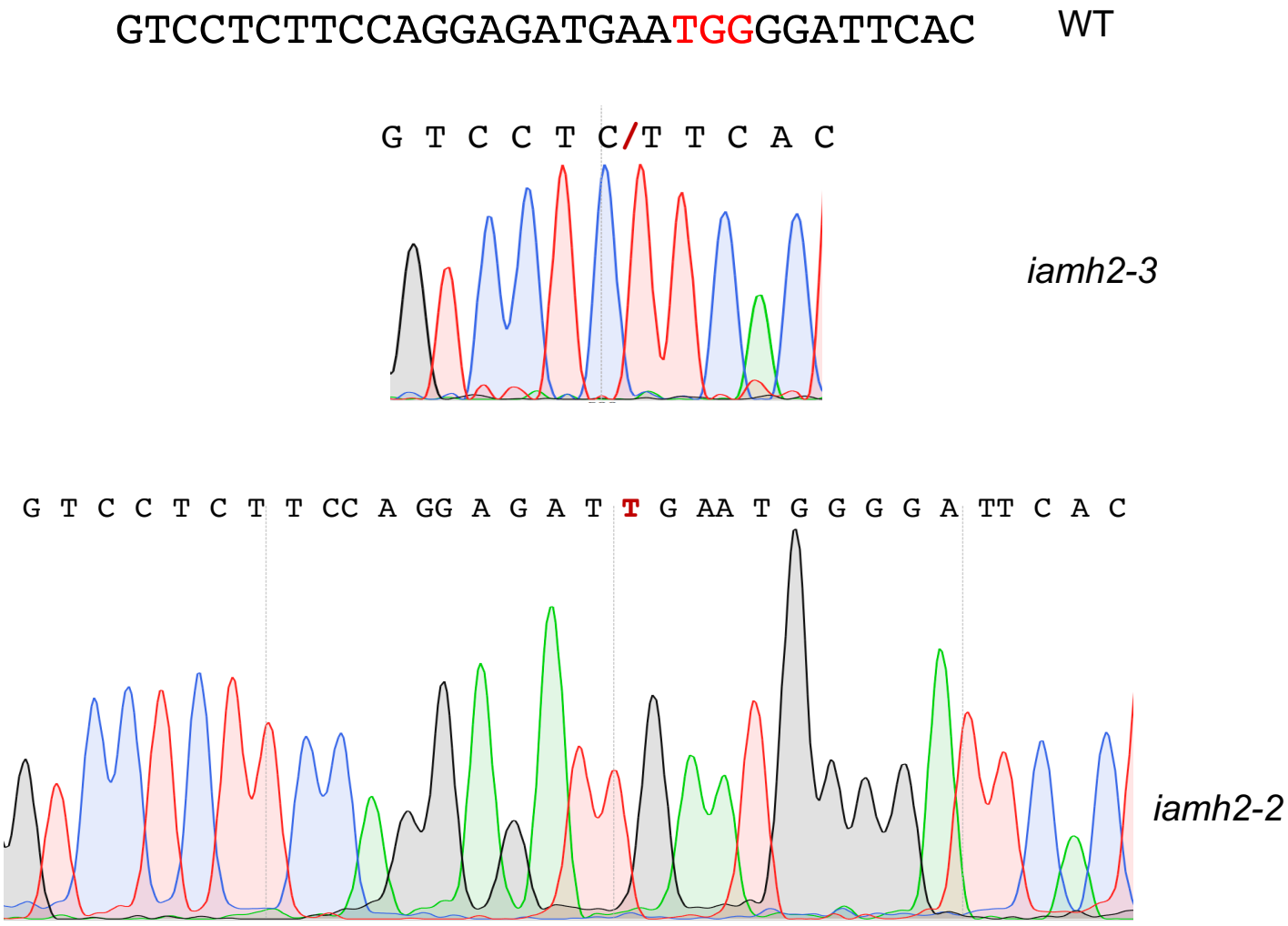

**SI Figure 1. Disruption of the *IAMH1* gene does not dramatically affect either Arabidopsis development or auxin reporter expression.** A) No obvious phenotypes were observed in the *iamh1-1* mutant. B) Expression of the auxin reporter *DR5:GUS* was not altered in the *iamh1-1* mutant.



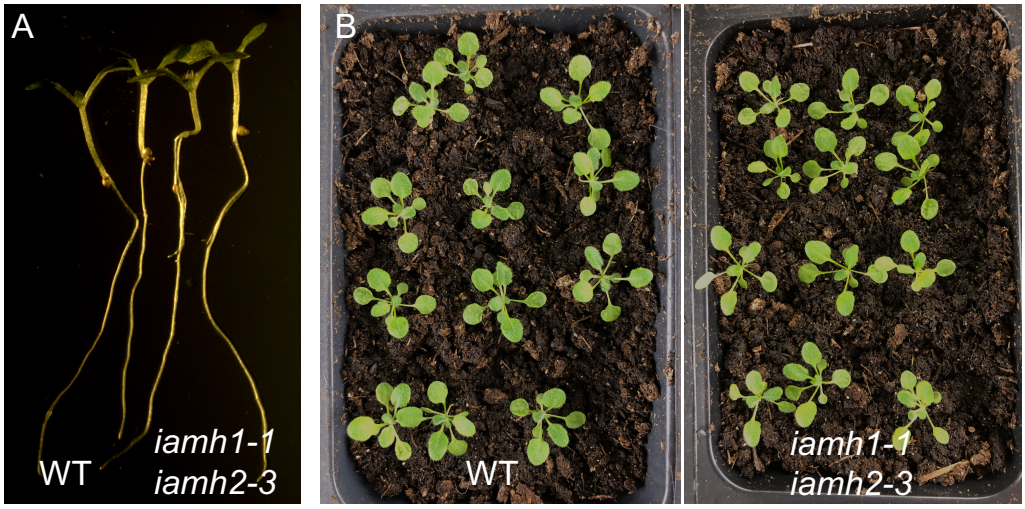

**SI Figure 2. Phylogenetic analysis of IAMH1 proteins across plant species**. The tree was generated using Clustal Omega online program. The shown tree is a Neighbour-joining tree without distance corrections.




**SI Figure 3. IAMH1 is highly conserved.** The multiple sequence alignment was generated using the Clustal Omega program (https://www.ebi.ac.uk/Tools/msa/clustalo/)




**SI Figure 4. Sequence analysis of *iamh2* CRISPR mutants.** The *iamh2-2* contained an T insertion. The *iamh2-3* had a 20-bpo deletion.




**SI Figure 5. The *iamh1 iamh2* double mutants grow similarly to WT plants.** A) The *iamh1-1 iamh2-3* double mutants did not display obvious phenotypes at seedling stages. B) Adult plants of *iamh1-1 iamh2-3* double mutants and WT were similar.