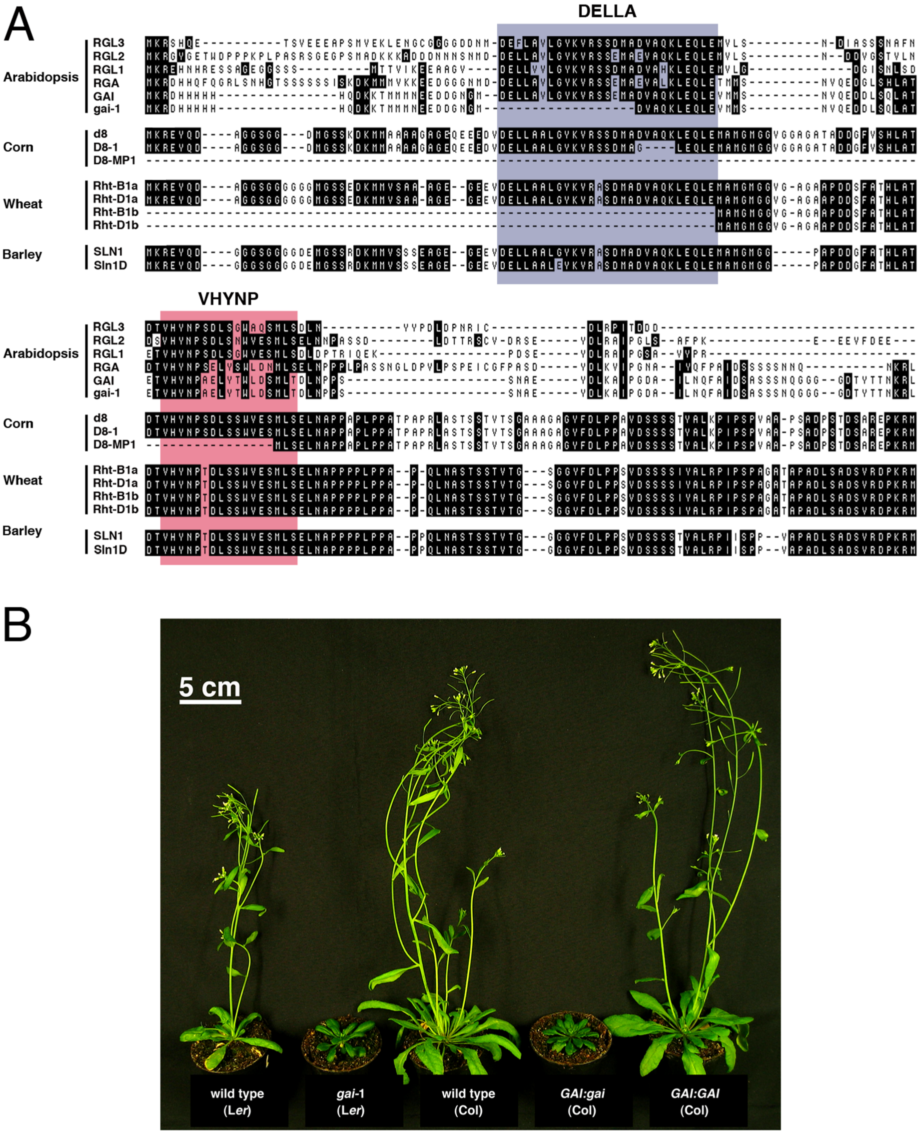
A
DELLA
Arabidopsis
RGL3
RGL2
RGL1
RGA
GAI
gai-1
Corn
d8
D8-1
D8-MP1
Wheat
Rht-B1a
Rht-D1a
Rht-B1b
Rht-D1b
Barley
SLN1
Sln1D
VHYNP
Arabidopsis
RGL3
RGL2
RGL1
RGA
GAI
gai-1
Corn
d8
D8-1
D8-MP1
Wheat
Rht-B1a
Rht-D1a
Rht-B1b
Rht-D1b
Barley
SLN1
Sln1D
B
5 cm
wild type (Ler)
gai-1 (Ler)
wild type (Col)
GAI:gai (Col)
GAI:GAI (Col)

Supplemental Figure 1. (A) Clustal alignment of the 140 N-terminal amino acid residues of Arabidopsis GAI with its orthologues from maize, wheat and barley. The amino acid sequences of the previously reported gain-of-function dwarfing alleles are shown below the respective wild type sequences. This alignment served as a basis for the design of the gai mutant variants examined in this manuscript (Figures 1 and 5). The highly conserved DELLA and VHYNP domains are boxed. (B) Transgenic GAI:gai plants mimic the phenotype of the *gai*-1 gain-of-function mutant. Four-week old wild type (ecotypes Columbia, Col, and Landsberg erecta, Ler), *gai*-1 mutant as well as GAI:gai and GAI:GAI transgenic plants are shown. Transgenic plants expressing the stabilized gai protein from the GAI:gai transgene (see Figure 1) are phenotypically indistinguishable from the *gai*-1 mutant whereas plants expressing the wild type GA responsive GAI protein from the GAI:GAI transgene are phenotypically wild type.