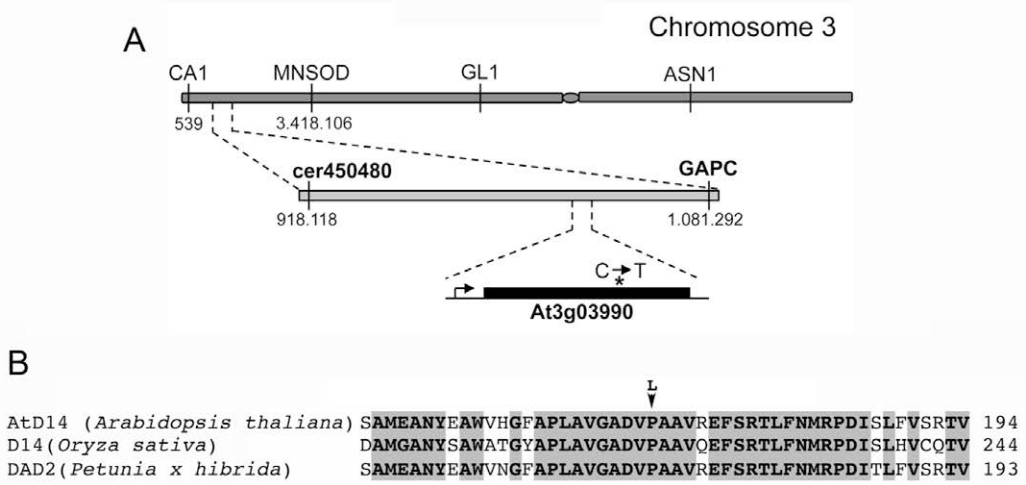
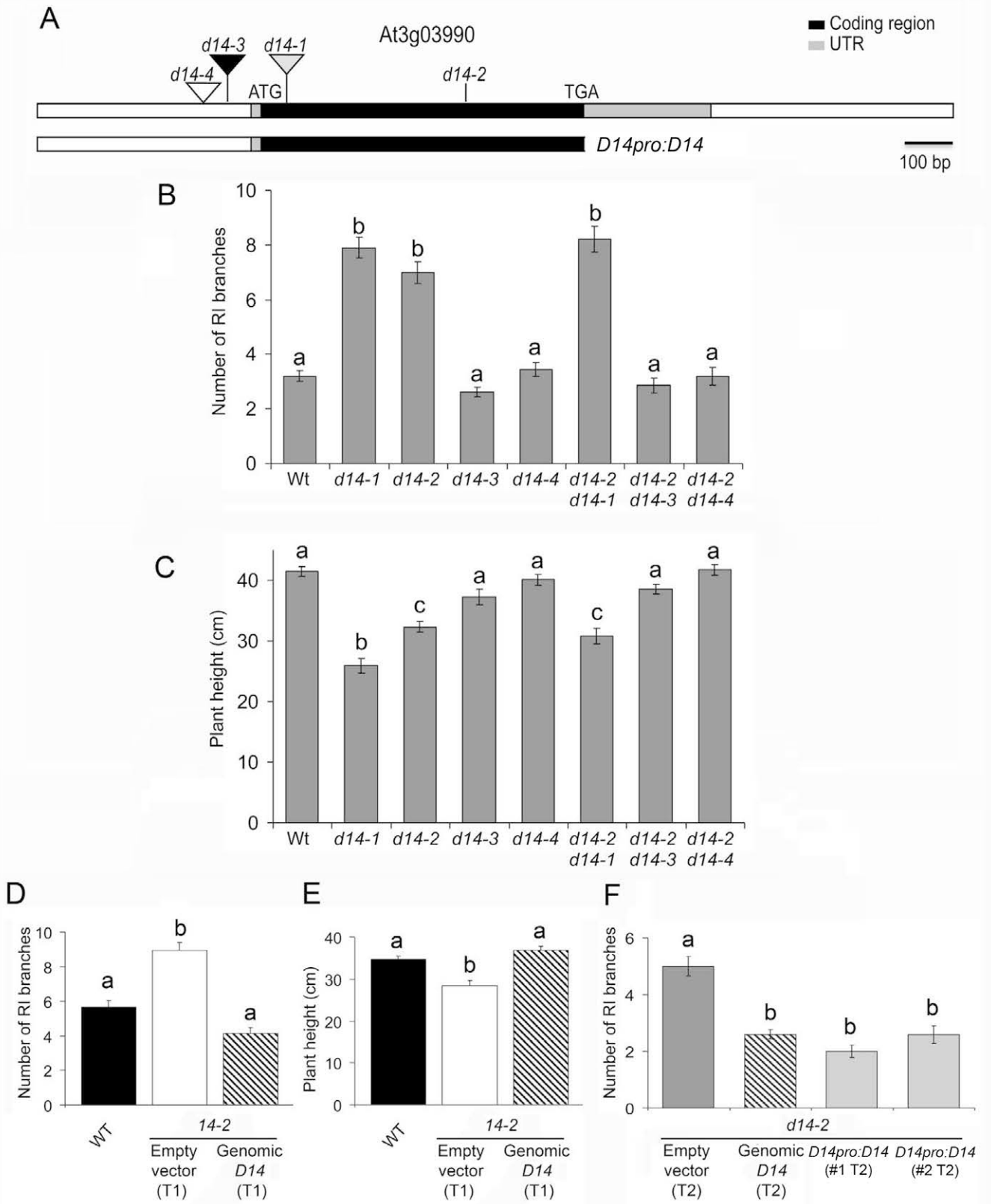
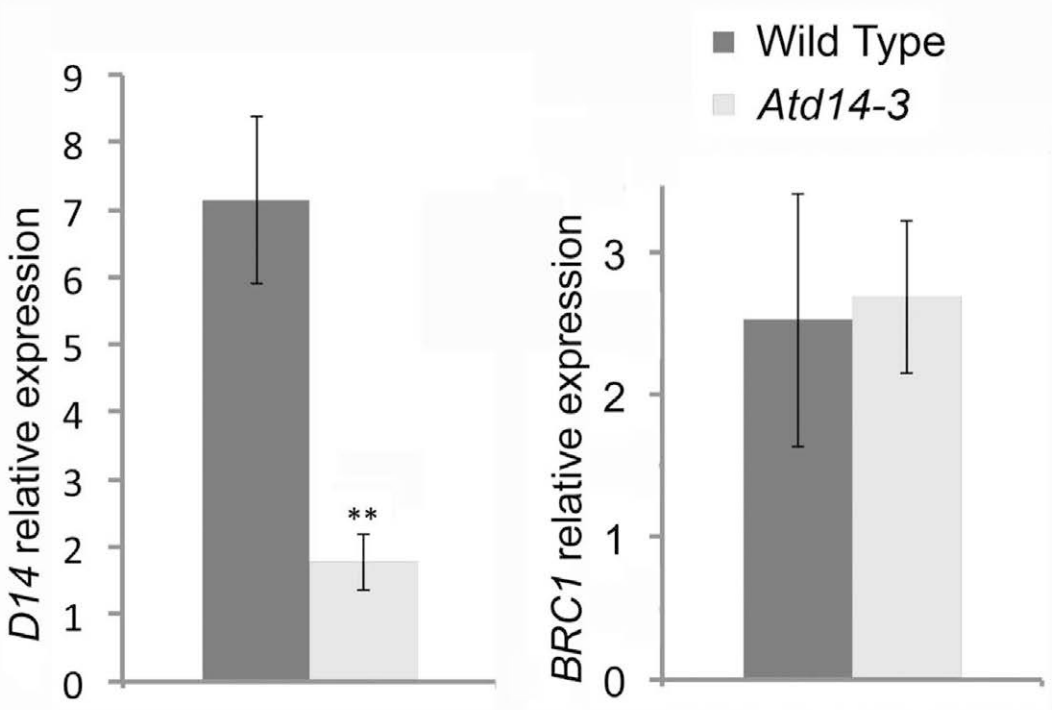


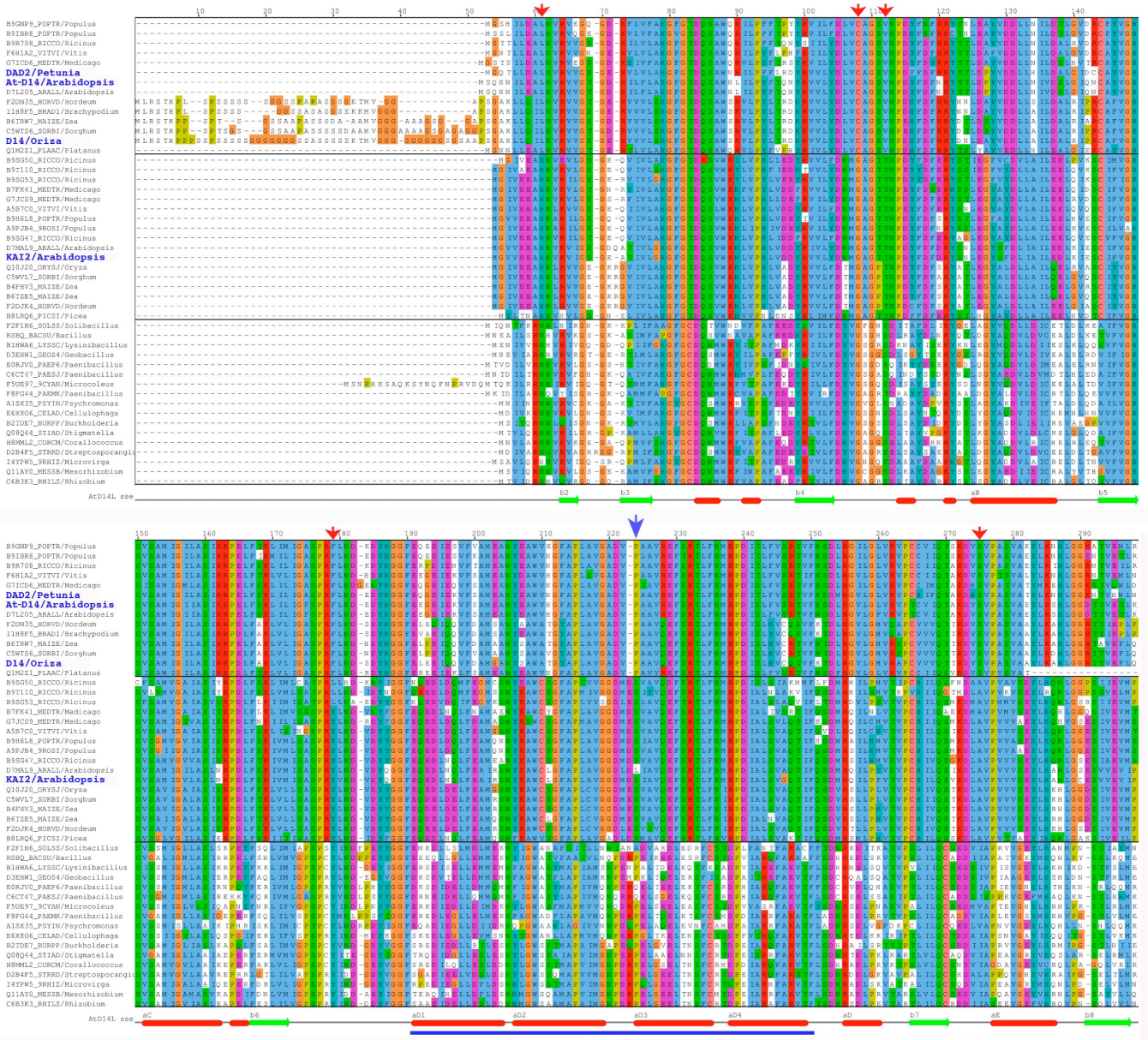

**Supplemental Figure 1. Mapping and cloning of the seto5 locus.**
A, Representation of chromosome 3 indicating the position of markers cer450480 and GAPC which delimited the 163 kb region to which seto5 was mapped. Numbers indicate kilo bases (Kb). The non-synonymous substitution in the gene At3G03990, responsible for the *seto5* mutation is indicated. B, Predicted peptide sequence of the At3g03990 protein where the *seto5* mutation is located. Rice D14 and DAD2 corresponding peptides are included for reference. Grey boxes highlight conserved residues. Numbers indicate amino acid positions for each protein. Black arrow indicates the predicted amino acid change of *seto5* mutants.



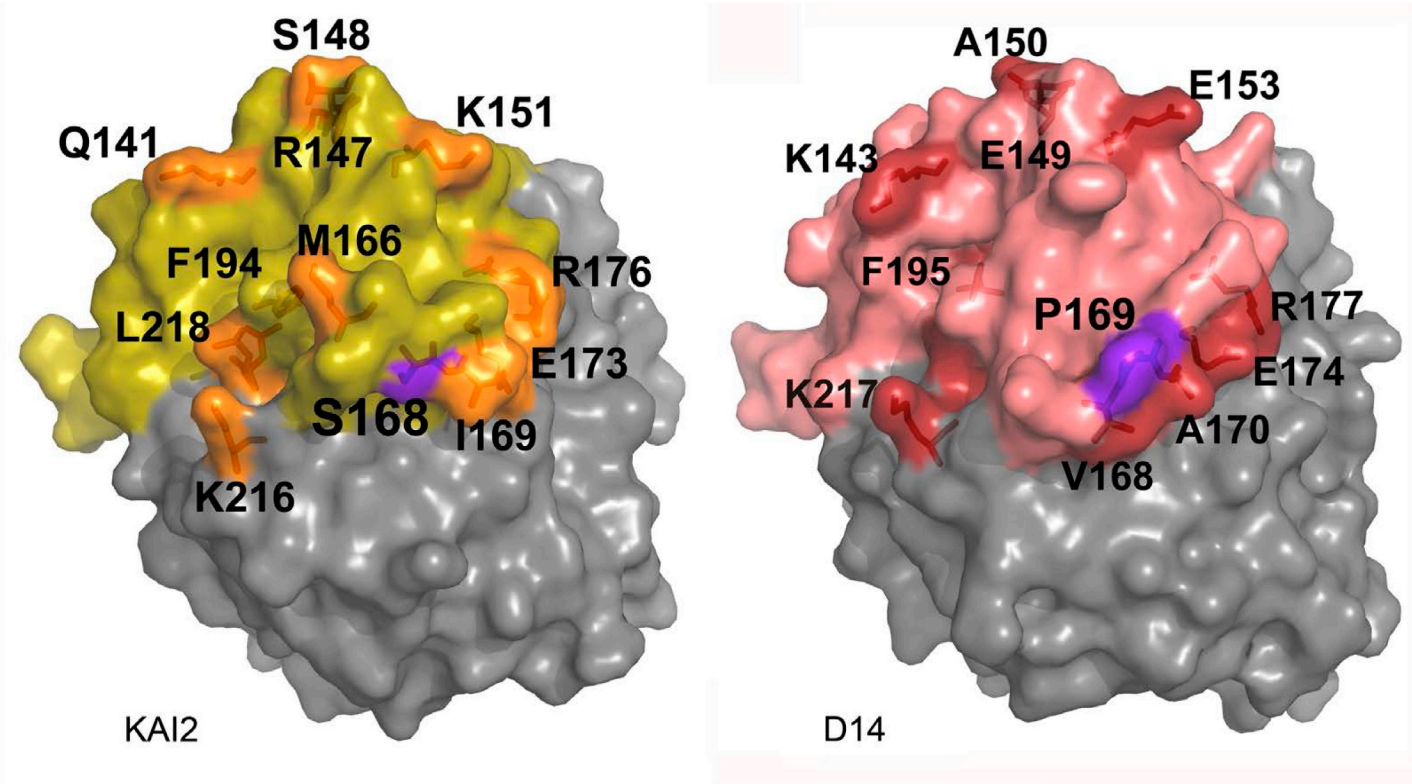

**Supplemental Figure 2. Complementation of the d14-2/seto5 mutant and D14 allelic series.**
A, Schematic representation of the genomic region flanking At3g03990 used to complement *d14-2/seto5* (*d14-2*). White bars indicate genomic regions upstream and downstream of the cDNA. Grey bars, 5´and 3´UTR regions, black bar, CDS. Mutations used in this study are also indicated: *d14-1*, a Wisconsin DsLox T-DNA insertion in the first 100 bp of the *D14* CDS in which full-length transcripts are undetectable (Waters et al. 2012b); *d14-2/seto5*, an EMS mutant (this work); *d14-3* is the SALK_057876 line; *d14-4*, is the Gabi-Kat insertion line GK-759C03. The construct containing only the 5´of the gene and CDS used to make GUS and GFP fusions is shown below. Shoot Branching phenotype (B) and height of same plants at maturity (C) of different *d14* alleles in homozygous condition or in heteroallelic combination with *d14-2/seto5* showing lack of phenotypic complementation. D, Branching phenotypes of wild-type (WT), *d14-2/seto5* mutant carrying one copy of an empty vector (T1) and *d14-2/seto5* plants carrying one copy of the genomic construct shown in A (T1). E, Height of the same set of plants at maturity. F, Shoot Branching phenotype of *d14-2/seto5* carrying one or two copies of an empty vector, the genomic construct used in D and E, and D14pro:D14 construct show in A. *D14pro:D14:GUS* and *D14pro:D14:GFP* lines behave similarly. Representative lines are shown. For B and C error bars represent SE (N≥10). For D, E and F, error bars represent SE (N=20). Different letters denote significant differences (One way ANOVA, Tukey test P<0.05).



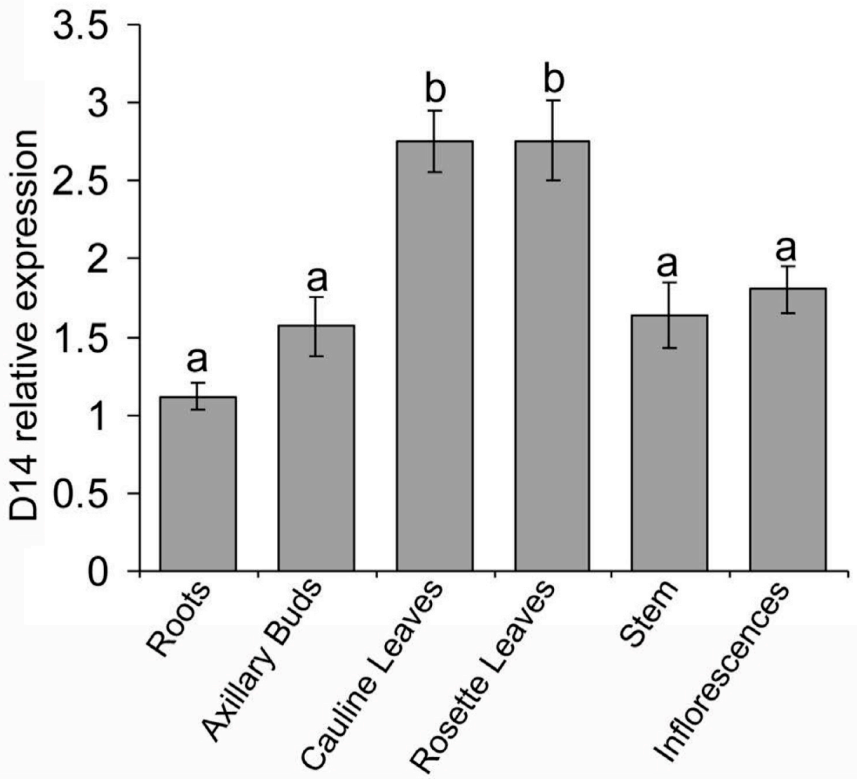

**Supplemental Figure 3. Relative *D14* and *BRC1* mRNA levels in axillary buds of the *d14-3* mutant, quantified by qPCR.** In spite of the significantly reduced transcript levels of *D14* relative to wild type, the mutants have a wild-type phenotype (Supplemental Figure 2B). Consistently, *BRC1* mRNA levels are wild type. Error bars represent SE from four biological replicates. Asterisks denote significant differences in Student's t-tests (**, P< 0.01).




**Supplemental Figure 4. Multiple sequence alignment of the D14 and KAI2 orthologs.** Multiple sequence alignment (MSA) of the closest D14 orthologs and KAI2 orthologs from several plant species, and proteins related to B. subtillisRSbQ. Numbers, indicate amino acid positions of the MSA. The blue arrow indicates the P169 position affected in the d14-2/seto5 allele. The red arrows indicate SDPs for D14 and KAI2. α-helices are indicated in red, β-sheets in green. Blue underline comprises the four cap helices. GI, NCBI GenInfo Identifier.

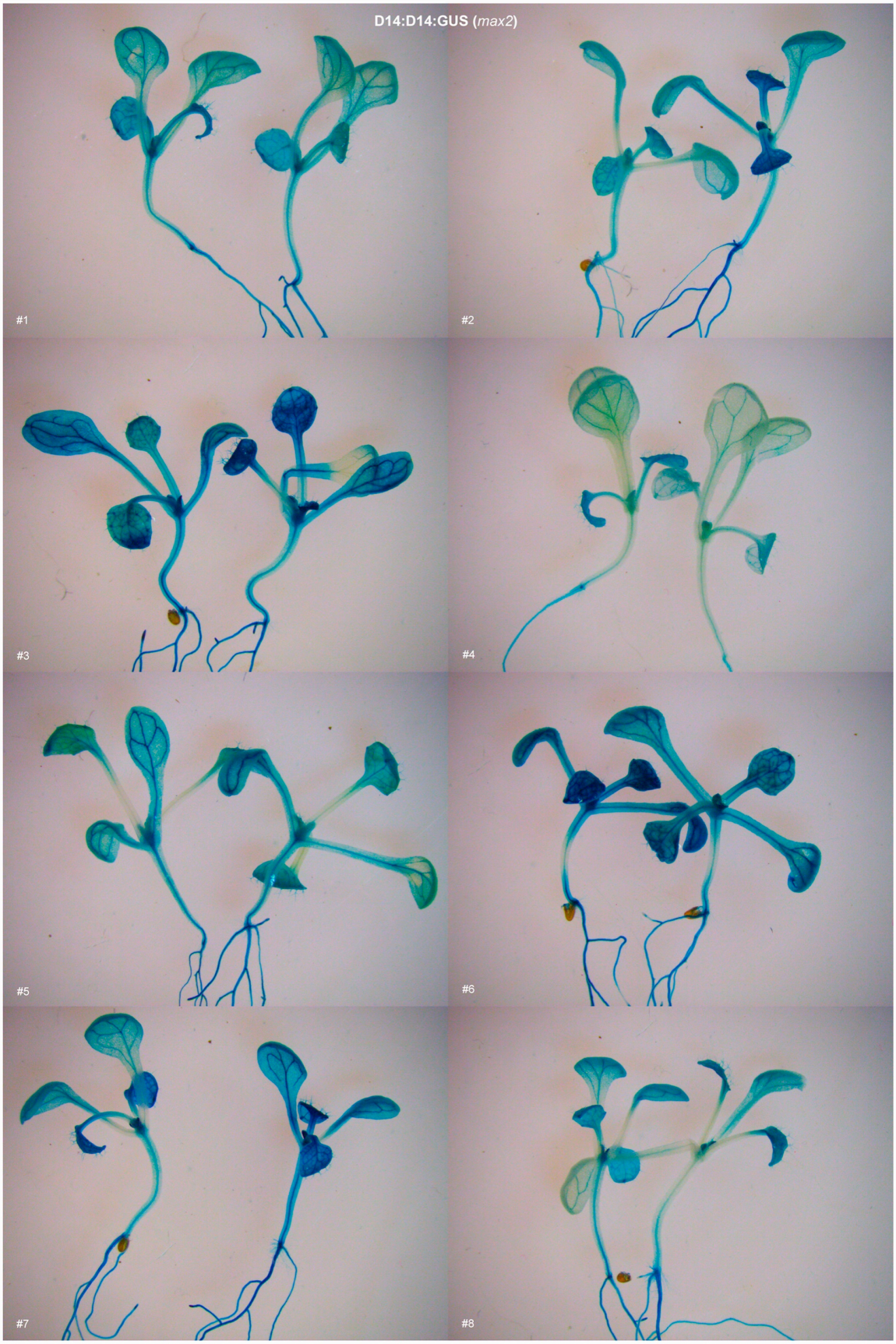



**Supplemental Figure 5. 3D structure of D14 and KAI2 and residues affected upon KAI1 binding.** KAI2 and D14 structures in surface representation. In KAI2, residues undergoing side-chain movement upon KAI1 binding are labelled and highlighted in orange; S168, purple; cap domain, yellow. In D14, residues equivalent to those highlighted in orange in KAI2 are labelled and highlighted in red; P169, purple; cap domain, pink.

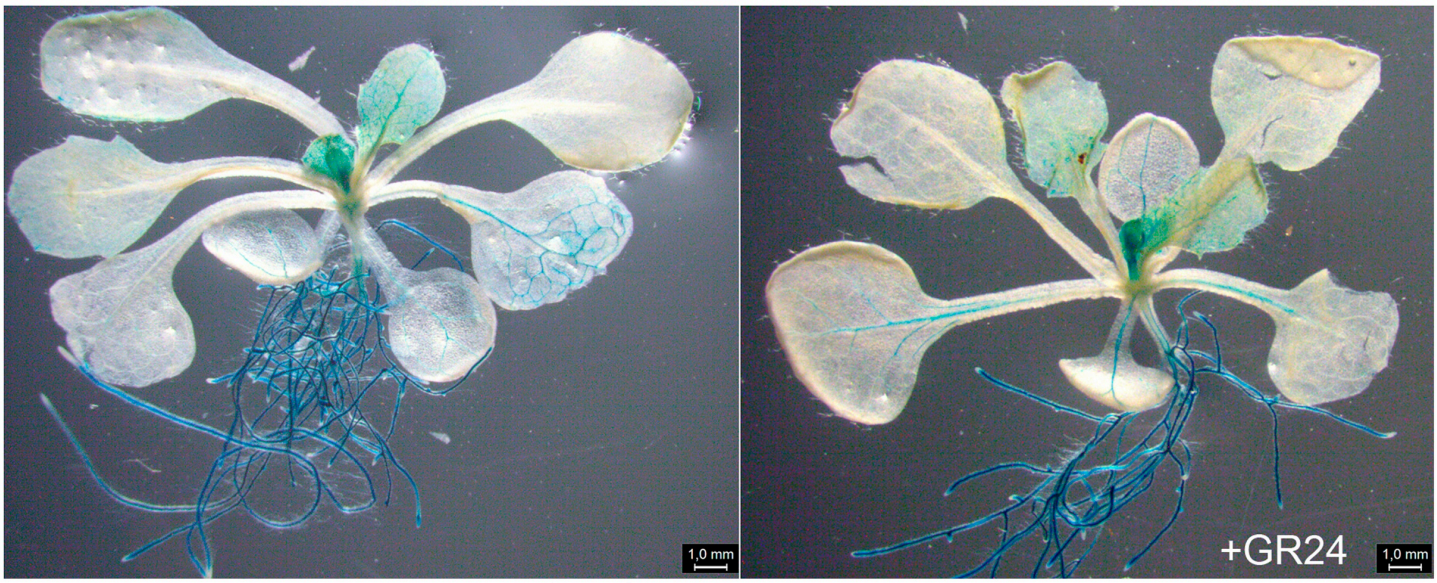



**Supplemental Figure 6. D14 relative mRNA levels in different tissues analysed by qPCR**. D14 relative mRNA levels in different tissues analysed by Q-PCR. Error bars represent SE from four biological replicates. Different letters denote significant differences (One-way ANOVA, Tukey test $P<0.05$).


**Supplemental Figure 7. The D14:GUS protein is destabilized by SL.** GUS histochemical activity of Arabidopsis D14pro:D14:GUS lines treated for 24 h with 5 µM GR24 (right) or with mock (left). Each panel corresponds to an independent homozygous transgenic line.




**Supplemental Figure 8. D14:GUS is not destabilized by SL in a *max2-1* background.** GUS histochemical activity of Arabidopsis *D14pro:D14:GUS* lines in a *max2-1* background treated for 24 h with 5 µM GR24 (right) or mock (left). Each panel corresponds to an independent homozygous transgenic line.




**Supplemental Figure 9. GUS is not destabilized by SL.** GUS histochemical activity of Arabidopsis *D14pro:GUS* plants treated for 24 h with mock control (left) or GR24 5 µM (right). No significant changes can be observed in GUS accumulation after the treatment.

| Method | ΔΔG (kcal/mol) | Effect of mutation |
|---|---|---|
| Concoord/PBSA | 2.35 | Destabilizing |
| FoldX | 1.84 | Destabilizing |
| I-Mutant3.0 (SVM2) | 0.38 | Neutral |
| I-Mutant2.0 | -0.28 | Neutral |
| SDM | -0.71 | Stabilizing |
| Eris (rigid) | -0.96 | Stabilizing |

**Supplemental Table I. Difference in free energy of unfolding between the wild-type D14 protein and mutant d14-2 protein.** Difference in free energy of unfolding (ΔΔG), between the wild-type D14 protein and mutant d14-2/seto5 protein, and predicted effect of the mutation. ΔΔG values obtained with different methods are indicated. Reference values: ΔΔG (kcal/mol)> 0.5 destabilizing, ΔΔG (kcal/mol) < -0.5 stabilizing, -0.5< ΔΔG (kcal/mol)< 0.5 neutral.

| Primer name | Primer sequence | Gene | Experiment |
|---|---|---|---|
| 3990CDSGTW-F | ggggacaagtttgtacaaaaaagcaggcttaATGAGTCAACACAACATCT | AtD14 | CDS amplification |
| 3990CDSGTW-R | ggggaccactttgtacaagaaagctgggtcGGCCCGAGGAAGAGCTCGCC | | |
| 3990GenoGTW-F | ggggacaagtttgtacaaaaaagcaggctCTCGTGACTCACCTATGTC | AtD14 | 2.3 Kb genomic amplification |
| 3990GenoGTW-R | ggggaccactttgtacaagaaagctgggtCTGCAGCCATACTGTTAGGT | | |
| 3990GenoGTW-F | ggggacaagtttgtacaaaaaagcaggctCTCGTGACTCACCTATGTC | AtD14 | Promoter amplification |
| 3990NewPromGTW-R | ggggaccactttgtacaagaaagctggGTTTTATGTGTTTGGGTTTGAGG | | |
| GTWMAX2-F | ggggacaagtttgtacaaaaaagcaggctTAATGGCTTCCACTACTCTCT | AtMAX2 | CDS amplification |
| GTWMAX2-R | ggggaccactttgtacaagaaagctgggtCTCAGTCAATGATGTTGCGGC | | |
| Seto5 Q 3rd F | TCGAAGAAAAGAAGGGCCTCT | AtD14 | RT-QPCR |
| Seto5 Q 3rd R | TGTGACAATGCCAAACTGTCCT | | |
| Brc1-L-QPCR-A | TTCCCAGTGATTAACCACCAT | AtBRC1 | RT-QPCR |
| Brc1-R-QPCR-A | TCCGTAAACTGATGCTGCTC | | |
| MAX2 Q5'B | CTCGTGATCTCTCCCTCGTC | AtMAX2 | RT-QPCR |
| MAX2 Q3'B | AGGTTCTGGTGATCGATTGG | | |
| MAX4 Q5'B | TGGAACATTGGAGACCACGA | AtMAX4 | RT-QPCR |
| MAX4 Q3'B | TGTGGAGTAGCCGTCGAAGAG | | |
| PIN1F Q-rt | CCTCAGGGGAATAGTAACGACA | AtPIN1 | RT-QPCR |
| PIN1R Q-rt | TCATCGTCTTTGTTACCGAAACT | | |
| IAA14-L-QPCR | CAAAGATGGTGACTGGATGC | | |
| IAA14-R-QPCR | GCATGACTCGACAAACATCG | | |
| SAND Q5'B | AACTCTATGCAGCATTTGATCCACT | AT2G28390 (SAND) | RT-QPCR (Reference gene) |
| SAND Q3'B | TGATTGCATATCTTTATCGCCATC | | |

Supplemental Table II. Primers used in this study