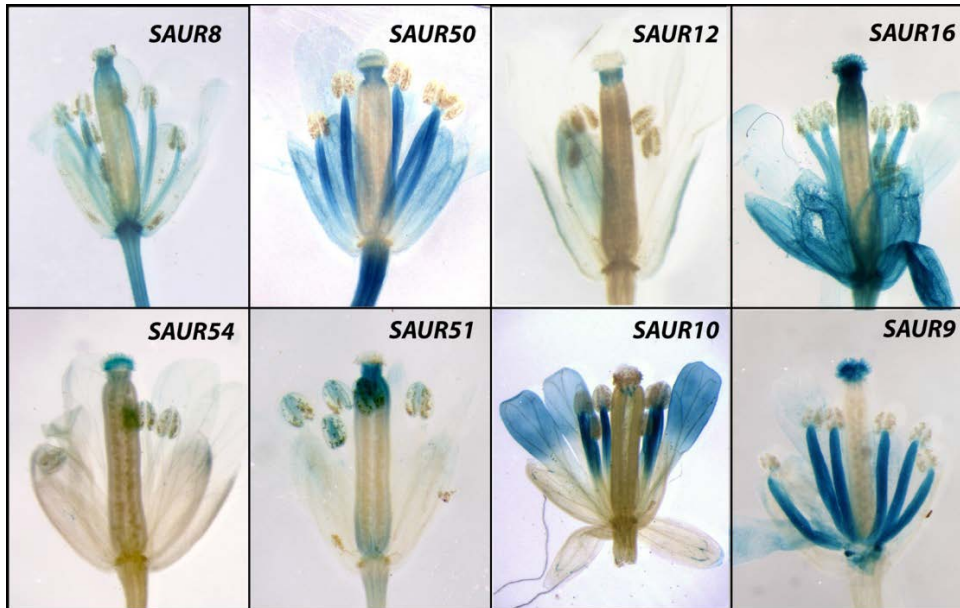
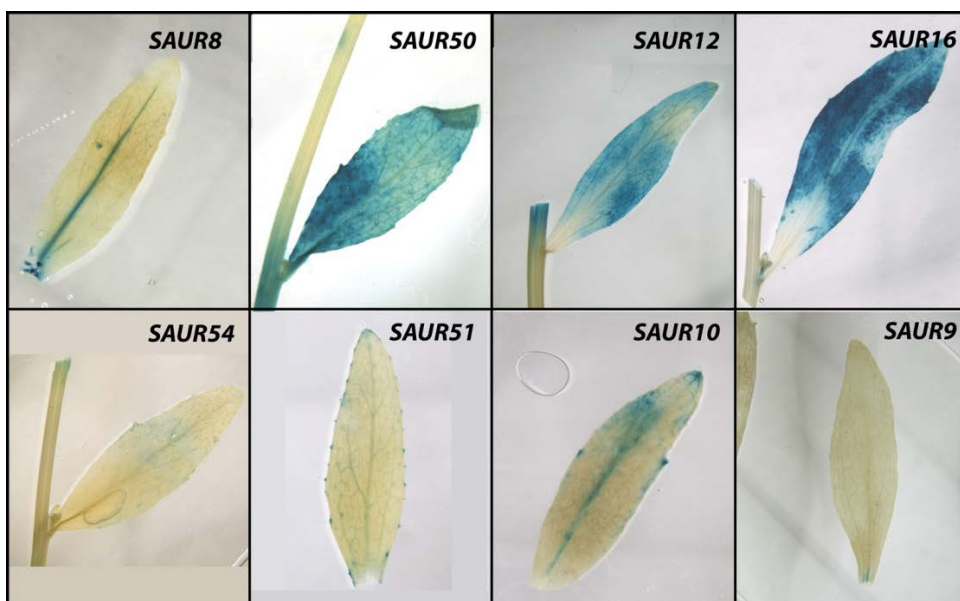
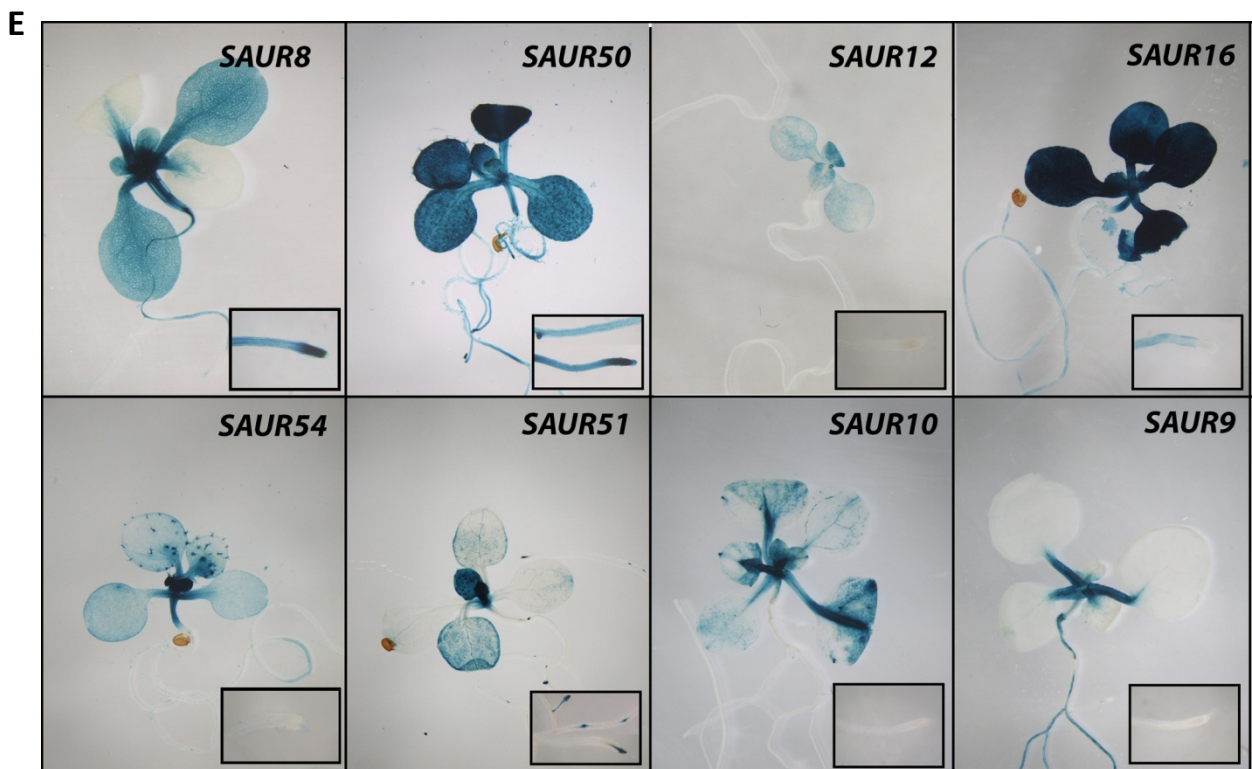
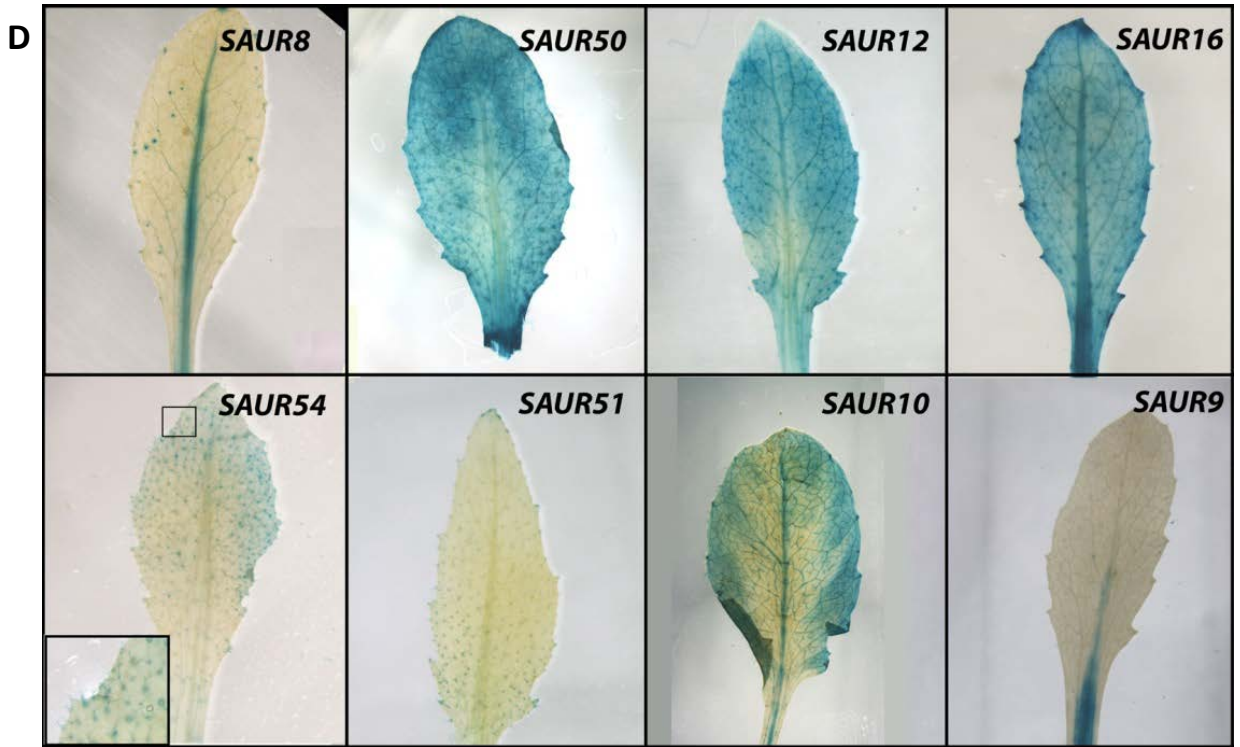
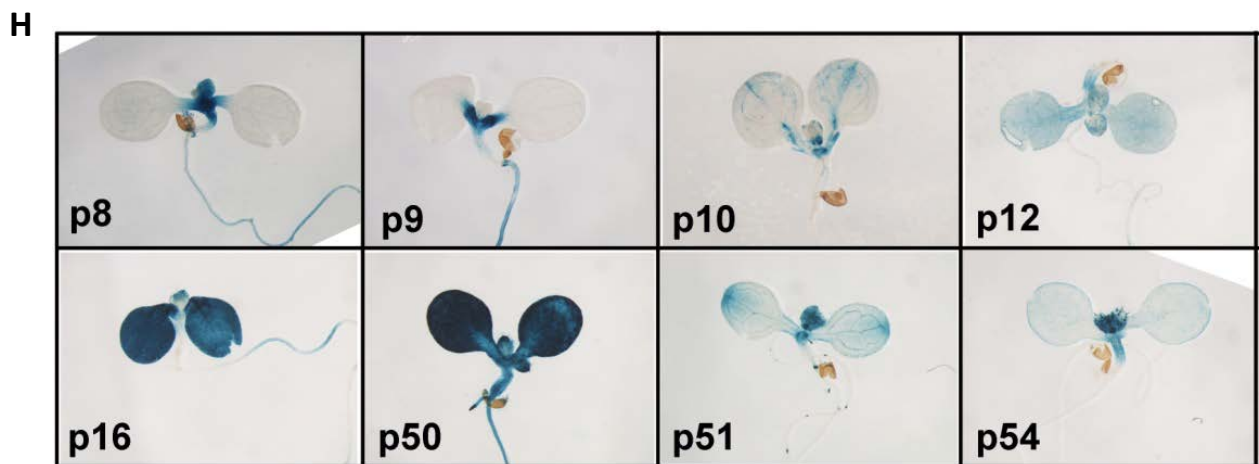
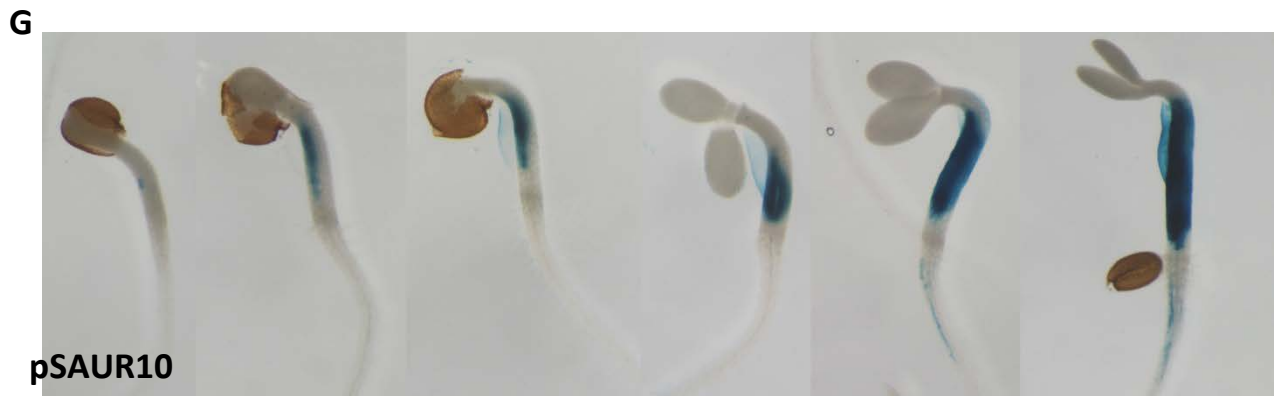
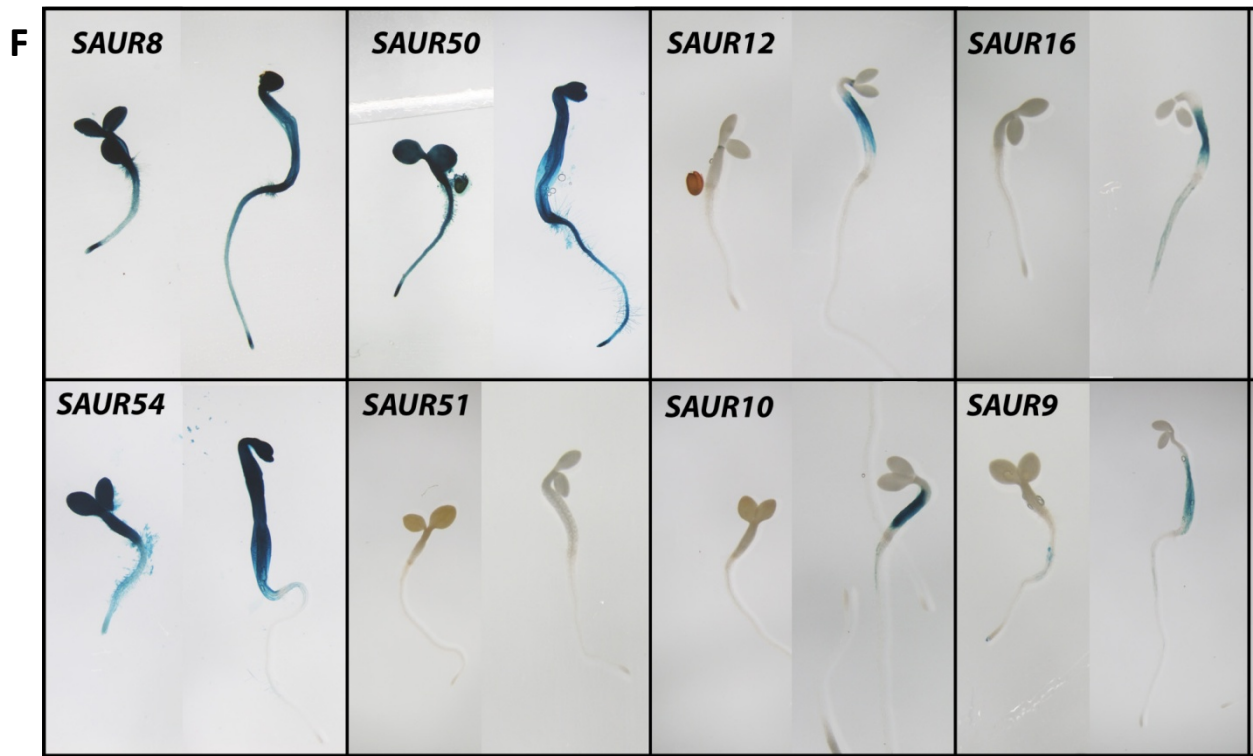
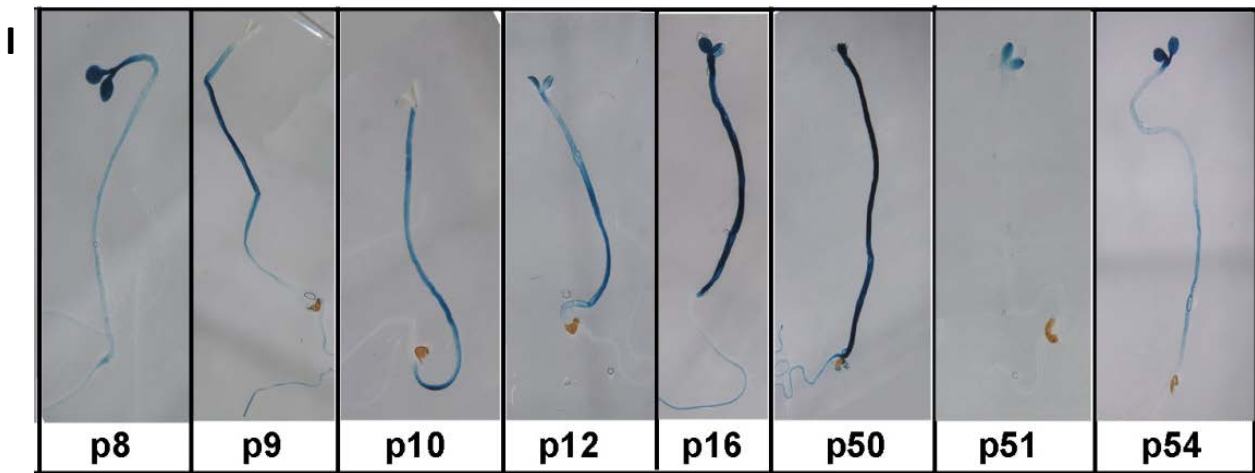


A**B****C**







Additional file 4: Figure S3. Expression patterns of the *pSAUR:GUS* lines. For every construct, at least two transgenic lines were tested. The tissue was stained in GUS buffer overnight. **A)** Mature flowers (stage 13), **B)** Flowers stage 11, **C)** Cauline leaves, **D)** Rosette leaves, **E)** Seedlings at 12 DAS (days after stratification), **F)** Seedlings 4 DAS. In each panel, the left depicted seedling was light-grown and the right one dark-grown. **G)** *pSAUR10* seedlings 2-4 DAS. For *pSAUR10*, a specific staining pattern in etiolated seedlings was observed, starting with a spot on one side of the hypocotyl and building up to expression throughout the hypocotyl. **H)** Light-grown seedlings at 7 DAS **I)** Etiolated seedlings at 7 DAS, **J)** Siliques stage 18. *pSAUR16* and *pSAUR50* show staining in this stage, while the other reporters are not active.