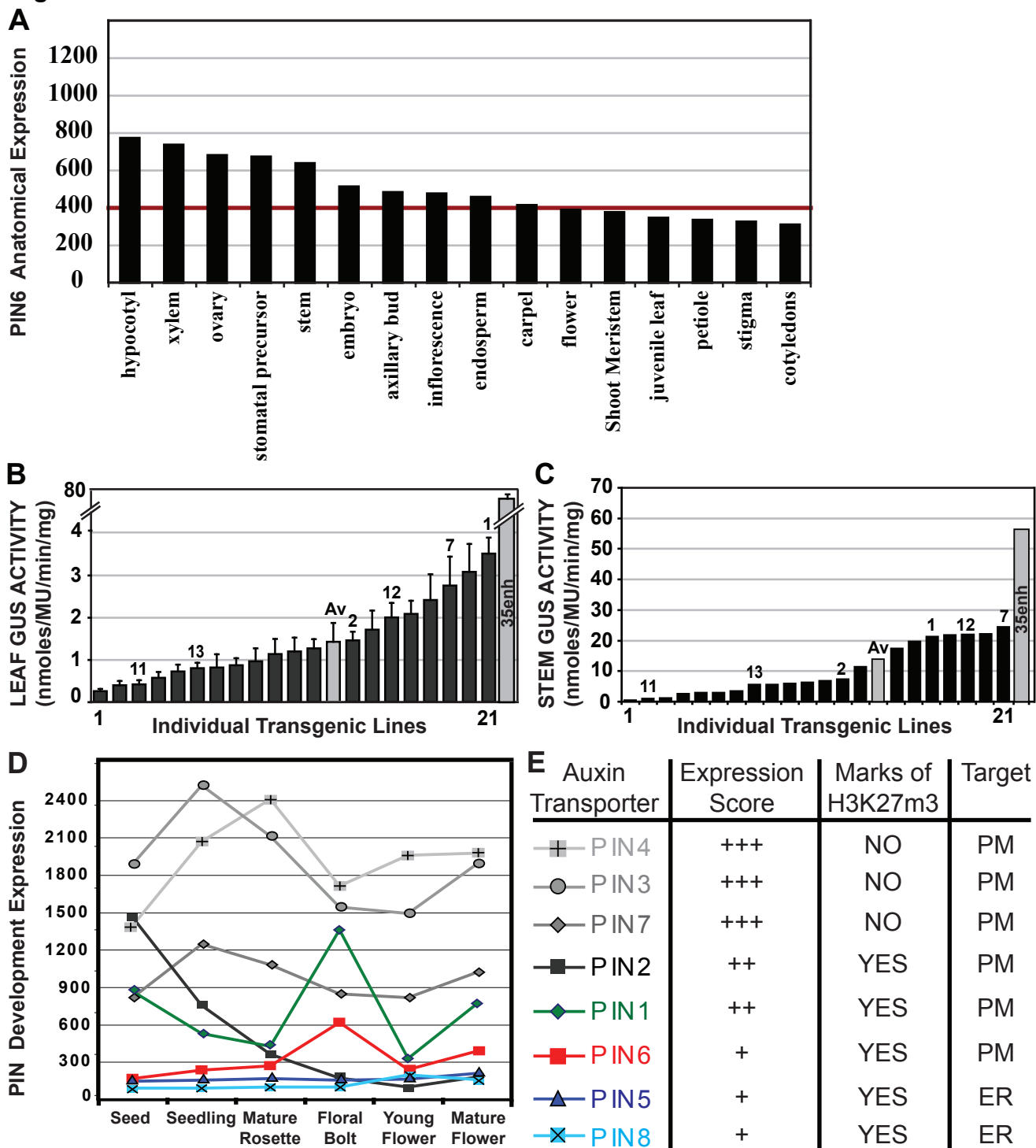


**Figure S2**

**Figure S2.** Characterisation of *PIN6* expression patterns. A) *PIN6* anatomical mRNA expression levels in wild type Columbia-O tissues. Genevestigator was used to generate an Arabidopsis *PIN6* transcript profile across a range of tissues and values >400 are considered to have medium expression levels (Hruz *et al.*, 2008). B) and C) Quantification of *PIN6* promoter-GUS activity in mature leaf and stem tissues, respectively. Tissues were harvested 28 DAG from multiple independent lines (n=21) and GUS activities expressed in nmoles 4MU/min/mg of soluble protein. Lines are presented in the order of increasing activity along the X-axis. Leaf error bars (B) represent  $\pm$ SE of three independent experiments (n=3) measuring pooled tissues from a single plant (hemizygous) in duplicate. Primary stem tissues were pooled from a single hemizygous plant and assayed in duplicate (SE bars not shown). A strong expressing CaMV35s::GUS line was included as a positive control and the average of the *PIN6*::GUS lines is displayed. Representative lines chosen for further analysis are displayed above the bars. D) *PIN* gene expression levels during plant development. GENEVESTIGATOR was used to collate published microarray data and report expression levels in germinating seeds, young seedlings, mature rosettes, floral bolts as well as young immature and older mature flowers. E) Summary of *PIN* expression, chromatin modifications and protein localisation. GENEVESTIGATOR expression levels were qualitatively scored as strong (+++), medium (++) and weak (++) and H3K27 trimethylation marks associated with repressive *PIN* gene expression were scored as absent (no) or present (yes) (<http://www.mcdb.ucla.edu/Research/Jacobsen/>). Subcellular targeting of the *PIN* genes to the plasma membrane (PM) or endoplasmic reticulum (ER) are shown.