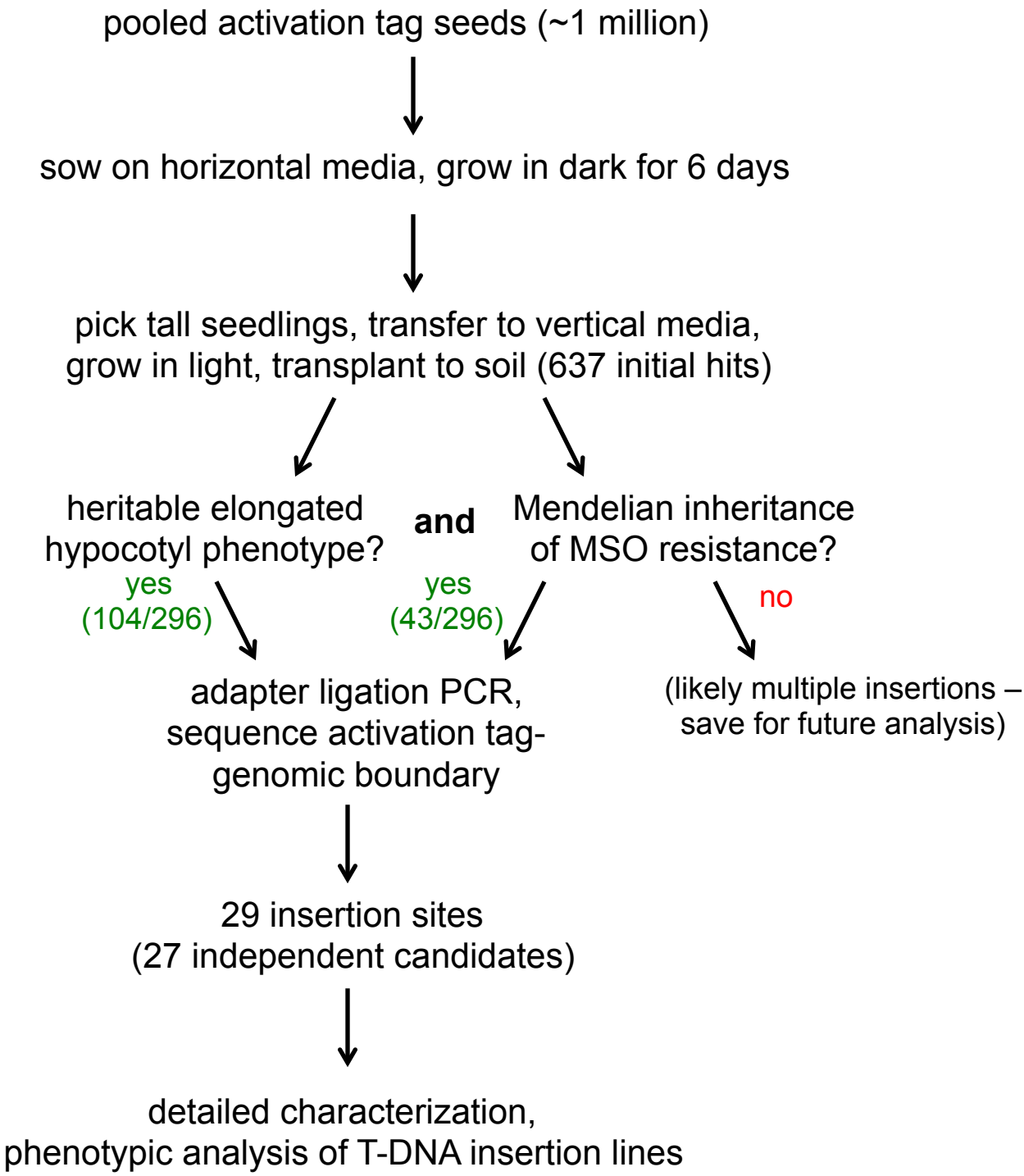
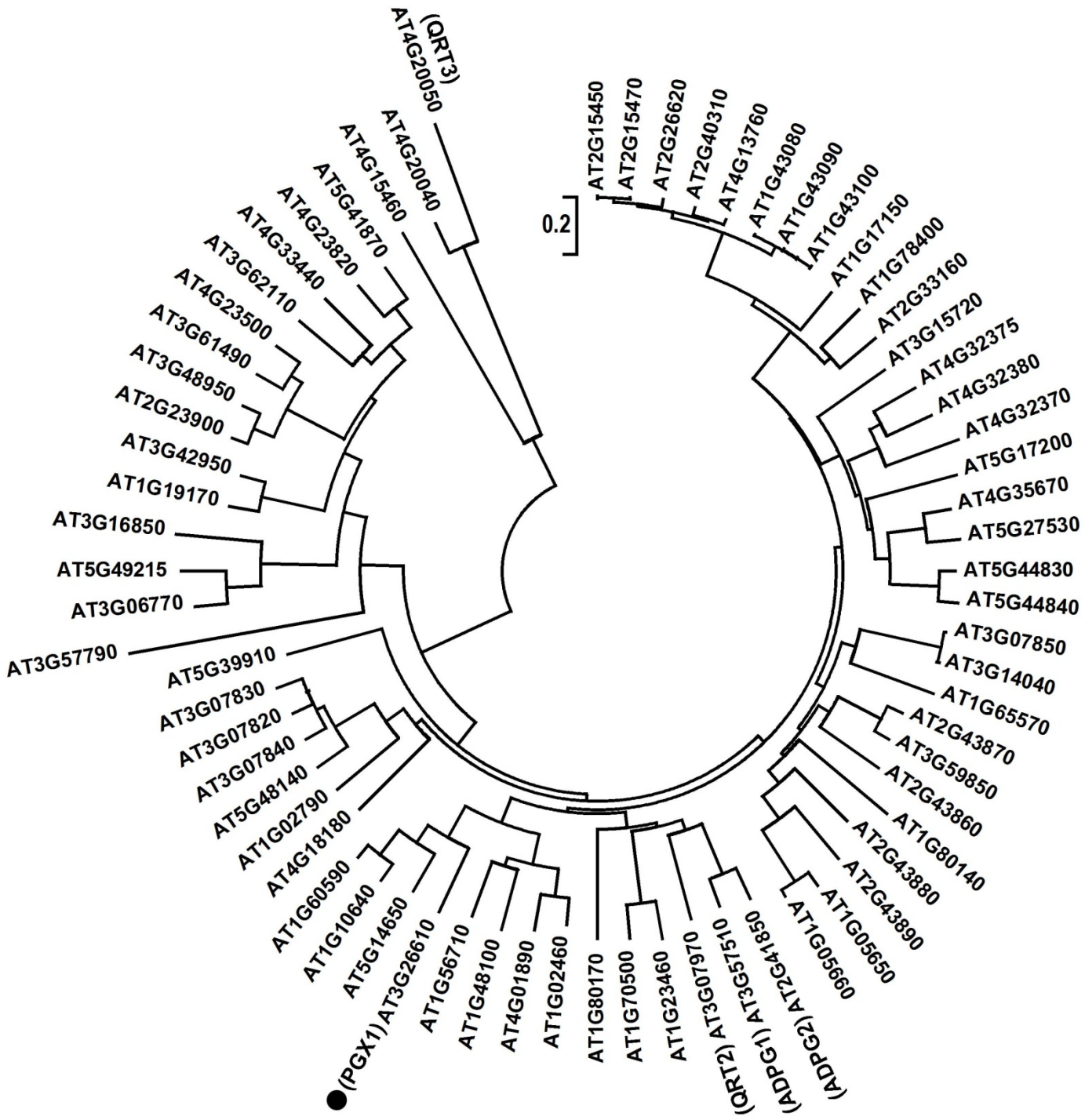
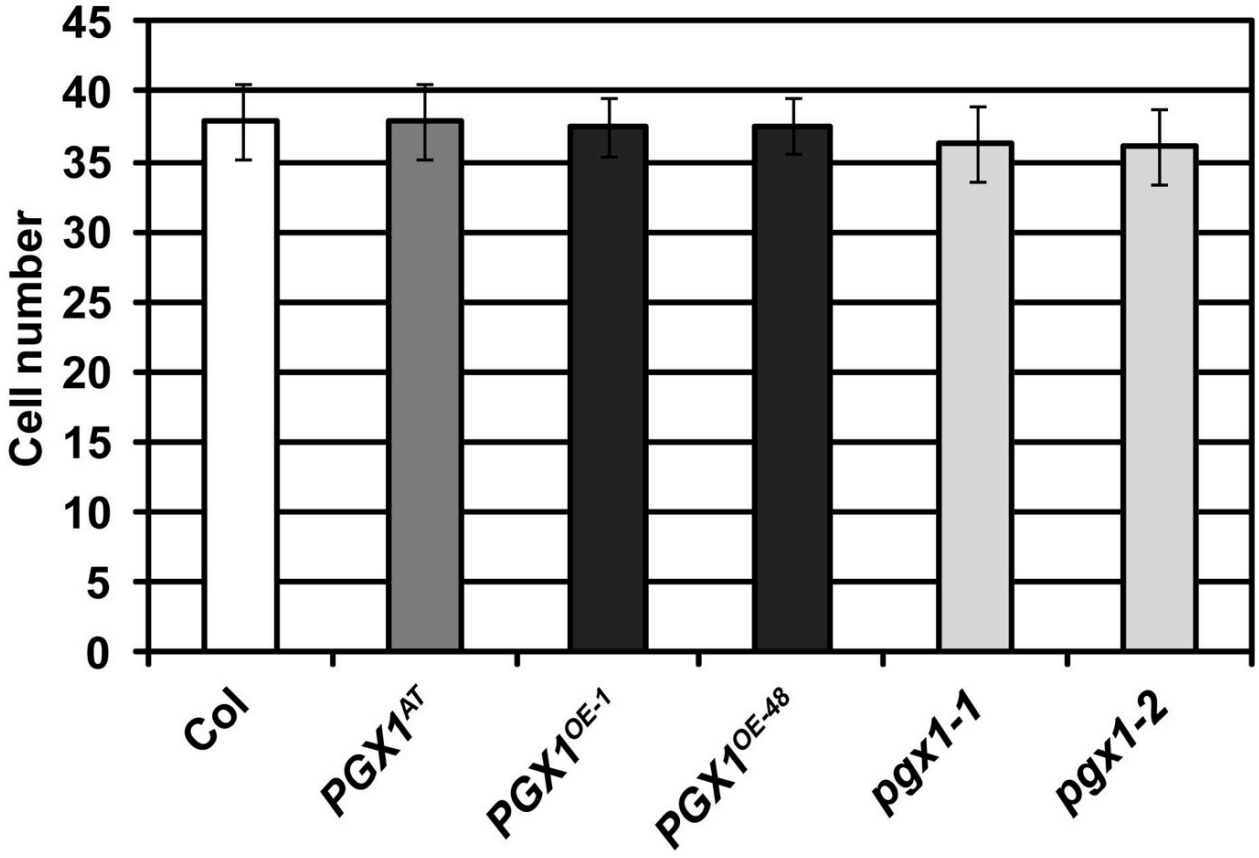


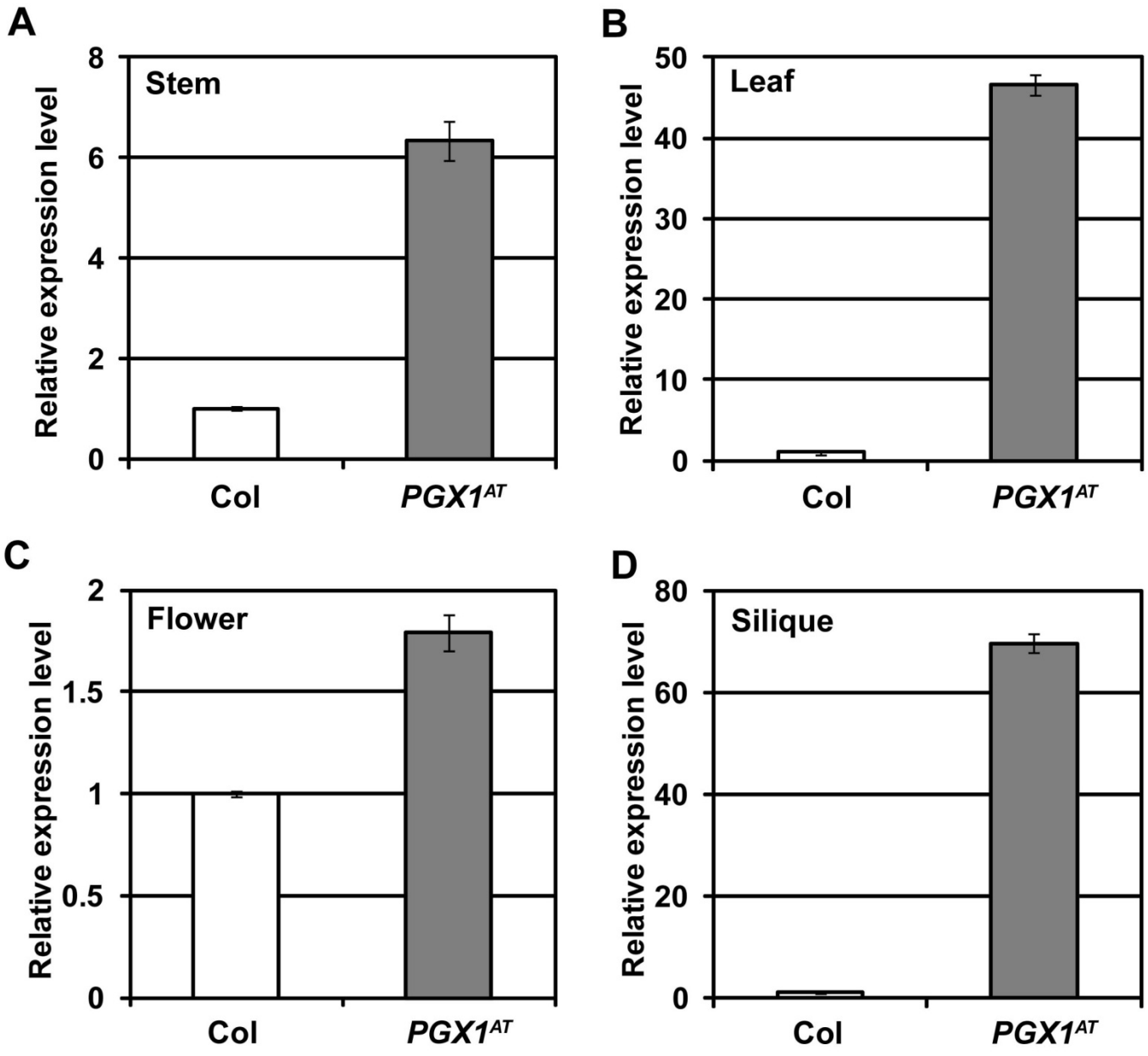
Supplemental Figure 1. Experimental Flow Chart for Activation Tag Screening for Genes Involved in Cell Expansion. See Results and Methods for experimental details.



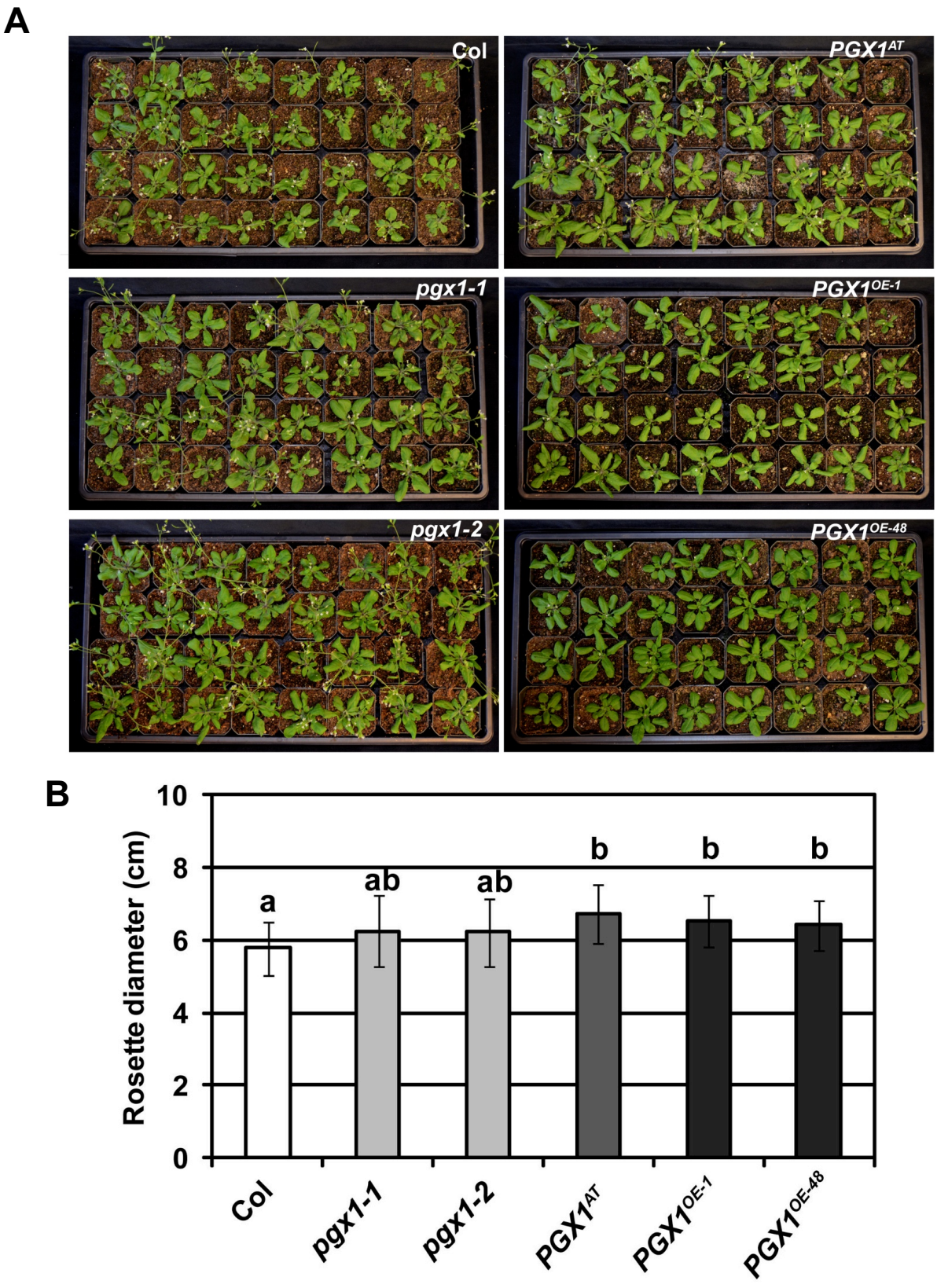
Supplemental Figure 2. Phylogenetic Analysis of *Arabidopsis* Putative PGs. The amino acid sequences of 69 Arabidopsis putative PGs were downloaded from TAIR (http://arabidopsis.org/). A multiple protein sequence alignment was conducted using ClustalW (see Supplemental Dataset 1), and a phylogenetic tree was generated by neighbor-joining (NJ) in the MEGA4 software package. The scale is 0.2 amino acid substitutions per site. QUARTET2 (QRT2) is essential for pollen grain separation (Rhee and Somerville, 1998), and QUARTET3 (QRT3) is involved in degradation of the pollen mother cell wall (Rhee et al., 2003). ARABIDOPSIS DEHISCENCE ZONE POLYGALACTURONASE1 (ADPG1) and ADPG2 contribute to silique dehiscence and floral organ abscission (Ogawa et al., 2009).



Supplemental Figure 3. Cell Number in Hypocotyls of 6-d-Old Etiolated Seedlings. Total cell numbers from the top to the bottom of hypocotyls of Col, *PGX1*^{AT}, *PGX1*$^{OE-1}$, *PGX1*$^{OE-48}$, *pgx1-1*, and *pgx1-2* seedlings were counted in transmitted light mode using a spinning disk confocal microscope with a 63X 1.40 NA oil-immersion objective. Error bars indicate SD (n=10 seedlings per genotype). No significant differences between genotypes were detected by t-test ($p>0.05$).



Supplemental Figure 4. Quantification of *PGX1* mRNA Expression in Adult Tissues of Col and *PGX1^{AT}* Plants. Total RNA was isolated from stems (A), leaves (B), flowers (C) and siliques (D) of six-week-old Col and *PGX1^{AT}* plants, and *PGX1* mRNA levels were quantified by qPCR. *ACT2* was used as an internal control. Expression levels of *PGX1* in Col plants were normalized to 1, and the relative expression levels of *PGX1* in *PGX1^{AT}* line were calculated relative to this value. The data show averages ± SD (n=3 replicates).



Supplemental Figure 5. *PGX1*^{AT} and *PGX1*^{OE} Rosettes Are Larger Than Wild-Type Rosettes. (A) Twenty-five-day-old Col, *pgx1-1*, *pgx1-2*, *PGX1*^{AT}, *PGX1*$^{OE-1}$ and *PGX1*$^{OE-48}$ plants grown in long-day conditions. **(B)** Quantification of whole rosette diameters. Error bars indicate SD (n=32 plants per genotype). Values annotated with different lowercase letters mean significant difference ($p<0.05$, one way ANOVA and Tukey test).

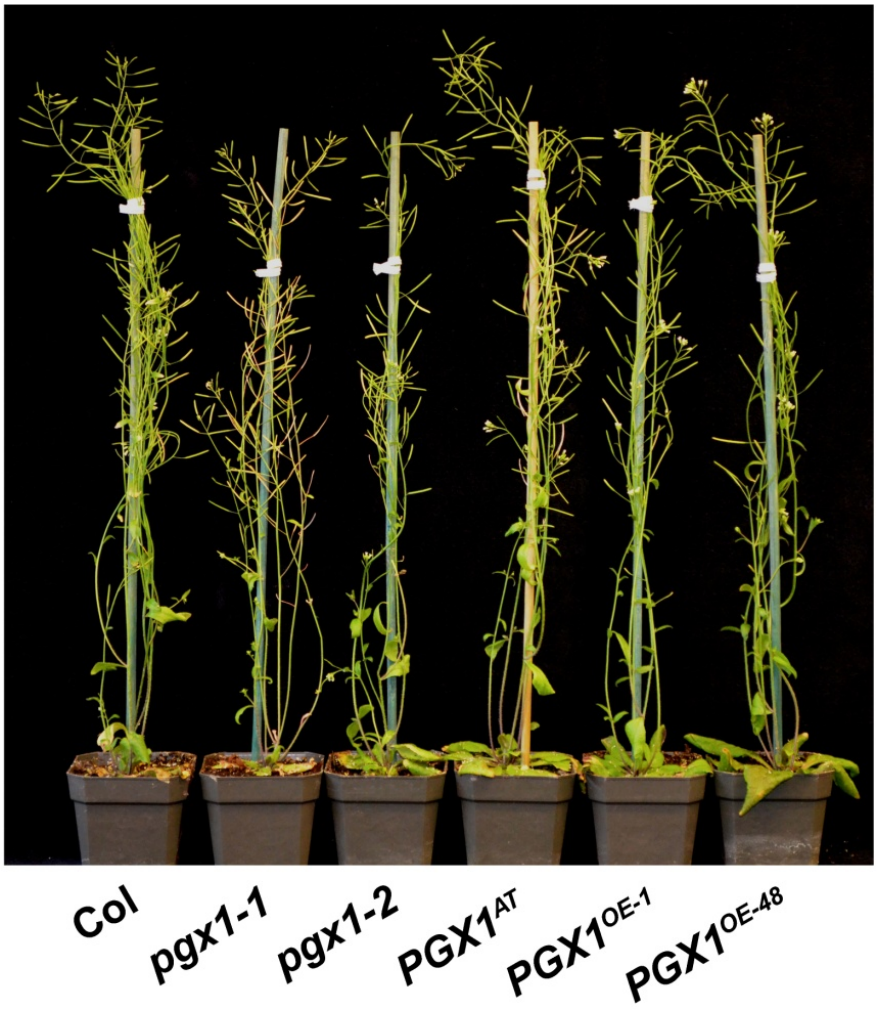
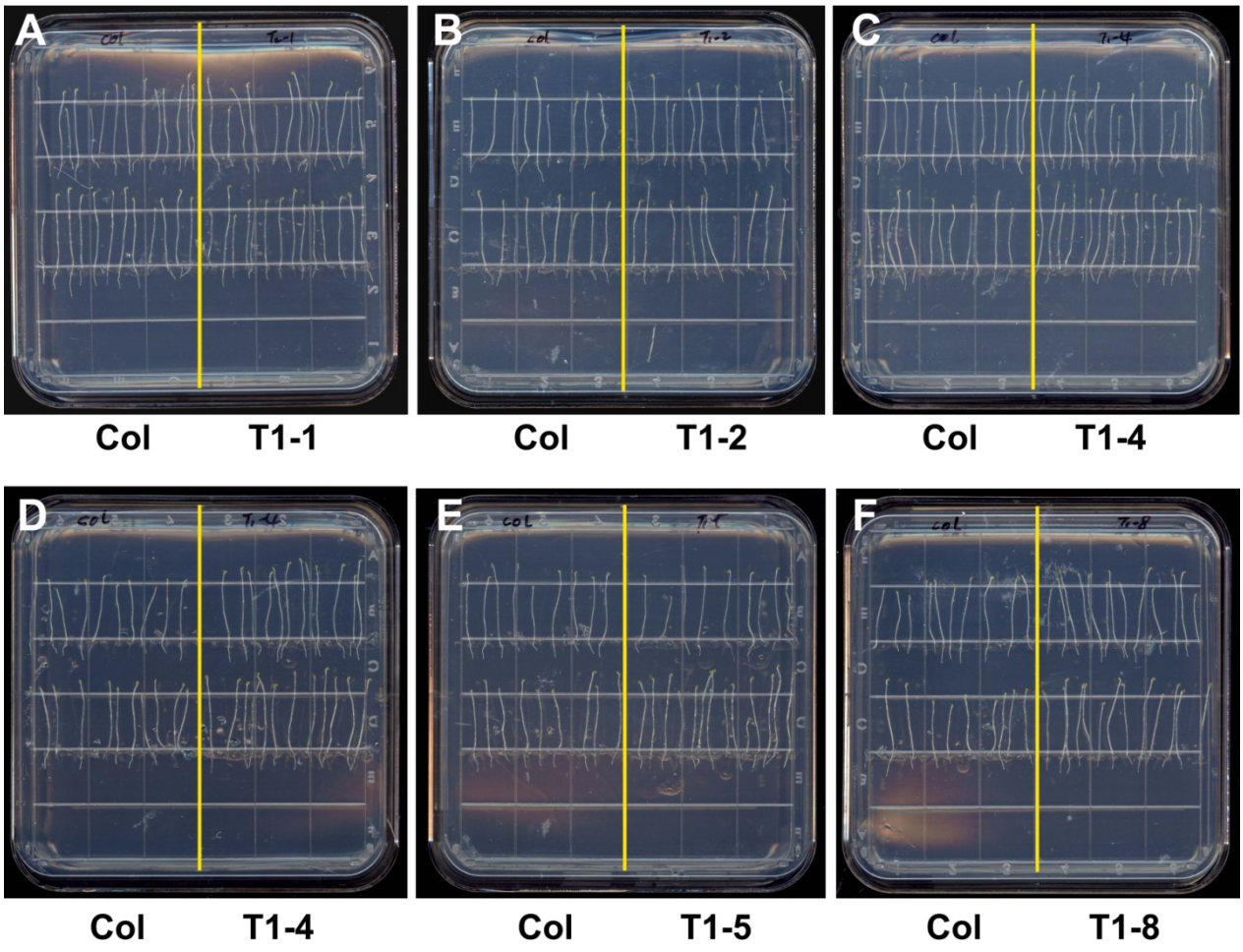


Figure S6. Forty-Five-Day-Old Plants of Col, *pgx1-1*, *pgx1-2*, *PGX1*^{AT}, *PGX1*$^{OE-1}$ and *PGX1*$^{OE-48}$ Grown in Long-Day Conditions. No significant differences in plant height were detected (n=32 plants per genotype, p>0.05, t-test).



Supplemental Figure 7. Hypocotyls of 6-d-Old Etiolated Seedlings of *PGX1*$_{pro}$*:PGX1-GFP* Complementation Lines are Comparable in Length to Wild-Type Hypocotyls. Lines T1-1, T1-2, and T1-4 in A, B, and C and lines T1-4, T1-5, and T1-8 in D, E, and F are independent heterozygous lines expressing *PGX1-GFP* driven by the endogenous *PGX1* promoter in the *pgx1-1* and *pgx1-2* mutant backgrounds, respectively. Hypocotyl lengths were quantified as shown in Figure 4.

Supplemental Table 1. Primers used in this study

Gene	Primer Name	Sequences (5'- 3')	Annotation
At3g26610	Wisc LB p745A	TCCGCAATGTGTTATTAAGTTGTC	genotyping
At3g26610	SALK LBb1.3	ATTTTGCCGATTTCGGAAC	genotyping
At3g26610	pSKI015LB_278-304rc	GAAGTTTCTCATCTAAGCCCCCATTTG	genotyping
At3g26610	pSKI015LB_136-159rc	TATAATAACGCTGCGGACATCTAC	genotyping
At3g26610 (*PGX1*)	CS850042LP	GGGGAAGCAAAAGGATACATC	genotyping
	CS850042RP	TGCTTTGGTTTGTGATCACAG	genotyping
	SALK_026818LP	TCAGCTGTTGGTTTGAACTCC	genotyping
	SALK_026818RP	GATTAGGGGTCGTCAAGAACC	genotyping
	PGX1LP	TGACAAAATTGGTCGAATTCTCA	genotyping
	PGX1RP	TGCATACTCTAATTCCAAAACAAGC	genotyping
	PGX1-promoter-F	ACATCCATGTTGTGGCACTCA	cloning
	PGX1-promoter-R	ATTTTCTTATAACTTTGTGTTATGTTTTTG	cloning
	PGX1-CDS-OP-F	AAGTTATAAGAAAAT-ATGAAGACAGTAAAGAGTTTACC	cloning
	PGX1-full-R	TGAAGGGCAAATCTTGTCATAG	cloning
	At3g26610-RP-F	GGTCTCAAGGT-ATGAAAACAGTGAAGTCTCTACCA	cloning
	At3g26610-RPN-R	CTCGAG-TTAAGAGGGACAGATCTTGTCGT	cloning
	PGX1-RT-F	CAACGGCACTTCGGTTTTAT	RT-PCR
	PGX1-RT-R	TTCGAACACCAGCAAGAGTG	RT-PCR
	PGX1-qF1	TCGGTAGTTTCACGGTGCAA	qPCR
	PGX1-qR1	CATGCATGGCACGTTGTTG	qPCR
	PGX1-qF2	TTGACCATCCAAGGCTCAGGGACTC	qPCR
	PGX1-qR2	CCGAAGTGCCGTTGGTTTCATTGGT	qPCR
	PGX1-OE-qF	GGGATTACAGACCCACCAGC	qPCR
	PGX1-OE-qR	TGGAAGATGGCACTAGGGGA	qPCR
At3g18780 (*ACT2*)	ACT2-RT-F	CACTGTGCCAATCTACGAGGGT	RT-PCR
	ACT2-RT-R	CACAAACGAGGGCTGGAACAAG	RT-PCR
	ACT2-qF	CTTGCACCAAGCAGCATGAA	qPCR
	ACT2-qR	CCGATCCAGACACTGTACTTCCTT	qPCR