Figure S1. Changes in Root angle in M82 and Penn do not represent skewing. Percentage of roots (y-axis) showing skew to the left or to the right in M82 (n=68) and PENN (n=78). No preference to skew to the left or the right is observed using a chi-square test and thus the null hypothesis is accepted.

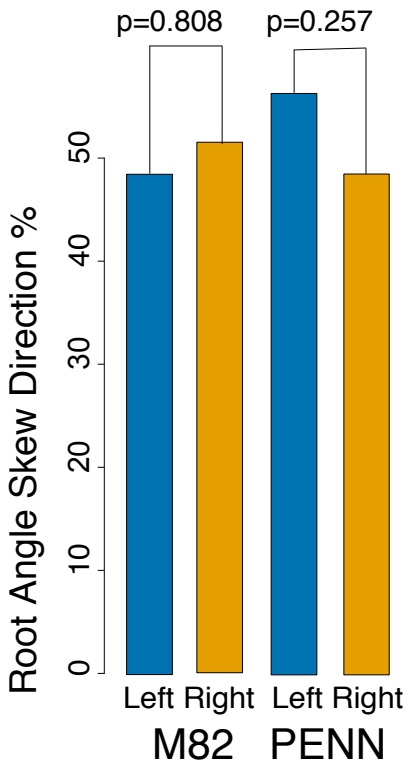
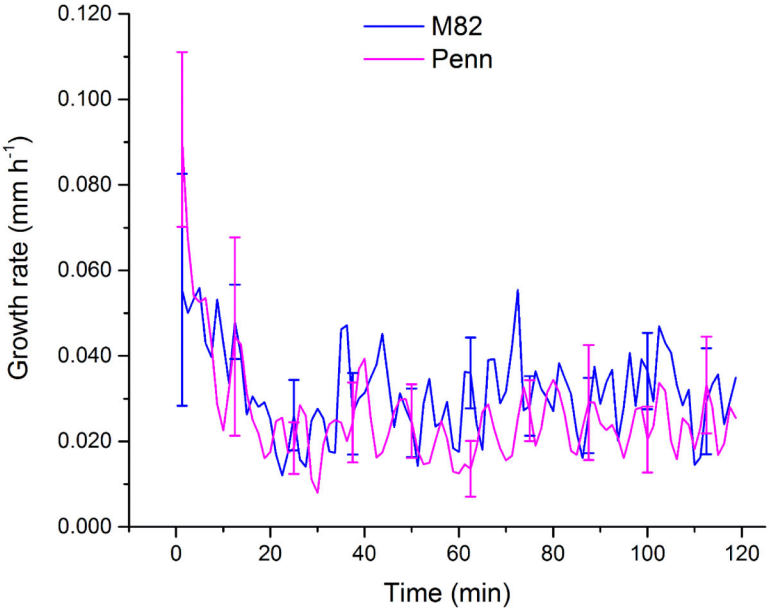


Figure S2: Mean root growth rate per time point in the two hours following rotation of M82 (n=89) **and PENN** (n=18).



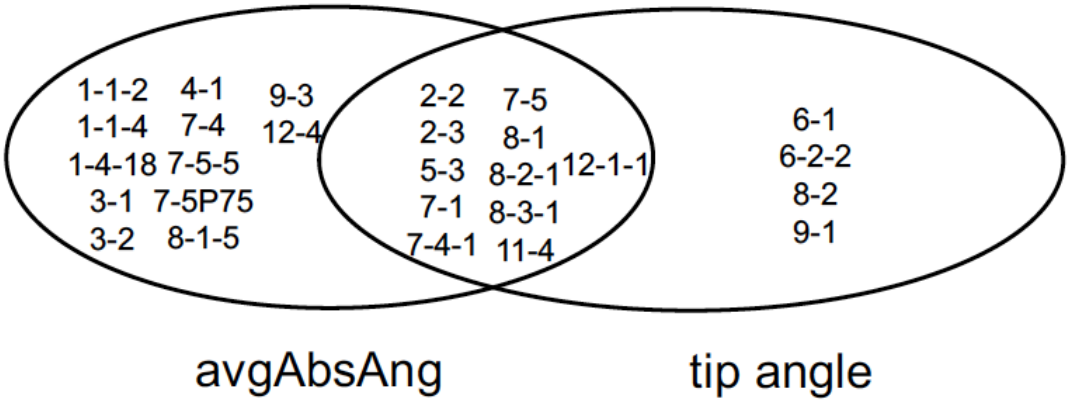


Figure S3. Overlap between average absolute angle QTL and root tip angle QTL. Venn diagram showing overlap between QTL identified for average absolute angle in this study compared to Ron et al. 2013.

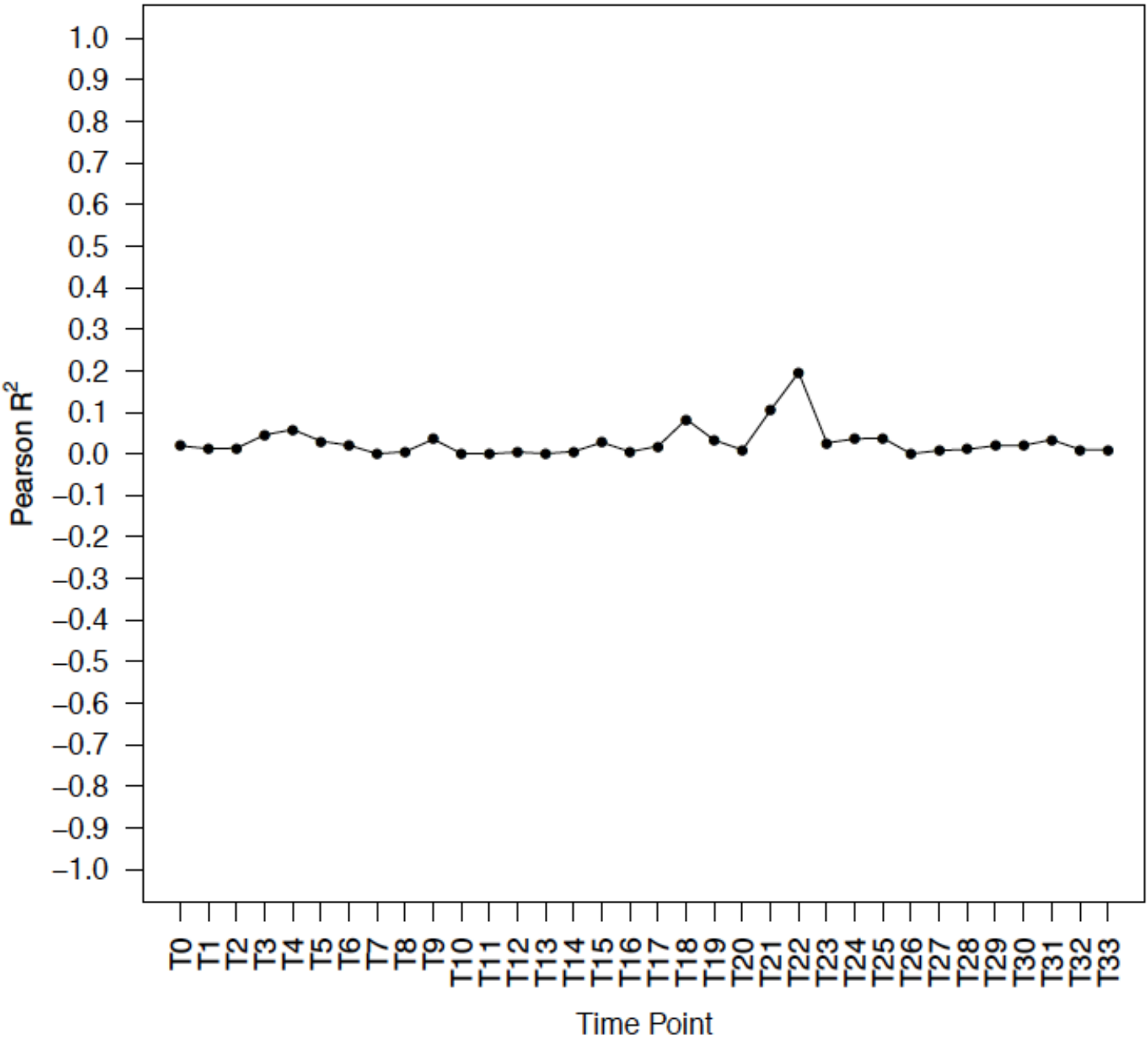


Figure S4. Pearson correlation of avgAbsAng with swing rate at each of the 34 time points.

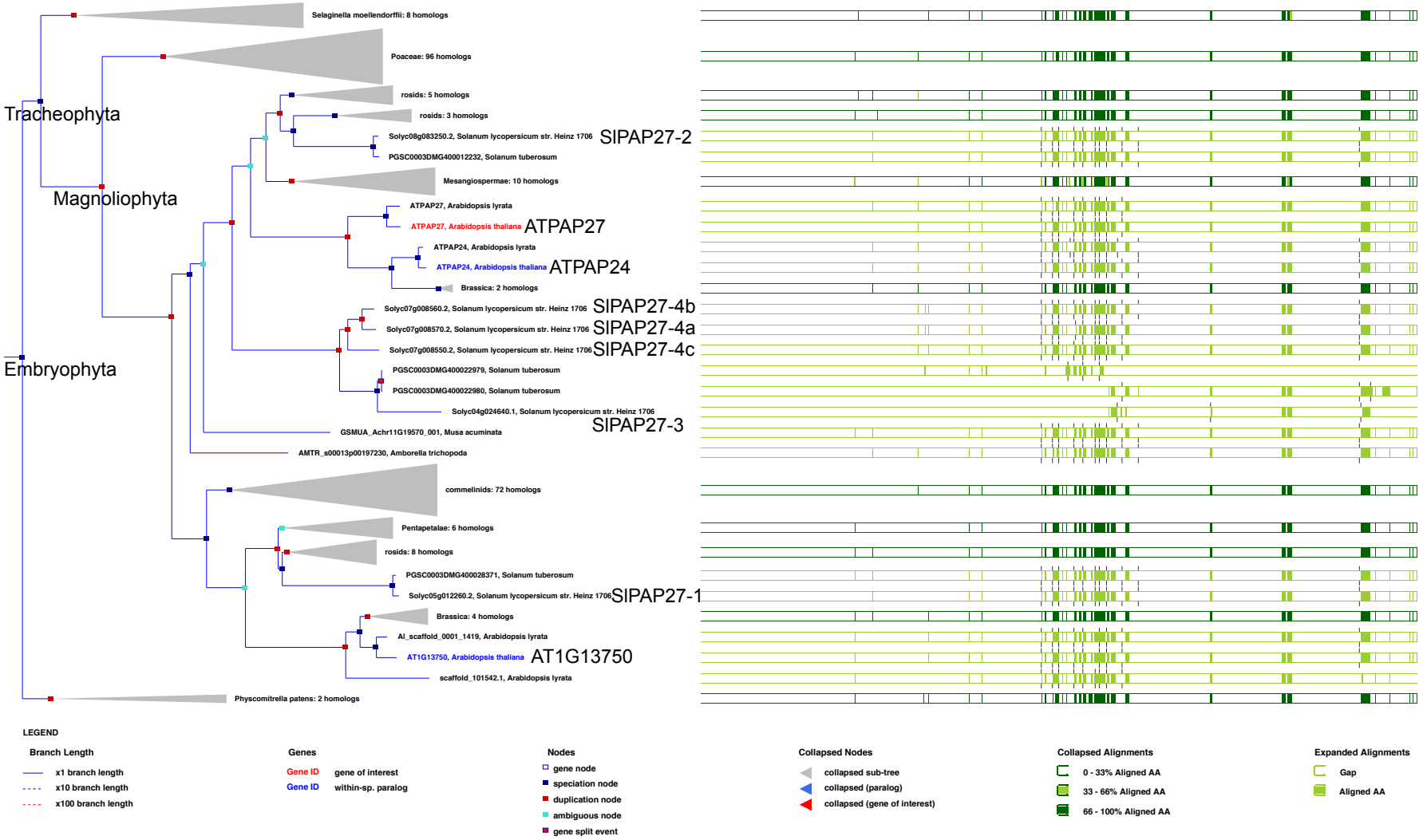


Figure S5: Precomputed phylogenetic tree of *AT5G50400 (PAP27)* and homologs in different species. Homology to the protein sequence of AT5G50400 [111, 112] is used. The taxon designation of the three highest nodes is shown. Subnodes that do not contain any genes from *A. thaliana* or *S. lycopersicum* are collapsed. PAP27 and its paralogs in *A. thaliana* and homologs in *S. lycopersicum* are called out in larger type. Alignments are shown to the right.

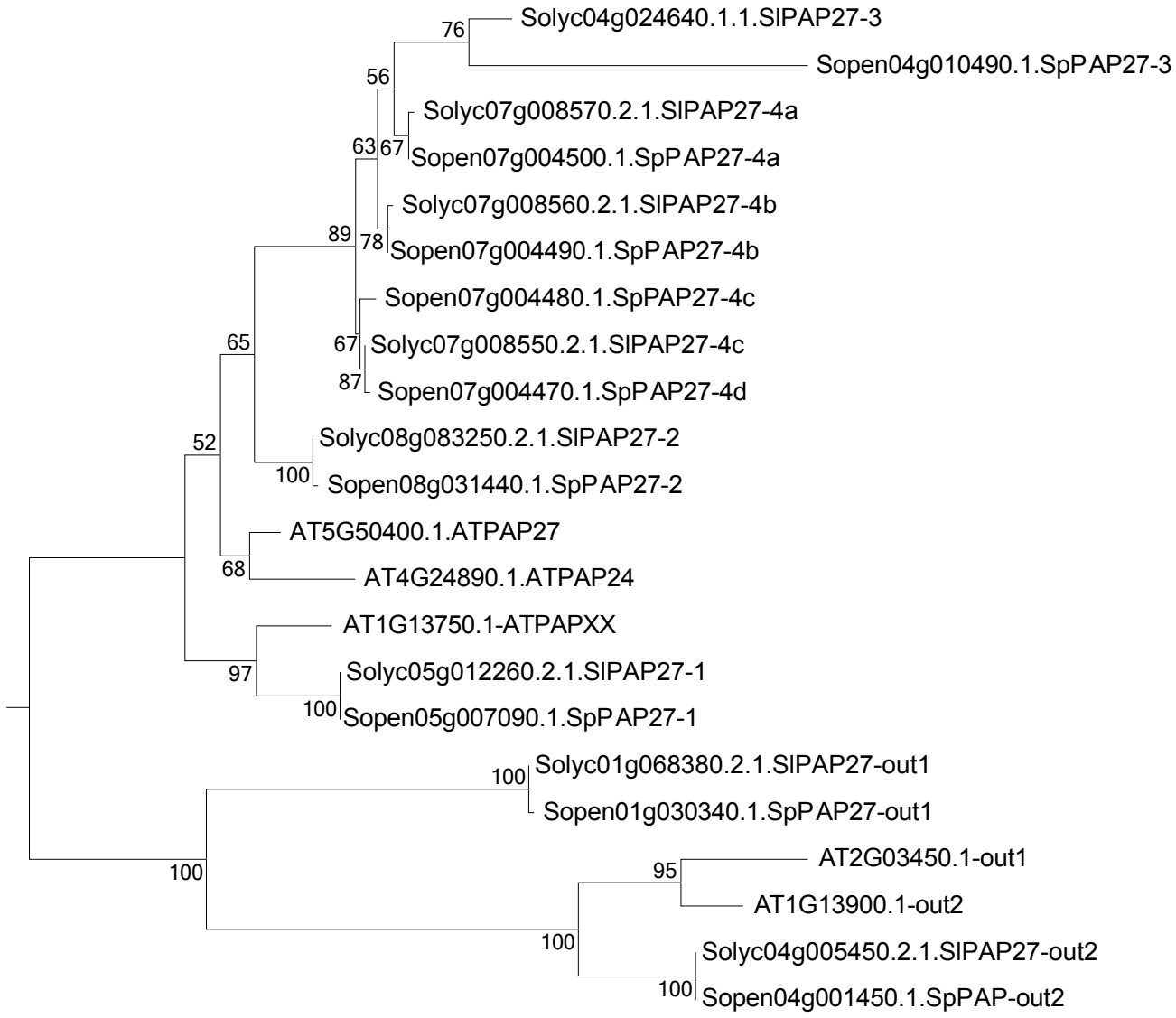


Figure S5: Maximum likelihood phylogenetic tree of *AT5G50400 (PAP27)* and homologs in *A. thaliana*, *S. lycopersicum*, and *S. pennellii*. Tree is computed with 200 bootstraps using MEGA (Tamura et al. 2011) from protein sequences. Suffixes "-out1" and "-out2" mark genes used as outgroups. Homologs were identified using the gene tree from Figure S5 and with BLAST+ (Camacho et al. 2009). Multiple alignment used Muscle (Edgar 2004).

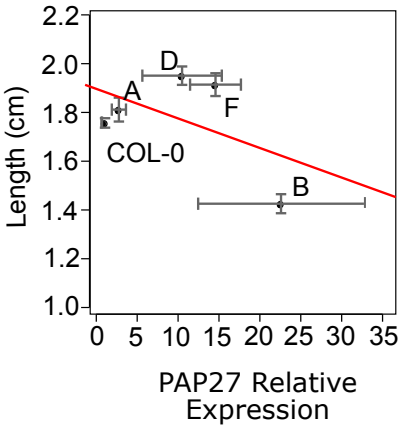
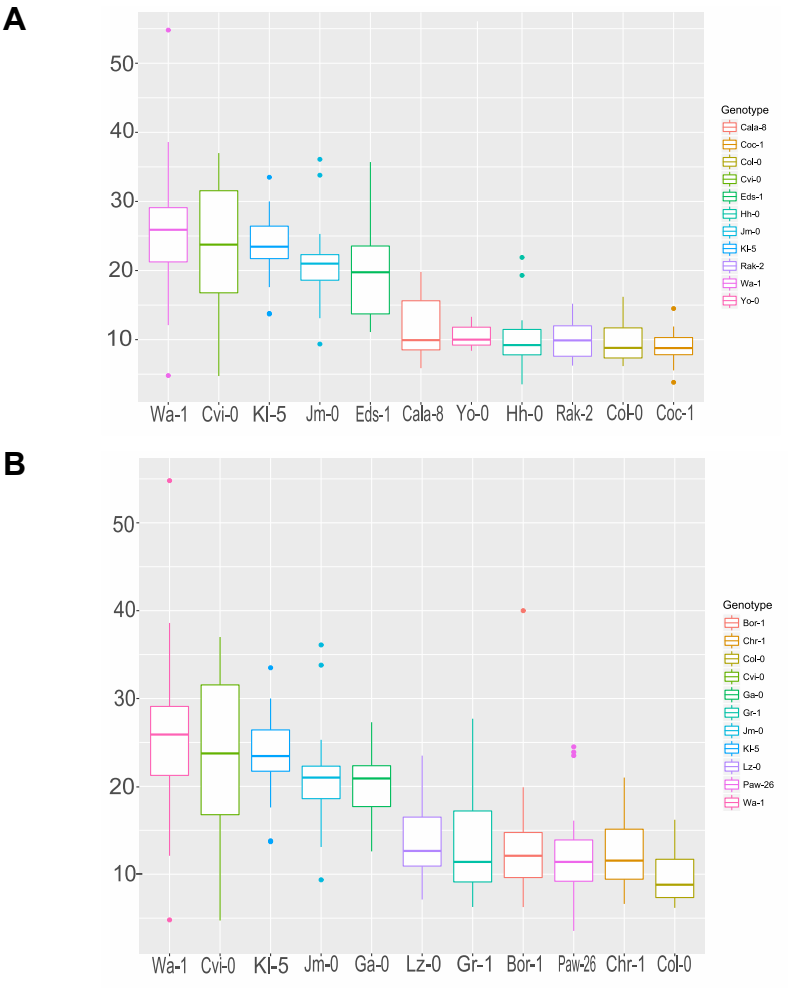


Figure S7. Root Length of *AtPAP27* overexpression lines does not linearly correlate with expression of *AtPAP27*. Error bars represent standard error of the mean, $n_{avgAbsAng}$(Col-0)=275, $n_{avgAbsAng}$(35S:AtPAP27/lineA)=11, $n_{avgAbsAng}$(35S:AtPAP27/lineB)=20, $n_{avgAbsAng}$(35S:AtPAP27/lineD)=83, $n_{avgAbsAng}$(35S:AtPAP27/lineF)=100; $n_{EXPRESSION}$(Col-0)=, $n_{EXPRESSION}$(35S:AtPAP27/lineA)=11, $n_{EXPRESSION}$(35S:AtPAP27/lineB)=20, $n_{EXPRESSION}$(35S:AtPAP27/lineD)=22, $n_{EXPRESSION}$(35S:AtPAP27/lineF)=7.

Figure S8. AvgAbsAng measurements capture the variation in the top and bottom 5 accessions for "Direction Index" (A) and "Root Angle". In each panel, the accessions with the highest "Direction Index" or "Root Angle" are shown on the left, while the accessions with the lowest "Direction Index" or "Root Angle" are shown on the right. n(Wa-1)=23, n(Cvi-0)=24, n(Kl-5)=24, n(Jm-0)=24, n(Eds-1)=18, n(Cala-8)=22, n(Yo-0)=21, n(Hh-0)=22, n(Rak-2)=20, n(Col-0)=22, n(Coc-1)=23.



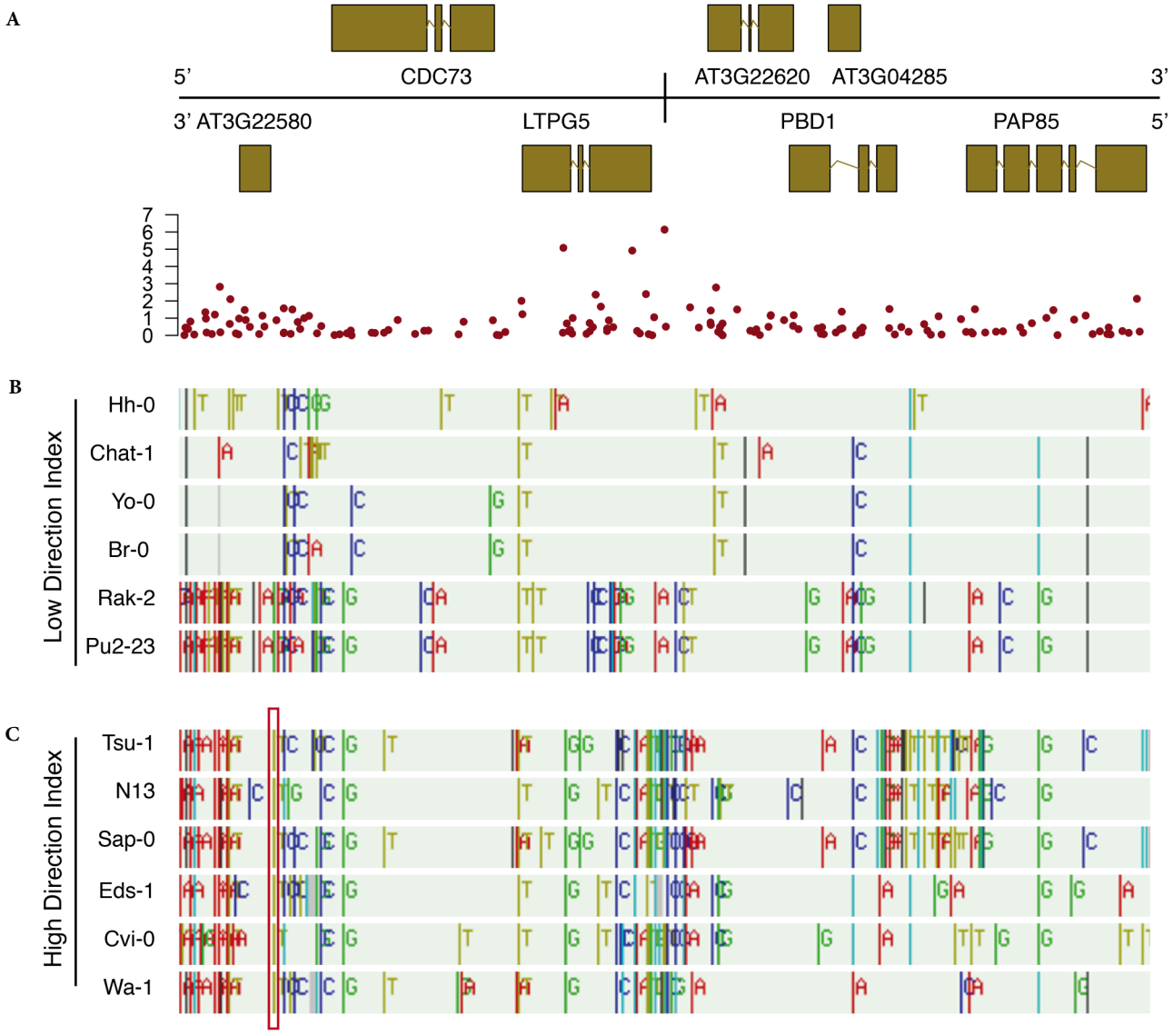


Figure S9. SNP patterns of contrasting accessions for direction index. **(A)** Gene models in the CDC73 region. **(B)** GWAS LOD score for the "median direction index day4" trait. **(C)** Exemplary accessions for low and high values of the direction index trait that was mapped using GWAS. A potentially relevant SNP that was not included in the original 250K SNP chip is indicated by the red box. Following criteria for the selection of the depicted accessions were used: 1) Genome sequence for accession is available on the http://signal.salk.edu/atg1001/3.0/gebrowser.php 2) For accessions with the lowest direction indexes: those having reference allele A/T (associated with low direction index) at the GWAS identified marker position (Chromosome 3, position 8008000) were selected. For accessions with highest direction indexes: those having marker SNP C/G (associated with high direction index). 3) For accessions with low direction index: examples from three haplotypes (inferred by fastPHASE) are shown with two exemplary accessions for each haplotype. Extreme accessions with the highest direction index belong (except Cvi-0) to the same predicted haplotype.

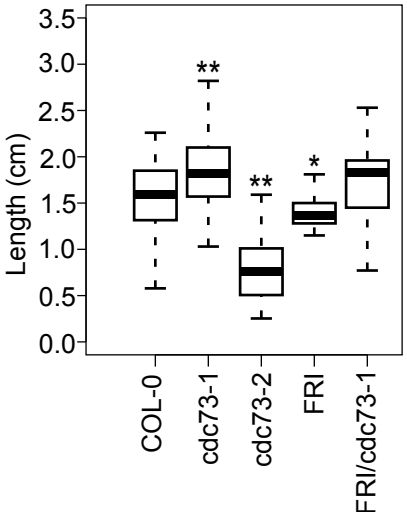


Figure S10: Root length of *cdc73* mutant alleles does not vary in a manner similar to root angle. Error bars represent standard error of the mean, n(Col-0)=144, n(cdc73-1)=85, n(cdc73-2)=26, n(FRI)=22, n(FRI/cdc73-1)=32. *p ≤ 0.05 **p ≤ 0.01 ***p ≤ 0.001 as determined using an ANOVA.