

Supplemental Material

Supplemental Figures

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 (Vilella et al. 2009; EBI 2015) 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 S6. 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 **Fig S3** 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, $n_{\text{avgAbsAng}}(\text{Col-0})=275$, $n_{\text{avgAbsAng}}(35\text{S:AtPAP27/lineA})=11$, $n_{\text{avgAbsAng}}(35\text{S:AtPAP27/lineB})=20$, $n_{\text{avgAbsAng}}(35\text{S:AtPAP27/lineD})=83$, $n_{\text{avgAbsAng}}(35\text{S:AtPAP27/lineF})=100$; $n_{\text{EXPRESSION}}(\text{Col-0})=$, $n_{\text{EXPRESSION}}(35\text{S:AtPAP27/lineA})=11$, $n_{\text{EXPRESSION}}(35\text{S:AtPAP27/lineB})=20$, $n_{\text{EXPRESSION}}(35\text{S:AtPAP27/lineD})=22$, $n_{\text{EXPRESSION}}(35\text{S:AtPAP27/lineF})=7$.

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(KI-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.

Supplemental Movie 1: <http://phytomorph.wisc.edu/results/Brady/M82.mp4>

Supplemental Movie 2: <http://phytomorph.wisc.edu/results/Brady/penn.mp4>

Supplemental Datasets

1. **S1_Dataset.zip:** zip file of code, input data, and output files for average absolute angle phenotype analysis.
2. **S2_Dataset.zip:** zip file of code, input data, and output files for rotation phenotype analysis.
3. **S3_Dataset.zip:** Normalized average expression of all genes in the 76 introgression lines.

4. **S4_Dataset.xlsx**: Dataset of p-values from GWAS on root direction index on DAG 4 of 257 accessions; Uncorrected genome-wide association p-values for each SNP tested. Minor allele count (MAC) refers to the number of accessions in the study panel carrying minor allele for the respective SNP. Minor allele frequency (MAF) refers to the frequency thereof.

Supplemental Tables

trait	genotype	N	mean	std. error	p-value	q-value
avgAbsAng	M82	60	16.85	1.37	NA	NA
avgAbsAng	PENN	78	47.88	1.53	0.000	0.000
avgAbsAng	IL1-1-2	13	26.92	3.22	0.010	0.037
avgAbsAng	IL1-1-4	34	22.18	2.12	0.002	0.010
avgAbsAng	IL1-4-18	25	26.29	2.28	0.000	0.001
avgAbsAng	IL2-2	23	28.54	2.15	0.000	0.001
avgAbsAng	IL2-3	29	24.52	2.35	0.001	0.006
avgAbsAng	IL3-1	34	23.55	1.95	0.004	0.016
avgAbsAng	IL3-2	22	25.17	2.28	0.015	0.050
avgAbsAng	IL4-1	34	27.39	3.20	0.000	0.000
avgAbsAng	IL5-3	29	25.38	2.54	0.001	0.006
avgAbsAng	IL7-1	37	23.09	1.67	0.008	0.030
avgAbsAng	IL7-4	29	24.88	2.77	0.002	0.009
avgAbsAng	IL7-4-1	34	37.76	2.90	0.000	0.000
avgAbsAng	IL7-5	28	26.81	2.31	0.000	0.000
avgAbsAng	IL7-5-5	35	27.15	2.15	0.000	0.000
avgAbsAng	IL7-5-P75	35	30.23	2.70	0.000	0.000
avgAbsAng	IL8-1	24	23.59	4.10	0.011	0.038
avgAbsAng	IL8-1-5	45	22.95	2.06	0.013	0.042
avgAbsAng	IL8-2-1	29	31.22	2.85	0.000	0.000
avgAbsAng	IL8-3-1	16	30.70	6.05	0.000	0.000
avgAbsAng	IL9-3	37	23.85	1.72	0.003	0.011

avgAbsAng	IL11-4	24	31.08	2.21	0.000	0.000
avgAbsAng	IL12-1-1	10	37.24	6.69	0.000	0.000
avgAbsAng	IL12-4	71	27.63	1.88	0.000	0.000

Table S1. Number of samples, mean, and standard error for root angle traits in *S. lycopersicum* cv. M82, *S. pennellii*, and all ILs significantly (q -value ≤ 0.05) different from M82, with p -values and their FDR-adjusted (Benjamini and Hochberg) q -values for the genotype contribution being significant. The comparison used the mixed-effect linear model "trait ~ genotype + collide + (1|germAge) + (1|plateDate)", where "trait" is the avgAbsAng, "genotype" is the plant genotype, "collide" is TRUE if the plant root collided with another plant's root during growth on the plate, "germAge" is the age since germination and is a random-effect variable, and "plateDate" is the date of plating and is also a random-effect.

genotype	peak swing rate	peak time (timepoint)
M82	3.9±0.12	29±1.7 (T7)
PENN	2.7±0.43	69±11 (T18)
All ILs	3.6±0.061	30±1.1 (T8)
IL1-1-2	4.4±0.19	21±2.3 (T5)
IL1-1-3	4±1.1	30±11 (T8)
IL1-3	4.7±0.16	20±3 (T5)
IL1-4	3.7±0.22	30±5.3 (T8)
IL1-4-18	3±0.22	67±8.7 (T17)
IL2-1	5±0.57	17±0.99 (T4)
IL2-1-1	4.5±0.15	16±2.6 (T4)
IL2-2	4.5±0.27	16±2.5 (T4)
IL2-3	3.5±0.3	22±5.2 (T5)
IL2-4	4±0.19	26±5.9 (T6)
IL2-6-5	3.5±0.15	18±5.3 (T4)
IL3-1	3.9±0.3	14±1.8 (T3)

IL3-5	3.5±0.23	29±3.3 (T7)
IL4-1	2.4±0.23	34±4.8 (T9)
IL4-1-1	2.6±0.21	24±5.8 (T6)
IL4-3	2.8±0.26	21±3.7 (T5)
IL4-3-2	3.9±0.25	15±1.2 (T4)
IL4-4	3.3±0.41	42±12 (T11)
IL5-1	3.7±0.34	36±14 (T9)
IL5-2	3.3±0.31	20±2.8 (T5)
IL5-3	4±0.76	18±3.6 (T4)
IL5-5	3.1±0.16	27±1.4 (T7)
IL6-1	4.2±0.49	31±5.3 (T8)
IL6-2	3.8±0.24	24±4.9 (T6)
IL6-4	2.8±0.21	43±6.8 (T11)
IL7-1	3.3±0.27	35±7.4 (T9)
IL7-3	3±0.41	43±10 (T11)
IL7-4	3.1±0.25	45±8.4 (T12)
IL7-4-1	3.6±0.18	49±15 (T13)
IL7-5	4.1±0.38	36±11 (T9)
IL7-5-1	3.5±0.82	46±12 (T12)
IL7-5-5	3.1±0.12	33±3.4 (T8)
IL7-5-P5	3.4±0.27	34±6.2 (T9)
IL8-1	3.8±0.21	21±2.1 (T5)
IL8-1-1	3.2±0.31	20±3.5 (T5)
IL8-1-5	3.1±0.26	28±3.6 (T7)
IL8-2-1	1.1±0.64	21±13 (T5)
IL8-3	4±0.37	20±2.6 (T5)
IL8-3-1	12±2.4	3.8±2.2 (T1)
IL9-1	3.1±0.18	25±2.4 (T6)
IL9-1-2	3.1±0.29	37±13 (T9)
IL9-1-3	NA	NA (NA)
IL9-2	4.6±0.34	23±4.8 (T6)
IL9-2-5	NA	NA (NA)

IL9-2-6	3.4±0.29	27±4.3 (T7)
IL9-3-1	3±0.33	44±12 (T11)
IL10-1	3.2±0.41	22±3.6 (T5)
IL10-1-1	3.7±0.23	38±15 (T10)
IL10-2	5.7±0.28	24±6.6 (T6)
IL10-2-2	4.2±0.59	41±15 (T10)
IL10-3	3.5±0.35	41±6.4 (T10)
IL11-1	3.5±0.16	29±3.9 (T7)
IL11-2	3.4±0.34	24±7.1 (T6)
IL11-4	3.5±0.36	49±12 (T13)
IL11-4-1	4±0.37	21±4.1 (T5)
IL12-1	3.6±0.21	25±3 (T6)
IL12-1-1	3.3±0.24	38±12 (T10)
IL12-2	2.4±0.25	41±12 (T10)
IL12-3	4.3±0.65	27±6.1 (T7)
IL12-3-1	4.6±0.34	15±3.4 (T4)
IL12-4	3.2±0.26	29±5.8 (T7)
IL12-4-1	3.5±0.38	33±3.4 (T8)

Table S2. Mean ± standard error of peak swing rates (degrees/3.75 mins) and mean time of peak swing rates ± standard error (mins) with timepoint shown for reference, for M82, *S. pennellii*, and ILs.

timepoint	genotype	N	mean	stderr	p-value	q-value
T0	M82	89	0.29	0.17	NA	NA
T0	PENN	18	0.35	0.41	0.87	0.97
T0	IL5-3	5	-2.3	0.73	0.00041	0.024
T1	M82	89	0.63	0.11	NA	NA
T1	PENN	18	0.64	0.27	0.96	0.96
T1	IL2-1-1	10	2	0.35	9.30E-05	0.0027
T1	IL7-4	8	-1.3	0.39	1.40E-06	8.20E-05
T2	M82	89	1.3	0.12	NA	NA
T2	PENN	18	1.1	0.3	0.45	0.71

T2	IL1-4-18	19	0.28	0.3	0.00038	0.0055
T2	IL2-1-1	10	3.4	0.39	2.60E-07	1.50E-05
T2	IL7-4	8	-0.44	0.43	4.60E-05	0.0013
T2	IL12-3-1	8	3.1	0.43	7.20E-05	0.0014
T3	M82	89	1.9	0.13	NA	NA
T3	PENN	18	1.2	0.32	0.028	0.13
T3	IL1-3	5	4.1	0.57	6.20E-05	0.00081
T3	IL1-4-18	19	0.56	0.31	3.70E-05	0.00072
T3	IL2-1	8	3.8	0.46	1.70E-05	0.00048
T3	IL2-1-1	10	3.8	0.41	2.00E-06	0.00012
T3	IL2-2	5	3.7	0.57	0.0014	0.011
T3	IL2-6-5	6	3.3	0.52	0.0063	0.041
T3	IL4-3-2	8	3.1	0.46	0.0059	0.041
T3	IL10-2	8	3.5	0.46	0.00044	0.0042
T3	IL12-3-1	8	3.7	0.46	7.00E-05	0.00081
T4	M82	89	2.2	0.13	NA	NA
T4	PENN	18	1	0.32	0.00042	0.0037
T4	IL1-3	5	4.2	0.57	0.00044	0.0037
T4	IL1-4-18	19	0.77	0.31	1.20E-05	0.00018
T4	IL2-1	8	4.5	0.46	2.70E-07	1.50E-05
T4	IL2-1-1	10	4	0.41	8.90E-06	0.00017
T4	IL4-3-2	8	3.4	0.46	0.0063	0.036
T4	IL9-2	13	3.3	0.37	0.0025	0.016
T4	IL10-2	8	4.2	0.46	6.80E-06	0.00017
T4	IL10-2-2	7	3.5	0.49	0.0068	0.036
T4	IL12-2	7	0.67	0.49	0.0025	0.016
T4	IL12-3-1	8	3.8	0.46	0.00039	0.0037
T5	M82	89	2.4	0.14	NA	NA
T5	PENN	18	0.83	0.34	2.80E-06	5.40E-05
T5	IL1-4-18	19	0.67	0.33	1.50E-07	8.70E-06
T5	IL2-1	8	4.7	0.48	2.50E-06	5.40E-05
T5	IL10-2	8	4.3	0.48	0.00013	0.0019
T6	M82	89	2.6	0.13	NA	NA
T6	PENN	18	0.44	0.32	7.10E-12	4.10E-10
T6	IL1-4-18	19	0.78	0.31	2.70E-09	7.80E-08
T6	IL4-1-1	10	1.5	0.41	0.0058	0.048
T6	IL4-3	14	1.7	0.35	0.0057	0.048

T6	IL6-1	23	1.4	0.29	7.60E-06	0.00015
T6	IL7-5-5	28	1.8	0.26	0.0016	0.024
T6	IL10-2	8	4	0.45	0.0021	0.024
T7	M82	89	2.9	0.12	NA	NA
T7	PENN	18	0.43	0.3	5.00E-16	2.90E-14
T7	IL1-4-18	19	0.86	0.29	5.80E-12	1.70E-10
T7	IL4-1-1	10	1.3	0.38	2.70E-05	0.00039
T7	IL4-3	14	1.6	0.33	6.20E-05	6.00E-04
T7	IL6-1	23	1.2	0.27	2.40E-10	4.70E-09
T7	IL7-3	8	1.6	0.42	0.003	0.022
T7	IL7-5-1	7	1.6	0.45	0.0037	0.024
T7	IL7-5-5	28	2	0.25	0.00036	0.003
T7	IL10-2	8	4.1	0.42	0.0044	0.026
T7	IL12-2	7	1.1	0.45	5.80E-05	6.00E-04
T8	M82	89	2.8	0.12	NA	NA
T8	PENN	18	0.53	0.29	1.70E-14	1.00E-12
T8	IL1-4-18	19	1.2	0.28	8.30E-09	1.60E-07
T8	IL2-1	8	1.6	0.41	0.0026	0.019
T8	IL4-1-1	10	1.3	0.37	5.40E-05	0.00063
T8	IL4-3	14	1.3	0.32	6.50E-06	9.40E-05
T8	IL4-3-2	8	1.6	0.41	0.0032	0.02
T8	IL6-1	23	1.1	0.26	4.40E-11	1.30E-09
T8	IL6-4	5	1.3	0.52	0.0046	0.026
T8	IL7-5-5	28	2	0.24	0.0017	0.014
T8	IL12-2	7	1.2	0.44	0.00032	0.0031
T9	M82	89	2.4	0.12	NA	NA
T9	PENN	18	0.34	0.3	7.60E-12	4.40E-10
T9	IL1-4-18	19	1.4	0.29	0.00054	0.01
T9	IL6-1	23	1.1	0.27	5.50E-07	1.60E-05
T10	M82	89	2.1	0.12	NA	NA
T10	PENN	18	0.079	0.3	1.70E-11	1.00E-09
T10	IL1-4-18	19	0.96	0.29	7.90E-05	0.0023
T10	IL6-1	23	1.1	0.27	0.00024	0.0046
T10	IL12-2	7	0.71	0.45	0.0018	0.027
T11	M82	89	1.9	0.12	NA	NA
T11	PENN	18	0.24	0.28	1.20E-08	6.80E-07
T11	IL1-4-18	19	0.72	0.28	3.60E-05	0.001

T12	M82	89	1.6	0.11	NA	NA
T12	PENN	18	0.32	0.27	2.50E-06	0.00015
T13	M82	89	1.4	0.1	NA	NA
T13	PENN	18	-0.16	0.24	9.30E-10	5.40E-08
T13	IL1-4-18	19	0.5	0.24	3.00E-04	0.0087
T14	M82	89	1.3	0.11	NA	NA
T14	PENN	18	-0.18	0.26	4.30E-08	2.50E-06
T15	M82	89	1.2	0.1	NA	NA
T15	PENN	18	0.34	0.24	0.001	0.029
T15	IL11-1	8	2.4	0.35	0.00024	0.014
T16	M82	89	0.99	0.1	NA	NA
T16	PENN	18	0.71	0.23	0.22	0.61
T16	IL4-4	11	-0.00076	0.29	0.00061	0.035
T17	M82	89	0.92	0.1	NA	NA
T17	PENN	18	0.43	0.24	0.042	0.41
T18	M82	89	0.89	0.1	NA	NA
T18	PENN	18	0.37	0.23	0.027	0.26
T18	IL11-4	5	2.7	0.42	1.40E-05	8.00E-04
T19	M82	89	0.85	0.1	NA	NA
T19	PENN	18	0.47	0.24	0.11	0.44
T19	IL11-4	5	2.3	0.42	8.00E-04	0.046
T20	M82	89	0.76	0.1	NA	NA
T20	PENN	18	0.29	0.23	0.047	0.28
T21	M82	89	0.44	0.09	NA	NA
T21	PENN	18	0.26	0.22	0.43	0.81
T21	IL1-4	9	-0.62	0.3	0.00049	0.0094
T21	IL1-4-18	19	1.3	0.22	0.00018	0.0052
T21	IL7-5-5	28	0.97	0.19	0.0044	0.043
T21	IL10-3	7	1.5	0.34	0.0011	0.013
T21	IL11-4	5	2	0.4	6.50E-05	0.0037
T21	IL12-3	11	-0.47	0.28	0.0011	0.013
T22	M82	89	0.35	0.1	NA	NA
T22	PENN	18	0.22	0.23	0.58	0.85
T22	IL1-4	9	-0.77	0.31	0.00038	0.022
T22	IL7-4-1	6	1.6	0.38	0.0015	0.044
T23	M82	89	0.22	0.1	NA	NA
T23	PENN	18	0.48	0.23	0.27	0.68

T24	M82	89	0.12	0.09	NA	NA
T24	PENN	18	0.63	0.23	0.029	0.4
T24	IL1-4-18	19	0.89	0.23	0.00069	0.04
T25	M82	89	0.11	0.09	NA	NA
T25	PENN	18	0.4	0.21	0.18	0.58
T25	IL1-4-18	19	0.75	0.21	0.0023	0.034
T25	IL6-1	23	0.72	0.19	0.0019	0.034
T25	IL7-4-1	6	1.3	0.35	0.00082	0.034
T25	IL11-4	5	1.3	0.38	0.0017	0.034
T26	M82	89	-0.0016	0.08	NA	NA
T26	PENN	18	0.42	0.2	0.033	0.19
T26	IL1-4	9	0.88	0.27	0.001	0.03
T26	IL1-4-18	19	0.93	0.19	1.90E-06	0.00011
T27	M82	89	0.082	0.08	NA	NA
T27	PENN	18	0.42	0.2	0.091	0.44
T27	IL1-4	9	0.89	0.27	0.0029	0.042
T27	IL1-4-18	19	0.95	0.2	1.10E-05	0.00066
T27	IL10-2-2	7	1.1	0.31	0.00056	0.016
T27	IL11-4-1	8	-0.83	0.29	0.0015	0.03
T28	M82	89	0.12	0.08	NA	NA
T28	PENN	18	0.018	0.2	0.61	0.91
T29	M82	89	0.092	0.08	NA	NA
T29	PENN	18	-0.14	0.2	0.24	0.71
T30	M82	89	0.19	0.09	NA	NA
T30	PENN	18	0.42	0.21	0.27	0.9
T30	IL7-5	9	1.2	0.28	0.00063	0.037
T31	M82	89	0.18	0.09	NA	NA
T31	PENN	18	0.36	0.21	0.38	0.78
T32	M82	89	0.076	0.08	NA	NA
T32	PENN	18	0.097	0.21	0.92	0.99
T33	M82	89	0.057	0.13	NA	NA
T33	PENN	18	0.33	0.32	0.41	0.85

Table S3. Number of samples, mean, and standard error for swing rate at all 34 timepoints in *S. lycopersicum* cv. M82, *S. pennellii*, and all ILs significantly (q -value ≤ 0.05) different from M82 for swing rate, with p -values and their FDR-adjusted (Benjamini and

Hochberg) q-values for the genotype contribution being significant. The comparison used the simple fixed-effect linear model "swing rate ~ genotype".

Name	ACC_ID	median_direction_index_DAG4
Hh-0	7169	0.1795
Coc-1	5729	0.183
Yo-0	6983	0.184
Rak-2	8365	0.1875
Cala-8	9152	0.189
Br-0	6904	0.194
Col-0	6909	0.194
Rev-1	8369	0.194
Bch-1	7028	0.196
Algutsrum	8230	0.1975
Pu2-23	6951	0.1995
Ost-0	8351	0.203
Benk-1	7008	0.2075
Mdn-1	1829	0.208
Chat-1	7071	0.211
Hau-0	7164	0.212
Do-0	7102	0.2125
Drall-1	8284	0.2135
Eden-2	6913	0.214
CrI-1	5731	0.2145
Bla-1	7015	0.22
Ren-11	6960	0.2235
Si-0	7337	0.224
Sq-1	6966	0.224
Hov4-1	8306	0.225
Ema-1	5736	0.225
Nw-0	8348	0.2255

Pent-1	2187	0.226
Bsch-0	7031	0.226
Bå5-1	8259	0.226
Ge-0	8297	0.227
Ct-1	6910	0.2275
Bå4-1	8258	0.2275
Ep-0	7123	0.228
Bor-4	6903	0.231
Ms-0	6938	0.231
Duk	6008	0.232
Es-0	7126	0.2335
Tottarp-2	6243	0.234
PHW-2	8243	0.235
Mir-0	8337	0.2355
Mt-0	6939	0.236
FOR-5	936	0.2365
Ste-3	2290	0.2375
Baa-1	7002	0.239
Boot-1	7026	0.241
Da-0	7094	0.2415
CUR-8	86	0.242
Rmx-A02	7524	0.2425
EM-183	461	0.243
Arby-1	6998	0.243
Bay-0	6899	0.2435
Gd-1	8296	0.244
Vår2-1	7516	0.2505
Pi-2	7299	0.251

Ra-0	6958	0.253
C24	6906	0.253
Kin-0	6926	0.253
Köln	8239	0.2545
Ca-0	7062	0.255
Fäb-4	6918	0.256
Kno-10	6927	0.256
Ren-1	6959	0.2575
Ri-0	7317	0.258
Van-0	6977	0.2585
Uod-7	6976	0.259
PAR-8	262	0.259
Or-0	7282	0.2605
Bor-1	5837	0.261
Stw-0	8388	0.2635
Wc-1	7404	0.2645
Ma-2	7246	0.266
Ove-0	7287	0.266
Bs-1	8270	0.266
MIB-86	224	0.267
St-0	8387	0.267
Ör-1	6074	0.2675
Lo-2	7242	0.27
Paw-26	2171	0.27
Nw-4	7262	0.2705
Ann-1	6994	0.2705
Map-42	2057	0.271
Kyl-1	5751	0.271

Ws-2	6981	0.272
Mnz-0	7244	0.273
Bå1-2	8256	0.273
Aa-0	7000	0.274
Lp2-2	7520	0.2745
Je-0	7181	0.2745
Kulturen-1	8240	0.275
MNF-Pot-80	1874	0.275
Ws-0	6980	0.275
La-1	7210	0.276
Old-1	7280	0.276
Pna-10	7526	0.276
RRS-10	7515	0.277
Drall-1	8285	0.278
Fei-0	8215	0.279
Oy-0	6946	0.2795
Pr-0	7310	0.28
Ba-1	7014	0.281
UII2-3	6973	0.283
Blh-1	8265	0.284
Nyl-2	6064	0.284
HR-10	6923	0.285
Bs-2	7004	0.285
HR-5	6924	0.2855
Hs-0	8310	0.2885
Sorbo	6963	0.289
Co	7081	0.29
Spr1-6	6965	0.29

WAR	7477	0.29
CIBC-17	6907	0.29
Bu-0	8271	0.2905
Seattle-0	8245	0.291
Per-1	8354	0.293
En-1	8290	0.294
Gel-1	7143	0.294
Uod-1	6975	0.295
Na-1	8343	0.295
Lu-1	8334	0.295
Ullapool-3	9308	0.2955
VOU-5	394	0.296
Hil-1	5745	0.296
Ei-2	6915	0.296
HSm	8236	0.2965
Tha-1	7353	0.297
TOU-J-3	383	0.298
Ob-0	7276	0.298
Com-1	7092	0.298
Hi-0	8304	0.299
Po-1	7309	0.3
Pla-0	7300	0.3
Mrk-0	6937	0.3015
Zu-1	7418	0.304
Krot-2	7205	0.305
Pna-17	7523	0.3055
Brö1-6	8231	0.306
Wt-5	6982	0.307

Kondara	6929	0.307
Gu-0	6922	0.307
Ha-0	7163	0.307
Lip-0	8325	0.3075
Tscha-1	7372	0.3075
Edinburgh-5	9302	0.308
NFA-10	6943	0.308
Pf-0	7297	0.308
Rhen-1	7316	0.309
Rmx-A180	7525	0.309
LAC-5	96	0.3095
Pa-2	7291	0.31
Hey-1	7166	0.31
Wei-0	6979	0.312
Li-7	7231	0.312
Dem-4	8233	0.3125
Nd-1	6942	0.3135
Jm-1	7178	0.314
Sq-8	6967	0.316
Pn-0	7307	0.317
Gy-0	8214	0.318
Nok-3	6945	0.3185
Liarum	8241	0.319
Zdr-6	6985	0.3195
NFA-8	6944	0.32
Ting-1	7354	0.32
Sha	6962	0.3205
Ag-0	6897	0.321

San-2	8247	0.321
Can-0	8274	0.3215
Cit-0	7075	0.322
Lp2-6	7521	0.322
Tiv-1	7355	0.3225
RAN	266	0.323
Ty-0	7351	0.325
Ts-1	6970	0.3255
HI-3	7172	0.3255
Kz-9	6931	0.3255
RRS-7	7514	0.326
Lz-0	6936	0.326
Frd-1	5742	0.3265
Pu2-7	6956	0.33
Mz-0	6940	0.331
MIB-60	204	0.3315
Lag1-6	9104	0.333
Kr-0	7201	0.333
Wil-1-Dean- Lab	100000	0.334
Mh-0	7255	0.335
Sh-0	7331	0.335
Is-1	7176	0.3355
Sapporo-0	7330	0.337
Lan-1	5752	0.338
Jl-3	7424	0.338
Utrecht	7382	0.339
Ts-5	6971	0.339

Lc-0	8323	0.34
Pa-1	8353	0.3415
Se-0	6961	0.342
Li-3	7224	0.3425
Kelsterbach-4	8420	0.3425
Kno-18	6928	0.343
Gie-0	7147	0.343
Sanna-2	8376	0.344
Tamm-27	6969	0.345
Mc-0	7252	0.3455
Rd-0	8366	0.3465
Rou-0	7320	0.347
Sg-1	7344	0.348
Est-1	6916	0.35
Uk-1	7378	0.3505
Kz-1	6930	0.351
Di-1	7098	0.352
Kni-1	6040	0.352
Rsch-4	8374	0.354
Bur-0	5719	0.355
Got-22	6920	0.355
Chr-1	5723	0.356
Ak-1	6987	0.357
In-0	8311	0.357
Kil-0	7192	0.3575
Amel-1	6990	0.359
Ker-38	1782	0.359
Ka-0	8314	0.359

Wilcox-4	2320	0.3595
Vimmerby	8249	0.3605
Te-0	7352	0.361
Truk-5	9165	0.362
Ors-1	7283	0.369
Zdr-1	6984	0.37
Np-0	7268	0.3705
Tamm-2	6968	0.373
An-1	6898	0.375
No-0	7275	0.376
Ven-1	7384	0.377
Ler-1	6932	0.378
Lm-2	8329	0.379
MOG-11	236	0.3795
Pog-0	7306	0.382
Pro-0	8213	0.3825
Tu-0	8395	0.39
Got-7	6921	0.3925
Tsu-1	6972	0.3955
LL-0	6933	0.3965
Ang-0	6992	0.4065
Ga-0	6919	0.416
N13	7438	0.417
LDV-58	149	0.418
Is-0	8312	0.4215
ÖMö2-3	7519	0.427
Gr-1	8300	0.427
CIBC-5	6730	0.43

Sap-0	8378	0.441
Mr-0	7522	0.441
Jm-0	8313	0.443
Eds-1	6016	0.447
Cvi-0	6911	0.473
Kl-5	7199	0.488
Wa-1	6978	0.518

Table S4. Median “Direction Index” on DAG 4 of 257 *Arabidopsis thaliana* accessions.

Name	ACC_ID	median_gravitropicDir_day_4
Wa-1	6978	-20.182
Cvi-0	6911	-16.659
Jm-0	8313	-16.314
Ga-0	6919	-15.165
CIBC-5	6730	-14.334
Tu-0	8395	-14.088
Sanna-2	8376	-13.459
Kl-5	7199	-13.404
Bur-0	5719	-13.124
Is-0	8312	-12.8915
Brö1-6	8231	-12.733
Np-0	7268	-12.075
Tsu-1	6972	-11.2945
Di-1	7098	-11.205
Wil-1-Dean-Lab	100000	-10.895
Ven-1	7384	-10.4735

Ler-1	6932	-10.391
Gie-0	7147	-10.278
Com-1	7092	-10.198
No-0	7275	-10.0125
Wilcox-4	2320	-9.9995
Zdr-1	6984	-9.914
Lan-1	5752	-9.887
San-2	8247	-9.801
LDV-58	149	-9.773
Sap-0	8378	-9.759
Ag-0	6897	-9.7
Kz-1	6930	-9.7
Est-1	6916	-9.478
Dralll-1	8285	-9.4285
Hil-1	5745	-9.1285
Tscha-1	7372	-9.05
Ge-0	8297	-9.027
Fei-0	8215	-8.791
Bs-1	8270	-8.584
Ts-1	6970	-8.5525
Mr-0	7522	-8.533
Edinburgh-5	9302	-8.346
Pro-0	8213	-8.213
RAN	266	-8.1005
Rmx-A02	7524	-7.8985
CUR-8	86	-7.897
Vår2-1	7516	-7.8035
LL-0	6933	-7.762

Kz-9	6931	-7.7505
Kil-0	7192	-7.708
Ann-1	6994	-7.7035
Ts-5	6971	-7.6885
Zu-1	7418	-7.619
Kelsterbach-4	8420	-7.396
Got-22	6920	-7.2645
Uod-1	6975	-7.036
Cit-0	7075	-6.981
NFA-10	6943	-6.973
Got-7	6921	-6.9545
Fäb-4	6918	-6.913
Ep-0	7123	-6.911
Utrecht	7382	-6.88
Kondara	6929	-6.808
Co	7081	-6.803
ÖMö2-3	7519	-6.7325
Sapporo-0	7330	-6.601
Truk-5	9165	-6.572
An-1	6898	-6.553
Pent-1	2187	-6.551
Kno-18	6928	-6.517
Köln	8239	-6.4205
Bå1-2	8256	-6.382
Ting-1	7354	-6.34
Ws-0	6980	-6.2855
Pa-1	8353	-6.208
Ha-0	7163	-6.187

Zdr-6	6985	-6.151
Tamm-2	6968	-6.092
C24	6906	-6.09
Rhen-1	7316	-6.083
Blh-1	8265	-6.0055
Pa-2	7291	-5.9525
Kr-0	7201	-5.932
Bay-0	6899	-5.92
Mz-0	6940	-5.901
Pog-0	7306	-5.881
Mdn-1	1829	-5.88
Arby-1	6998	-5.812
Ost-0	8351	-5.794
Ra-0	6958	-5.7575
TOU-J-3	383	-5.755
VOU-5	394	-5.662
Oy-0	6946	-5.5825
HI-3	7172	-5.42
Ty-0	7351	-5.416
Sorbo	6963	-5.398
Bsch-0	7031	-5.3415
Rev-1	8369	-5.312
Lm-2	8329	-5.243
Ct-1	6910	-5.146
Wt-5	6982	-5.088
Duk	6008	-5.059
Hi-0	8304	-4.997
Gd-1	8296	-4.948

Rd-0	8366	-4.8815
Ak-1	6987	-4.764
En-1	8290	-4.681
Jl-3	7424	-4.612
Nyl-2	6064	-4.516
N13	7438	-4.49
Eden-2	6913	-4.4745
Sh-0	7331	-4.47
MOG-11	236	-4.469
Es-0	7126	-4.392
Da-0	7094	-4.2505
Ws-2	6981	-4.227
Algutsrum	8230	-4.212
Sq-8	6967	-4.203
Rak-2	8365	-4.1615
EM-183	461	-4.16
CrI-1	5731	-4.1445
Hh-0	7169	-4.132
Sg-1	7344	-4.086
Stw-0	8388	-4.081
Yo-0	6983	-4.049
Eds-1	6016	-3.994
Ca-0	7062	-3.948
Tiv-1	7355	-3.838
Tottarp-2	6243	-3.78
Bs-2	7004	-3.739
Rmx-A180	7525	-3.734
NFA-8	6944	-3.576

In-0	8311	-3.532
Tha-1	7353	-3.493
Sha	6962	-3.4835
Old-1	7280	-3.4545
Krot-2	7205	-3.443
Spr1-6	6965	-3.4375
Li-7	7231	-3.347
Rou-0	7320	-3.344
Ör-1	6074	-3.337
Nd-1	6942	-3.185
Is-1	7176	-3.145
Lc-0	8323	-3.126
Wc-1	7404	-3.0835
Hey-1	7166	-3.0025
Kni-1	6040	-3.002
PAR-8	262	-2.9945
Ma-2	7246	-2.964
Mc-0	7252	-2.9355
Ors-1	7283	-2.931
Mnz-0	7244	-2.7975
Lo-2	7242	-2.791
Ei-2	6915	-2.713
Po-1	7309	-2.712
Uk-1	7378	-2.7105
Ove-0	7287	-2.705
Gy-0	8214	-2.693
MIB-86	224	-2.688
Ullapool-3	9308	-2.681

HR-10	6923	-2.68
Liarum	8241	-2.6025
Si-0	7337	-2.591
Bu-0	8271	-2.5475
Ang-0	6992	-2.535
CIBC-17	6907	-2.529
FOR-5	936	-2.484
Lp2-2	7520	-2.443
Pi-2	7299	-2.373
Boot-1	7026	-2.3665
PHW-2	8243	-2.337
Bor-4	6903	-2.296
RRS-10	7515	-2.19
Br-0	6904	-2.085
HR-5	6924	-2.0665
Te-0	7352	-2.035
Bå4-1	8258	-1.978
Ba-1	7014	-1.9295
Do-0	7102	-1.8135
Gu-0	6922	-1.811
Hau-0	7164	-1.79
Frd-1	5742	-1.781
Vimmerby	8249	-1.751
Amel-1	6990	-1.7245
Ka-0	8314	-1.721
Ema-1	5736	-1.675
Ker-38	1782	-1.667
Col-0	6909	-1.639

Mrk-0	6937	-1.538
Lp2-6	7521	-1.4565
LAC-5	96	-1.4495
St-0	8387	-1.408
Mt-0	6939	-1.358
Pla-0	7300	-1.257
Kyl-1	5751	-1.245
Or-0	7282	-1.1215
Chat-1	7071	-1.082
Jm-1	7178	-1.049
Je-0	7181	-1.0155
Ste-3	2290	-0.944
Ob-0	7276	-0.937
Van-0	6977	-0.907
Drall-1	8284	-0.8735
UII2-3	6973	-0.862
Map-42	2057	-0.861
Coc-1	5729	-0.849
Bla-1	7015	-0.8225
Pna-10	7526	-0.753
Can-0	8274	-0.7225
Na-1	8343	-0.6005
Tamm-27	6969	-0.383
WAR	7477	-0.2485
Aa-0	7000	-0.1495
Sq-1	6966	-0.122
Nw-0	8348	-0.013
Ren-1	6959	0.086

Benk-1	7008	0.0985
Kin-0	6926	0.138
Nok-3	6945	0.194
Mh-0	7255	0.235
Li-3	7224	0.2435
Kno-10	6927	0.2825
Baa-1	7002	0.365
Cala-8	9152	0.495
Lip-0	8325	0.5275
MIB-60	204	0.609
Rsch-4	8374	0.823
Pf-0	7297	0.8845
Pu2-23	6951	1.113
Se-0	6961	1.137
Ri-0	7317	1.2275
Hs-0	8310	1.5085
Bå5-1	8259	1.739
Hov4-1	8306	1.836
Per-1	8354	1.888
HSm	8236	1.932
Pr-0	7310	1.959
Bch-1	7028	1.966
Uod-7	6976	2.15
La-1	7210	2.151
Lag1-6	9104	2.2465
Seattle-0	8245	2.307
Gel-1	7143	2.423
Pna-17	7523	2.689

Ren-11	6960	2.7725
Nw-4	7262	2.878
Ms-0	6938	3.0755
Kulturen-1	8240	3.106
Paw-26	2171	3.12
MNF-Pot-80	1874	3.232
Pu2-7	6956	3.232
Dem-4	8233	3.4155
Wei-0	6979	3.569
Lu-1	8334	3.596
Bor-1	5837	3.755
RRS-7	7514	4.6
Mir-0	8337	4.6705
Pn-0	7307	4.708
Gr-1	8300	5.059
Lz-0	6936	5.67
Chr-1	5723	6.5405

Table S5. Median “Root Angle” on DAG 4 of 257 *Arabidopsis thaliana* accessions.

Name	Origin	ACC_ID
Aa-0	GER	7000
Ag-0	FR	6897
Ak-1	GER	6987
Algutsrum	SWE	8230
Amel-1	NLD	6990
An-1	BEL	6898
Ang-0	BEL	6992

Ann-1	FR	6994
Arby-1	SWE	6998
Ba-1	UK	7014
Bå1-2	SWE	8256
Bå4-1	SWE	8258
Bå5-1	SWE	8259
Baa-1	NLD	7002
Bay-0	GER	6899
Bch-1	GER	7028
Benk-1	NLD	7008
Bla-1	ESP	7015
Blh-1	CZ	8265
Boot-1	UK	7026
Bor-1	CZE	5837
Bor-4	CZE	6903
Br-0	CZE	6904
Brö1-6	SWE	8231
Bs-1	SUI	8270
Bs-2	SUI	7004
Bsch-0	GER	7031
Bu-0	GER	8271
Bur-0	IRL	5719
C24	POR	6906
Ca-0	GER	7062
Cala-8	ESP	9152
Can-0	ESP	8274
Chat-1	FRA	7071
Chr-1	UK	5723
CIBC-17	UK	6907

CIBC-5	UK	6730
Cit-0	FRA	7075
Co	POR	7081
Coc-1	ESP	5729
Col-0	USA	6909
Com-1	FRA	7092
CrI-1	UK	5731
Ct-1	ITA	6910
CUR-8	FRA	86
Cvi-0	CPV	6911
Da-0	GER	7094
Dem-4	USA	8233
Di-1	FRA	7098
Do-0	GER	7102
Drall-1	CZE	8284
Dralll-1	CZE	8285
Duk	CZE	6008
Eden-2	SWE	6913
Edinburgh-5	UK	9302
Eds-1	SWE	6016
Ei-2	GER	6915
EM-183	UK	461
Ema-1	UK	5736
En-1	GER	8290
Ep-0	GER	7123
Es-0	FIN	7126
Est-1	RUS	6916
Fäb-4	SWE	6918
Fei-0	POR	8215

FOR-5	UK	936
Frd-1	UK	5742
Ga-0	GER	6919
Gd-1	GER	8296
Ge-0	SUI	8297
Gel-1	NLD	7143
Gie-0	GER	7147
Got-22	GER	6920
Got-7	GER	6921
Gr-1	AUT	8300
Gu-0	GER	6922
Gy-0	FRA	8214
Ha-0	GER	7163
Hau-0	DEK	7164
Hey-1	NLD	7166
Hh-0	GER	7169
Hi-0	NLD	8304
Hil-1	UK	5745
HI-3	GER	7172
Hov4-1	SWE	8306
HR-10	UK	6923
HR-5	UK	6924
Hs-0	GER	8310
HSm	CZE	8236
In-0	AUT	8311
Is-0	GER	8312
Is-1	DE	7176
Je-0	GER	7181
Jl-3	CZE	7424

Jm-0	CZE	8313
Jm-1	CZE	7178
Ka-0	AUT	8314
Kelsterbach-4	GER	8420
Ker-38	USA	1782
Kil-0	UK	7192
Kin-0	USA	6926
KI-5	GER	7199
Kni-1	SWE	6040
Kno-10	USA	6927
Kno-18	USA	6928
Köln	GER	8239
Kondara	TJK	6929
Kr-0	GER	7201
Krot-2	GER	7205
Kulturen-1	SWE	8240
Kyl-1	UK	5751
Kz-1	KAZ	6930
Kz-9	KAZ	6931
La-1	GER	7210
LAC-5	LAC	96
Lag1-6	GEO	9104
Lan-1	UK	5752
Lc-0	UK	8323
LDV-58	FRA	149
Ler-1	GER	6932
Li-3	GER	7224
Li-7	GER	7231
Liarum	SWE	8241

Lip-0	POL	8325
LL-0	ESP	6933
Lm-2	FRA	8329
Lo-2	GER	7242
Lp2-2	CZ	7520
Lp2-6	CZE	7521
Lu-1	SE	8334
Lz-0	FR	6936
Ma-2	DE	7246
Map-42	USA	2057
Mc-0	UK	7252
Mdn-1	USA	1829
Mh-0	PL	7255
MIB-60	FR	204
MIB-86	FR	224
Mir-0	IT	8337
MNF-Pot-80	USA	1874
Mnz-0	DE	7244
MOG-11	FR	236
Mr-0	ITA	7522
Mrk-0	GER	6937
MS-0	RU	6938
Mt-0	LY	6939
Mz-0	DE	6940
N13	RUS	7438
Na-1	FR	8343
Nd-1	CH	6942
NFA-10	UK	6943
NFA-8	UK	6944

No-0	DE	7275
Nok-3	NLD	6945
Np-0	DE	7268
Nw-0	DE	8348
Nw-4	DE	7262
Nyl-2	SWE	6064
Ob-0	DE	7276
Old-1	DE	7280
ÖMö2-3	SWE	7519
Or-0	DE	7282
Ör-1	SWE	6074
Ors-1	ROM	7283
Ost-0	SWE	8351
Ove-0	DE	7287
Oy-0	NO	6946
Pa-1	ITA	8353
Pa-2	IT	7291
PAR-8	FR	262
Paw-26	US	2171
Pent-1	USA	2187
Per-1	RU	8354
Pf-0	DE	7297
PHW-2	IT	8243
Pi-2	AT	7299
Pla-0	ES	7300
Pn-0	FR	7307
Pna-10	USA	7526
Pna-17	USA	7523
Po-1	DE	7309

Pog-0	CA	7306
Pr-0	DE	7310
Pro-0	ESP	8213
Pu2-23	CZ	6951
Pu2-7	CZ	6956
Ra-0	FR	6958
Rak-2	CZE	8365
RAN	FR	266
Rd-0	DE	8366
Ren-1	FR	6959
Ren-11	FR	6960
Rev-1	SWE	8369
Rhen-1	NLD	7316
Ri-0	CA	7317
Rmx-A02	USA	7524
Rmx-A180	US	7525
Rou-0	FR	7320
RRS-10	USA	7515
RRS-7	USA	7514
Rsch-4	RU	8374
San-2	SWE	8247
Sanna-2	SWE	8376
Sap-0	CZ	8378
Sapporo-0	JP	7330
Se-0	ES	6961
Seattle-0	US	8245
Sg-1	DE	7344
Sh-0	DE	7331
Shahdara	TJ	6962

Si-0	DE	7337
Sorbo	TJ	6963
Spr1-6	SWE	6965
Sq-1	UK	6966
Sq-8	UK	6967
St-0	SE	8387
Ste-3	US	2290
Stw-0	RU	8388
Tamm-2	FIN	6968
Tamm-27	FIN	6969
Te-0	FI	7352
Tha-1	NL	7353
Ting-1	SWE	7354
Tiv-1	ITA	7355
Tottarp-2	SE	6243
TOU-J-3	FRA	383
Truk-5	UA	9165
Ts-1	ES	6970
Ts-5	ESP	6971
Tscha-1	AT	7372
Tsu-1	JP	6972
Tu-0	IT	8395
Ty-0	UK	7351
Uk-1	DE	7378
UII2-3	SE	6973
Ullapol-3	UK	9308

Table S6. RegMap panel accessions used in the GWAS.

T-DNA	avgAbsAng P Value	Significant	COL-0 Mean	T-DNA Mean	ATI	Gene Name
CS859638	0.485		13.5	14.2	AT1G32050	ATSCAMP5
SALK_053469C	0.729		14.5	13.8	AT1G32080	ATLRGB
SALK_035509	0.325		16	14.5	AT1G32210	ATDAD1
SALK_104469C	0.88		13.9	13.6	AT1G32220	
SALK_146277C	0.0474	*	14.2	12.2	AT2G03820	ATNMD3
SALK_094846	0.102		13.8	11.9	AT2G34930	
SALK_042714C	0.0107	*	14.7	11.9	AT3G01690	
SALK_008357	9.2E-10	***	13	22.2	AT3G22590	PHP, CDC73
SALK_150644C	0.000000843	***	12.3	16.6	AT3G22590	PHP, CDC73
SALK_007462C	0.899		13	13.1	AT3G22600	LTPG5
SALK_150636C	0.111		12.5	10.5	AT3G58180	
SALK_135752	0.356		11	12.2	AT4G17030	AEXLB1,EXPR,AT- EXPR,ATEXPR1,ATHEXPBETA3.1,EXLB1
SALK_081121C	0.659		12.3	11.8	AT4G17070	
SALK_119615C	0.267		12.3	11.2	AT4G24880	
SALK_038436C	0.471		13.3	12.5	AT5G11420	
SALK_119093C	0.0166	*	14.6	11.6	AT5G43710	MNS4
SALK_129775C	0.0421	*	15.4	12.6	AT5G55160	SUM2,SUMO2,SUMO2,ATSUMO2

Table S7. T-DNA lines and their angles.

Line	Direction	Sequence
PAP27_F	Forward	CACCATGGCTAGGAATTTCTTGTTAGTG
PAP27_R	Reverse	TGAAGCTAATGTGGTTGGCTC
<i>AtEF1α</i>	Forward	TGAGCACGCTCTTCTTGCTTTCA
<i>AtEF1α</i>	Reverse	GGTGGTGGCATCCATCTTGTTACA

Table S8. Primer sequences

<i>S. lycopersicum</i>				<i>S. pennellii</i>			
Gene	Symbol	Expr. Count	Expr. Z	Gene	Symbol	Expr. Count	Expr. Z
Solyc05g012260	SIPAP27-1	1880	0.66	Sopen05g007090	SpPAP27-1	1289	0.49
Solyc08g083250	SIPAP27-2	553	0.0015	Sopen08g031440	SpPAP27-2	753	0.16
Solyc04g024640	SIPAP27-3	0	-0.27	Sopen04g010490	SpPAP27-3	1	-0.31
Solyc07g008570	SIPAP27-4a	325	-0.11	Sopen07g004500	SpPAP27-4a	1097	0.37

Solyc07g008560	SIPAP27-4b	NA	NA	Sopen07g004490	SpPAP27-4b	NA	NA
Solyc07g008550	SIPAP27-4c	554	0.002	Sopen07g004480	SpPAP27-4c	207	-0.18
(none)		207	-0.18	Sopen07g004470	SpPAP27-4d	NA	NA

Table S9. Homologous pairs, symbol names, and root tissue expression levels for selected purple acid phosphatase genes. Each row is pair of homologous genes in the two species. Based on these genes' similarities to ATPAP27 (AT5G50400) and on phylogenetic trees of these genes (**Figure S4, S5**), we assigned the symbolic names shown here to these genes. Expression values are RNA-seq for root tip tissue, normalized counts and Z-scaled (mean 0, standard deviation 1).