Supporting Information

Rosas et al. 10.1073/pnas.1305883110

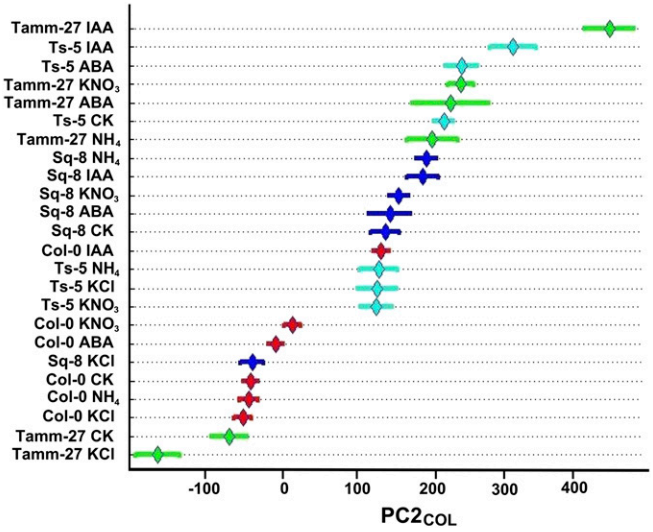

Fig. S1. PC2$_{COL}$ plasticity in four *Arabidopsis* accessions. Bars indicate SE.

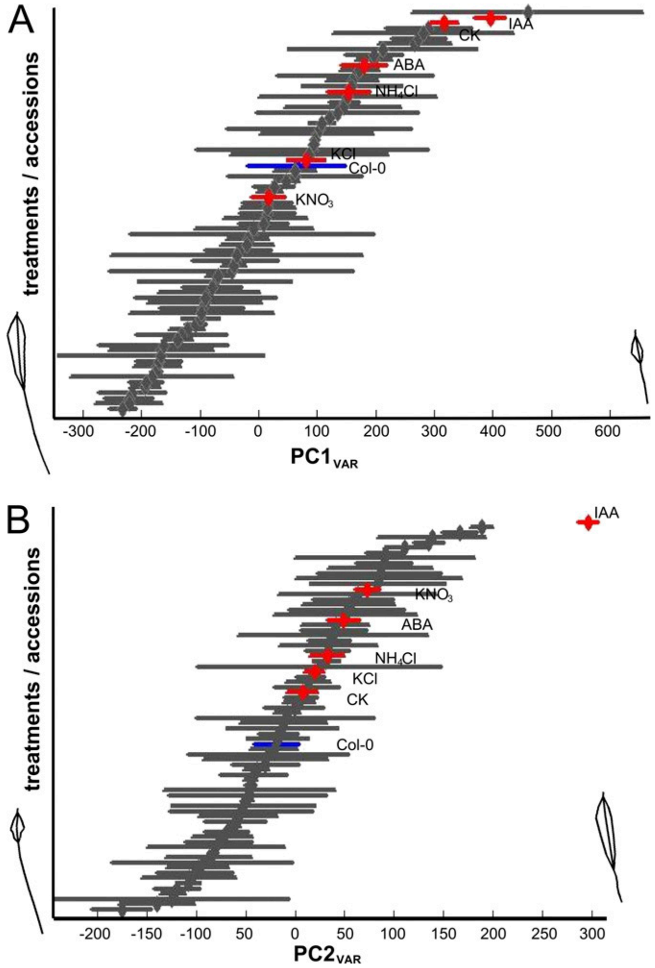

Fig. S2. Root plasticity and natural variation projected on the PC1$_{VAR}$ and PC2$_{VAR}$ spaces. (*A* and *B*) Bars indicate SE. Red bars, Col-0 in the five treatments IAA, CK, ABA, KNO$_3$, NH$_4$Cl, and a KCl control; gray bars, phenotypes of *Arabidopsis* accessions grown under a single (KNO$_3$) condition; blue bars, reference Col-0 accession. Morphometrics modeled root systems architecture phenotypes, and those corresponding to extreme root PC1$_{VAR}$ and PC2$_{VAR}$ phenotypes are shown.

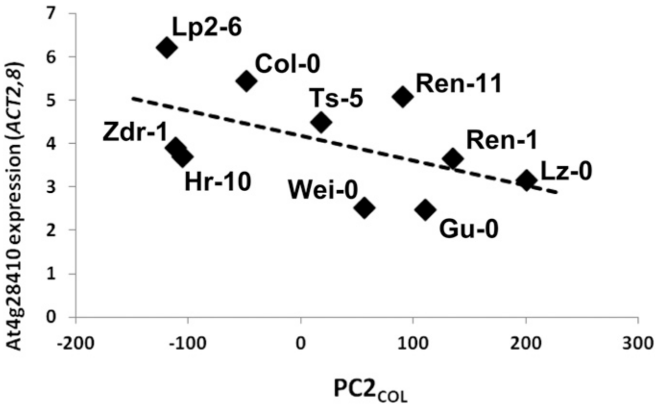

Fig. S3. *RSA1* (At4g28410) normalized gene expression in several *Arabidopsis* accessions. Pearson correlation = −0.52, ($P = 0.05$).

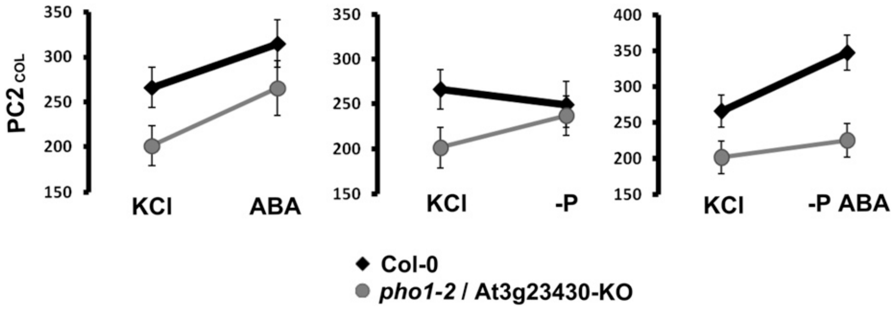

Fig. S4. *pho1-2* mutant phenotypes in the presence or absence of ABA and inorganic phosphate (KH_2PO_4). We prepared custom media according to the manufacturer's recipe (www.invitrogen.com/site/us/en/home/support/Product-Technical-Resources/media_formulation.129.html), substituting the moles of $^{-}PO_4$ in KH_2PO_4 with moles of KOH under the phosphate (P) deprivation condition. We mimicked our conditions to characterize phenotypic plasticity by growing the seedlings in full MS media containing phosphate for 10 d (GibcoBRL), transferring the plants to the treatments for 4 d, and phenotyping the roots on the 14th day. The treatments were (*i*) +ABA +P, (*ii*) +ABA –P, (*iii*) –ABA +P, and (*iv*) –ABA –P in the wild-type and the *pho1-2* mutant (total: $n = 188$). A three-way analysis of variance with interactions with full combinatorial effects gave significant differences due to genotype ($P = 0.0005$) and ABA treatment ($P = 0.0048$), but not due to phosphate ($P = 0.847$) or any interactions (i.e., genotype*ABA*phosphate $P = 0.0767$) under our experimental conditions.

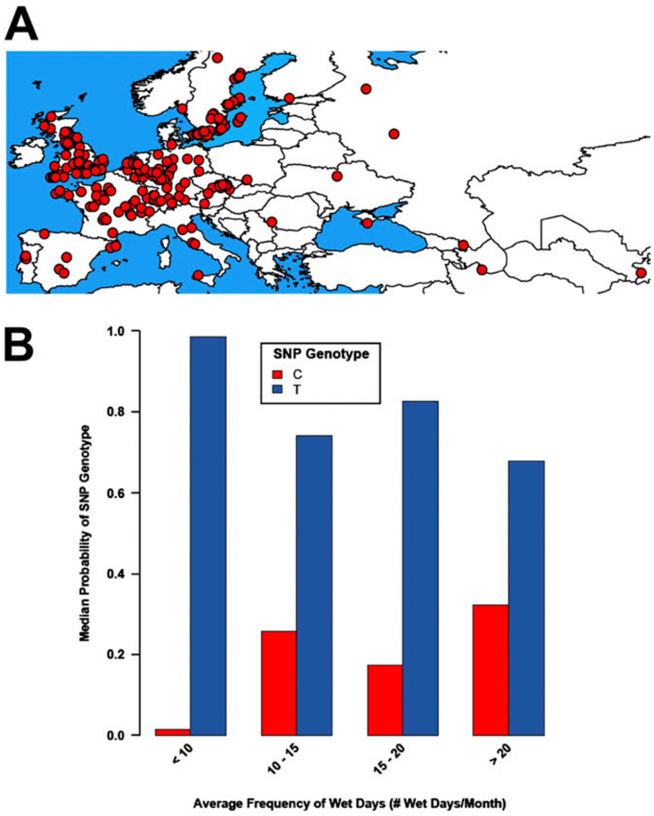

Fig. S5. Median probabilities of occurrence of the two *PHO1* SNP alleles at different frequencies of wet days. (*A*) The locations of origin of the 726 accessions used in the landscape genetics study. (*B*) The probabilities were calculated by applying a logistic function to the fitted values from the logistic regression analysis. For each level of wet day frequency represented by a bar in the bar graph, the median probability was calculated using all of the accessions originating from areas with that frequency of wet days. We used a list of accessions and geographic coordinates of their origins (1) and intersected this list with those for which SNP genotype information is available at the two SNP loci of interest (2). We limited this list to accessions falling within the native range of *Arabidopsis thaliana* in Europe and Asia (−11° to 86° E and 35° to 71° N). We then filtered this list by the "red list" and "yellow list" of putative misidentified accessions previously flagged by Anastasio et al. (1). There were a total of 726 accessions that remained after intersecting and filtering.

1. Anastasio AE, et al. (2011) Source verification of mis-identified *Arabidopsis* thaliana accessions. *Plant J* 67(3):554–566.
2. Atwell S, et al. (2010) Genome-wide association study of 107 phenotypes in *Arabidopsis* thaliana inbred lines. *Nature* 465(7298):627–631.

Other Supporting Information Files

Table S1 (DOCX)
Table S2 (DOCX)
Table S3 (DOCX)
Table S4 (DOCX)
Table S5 (DOCX)
Dataset S1 (XLSX)