Supplemental Figure S1: Phylogenetic relationship among His phosphotransfer proteins across Viridiplantae. Phylogenetic tree showing AHP and PHP proteins across the following lineages: yeast (dark blue), algae (purple), bryophytes (red), lycophytes (mint), ferns (pink), gymnosperms (dark green), early diverging angiosperms (light green), monocots (light blue), and dicots (orange). Branch numbers are branch support values, shown as a percentage. The scale bar represents evolutionary distance. See Supplemental Table S2 for gene list.
Supplemental Figure S2: Alignment of putative PHPs. Multiple sequence alignment for all putative PHPs proteins from Supplemental Figure 1.
Supplemental Figure S3: Spatial expression pattern of PHP1-PHP3.

Expression pattern along the longitudinal and radial root axis based on laser microdissection of ten-day-old crown roots. The radial tissues are divided into three radial tissue types at two developmental stages. The data has been extracted from the RiceXPro database (Sato et al., 2011) based on dataset RXP_4001 (Takehisa et al., 2012). On the right is the RNA-Seq expression profile across nine tissues types based on the Rice Expression database (Xia et al., 2017).
Supplementary Figure S4: Analysis of root cross-sections.
Quantification of root anatomical measurements for primary (A – H) or the first crown root (I – P) in wild-type (Kitaake) and two php1,2,3 triple mutant plants. At least nine plants per genotype were grown for two weeks on agar plates, sectioned 5 cm above the root tip, imaged, and anatomical measurements calculated using PHIV Rootcell plugin in ImageJ (Lartaud et al., 2015). Significance was tested using one-way ANOVA and Tukey’s multiple comparisons test.
**Supplementary Figure S5**: Analysis of root architecture in wild type and *php* mutants

Quantification of various aspects of root architecture in wild-type (Kitaake) and two *php1,2,3* triple mutant lines. 18 plants per genotype were grown for two weeks on plates, imaged, and root number (A) length (B) and convex hull (E) calculated using RootNav (Pound et al., 2013) software. Lateral density (C) was calculated manually from segments between 5 and 7 cm from the primary root tip of 12 plants per genotype, and expressed as length (in pixels) between lateral roots. Root hair length (D) was calculated from primary root segments 5 to 6 cm above the root tip, from 5 individual plants, taking 5 root hairs per individual. Lengths were calculated using ImageJ. Significance was tested using Students t-tests.
Supplemental Figure S6: Cytokinin response assay.
Rice seedling were grown on agar media in the presence of increasing concentrations of the cytokinin BA (or an NaOH vehicle control). After seven days, the plants were photographed and primary root length, crown root number, and shoot length measured. Data is presented as the mean ± SEM (n ≥ 9).
Supplemental Figure 7: Expression of type-A RRs and CKX genes in wild-type and php1,2,3 mutant roots.
Normalized expression values for the type-A RRs (A) and the CKX genes (B) in wild-type and php1,2,3 triple mutant roots treated with the indicated concentration of BA (note: this data is derived from the RNA-Seq data). Red asterisks indicate statistical significance (FDR ≤ .05) for the comparison of wild-type and php1,2,3 in the untreated control condition. Error bars reflect the standard error. Genes with very low expression counts (<50 normalized reads in all samples) were omitted.