Table S1. Selected chemical properties of the Gorbea series soils used in the rhizobox experiment

Available P (mg kg^{-1})[A]	17.4
Total P (mg kg^{-1})[B]	3910
Organic P (mg kg^{-1})[C]	1870
pH[D]	4.92
Organic matter (%)[E]	11.4
Exchangeable cations (cmol(+) kg^{-1}):	
K[F]	0.31
Na[F]	0.04
Ca[F]	0.91
Mg[F]	0.34
Al[G]	0.32
Al saturation (%)	16.7
Base saturation (cmol(+) kg^{-1})	1.6

All analytical techniques were carried out according to the Normalisation and Accreditation Commission of the Chilean Soil Science Society (Sadzawka *et al.*, 2006). ECEC, Effective cation exchange capacity. [A] Extractable by Olsen method. [B] Determined by soil oxidation with sodium hypobromite. [C] Determined by Hedley fractionation procedure. [D] Measured in H_2O. [E] Walkley–Black method. [F] Extracted by 1 M ammonium acetate. [G] Extracted by 1M potassium chloride.

Table S2. Primer sequences used in the real-time qPCR analysis.

Gene	primer (5' → 3')	˚C	Reference
TaPht1;2a/b	CGACACCATTGCTCCGACTG TCAARCACACCAACMATGCACG	58	Grün *et al.* (2017)
TaPht1;10	CTAACTCTGACGCCCAAGAG CGGAACTGCTTATGCGTSG	58	Grün *et al.* (2017)
TaIPS1	CAGTACCAGCTGCATGCCTG CTAGCCAACGCCGGATCCA	58	Ouyang *et al.* (2016)
Tae-miR399	GGAGGCATGCATGTACTGATG GGCAATTCTCCTTTGGCACG	58	Ouyang *et al.* (2016)
TaPHO2	GGAGAAGAACTCCATCACGTACAACG GGCAAGTGAAGTGCTCCTTGACGA	54	Ouyang *et al.* (2016)
TaPHO1	GAGTGGCTACCACAAATTGAATC TATTTTTACATCCATGTCAAAGGTG	58	Ouyang *et al.* (2016)
TaD27	CATGTGAGGTCAGGGAATCTG TCATCTCGCAGCTCATGTCT	55	This work
TaCCD8	AAGGGCTCCATCGTCGTC CAGCGTCCAGAGGTCGGTGTC	58	This work
TaPHO2 1A	GTATAAGGATGATGGAATTGAAGTA CATTCTTAGTACTCTCATGGTGAT	55	Ouyang *et al.* (2016)
TaPHO2 1B	GGTTTAGCTTCAGTCCTGTCAG CAGCCTTTGAACAGCGGTC	58	Ouyang *et al.* (2016)
TaPHO2 1D	CTCGGCGGTGATCTCATTG AGGCGATCCCAGCTTCGC	58	Ouyang *et al.* (2016)
TahnrRNPQ	TCACCTTCGCCAAGCTCAGAACTA AGTTGAACTTGCCCGAAACATGCC	58	Grün *et al.* (2017)

Table S3. Effects of Pi starvation in Crac and Tukan grown in hydroponics. Plants were grown in Pi-sufficient conditions (200 μM) for 2 weeks, and then half of them subjected to Pi deprivation (10 μM) for 3 weeks. Values (%) of growth rate, root system architecture, and Pi acquisition were calculated as the difference between individual plants in both conditions. Asterisks indicate the significance of differences between the genotypes in the same condition, as determined by Student's t test analysis: * $P<0.05$, *** $P<0.001$.

cv	Shoot Weight	Root Weight	Total Weight	Root: Shoot	Root Length	Root Area	Shoot P (mg)	Shoot P ($mg.g^{-1}$)	Root P (mg)	Root P ($mg.g^{-1}$)	Plant P (mg)	Plant P ($mg.g^{-1}$)
Crac	-23%	59%	-11%	128%	113%	98%	-46%	-25%	-34%	-49%	-46%	-36%
Tukan	-37%	31%	-26%	87%	80%	77%	-57%	-36%	-48%	-60%	-57%	-45%
p-value	*	*	***	*	*	*	*	n.s.	*	*	*	*

Fig. S1. Growth performance wheat plants under different experimental conditions. (A) Hydroponically and (B) pot grown plants for phenotyping experiments; and (C) hydroponically grown plants for molecular analysis.

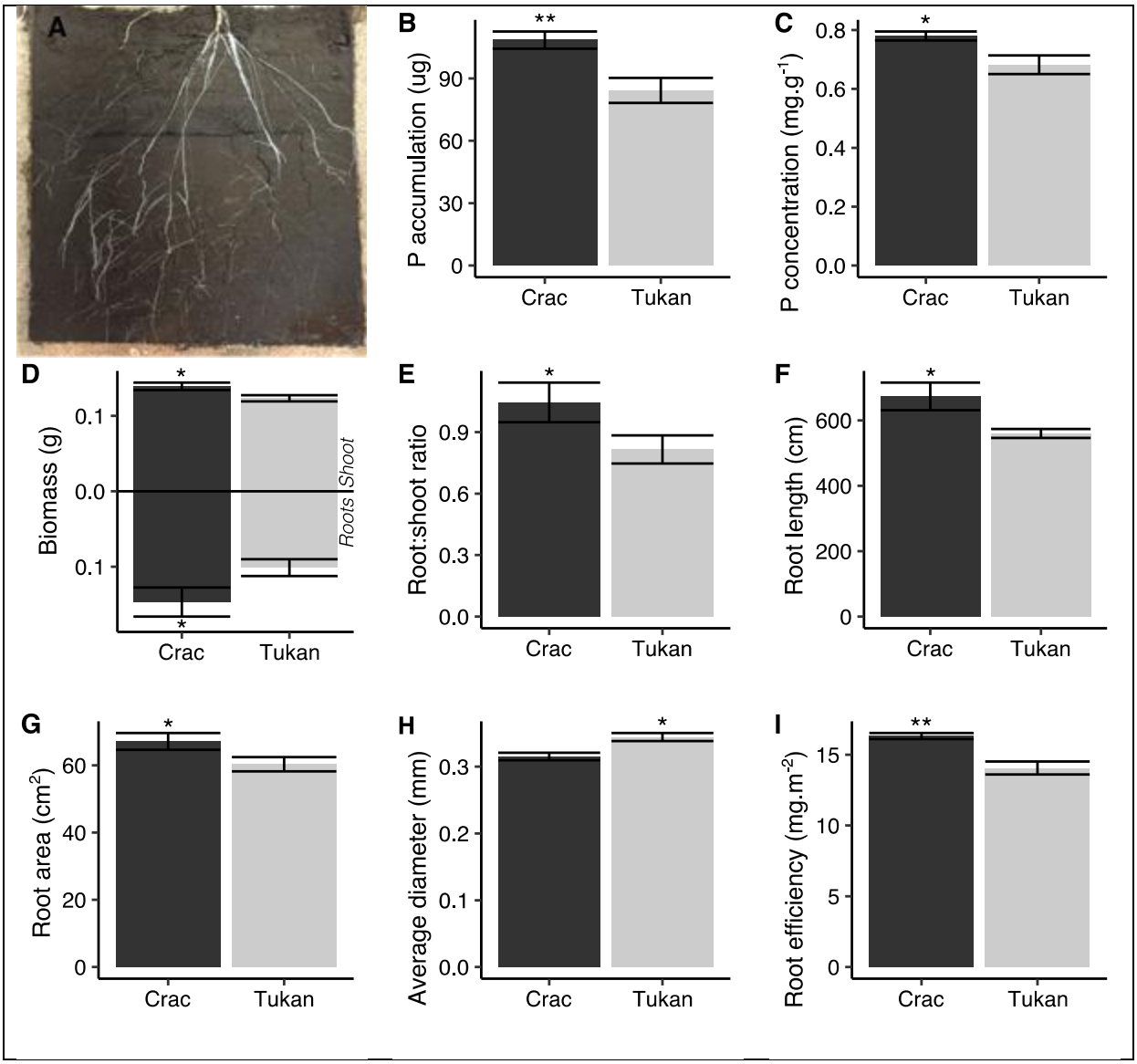


Fig. S2. Rhizobox experiment to analyze the effect of Pi starvation in Crac (dark bars) and Tukan (light bars). Plants were grown for 8 weeks in a high P-fixing acidic soil without Pi addition. (A) Visual representation of rhizobox growth system; (B) Shoot Pi accumulation; (C) Shoot Pi concentration; (D) Shoot and root biomass production; (E) Root-to-shoot ratio; (F) Total root length; (G) Root area; (H) Average root diameter; and (I) Root efficiency in Shoot Pi accumulation. Data represent the means of five independent replicates (±SE). Asterisks indicate the significance of differences between the genotypes, as determined by Student's t test analysis: * P<0.05, ** P<0.01, *** P<0.001.

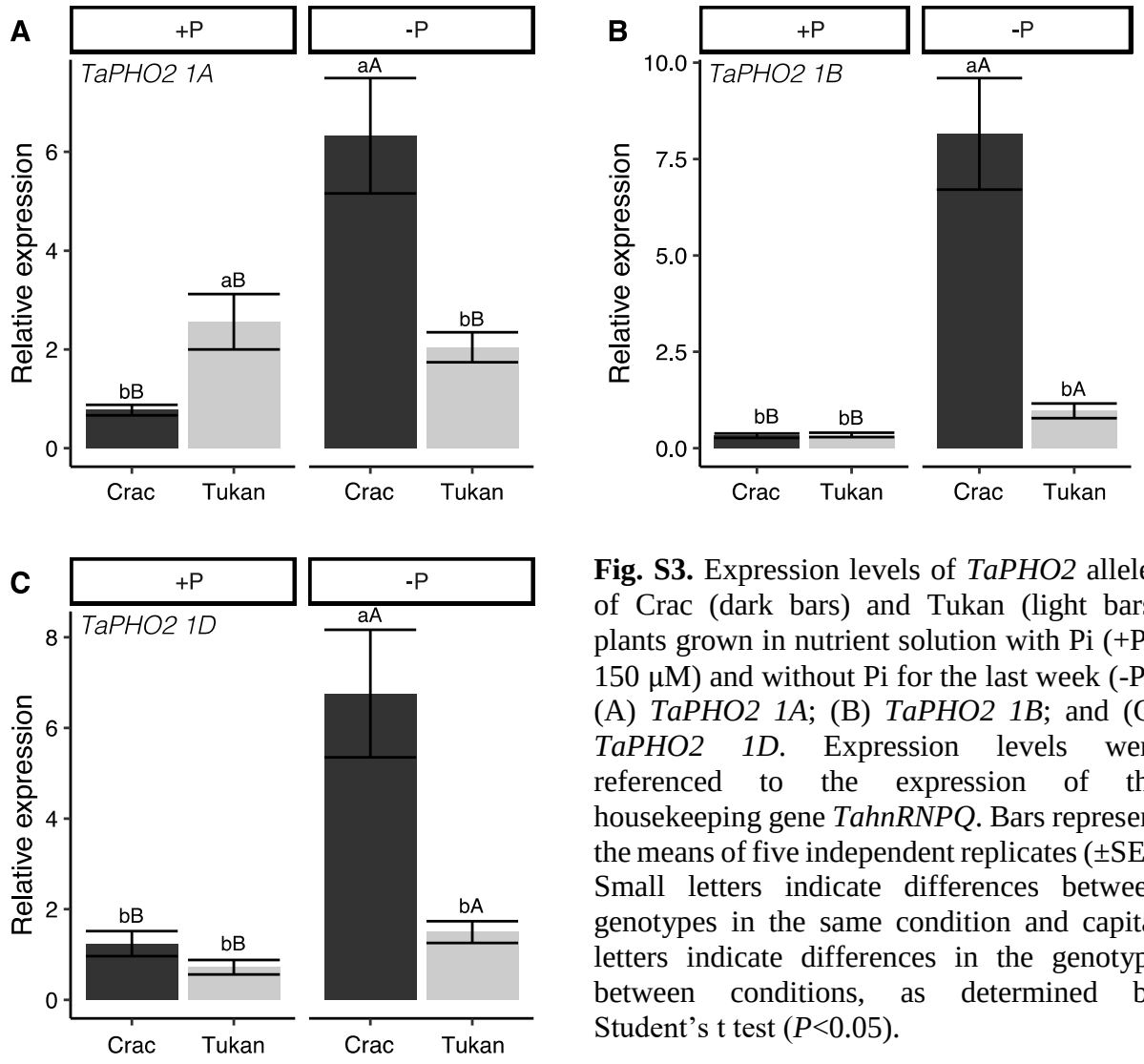
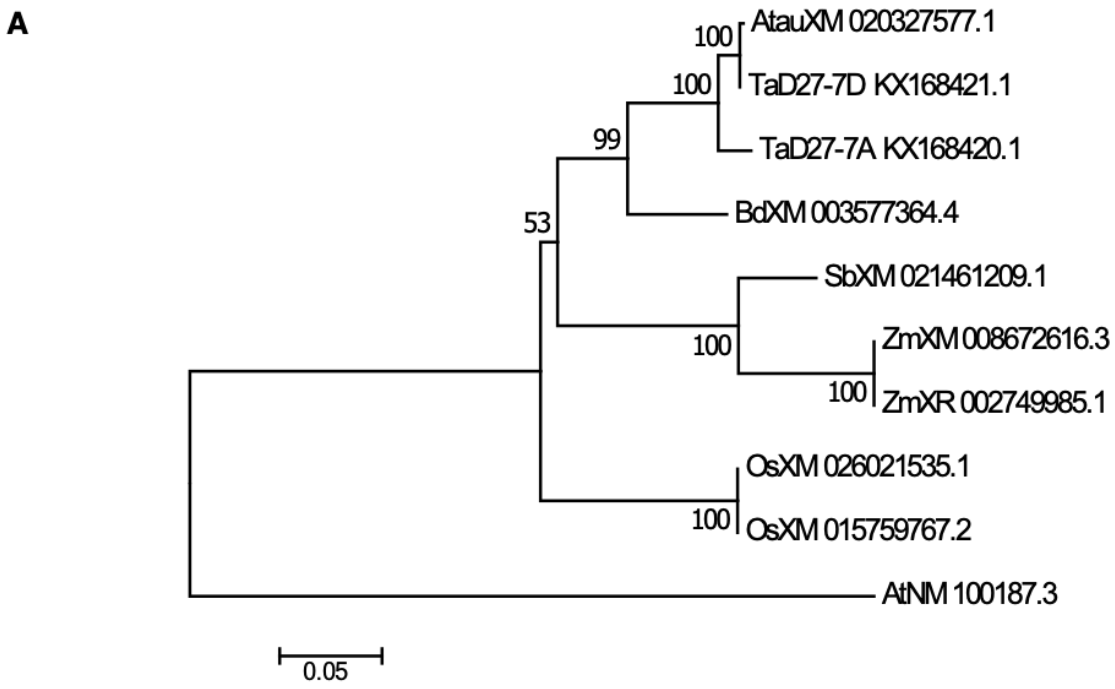


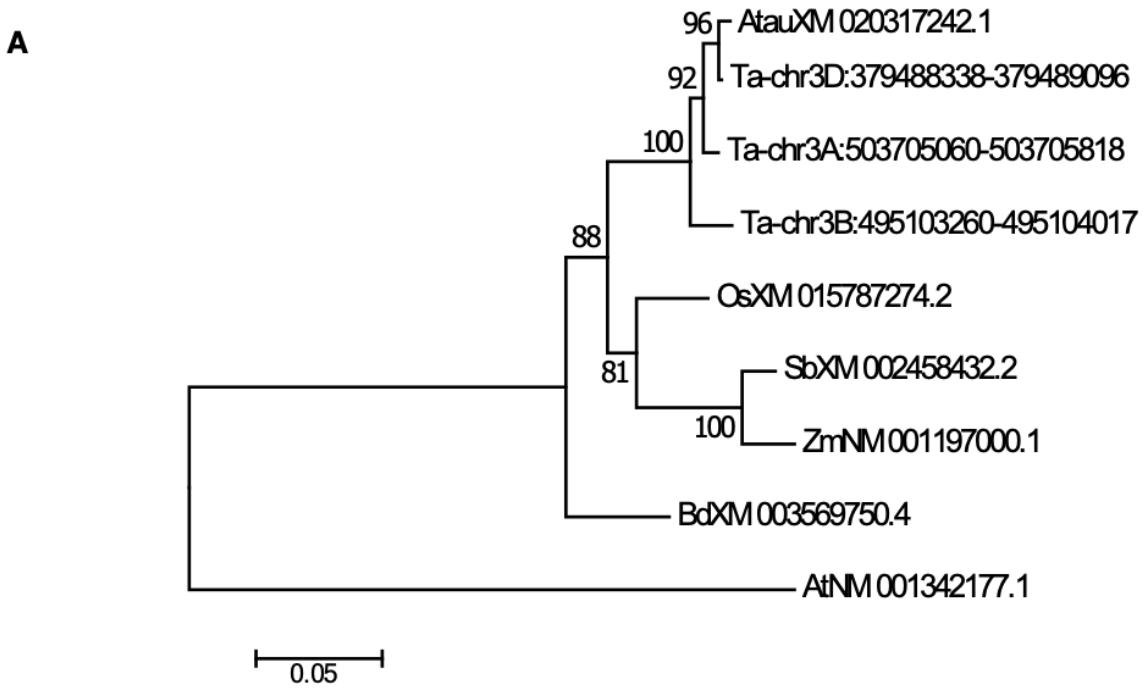
Fig. S3. Expression levels of *TaPHO2* alleles of Crac (dark bars) and Tukan (light bars) plants grown in nutrient solution with Pi (+Pi; 150 μM) and without Pi for the last week (-P). (A) *TaPHO2 1A*; (B) *TaPHO2 1B*; and (C) *TaPHO2 1D*. Expression levels were referenced to the expression of the housekeeping gene *TahnRNPQ*. Bars represent the means of five independent replicates (±SE). Small letters indicate differences between genotypes in the same condition and capital letters indicate differences in the genotype between conditions, as determined by Student's t test (P<0.05).



B

A I N **Met** E A T A L V L L P H S H S G L T A R A P P C V G G S S A **Met** K R	35
S Y V R R I K R S S T V R G V **Met** A R P Q E A T L A R V P A P A P T R P V	71
R E T A A A T T T T K T V Y H D T W F D N L A I G Y L S R K L Q E A S G I K	109
G K H G Y Q G L I E A A V A I S R I F R L D T Q C E V V A G A L E R	143
A **Met** P S Y I V T **Met** I K V **Met** **Met** P P S K F S R E Y F A A F T T I F F P	176
W L V G P C E V R E S E V D G T R E K N V V Y I P K C R F L E S T N C V	212
G **Met** C T N L C K I P S Q K F **Met** Q D S L G V S V Y **Met** S P N F E	242
D **Met** S C E **Met** I F G Q Q P P E D D P A L K Q P C F S T K C I A K Q D Y	276
G V N C **Stop**	281

Fig. S4. Phylogenetic analysis of *D27* sequences from *Aegilops tauschii* (Atau), *Arabidopsis thaliana* (At), *Brachypodium distachyon* (Bd), *Oryza sativa* (Os), *Sorghum bicolor* (Sb), *Zea mays* (Zm), and *Triticum aestivum* (A); and Amino acidic sequence of *TaD27* (B). In red, sequence encoding for DUF4033 superfamily. The tree was inferred using the Neighbor-Joining method (Saitou and Nei, 1987). The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) is shown next to the branches (Fellsenstein, 2009). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Maximum Composite Likelihood method (Tamura *et al.*, 2004) and are in the units of the number of base substitutions per site. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA7 (Kumar *et al.*, 2016).



B

A L L Q D G T Y L R N G P G L W D L G D Y G F R H L F D G Y A T L V R V	36
S F R D G R A V G A H R Q I E S E A Y K A A R R H G K V C Y R E F S E V	72
P K P D S F K S F V G Q L A S L F S G N S L T D N S N T G V V R L G D G	108
R V L C L T E T V K G S I V V D P D T L D T V S K F E Y E D K L G G L I H	145
S A H P I V T D T E F W T L I P D L I R P G Y V V A R **Met** D A G S N E R Q	181
F V G R V D C R G G P A P G W V H S F P V T E N Y V V V P E **Met** P L R	215
Y C A A N L L R A E P T P L Y K F Q W H L E S G S Y **Met** H V **Met** C K A S	249
G K I	252

Fig. S5. Phylogenetic analysis of partial *CCD8* sequences from *Aegilops tauschii* (Atau), *Arabidopsis thaliana* (At), *Brachypodium distachyon* (Bd), *Oryza sativa* (Os), *Sorghum bicolor* (Sb), *Zea mays* (Zm), and *Triticum aestivum* (A); and Partial amino acidic sequence of *TaCCD8* (B). In red sequence encoding for RPE65 superfamily. The tree was constructed as described in Figure S4.

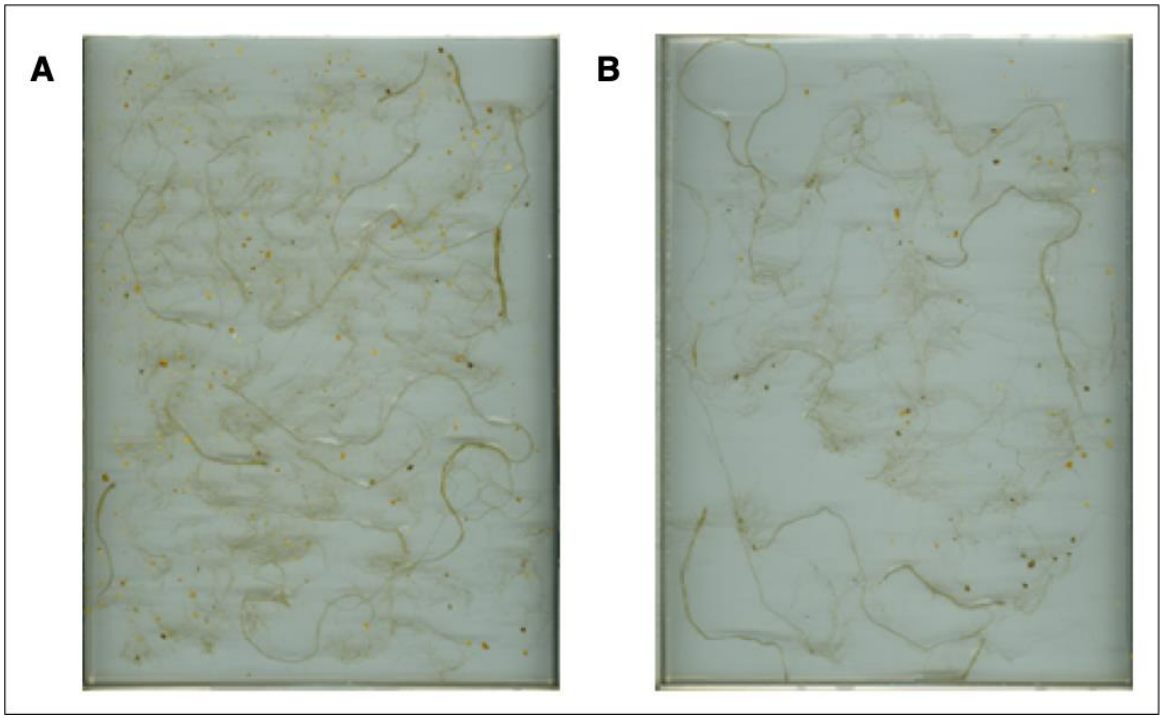


Fig. S6. Transparent tray containing the root systems of a single Crac (A) and Tukan (B) plant grown for 5 weeks in pots filled with sand/vermiculite and exposed to low Pi stress (10 µM). Root systems from individual plants were cut before the analysis in order to minimize overlaps in the scanner.

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