

Table S1. Description of the sixteen root, biomass, and phosphorus index traits accessed in the study.

S.No .	Trait abbreviated form	Full Name	Unit	Description	Reference
1	TRL	Total root length	cm plant ⁻¹	Sum of the path length of primary root (PR) and lateral roots (LRs)	[70]
2	TSA	Total root surface area	cm ² plant ⁻¹	Real surface of root that is in contact with the water	[27]
3	AVD	Average diameter	mm plant ⁻¹	Projected area (2D measurement of the area occupied by roots) divided by Total Root length	[74]
4	TIP	Total root tips	Number	Total number of tips (where a link end without any other link connection)	[74]
5	RVL	Total root volume	cm ³ plant ⁻¹	$\pi \times (\text{Half of the avg. diameter}/2)^2 \times \text{TRL}$	[70]
6	PRL	Primary root length	cm plant ⁻¹	Sum of the path length of primary root or longest root per wheat plant	[70]
7	RDW	Root dry weight	g plant ⁻¹	-	-
8	SDW	Shoot dry weight	g plant ⁻¹	-	-
9	TBM	Total biomass	g plant ⁻¹	Sum of SDW and RDW	-
10	RMR	Root mass ratio	Ratio	Ratio of root dry mass to total plant dry mass	[27]
11	P CON	Tissue P concentration	mg P g ⁻¹ dry matter	Amount of P content per gram of Dry Matter (Tissue P concentration)	-
12	TPU	Total P uptake	mg P plant ⁻¹	Total amount of phosphorus in the plant	[48]
13	PER	P efficiency ratio	g dry weight mg ⁻¹ P	Total plant dry mass divided by total P accumulation	[7]
14	PUtE	Phosphorus utilization efficiency	g dry matter g ⁻¹ P taken up	(Total plant dry mass divided by tissue P concentration) *100	[75]
15	PUpE	P uptake efficiency	mg P g ⁻¹ root Dry matter	Total P accumulation divided by root dry mass	[75]
16.	SRL	Specific root length	cm g ⁻¹ root dry matter	The total root length divided by the root dry weight	[58]

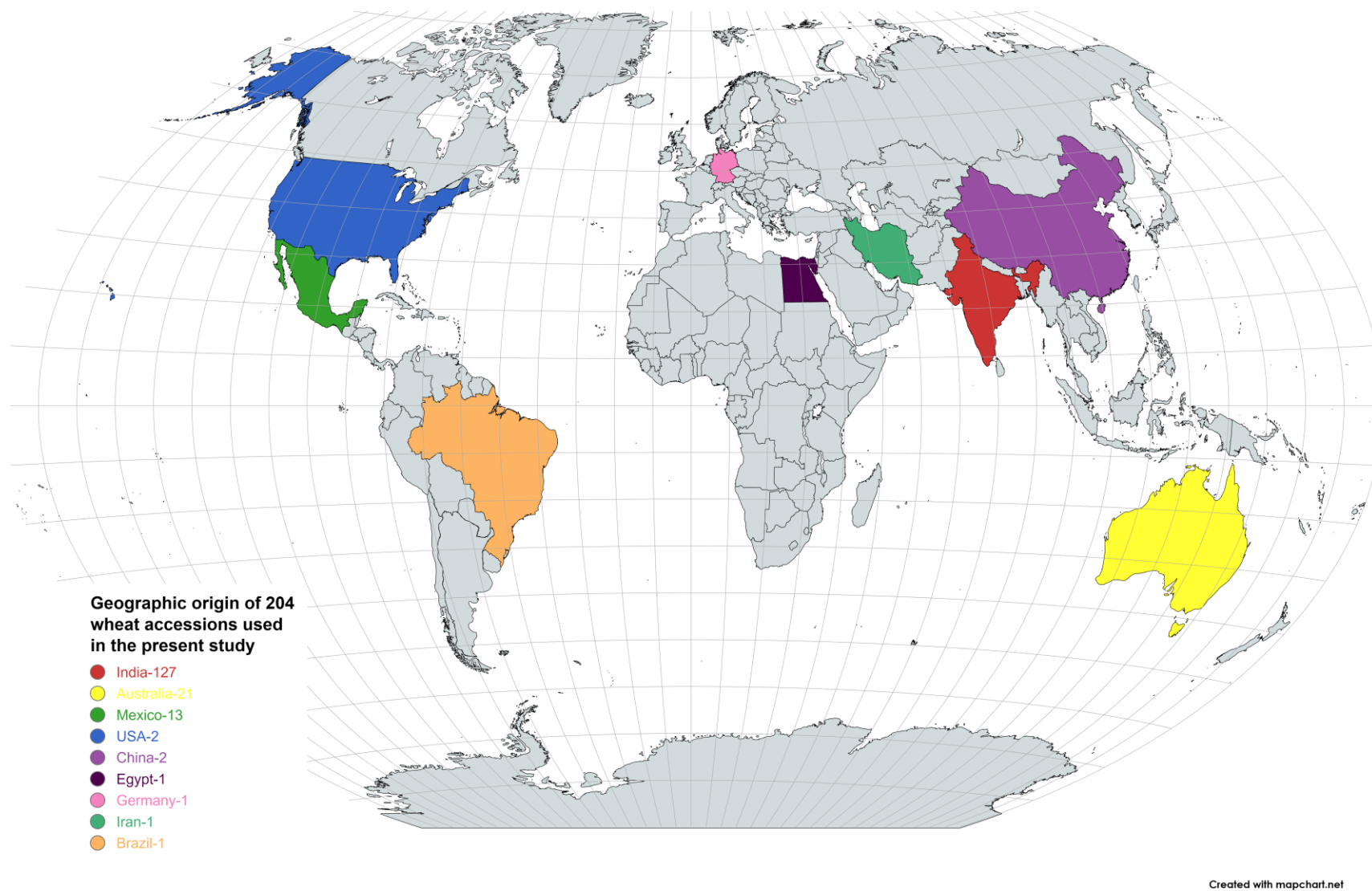


Figure S1. Geographic origin of 204 wheat accessions used in the present study. Colour indicates the country of origin. The geographic distributions of accessions are visualized by <https://www.mapchart.net/world-advanced.html>. (Source: mapchart.net). [Note: 35 genotypes origin details were not available].

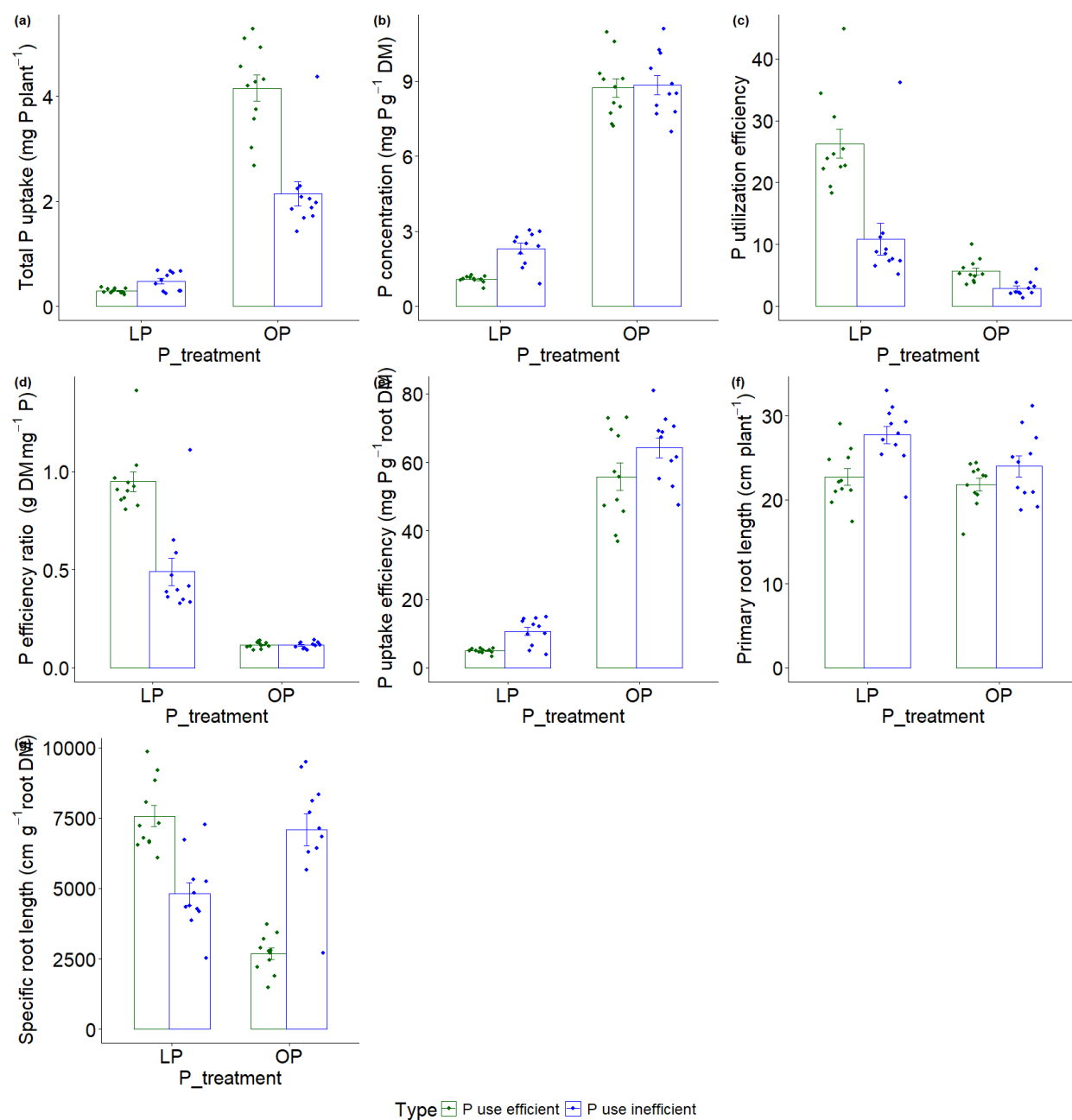


Figure S2. Bar plot showing variation of P use efficient and inefficient genotypes under low and optimum P in (a) Total P uptake (TPU), (b) P concentration (P CON), (c) P utilization efficiency (PUtE), (d) P efficiency ratio (PER), (e) P uptake efficiency (PUpE), (f) Primary root length (PRL), (g) Specific root length (SRL). Bar plot show the mean and error bars indicate standard errors.

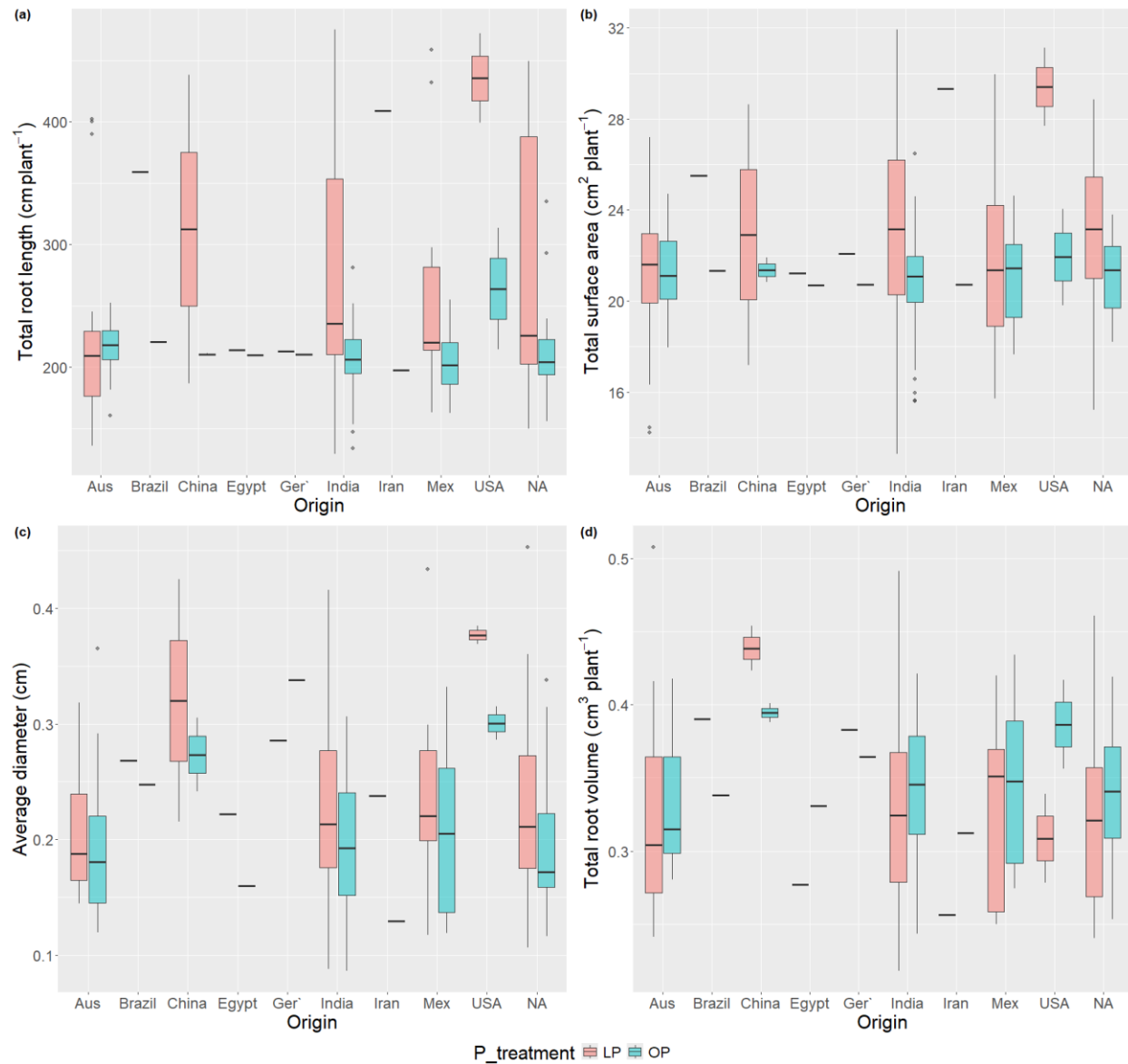


Figure S3a-d. Variation among the nine countries of origin in (a) Total root length, (b) Total surface area, (c) Average diameter, (d) Total root volume in 204 wheat genotypes grown in a hydroponic phenotyping platform for 21 days. The boxplots were confined to the first and third quartile with the middle lines being the median. The number of genotypes in each country varied and ranged from one to 127 (see Table S2) [Note: Aus-Australia, Mex- Mexico, Ger, Germany].

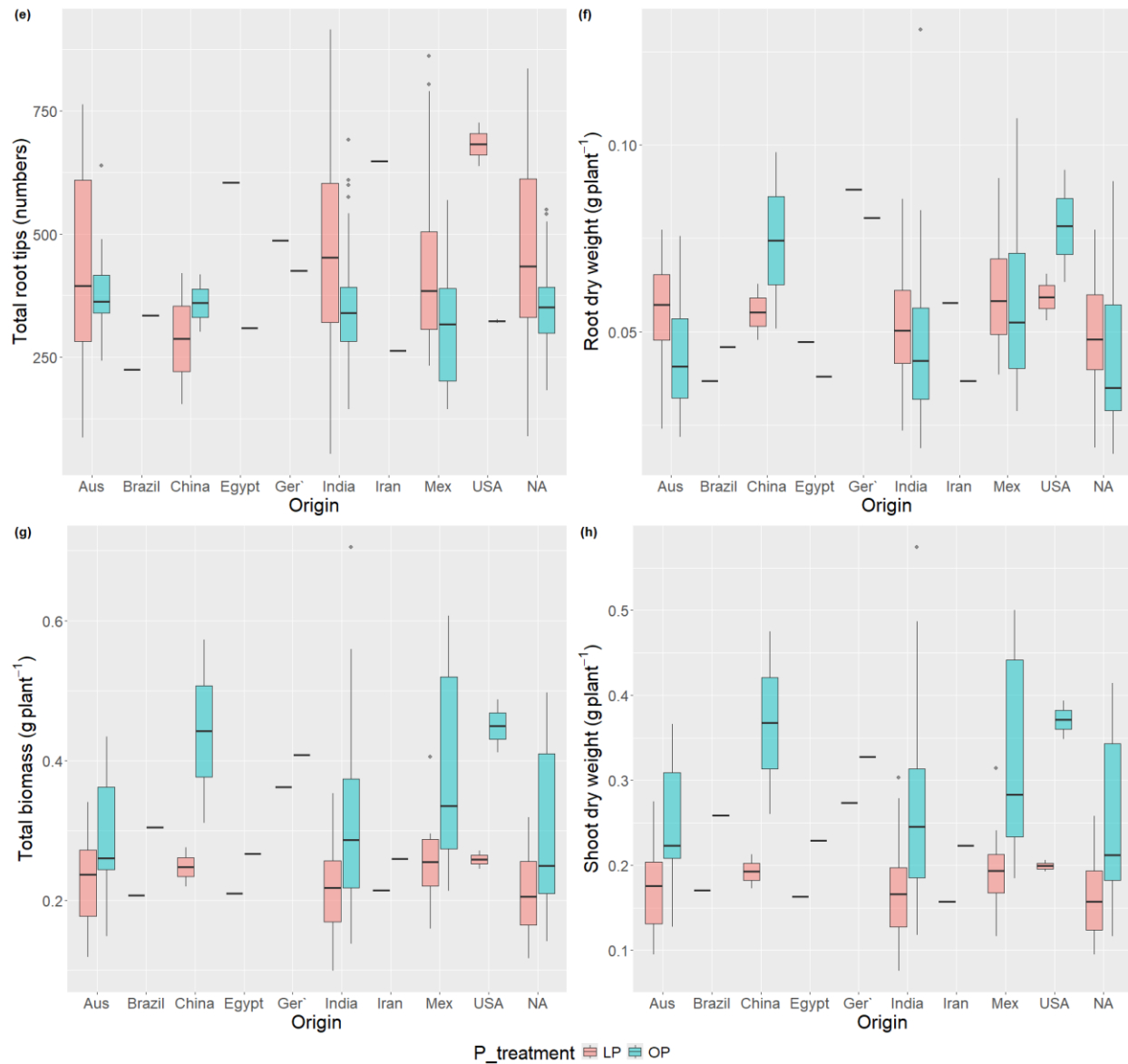


Figure S3e-h. Variation among the nine countries of origin in (e) Total root tips, (f) Root dry weight, (g) Total biomass, (h) Shoot dry weight in 204 wheat genotypes grown in a hydroponic phenotyping platform for 21 days. The boxplots were confined to the first and third quartile with the middle lines being the median. The number of genotypes in each country varied and ranged from one to 127 (see Table S2) [Note: Aus-Australia, Mex- Mexico, Ger, Germany].

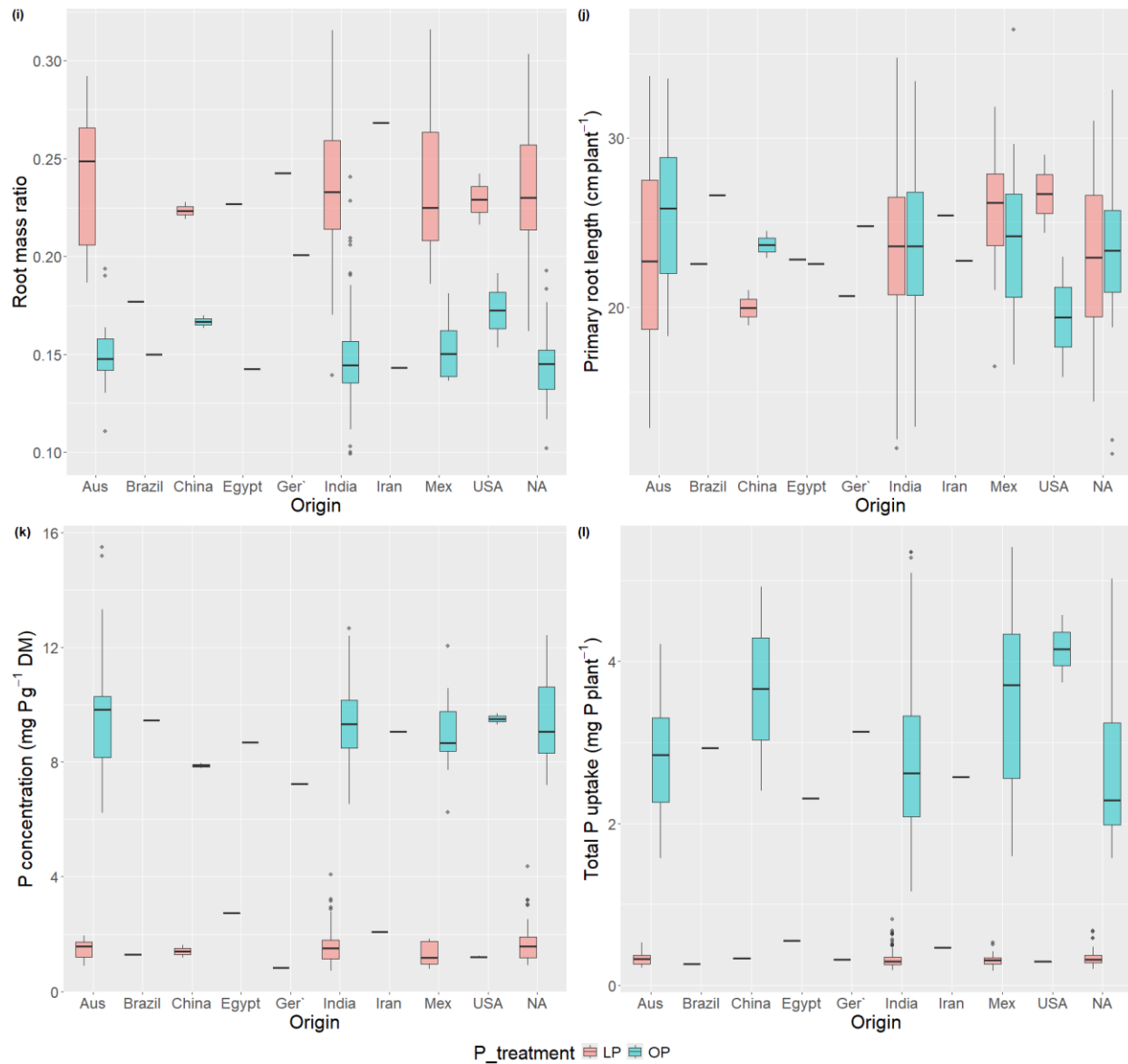


Figure S3i-l. Variation among the nine countries of origin in (i) Root mass ratio, (j) Primary root length, (k) P concentration, (l) Total P uptake in 204 wheat genotypes grown in a hydroponic phenotyping platform for 21 days. The boxplots were confined to the first and third quartile with the middle lines being the median. The number of genotypes in each country varied and ranged from one to 127 (see Table S2) [Note: Aus-Australia, Mex- Mexico, Ger, Germany].

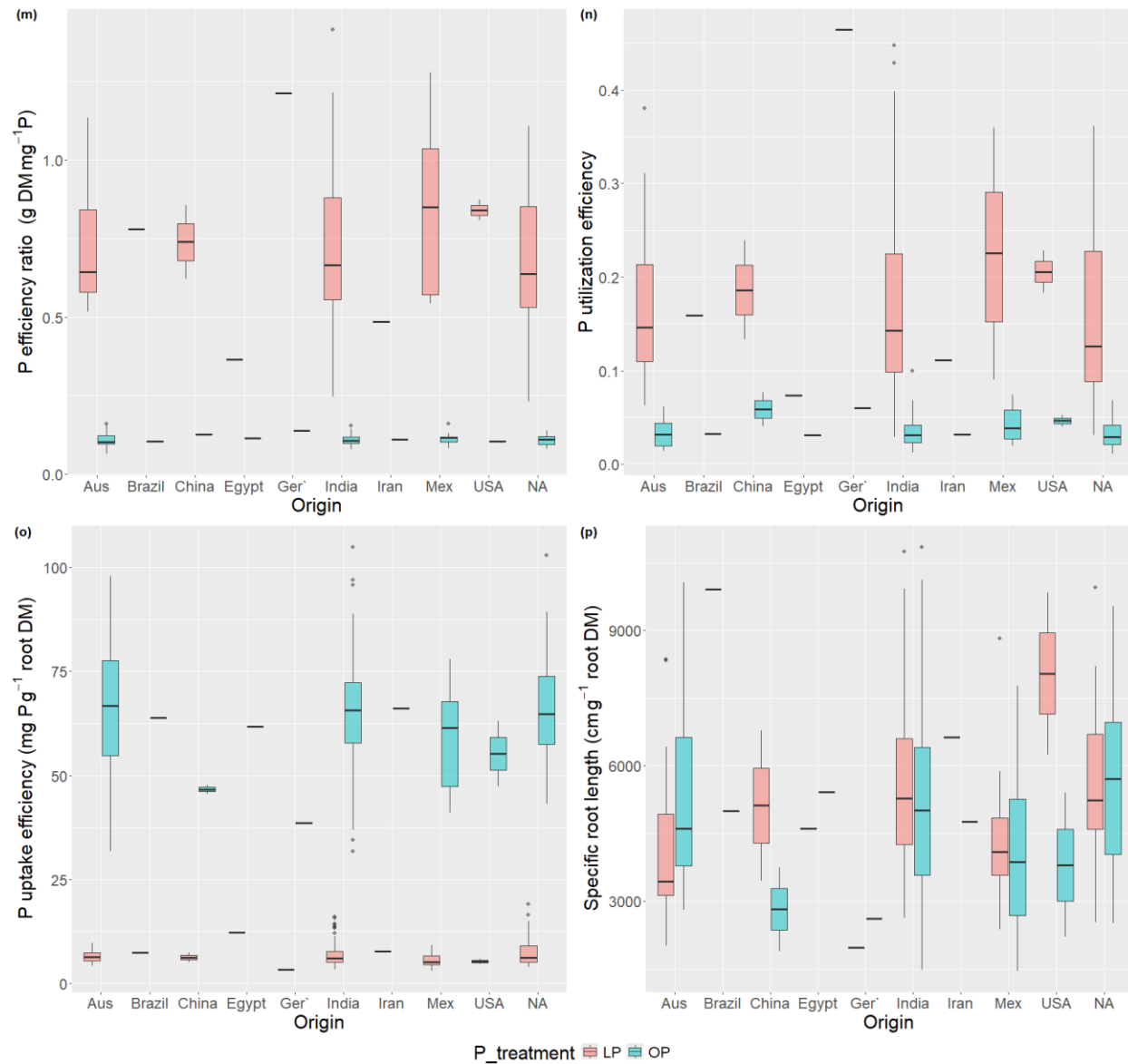


Figure S3m-p. Variation among the nine countries of origin in (m) P efficiency ratio, (n) P utilization efficiency, (o) P uptake efficiency, (p) specific root length in 204 wheat genotypes grown in a hydroponic phenotyping platform for 21 days. The boxplots were confined to the first and third quartile with the middle lines being the median. The number of genotypes in each country varied and ranged from one to 127 (see Table S2) [Note: Aus-Australia, Mex- Mexico, Ger, Germany].