SUPPLEMENTARY INFORMATION

The Phosphate Deprivation Response is Mediated by an Interaction between Brassinosteroid Signaling and Zinc in Tomato

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Supplementary Figures

A

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	1.734	<0.0001	****	Yes	
Genotype	78.50	<0.0001	****	Yes	
P treatment	2.378	<0.0001	****	Yes	
ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	52.75	1	52.75	F (1, 185) = 19.20	P<0.0001
Genotype	2388	1	2388	F (1, 185) = 869.4	P<0.0001
P treatment	72.34	1	72.34	F (1, 185) = 26.34	P<0.0001
Residual	508.1	185	2.747		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	2.307	1.448 to 3.167	Yes	<0.0001
M82:P+ vs. Penn:P+	8.213	7.354 to 9.073	Yes	<0.0001
M82:P+ vs. Penn:P-	8.395	7.477 to 9.313	Yes	<0.0001
M82:P- vs. Penn:P+	5.906	5.047 to 6.765	Yes	<0.0001
M82:P- vs. Penn:P-	6.088	5.170 to 7.006	Yes	<0.0001
Penn:P+ vs. Penn:P-	0.1818	-0.7361 to 1.100	No	0.9558

B

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	5.373	0.0010	**	Yes	
Genotype	2.642	0.0206	*	Yes	
P treatment	2.057	0.0407	*	Yes	
ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	43.99	1	43.99	F (1, 185) = 11.09	P=0.0010
Genotype	21.63	1	21.63	F (1, 185) = 5.454	P=0.0206
P treatment	16.84	1	16.84	F (1, 185) = 4.246	P=0.0407
Residual	733.7	185	3.966		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	-1.571	-2.604 to -0.5384	Yes	0.0007
M82:P+ vs. Penn:P+	-0.2900	-1.323 to 0.7426	No	0.8857
M82:P+ vs. Penn:P-	0.08006	-1.023 to 1.183	No	0.9976
M82:P- vs. Penn:P+	1.281	0.2484 to 2.314	Yes	0.0083
M82:P- vs. Penn:P-	1.651	0.5480 to 2.754	Yes	0.0008
Penn:P+ vs. Penn:P-	0.3701	-0.7330 to 1.473	No	0.8205

C

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	22.70	<0.0001	****	Yes	
Genotype	62.58	<0.0001	****	Yes	
P treatment	4.871	<0.0001	****	Yes	
ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	1.093	1	1.093	F (1, 75) = 169.0	P<0.0001
Genotype	3.015	1	3.015	F (1, 75) = 466.1	P<0.0001
P treatment	0.2347	1	0.2347	F (1, 75) = 36.28	P<0.0001
Residual	0.4851	75	0.0065		

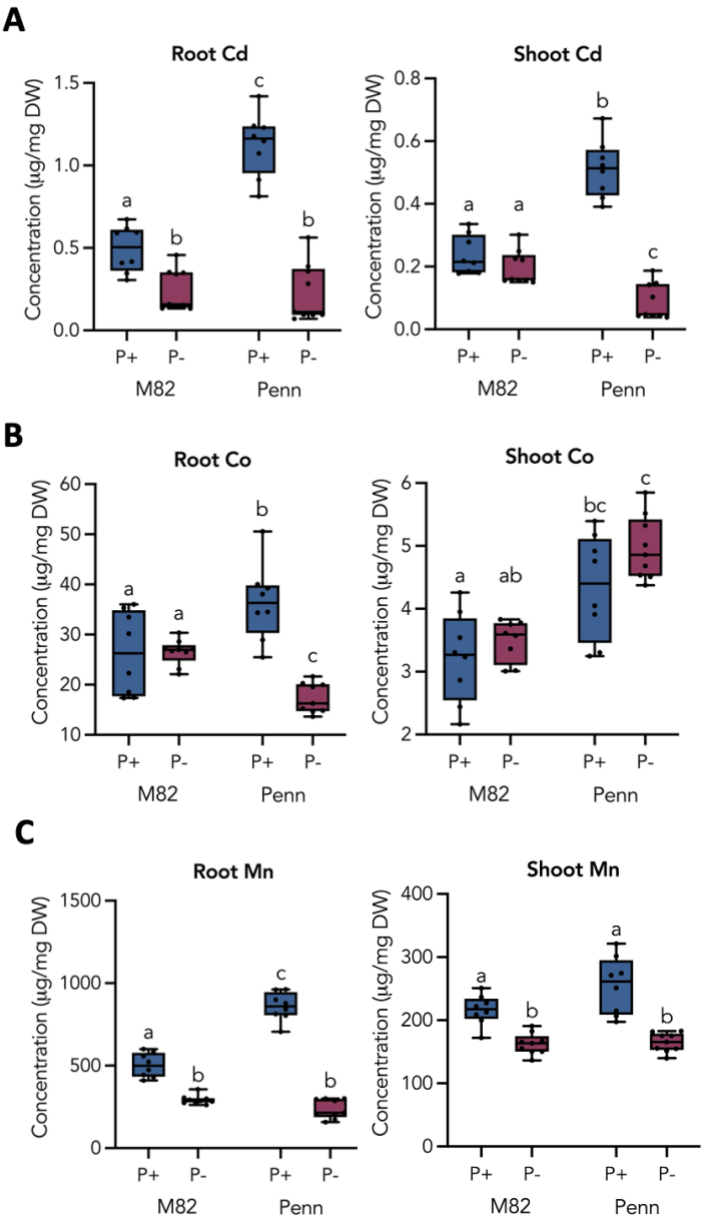
Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	-0.1263	-0.1940 to -0.05862	Yes	<0.0001
M82:P+ vs. Penn:P+	-0.6262	-0.6939 to -0.5585	Yes	<0.0001
M82:P+ vs. Penn:P-	-0.2818	-0.3495 to -0.2141	Yes	<0.0001
M82:P- vs. Penn:P+	-0.4998	-0.5667 to -0.4330	Yes	<0.0001
M82:P- vs. Penn:P-	-0.1554	-0.2223 to -0.08862	Yes	<0.0001
Penn:P+ vs. Penn:P-	0.3444	0.2776 to 0.4112	Yes	<0.0001

D

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	9.773	0.0142	*	Yes	
Genotype	25.92	0.0005	***	Yes	
P treatment	50.02	<0.0001	****	Yes	
ANOVA table	SS	DF	MS	F (DFn, DFd)	P value
Interaction	4.530	1	4.530	F (1, 12) = 8.206	P=0.0142
Genotype	12.01	1	12.01	F (1, 12) = 21.76	P=0.0005
P treatment	23.18	1	23.18	F (1, 12) = 42.00	P<0.0001
Residual	6.624	12	0.5520		

Tukey's multiple comparisons	Mean Diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	-3.472	-5.031 to -1.912	Yes	0.0001
M82:P+ vs. Penn:P+	-2.797	-4.357 to -1.237	Yes	0.0009
M82:P+ vs. Penn:P-	-4.140	-5.700 to -2.581	Yes	<0.0001
M82:P- vs. Penn:P+	0.6746	-0.8851 to 2.234	No	0.5893
M82:P- vs. Penn:P-	-0.6687	-2.228 to 0.8910	No	0.5958
Penn:P+ vs. Penn:P-	-1.343	-2.903 to 0.2164	No	0.1005

Supp. Fig 1: Statistical analysis of Figure 1. A) Figure 1 Panel A (primary root length). **B)** Figure 1 Panel B (total lateral root length). **C)** Figure 1 Panel D (mature root hair length). **D)** Figure 1 Panel G (pNPP assay).



Supp. Fig. 2: ICP-MS results of Cd, Co, and Mn roots and shoots in P sufficiency or deficiency. A) Root and shoot Cd **B)** Root and shoot Co and **C)** Root and shoot Mn profile of M82 and Penn in P-sufficient and P-limiting conditions. N= 6 for all plots. Letters represent statistically significant differences as determined by a two-way ANOVA and a post-hoc Tukey test, $p<0.01$.

A

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	0.7111	0.2247	ns	No	
Genotype	1.427	0.0894	ns	No	
P treatment	85.68	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	4.420	1	4.420	F (1, 29) = 1.539	P=0.2247
Genotype	8.869	1	8.869	F (1, 29) = 3.089	P=0.0894
P treatment	532.5	1	532.5	F (1, 29) = 185.5	P<0.0001
Residual	83.27	29	2.871		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	7.341	5.098 to 9.585	Yes	<0.0001
M82:P+ vs. Penn:P+	-1.778	-4.168 to 0.6111	No	0.2013
M82:P+ vs. Penn:P-	7.035	4.792 to 9.278	Yes	<0.0001
M82:P- vs. Penn:P+	-9.120	-11.45 to -6.793	Yes	<0.0001
M82:P- vs. Penn:P-	-0.3065	-2.483 to 1.870	No	0.9804
Penn:P+ vs. Penn:P-	8.813	6.487 to 11.14	Yes	<0.0001

B

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	1.093	0.0259	*	Yes	
Genotype	3.785	0.0001	***	Yes	
P treatment	91.39	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	6.270	1	6.270	F (1, 29) = 5.514	P=0.0259
Genotype	21.72	1	21.72	F (1, 29) = 19.10	P=0.0001
P treatment	524.3	1	524.3	F (1, 29) = 461.0	P<0.0001
Residual	32.98	29	1.137		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	7.138	5.726 to 8.550	Yes	<0.0001
M82:P+ vs. Penn:P+	-2.508	-4.011 to -1.004	Yes	0.0005
M82:P+ vs. Penn:P-	6.383	4.972 to 7.795	Yes	<0.0001
M82:P- vs. Penn:P+	-9.646	-11.11 to -8.181	Yes	<0.0001
M82:P- vs. Penn:P-	-0.7546	-2.124 to 0.6150	No	0.4498
Penn:P+ vs. Penn:P-	8.891	7.427 to 10.36	Yes	<0.0001

C

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	0.1872	0.7538	ns	No	
Genotype	0.4804	0.6159	ns	No	
P treatment	45.60	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.04914	1	0.04914	F (1, 29) = 0.1002	P=0.7538
Genotype	0.1261	1	0.1261	F (1, 29) = 0.2572	P=0.6159
P treatment	11.97	1	11.97	F (1, 29) = 24.41	P<0.0001
Residual	14.22	29	0.4903		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	-1.133	-2.060 to -0.2063	Yes	0.0120
M82:P+ vs. Penn:P+	0.2019	-0.7855 to 1.189	No	0.9439
M82:P+ vs. Penn:P-	-1.087	-2.014 to -0.1596	Yes	0.0168
M82:P- vs. Penn:P+	1.335	0.3738 to 2.297	Yes	0.0038
M82:P- vs. Penn:P-	0.04670	-0.8526 to 0.9460	No	0.9990
Penn:P+ vs. Penn:P-	-1.288	-2.250 to -0.3271	Yes	0.0053

D

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	0.3997	0.6452	ns	No	
Genotype	9.799	0.0288	*	Yes	
P treatment	38.05	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.0005324	1	0.0005324	F (1, 28) = 0.2167	P=0.6452
Genotype	0.01305	1	0.01305	F (1, 28) = 5.312	P=0.0288
P treatment	0.05069	1	0.05069	F (1, 28) = 20.63	P<0.0001
Residual	0.06881	28	0.002457		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	-0.07172	-0.1375 to -0.005957	Yes	0.0286
M82:P+ vs. Penn:P+	-0.03236	-0.1024 to 0.03768	No	0.5942
M82:P+ vs. Penn:P-	-0.1205	-0.1881 to -0.05280	Yes	0.0002
M82:P- vs. Penn:P+	0.03936	-0.02885 to 0.1076	No	0.4083
M82:P- vs. Penn:P-	-0.04875	-0.1145 to 0.01702	No	0.2036
Penn:P+ vs. Penn:P-	-0.08811	-0.1582 to -0.01806	Yes	0.0095

E

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	48.02	<0.0001	****	Yes	
Genotype	18.37	0.0002	***	Yes	
P treatment	11.92	0.0018	**	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.8472	1	0.8472	F (1, 29) = 47.84	P<0.0001
Genotype	0.3241	1	0.3241	F (1, 29) = 18.30	P=0.0002
P treatment	0.2103	1	0.2103	F (1, 29) = 11.87	P=0.0018
Residual	0.5136	29	0.01771		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	-0.1617	-0.3379 to 0.01452	No	0.0810
M82:P+ vs. Penn:P+	-0.5215	-0.7091 to -0.3338	Yes	<0.0001
M82:P+ vs. Penn:P-	-0.03875	-0.2149 to 0.1374	No	0.9315
M82:P- vs. Penn:P+	-0.3598	-0.5425 to -0.1771	Yes	<0.0001
M82:P- vs. Penn:P-	0.1229	-0.04801 to 0.2938	No	0.2266
Penn:P+ vs. Penn:P-	0.4827	0.3000 to 0.6654	Yes	<0.0001

F

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	28.51	<0.0001	****	Yes	
Genotype	46.09	<0.0001	****	Yes	
P treatment	22.03	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.07443	1	0.07443	F (1, 29) = 63.02	P<0.0001
Genotype	0.1203	1	0.1203	F (1, 29) = 101.9	P<0.0001
P treatment	0.05750	1	0.05750	F (1, 29) = 48.69	P<0.0001
Residual	0.03425	29	0.001181		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	-0.01156	-0.05705 to 0.03394	No	0.8993
M82:P+ vs. Penn:P+	-0.2169	-0.2654 to -0.1684	Yes	<0.0001
M82:P+ vs. Penn:P-	-0.03748	-0.08298 to 0.008019	No	0.1353
M82:P- vs. Penn:P+	-0.2054	-0.2525 to -0.1582	Yes	<0.0001
M82:P- vs. Penn:P-	-0.02592	-0.07006 to 0.01822	No	0.3944
Penn:P+ vs. Penn:P-	0.1794	0.1322 to 0.2266	Yes	<0.0001

Supp. Fig 3: Statistical analysis of Figure 3. A) Figure 3 Panel A (Root P). **B)** Figure 3 Panel B (Shoot P). **C)** Figure 3 Panel C (Root Fe). **D)** Figure 3 Panel D (Shoot Fe). **E)** Figure 3 Panel E (Root Zn). **F)** Figure 3 Panel F (Shoot Zn).

A

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	0.7683	0.2444	ns	No	
Zn treatment	0.8349	0.2251	ns	No	
P treatment	34.88	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	5.141	1	5.141	F (1, 113) = 1.369	P=0.2444
Zn treatment	5.586	1	5.586	F (1, 113) = 1.488	P=0.2251
P treatment	233.3	1	233.3	F (1, 113) = 62.15	P<0.0001
Residual	424.3	113	3.755		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82 Zn+:P+ vs. M82 Zn+:P-	2.410	1.080 to 3.740	Yes	<0.0001
M82 Zn+:P+ vs. M82 Zn-:P+	-0.8578	-2.141 to 0.4256	No	0.3066
M82 Zn+:P+ vs. M82 Zn-:P-	2.392	1.075 to 3.709	Yes	<0.0001
M82 Zn+:P- vs. M82 Zn-:P+	-3.268	-4.598 to -1.937	Yes	<0.0001
M82 Zn+:P- vs. M82 Zn-:P-	-0.01780	-1.381 to 1.345	No	>0.9999
M82 Zn-:P+ vs. M82 Zn-:P-	3.250	1.932 to 4.567	Yes	<0.0001

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	0.4863	0.4343	ns	No	
Zn treatment	0.8453	0.3031	ns	No	
P treatment	0.6541	0.3648	ns	No	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.8244	1	0.8244	F (1, 124) = 0.6152	P=0.4343
Zn treatment	1.433	1	1.433	F (1, 124) = 1.069	P=0.3031
P treatment	1.109	1	1.109	F (1, 124) = 0.8275	P=0.3648
Residual	166.2	124	1.340		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
Penn Zn+:P+ vs. Penn Zn+:P-	-0.3481	-1.127 to 0.4307	No	0.6507
Penn Zn+:P+ vs. Penn Zn-:P+	-0.3737	-1.139 to 0.3921	No	0.5832
Penn Zn+:P+ vs. Penn Zn-:P-	-0.3994	-1.133 to 0.3346	No	0.4912
Penn Zn+:P- vs. Penn Zn-:P+	-0.02557	-0.8044 to 0.7533	No	0.9998
Penn Zn+:P- vs. Penn Zn-:P-	-0.05133	-0.7990 to 0.6964	No	0.9980
Penn Zn-:P+ vs. Penn Zn-:P-	-0.02575	-0.7598 to 0.7083	No	0.9997

B

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	0.02565	0.8503	ns	No	
Genotype	0.6825	0.3314	ns	No	
P treatment	28.53	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.04753	1	0.04753	F (1, 98) = 0.03580	P=0.8503
Zn treatment	1.265	1	1.265	F (1, 98) = 0.9527	P=0.3314
P treatment	52.86	1	52.86	F (1, 98) = 39.82	P<0.0001
Residual	130.1	98	1.327		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82 Zn+:P+ vs. M82 Zn+:P-	-1.493	-2.372 to -0.6146	Yes	0.0001
M82 Zn+:P+ vs. M82 Zn-:P+	-0.2677	-1.146 to 0.6110	No	0.8559
M82 Zn+:P+ vs. M82 Zn-:P-	-1.674	-2.503 to -0.8454	Yes	<0.0001
M82 Zn+:P- vs. M82 Zn-:P+	1.226	0.3563 to 2.095	Yes	0.0021
M82 Zn+:P- vs. M82 Zn-:P-	-0.1808	-0.9995 to 0.6380	No	0.9387
M82 Zn-:P+ vs. M82 Zn-:P-	-1.406	-2.225 to -0.5876	Yes	0.0001

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	9.415	<0.0001	****	Yes	
Genotype	12.17	<0.0001	****	Yes	
P treatment	0.1294	0.6351	ns	No	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	15.83	1	15.83	F (1, 133) = 16.47	P<0.0001
Zn treatment	20.46	1	20.46	F (1, 133) = 21.29	P<0.0001
P treatment	0.2175	1	0.2175	F (1, 133) = 0.2263	P=0.6351
Residual	127.8	133	0.9612		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
Penn Zn+:P+ vs. Penn Zn+:P-	0.7684	0.1754 to 1.361	Yes	0.0054
Penn Zn+:P+ vs. Penn Zn-:P+	-0.09424	-0.7470 to 0.5585	No	0.9819
Penn Zn+:P+ vs. Penn Zn-:P-	-0.7014	-1.294 to -0.1084	Yes	0.0134
Penn Zn+:P- vs. Penn Zn-:P+	-0.8627	-1.515 to -0.2099	Yes	0.0043
Penn Zn+:P- vs. Penn Zn-:P-	-1.470	-2.063 to -0.8768	Yes	<0.0001
Penn Zn-:P+ vs. Penn Zn-:P-	-0.6072	-1.260 to 0.04560	No	0.0782

C

Source of Variation	% of total variation	P value	P value summary	Significant?	
Zn treatment	0.2871	0.6877	ns	No	
P treatment	20.80	0.0013	**	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Zn treatment	0.001562	1	0.001562	F (1, 45) = 0.1637	P=0.6877
P treatment	0.1132	1	0.1132	F (1, 45) = 11.86	P=0.0013
Residual	0.4294	45	0.009542		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
Zn+:P+ vs. Zn+:P-	-0.09712	-0.1723 to -0.02190	Yes	0.0066
Zn+:P+ vs. Zn-:P+	0.01141	-0.06382 to 0.08664	No	0.9773
Zn+:P+ vs. Zn-:P-	-0.08571	-0.1921 to 0.02067	No	0.1534
Zn+:P- vs. Zn-:P+	0.1085	0.002148 to 0.2149	Yes	0.0440
Zn+:P- vs. Zn-:P-	0.01141	-0.06382 to 0.08664	No	0.9773
Zn-:P+ vs. Zn-:P-	-0.09712	-0.1723 to -0.02190	Yes	0.0066

Source of Variation	% of total variation	P value	P value summary	Significant?	
Zn treatment	13.10	0.0104	*	Yes	
P treatment	6.902	0.0585	ns	No	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Zn treatment	0.08090	1	0.08090	F (1, 44) = 7.164	P=0.0104
P treatment	0.04262	1	0.04262	F (1, 44) = 3.774	P=0.0585
Residual	0.4968	44	0.01129		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
Zn+:P+ vs. Zn+:P-	0.06037	-0.02260 to 0.1433	No	0.2255
Zn+:P+ vs. Zn-:P+	0.08317	0.0002053 to 0.1661	Yes	0.0492
Zn+:P+ vs. Zn-:P-	0.1435	0.02472 to 0.2624	Yes	0.0122
Zn+:P- vs. Zn-:P+	0.02280	-0.09302 to 0.1386	No	0.9524
Zn+:P- vs. Zn-:P-	0.08317	0.0002053 to 0.1661	Yes	0.0492
Zn-:P+ vs. Zn-:P-	0.06037	-0.02260 to 0.1433	No	0.2255

Supp. Fig 4: Statistical analysis of Fig 4. A) Primary root responses of M82 (left) and *S. pennellii* (right) **B)** Total lateral root length responses of M82 (left) and *S. pennellii* (right) **C)** Mature root hair length responses of M82 (left) and *S. pennellii* (right) in P sufficiency or deficiency when Zn is absent or present.

Derivative	Source	p.value	adjusted_p.value
CR	P treatment	0.9029	0.9612
CN	P treatment	0.4129	0.7570
6-deoxoCT	P treatment	0.9786	0.9786
6-deoxoTY	P treatment	0.2105	0.4961
6-oxoCN	P treatment	0.2634	0.5433
CS	P treatment	0.5973	0.7884
BL	P treatment	0.7968	0.9067
homoCS	P treatment	0.2421	0.5326
norTE	P treatment	0.0068	0.0448
norCS	P treatment	0.1250	0.4126
homoBL	P treatment	0.2010	0.4961
CR	Species	0.0003	0.0035
CN	Species	0.0199	0.0937
6-deoxoCT	Species	0.0772	0.3186
6-deoxoTY	Species	0.0001	0.0020
6-oxoCN	Species	0.4706	0.7727
CS	Species	0.1433	0.4298
BL	Species	0.0056	0.0448
homoCS	Species	0.6732	0.8545
norTE	Species	0.5475	0.7727
norCS	Species	0.0000	0.0009
homoBL	Species	0.4955	0.7727
CR	Interaction	0.4771	0.7727
CN	Interaction	0.3277	0.6361
6-deoxoCT	Interaction	0.1583	0.4354
6-deoxoTY	Interaction	0.7339	0.8764
6-oxoCN	Interaction	0.8375	0.9212
CS	Interaction	0.0138	0.0760
BL	Interaction	0.5439	0.7727
homoCS	Interaction	0.7436	0.8764
norTE	Interaction	0.1182	0.4126
norCS	Interaction	0.9737	0.9786
homoBL	Interaction	0.5619	0.7727

Supp. Fig 5: Statistical analysis of BR levels in M82 and *S. pennellii* (Figure 5C). P-values are obtained from a two-way ANOVA analysis. BL is highlighted as one of my main types of BRs. The samples were clustered as follows: z-scores were calculated for each BR level, Euclidean distances between samples were calculated and hierarchical clustering was performed using the complete method. Hypothesis testing: Two-way ANOVA was performed for each BR with P and Species as main factors and their interaction. For each BR with significant effect, post hoc comparisons were performed using Tukey's HSD test. Fig. 5A,B For each species one way analysis of variance was performed with hormone concentration as the independent variable. When significant the ANOVA was followed by Tukey's HSD test to compare between the different concentration pairs. Fig 5 D,E - For M82, two independent experiments were analyzed. Thus, to determine the effect of P and BRZ on LR, mixed model analysis of variance (ANOVA) was performed with P, BRZ and their interaction as fixed factors and the batch as random factor. Post-hoc analysis was performed using pairwise differences of LS-mean as implemented in the lmerTest R package. P-values are based on the t-distribution using degrees of freedom according to Satterthwaites method. P-values that passed correction for multiple comparisons using the False Discovery Rate procedure with alpha<0 are indicated by letters. For Penn two-way ANOVA was performed with P and BRZ treatments as main factors and their interaction.

A

M82 BL p values

	diff	lwr	upr	p adj
0.01-0	-0.1188333	-2.147240	1.9095738	0.9997857
0.1-0	-0.2318333	-2.095492	1.6318256	0.9958823
1-0	-0.1673333	-2.101344	1.7666769	0.9989998
10-0	-1.7234333	-3.751840	0.3049738	0.1232693
0.1-0.01	-0.1130000	-2.074444	1.8484444	0.9997995
1-0.01	-0.0485000	-2.076907	1.9799071	0.9999940
10-0.01	-1.6046000	-3.723202	0.5140021	0.2025182
1-0.1	0.0645000	-1.799159	1.9281589	0.9999736
10-0.1	-1.4916000	-3.453044	0.4698444	0.1993606
10-1	-1.5561000	-3.584507	0.4723071	0.1926136

Penn BL p values

	diff	lwr	upr	p adj
0.01-0	0.77875000	-0.2395590	1.7970590	0.2078131
0.1-0	-1.83175000	-2.9350599	-0.7284401	0.0002297
1-0	-1.74339286	-2.9472027	-0.5395830	0.0015024
10-0	-1.61337500	-2.7763658	-0.4503842	0.0025271
0.1-0.01	-2.61050000	-3.5600780	-1.6609220	0.0000000
1-0.01	-2.52214286	-3.5868323	-1.4574534	0.0000003
10-0.01	-2.39212500	-3.4104340	-1.3738160	0.0000004
1-0.1	0.08835714	-1.0578991	1.2346134	0.9994635
10-0.1	0.21837500	-0.8849349	1.3216849	0.9796175
10-1	0.13001786	-1.0737920	1.3338277	0.9979800

B

M82 BRZ p values

	diff	lwr	upr	p adj
0.003-0	2.0091667	0.1756713	3.8426620	0.0271323
0.03-0	-0.4476333	-2.1676044	1.2723377	0.9359405
0.3-0	-0.1285000	-1.7684281	1.5114281	0.9992991
3-0	-3.5875000	-5.2274281	-1.9475719	0.0000144
0.03-0.003	-2.4568000	-4.3622242	-0.5513758	0.0073857
0.3-0.003	-2.1376667	-3.9711620	-0.3041713	0.0170820
3-0.003	-5.5966667	-7.4301620	-3.7631713	0.0000001
0.3-0.03	0.3191333	-1.4008377	2.0391044	0.9807287
3-0.03	-3.1398667	-4.8598377	-1.4198956	0.0001718
3-0.3	-3.4590000	-5.0989281	-1.8190719	0.0000244

Penn BRZ p values

	diff	lwr	upr	p adj
0.003-0	0.53619444	-0.5375301	1.6099190	0.6216528
0.03-0	0.09305000	-0.9551060	1.1412060	0.9990875
0.3-0	0.05008333	-0.9585053	1.0586719	0.9999087
3-0	0.01521667	-0.9521875	0.9826209	0.9999991
0.03-0.003	-0.44314444	-1.4584347	0.5721458	0.7305423
0.3-0.003	-0.48611111	-1.4605003	0.4882780	0.6225262
3-0.003	-0.52097778	-1.4526720	0.4107165	0.5148184
0.3-0.03	-0.04296667	-0.9891066	0.9031733	0.9999360
3-0.03	-0.07783333	-0.9799424	0.8242757	0.9991844
3-0.3	-0.03486667	-0.8906825	0.8209491	0.9999585

C

Source of Variation	% of total variation	P value	P value summary	Significant?
Interaction	18.80	<0.0001	****	Yes
Genotype	22.05	<0.0001	****	Yes
BRZ treatment	13.44	<0.0001	****	Yes

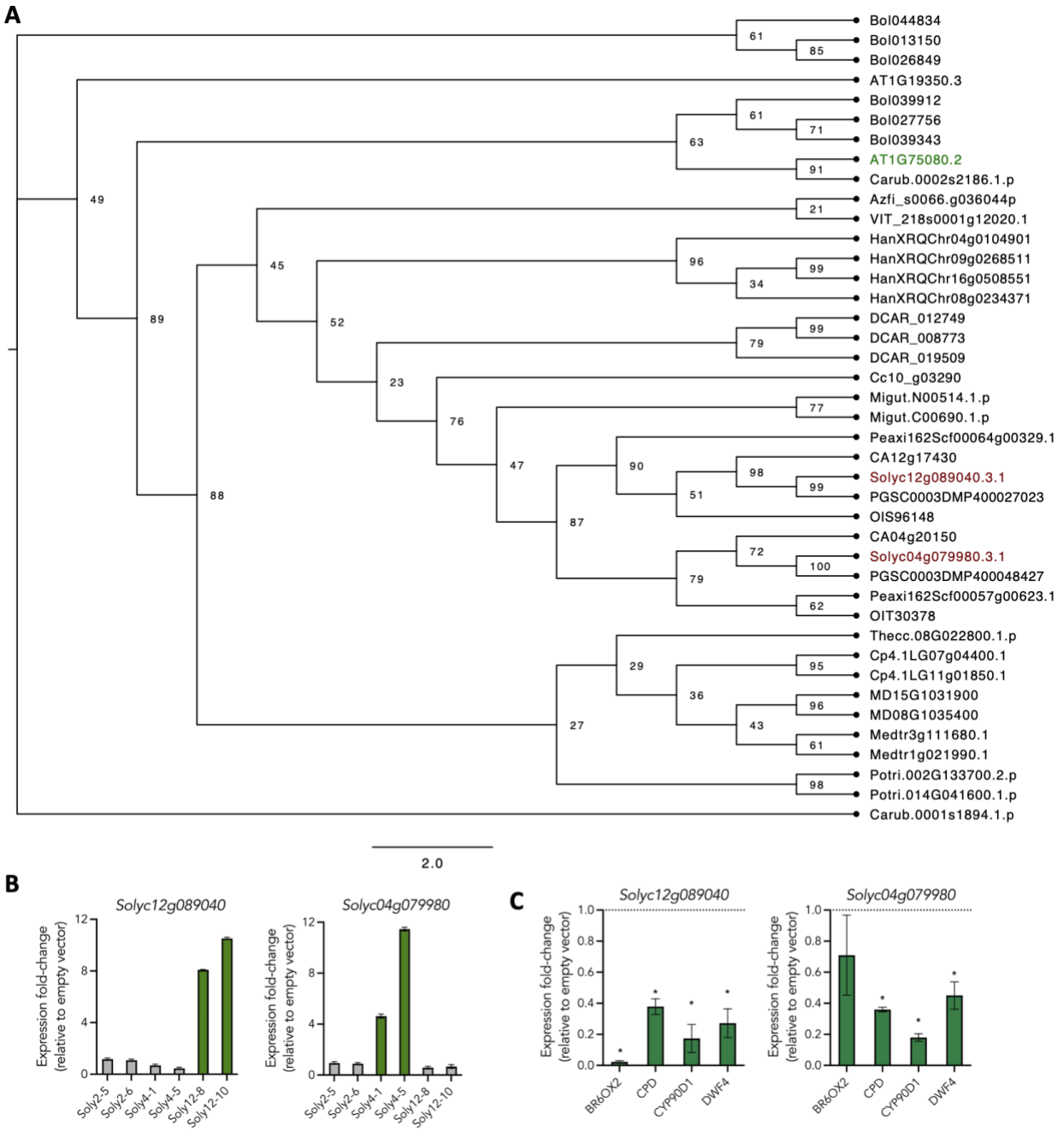
ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	221.5	3	73.83	F (3, 95) = 12.67	P<0.0001
Genotype	259.8	1	259.8	F (1, 95) = 44.58	P<0.0001
BRZ treatment	158.3	3	52.78	F (3, 95) = 9.058	P<0.0001
Residual	553.5	95	5.827		

D

Source of Variation	% of total variation	P value	P value summary	Significant?
Interaction	10.18	0.0001	***	Yes
Genotype	7.896	<0.0001	****	Yes
BRZ treatment	9.508	0.0002	***	Yes

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	183.4	3	61.13	F (3, 143) = 7.478	P=0.0001
Genotype	142.3	1	142.3	F (1, 143) = 17.40	P<0.0001
BRZ treatment	171.3	3	57.11	F (3, 143) = 6.985	P=0.0002
Residual	1169	143	8.176		

Supp. Fig 6: Statistical analysis of Figure 5 for A) M82 and Penn primary root length measurement upon BL and **B)** BRZ treatment. **C)** LR number and **D)** LR length of mock and BRZ-treated (3 µM) M82 and Penn plants.



Supp. Fig 7: BZR1/BES1 phylogeny in tomato. A) *Solyc12g089040* and *Solyc04g079980* genes were mutated in tomato hairy root lines. **B)** qPCR validation of overexpression of *Solyc12g089040* and *Solyc04g079980* in mutant hairy root lines. Soly12-8 and Soly12-10 lines showing promising results for *Solyc12g089040,* and Soly4-1 and Soly4-5 showing promising results for *Solyc04g079980.* **C)** Soly12-10 and Soly4-5 lines were used to check expression of downstream BZR1 target genes using qPCR, and stable mutants of these lines were generated.

A

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	7.171	0.0003	***	Yes	
Genotype	13.61	<0.0001	****	Yes	
BRZ treatment	65.16	<0.0001	****	Yes	
ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	27.32	1	27.32	F (1, 53) = 14.87	P=0.0003
Genotype	51.85	1	51.85	F (1, 53) = 28.22	P<0.0001
BRZ treatment	248.3	1	248.3	F (1, 53) = 135.1	P<0.0001
Residual	97.37	53	1.837		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
WT:BRZ- vs. WT:BRZ+	5.698	4.186 to 7.210	Yes	<0.0001
WT:BRZ- vs. SlBZR1-D:BRZ-	-0.5360	-1.878 to 0.8064	No	0.7156
WT:BRZ- vs. SlBZR1-D:BRZ+	2.323	1.015 to 3.632	Yes	0.0001
WT:BRZ+ vs. SlBZR1-D:BRZ-	-6.234	-7.683 to -4.785	Yes	<0.0001
WT:BRZ+ vs. SlBZR1-D:BRZ+	-3.375	-4.793 to -1.957	Yes	<0.0001
SlBZR1-D:BRZ- vs. SlBZR1-D:BRZ+	2.859	1.624 to 4.095	Yes	<0.0001

B

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	16.02	<0.0001	****	Yes	
Genotype	3.437	0.0039	**	Yes	
P treatment	22.50	<0.0001	****	Yes	
ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	119.9	1	119.9	F (1, 147) = 40.09	P<0.0001
Genotype	25.72	1	25.72	F (1, 147) = 8.598	P=0.0039
P treatment	168.4	1	168.4	F (1, 147) = 56.29	P<0.0001
Residual	439.8	147	2.992		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
wt:P+ vs. wt:P-	3.895	2.850 to 4.940	Yes	<0.0001
wt:P+ vs. bzr1:P+	0.9572	-0.07431 to 1.989	No	0.0793
wt:P+ vs. bzr1:P-	1.287	0.2489 to 2.325	Yes	0.0084
wt:P- vs. bzr1:P+	-2.938	-3.970 to -1.907	Yes	<0.0001
wt:P- vs. bzr1:P-	-2.609	-3.647 to -1.570	Yes	<0.0001
bzr1:P+ vs. bzr1:P-	0.3298	-0.6947 to 1.354	No	0.8370

C

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	7.722	0.0001	***	Yes	
Genotype	2.972	0.0146	*	Yes	
P treatment	17.43	<0.0001	****	Yes	
ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	265.9	1	265.9	F (1, 149) = 15.85	265.9
Genotype	102.3	1	102.3	F (1, 149) = 6.101	102.3
P treatment	600.0	1	600.0	F (1, 149) = 35.78	600.0
Residual	2499	149	16.77		2499

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
wt:P+ vs. wt:P-	-6.601	-9.074 to -4.127	Yes	<0.0001
wt:P+ vs. bzr1:P+	-1.002	-3.428 to 1.425	No	0.7070
wt:P+ vs. bzr1:P-	-2.326	-4.768 to 0.1153	No	0.0680
wt:P- vs. bzr1:P+	5.599	3.172 to 8.026	Yes	<0.0001
wt:P- vs. bzr1:P-	4.274	1.832 to 6.716	Yes	<0.0001
bzr1:P+ vs. bzr1:P-	-1.325	-3.719 to 1.069	No	0.4779

D

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	65.82	<0.0001	****	Yes	
Genotype	7.008	<0.0001	****	Yes	
P treatment	2.014	<0.0001	****	Yes	
ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	63.12	1	63.12	F (1, 779) = 2002	P<0.0001
Genotype	6.720	1	6.720	F (1, 779) = 213.2	P<0.0001
P treatment	1.931	1	1.931	F (1, 779) = 61.24	P<0.0001
Residual	24.56	779	0.03153		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	-0.6808	-0.7280 to -0.6337	Yes	<0.0001
M82:P+ vs. bzr1:P+	-0.7686	-0.8169 to -0.7202	Yes	<0.0001
M82:P+ vs. bzr1:P-	-0.2904	-0.3328 to -0.2481	Yes	<0.0001
M82:P- vs. bzr1:P+	-0.08773	-0.1392 to -0.0362	Yes	<0.0001
M82:P- vs. bzr1:P-	0.3904	0.3445 to 0.4363	Yes	<0.0001
bzr1:P+ vs. bzr1:P-	0.4781	0.4309 to 0.5253	Yes	<0.0001

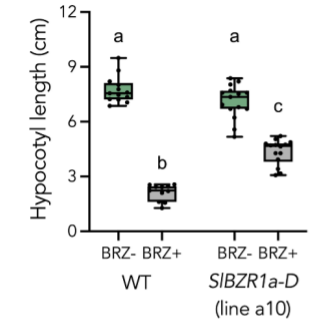
E

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	6.276	<0.0001	****	Yes	
Genotype	19.91	<0.0001	****	Yes	
P treatment	69.91	<0.0001	****	Yes	
ANOVA table	SS	DF	MS	F (DFn, DFd)	P value
Interaction	7416744	1	7416744	F (1, 96) = 154.4	P<0.0001
Genotype	23531910	1	23531910	F (1, 96) = 489.8	P<0.0001
P treatment	82621374	1	82621374	F (1, 96) = 1720	P<0.0001
Residual	4612413	96	48046		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	-1273	-1435 to -1111	Yes	<0.0001
M82:P+ vs. bzr1:P+	-425.5	-587.6 to -263.4	Yes	<0.0001
M82:P+ vs. bzr1:P-	-2788	-2950 to -2626	Yes	<0.0001
M82:P- vs. bzr1:P+	847.7	685.6 to 1010	Yes	<0.0001
M82:P- vs. bzr1:P-	-1515	-1677 to -1353	Yes	<0.0001
bzr1:P+ vs. bzr1:P-	-2363	-2525 to -2201	Yes	<0.0001

Supp. Fig 8: Statistical analysis of Figure 6. A) Figure 6 Panel A (hypocotyl length). **B)** Figure 6 Panel C (primary root length). **C)** Figure 6 Panel D (total lateral root length). **D)** Figure 6 Panel E (mature root hair length). **E)** Figure 6 Panel F (BCIP staining intensity).

A



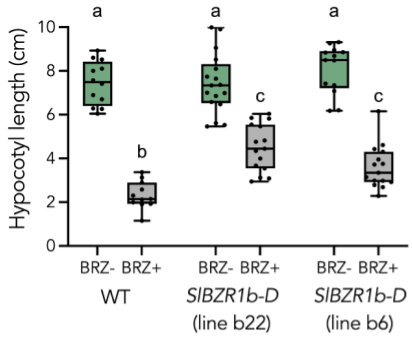
B

Source of Variation	% of total variation	P value	P value summary	Significant?
Interaction	9.768	<0.0001	****	Yes
Genotype	2.977	0.0003	***	Yes
BRZ treatment	83.39	<0.0001	****	Yes

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)
Interaction	26.75	1	26.75	F (1, 49) = 48.79
Genotype	8.153	1	8.153	F (1, 49) = 14.87
BRZ treatment	228.4	1	228.4	F (1, 49) = 416.5
Residual	26.87	49	0.5483	

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
WT:BRZ- vs. WT:BRZ+	5.610	4.803 to 6.417	Yes	<0.0001
WT:BRZ- vs. SlBZR1-D:BRZ-	0.6407	-0.1055 to 1.387	No	0.1159
WT:BRZ- vs. SlBZR1-D:BRZ+	3.390	2.631 to 4.148	Yes	<0.0001
WT:BRZ+ vs. SlBZR1-D:BRZ-	-4.969	-5.751 to -4.187	Yes	<0.0001
WT:BRZ+ vs. SlBZR1-D:BRZ+	-2.220	-3.013 to -1.427	Yes	<0.0001
SlBZR1-D:BRZ- vs. SlBZR1-D:BRZ+	2.749	2.017 to 3.481	Yes	<0.0001

C



D

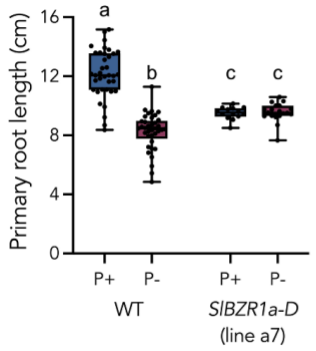
Source of Variation	% of total variation	P value	P value summary	Significant?
Interaction	3.889	0.0009	***	Yes
Genotype	3.781	0.0011	**	Yes
BRZ treatment	76.38	<0.0001	****	Yes

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)
Interaction	18.02	2	9.009	F (2, 77) = 7.721
Genotype	17.52	2	8.759	F (2, 77) = 7.507
BRZ treatment	353.9	1	353.9	F (1, 77) = 303.3
Residual	89.84	77	1.167	

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
WT:BRZ- vs. WT:BRZ+	5.123	3.805 to 6.440	Yes	<0.0001
WT:BRZ- vs. SlBZR1b-D b22:BRZ-	0.02487	-1.165 to 1.215	No	>0.9999
WT:BRZ- vs. SlBZR1b-D b22:BRZ+	2.947	1.725 to 4.170	Yes	<0.0001
WT:BRZ- vs. SlBZR1b-D b6:BRZ-	-0.6402	-1.904 to 0.6236	No	0.6776
WT:BRZ- vs. SlBZR1b-D b6:BRZ+	3.840	2.617 to 5.062	Yes	<0.0001
WT:BRZ+ vs. SlBZR1b-D b22:BRZ-	-5.098	-6.319 to -3.876	Yes	<0.0001
WT:BRZ+ vs. SlBZR1b-D b22:BRZ+	-2.175	-3.428 to -0.9220	Yes	<0.0001
WT:BRZ+ vs. SlBZR1b-D b6:BRZ-	-5.763	-7.056 to -4.469	Yes	<0.0001
WT:BRZ+ vs. SlBZR1b-D b6:BRZ+	-1.283	-2.536 to -0.02965	Yes	0.0417
SlBZR1b-D b22:BRZ- vs. SlBZR1b-D b22:BRZ+	2.923	1.804 to 4.041	Yes	<0.0001
SlBZR1b-D b22:BRZ- vs. SlBZR1b-D b6:BRZ-	-0.6651	-1.828 to 0.4981	No	0.5548
SlBZR1b-D b22:BRZ- vs. SlBZR1b-D b6:BRZ+	3.815	2.696 to 4.933	Yes	<0.0001
SlBZR1b-D b22:BRZ+ vs. SlBZR1b-D b6:BRZ-	-3.588	-4.784 to -2.391	Yes	<0.0001
SlBZR1b-D b22:BRZ+ vs. SlBZR1b-D b6:BRZ+	0.8923	-0.2605 to 2.045	No	0.2223
SlBZR1b-D b6:BRZ- vs. SlBZR1b-D b6:BRZ+	4.480	3.284 to 5.676	Yes	<0.0001

Supp. Fig. 9: BRZ treatment of second *Slbzr1a-D* independent line and *Slbzr1b-D* lines. A) Hypocotyl length of M82 WT and *Slbzr1a-D* line a10 upon BRZ treatment grown in dark for 7 days. **B)** Statistical analysis results of Panel A. **C)** Hypocotyl length of M82 WT and *Slbzr1b-D* lines b22 and b6 upon BRZ treatment grown in dark for 7 days. **D)** Statistical analysis results of Panel C.

A



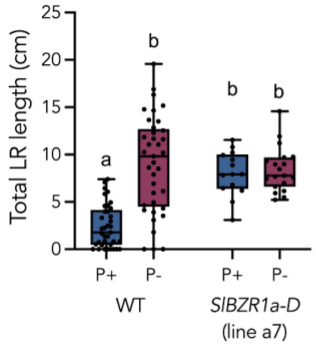
B

Source of Variation	% of total variation	P value	P value summary	Significant?
Interaction	19.20	<0.0001	****	Yes
Genotype	2.263	0.0124	*	Yes
P treatment	18.29	<0.0001	****	Yes

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)
Interaction	87.28	1	87.28	F (1, 103) = 55.00
Genotype	10.28	1	10.28	F (1, 103) = 6.481
P treatment	83.14	1	83.14	F (1, 103) = 52.39
Residual	163.5	103	1.587	

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
wt:P+ vs. wt:P-	3.895	3.131 to 4.660	Yes	<0.0001
wt:P+ vs. SlBZR1a-D a7:P+	2.648	1.616 to 3.680	Yes	<0.0001
wt:P+ vs. SlBZR1a-D a7:P-	2.601	1.672 to 3.529	Yes	<0.0001
wt:P- vs. SlBZR1a-D a7:P+	-1.247	-2.280 to -0.2151	Yes	0.0111
wt:P- vs. SlBZR1a-D a7:P-	-1.295	-2.223 to -0.3662	Yes	0.0024
SlBZR1a-D a7:P+ vs. SlBZR1a-D a7:P-	-0.04729	-1.206 to 1.111	No	0.9996

C



D

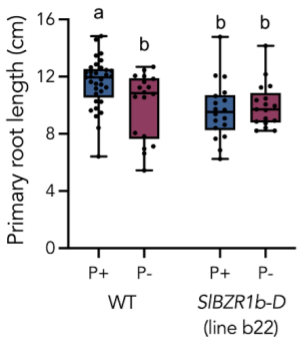
Source of Variation	% of total variation	P value	P value summary	Significant?
Interaction	9.586	<0.0001	****	Yes
Genotype	6.229	0.0012	**	Yes
P treatment	12.25	<0.0001	****	Yes

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)
Interaction	215.6	1	215.6	F (1, 103) = 17.14
Genotype	140.1	1	140.1	F (1, 103) = 11.14
P treatment	275.5	1	275.5	F (1, 103) = 21.90
Residual	1296	103	12.58	

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
wt:P+ vs. wt:P-	-6.601	-8.754 to -4.447	Yes	<0.0001
wt:P+ vs. SlBZR1a-D a7:P+	-5.596	-8.502 to -2.690	Yes	<0.0001
wt:P+ vs. SlBZR1a-D a7:P-	-6.000	-8.614 to -3.386	Yes	<0.0001
wt:P- vs. SlBZR1a-D a7:P+	1.005	-1.901 to 3.911	No	0.8032
wt:P- vs. SlBZR1a-D a7:P-	0.6007	-2.013 to 3.215	No	0.9318
SlBZR1a-D a7:P+ vs. SlBZR1a-D a7:P-	-0.4042	-3.666 to 2.858	No	0.9882

Supp. Fig. 10: RSA response of second *Slbzr1a-D* independent line (a7) to P-limiting conditions. A) Primary root length of M82 WT and *Slbzr1a-D* line a7 under P sufficiency or deficiency. **B)** Statistical analysis results of Panel A. **C)** Total lateral root length of M82 WT and *Slbzr1a-D* line a7 under P sufficiency or deficiency. **D)** Statistical analysis results of Panel C.

A



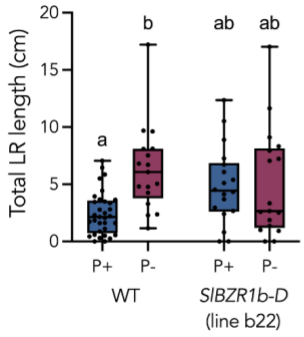
B

Source of Variation	% of total variation	P value	P value summary	Significant?
Interaction	5.066	0.0282	*	Yes
Genotype	5.404	0.0235	*	Yes
P treatment	2.050	0.1590	ns	No

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)
Interaction	18.14	1	18.14	F (1, 82) = 4.993
Genotype	19.35	1	19.35	F (1, 82) = 5.327
P treatment	7.340	1	7.340	F (1, 82) = 2.020
Residual	297.9	82	3.633	

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
WT:P+ vs. WT:P-	1.559	0.09445 to 3.024	Yes	0.0324
WT:P+ vs. SlBZR1b-D b22:P+	1.937	0.4725 to 3.402	Yes	0.0046
WT:P+ vs. SlBZR1b-D b22:P-	1.590	0.09814 to 3.083	Yes	0.0321
WT:P- vs. SlBZR1b-D b22:P+	0.3781	-1.288 to 2.044	No	0.9333
WT:P- vs. SlBZR1b-D b22:P-	0.03131	-1.659 to 1.722	No	>0.9999
SlBZR1b-D b22:P+ vs. SlBZR1b-D b22:P-	-0.3467	-2.037 to 1.344	No	0.9495

C



D

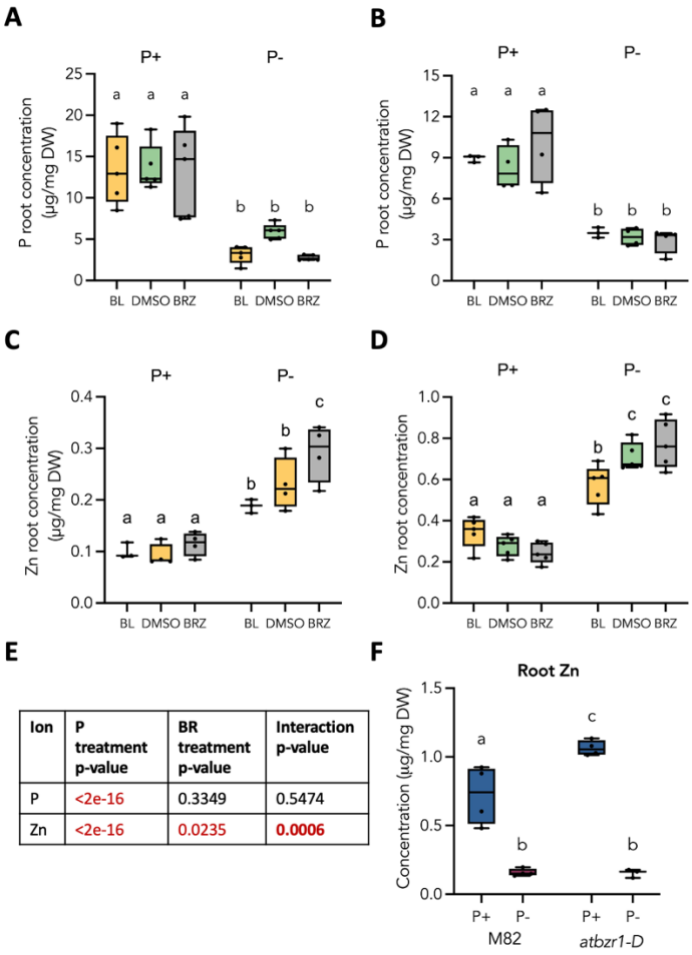
Source of Variation	% of total variation	P value	P value summary	Significant?
Interaction	6.486	0.0133	*	Yes
Genotype	0.5110	0.4792	ns	No
P treatment	7.154	0.0094	**	Yes

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)
Interaction	71.11	1	71.11	F (1, 81) = 6.413
Genotype	5.602	1	5.602	F (1, 81) = 0.5053
P treatment	78.43	1	78.43	F (1, 81) = 7.074
Residual	898.1	81	11.09	

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
WT:P+ vs. WT:P-	-3.900	-6.507 to -1.292	Yes	0.0010
WT:P+ vs. SlBZR1b-D b22:P+	-2.436	-4.995 to 0.1235	No	0.0680
WT:P+ vs. SlBZR1b-D b22:P-	-2.531	-5.139 to 0.07615	No	0.0603
WT:P- vs. SlBZR1b-D b22:P+	1.464	-1.490 to 4.418	No	0.5658
WT:P- vs. SlBZR1b-D b22:P-	1.368	-1.628 to 4.364	No	0.6299
SlBZR1b-D b22:P+ vs. SlBZR1b-D b22:P-	-0.09557	-3.050 to 2.858	No	0.9998

Supp. Fig. 11: RSA response of *Slbzr1b-D* line (b22) to P-limiting conditions. A) Primary root length of M82 WT and *Slbzr1b-D* line b22 under P sufficiency or deficiency. **B)** Statistical analysis results of Panel A. **C)** Total lateral root length of M82 WT and *Slbzr1b-D* line b22 under P sufficiency or deficiency. **D)** Statistical analysis results of Panel C.

Supp. Fig. 12: Amino acid sequence comparison of *Solyc12g089040* and *Solyc04g079980* with *S. pennellii* BZR1 orthologs shows no mutation in the predicted phosphorylation sites.



Ion	P treatment p-value	BR treatment p-value	Interaction p-value
P	<2e-16	0.3349	0.5474
Zn	<2e-16	0.0235	**0.0006**

Supp. Fig 13: Two additional replicates for M82 BL/BRZ treatment ICP-MS results. A) Second **B)** and third replicate for P root concentration. **C)** Second **D)** and third replicate for Zn root concentration. **E)** Three independent experiments (batches) were analyzed. Thus, to determine the effect of P treatment and BRZ or BL (BR) treatment on P and Zn concentrations in the root, mixed model analysis of variance (ANOVA) was performed with P, BR and their interaction as fixed factors and the batch as random factor, followed by Correction for multiple comparisons. Post-hoc analysis was performed using pairwise differences of LS-mean as implemented in the lmerTest R package. P-values are based on the t-distribution using degrees of freedom according to Satterthwaites method. P-values that passed correction for multiple comparisons using the False Discovery Rate procedure with alpha<0.05 are indicated by letters. F) Arabidopsis *atbzr1-D* accumulates Zn in P sufficient conditions compared to Col-0 wild-type.

A

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	0.05551	0.8495	ns	No	
Genotype	10.52	0.0204	*	Yes	
P treatment	71.69	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.01843	1	0.01843	F (1, 12) = 0.03757	P=0.8495
Genotype	3.494	1	3.494	F (1, 12) = 7.124	P=0.0204
P treatment	23.80	1	23.80	F (1, 12) = 48.53	P<0.0001
Residual	5.886	12	0.4905		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	2.507	0.9517 to 4.063	Yes	0.0017
M82:P+ vs. *bzr1*:P+	1.003	-0.5531 to 2.558	No	0.3352
M82:P+ vs. *bzr1*:P-	3.374	1.818 to 4.930	Yes	0.0001
M82:P- vs. *bzr1*:P+	-1.505	-3.060 to 0.05085	No	0.0602
M82:P- vs. *bzr1*:P-	0.8668	-0.6888 to 2.422	No	0.4880
bzr1:P+ vs. *bzr1*:P-	2.372	0.8159 to 3.927	Yes	0.0026

B

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	0.0001080	0.9803	ns	No	
Genotype	0.8588	0.0444	*	Yes	
P treatment	97.10	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	3.906e-005	1	3.906e-005	F (1, 12) = 0.0006342	P=0.9803
Genotype	0.3105	1	0.3105	F (1, 12) = 5.041	P=0.0444
P treatment	35.11	1	35.11	F (1, 12) = 570.0	P<0.0001
Residual	0.7392	12	0.06160		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	2.960	2.408 to 3.511	Yes	<0.0001
M82:P+ vs. *bzr1*:P+	0.2755	-0.2758 to 0.8268	No	0.6022
M82:P+ vs. *bzr1*:P-	3.241	2.690 to 3.793	Yes	<0.0001
M82:P- vs. *bzr1*:P+	-2.684	-3.235 to -2.133	Yes	<0.0001
M82:P- vs. *bzr1*:P-	0.2818	-0.2695 to 0.8330	No	0.5793
bzr1:P+ vs. *bzr1*:P-	2.966	2.414 to 3.517	Yes	<0.0001

C

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	4.459	0.1540	ns	No	
Genotype	6.667	0.0875	ns	No	
P treatment	65.76	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.009752	1	0.009752	F (1, 12) = 2.315	P=0.1540
Genotype	0.01458	1	0.01458	F (1, 12) = 3.461	P=0.0875
P treatment	0.1438	1	0.1438	F (1, 12) = 34.14	P<0.0001
Residual	0.05055	12	0.004212		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	-0.2390	-0.3832 to -0.09484	Yes	0.0013
M82:P+ vs. *bzr1*:P+	-0.1098	-0.2539 to 0.03441	No	0.1877
M82:P+ vs. *bzr1*:P-	-0.2500	-0.3942 to -0.1058	Yes	0.0009
M82:P- vs. *bzr1*:P+	0.1293	-0.01491 to 0.2734	No	0.0898
M82:P- vs. *bzr1*:P-	-0.01100	-0.1552 to 0.1332	No	>0.9999
bzr1:P+ vs. *bzr1*:P-	-0.1403	-0.2844 to 0.003913	No	0.0584

D

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	8.414	<0.0001	****	Yes	
Genotype	1.628	0.0091	**	Yes	
P treatment	87.93	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	3.136	1	3.136	F (1, 12) = 49.83	P<0.0001
Genotype	0.6068	1	0.6068	F (1, 12) = 9.640	P=0.0091
P treatment	32.78	1	32.78	F (1, 12) = 520.7	P<0.0001
Residual	0.7554	12	0.06295		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	-3.748	-4.305 to -3.191	Yes	<0.0001
M82:P+ vs. *bzr1*:P+	-0.4960	-1.053 to 0.06128	No	0.0932
M82:P+ vs. *bzr1*:P-	-2.473	-3.030 to -1.916	Yes	<0.0001
M82:P- vs. *bzr1*:P+	3.252	2.695 to 3.809	Yes	<0.0001
M82:P- vs. *bzr1*:P-	1.275	0.7177 to 1.832	Yes	<0.0001
bzr1:P+ vs. *bzr1*:P-	-1.977	-2.534 to -1.420	Yes	<0.0001

E

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	65.00	<0.0001	****	Yes	
Genotype	13.76	0.0161	*	Yes	
P treatment	0.1604	0.7677	ns	No	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.1206	1	0.1206	F (1, 12) = 37.01	P<0.0001
Genotype	0.02552	1	0.02552	F (1, 12) = 7.832	P=0.0161
P treatment	0.0002976	1	0.0002976	F (1, 12) = 0.09132	P=0.7677
Residual	0.03910	12	0.003258		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	-0.1650	-0.2918 to -0.03821	Yes	0.0090
M82:P+ vs. *bzr1*:P+	-0.2535	-0.3803 to -0.1267	Yes	0.0002
M82:P+ vs. *bzr1*:P-	-0.07125	-0.1980 to 0.05554	No	0.4789
M82:P- vs. *bzr1*:P+	-0.08850	-0.2153 to 0.03829	No	0.2592
M82:P- vs. *bzr1*:P-	0.09375	-0.03304 to 0.2205	No	0.2103
bzr1:P+ vs. *bzr1*:P-	0.1823	0.05546 to 0.3090	Yes	0.0042

F

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	81.53	<0.0001	****	Yes	
Genotype	1.686	0.1288	ns	No	
P treatment	9.174	0.0025	**	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	22.50	1	22.50	F (1, 12) = 128.7	P<0.0001
Genotype	0.4651	1	0.4651	F (1, 12) = 2.660	P=0.1288
P treatment	2.531	1	2.531	F (1, 12) = 14.48	P=0.0025
Residual	2.098	12	0.1749		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
M82:P+ vs. M82:P-	-1.576	-2.505 to -0.6472	Yes	0.0011
M82:P+ vs. *bzr1*:P+	-2.031	-2.959 to -1.102	Yes	0.0001
M82:P+ vs. *bzr1*:P-	1.137	0.2077 to 2.065	Yes	0.0139
M82:P- vs. *bzr1*:P+	-0.4545	-1.383 to 0.4743	No	0.6234
M82:P- vs. *bzr1*:P-	2.713	1.784 to 3.641	Yes	<0.0001
bzr1:P+ vs. *bzr1*:P-	3.167	2.238 to 4.096	Yes	<0.0001

Supp. Fig 14: Statistical analysis of Figure 7. A) Figure 7 Panel C (Root P). **B)** Figure 7 Panel D (Shoot P). **C)** Figure 7 Panel E (Root Fe). **D)** Figure 7 Panel F (Shoot Fe). **E)** Figure 7 Panel G (Root Zn). **F)** Figure 7 Panel H (Shoot Zn).

A

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	1.768	0.1072	ns	No	
Zn treatment	9.510	0.0003	***	Yes	
P treatment	24.53	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	40.08	1	40.08	F (1, 96) = 2.644	P=0.1072
Zn treatment	215.6	1	215.6	F (1, 96) = 14.22	P=0.0003
P treatment	556.2	1	556.2	F (1, 96) = 36.69	P<0.0001
Residual	1455	96	15.16		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
Zn+:P+ vs. Zn+:P-	5.983	3.103 to 8.862	Yes	<0.0001
Zn+:P+ vs. Zn-:P+	4.203	1.324 to 7.082	Yes	0.0014
Zn+:P+ vs. Zn-:P-	7.653	4.774 to 10.53	Yes	<0.0001
Zn+:P- vs. Zn-:P+	-1.780	-4.659 to 1.100	No	0.3745
Zn+:P- vs. Zn-:P-	1.671	-1.209 to 4.550	No	0.4314
Zn-:P+ vs. Zn-:P-	3.450	0.5711 to 6.330	Yes	0.0121

B

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	0.3818	0.4424	ns	No	
Zn treatment	2.446	0.0536	ns	No	
P treatment	27.54	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	7.477	1	7.477	F (1, 108) = 0.5945	P=0.4424
Zn treatment	47.91	1	47.91	F (1, 108) = 3.809	P=0.0536
P treatment	539.3	1	539.3	F (1, 108) = 42.88	P<0.0001
Residual	1358	108	12.58		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
Zn+:P+ vs. Zn+:P-	-3.874	-6.393 to -1.356	Yes	0.0006
Zn+:P+ vs. Zn-:P+	-0.7918	-3.267 to 1.683	No	0.8378
Zn+:P+ vs. Zn-:P-	-5.700	-8.175 to -3.225	Yes	<0.0001
Zn+:P- vs. Zn-:P+	3.083	0.6077 to 5.558	Yes	0.0083
Zn+:P- vs. Zn-:P-	-1.826	-4.301 to 0.6490	No	0.2236
Zn-:P+ vs. Zn-:P-	-4.909	-7.339 to -2.478	Yes	<0.0001

C

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	0.8841	0.0085	**	Yes	
Zn treatment	1.271	0.0016	**	Yes	
P treatment	47.76	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	0.8273	1	0.8273	F (1, 396) = 6.991	P=0.0085
Zn treatment	1.190	1	1.190	F (1, 396) = 10.05	P=0.0016
P treatment	44.69	1	44.69	F (1, 396) = 377.7	P<0.0001
Residual	46.87	396	0.1183		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
Zn+:P+ vs. Zn+:P-	-0.7595	-0.8850 to -0.6340	Yes	<0.0001
Zn+:P+ vs. M82:P+	0.01812	-0.1074 to 0.1436	No	0.9824
Zn+:P+ vs. M82:P-	-0.5595	-0.6850 to -0.4339	Yes	<0.0001
Zn+:P- vs. M82:P+	0.7776	0.6521 to 0.9031	Yes	<0.0001
Zn+:P- vs. M82:P-	0.2000	0.07451 to 0.3256	Yes	0.0003
M82:P+ vs. M82:P-	-0.5776	-0.7031 to -0.4521	Yes	<0.0001

D

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	0.8823	0.0108	*	Yes	
Zn treatment	0.4410	0.0690	ns	No	
P treatment	86.16	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	342260	1	342260	F (1, 96) = 6.765	P=0.0108
Zn treatment	171090	1	171090	F (1, 96) = 3.382	P=0.0690
P treatment	33422620	1	33422620	F (1, 96) = 660.6	P<0.0001
Residual	4856884	96	50593		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
Zn+:P+ vs. Zn+:P-	-1273	-1440 to -1107	Yes	<0.0001
Zn+:P+ vs. M82:P+	-34.28	-200.6 to 132.1	No	0.9493
Zn+:P+ vs. M82:P-	-1074	-1240 to -907.2	Yes	<0.0001
Zn+:P- vs. M82:P+	1239	1073 to 1405	Yes	<0.0001
Zn+:P- vs. M82:P-	199.7	33.39 to 366.1	Yes	0.0119
M82:P+ vs. M82:P-	-1039	-1206 to -872.9	Yes	<0.0001

E

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	7.709	0.0011	**	Yes	
Zn treatment	18.53	<0.0001	****	Yes	
P treatment	8.611	0.0006	***	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	137.7	1	137.7	F (1, 96) = 11.36	P=0.0011
Zn treatment	330.9	1	330.9	F (1, 96) = 27.30	P<0.0001
P treatment	153.8	1	153.8	F (1, 96) = 12.69	P=0.0006
Residual	1164	96	12.12		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
Zn+:P+ vs. Zn+:P-	0.1335	-2.441 to 2.708	No	0.9991
Zn+:P+ vs. Zn-:P+	1.291	-1.283 to 3.866	No	0.5579
Zn+:P+ vs. Zn-:P-	6.118	3.544 to 8.693	Yes	<0.0001
Zn+:P- vs. Zn-:P+	1.158	-1.417 to 3.732	No	0.6434
Zn+:P- vs. Zn-:P-	5.985	3.410 to 8.559	Yes	<0.0001
Zn-:P+ vs. Zn-:P-	4.827	2.252 to 7.401	Yes	<0.0001

F

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	7.535	0.0021	**	Yes	
Zn treatment	3.619	0.0314	*	Yes	
P treatment	6.568	0.0040	**	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	89.48	1	89.48	F (1, 108) = 9.901	P=0.0021
Zn treatment	42.98	1	42.98	F (1, 108) = 4.755	P=0.0314
P treatment	78.00	1	78.00	F (1, 108) = 8.630	P=0.0040
Residual	976.1	108	9.038		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
Zn+:P+ vs. Zn+:P-	0.1187	-1.997 to 2.235	No	0.9989
Zn+:P+ vs. Zn-:P+	0.5489	-1.549 to 2.647	No	0.9035
Zn+:P+ vs. Zn-:P-	-2.909	-5.025 to -0.7929	Yes	0.0028
Zn+:P- vs. Zn-:P+	0.4302	-1.648 to 2.509	No	0.9490
Zn+:P- vs. Zn-:P-	-3.028	-5.124 to -0.9309	Yes	0.0015
Zn-:P+ vs. Zn-:P-	-3.458	-5.536 to -1.379	Yes	0.0002

G

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	10.17	<0.0001	****	Yes	
Zn treatment	24.23	<0.0001	****	Yes	
P treatment	14.81	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	5.105	1	5.105	F (1, 396) = 79.35	P<0.0001
Zn treatment	12.16	1	12.16	F (1, 396) = 189.0	P<0.0001
P treatment	7.433	1	7.433	F (1, 396) = 115.5	P<0.0001
Residual	25.48	396	0.06433		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
Zn+:P+ vs. Zn+:P-	0.4986	0.4060 to 0.5911	Yes	<0.0001
Zn+:P+ vs. bzr1:P+	0.5746	0.4821 to 0.6672	Yes	<0.0001
Zn+:P+ vs. bzr1:P-	0.6213	0.5288 to 0.7139	Yes	<0.0001
Zn+:P- vs. bzr1:P+	0.07607	-0.01648 to 0.1686	No	0.1483
Zn+:P- vs. bzr1:P-	0.1228	0.03021 to 0.2153	Yes	0.0038
bzr1:P+ vs. bzr1:P-	0.04669	-0.04586 to 0.1392	No	0.5624

H

Source of Variation	% of total variation	P value	P value summary	Significant?	
Interaction	0.4573	0.0070	**	Yes	
Zn treatment	0.08228	0.2456	ns	No	
P treatment	93.67	<0.0001	****	Yes	

ANOVA table	SS (Type III)	DF	MS	F (DFn, DFd)	P value
Interaction	787479	1	787479	F (1, 96) = 7.584	P=0.0070
Zn treatment	141677	1	141677	F (1, 96) = 1.365	P=0.2456
P treatment	161300160	1	161300160	F (1, 96) = 1554	P<0.0001
Residual	9967504	96	103828		

Tukey's multiple comparisons	Predicted mean diff.	95.00% CI of diff.	Below threshold?	Adjusted P Value
Zn+:P+ vs. Zn+:P-	-2363	-2601 to -2124	Yes	<0.0001
Zn+:P+ vs. Zn-:P+	252.8	14.47 to 491.1	Yes	0.0332
Zn+:P+ vs. Zn-:P-	-2465	-2703 to -2227	Yes	<0.0001
Zn+:P- vs. Zn-:P+	2615	2377 to 2854	Yes	<0.0001
Zn+:P- vs. Zn-:P-	-102.2	-340.5 to 136.1	No	0.6773
Zn-:P+ vs. Zn-:P-	-2718	-2956 to -2479	Yes	<0.0001

Supp. Fig 15: Statistical analysis of Figure 8 of A) Primary root length **B)** Total lateral root length **C)** Mature root hair length and **D)** APase activity of M82 WT in P-sufficient or P-deficient conditions when Zn is present or absent. **E)** Primary root length **F)** Total lateral root length **G)** Mature root hair length and **H)** APase activity of *Slbzr1a-D* in P-sufficient or P-deficient conditions when Zn is present or absent.