

Appendix

Summary statistics for the transcript abundance of *COPT2* in the *copt2-1*, *copt2-2* and *copt2-3* lines are shown in Table S1, below, normalised to the wild-type (WT) expression level. The *copt2-2* had significantly higher expression of *COPT2* transcript compared to *copt2-3*, but there were no other significant differences noted following assessment using a Wilcoxon rank-sum test, shown in Table S2.

Table S1. Summary statistics of the *COPT2* transcript abundance in two-week old Arabidopsis rosette leaves from WT (Col0), *copt2-1*, *copt2-2* or *copt2-3*.

Line	Mean	Std	N	Se
Col0	1	-	-	-
<i>copt2-1</i>	0.4038	0.1772	5	0.0793
<i>copt2-2</i>	0.3871	0.0753	5	0.0337
<i>copt2-3</i>	0.2922	0.0422	5	0.0189

Table S2. Results of a Wilcoxon rank-sum test comparing the medians between the *COPT2* transcript abundance in the two-week old rosette tissue of Arabidopsis WT (Col0), *copt2-1*, *copt2-2* or *copt2-3*. Significance is denoted by: (*) $p < 0.05$; (**) $p < 0.01$; (***) $p < 0.001$.

Pairwise comparison	Col0	<i>copt2-1</i>	<i>copt2-2</i>
<i>copt2-1</i>	0.049 (*)	-	-
<i>copt2-2</i>	0.049 (*)	0.421	-
<i>copt2-3</i>	0.049 (*)	0.181	0.049 (*)

Root characterisation of *Arabidopsis COPT2* on Au

Arabidopsis WT and the three *copt2* genotypes were grown on undosed ½MS(A) plates, or plates containing a range of Cu or Au concentrations. Root architecture was calculated by dividing the number of lateral root branches by the root length to calculate the number of branches per mm of root. The summary statistics for the root length data are shown in Table S3, for the number of lateral root branches in Table S4, and for the root architecture in Table S5. Tests for homogeneity of variances and normal distributions were performed for each concentration tested (Levene's and Shapiro-Wilk test, respectively) and used to inform statistical analysis. Comparisons were made using a two-way ANOVA test to investigate whether the interaction of concentration and genotype influenced root length (Table S6), number of lateral root branches (Table S7) or root architecture (Table S8). All values were normalised to the 0 µM mean value to evaluate differences in the root phenotype in response to the metal treatment.

Table S3. Summary statistics of Arabidopsis root length of Col0 or *copt2* lines grown on Cu or Au (normalised to the mean value of each genotype at 0 uM)

Genotype	Condition	Concentration	Length	STD	N	SE
Col0	Cu	0	1	0.09	63	0.01
Col0	Cu	10	0.95	0.13	29	0.02
Col0	Cu	20	0.63	0.13	30	0.02
Col0	Cu	30	0.61	0.17	17	0.04
Col0	Cu	40	0.32	0.13	23	0.03
<i>copt2-1</i>	Cu	0	1	0.12	26	0.02
<i>copt2-1</i>	Cu	10	0.97	0.07	25	0.01
<i>copt2-1</i>	Cu	20	0.58	0.13	26	0.03
<i>copt2-1</i>	Cu	30	0.57	0.17	22	0.04
<i>copt2-1</i>	Cu	40	0.32	0.10	18	0.02
<i>copt2-2</i>	Cu	0	1	0.08	27	0.02
<i>copt2-2</i>	Cu	10	0.96	0.10	30	0.02
<i>copt2-2</i>	Cu	20	0.64	0.10	30	0.02
<i>copt2-2</i>	Cu	30	0.55	0.14	26	0.03
<i>copt2-2</i>	Cu	40	0.39	0.10	23	0.02
<i>copt2-3</i>	Cu	0	-0.05	7.16	26	1.40
<i>copt2-3</i>	Cu	10	4.58	10.53	24	2.15
<i>copt2-3</i>	Cu	20	-24.32	9.66	25	1.93
<i>copt2-3</i>	Cu	30	-28.31	13.53	23	2.82
<i>copt2-3</i>	Cu	40	-41.63	8.93	11	2.69
Col0	Au	0	0.99	0.09	50	0.01
Col0	Au	100	0.79	0.09	60	0.01
Col0	Au	150	0.55	0.09	52	0.01
Col0	Au	200	0.36	0.06	54	0.01
Col0	Au	50	0.70	0.12	56	0.02
<i>copt2-1</i>	Au	0	1	0.12	26	0.02
<i>copt2-1</i>	Au	100	0.76	0.08	26	0.01
<i>copt2-1</i>	Au	150	0.54	0.07	27	0.01
<i>copt2-1</i>	Au	200	0.33	0.05	21	0.01
<i>copt2-1</i>	Au	50	0.50	0.14	27	0.03
<i>copt2-2</i>	Au	0	1	0.08	27	0.02
<i>copt2-2</i>	Au	100	0.78	0.07	25	0.01
<i>copt2-2</i>	Au	150	0.53	0.08	23	0.02
<i>copt2-2</i>	Au	200	0.39	0.07	25	0.01
<i>copt2-2</i>	Au	50	0.67	0.11	28	0.02
<i>copt2-3</i>	Au	0	1	0.10	27	0.02
<i>copt2-3</i>	Au	100	0.78	0.07	26	0.01
<i>copt2-3</i>	Au	150	0.55	0.08	28	0.02
<i>copt2-3</i>	Au	200	0.42	0.06	27	0.01
<i>copt2-3</i>	Au	50	0.67	0.08	27	0.02

Table S4. Summary statistics of the number of lateral root branches of Arabidopsis Col0 or *copt2* lines grown on Cu or Au (normalised to the mean value of each genotype at 0 uM)

Genotype	Condition	Concentration	Number of lateral root branches	STD	n	SE
Col0	Cu	0	1.00	0.58	63	0.07
<i>copt2-1</i>	Cu	0	1.00	0.50	26	0.10
<i>copt2-2</i>	Cu	0	1.00	0.52	27	0.10
<i>copt2-3</i>	Cu	0	1.00	0.44	26	0.09
Col0	Cu	10	1.00	0.33	29	0.06
<i>copt2-1</i>	Cu	10	1.09	0.38	25	0.08
<i>copt2-2</i>	Cu	10	1.46	0.47	30	0.09
<i>copt2-3</i>	Cu	10	1.21	0.34	24	0.07
Col0	Cu	20	0.22	0.15	30	0.03
<i>copt2-1</i>	Cu	20	0.21	0.14	26	0.03
<i>copt2-2</i>	Cu	20	0.35	0.22	30	0.04
<i>copt2-3</i>	Cu	20	0.24	0.19	25	0.04
Col0	Cu	30	0.21	0.12	17	0.03
<i>copt2-1</i>	Cu	30	0.15	0.11	22	0.02
<i>copt2-2</i>	Cu	30	0.21	0.16	26	0.03
<i>copt2-3</i>	Cu	30	0.18	0.12	23	0.03
Col0	Cu	40	0.10	0.04	23	0.01
<i>copt2-1</i>	Cu	40	0.10	0.00	18	0.00
<i>copt2-2</i>	Cu	40	0.10	0.00	23	0.00
<i>copt2-3</i>	Cu	40	0.09	0.00	11	0.00
Col0	Au	0	1.00	0.55	38	0.08
Col0	Au	100	0.59	0.47	60	0.06
Col0	Au	150	0.40	0.33	52	0.05
Col0	Au	200	0.29	0.23	54	0.03
Col0	Au	50	0.62	0.47	56	0.06
<i>copt2-1</i>	Au	0	1.00	0.50	26	0.10
<i>copt2-1</i>	Au	100	0.99	0.30	26	0.06
<i>copt2-1</i>	Au	150	0.68	0.25	27	0.05
<i>copt2-1</i>	Au	200	0.39	0.12	21	0.03
<i>copt2-1</i>	Au	50	0.45	0.22	27	0.04
<i>copt2-2</i>	Au	0	1.00	0.52	27	0.10
<i>copt2-2</i>	Au	100	1.05	0.52	25	0.10
<i>copt2-2</i>	Au	150	0.63	0.24	23	0.05
<i>copt2-2</i>	Au	200	0.61	0.32	25	0.06
<i>copt2-2</i>	Au	50	0.83	0.41	28	0.08
<i>copt2-3</i>	Au	0	1.00	0.43	27	0.08
<i>copt2-3</i>	Au	100	0.92	0.29	26	0.06
<i>copt2-3</i>	Au	150	0.69	0.22	28	0.04
<i>copt2-3</i>	Au	200	0.52	0.22	27	0.04
<i>copt2-3</i>	Au	50	0.75	0.27	27	0.05

Table S5. Summary statistics of the root architecture of Arabidopsis Col0 or *copt2* lines (number of branches per mm of root length) grown on Cu or Au (normalised to the mean value of each genotype at 0 uM)

Genotype	Condition	Concentration	Architecture	STD	n	SE
Col0	Cu	0	0.99	0.56	63	0.07
<i>copt2-1</i>	Cu	0	1.01	0.48	26	0.10
<i>copt2-2</i>	Cu	0	1.00	0.53	27	0.10
<i>copt2-3</i>	Cu	0	1.01	0.46	26	0.09
Col0	Cu	10	1.06	0.33	29	0.06
<i>copt2-1</i>	Cu	10	1.14	0.43	25	0.09
<i>copt2-2</i>	Cu	10	1.52	0.46	30	0.08
<i>copt2-3</i>	Cu	10	1.16	0.36	24	0.07
Col0	Cu	20	0.34	0.18	30	0.03
<i>copt2-1</i>	Cu	20	0.36	0.19	26	0.04
<i>copt2-2</i>	Cu	20	0.54	0.29	30	0.05
<i>copt2-3</i>	Cu	20	0.38	0.29	25	0.06
Col0	Cu	30	0.35	0.18	17	0.04
<i>copt2-1</i>	Cu	30	0.30	0.22	22	0.05
<i>copt2-2</i>	Cu	30	0.40	0.29	26	0.06
<i>copt2-3</i>	Cu	30	0.33	0.23	23	0.05
Col0	Cu	40	0.37	0.13	23	0.03
<i>copt2-1</i>	Cu	40	0.33	0.09	18	0.02
<i>copt2-2</i>	Cu	40	0.27	0.07	23	0.01
<i>copt2-3</i>	Cu	40	0.23	0.08	11	0.02
Col0	Au	0	1.00	0.54	38	0.09
<i>copt2-1</i>	Au	0	1.01	0.48	26	0.10
<i>copt2-2</i>	Au	0	1.00	0.53	27	0.10
<i>copt2-3</i>	Au	0	1.01	0.45	27	0.09
Col0	Au	50	0.87	0.66	56	0.09
<i>copt2-1</i>	Au	50	0.92	0.41	27	0.08
<i>copt2-2</i>	Au	50	1.26	0.72	28	0.14
<i>copt2-3</i>	Au	50	1.12	0.38	27	0.07
Col0	Au	100	0.73	0.57	60	0.07
<i>copt2-1</i>	Au	100	1.30	0.35	26	0.07
<i>copt2-2</i>	Au	100	1.32	0.64	25	0.13
<i>copt2-3</i>	Au	100	1.18	0.35	26	0.07
Col0	Au	150	0.72	0.57	52	0.08
<i>copt2-1</i>	Au	150	1.24	0.40	27	0.08
<i>copt2-2</i>	Au	150	1.16	0.39	23	0.08
<i>copt2-3</i>	Au	150	1.27	0.35	28	0.07
Col0	Au	200	0.78	0.59	54	0.08
<i>copt2-1</i>	Au	200	1.19	0.29	21	0.06
<i>copt2-2</i>	Au	200	1.51	0.65	25	0.13
<i>copt2-3</i>	Au	200	1.22	0.47	27	0.09

Table S6. Two-way ANOVA analysis results on root length of Col0 and *copt2* lines in the presence of Au. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Within condition, between genotype							
Concentration 1	Genotype 1	Concentration 2	Genotype 2	Diff	Lwr	Upr	p-value
50	<i>copt2-1</i>	50	Col0	- 0.199	- 0.275	- 0.123	0.000
Within genotype, between condition							
50	Col0	0	Col0	- 0.294	- 0.357	- 0.231	0.000
100	Col0	0	Col0	- 0.203	- 0.265	- 0.141	0.000
150	Col0	0	Col0	- 0.440	- 0.504	- 0.376	0.000
200	Col0	0	Col0	- 0.635	- 0.698	- 0.572	0.000
100	Col0	50	Col0	0.091	0.031	0.151	0.000
150	Col0	50	Col0	- 0.146	- 0.208	- 0.084	0.000
200	Col0	50	Col0	- 0.341	- 0.402	- 0.279	0.000
150	Col0	100	Col0	- 0.237	- 0.298	- 0.176	0.000
200	Col0	100	Col0	- 0.432	- 0.492	- 0.371	0.000
200	Col0	150	Col0	- 0.195	- 0.257	- 0.132	0.000
50	<i>copt2-1</i>	0	<i>copt2-1</i>	- 0.499	- 0.588	- 0.410	0.000
100	<i>copt2-1</i>	0	<i>copt2-1</i>	- 0.240	- 0.330	- 0.150	0.000
150	<i>copt2-1</i>	0	<i>copt2-1</i>	- 0.460	- 0.549	- 0.371	0.000
200	<i>copt2-1</i>	0	<i>copt2-1</i>	- 0.672	- 0.767	- 0.577	0.000
100	<i>copt2-1</i>	50	<i>copt2-1</i>	0.259	0.170	0.348	0.000
200	<i>copt2-1</i>	50	<i>copt2-1</i>	- 0.173	- 0.267	- 0.079	0.000
150	<i>copt2-1</i>	100	<i>copt2-1</i>	- 0.220	- 0.309	- 0.131	0.000
200	<i>copt2-1</i>	100	<i>copt2-1</i>	- 0.432	- 0.527	- 0.337	0.000
200	<i>copt2-1</i>	150	<i>copt2-1</i>	- 0.212	- 0.306	- 0.118	0.000
50	<i>copt2-2</i>	0	<i>copt2-2</i>	- 0.329	- 0.416	- 0.242	0.000
100	<i>copt2-2</i>	0	<i>copt2-2</i>	- 0.216	- 0.305	- 0.126	0.000
150	<i>copt2-2</i>	0	<i>copt2-2</i>	- 0.466	- 0.557	- 0.374	0.000
200	<i>copt2-2</i>	0	<i>copt2-2</i>	- 0.609	- 0.699	- 0.520	0.000
100	<i>copt2-2</i>	50	<i>copt2-2</i>	0.114	0.025	0.203	0.001
150	<i>copt2-2</i>	50	<i>copt2-2</i>	- 0.137	- 0.227	- 0.046	0.000
200	<i>copt2-2</i>	50	<i>copt2-2</i>	- 0.280	- 0.369	- 0.191	0.000
150	<i>copt2-2</i>	100	<i>copt2-2</i>	- 0.250	- 0.344	- 0.157	0.000
200	<i>copt2-2</i>	100	<i>copt2-2</i>	- 0.394	- 0.485	- 0.302	0.000

200	<i>copt2-2</i>	150	<i>copt2-2</i>	-	-	-	0.000
				0.143	0.237	0.050	
50	<i>copt2-3</i>	0	<i>copt2-3</i>	-	-	-	0.000
				0.325	0.413	0.237	
100	<i>copt2-3</i>	0	<i>copt2-3</i>	-	-	-	0.000
				0.217	0.306	0.128	
150	<i>copt2-3</i>	0	<i>copt2-3</i>	-	-	-	0.000
				0.454	0.541	0.367	
200	<i>copt2-3</i>	0	<i>copt2-3</i>	-	-	-	0.000
				0.580	0.668	0.492	
100	<i>copt2-3</i>	50	<i>copt2-3</i>	0.108	0.019	0.197	0.003
150	<i>copt2-3</i>	50	<i>copt2-3</i>	-	-	-	0.000
				0.129	0.216	0.041	
200	<i>copt2-3</i>	50	<i>copt2-3</i>	-	-	-	0.000
				0.255	0.342	0.167	
150	<i>copt2-3</i>	100	<i>copt2-3</i>	-	-	-	0.000
				0.237	0.325	0.149	
200	<i>copt2-3</i>	100	<i>copt2-3</i>	-	-	-	0.000
				0.363	0.451	0.274	
200	<i>copt2-3</i>	150	<i>copt2-3</i>	-	-	-	0.000
				0.126	0.213	0.039	

Table S7. Two-way ANOVA analysis results on number of lateral root branches of Col0 and *copt2* lines in the presence of Au. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotype							
100	COPT21	100	Col0	0.4018	0.0861	0.7175	0.0012
100	COPT22	100	Col0	0.4570	0.1369	0.7770	0.0001
Within genotype, between condition							
50	Col0	0	Col0	-0.3829	-0.6655	-0.1003	0.0003
100	Col0	0	Col0	-0.4090	-0.6877	-0.1302	0.0000
150	Col0	0	Col0	-0.5965	-0.8834	-0.3095	0.0000
200	Col0	0	Col0	-0.7120	-0.9967	-0.4273	0.0000
200	Col0	50	Col0	-0.3291	-0.5855	-0.0726	0.0010
200	Col0	100	Col0	-0.3030	-0.5552	-0.0508	0.0036
50	COPT21	0	COPT21	-0.5509	-0.9203	-0.1814	0.0000
200	COPT21	0	COPT21	-0.6059	-1.0004	-0.2114	0.0000
100	COPT21	50	COPT21	0.5435	0.1740	0.9129	0.0000
200	COPT21	100	COPT21	-0.5985	-0.9930	-0.2040	0.0000
150	COPT22	100	COPT22	-0.4193	-0.8078	-0.0308	0.0191
200	COPT22	100	COPT22	-0.4403	-0.8205	-0.0600	0.0067
200	COPT23	0	COPT23	-0.4833	-0.8492	-0.1173	0.0006
200	COPT23	100	COPT23	-0.4059	-0.7753	-0.0365	0.0149

Table S8. Two-way ANOVA analysis results on the root architecture of Col0 and *copt2* lines in the presence of Au. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
100	<i>COPT21</i>	100	Col0	0.57	0.13	1.01	0.00
100	<i>COPT22</i>	100	Col0	0.59	0.15	1.04	0.00
150	<i>COPT21</i>	150	Col0	0.53	0.08	0.97	0.00
150	<i>COPT23</i>	150	Col0	0.55	0.12	0.99	0.00
200	<i>COPT22</i>	200	Col0	0.72	0.27	1.18	0.00
Within genotype, between conditions							
No significant differences							

Analysis of element uptake in *Arabidopsis copt2* grown in the presence of Au

To analyse the concentration of Au, Fe and Cu in the shoot or root tissues of five-week-old hydroponically grown *Arabidopsis* WT, *copt2-1*, *copt2-2* and *copt2-3* plants, analysis was performed using ICP-OES normalised to dry weight (g). Tests for homogeneity and normal distribution were performed on the concentration data (Table S9). Comparisons were made using a one-way ANOVA (for data that fit the assumptions) or a Kruskal-Wallis test (the non-parametric alternative) (Table S10), post-hoc tests were used to determine the direction of any significant differences (Table S11).

Table S9. Results of the Levene's and Shapiro Wilk tests for homogeneity of variance and normal distribution, respectively, on element concentration data from five-week-old shoot and root tissue of Arabidopsis WT, *copt2-1*, *copt2-2* or *copt2-3* grown in a hydroponic system dosed with Au

Tissue	Element (nm)	Test	p-value	Test stat	Stats test to use
Shoot	Au (242)	Levene's	> 0.05	1.9501	one-way ANOVA
Shoot	Au (242)	Shapiro-Wilk	> 0.05	0.909	one-way ANOVA
Shoot	Au (267)	Levene's	> 0.05	1.7757	one-way ANOVA
Shoot	Au (267)	Shapiro-Wilk	> 0.05	0.9988	one-way ANOVA
Shoot	Cu (324)	Levene's	> 0.05	1.1831	one-way ANOVA
Shoot	Cu (324)	Shapiro-Wilk	> 0.05	0.9461	one-way ANOVA
Shoot	Fe (239)	Levene's	> 0.05	0.5757	Kruksal-Wallis
Shoot	Fe (239)	Shapiro-Wilk	< 0.05	0.7324	Kruksal-Wallis
Root	Au (267)	Levene's	> 0.05	0.7176	one-way ANOVA
Root	Au (267)	Shapiro-Wilk	> 0.05	0.9467	one-way ANOVA
Root	Cu (324)	Levene's	> 0.05	0.0575	one-way ANOVA
Root	Cu (324)	Shapiro-Wilk	> 0.05	0.9678	one-way ANOVA
Root	Fe (239)	Levene's	> 0.05	0.2539	one-way ANOVA
Root	Fe (239)	Shapiro-Wilk	> 0.05	0.9502	one-way ANOVA

Table S10. Results of ANOVA tests on element concentration data from five-week-old shoot and root tissue of Arabidopsis WT, *copt2-1*, *copt2-2* or *copt2-3* grown in a hydroponic system dosed with Au. Significant results were further examined by a Tukey's HSD test.

Tissue	Element (nm)	Test	Test value	d.f.	p-value	sig
Shoot	Au (242)	one-way ANOVA	3.378	3, 14	< 0.05	*
Shoot	Au (267)	one-way ANOVA	2.577	3, 14	> 0.05	ns
Shoot	Cu (324)	one-way ANOVA	12.96	3, 16	< 0.05	*
Shoot	Fe (239)	Kruskal-Wallis	4.3486	3, 14	> 0.05	ns
Root	Au (267)	one-way ANOVA	2.068	3, 16	> 0.05	ns
Root	Cu (324)	one-way ANOVA	10.78	3, 14	< 0.05	*
Root	Fe (239)	one-way ANOVA	1.639	3, 14	> 0.05	Ns

Table S11. Significant results of Tukey's HSD tests on element concentration data from five-week-old shoot and root tissue of *Arabidopsis* WT, *copt2-1*, *copt2-2* or *copt2-3* grown in a hydroponic system dosed with Au.

Tissue	Element (nm)	Pairwise comparison	Difference	Lower limit	Upper limit	p-value	sig
Shoot	Au (242)	<i>copt2-2</i> : Col0	0.1872	0.0136	0.3607	< 0.05	*
Shoot	Cu (324)	<i>copt2-2</i> : Col0	0.1162	0.0377	0.1946	< 0.01	**
Shoot	Cu (324)	<i>copt2-3</i> : Col0	0.1336	0.0551	0.212	< 0.001	***
Root	Cu (324)	<i>copt2-1</i> : Col0	0.285	0.1058	0.4641	< 0.01	**
Root	Cu (324)	<i>copt2-2</i> : Col0	0.3106	0.1314	0.4898	< 0.001	***
Root	Cu (324)	<i>copt2-3</i> : Col0	0.3108	0.1316	0.49	< 0.001	***

Measurements of ROS accumulation in Arabidopsis WT and *COPT2*

To investigate the effect further, the fluorescent indicator H₂DCFDA was used to visualise the presence of ROS in response to metal treatment. Roots were submerged in Cu or Au (25 µM Cu; 25 µM or 50 µM Au), then treated with H₂DCF for 30 minutes. Samples were exposed to peroxides in the root tissue and the fluorescence signal measured by epifluorescence microscopy. ImageJ was used to quantify the fluorescence. Fluorescence was quantified on a minimum of three images from the untreated, 30 µM Cu, and 25 µM Au conditions. There were significant differences between the Untreated and Au-treated conditions (Tukey's HSD test: p-value < 0.05), and between the Au- and Cu-treated conditions (p-value < 0.05) (Table S12).

Table S12. Significant results of a Tukey's HSD multiple comparisons test on the outcome of a two-way ANOVA on the interaction of genotype and treatment, genotype, or treatment on the CTCF value in the root tips of Arabidopsis following metal treatment (Cu or Au). Signif. codes: (***) 0.001, (**) 0.01, (*) 0.05

Comparison					
Treatment					
Comparison	Difference	Lower	Upper	p-value	Sig
Au-Untreated	1.0418	0.0619	2.0216	0.0367	*
Au-Cu	1.078	0.1614	1.9946	0.0209	*
Treatment:Condition					
Comparison	Difference	Lower	Upper	p-value	Sig
Au:Col0 - Untreated:Col0	1.9468	0.2103	3.6834	0.0243	*
Au:Col0 - Cu:Col0	1.6569	0.0325	3.2813	0.0444	*

Investigating *COPT2* expression in Arabidopsis 35S-*COPT2* lines by qPCR

To monitor expression of *optCOPT2* qPCR was performed using the previously characterised C2Ds1 primers on *copt2-1*, *copt2-2* or *copt2-3* cDNA from soil. A Tukey's HSD test was performed to identify the direction of the significant differences (Table S13).

Table S13. Significant results of the Tukey's HSD test on the results of one-way ANOVA on the level of *COPT2* expression in Arabidopsis Col0, 35S-*COPT2A*, 35S-*COPT2B*, 35S-*COPT2C*

Comparison	Difference	Lower	Upper	Adjusted P value	Sig
35S- <i>COPT2A</i> : Col0	22,752	-4,498	50,003	0.0000	***
35S- <i>COPT2B</i> : Col0	67,663	39,990	95,337	0.0000	***
35S- <i>COPT2C</i> : Col0	99,56	-17,294	37,207	0.0000	***

Root characterisation using three Arabidopsis 35S-COPT2 genotypes on Cu and Au

To examine whether increased expression of Arabidopsis *COPT2* changes the phenotypic response of plants to Au, the 35S-*COPT2* overexpression lines and WT, were grown on $\frac{1}{2}$ MS(A) media containing a range of Cu or Au concentrations, and the primary root length, number of lateral root branches and root architecture investigated. The summary statistics for root length are shown in Table S14, number of lateral root branches in Table S15 or the root architecture in Table S16. The two-way ANOVA test results for root length (Table S17), number of lateral root branches (Table S18) or the root architecture (Table S19) were performed with a more conservative test statistic ($p = 0.02$).

Table S14. Summary statistics of the root length on Au (normalised to the mean value of each Analysis of element uptake in three Arabidopsis 35S-COPT2 genotypes grown in the presence of Au genotype at 0 uM

Genotype	Condition	Conc	Root length	STD	n	SE
Col0	Au	0	0.99	0.08	38	0.01
35S-COPT2A	Au	0	1.00	0.16	32	0.03
35S-COPT2B	Au	0	1.00	0.16	31	0.03
35S-COPT2C	Au	0	1.00	0.24	40	0.04
Col0	Au	50	0.70	0.12	56	0.02
35S-COPT2A	Au	50	1.01	0.19	40	0.03
35S-COPT2B	Au	50	0.67	0.33	39	0.05
35S-COPT2C	Au	50	0.72	0.29	43	0.04
Col0	Au	100	0.79	0.09	60	0.01
35S-COPT2A	Au	100	0.65	0.31	39	0.05
35S-COPT2B	Au	100	0.50	0.29	33	0.05
35S-COPT2C	Au	100	0.45	0.20	45	0.03
Col0	Au	150	0.55	0.09	52	0.01
35S-COPT2A	Au	150	0.62	0.23	41	0.04
35S-COPT2B	Au	150	0.48	0.19	37	0.03
35S-COPT2C	Au	150	0.39	0.18	45	0.03
Col0	Au	200	0.36	0.06	54	0.01
35S-COPT2A	Au	200	0.52	0.24	31	0.04
35S-COPT2B	Au	200	0.38	0.22	52	0.03
35S-COPT2C	Au	200	0.32	0.19	37	0.03

Table S15. Summary statistics of the number of lateral root on Au (normalised to the mean value of each genotype at 0 uM) of Arabidopsis Col0 or 35S-COPT2 genotypes

Genotype	Condition	Conc	Lateral root branches	STD	n	SE
Col0	Au	0	1.00	0.55	38	0.09
35S-COPT2A	Au	0	1.00	0.37	14	0.10
35S-COPT2B	Au	0	1.00	0.38	31	0.07
35S-COPT2C	Au	0	1.00	0.92	30	0.17
Col0	Au	50	0.62	0.47	56	0.06
35S-COPT2A	Au	50	1.03	0.59	12	0.17
35S-COPT2B	Au	50	0.22	0.16	39	0.03
35S-COPT2C	Au	50	1.14	1.10	43	0.17
Col0	Au	100	0.59	0.47	60	0.06
35S-COPT2A	Au	100	0.35	0.26	39	0.04
35S-COPT2B	Au	100	0.23	0.16	33	0.03
35S-COPT2C	Au	100	0.56	0.27	45	0.04
Col0	Au	150	0.40	0.33	52	0.05
35S-COPT2A	Au	150	0.34	0.29	41	0.05
35S-COPT2B	Au	150	0.20	0.12	37	0.02
35S-COPT2C	Au	150	0.52	0.21	45	0.03
Col0	Au	200	0.29	0.23	54	0.03
35S-COPT2A	Au	200	0.26	0.20	31	0.04
35S-COPT2B	Au	200	0.15	0.19	52	0.03
35S-COPT2C	Au	200	0.63	0.34	37	0.06

Table S16. Summary statistics of the root architecture (normalised to the mean value of each genotype at 0 μ M) of Arabidopsis Col0 or 35S-COPT2 genotypes on Au

Genotype	Condition	Concentration	Architecture	STD	n	SE
Col0	Au	0	1.00	0.54	38	0.09
35S-COPT2A	Au	0	1.11	0.52	14	0.14
35S-COPT2B	Au	0	1.03	0.43	31	0.08
35S-COPT2C	Au	0	1.06	0.97	30	0.18
Col0	Au	50	0.87	0.66	56	0.09
35S-COPT2A	Au	50	1.04	0.60	12	0.17
35S-COPT2B	Au	50	0.29	0.19	35	0.03
35S-COPT2C	Au	50	2.66	4.12	43	0.63
Col0	Au	100	0.73	0.57	60	0.07
35S-COPT2A	Au	100	0.45	0.31	34	0.05
35S-COPT2B	Au	100	0.59	0.75	28	0.14
35S-COPT2C	Au	100	1.71	2.29	43	0.35
Col0	Au	150	0.72	0.57	52	0.08
35S-COPT2A	Au	150	0.55	0.45	38	0.07
35S-COPT2B	Au	150	0.55	0.47	37	0.08
35S-COPT2C	Au	150	2.06	2.05	45	0.31
Col0	Au	200	0.78	0.59	54	0.08
35S-COPT2A	Au	200	0.50	0.38	28	0.07
35S-COPT2B	Au	200	0.48	0.68	52	0.09
35S-COPT2C	Au	200	2.39	2.29	32	0.41

Table S17. Two-way ANOVA analysis results on the root length of Col0 and 35S-COPT2 genotypes in the presence of Au. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
50	35S-COPT2A	50	Col0	0.3134	0.1652	0.4616	0.0000
100	35S-COPT2B	100	Col0	-0.2921	-0.4472	-0.1369	0.0000
100	35S-COPT2C	100	Col0	-0.3433	-0.4844	-0.2021	0.0000
150	35S-COPT2C	150	Col0	-0.1626	-0.3083	-0.0168	0.0119
Within genotype, between conditions							
50	Col0	0	Col0	-0.2923	-0.4427	-0.1418	0.0000
100	Col0	0	Col0	-0.2014	-0.3498	-0.0530	0.0003
150	Col0	0	Col0	-0.4385	-0.5913	-0.2857	0.0000
200	Col0	0	Col0	-0.6332	-0.7847	-0.4816	0.0000
200	Col0	50	Col0	-0.3409	-0.4774	-0.2044	0.0000
150	Col0	100	Col0	-0.2371	-0.3728	-0.1015	0.0000
200	Col0	100	Col0	-0.4318	-0.5661	-0.2975	0.0000
200	Col0	150	Col0	-0.1947	-0.3337	-0.0556	0.0001
100	35S-COPT2A	0	35S-COPT2A	-0.3550	-0.5257	-0.1842	0.0000
150	35S-COPT2A	0	35S-COPT2A	-0.3790	-0.5478	-0.2101	0.0000
200	35S-COPT2A	0	35S-COPT2A	-0.4779	-0.6583	-0.2975	0.0000
100	35S-COPT2A	50	35S-COPT2A	-0.3685	-0.5296	-0.2074	0.0000
150	35S-COPT2A	50	35S-COPT2A	-0.3925	-0.5516	-0.2334	0.0000
200	35S-COPT2A	50	35S-COPT2A	-0.4914	-0.6627	-0.3201	0.0000
50	35S-COPT2B	0	35S-COPT2B	-0.3276	-0.4999	-0.1554	0.0000
100	35S-COPT2B	0	35S-COPT2B	-0.5012	-0.6802	-0.3221	0.0000
150	35S-COPT2B	0	35S-COPT2B	-0.5218	-0.6961	-0.3475	0.0000
200	35S-COPT2B	0	35S-COPT2B	-0.6176	-0.7801	-0.4552	0.0000
150	35S-COPT2B	50	35S-COPT2B	-0.1941	-0.3584	-0.0298	0.0047
200	35S-COPT2B	50	35S-COPT2B	-0.2900	-0.4416	-0.1384	0.0000
50	35S-COPT2C	0	35S-COPT2C	-0.2809	-0.4382	-0.1237	0.0000
100	35S-COPT2C	0	35S-COPT2C	-0.5523	-0.7079	-0.3968	0.0000
150	35S-COPT2C	0	35S-COPT2C	-0.6087	-0.7643	-0.4532	0.0000
200	35S-COPT2C	0	35S-COPT2C	-0.6772	-0.8405	-0.5139	0.0000
100	35S-COPT2C	50	35S-COPT2C	-0.2714	-0.4241	-0.1188	0.0000
150	35S-COPT2C	50	35S-COPT2C	-0.3278	-0.4805	-0.1752	0.0000
200	35S-COPT2C	50	35S-COPT2C	-0.3963	-0.5568	-0.2357	0.0000

Table S18. Two-way ANOVA analysis results on the number of lateral root branches of Col0 and 35S-COPT2 genotypes in the presence of Au. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
50	35S-COPT2B	50	Col0	-0.3982	-0.7266	-0.0698	0.0030
50	35S-COPT2C	50	Col0	0.5194	0.2002	0.8386	0.0000
Within genotype, between conditions							
50	Col0	0	Col0	-0.3829	-0.7138	-0.0520	0.0067
100	Col0	0	Col0	-0.4090	-0.7354	-0.0826	0.0016
150	Col0	0	Col0	-0.5965	-0.9325	-0.2605	0.0000
200	Col0	0	Col0	-0.7120	-1.0454	-0.3786	0.0000
200	Col0	50	Col0	-0.3291	-0.6294	-0.0288	0.0154
200	Col0	100	Col0	-0.3030	-0.5983	-0.0077	0.0369
100	35S-COPT2A	0	35S-COPT2A	-0.6512	-1.1417	-0.1606	0.0005
150	35S-COPT2A	0	35S-COPT2A	-0.6602	-1.1475	-0.1728	0.0003
200	35S-COPT2A	0	35S-COPT2A	-0.7418	-1.2488	-0.2348	0.0000
100	35S-COPT2A	50	35S-COPT2A	-0.6854	-1.2051	-0.1657	0.0006
150	35S-COPT2A	50	35S-COPT2A	-0.6944	-1.2112	-0.1777	0.0004
200	35S-COPT2A	50	35S-COPT2A	-0.7760	-1.3113	-0.2407	0.0001
50	35S-COPT2B	0	35S-COPT2B	-0.7820	-1.1608	-0.4031	0.0000
100	35S-COPT2B	0	35S-COPT2B	-0.7740	-1.1678	-0.3802	0.0000
150	35S-COPT2B	0	35S-COPT2B	-0.7985	-1.1819	-0.4152	0.0000
200	35S-COPT2B	0	35S-COPT2B	-0.8512	-1.2084	-0.4939	0.0000

Table S19. Two-way ANOVA analysis results on the root architecture of Col0 and 35S-COPT2 genotypes in the presence of Au. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
50	35SCOPT2C	50	Col0	1.7821	0.7660	2.7982	0.0000
150	35SCOPT2C	150	Col0	1.3391	0.3188	2.3594	0.0006
200	35SCOPT2C	200	Col0	1.6015	0.4836	2.7195	0.0001
Within genotype, between conditions							
50	35SCOPT2C	0	35SCOPT2C	1.6005	0.4084	2.7926	0.0004

Analysis of element uptake in Arabidopsis 35S-COPT2 grown in the presence of Au

The 35S-COPT2 lines were grown hydroponically (with roots submerged in 1mM Au containing media) to assess metal uptake. To analyse the concentration of Au, Fe and Cu in the shoot or root tissues of five-week-old hydroponically grown Arabidopsis 35S-COPT2A, 35S-COPT2B and 35S-COPT2C seedlings, analysis was performed using ICP-OES. Tests for homogeneity and normal distribution were performed on the concentration data (Table S20). Comparisons were made using a one-way ANOVA (for data that fit the assumptions) or a Kruskal-Wallis test (the non-parametric alternative to the one-way ANOVA) (Table S21). These were followed by post-hoc tests to determine the direction of any significant differences (Table S22).

Table S20. Results of the Levene's and Shapiro Wilk tests for homogeneity of variance and normal distribution, respectively, on element concentration data from five-week-old shoot and root tissue of Arabidopsis WT, *35S-COPT2A*, *35S-COPT2B*, *35S-COPT2C* grown in a hydroponic system dosed with Au

Tissue	Element (nm)	Test	p-value	Test stat	Stats test to use
Shoot	Au (242)	Levene's	> 0.05	0.9288	Kruskal-Wallis
Shoot	Au (242)	Shapiro-Wilk	< 0.05	0.5695	Kruskal-Wallis
Shoot	Au (267)	Levene's	> 0.05	0.2191	Kruskal-Wallis
Shoot	Au (267)	Shapiro-Wilk	< 0.05	0.8821	Kruskal-Wallis
Shoot	Cu (324)	Levene's	> 0.05	0.2384	one-way ANOVA
Shoot	Cu (324)	Shapiro-Wilk	> 0.05	0.9392	one-way ANOVA
Shoot	Fe (239)	Levene's	> 0.05	1.2433	Kruskal-Wallis
Shoot	Fe (239)	Shapiro-Wilk	< 0.05	0.8061	Kruskal-Wallis
Root	Au (267)	Levene's	> 0.05	0.3799	one-way ANOVA
Root	Au (267)	Shapiro-Wilk	> 0.05	0.9411	one-way ANOVA
Root	Cu (324)	Levene's	> 0.05	2.0893	one-way ANOVA
Root	Cu (324)	Shapiro-Wilk	> 0.05	0.9662	one-way ANOVA
Root	Fe (239)	Levene's	> 0.05	0.238	Kruskal-Wallis
Root	Fe (239)	Shapiro-Wilk	< 0.05	0.7943	Kruskal-Wallis

Table S21. Results of ANOVA tests on element concentration data from five-week-old shoot and root tissue of *Arabidopsis* WT, *35S-COPT2A*, *35S-COPT2B*, *35S-COPT2C* grown in a hydroponic system dosed with Au. Significant results were further examined by a Tukey's HSD test

Tissue	Element (nm)	Test	Test value	d.f.	p-value	sig
Shoot	Au (242)	Kruskal-Wallis	14.267	3, 14	< 0.05	*
Shoot	Au (267)	Kruskal-Wallis	12.61	3, 14	< 0.05	*
Shoot	Cu (324)	one-way ANOVA	16.99	3, 16	< 0.05	*
Shoot	Fe (239)	Kruskal-Wallis	4.04	3, 14	> 0.05	ns
Root	Au (267)	one-way ANOVA	0.197	3, 16	> 0.05	ns
Root	Cu (324)	one-way ANOVA	6.067	3, 14	< 0.05	*
Root	Fe (239)	Kruskal-Wallis	5.8468	3, 14	> 0.05	ns

Table S22. Significant results of Tukey's HSD tests on element concentration data from five-week-old shoot and root tissue of Arabidopsis WT compared to 35S-COPT2A, 35S-COPT2B, 35S-COPT2C grown in a hydroponic system dosed with Au.

Tissue	Element (nm)	Test	Comparison	p-value	sig
Shoot	Au (242)	Wilcoxon sum rank	35S-COPT2B - Col0	< 0.05	*
Shoot	Au (242)	Wilcoxon sum rank	35S-COPT2C - Col0	< 0.05	*
Shoot	Au (267)	Wilcoxon sum rank	35S-COPT2B - Col0	< 0.05	*
Shoot	Au (267)	Wilcoxon sum rank	35S-COPT2C - Col0	< 0.05	*
Shoot	Cu (324)	Tukey's HSD	35S-COPT2A - Col0	< 0.001	***
Shoot	Cu (324)	Tukey's HSD	35S- COPT2B - Col0	< 0.001	***
Shoot	Cu (324)	Tukey's HSD	35S- COPT2C - Col0	< 0.001	***
Root	Cu (324)	Tukey's HSD	35S-COPT2A - Col0	< 0.05	*
Root	Cu (324)	Tukey's HSD	35S-COPT2B - Col0	< 0.01	**

Root architecture characterisation of Arabidopsis 35S-GP lines on Cu or Au

To examine whether the expression of the short, synthetic GP would change the phenotypic response of plants to Au due to increased NP formation, Arabidopsis Col0, 35S-GPA, 35S-GPB and 35S-GPC lines were grown on ½ MS(A) media containing Au (0, 50, 100, 150 or 200 µM) and the primary root length, number of lateral root branches and the interaction between length and branching investigated. The summary statistics for root length are shown in Table S23, number of lateral root branches in Table S24, or the root architecture in Table S25. The two-way ANOVA test results for root length (Table S26), number of lateral root branches (Table S27) or the root architecture (Table S28) were performed with a more conservative test statistic ($p = 0.02$).

Table S23. Summary statistics of the root length (normalised to the mean value of each genotype at 0 uM) of Arabidopsis Col0 or 35S-GP genotypes on Au

Genotype	Condition	Conc	Root length	STD	n	SE
Col0	Au	0	0.99	0.08	38	0.01
35S-GPA	Au	0	1.00	0.23	29	0.04
35S-GPB	Au	0	1.00	0.11	25	0.02
35S-GPC	Au	0	1.00	0.18	17	0.04
Col0	Au	50	0.70	0.12	56	0.02
35S-GPA	Au	50	1.01	0.13	33	0.02
35S-GPB	Au	50	1.09	0.11	31	0.02
35S-GPC	Au	50	0.71	0.11	3	0.06
Col0	Au	100	0.79	0.09	60	0.01
35S-GPA	Au	100	0.81	0.27	27	0.05
35S-GPB	Au	100	0.76	0.13	26	0.02
Col0	Au	150	0.55	0.09	52	0.01
35S-GPA	Au	150	0.57	0.13	24	0.03
35S-GPB	Au	150	0.51	0.08	14	0.02
Col0	Au	200	0.36	0.06	54	0.01
35S-GPA	Au	200	0.34	0.11	23	0.02
35S-GPB	Au	200	0.35	0.08	18	0.02
35S-GPC	Au	200	0.28	0.05	21	0.01

Table S24. Summary statistics of the number of lateral root branches (normalised to the mean value of each genotype at 0 μ M) of Arabidopsis Col0 or 35S-GP genotypes on Au

Genotype	Condition	Conc	Lateral root branches	STD	n	SE
Col0	Au	0	1.00	0.55	38	0.09
35S-GPA	Au	0	1.00	0.29	29	0.05
35S-GPB	Au	0	1.00	0.26	25	0.05
35S-GPC	Au	0	1.00	0.22	17	0.05
Col0	Au	50	0.62	0.47	56	0.06
35S-GPA	Au	50	1.23	0.54	33	0.09
35S-GPB	Au	50	0.89	0.30	31	0.05
35S-GPC	Au	50	0.40	0.08	3	0.05
Col0	Au	100	0.59	0.47	60	0.06
35S-GPA	Au	100	0.71	0.50	27	0.10
35S-GPB	Au	100	0.85	0.20	26	0.04
Col0	Au	150	0.40	0.33	52	0.05
35S-GPA	Au	150	0.60	0.25	24	0.05
35S-GPB	Au	150	0.80	0.18	14	0.05
Col0	Au	200	0.39	0.18	40	0.03
35S-GPA	Au	200	0.18	0.14	23	0.03
35S-GPB	Au	200	0.54	0.13	18	0.03
35S-GPC	Au	200	0.34	0.09	21	0.02

Table S25. Summary statistics of the complexity of root architecture (normalised to the mean value of each genotype at 0 μ M) of Arabidopsis Col0 or 35S-GP genotypes on Au

Genotype	Condition	Conc	Root architecture	STD	n	SE
Col0	Au	0	1.00	0.54	38	0.09
35S-GPA	Au	0	1.08	0.55	29	0.10
35S-GPB	Au	0	1.00	0.23	25	0.05
35S-GPC	Au	0	1.03	0.30	17	0.07
Col0	Au	50	0.87	0.66	56	0.09
35S-GPA	Au	50	1.25	0.57	33	0.10
35S-GPB	Au	50	0.82	0.25	31	0.05
35S-GPC	Au	50	0.56	0.04	3	0.02
Col0	Au	100	0.73	0.57	60	0.07
35S-GPA	Au	100	0.82	0.56	27	0.11
35S-GPB	Au	100	1.13	0.27	26	0.05
Col0	Au	150	0.72	0.57	52	0.08
35S-GPA	Au	150	1.05	0.35	24	0.07
35S-GPB	Au	150	1.58	0.36	14	0.10
Col0	Au	200	1.06	0.42	40	0.07
35S-GPA	Au	200	0.49	0.32	23	0.07
35S-GPB	Au	200	1.59	0.45	18	0.11
35S-GPC	Au	200	1.27	0.40	21	0.09

Table S26. Two-way ANOVA analysis results on the root length (normalised to the mean value of each genotype at 0 uM) of Col0 and 35S-GP genotypes in the presence of Au. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
50	35S-GPA	50	Col0	0.3056	0.2055	0.4058	0.0000
50	35S-GPB	50	Col0	0.3858	0.2836	0.4880	0.0000
Within genotype, between conditions							
50	Col0	0	Col0	-0.2923	-0.3882	-0.1964	0.0000
100	Col0	0	Col0	-0.2014	-0.2960	-0.1068	0.0000
150	Col0	0	Col0	-0.4385	-0.5359	-0.3411	0.0000
200	Col0	0	Col0	-0.6332	-0.7298	-0.5365	0.0000
150	Col0	50	Col0	-0.1462	-0.2341	-0.0583	0.0000
200	Col0	50	Col0	-0.3409	-0.4279	-0.2538	0.0000
150	Col0	100	Col0	-0.2371	-0.3236	-0.1507	0.0000
200	Col0	100	Col0	-0.4318	-0.5174	-0.3462	0.0000
200	Col0	150	Col0	-0.1947	-0.2833	-0.1060	0.0000
100	35S-GPA	0	35S-GPA	-0.1853	-0.3073	-0.0632	0.0000
150	35S-GPA	0	35S-GPA	-0.4341	-0.5600	-0.3082	0.0000
200	35S-GPA	0	35S-GPA	-0.6600	-0.7875	-0.5326	0.0000
100	35S-GPA	50	35S-GPA	-0.1910	-0.3094	-0.0725	0.0000
150	35S-GPA	50	35S-GPA	-0.4398	-0.5622	-0.3174	0.0000
200	35S-GPA	50	35S-GPA	-0.6657	-0.7897	-0.5418	0.0000
150	35S-GPA	100	35S-GPA	-0.2488	-0.3769	-0.1208	0.0000
200	35S-GPA	100	35S-GPA	-0.4748	-0.6043	-0.3453	0.0000
200	35S-GPA	150	35S-GPA	-0.2259	-0.3591	-0.0928	0.0000
100	35S-GPB	0	35S-GPB	-0.2390	-0.3668	-0.1111	0.0000
150	35S-GPB	0	35S-GPB	-0.4916	-0.6440	-0.3393	0.0000
200	35S-GPB	0	35S-GPB	-0.6496	-0.7907	-0.5085	0.0000
100	35S-GPB	50	35S-GPB	-0.3249	-0.4463	-0.2035	0.0000
150	35S-GPB	50	35S-GPB	-0.5776	-0.7246	-0.4306	0.0000
200	35S-GPB	50	35S-GPB	-0.7356	-0.8708	-0.6003	0.0000
150	35S-GPB	100	35S-GPB	-0.2527	-0.4040	-0.1014	0.0000
200	35S-GPB	100	35S-GPB	-0.4107	-0.5506	-0.2707	0.0000
200	35S-GPC	0	35S-GPC	-0.7221	-0.8710	-0.5732	0.0000
200	35S-GPC	50	35S-GPC	-0.4338	-0.7155	-0.1521	0.0000

Table S27. Two-way ANOVA analysis results on the number of lateral root branches (normalised to the mean value of each genotype at 0 μ M) of Col0 and 35S-GP genotypes in the presence of Au. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
50	35S-GPA	50	Col0	0.6171	0.3299	0.9042	0.0000
Within genotype, between conditions							
50	Col0	0	Col0	-0.3829	-0.6579	-0.1079	0.0002
100	Col0	0	Col0	-0.4090	-0.6803	-0.1377	0.0000
150	Col0	0	Col0	-0.5965	-0.8757	-0.3172	0.0000
200	Col0	0	Col0	-0.6111	-0.9075	-0.3147	0.0000
100	Col0	50	Col0	-0.0261	-0.2692	0.2170	1.0000
150	Col0	50	Col0	-0.2136	-0.4656	0.0384	0.2254
200	Col0	50	Col0	-0.2282	-0.4991	0.0427	0.2352
150	Col0	100	Col0	-0.1875	-0.4354	0.0604	0.4348
200	Col0	100	Col0	-0.2021	-0.4692	0.0650	0.4337
200	Col0	150	Col0	-0.0146	-0.2898	0.2606	1.0000
150	35S-GPA	0	35S-GPA	-0.4046	-0.7657	-0.0435	0.0112
200	35S-GPA	0	35S-GPA	-0.8246	-1.1899	-0.4592	0.0000
100	35S-GPA	50	35S-GPA	-0.5246	-0.8641	-0.1850	0.0000
150	35S-GPA	50	35S-GPA	-0.6392	-0.9902	-0.2881	0.0000
200	35S-GPA	50	35S-GPA	-1.0591	-1.4146	-0.7037	0.0000
200	35S-GPA	100	35S-GPA	-0.5346	-0.9058	-0.1633	0.0001
200	35S-GPA	150	35S-GPA	-0.4200	-0.8018	-0.0382	0.0147
200	35S-GPB	0	35S-GPB	-0.4599	-0.8643	-0.0554	0.0089
200	35S-GPC	0	35S-GPC	-0.6571	-1.0840	-0.2302	0.0000

Table S28. Two-way ANOVA analysis results on the root architecture (normalised to the mean value of each genotype at 0 μ M) of Col0 and 35S-GP genotypes in the presence of Au. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
150	35S-GPB	150	Col0	0.8678	0.3424	1.3932	0.0000
200	35S-GPA	200	Col0	-0.5657	-1.0224	-0.1091	0.0021
Within genotype, between conditions							
200	35S-GPA	0	35S-GPA	-0.5912	-1.0784	-0.1039	0.0030
200	35S-GPA	50	35S-GPA	-0.7554	-1.2294	-0.2814	0.0000
200	35S-GPA	150	35S-GPA	-0.5584	-1.0676	-0.0492	0.0153
200	35S-GPB	0	35S-GPB	0.5907	0.0512	1.1301	0.0157
150	35S-GPB	50	35S-GPB	0.7687	0.2068	1.3307	0.0003
200	35S-GPB	50	35S-GPB	0.7746	0.2575	1.2917	0.0000

Analysis of element uptake in Arabidopsis 35S-GP lines grown in the presence of Au

Following the analysis of 35S-GP lines on agar plates containing Au and having established that the root phenotype of 35S-GP lines differs to the WT root phenotype, these lines were grown hydroponically. To analyse the concentration of Au, Fe and Cu in the shoot or root tissues of five-week-old hydroponically grown Arabidopsis 35S-GPA, 35S-GPB and 35S-GPC, analysis was performed using ICP-OES. Tests for homogeneity and normal distribution were performed on the concentration data (Table S29). Comparisons were made using a one-way ANOVA (for data that fit the assumptions) or a Kruskal-Wallis test (the non-parametric alternative to the one-way ANOVA) (Table S30). These were followed by post-hoc tests to determine the direction of any significant differences (Table S31).

Table S29. Results of the Levene's and Shapiro Wilk tests for homogeneity of variance and normal distribution, respectively, on element concentration data from five-week-old shoot and root tissue of *Arabidopsis* WT, 35S-GPA, 35S-GPB, 35S-GPC grown in a hydroponic system dosed with Au

Tissue	Element (nm)	Test	p-value	test value	stats test
Shoot	Au (242)	Levene's	> 0.05	0.8196	one-way ANOVA
Shoot	Au (242)	Shapiro-Wilk	> 0.05	0.9676	one-way ANOVA
Shoot	Au (267)	Levene's	> 0.05	0.5079	one-way ANOVA
Shoot	Au (267)	Shapiro-Wilk	> 0.05	0.9363	one-way ANOVA
Shoot	Cu (324)	Levene's	> 0.05	0.3108	one-way ANOVA
Shoot	Cu (324)	Shapiro-Wilk	> 0.05	0.9632	one-way ANOVA
Shoot	Fe (239)	Levene's	> 0.05	1.1306	Kruskal-Wallis
Shoot	Fe (239)	Shapiro-Wilk	< 0.05	0.8061	Kruskal-Wallis
Root	Au (267)	Levene's	> 0.05	0.1709	one-way ANOVA
Root	Au (267)	Shapiro-Wilk	> 0.05	0.9742	one-way ANOVA
Root	Cu (324)	Levene's	> 0.05	0.6584	one-way ANOVA
Root	Cu (324)	Shapiro-Wilk	> 0.05	0.9457	one-way ANOVA
Root	Fe (239)	Levene's	> 0.05	0.7347	one-way ANOVA
Root	Fe (239)	Shapiro-Wilk	> 0.05	0.9043	one-way ANOVA

Table S30. Results of ANOVA tests on element concentration data from five-week-old shoot and root tissue of *Arabidopsis* WT, *35S-GPA*, *35S-GPB*, *35S-GPC* grown in a hydroponic system dosed with Au. Significant results were further examined by a Tukey's HSD test.

Tissue	Element (nm)	Test	p-value	test value	d.f.	sig
Shoot	Au (242)	one-way ANOVA	> 0.05	5.619	3, 15	ns
Shoot	Au (267)	one-way ANOVA	< 0.05	4.158	3, 15	ns
Shoot	Cu (324)	one-way ANOVA	< 0.05	19.780	3, 15	ns
Shoot	Fe (239)	Kruskal-Wallis	> 0.05	4.040	3, 15	ns
Root	Au (267)	one-way ANOVA	< 0.05	10.600	3, 13	ns
Root	Cu (324)	one-way ANOVA	< 0.05	12.840	3, 13	ns
Root	Fe (239)	one-way ANOVA	> 0.05	0.111	3, 13	ns

Table S31. Significant results of Tukey's HSD tests on element concentration data from five-week-old shoot and root tissue of Arabidopsis WT compared to 35S-GPA, 35S-GPB, 35S-GPC grown in a hydroponic system dosed with Au.

Tissue	Element (nm)	Test	Comparison	Diff	Upper	Lower	p-value	sig
Shoot	Au (267)	Tukey's HSD	35S-GPC : Col0	0.069	0.011	0.128	0.018	*
Shoot	Cu (324)	Tukey's HSD	35S-GPA : Col0	0.130	0.077	0.184	0.000	***
Shoot	Cu (324)	Tukey's HSD	35S-GPB : Col0	0.111	0.055	0.168	0.000	***
Shoot	Cu (324)	Tukey's HSD	35S-GPC : Col0	0.106	0.052	0.159	0.000	***
Root	Au (267)	Tukey's HSD	35S-GPC : Col0	78	36	120	0.000	***
Root	Cu (324)	Tukey's HSD	35S-GPA : Col0	0.315	0.154	0.476	0.000	***
Root	Cu (324)	Tukey's HSD	35S-GPB : Col0	0.274	0.106	0.442	0.002	**
Root	Cu (324)	Tukey's HSD	35S-GPC : Col0	0.288	0.127	0.448	0.001	**

Root characterisation of 35S-GPC genotypes grown on Cu or Au

To examine whether the combination of a higher expression of Arabidopsis *COPT2* combined with the expression of the synthetic AuNP forming peptide (*GP*) resulted in an altered phenotypic response to Au, Arabidopsis Col0 and 35S-GPC genotypes were grown on ½MS(A) media containing a range of Au concentrations and the number of root length and lateral root branches recorded. The summary statistics for root length are shown in Table S32, number of lateral root branches are shown in Table S33, and root architecture are shown in Table S34. The results of the two-way ANOVA analyses for root length, number of lateral root branches and root architecture are shown in Table S35, Table S36 and Table S37, respectively. The two-way ANOVA test was performed with a more conservative test statistic ($p = 0.02$).

Table S32. Summary statistics of the root length (normalised to the mean value of each genotype at 0 μ M) of Arabidopsis Col0 or 35S-GPC genotypes on Au

Genotype	Condition	Conc	Root length	STD	n	SE
Col0	Au	0	0.99	0.08	38	0.01
35S-GPCA	Au	0	1.00	0.33	19	0.071
35S-GPCB	Au	0	0.99	0.31	26	0.06
35S-GPCC	Au	0	1.00	0.45	20	0.10
Col0	Au	50	0.70	0.12	56	0.01
35S-GPCA	Au	50	0.97	0.32	9	0.10
35S-GPCB	Au	50	1.11	0.55	21	0.12
35S-GPCC	Au	50	0.47	0.10	20	0.02
Col0	Au	100	0.79	0.09	60	0.01
35S-GPCA	Au	100	0.23	0.14	17	0.03
35S-GPCB	Au	100	0.60	0.23	19	0.05
35S-GPCC	Au	100	0.57	0.26	18	0.06
Col0	Au	150	0.55	0.09	52	0.01
35S-GPCA	Au	150	0.33	0.15	21	0.03
35S-GPCB	Au	150	0.84	0.28	16	0.07
35S-GPCC	Au	150	0.39	0.11	16	0.02
Col0	Au	200	0.35	0.06	54	0.00
35S-GPCA	Au	200	0.37	0.05	25	0.01
35S-GPCC	Au	200	0.23	0.15	12	0.04

Table S33. Summary statistics of the number of lateral root branches (normalised to the mean value of each genotype at 0 μ M) of *Arabidopsis* Col0 or 35S-GPC genotypes on Au

Genotype	Condition	Conc	Lateral root branches	STD	n	SE
Col0	Au	0	1.00	0.55	38	0.09
35S-GPCA	Au	0	1.00	0.31	19	0.07
35S-GPCB	Au	0	1.00	0.53	26	0.10
35S-GPCC	Au	0	1.00	0.40	20	0.09
Col0	Au	50	0.77	0.39	45	0.06
35S-GPCA	Au	50	0.69	0.37	9	0.12
35S-GPCB	Au	50	0.50	0.46	21	0.10
35S-GPCC	Au	50	0.63	0.25	20	0.06
Col0	Au	100	0.79	0.38	45	0.06
35S-GPCA	Au	100	0.10	0.04	17	0.01
35S-GPCB	Au	100	0.68	0.31	19	0.07
35S-GPCC	Au	100	0.56	0.26	18	0.06
Col0	Au	150	0.57	0.25	37	0.04
35S-GPCA	Au	150	0.18	0.12	21	0.03
35S-GPCB	Au	150	0.69	0.27	16	0.07
35S-GPCC	Au	150	0.34	0.10	16	0.03
Col0	Au	200	0.39	0.18	40	0.03
35S-GPCA	Au	200	0.72	0.20	25	0.04
35S-GPCC	Au	200	0.15	0.09	12	0.03

Table S34. Summary statistics of the root architecture (normalised to the mean value of each genotype at 0 uM) of Arabidopsis Col0 or 35S-GPC genotypes on Au

Genotype	Condition	Conc	Root architecture	STD	n	SE
Col0	Au	0	1.00	0.54	38	0.09
35S-GPCA	Au	0	1.07	0.37	19	0.08
35S-GPCB	Au	0	0.99	0.39	26	0.08
35S-GPCC	Au	0	1.10	0.38	20	0.09
Col0	Au	50	1.09	0.55	45	0.08
35S-GPCA	Au	50	0.70	0.39	9	0.13
35S-GPCB	Au	50	0.44	0.26	21	0.06
35S-GPCC	Au	50	1.34	0.43	20	0.10
Col0	Au	100	0.98	0.44	45	0.06
35S-GPCA	Au	100	0.57	0.36	17	0.09
35S-GPCB	Au	100	1.17	0.43	19	0.10
35S-GPCC	Au	100	1.01	0.30	18	0.07
Col0	Au	150	1.01	0.40	37	0.07
35S-GPCA	Au	150	0.52	0.27	21	0.06
35S-GPCB	Au	150	0.88	0.39	16	0.10
35S-GPCC	Au	150	0.91	0.27	16	0.07
Col0	Au	200	1.06	0.42	40	0.07
35S-GPCA	Au	200	1.96	0.56	25	0.11
35S-GPCC	Au	200	0.72	0.29	12	0.08

Table S35. Two-way ANOVA analysis results on the root length (normalised to the mean value of each genotype at 0 μ M) of Col0 and 35S-GPC genotypes in the presence of Au. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 1	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
50	35S-GPCB	50	Col0	0.4105	0.2169	0.6041	0.0000
50	35S-GPCC	50	Col0	-0.2280	-0.4250	-0.0309	0.0068
100	35S-GPCA	100	Col0	-0.5563	-0.7642	-0.3485	0.0000
150	35S-GPCA	150	Col0	-0.2176	-0.4132	-0.0220	0.0125
150	35S-GPCB	150	Col0	0.2926	0.0763	0.5089	0.0003
Within genotype, between conditions							
50	Col0	0	Col0	-0.2923	-0.4513	-0.1333	0.0000
100	Col0	0	Col0	-0.2014	-0.3582	-0.0446	0.0010
150	Col0	0	Col0	-0.4385	-0.6000	-0.2771	0.0000
200	Col0	0	Col0	-0.6332	-0.7934	-0.4730	0.0000
200	Col0	50	Col0	-0.3409	-0.4852	-0.1966	0.0000
150	Col0	100	Col0	-0.2371	-0.3805	-0.0938	0.0000
200	Col0	100	Col0	-0.4318	-0.5737	-0.2899	0.0000
200	Col0	150	Col0	-0.1947	-0.3416	-0.0477	0.0005
100	35S-GPCA	0	35S-GPCA	-0.7653	-1.0178	-0.5127	0.0000
150	35S-GPCA	0	35S-GPCA	-0.6637	-0.9032	-0.4241	0.0000
200	35S-GPCA	0	35S-GPCA	-0.6257	-0.8559	-0.3954	0.0000
100	35S-GPCA	50	35S-GPCA	-0.7433	-1.0552	-0.4315	0.0000
150	35S-GPCA	50	35S-GPCA	-0.6417	-0.9431	-0.3403	0.0000
200	35S-GPCA	50	35S-GPCA	-0.6037	-0.8978	-0.3097	0.0000
100	35S-GPCB	0	35S-GPCB	-0.3923	-0.6206	-0.1640	0.0000
100	35S-GPCB	50	35S-GPCB	-0.5032	-0.7427	-0.2636	0.0000
50	35S-GPCC	0	35S-GPCC	-0.5278	-0.7671	-0.2886	0.0000
100	35S-GPCC	0	35S-GPCC	-0.4218	-0.6676	-0.1760	0.0000
150	35S-GPCC	0	35S-GPCC	-0.6097	-0.8634	-0.3560	0.0000
200	35S-GPCC	0	35S-GPCC	-0.7673	-1.0436	-0.4911	0.0000
200	35S-GPCC	100	35S-GPCC	-0.3455	-0.6275	-0.0636	0.0025

Table S36. Two-way ANOVA analysis results on the number of lateral root branches (normalised to the mean value of each genotype at 0 uM) of Col0 and 35S-GPC genotypes in the presence of Au. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
100	35S-GPCA	100	Col0	-0.6956	-1.0373	-0.3489	0.0000
150	35S-GPCA	150	Col0	-0.3885	-0.7193	-0.0586	0.0051
Within genotype, between conditions							
150	Col0	0	Col0	-0.4356	-0.7121	-0.1535	0.0000
200	Col0	0	Col0	-0.6125	-0.8850	-0.3372	0.0000
200	Col0	50	Col0	-0.3711	-0.6418	-0.1163	0.0001
200	Col0	100	Col0	-0.3923	-0.6620	-0.1364	0.0000
100	35S-GPCA	0	35S-GPCA	-0.9091	-1.3085	-0.5011	0.0000
150	35S-GPCA	0	35S-GPCA	-0.8273	-1.2043	-0.4386	0.0000
100	35S-GPCA	50	35S-GPCA	-0.5954	-1.0943	-0.0974	0.0040
200	35S-GPCA	100	35S-GPCA	0.6219	0.2438	1.0040	0.0000
200	35S-GPCA	150	35S-GPCA	0.5465	0.1827	0.8985	0.0000
50	35S-GPCB	0	35S-GPCB	-0.5066	-0.8577	-0.1482	0.0001
100	35S-GPCC	0	35S-GPCC	-0.4391	-0.8290	-0.0433	0.0129
150	35S-GPCC	0	35S-GPCC	-0.6580	-1.0635	-0.2524	0.0000
200	35S-GPCC	0	35S-GPCC	-0.8507	-1.2923	-0.4092	0.0000
200	35S-GPCC	50	35S-GPCC	-0.4826	-0.9241	-0.0411	0.0161

Table S37. Two-way ANOVA analysis results on the root architecture (normalised to the mean value of each genotype at 0 uM) of Col0 and 35S-GPC genotypes in the presence of Au. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
50	35S-GPCB	50	Col0	-0.6499	-1.0514	-0.2484	0.0000
150	35S-GPCA	150	Col0	-0.4823	-0.8974	-0.0672	0.0064
200	35S-GPCA	200	Col0	0.9052	0.5179	1.2926	0.0000
Within genotype, between conditions							
150	35S-GPCA	0	35S-GPCA	-0.5487	-1.0297	-0.0677	0.0086
200	35S-GPCA	0	35S-GPCA	0.8906	0.4282	1.3530	0.0000
200	35S-GPCA	50	35S-GPCA	1.2656	0.6750	1.8562	0.0000
200	35S-GPCA	100	35S-GPCA	1.3947	0.9171	1.8723	0.0000
200	35S-GPCA	150	35S-GPCA	1.4393	0.9896	1.8890	0.0000
50	35S-GPCB	0	35S-GPCB	-0.5563	-1.0020	-0.1105	0.0018
100	35S-GPCB	50	35S-GPCB	0.7290	0.2480	1.2101	0.0000
200	35S-GPCC	50	35S-GPCC	-0.6230	-1.1778	-0.0683	0.0109

Analysis of element uptake in Arabidopsis 35S-GPC lines grown in the presence of Au

Following the analysis of 35S-GPC lines on agar plates containing Au and having established that the root phenotype of 35S-GPC lines differs to the WT root phenotype, these lines were grown hydroponically. To analyse the concentration of Au, Fe and Cu in the shoot or root tissues of five-week-old hydroponically grown Arabidopsis 35S-GPCA, 35S-GPCB and 35S-GPCC, analysis was performed using ICP-OES. Tests for homogeneity and normal distribution were performed on the concentration data (Table S38). Comparisons were made using a one-way ANOVA (for data that fit the assumptions) or a Kruskal-Wallis test (the non-parametric alternative to the one-way ANOVA) (Table S39). These were followed by post-hoc tests to determine the direction of any significant differences (Table S40).

Table S38. Results of the Levene's and Shapiro Wilk tests for homogeneity of variance and normal distribution, respectively, on element concentration data from five-week-old shoot and root tissue of *Arabidopsis* WT, *35S-GPCA*, *35S-GPCB*, *35S-GPCC* grown in a hydroponic system dosed with Au

Tissue	Element (nm)	Test	p-value	test value	stats test
Shoot	Au (242)	Levene's	< 0.05	6.260	Kruskal-Wallis
Shoot	Au (242)	Shapiro-Wilk	> 0.05	0.906	Kruskal-Wallis
Shoot	Au (267)	Levene's	< 0.05	0.009	Kruskal-Wallis
Shoot	Au (267)	Shapiro-Wilk	> 0.05	0.906	Kruskal-Wallis
Shoot	Cu (324)	Levene's	> 0.05	0.386	one-way ANOVA
Shoot	Cu (324)	Shapiro-Wilk	> 0.05	0.977	one-way ANOVA
Shoot	Fe (239)	Levene's	< 0.05	5.131	Kruskal-Wallis
Shoot	Fe (239)	Shapiro-Wilk	> 0.05	0.924	Kruskal-Wallis
Root	Au (267)	Levene's	> 0.05	0.531	one-way ANOVA
Root	Au (267)	Shapiro-Wilk	> 0.05	0.972	one-way ANOVA
Root	Cu (324)	Levene's	> 0.05	0.322	Kruskal-Wallis
Root	Cu (324)	Shapiro-Wilk	< 0.05	0.887	Kruskal-Wallis
Root	Fe (239)	Levene's	> 0.05	0.596	one-way ANOVA
Root	Fe (239)	Shapiro-Wilk	> 0.05	0.962	one-way ANOVA

Table S39. Results of ANOVA tests on element concentration data from five-week-old shoot and root tissue of *Arabidopsis* WT, *35S-GPCA*, *35S-GPCB*, *35S-GPCC* grown in a hydroponic system dosed with Au. Significant results were further examined by a Tukey's HSD test

Tissue	Element (nm)	Test	p-value	test value	d.f.	sig
Shoot	Au (242)	one-way ANOVA	< 0.05	10.342	3, 14	*
Shoot	Au (267)	one-way ANOVA	< 0.05	9.6526	3, 14	*
Shoot	Cu (324)	one-way ANOVA	< 0.001	12.04	3, 14	***
Shoot	Fe (239)	Kruskal-Wallis	> 0.05	2.7529	3, 14	ns
Root	Au (267)	one-way ANOVA	> 0.05	1.422	3, 14	ns
Root	Cu (324)	one-way ANOVA	< 0.05	9.8843	3, 14	*
Root	Fe (239)	one-way ANOVA	> 0.05	17.06	3, 13	ns

Table S40. Significant results of Tukey's HSD tests on element concentration data from five-week-old shoot and root tissue of Arabidopsis WT compared to 35S-GPCA, 35S-GPCB, 35S-GPCC grown in a hydroponic system dosed with Au.

Tissue	Element (nm)	Test	Comparison	Diff	Upper	Lower	p-value	sig
Shoot	Au (242)	Wilcoxon sum rank	35S-GPCA - Col0	NA	NA	NA	< 0.05	*
Shoot	Au (242)	Wilcoxon sum rank	35S-GPCC - Col0	NA	NA	NA	< 0.05	*
Shoot	Au (267)	Wilcoxon sum rank	35S-GPCA - Col0	NA	NA	NA	< 0.05	*
Shoot	Au (267)	Wilcoxon sum rank	35S-GPCC - Col0	NA	NA	NA	< 0.05	*
Shoot	Cu (324)	Tukey's HSD	35S-GPCA : Col0	0.119	0.043	0.194	< 0.05	*
Shoot	Cu (324)	Tukey's HSD	35S-GPCB : Col0	0.128	0.483	0.208	< 0.05	*
Shoot	Cu (324)	Tukey's HSD	35S-GPCC : Col0	0.141	0.061	0.221	< 0.01	**

Root architecture characterisation of *Arabidopsis copt2* mutant lines on Pd

The *Arabidopsis copt2* mutant lines were grown on $\frac{1}{2}$ MS(A) media containing Pd (0, 5, 10, 15 or 20 μ M) and the primary root length, number of lateral root branches and the interaction between length and branching investigated. The summary statistics for root length are shown in Table S41, number of lateral root branches in Table S42, or the root architecture in Table S43. The two-way ANOVA test results for root length (Table S44), number of lateral root branches (Table S45) or the root architecture (Table S46) were performed with a more conservative test statistic ($p = 0.02$).

Table S41. Summary statistics of the root length (normalised to the mean value of each genotype at 0 uM) of Arabidopsis Col0 or *copt2* mutant genotypes on Pd

Genotype	Condition	Conc	Root length	STD	n	SE
Col0	Pd	0	1.00	0.15	31	0.03
<i>copt2-1</i>	Pd	0	1.00	0.17	28	0.03
<i>copt2-2</i>	Pd	0	1.00	0.07	25	0.01
<i>copt2-3</i>	Pd	0	1.00	0.14	29	0.03
Col0	Pd	5	1.19	0.15	59	0.02
<i>copt2-1</i>	Pd	5	1.00	0.18	29	0.03
<i>copt2-2</i>	Pd	5	1.17	0.12	29	0.02
<i>copt2-3</i>	Pd	5	1.19	0.14	29	0.03
Col0	Pd	10	1.25	0.23	71	0.03
<i>copt2-1</i>	Pd	10	0.90	0.12	30	0.02
<i>copt2-2</i>	Pd	10	1.08	0.13	27	0.03
<i>copt2-3</i>	Pd	10	1.07	0.10	28	0.02
Col0	Pd	15	1.15	0.20	46	0.03
<i>copt2-1</i>	Pd	15	0.88	0.16	27	0.03
<i>copt2-2</i>	Pd	15	0.98	0.18	28	0.03
<i>copt2-3</i>	Pd	15	0.97	0.18	29	0.03
Col0	Pd	20	1.04	0.19	42	0.03
<i>copt2-1</i>	Pd	20	0.72	0.10	28	0.02
<i>copt2-2</i>	Pd	20	0.83	0.14	28	0.03
<i>copt2-3</i>	Pd	20	0.75	0.26	23	0.05

Table S42. Summary statistics of the number of lateral root branches (normalised to the mean value of each genotype at 0 uM) of Arabidopsis Col0 or *copt2* mutant genotypes on Pd

Genotype	Condition	Conc	Lateral root branches	STD	n	SE
Col0	Pd	0	1.00	0.24	31	0.04
<i>copt2-1</i>	Pd	0	1.00	0.80	28	0.15
<i>copt2-2</i>	Pd	0	1.00	0.60	25	0.12
<i>copt2-3</i>	Pd	0	1.00	0.63	29	0.12
Col0	Pd	5	0.59	0.33	59	0.04
<i>copt2-1</i>	Pd	5	1.03	0.88	29	0.16
<i>copt2-2</i>	Pd	5	1.33	0.75	29	0.14
<i>copt2-3</i>	Pd	5	0.96	0.58	29	0.11
Col0	Pd	10	0.49	0.26	71	0.03
<i>copt2-1</i>	Pd	10	0.83	0.71	30	0.13
<i>copt2-2</i>	Pd	10	0.79	0.53	27	0.10
<i>copt2-3</i>	Pd	10	0.59	0.50	28	0.10
Col0	Pd	15	0.29	0.23	46	0.03
<i>copt2-1</i>	Pd	15	0.45	0.53	27	0.10
<i>copt2-2</i>	Pd	15	0.54	0.42	28	0.08
<i>copt2-3</i>	Pd	15	0.38	0.27	29	0.05
Col0	Pd	20	0.27	0.23	42	0.04
<i>copt2-1</i>	Pd	20	0.52	0.35	28	0.07
<i>copt2-2</i>	Pd	20	0.35	0.24	28	0.04
<i>copt2-3</i>	Pd	20	0.53	0.51	23	0.11

Table S43. Summary statistics of the root architecture (normalised to the mean value of each genotype at 0 uM) of Arabidopsis Col0 or *copt2* mutant genotypes on Pd

Genotype	Condition	Con	Root architecture	STD	n	SE
Col0	Pd	0	1.02	0.27	31	0.05
<i>copt2-1</i>	Pd	0	0.99	0.76	28	0.14
<i>copt2-2</i>	Pd	0	1.00	0.62	25	0.12
<i>copt2-3</i>	Pd	0	0.99	0.62	29	0.12
Col0	Pd	5	0.49	0.27	59	0.04
<i>copt2-1</i>	Pd	5	1.02	0.86	29	0.16
<i>copt2-2</i>	Pd	5	1.13	0.61	29	0.11
<i>copt2-3</i>	Pd	5	0.79	0.49	29	0.09
Col0	Pd	10	0.41	0.24	71	0.03
<i>copt2-1</i>	Pd	10	0.88	0.70	30	0.13
<i>copt2-2</i>	Pd	10	0.71	0.44	27	0.09
<i>copt2-3</i>	Pd	10	0.54	0.47	28	0.09
Col0	Pd	15	0.25	0.19	46	0.03
<i>copt2-1</i>	Pd	15	0.49	0.55	27	0.11
<i>copt2-2</i>	Pd	15	0.53	0.35	28	0.07
<i>copt2-3</i>	Pd	15	0.37	0.22	29	0.04
Col0	Pd	20	0.25	0.20	42	0.03
<i>copt2-1</i>	Pd	20	0.72	0.46	28	0.09
<i>copt2-2</i>	Pd	20	0.43	0.25	28	0.05
<i>copt2-3</i>	Pd	20	0.80	0.99	23	0.21

Table S44. Two-way ANOVA analysis results on the root length (normalised to the mean value of each genotype at 0 uM) of Col0 and *copt2* mutant genotypes in the presence of Pd. Diff: difference between mean values; Lwr: the lower limit; Upr: the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 1	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
5	<i>copt2-1</i>	5	Col0	-0.1906	-0.3259	-0.0554	0.0001
10	<i>copt2-1</i>	10	Col0	-0.3512	-0.4811	-0.2213	0.0000
10	<i>copt2-2</i>	10	Col0	-0.1684	-0.3033	-0.0335	0.0017
10	<i>copt2-3</i>	10	Col0	-0.1759	-0.3090	-0.0428	0.0005
15	<i>copt2-1</i>	15	Col0	-0.2738	-0.4184	-0.1292	0.0000
15	<i>copt2-2</i>	15	Col0	-0.1764	-0.3194	-0.0334	0.0022
15	<i>copt2-3</i>	15	Col0	-0.1850	-0.3265	-0.0436	0.0007
20	<i>copt2-1</i>	20	Col0	-0.3109	-0.4565	-0.1654	0.0000
20	<i>copt2-2</i>	20	Col0	-0.2050	-0.3505	-0.0594	0.0001
20	<i>copt2-3</i>	20	Col0	-0.2884	-0.4432	-0.1337	0.0000
Within genotype, between conditions							
5	Col0	0	Col0	0.1932	0.0609	0.3255	0.0000
10	Col0	0	Col0	0.2508	0.1224	0.3792	0.0000
15	Col0	0	Col0	0.1548	0.0162	0.2935	0.0116
20	Col0	5	Col0	-0.1574	-0.2779	-0.0370	0.0007
20	Col0	10	Col0	-0.2150	-0.3311	-0.0989	0.0000
20	<i>copt2-1</i>	0	<i>copt2-1</i>	-0.2751	-0.4345	-0.1157	0.0000
20	<i>copt2-1</i>	5	<i>copt2-1</i>	-0.2777	-0.4358	-0.1197	0.0000
20	<i>copt2-1</i>	10	<i>copt2-1</i>	-0.1747	-0.3315	-0.0180	0.0120
15	<i>copt2-2</i>	5	<i>copt2-2</i>	-0.1883	-0.3463	-0.0303	0.0041
20	<i>copt2-2</i>	5	<i>copt2-2</i>	-0.3359	-0.4940	-0.1779	0.0000
20	<i>copt2-2</i>	10	<i>copt2-2</i>	-0.2516	-0.4125	-0.0907	0.0000
5	<i>copt2-3</i>	0	<i>copt2-3</i>	0.1907	0.0340	0.3473	0.0028
20	<i>copt2-3</i>	0	<i>copt2-3</i>	-0.2526	-0.4192	-0.0861	0.0000
15	<i>copt2-3</i>	5	<i>copt2-3</i>	-0.2208	-0.3775	-0.0642	0.0001
20	<i>copt2-3</i>	5	<i>copt2-3</i>	-0.4433	-0.6099	-0.2768	0.0000
20	<i>copt2-3</i>	10	<i>copt2-3</i>	-0.3276	-0.4954	-0.1597	0.0000
20	<i>copt2-3</i>	15	<i>copt2-3</i>	-0.2225	-0.3890	-0.0559	0.0004

Table S45. Two-way ANOVA analysis results on the number of lateral root branches (normalised to the mean value of each genotype at 0 uM) of Col0 and *copt2* mutant genotypes in the presence of Pd. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
5	<i>copt2-1</i>	5	Col0	0.4391	0.0443	0.8339	0.0124
5	<i>copt2-2</i>	5	Col0	0.7468	0.3519	1.1416	0.0000
Within genotype, between conditions							
10	Col0	0	Col0	-0.5099	-0.8847	-0.1351	0.0003
15	Col0	0	Col0	-0.7122	-1.1168	-0.3077	0.0000
20	Col0	0	Col0	-0.7301	-1.1423	-0.3179	0.0000
15	<i>copt2-1</i>	0	<i>copt2-1</i>	-0.5536	-1.0232	-0.0840	0.0049
15	<i>copt2-1</i>	5	<i>copt2-1</i>	-0.5786	-1.0442	-0.1130	0.0019
20	<i>copt2-1</i>	5	<i>copt2-1</i>	-0.5022	-0.9634	-0.0409	0.0169
20	<i>copt2-2</i>	0	<i>copt2-2</i>	-0.6417	-1.1207	-0.1627	0.0004
10	<i>copt2-2</i>	5	<i>copt2-2</i>	-0.5460	-1.0116	-0.0804	0.0054
15	<i>copt2-2</i>	5	<i>copt2-2</i>	-0.7910	-1.2523	-0.3298	0.0000
20	<i>copt2-2</i>	5	<i>copt2-2</i>	-0.9790	-1.4402	-0.5177	0.0000
15	<i>copt2-3</i>	0	<i>copt2-3</i>	-0.6244	-1.0816	-0.1673	0.0003
15	<i>copt2-3</i>	5	<i>copt2-3</i>	-0.5802	-1.0374	-0.1230	0.0013

Table S46. Two-way ANOVA analysis results on the root architecture (normalised to the mean value of each genotype at 0 uM) of Col0 and *copt2* mutant genotypes in the presence of Pd. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
5	<i>copt2-1</i>	5	Col0	0.5271	0.1338	0.9203	0.0004
5	<i>copt2-2</i>	5	Col0	0.6431	0.2498	1.0363	0.0000
10	<i>copt2-1</i>	10	Col0	0.4758	0.0981	0.8534	0.0015
20	<i>copt2-1</i>	20	Col0	0.4675	0.0444	0.8905	0.0137
20	<i>copt2-3</i>	20	Col0	0.5530	0.1032	1.0029	0.0023
Within genotype, between conditions							
5	Col0	0	Col0	-0.5255	-0.9102	-0.1409	0.0003
10	Col0	0	Col0	-0.6084	-0.9817	-0.2351	0.0000
15	Col0	0	Col0	-0.7663	-1.1692	-0.3633	0.0000
20	Col0	0	Col0	-0.7644	-1.1750	-0.3538	0.0000
15	<i>copt2-1</i>	5	<i>copt2-1</i>	-0.5223	-0.9860	-0.0585	0.0103
20	<i>copt2-2</i>	0	<i>copt2-2</i>	-0.5770	-1.0541	-0.0998	0.0032
15	<i>copt2-2</i>	5	<i>copt2-2</i>	-0.6053	-1.0648	-0.1459	0.0006
20	<i>copt2-2</i>	5	<i>copt2-2</i>	-0.7052	-1.1647	-0.2458	0.0000
15	<i>copt2-3</i>	0	<i>copt2-3</i>	-0.6154	-1.0708	-0.1600	0.0003

Root architecture characterisation of Arabidopsis 35S-COPT2 lines on Pd

The Arabidopsis 35S-COPT2 lines were grown on ½MS(A) media containing Pd (0, 5, 10, 15 or 20 µM) and the primary root length, number of lateral root branches and the interaction between length and branching investigated. The summary statistics for root length are shown in Table S47, number of lateral root branches in Table S48, or the root architecture in Table S49. The two-way ANOVA test results for root length (Table S50), number of lateral root branches (Table S51) or the root architecture (Table S52) were performed with a more conservative test statistic ($p = 0.02$).

Table S47. Summary statistics of the root length (normalised to the mean value of each genotype at 0 µM) of Arabidopsis Col0 or 35S-COPT2 genotypes on Pd

Genotype	Condition	Con	Root length	STD	n	SE
Col0	Pd	0	1.00	0.15	31	0.03
35S-COPT2A	Pd	0	1.00	0.12	21	0.03
35S-COPT2B	Pd	0	1.00	0.18	25	0.04
35S-COPT2C	Pd	0	1.00	0.30	18	0.07
Col0	Pd	5	1.19	0.15	59	0.02
35S-COPT2A	Pd	5	1.01	0.23	31	0.04
35S-COPT2B	Pd	5	1.02	0.31	8	0.11
35S-COPT2C	Pd	5	1.12	0.25	20	0.06
Col0	Pd	10	1.25	0.23	71	0.03
35S-COPT2A	Pd	10	1.05	0.23	29	0.04
35S-COPT2B	Pd	10	0.94	0.38	29	0.07
35S-COPT2C	Pd	10	1.17	0.16	23	0.03
Col0	Pd	15	1.15	0.20	46	0.03
35S-COPT2A	Pd	15	1.00	0.22	35	0.04
35S-COPT2B	Pd	15	0.87	0.31	21	0.07
35S-COPT2C	Pd	15	1.07	0.28	26	0.05
Col0	Pd	20	1.04	0.19	42	0.03
35S-COPT2A	Pd	20	0.83	0.21	20	0.05
35S-COPT2B	Pd	20	0.93	0.28	34	0.05
35S-COPT2C	Pd	20	1.11	0.25	21	0.05

Table S48. Summary statistics of the number of lateral root branches (normalised to the mean value of each genotype at 0 uM) of Arabidopsis Col0 or 35S-COPT2 genotypes on Pd

Genotype	Condition	Conc	Lateral root branches	STD	n	SE
Col0	Pd	0	1.00	0.24	31	0.04
35S-COPT2A	Pd	0	1.00	0.37	21	0.08
35S-COPT2B	Pd	0	1.00	0.47	25	0.09
35S-COPT2C	Pd	0	1.00	0.99	18	0.23
Col0	Pd	5	0.59	0.33	59	0.04
35S-COPT2A	Pd	5	0.81	0.47	31	0.08
35S-COPT2B	Pd	5	1.01	0.61	8	0.21
35S-COPT2C	Pd	5	1.35	1.18	20	0.26
Col0	Pd	10	0.49	0.26	71	0.03
35S-COPT2A	Pd	10	0.41	0.34	29	0.06
35S-COPT2B	Pd	10	0.32	0.21	29	0.04
35S-COPT2C	Pd	10	1.81	1.72	23	0.36
Col0	Pd	15	0.29	0.23	46	0.03
35S-COPT2A	Pd	15	0.53	0.23	35	0.04
35S-COPT2B	Pd	15	0.40	0.20	21	0.04
35S-COPT2C	Pd	15	1.44	1.05	26	0.21
Col0	Pd	20	0.27	0.23	42	0.04
35S-COPT2A	Pd	20	0.30	0.23	20	0.05
35S-COPT2B	Pd	20	0.49	0.46	34	0.08
35S-COPT2C	Pd	20	2.70	2.03	21	0.44

Table S49. Summary statistics of the root architecture (normalised to the mean value of each genotype at 0 uM) of Arabidopsis Col0 or 35S-COPT2 genotypes on Pd

Genotype	Condition	Conc	Root architecture	STD	n	SE
Col0	Pd	0	1.02	0.27	31	0.05
35S-COPT2A	Pd	0	1.01	0.36	21	0.08
35S-COPT2B	Pd	0	0.98	0.43	25	0.09
35S-COPT2C	Pd	0	1.08	0.94	18	0.22
Col0	Pd	5	0.49	0.27	59	0.04
35S-COPT2A	Pd	5	0.79	0.45	31	0.08
35S-COPT2B	Pd	5	0.93	0.43	8	0.15
35S-COPT2C	Pd	5	1.21	0.95	20	0.21
Col0	Pd	10	0.41	0.24	71	0.03
35S-COPT2A	Pd	10	0.39	0.32	29	0.06
35S-COPT2B	Pd	10	0.61	0.88	29	0.16
35S-COPT2C	Pd	10	1.46	1.24	23	0.26
Col0	Pd	15	0.25	0.19	46	0.03
35S-COPT2A	Pd	15	0.54	0.22	35	0.04
35S-COPT2B	Pd	15	0.69	0.85	21	0.19
35S-COPT2C	Pd	15	1.42	1.13	26	0.22
Col0	Pd	20	0.25	0.20	42	0.03
35S-COPT2A	Pd	20	0.36	0.26	20	0.06
35S-COPT2B	Pd	20	0.54	0.40	34	0.07
35S-COPT2C	Pd	20	2.34	1.73	21	0.38

Table S50. Two-way ANOVA analysis results on the root length (normalised to the mean value of each genotype at 0 uM) of Col0 and 35S-COPT2 genotypes in the presence of Pd. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition. Between genotypes							
10	35S-COPT2A	10	Col0	-0.2035	-0.3843	-0.0227	0.0104
10	35S-COPT2B	10	Col0	-0.3104	-0.4913	-0.1296	0.0000
15	35S-COPT2B	15	Col0	-0.2831	-0.4992	-0.0670	0.0007
Within genotype, between conditions							
10	Col0	0	Col0	0.2508	0.0741	0.4274	0.0001
20	Col0	10	Col0	-0.2150	-0.3747	-0.0553	0.0004

Table S51. Two-way ANOVA analysis results on the number of lateral root branches (normalised to the mean value of each genotype at 0 μ M) of Col0 and 35S-COPT2 genotypes in the presence of Pd. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
5	35S-COPT2C	5	Col0	0.7635	0.1436	1.3835	0.0023
10	35S-COPT2C	10	Col0	1.3157	0.7408	1.8905	0.0000
15	35S-COPT2C	15	Col0	1.1499	0.5620	1.7377	0.0000
Within genotype, between conditions							
15	Col0	0	Col0	-0.7122	-1.2690	-0.1555	0.0011
20	Col0	0	Col0	-0.7301	-1.2974	-0.1628	0.0010
20	35S-COPT2C	0	35S-COPT2C	1.7033	0.9337	2.4729	0.0000
20	35S-COPT2C	5	35S-COPT2C	1.3533	0.6047	2.1019	0.0000
20	35S-COPT2C	10	35S-COPT2C	0.8973	0.1741	1.6204	0.0020
20	35S-COPT2C	15	35S-COPT2C	1.2654	0.5625	1.9684	0.0000

Table S52. Two-way ANOVA analysis results on the root architecture (normalised to the mean value of each genotype at 0 μ M) of Col0 and 35S-COPT2 genotypes in the presence of Pd. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
5	35S-COPT2C	5	Col0	0.7176	0.1389	1.2963	0.0020
10	35S-COPT2C	10	Col0	1.0495	0.5128	1.5861	0.0000
15	35S-COPT2C	15	Col0	1.1693	0.6205	1.7181	0.0000
20	35S-COPT2C	20	Col0	2.0888	1.4911	2.6866	0.0000
Within genotype, between conditions							
10	Col0	0	Col0	-0.6084	-1.0899	-0.1269	0.0014
15	Col0	0	Col0	-0.7663	-1.2860	-0.2465	0.0000
20	Col0	0	Col0	-0.7644	-1.2940	-0.2348	0.0001
20	35S-COPT2C	0	35S-COPT2C	1.2555	0.5370	1.9739	0.0000
20	35S-COPT2C	5	35S-COPT2C	1.1323	0.4335	1.8312	0.0000

Root architecture characterisation of Arabidopsis 35S-GP lines on Pd

The Arabidopsis 35S-GP lines were grown on $\frac{1}{2}$ MS(A) media containing Pd (0, 5, 10, 15 or 20 μ M) and the primary root length, number of lateral root branches and the interaction between length and branching investigated. The summary statistics for root length are shown in Table S53, number of lateral root branches in Table S54, or the root architecture in Table S55. The two-way ANOVA test results for root length (Table S56), number of lateral root branches (Table S57) or the root architecture (Table S58) were performed with a more conservative test statistic ($p = 0.02$).

Table S53. Summary statistics of the root length (normalised to the mean value of each genotype at 0 μ M) of Arabidopsis Col0 or 35S-GP genotypes on Pd

Genotype	Condition	Conc	Root length	STD	n	SE
Col0	Pd	0	1.00	0.15	31	0.03
35S-GPA	Pd	0	1.00	0.26	24	0.05
35S-GPB	Pd	0	1.00	0.41	20	0.09
35S-GPC	Pd	0	1.00	0.29	20	0.06
Col0	Pd	5	1.19	0.15	59	0.02
35S-GPA	Pd	5	0.72	0.50	22	0.11
35S-GPB	Pd	5	1.30	0.47	26	0.09
35S-GPC	Pd	5	0.74	0.24	25	0.05
Col0	Pd	10	1.25	0.23	71	0.03
35S-GPA	Pd	10	0.97	0.46	12	0.13
35S-GPB	Pd	10	1.44	0.62	26	0.12
35S-GPC	Pd	10	0.33	0.40	27	0.08
Col0	Pd	15	1.15	0.20	46	0.03
35S-GPA	Pd	15	0.60	0.57	24	0.12
35S-GPB	Pd	15	1.82	0.23	11	0.07
35S-GPC	Pd	15	0.12	0.09	31	0.02
Col0	Pd	20	1.04	0.19	42	0.03
35S-GPA	Pd	20	0.39	0.44	8	0.16
35S-GPB	Pd	20	1.31	0.41	2	0.29
35S-GPC	Pd	20	0.18	0.19	37	0.03

Table S54. Summary statistics of the number of lateral root branches (normalised to the mean value of each genotype at 0 μ M) of *Arabidopsis* Col0 or 35S-GP genotypes on Pd

Genotype	Condition	Conc	Lateral root branches	STD	n	SE
Col0	Pd	0	1.00	0.24	31	0.04
35S-GPA	Pd	0	1.00	0.59	24	0.12
35S-GPB	Pd	0	1.00	0.53	20	0.12
35S-GPC	Pd	0	1.00	0.48	20	0.11
Col0	Pd	5	0.59	0.33	59	0.04
35S-GPA	Pd	5	0.47	0.50	22	0.11
35S-GPB	Pd	5	1.14	0.81	26	0.16
35S-GPC	Pd	5	1.14	0.56	25	0.11
Col0	Pd	10	0.49	0.26	71	0.03
35S-GPA	Pd	10	0.78	0.59	12	0.17
35S-GPB	Pd	10	1.38	0.85	26	0.17
35S-GPC	Pd	10	0.28	0.43	27	0.08
Col0	Pd	15	0.29	0.23	46	0.03
35S-GPA	Pd	15	0.48	0.47	24	0.10
35S-GPB	Pd	15	1.68	0.83	11	0.25
35S-GPC	Pd	15	0.16	0.05	31	0.01
Col0	Pd	20	0.27	0.23	42	0.04
35S-GPA	Pd	20	0.19	0.15	8	0.05
35S-GPB	Pd	20	0.35	0.33	2	0.24
35S-GPC	Pd	20	0.26	0.26	37	0.04

Table S55. Summary statistics of the root architecture (normalised to the mean value of each genotype at 0 uM) of Arabidopsis Col0 or 35S-GP genotypes on Pd

Genotype	Condition	Conc	Root architecture	STD	n	SE
Col0	Pd	0	1.02	0.27	31	0.05
35S-GPA	Pd	0	0.97	0.44	24	0.09
35S-GPB	Pd	0	1.05	0.42	20	0.09
35S-GPC	Pd	0	1.08	0.64	20	0.14
Col0	Pd	5	0.49	0.27	59	0.04
35S-GPA	Pd	5	1.23	1.19	22	0.25
35S-GPB	Pd	5	0.77	0.46	26	0.09
35S-GPC	Pd	5	1.59	0.73	25	0.15
Col0	Pd	10	0.41	0.24	71	0.03
35S-GPA	Pd	10	1.17	1.02	12	0.29
35S-GPB	Pd	10	1.12	0.85	26	0.17
35S-GPC	Pd	10	1.53	0.97	27	0.19
Col0	Pd	15	0.25	0.19	46	0.03
35S-GPA	Pd	15	1.52	1.05	24	0.22
35S-GPB	Pd	15	0.89	0.41	11	0.12
35S-GPC	Pd	15	2.10	1.33	31	0.24
Col0	Pd	20	0.25	0.20	42	0.03
35S-GPA	Pd	20	1.81	2.43	8	0.86
35S-GPB	Pd	20	0.33	0.36	2	0.25
35S-GPC	Pd	20	1.98	1.25	37	0.21

Table S56. Two-way ANOVA analysis results on the root length (normalised to the mean value of each genotype at 0 uM) of Col0 and 35S-GP genotypes in the presence of Pd. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 1	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
5	35S-GPA	5	Col0	-0.4735	-0.7560	-0.1910	0.0000
5	35S-GPC	5	Col0	-0.4501	-0.7200	-0.1802	0.0000
10	35S-GPC	10	Col0	-0.9246	-1.1803	-0.6689	0.0000
15	35S-GPA	15	Col0	-0.5507	-0.8355	-0.2659	0.0000
15	35S-GPB	15	Col0	0.6683	0.2887	1.0478	0.0000
15	35S-GPC	15	Col0	-1.0343	-1.2971	-0.7715	0.0000
20	35S-GPA	20	Col0	-0.6428	-1.0791	-0.2065	0.0000
20	35S-GPC	20	Col0	-0.8579	-1.1129	-0.6029	0.0000
Within genotype, between condition							
15	35S-GPA	0	35S-GPA	-0.3958	-0.7223	-0.0694	0.0030
20	35S-GPA	0	35S-GPA	-0.6070	-1.0687	-0.1453	0.0006
20	35S-GPA	10	35S-GPA	-0.5759	-1.0921	-0.0597	0.0119
10	35S-GPB	0	35S-GPB	0.4443	0.1079	0.7807	0.0006
15	35S-GPB	0	35S-GPB	0.8231	0.3986	1.2477	0.0000
15	35S-GPB	5	35S-GPB	0.5240	0.1173	0.9308	0.0009
10	35S-GPC	0	35S-GPC	-0.6738	-1.0074	-0.3401	0.0000
15	35S-GPC	0	35S-GPC	-0.8794	-1.2037	-0.5550	0.0000
20	35S-GPC	0	35S-GPC	-0.8221	-1.1360	-0.5082	0.0000
10	35S-GPC	5	35S-GPC	-0.4169	-0.7308	-0.1030	0.0005
15	35S-GPC	5	35S-GPC	-0.6225	-0.9265	-0.3185	0.0000
20	35S-GPC	5	35S-GPC	-0.5652	-0.8580	-0.2724	0.0000

Table S57. Two-way ANOVA analysis results on the number of lateral root branches (normalised to the mean value of each genotype at 0 μ M) of Col0 and 35S-GP genotypes in the presence of Pd. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
5	35S-GPB	5	Col0	0.5538	0.1841	0.9235	0.0000
5	35S-GPC	5	Col0	0.5564	0.1816	0.9312	0.0000
10	35S-GPB	10	Col0	0.8898	0.5298	1.2498	0.0000
15	35S-GPB	15	Col0	1.3911	0.8640	1.9182	0.0000
Within genotype, between conditions							
5	Col0	0	Col0	-0.4138	-0.7622	-0.0654	0.0044
10	Col0	0	Col0	-0.5099	-0.8480	-0.1718	0.0000
15	Col0	0	Col0	-0.7122	-1.0772	-0.3473	0.0000
20	Col0	0	Col0	-0.7301	-1.1020	-0.3582	0.0000
5	35S-GPA	0	35S-GPA	-0.5317	-0.9953	-0.0682	0.0078
15	35S-GPA	0	35S-GPA	-0.5148	-0.9681	-0.0614	0.0091
20	35S-GPA	0	35S-GPA	-0.8095	-1.4506	-0.1683	0.0014
15	35S-GPB	0	35S-GPB	0.6791	0.0896	1.2687	0.0073
10	35S-GPC	0	35S-GPC	-0.7160	-1.1793	-0.2526	0.0000
15	35S-GPC	0	35S-GPC	-0.8399	-1.2904	-0.3895	0.0000
20	35S-GPC	0	35S-GPC	-0.7399	-1.1758	-0.3040	0.0000
10	35S-GPC	5	35S-GPC	-0.8588	-1.2947	-0.4229	0.0000
15	35S-GPC	5	35S-GPC	-0.9828	-1.4049	-0.5606	0.0000
20	35S-GPC	5	35S-GPC	-0.8827	-1.2893	-0.4761	0.0000

Table S58. Two-way ANOVA analysis results on the root architecture (normalised to the mean value of each genotype at 0 uM) of Col0 and 35S-GP genotypes in the presence of Pd. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
5	35S-GPC	5	Col0	1.0955	0.4552	1.7357	0.0000
10	35S-GPB	10	Col0	0.7164	0.1014	1.3314	0.0061
10	35S-GPC	10	Col0	1.1203	0.5137	1.7270	0.0000
15	35S-GPA	15	Col0	1.2684	0.5929	1.9440	0.0000
15	35S-GPC	15	Col0	1.8470	1.2236	2.4705	0.0000
20	35S-GPA	20	Col0	1.5559	0.5209	2.5908	0.0000
20	35S-GPC	20	Col0	1.7290	1.1241	2.3339	0.0000
Within genotypes, between conditions							
15	Col0	0	Col0	-0.7663	-1.3897	-0.1428	0.0024
20	Col0	0	Col0	-0.7644	-1.3997	-0.1291	0.0035
15	35S-GPC	0	35S-GPC	1.0172	0.2477	1.7867	0.0006
20	35S-GPC	0	35S-GPC	0.9010	0.1564	1.6456	0.0032

Root architecture characterisation of Arabidopsis 35S-GPC lines on Pd

The Arabidopsis 35S-GPC lines were grown on $\frac{1}{2}$ MS(A) media containing Pd (0, 5, 10, 15 or 20 μ M) and the primary root length, number of lateral root branches and the interaction between length and branching investigated. The summary statistics for root length are shown in Table S59, number of lateral root branches in Table S60, or the root architecture in Table S61. The two-way ANOVA test results for root length are in Table S62, number of lateral root branches in Table S63 or the root architecture Table S64, and were performed with a more conservative test statistic ($p = 0.02$).

Table S59. Summary statistics of the root length (normalised to the mean value of each genotype at 0 μ M) of Arabidopsis Col0 or 35S-GPC genotypes on Pd

Genotype	Condition	Conc	Root length	STD	n	SE
Col0	Pd	0	1.00	0.15	31	0.03
35S-GPCA	Pd	0	1.00	0.46	21	0.10
35S-GPCB	Pd	0	1.00	0.31	26	0.06
35S-GPCC	Pd	0	1.00	0.49	51	0.07
Col0	Pd	5	1.19	0.15	59	0.02
35S-GPCA	Pd	5	0.91	0.36	17	0.09
35S-GPCB	Pd	5	0.57	0.88	16	0.22
35S-GPCC	Pd	5	1.59	0.58	30	0.11
Col0	Pd	10	1.25	0.23	71	0.03
35S-GPCA	Pd	10	1.15	0.68	25	0.14
35S-GPCB	Pd	10	0.18	0.21	33	0.04
35S-GPCC	Pd	10	0.83	0.59	23	0.12
Col0	Pd	15	1.15	0.20	46	0.03
35S-GPCA	Pd	15	0.83	0.49	40	0.08
35S-GPCB	Pd	15	0.25	0.22	24	0.05
35S-GPCC	Pd	15	0.62	0.34	20	0.08
Col0	Pd	20	1.04	0.19	42	0.03
35S-GPCA	Pd	20	0.63	0.43	33	0.08
35S-GPCB	Pd	20	0.19	0.15	27	0.03
35S-GPCC	Pd	20	0.26	0.12	27	0.02

Table S60. Summary statistics of the number of lateral root branches (normalised to the mean value of each genotype at 0 μ M) of *Arabidopsis* Col0 or 35S-GPC genotypes on Pd

Genotype	Condition	Conc	Lateral root branches	STD	n	SE
Col0	Pd	0	1.0003	0.2417	31	0.0434
35S-GPCA	Pd	0	1.0005	0.8672	21	0.1892
35S-GPCB	Pd	0	0.9942	0.5271	26	0.1034
35S-GPCC	Pd	0	1.0007	0.5725	51	0.0802
Col0	Pd	5	0.5865	0.3270	59	0.0426
35S-GPCA	Pd	5	1.4590	0.6357	17	0.1542
35S-GPCB	Pd	5	0.2476	0.1648	16	0.0412
35S-GPCC	Pd	5	0.3509	0.3228	30	0.0589
Col0	Pd	10	0.4903	0.2564	71	0.0304
35S-GPCA	Pd	10	1.1122	1.0182	25	0.2036
35S-GPCB	Pd	10	0.2401	0.1181	33	0.0206
35S-GPCC	Pd	10	0.4923	0.2717	23	0.0566
Col0	Pd	15	0.2880	0.2291	46	0.0338
35S-GPCA	Pd	15	0.4739	0.4760	40	0.0753
35S-GPCB	Pd	15	0.2516	0.1065	24	0.0217
35S-GPCC	Pd	15	0.4864	0.2903	20	0.0649
Col0	Pd	20	0.2701	0.2271	42	0.0350
35S-GPCA	Pd	20	0.3686	0.4302	33	0.0749
35S-GPCB	Pd	20	0.2236	0.0747	27	0.0144
35S-GPCC	Pd	20	0.3072	0.1528	27	0.0294

Table S61. Summary statistics of the root architecture (normalised to the mean value of each genotype at 0 μ M) of Arabidopsis Col0 or 35S-GPC genotypes on Pd

Genotype	Condition	Conc	Root architecture	STD	n	SE
Col0	Pd	0	1.02	0.27	31	0.05
35S-GPCA	Pd	0	1.02	0.75	21	0.16
35S-GPCB	Pd	0	0.99	0.39	26	0.08
35S-GPCC	Pd	0	1.06	0.50	51	0.07
Col0	Pd	5	0.49	0.27	59	0.04
35S-GPCA	Pd	5	1.63	0.67	17	0.16
35S-GPCB	Pd	5	2.55	2.27	16	0.57
35S-GPCC	Pd	5	0.24	0.20	30	0.04
Col0	Pd	10	0.41	0.24	71	0.03
35S-GPCA	Pd	10	0.99	0.72	25	0.14
35S-GPCB	Pd	10	2.51	1.29	33	0.22
35S-GPCC	Pd	10	0.94	0.72	23	0.15
Col0	Pd	15	0.25	0.19	46	0.03
35S-GPCA	Pd	15	0.71	0.60	40	0.09
35S-GPCB	Pd	15	2.52	2.77	24	0.57
35S-GPCC	Pd	15	0.88	0.45	20	0.10
Col0	Pd	20	0.25	0.20	42	0.03
35S-GPCA	Pd	20	0.79	0.63	33	0.11
35S-GPCB	Pd	20	1.84	1.19	27	0.23
35S-GPCC	Pd	20	1.40	0.74	27	0.14

Table S62. Two-way ANOVA analysis results on the root length (normalised to the mean value of each genotype at 0 μ M) of Col0 and 35S-GPC genotypes in the presence of Pd. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
5	35S-GPCB	5	Col0	-0.6224	-0.9997	-0.2451	0.0000
5	35S-GPCC	5	Col0	0.3999	0.0998	0.7001	0.0005
10	35S-GPCB	10	Col0	-1.0684	-1.3504	-0.7864	0.0000
10	35S-GPCC	10	Col0	-0.4171	-0.7382	-0.0959	0.0008
15	35S-GPCB	15	Col0	-0.9075	-1.2446	-0.5705	0.0000
15	35S-GPCC	15	Col0	-0.5361	-0.8946	-0.1775	0.0000
20	35S-GPCA	20	Col0	-0.4012	-0.7126	-0.0898	0.0009
20	35S-GPCB	20	Col0	-0.8462	-1.1764	-0.5161	0.0000
20	35S-GPCC	20	Col0	-0.7746	-1.1048	-0.4444	0.0000
Within genotype, between conditions							
20	35S-GPCA	10	35S-GPCA	-0.5174	-0.8723	-0.1625	0.0001
10	35S-GPCB	0	35S-GPCB	-0.8174	-1.1684	-0.4664	0.0000
15	35S-GPCB	0	35S-GPCB	-0.7524	-1.1313	-0.3735	0.0000
20	35S-GPCB	0	35S-GPCB	-0.8102	-1.1780	-0.4424	0.0000
5	35S-GPCC	0	35S-GPCC	0.5930	0.2850	0.9009	0.0000
15	35S-GPCC	0	35S-GPCC	-0.3814	-0.7345	-0.0282	0.0190
20	35S-GPCC	0	35S-GPCC	-0.7390	-1.0576	-0.4204	0.0000
10	35S-GPCC	5	35S-GPCC	-0.7594	-1.1304	-0.3885	0.0000
15	35S-GPCC	5	35S-GPCC	-0.9743	-1.3607	-0.5879	0.0000
20	35S-GPCC	5	35S-GPCC	-1.3320	-1.6870	-0.9769	0.0000
20	35S-GPCC	10	35S-GPCC	-0.5725	-0.9523	-0.1927	0.0000

Table S63. Two-way ANOVA analysis results on the number of lateral root branches (normalised to the mean value of each genotype at 0 μ M) of Col0 and 35S-GPC genotypes in the presence of Pd. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition, between genotypes							
5	35S-GPCA	5	Col0	0.8725	0.4677	1.2773	0.0000
10	35S-GPCA	10	Col0	0.6218	0.2798	0.9638	0.0000
Within genotype, between conditions							
5	Col0	0	Col0	-0.4138	-0.7400	-0.0876	0.0013
10	Col0	0	Col0	-0.5099	-0.8265	-0.1933	0.0000
15	Col0	0	Col0	-0.7122	-1.0540	-0.3705	0.0000
20	Col0	0	Col0	-0.7301	-1.0783	-0.3819	0.0000
15	35S-GPCA	0	35S-GPCA	-0.5266	-0.9229	-0.1303	0.0005
20	35S-GPCA	0	35S-GPCA	-0.6319	-1.0424	-0.2214	0.0000
15	35S-GPCA	5	35S-GPCA	-0.9850	-1.4108	-0.5593	0.0000
20	35S-GPCA	5	35S-GPCA	-1.0904	-1.5294	-0.6513	0.0000
15	35S-GPCA	10	35S-GPCA	-0.6382	-1.0132	-0.2633	0.0000
20	35S-GPCA	10	35S-GPCA	-0.7435	-1.1335	-0.3536	0.0000
5	35S-GPCB	0	35S-GPCB	-0.7466	-1.2138	-0.2793	0.0000
10	35S-GPCB	0	35S-GPCB	-0.7541	-1.1397	-0.3684	0.0000
15	35S-GPCB	0	35S-GPCB	-0.7426	-1.1589	-0.3263	0.0000
20	35S-GPCB	0	35S-GPCB	-0.7706	-1.1747	-0.3665	0.0000
5	35S-GPCC	0	35S-GPCC	-0.6498	-0.9882	-0.3115	0.0000
10	35S-GPCC	0	35S-GPCC	-0.5084	-0.8778	-0.1390	0.0002
15	35S-GPCC	0	35S-GPCC	-0.5143	-0.9023	-0.1263	0.0005
20	35S-GPCC	0	35S-GPCC	-0.6936	-1.0436	-0.3435	0.0000

Table S64. Two-way ANOVA analysis results on the root architecture (normalised to the mean value of each genotype at 0 uM) of Col0 and 35S-GPC genotypes in the presence of Pd. Diff: difference between mean values; Lwr: the lower limit; Upr; the upper limit; p-value: probability value. Only significant results are shown ($p < 0.02$).

Conc 1	Genotype 1	Conc 2	Genotype 2	Diff	Lwr	Upr	p-value
Within condition. Between genotypes							
5	35S-GPCA	5	Col0	1.1404	0.3092	1.9715	0.0002
5	35S-GPCB	5	Col0	2.0585	1.2074	2.9095	0.0000
10	35S-GPCB	10	Col0	2.1053	1.4691	2.7414	0.0000
15	35S-GPCB	15	Col0	2.2697	1.5094	3.0300	0.0000
20	35S-GPCB	20	Col0	1.5876	0.8429	2.3324	0.0000
20	35S-GPCC	20	Col0	1.1506	0.4058	1.8954	0.0000
Within genotype, between condition							
15	Col0	0	Col0	-0.7663	-1.4679	-0.0646	0.0162
5	35S-GPCB	0	35S-GPCB	1.5606	0.6012	2.5200	0.0000
10	35S-GPCB	0	35S-GPCB	1.5245	0.7327	2.3163	0.0000
15	35S-GPCB	0	35S-GPCB	1.5311	0.6764	2.3858	0.0000
5	35S-GPCC	0	35S-GPCC	-0.8197	-1.5144	-0.1250	0.0049
20	35S-GPCC	5	35S-GPCC	1.1636	0.3626	1.9646	0.0001

Analysis of element uptake of Arabidopsis *COPT2* and *35S-COPT2* lines grown in the presence of Pd

Analysis of element uptake was performed using the Arabidopsis *COPT2* and transgenic genotypes alongside WT. A one-way ANOVA was performed for each tissue type (shoot or root) and wavelength (Pd: 340 nm, 342 nm; Cu: 324 nm; Fe: 239 nm) (Table S65). Homogeneity of variances for each subset of data was analysed by a Levene's test, and the normality of data was investigated using a Shapiro-Wilk test on the residuals of the one-way ANOVA analysis (Table S66, Table S67). The data produced a significant ($p < 0.05$) result from either of the tests of assumptions a non-parametric test, Kruskal-Wallis, was performed; otherwise, data was analysed by a one-way ANOVA followed by a Tukey's HSD test (Table S68). All data subsets excluding the root measurement of Pd at 342 nm were analysed by a Kruskal-Wallis test. The Pd measurements both produced significant results, but the subsequent Wilcoxon rank sum test did not show any significant differences (Table S68). There was one significant comparison within the root Pd concentration measured at 342 nm, Arabidopsis Col0 contained a significantly higher concentration of Pd comparative to *copt2-2* (Table S68).

Table S65. Results of individual one-way ANOVA tests on the element concentration in shoot or root tissue of Arabidopsis genotypes grown in a hydroponic system with 1mM Pd

ANOVA results (one-way)											
Tissue	Element	Wavelength (nm)	d.f.	Sum squares	Mean Sq	F value	p-value	Sig	Homogeneity of variances?	Normal distribution?	Chosen test
shoot	Pd	340	12, 52	5.9830	0.4985	2.9330	0.0036	***	FALSE	FALSE	Non-parametric
shoot	Pd	342	12, 52	5.2850	0.4404	3.6280	0.0006	***	TRUE	FALSE	Non-parametric
shoot	Cu	324	12, 52	0.0231	0.0019	1.2650	0.2670	ns	FALSE	FALSE	Non-parametric
shoot	Fe	239	12, 52	112.4000	9.3640	0.6670	0.7750	ns	TRUE	FALSE	Non-parametric
root	Pd	340	12, 49	6590.0000	549.2000	0.8980	0.5550	ns	TRUE	FALSE	Non-parametric
root	Pd	342	12, 43	6530.0000	544.1000	2.0570	0.0418	*	TRUE	TRUE	One-way ANOVA
root	Cu	324	12,52	0.2490	0.0208	0.3080	0.9850	ns	TRUE	FALSE	Non-parametric
root	Fe	239	12, 48	1437.0000	119.8000	0.5420	0.8760	ns	TRUE	FALSE	Non-parametric

Table S66. Results of Levene's tests for the homogeneity of variances on the element concentration in shoot or root tissue of Arabidopsis genotypes grown in a hydroponic system with 1mM Pd

Levene's test for homogeneity of variances						
Tissue	Element	Wavelength (nm)	d.f.	f value	p-value	Sig
shoot	Pd	340	12, 52	2.0978	0.0333	*
shoot	Pd	340	12, 52	1.6410	0.1089	ns
shoot	Cu	324	12, 52	2.5461	0.0100	*
shoot	Fe	239	12, 52	0.5671	0.8579	ns
root	Pd	340	12, 49	1.0583	0.4143	ns
root	Pd	342	12, 43	0.8925	0.5611	ns
root	Cu	324	12, 52	0.7543	0.6927	ns
root	Fe	239	12, 48	0.7010	0.7425	ns

Table S67. Results of individual Shapiro-Wilk tests on the residuals of a one-way ANOVA performed on the element concentration in shoot or root tissue of Arabidopsis genotypes grown in a hydroponic system with 1mM Pd

Shapiro-Wilk test for normal distribution					
Tissue	Element	Wavelength (nm)	W	p-value	Sig
shoot	Pd	340	0.8958	0.0000	***
shoot	Pd	340	0.8547	0.0000	***
shoot	Cu	324	0.8689	0.0000	***
shoot	Fe	239	0.8716	0.0000	***
root	Pd	340	0.8001	0.0000	***
root	Pd	342	0.9738	0.2595	ns
root	Cu	324	0.8815	0.0000	***
root	Fe	239	0.9006	0.0001	***

Table S68. Results of Kruskal-Wallis test, the non-parametric alternative to the one-way ANOVA, and a Tukey's HSD test on the element concentration in shoot or root tissue of Arabidopsis genotypes grown in a hydroponic system with 1mM Pd

Kruskal-Wallis test								
Tissue	Element	Wavelength (nm)	X ²	d.f.	p-value	Sig	Wilcoxon sig. comparisons	p-value
shoot	Pd	340	23.462	12	0.02405	*	ns	NA
shoot	Pd	342	25.863	12	0.01122	*	ns	NA
shoot	Cu	324	7.9803	12	0.7867	ns	NA	NA
shoot	Fe	239	13.258	12	0.3506	ns	NA	NA
root	Pd	340	14.435	12	0.2738	ns	NA	NA
root	Cu	324	7.3922	12	0.8306	ns	NA	NA
root	Fe	239	7.8453	12	0.7971	ns	NA	NA
Tukey's HSD test								
Tissue	Element	Wavelength (nm)	Comp	Difference	Lower	Upper	p-value	Sig
root	Pd	342	<i>copt2-2-Col0</i>	-42.0147	-78.0647	-5.96465	0.0104	*