Table S1. QTL analyses

QTL	Trait <sup>a</sup>	Chromosome	QTL position (cM) <sup>b</sup>	Marker <sup>c</sup>	LOD score	R <sup>2</sup> value <sup>d</sup>	a <sup>e</sup>
ZnT1	RelPR <sub>150</sub>	1	55.6	F5I14	5.99	12	3.66
ZnT2	RelPR <sub>150</sub>	3	6.0	ATHCHIB2	14.1	29	5.58
ZnT3	RelPR <sub>150</sub>	5	51.2	MSAT5.9	6.94	16	4.13

- a. Relative variation of the Primary Root length between 150 μM Zn and control condition (RelPR<sub>150</sub>)
- b. The position of the QTL is expressed in cM from the 1st marker of the chromosome
- c. Name of the closest marker, according to the initial mapping approach
- d. Percentage of variance explained by the QTL
- e. Additive effect. Positive value indicates that for the three QTLs, the presence of the Sha allele at QTL decreases root length in the presence of Zn.