

CORRECTION

# Correction: Mapping Quantitative Trait Loci Associated with Root Traits Using Sequencing-Based Genotyping Chromosome Segment Substitution Lines Derived from 9311 and Nipponbare in Rice (*Oryza sativa* L.)

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There are errors in the title. The correct title is: Mapping Quantitative Trait Loci Associated with Root Traits Using High Throughput Genotyped Chromosome Segment Substitution Lines Derived from 9311 and Nipponbare in Rice (*Oryza sativa* L.). The correct citation is: Zhou Y, Dong G, Tao Y, Chen C, Yang B, Wu Y, et al. (2016) Mapping Quantitative Trait Loci Associated with Root Traits Using High Throughput Genotyped Chromosome Segment Substitution Lines Derived from 9311 and Nipponbare in Rice (*Oryza sativa* L.). PLoS ONE 11(3): e0151796. doi:[10.1371/journal.pone.0151796](https://doi.org/10.1371/journal.pone.0151796).

In [Table 3](#), the column “TRL” is missing. Please see the corrected [Table 3](#) here.



## OPEN ACCESS

**Citation:** Zhou Y, Dong G, Tao Y, Chen C, Yang B, Wu Y, et al. (2016) Correction: Mapping Quantitative Trait Loci Associated with Root Traits Using Sequencing-Based Genotyping Chromosome Segment Substitution Lines Derived from 9311 and Nipponbare in Rice (*Oryza sativa* L.). PLoS ONE 11(5): e0155280. doi:[10.1371/journal.pone.0155280](https://doi.org/10.1371/journal.pone.0155280)

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**Table 3. Correlation analysis among seven root traits and six yield-related traits in the CSSL population.**

	RN	TRL	RDW	RTH	MRL	TAA	RV
PN	- 0.132	0.194*	- 0.043	0.116	0.167	0.001	0.057
SPP	- 0.059	0.003	0.119	0.094	0.072	- 0.099	- 0.132
GW	0.042	0.137	0.085	0.015	0.224*	0.171	0.104
SSR	0.162	0.138	- 0.004	0.195*	0.024	0.193*	- 0.046
BY	0.017	0.194*	0.220*	0.023	0.386**	- 0.090	- 0.071
GY	0.001	0.209*	0.056	0.194*	0.201*	0.103	- 0.056

\* Correlation is significant at the 0.05 level (two-tailed).

\*\* Correlation is significant at the 0.01 level (two-tailed).

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## Reference

1. Zhou Y, Dong G, Tao Y, Chen C, Yang B, Wu Y, et al. (2016) Mapping Quantitative Trait Loci Associated with Root Traits Using Sequencing-Based Genotyping Chromosome Segment Substitution Lines Derived from 9311 and Nipponbare in Rice (*Oryza sativa* L.). PLoS ONE 11(3): e0151796. doi: [10.1371/journal.pone.0151796](https://doi.org/10.1371/journal.pone.0151796) PMID: [27010823](https://pubmed.ncbi.nlm.nih.gov/27010823/)