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CORRECTION

Correction: A Metatranscriptomic Approach to the Identification of Microbiota Associated with the Ant *Formica exsecta*

The *PLOS ONE* Staff

In Table 1, there is an error in the title. Additionally, there are errors in the numbers of the FIMM and BGI columns of the New Stage in Caste/sex Queen. Please view a corrected version of Table 1 here.

Table 1. Number of individuals pooled in each of the total of 14 libraries sequenced by FIMM or BGI.

Caste/sex	Stage	FIMM	BGI
Queen	Old overwintered	6 (6)	4 (4)
	New	10 (5)	8 (4)
	Old cocoon	8 (4)	6 (3)
	Intermediate cocoon	8 (4)	6 (3)
	Young cocoon	8 (4)	6 (3)
Worker	Old overwintered	18 (6)	30 (8)
	New	10 (5)	15 (6)
	Old cocoon	8 (4)	6 (3)
	Intermediate cocoon	8 (4)	6 (3)
	Young cocoon	8 (4)	6 (3)
Male	Adult	3 (3)	3 (3)
	Old cocoon	3 (3)	3 (3)
	Intermediate cocoon	3 (3)	3 (3)
	Young cocoon	3 (3)	3 (3)

Castes and developmental classes of *F*. *exsecta* are given together with number of source colonies in parentheses.

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Reference

1. Johansson H, Dhaygude K, Lindström S, Helanterä H, Sundström L, Trontti K (2013) A Metatranscriptomic Approach to the Identification of Microbiota Associated with the Ant *Formica exsecta*. PLoS ONE 8(11): e79777. doi: 10.1371/journal.pone.0079777 PMID: 24260298

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