

CORRECTION

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Correction: Maptcha: an efficient parallel workflow for hybrid genome scaffolding

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The original article can be found online at <https://doi.org/10.1186/s12859-024-05878-4>.

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Following publication of the original article [1], the authors identified that the data in Table 3 was measured in minutes and not in seconds. The correct table is given below. The original article [1] has been corrected.



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Table 3 Performance comparison of the output scaffolds generated by the different tools on the different inputs

		Time taken (in mins)	Peak Memory (in GB)
<i>T. crassiceps</i>	LRScaf	10.13	10.87
		10.32	16.01
		10.33	12.33
	Pilon	10.18	11.02
		10.22	18.01
		10.27	12.11
	Pilon	10.54	12.48
		10.54	12.48
		10.54	12.48

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Reference

1. Bhowmik O, et al. Maptcha: an efficient parallel workflow for hybrid genome scaffolding. *BMC Bioinformatics*. 2024;25:263. <https://doi.org/10.1186/s12859-024-05878-4>.

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