

ERRATUM

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# Erratum to: OrthoFiller: utilising data from multiple species to improve the completeness of genome annotations

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## Erratum

After publication of the original article [1] the authors found the following errors had occurred:

1. *Saccaromyces* should be spelt *Saccharomyces* in Table 1. (Table 1)
2. *Kluveromyces* should be spelt *Kluyveromyces* in Table 1. (Table 1)
3. Table 4, columns 3, 5, 7 and 9: All values within these columns should be placed in brackets to indicate the standard deviation. (Table 4)
4. The legend for Table 4 should read: 'Numbers shown are rounded mean values from 5 disjoint removed subsets of genes, with standard deviations bracketed and not '10 removed subsets' as per the original article. (Table 4)

The original article has been corrected.

Corrected versions of all figures and tables are included in this Erratum:

Corrected Table 1

**Table 1** Species Set A, fungal species used for algorithm validation

Species Name	Source	Strain	Taxonomy ID	References
<i>Eremothecium gossypii</i>	JGI <sup>a</sup>	ATCC10895	284,811	[12]
<i>Debaromyces hansenii</i>	JGI	CBS767	284,592	[13] [14]
<i>Kluyveromyces lactis</i>	JGI	CLIB210	284,590	[13]
<i>Saccharomyces cerevisiae</i>	SGD <sup>b</sup>	S288C	559,292	[24]
<i>Yarrowia lipolytica</i>	JGI	CLIB122	284,591	[13]

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## Corrected Table 4

**Table 4** Recovery of removed genes in *A. thaliana*, averaged over five runs

	10% annotations removed				90% annotations removed			
	OrthoFiller		de novo		OrthoFiller		de novo	
No. genes removed	2410		2410		21,683		21,683	
Total genes found <sup>a</sup>	1233	(37.5)	13,184	(426.7)	11,480	(96.2)	42,504	(223.5)
Found genes which overlap removed genes <sup>a</sup>	1106	(37.5)	4918	(130.4)	11,343	(89.0)	35,609	(149.5)
Total recovered genes <sup>a</sup>	1035	(31.72)	2268	(16.4)	10,380	(59.7)	20,430	(33.0)
Number of split genes <sup>a</sup>	67	(5.4)	1213	(23.6)	944	(34.4)	7451	(37.7)
Mean pF-score of found genes <sup>a</sup>	0.75	(0.01)	0.45	(<0.01)	0.70	(<0.01)	0.55	(<0.01)
Mean oF-score of found genes <sup>a</sup>	0.94	(<0.01)	0.51	(<0.01)	0.89	(<0.01)	0.64	(<0.01)
High-quality found genes (pF-score $\geq$ 0.95) <sup>a</sup>	432.0	(29.3)	640.8	(27.4)	3419.8	(21.3)	9079.6	(99.5)
Lower-quality found genes (pF-score < 0.95) <sup>a</sup>	674.6	(32.1)	4277.2	(147.8)	7923.8	(99.5)	26,529.8	(201.3)
Mean pF-score of lower-quality genes <sup>a</sup>	0.61	(0.02)	0.31	(<0.01)	0.57	(<0.01)	0.33	(<0.01)
% of lower-quality genes with oF-score < 0.95 <sup>a</sup>	34.6	(1.9)	81.1	(0.9)	43.4	(0.6)	73.9	(0.1)

<sup>a</sup>Numbers shown are rounded mean values from 5 disjoint removed subsets of genes, with standard deviations bracketed

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## Reference

1. Dunne M, Kelly S. OrthoFiller: utilising data from multiple species to improve the completeness of genome annotations. *BMC Genomics*. 2017; 18:390. doi:10.1186/s12864-017-3771-x.