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Erratum to: BicPAMS: software for biological data analysis with pattern-based biclustering

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Erratum

Upon publication of this article [1], it was brought to our attention that the online version of Table 8 contained an error. The correct Table 8 is shown below:

Table 8 has been corrected in the original article.

Reference
1. Henriques R, et al. BicPAMS: software for biological data analysis with pattern-based biclustering. BMC Bioinformatics. 2017;18:82. doi:10.1186/s12859-017-1493-3.

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Table 8 Biological networks used to experimentally assess BicPAMS

Type	Source	Organism	#Nodes	#Interactions	Density	Notes on the weight of interactions
GI (gene interactions)	DryGIN	Yeast	4455	191309	1.0%	Weights (65% negative) from double-mutant arrays [36].
GI (gene interactions)	STRING	Yeast	6314	3759902	1.1%	Known and predicted associations benchmarked from multiple data sources and literature (text mining), and combined through an integrative score [37].
PPI (protein interactions)	STRING	E. Coli	8428	3293416	4.6%	
PPI (protein interactions)	STRING	Human	19247	8548002	2.3%	