# CORRECTION Open Access



# Correction to: Identification of new signalling peptides through a genome-wide survey of 250 fungal secretomes

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### **Correction to: BMC Genomics**

## https://doi.org/10.1186/s12864-018-5414-2

Following the publication of this article [1] the authors noted that the image in Fig. 1 was incorrect. Due to a typesetting error an incorrect image was processed as Fig. 1, and the publisher apologizes to the authors and readers for the inconvenience. The correct figure is reproduced in this erratum:

The original article has been corrected.

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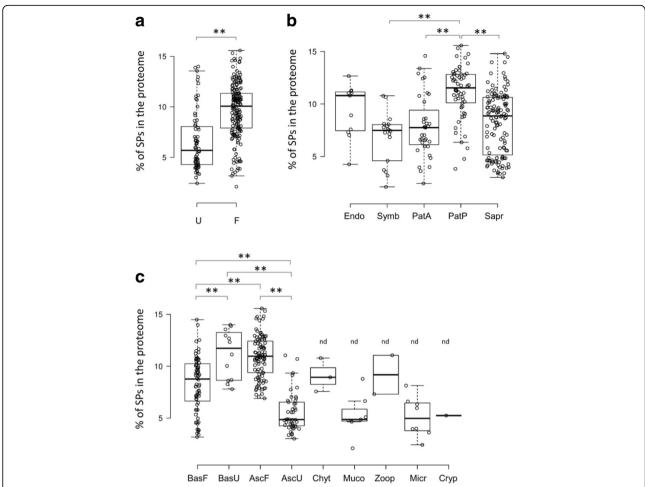
### Reference

 Le Marquer, et al. Identification of new signalling peptides through a genome-wide survey of 250 fungal secretomes. BMC Genomics. 2019;20:64 https://doi.org/10.1186/s12864-018-5414-2.

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**Fig. 1** Proportion of secreted proteins (SPs) in 250 fungal species, with regard to fungal morphology (**a**), lifestyle (**b**) and lineage (**c**). U: yeasts, yeast-like and unicellular fungi, F: filamentous fungi, Endo: endophytes, Symb: symbionts, PatP: plant pathogens, PatA: animal pathogens, Sapr: saprotrophs, BasF: filamentous Basidiomycota, BasU: yeast, yeast-like and unicellular Basidiomycota, AscF: filamentous Ascomycota, AscU: yeast, yeast-like and unicellular Ascomycota, Chyt: Chytridiomycota, Muco: Mucoromycota, Zoop: Zoopagomycota, Micr: Microsporidia, Cryp: Cryptomycota. Statistical analysis was performed with one-way analysis of variance with post-hoc Tukey HSD test; \*\*: p < 0.01). nd: fungal phylum for which statistical comparisons were not performed