Correction

Patterns of Genomic Variation in the Opportunistic Pathogen Candida glabrata Suggest the Existence of Mating and a Secondary Association with Humans

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After the original publication of this article, and due to new analysis re-using the data, we noted an error in our calculation of unique genes in the analyzed strains that was caused by a program bug in our analysis of OrthoMCL output. As a result, two sentences in the text contain several erroneous numbers that we now wish to correct.

The sentences “We found that 580 protein-coding genes from the reference strain (CBS138) are unique to this genome. Similarly, a range of 302–580 predicted genes (average 342) are unique for each strain, totaling 9,915 strain-specific genes among the 29 strains considered.” should be “We found that 291 protein-coding genes from the reference strain (CBS138) are unique to this genome. A range of 2–291 predicted genes (average 42) are unique for each strain, totaling 1,224 strain-specific genes among the 29 strains considered.”

No other calculations were affected, and this error does not affect other analyses or the conclusions of the article. We apologize for the error and the confusion it may have caused.