

CORRECTION

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# Correction: Chromosome-level genome assemblies of *Cutaneotrichosporon* spp. (Trichosporonales, Basidiomycota) reveal imbalanced evolution between nucleotide sequences and chromosome synteny

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**Correction:** *BMC Genomics* 24, 609 (2023)  
<https://doi.org/10.1186/s12864-023-09718-2>

Following publication of the original article [1], it was reported that part of the figure captions for Figs. 1, 2, 3, 4 and 5 were mistakenly inserted into the article body.

Part of the caption of Fig. 1 appeared in the sub-section “Sequencing and assembly results” and was processed as the paragraph directly preceding the beginning with

“The self-synteny plot of the *Cutaneotrichosporon* genome showed no obvious centromeric repeats ...”

Part of the caption of Fig. 2 appeared as the final paragraph of the sub-section “Comparison of nuclear genomes.”

Part of the caption of Fig. 3 appeared as the final paragraph of the sub-section “Quantification of differences in genomes using different criteria.”

The captions of Fig. 4 and 5 appeared as the final two paragraphs of the sub-section “Genes and synteny of mitochondrial genomes.”

The correct Figs. 1-5 with their captions are given in this Correction article and the original article [1] has been updated.

The original article can be found online at <https://doi.org/10.1186/s12864-023-09718-2>.

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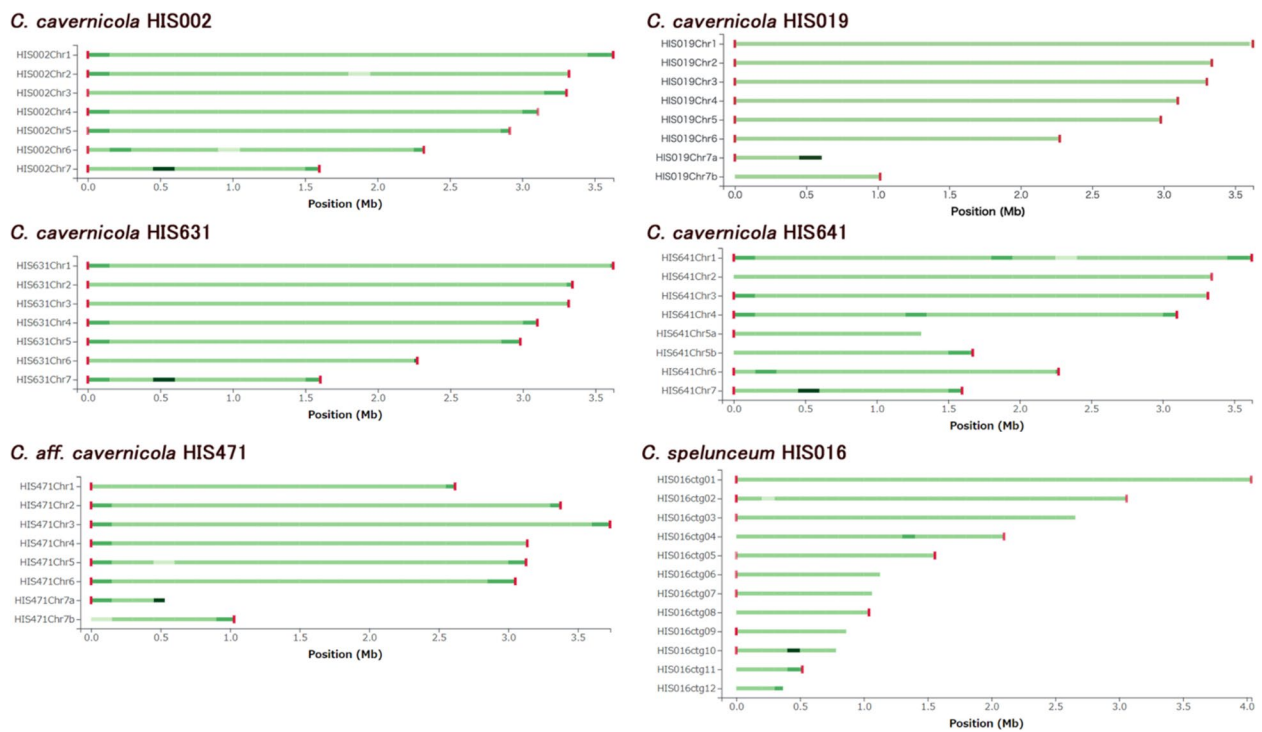
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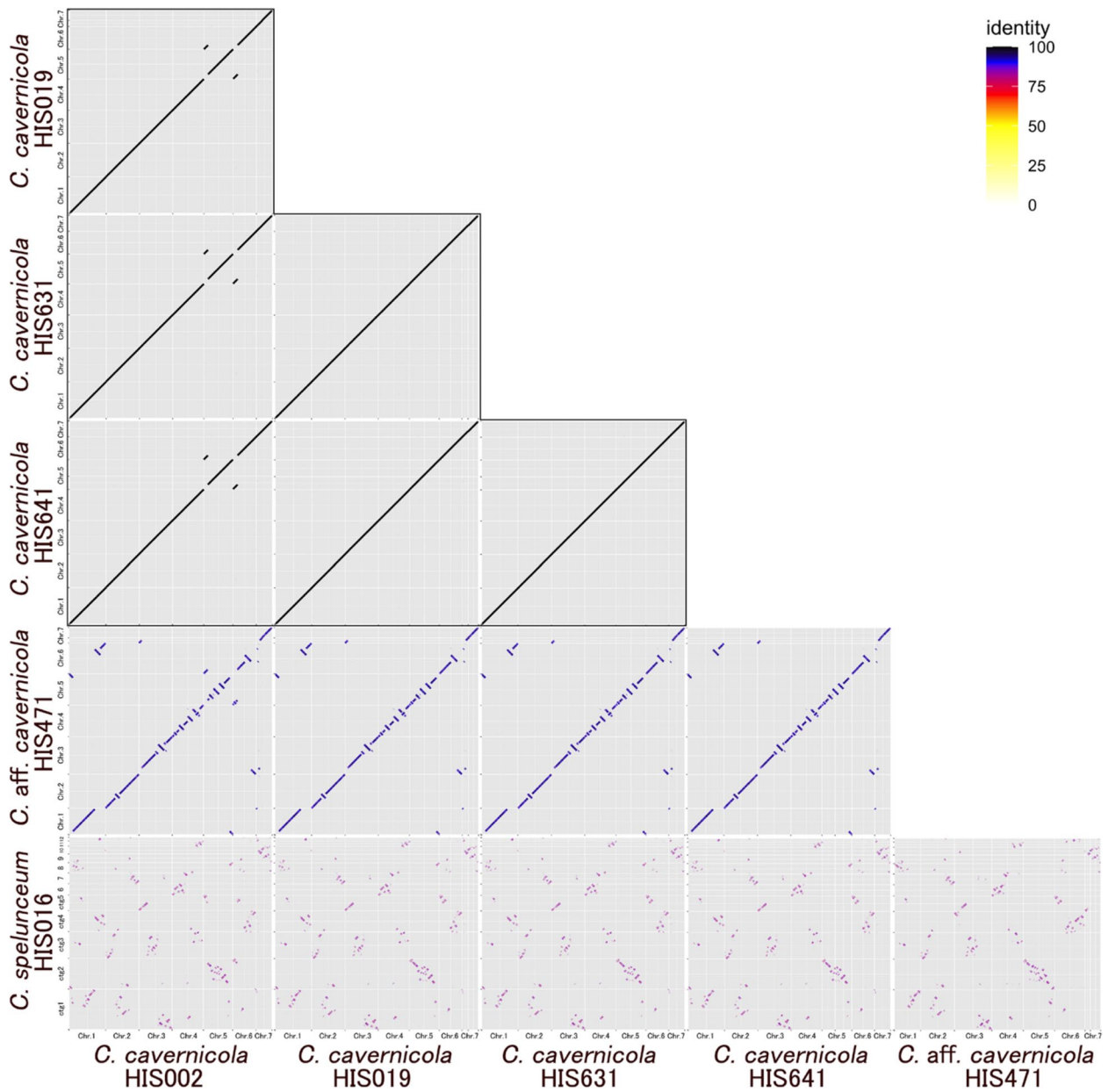
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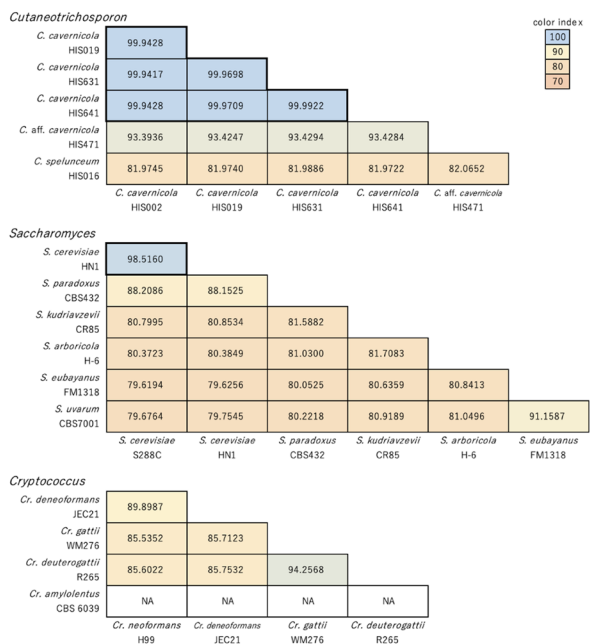


**Fig. 1** Chromosome continuity of genomes assemblies. Telomere sequence and sequencing depth was illustrated using Tapestry 1.0.0. Red rectangles at the termini stand for telomere repeat sequences (CCCTAA/ TTAGGG). The intensity of the green lines indicates the depth of sequencing reads. The dark-coloured region on Chr.7 in the genomes of HIS002, HIS019, HIS631, HIS641, and HIS471, and on ctg.10 in the genome of HIS016 correspond to rDNA repeats

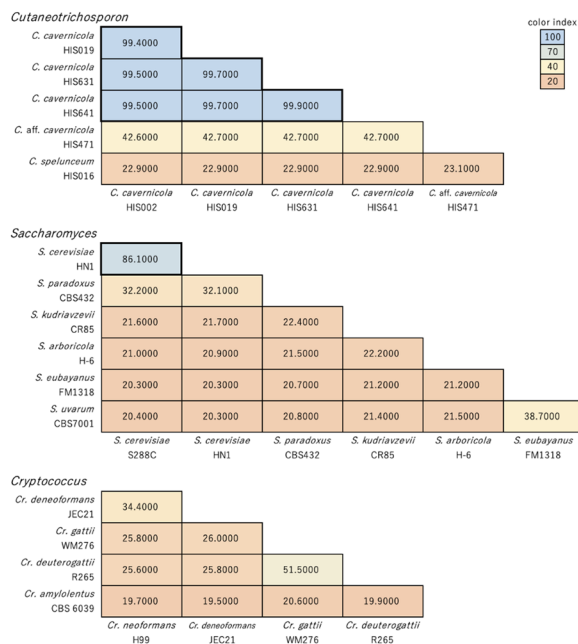


**Fig. 2** Plots of chromosome synteny based on pairwise BLASTN alignment among *Cutaneotrichosporon* strains. The line colour reflects the percentage of nucleotide identity in the alignment as shown in the legend

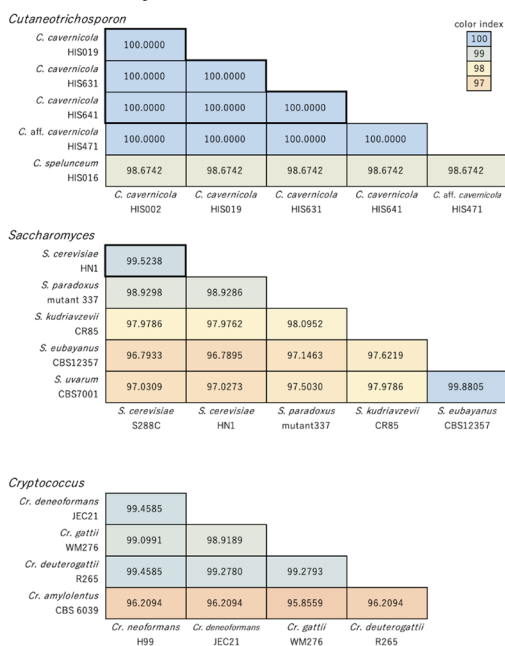
A. ANI



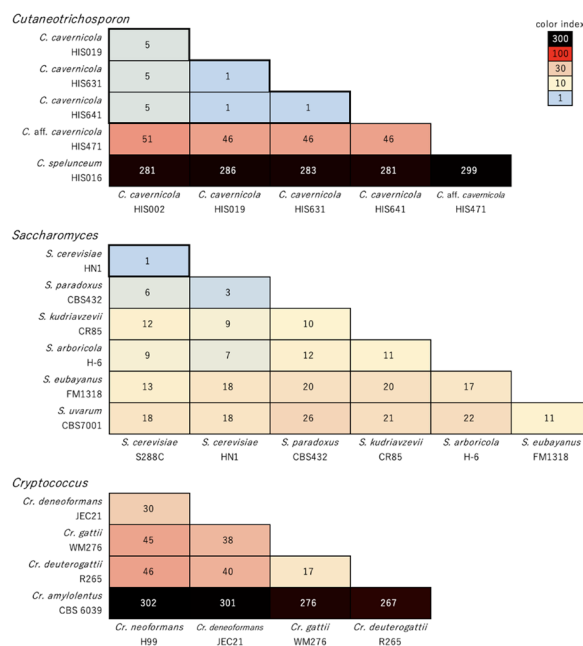
B. Digital DDH based on GGDC



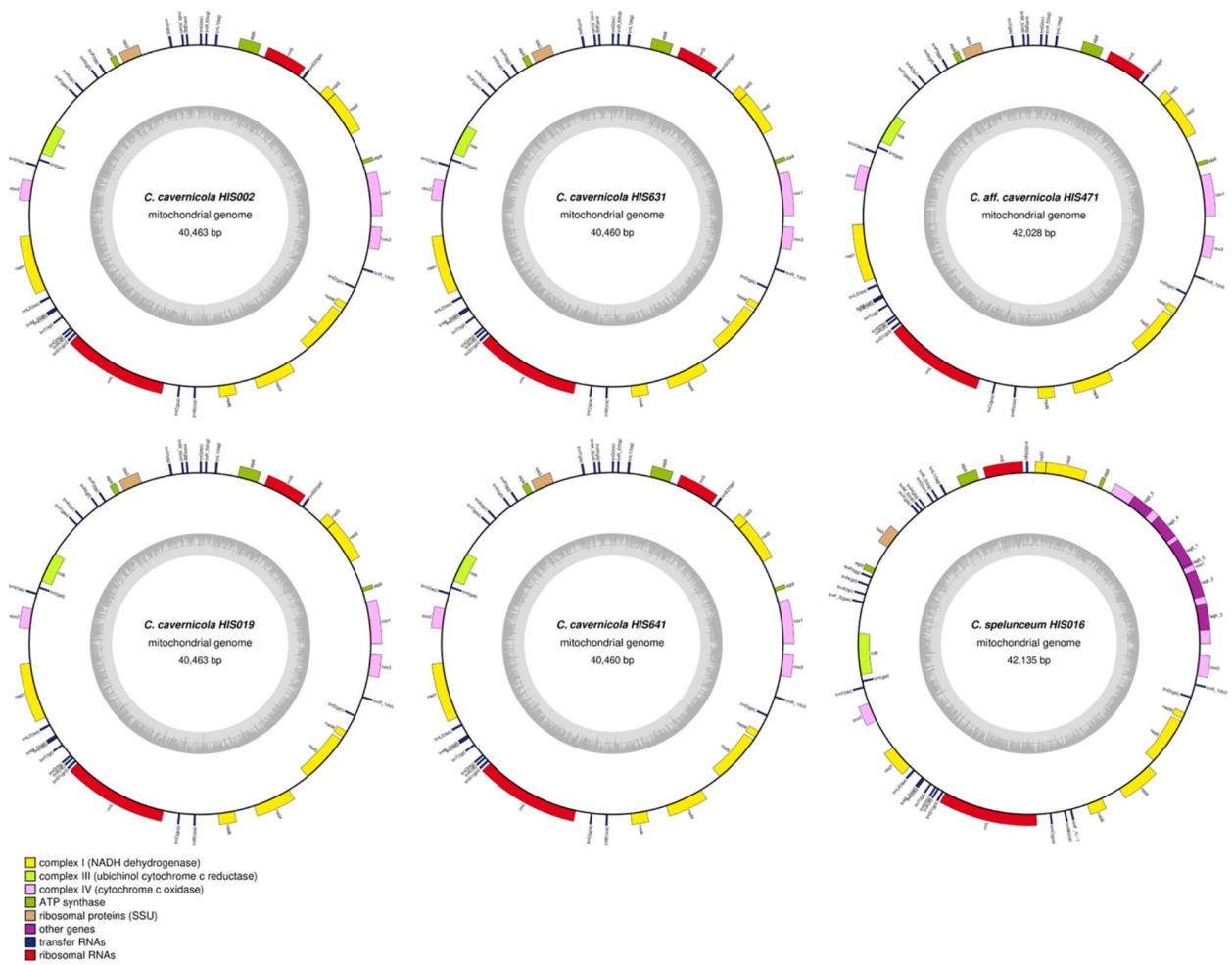
C. % identity of ITS



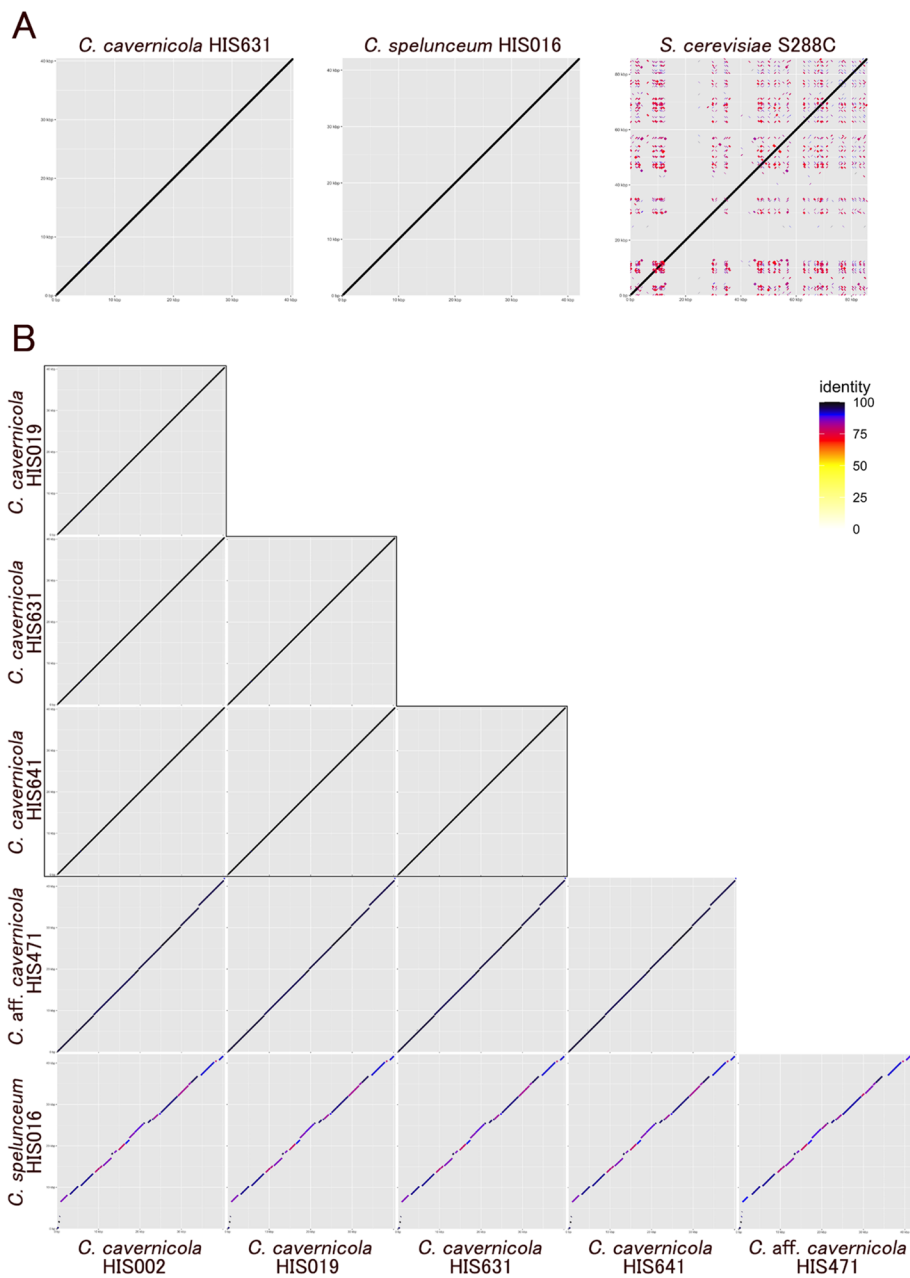
D. Number of LCBs



**Fig. 3** Genome similarities based on multiple criteria among *Cutaneotrichosporon* strains compared with reference *Saccharomyces* and *Cryptococcus*. Thick-bordered areas in the *Cutaneotrichosporon* and *Saccharomyces* panels indicate intraspecific comparisons among the *C. cavernicola* standard strains and *S. cerevisiae*, respectively. Box colours identify identical genomes (blue) and the most distant interspecific comparison (orange) in *Saccharomyces*. **A**; ANI score. **B**; GBDP score calculated with GGDC. The scores for formula 2 are shown according to the recommendation in Henz et al. [9], and scores by all three formulae are shown in Fig. S6. **C**; Percentage identity in the ITS sequence. **D**; Number of LCBs with a minimum weight of 10 kb



**Fig. 4** Mitochondrial genomes of *Cutaneotrichosporon* strains. Genes projecting outward from the outer circles indicate genes transcribed in the forward direction; genes projecting inward from the outer circles indicate genes transcribed in the reverse direction. Gene families are identified by colour as shown in the legend. The inner circles represent the GC content of the sequences



**Fig. 5** Plots of mitochondrial genome synteny based on pairwise BLASTN alignments. Line colour reflects the percentage of nucleotide identity in the alignment as shown in the legend. **A**, Self synteny of *C. cavernicola* HIS631, *C. spelunceum* HIS016, and the reference *S. cerevisiae* S288C. **B**; Pairwise synteny plots among *Cutaneotrichosporon* mitogenomes

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#### Reference

1. Kobayashi Y, et al. Chromosome-level genome assemblies of *Cutaneotrichosporon* spp. (Trichosporonales, Basidiomycota) reveal imbalanced evolution between nucleotide sequences and chromosome synteny. BMC Genomics. 2023;24:609. <https://doi.org/10.1186/s12864-023-09718-2>.