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# Corrigendum: Patterns of within-host spread of *Chlamydia trachomatis* between vagina, endocervix and rectum revealed by comparative genomic analysis

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*Chlamydia trachomatis*, single nucleotide polymorphisms, single variable polymorphisms, sexually transmitted diseases, chlamydiae

# A corrigendum on

Patterns of within-host spread of *Chlamydia trachomatis* between vagina, endocervix and rectum revealed by comparative genomic analysis

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In the published article, there was an error in Figure 2 as published. Some of the colors in the "ompA genotype" column of the heatmap did not match the true genotype of strain in the phylogenetic tree. The corrected Figure 2 and its caption appear below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated

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### FIGURE 2

Global phylogeny with clade designations. The global phylogeny of high-quality C. trachomatis Fiji genomes plus selected complete C. trachomatis reference and clinical genomes representing global diversity from the National Center for Biotechnology Information (NCBI). Sample names are < ompA genotype > - < participant ID > - < body site code, where C = endocervix, R = rectum and V = vagina >. The round tips are colored by the 4 clade designations [LGV, ocular, prevalent- urogenital and anorectal (P-UA), non-prevalent urogenital and anorectal (NP-UA)]. The first column to the right of the tree denotes the ompA genotype with code at the lower right; the second column represents the source of the genomes from NCBI or the Fijian samples.