Author Correction: Short tRNA anticodon stem and mutant eRF1 allow stop codon reassignment

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Check for updates

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After this article was published, we were alerted by Estienne Swart that the putative *C. magnum* 5-bp-long AS $tRNA^{Trp}_{CCA}$, which we used as a negative control in Fig. 3d and 3f, most likely originated from a bacterial contaminant in the ciliate genome assembly. Using a metagenome binning strategy, we found that the contig containing the respective tRNA gene indeed belongs to a single bacterial metagenome-assembled genome (MAG) reconstructed from the whole-genome data. This high-quality MAG corresponds to an unidentified alphaproteobacterium not closely related to previously described taxa. We thus confirmed the bacterial origin of 5-bp AS $tRNA^{Trp}$. Regrettably, the presence of contaminating bacterial sequences in the *C. magnum* genome assembly was not obvious from the original paper[1] when we were working on the original manuscript.

Nonetheless, it is important to stress that the bacterial origin of analyzed 5-bp-long AS $tRNA^{Trp}_{CCA}$ does not affect the validity of our conclusions. In fact, the complete loss of the canonical 5-bp-long AS $tRNA^{Trp}$ in the evolutionary lineage leading to *C. magnum* further underscores the essentiality of the 4-bp-long AS $tRNA^{Trp}_{CCA}$ for UGA translation as Trp in this organism.

To address this issue, we took the genuine and only existing 4-bp-long AS variant of *C. magnum* $tRNA^{Trp}_{CCA}$ and its 5-bp-long AS variant that we created by the U26G substitution, and remeasured stop codon readthrough (SC-RT) efficiency that these two tRNAs allow in *T. brucei* and *S. cerevisiae*, following the original setup. As anticipated and in full agreement with one of the main conclusions of this article, the 5-bp-long AS $tRNA^{Trp}$ mutant variant was a several-fold less potent stimulator of SC-RT when compared to its *C. magnum* wild-type 4-bp-long AS variant. These new measurements expressed in plots replaced the originally reported plots in Fig. 3d and 3f. We also modified the corresponding text in the "UGA reassignment involves 4-bp $tRNA^{Trp}$" section, removed the bacterial contaminant 5-bp $tRNA^{Trp}_{CCA}$ from Fig. 3a, and replaced the northern blot data in Extended Data Figs. 7 and 9, the original raw data in Supplementary Figure 1 (pages 7–31), the source data in the Source Data Extended Data Figs. 7 and 9 Excel file (Worksheets 4 [7b – Condylostoma] and 5 [9b]) and in the Source Data Extended Data Figs. 3 and 4 and Extended Fig. 8 Excel file (Worksheets 2 [3d] and 4 [3f]), and corresponding cloning details in the Supplementary Information file. The changes have been made in the HTML and PDF versions of the article.

1. Swart, E. C., Serra, V., Petroni, G. & Nowacki, M. Genetic codes with no dedicated stop codon: context-dependent translation termination. *Cell* **166**, 691–702 (2016).