



Author Correction: Phylogenomics provides robust support for a two-domains tree of life

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Correction to: *Nature Ecology & Evolution* <https://doi.org/10.1038/s41559-019-1040-x>, published online 9 December 2019.

In the version of this Article originally published, there was an error in the calculation of the summed quartet distance for the ASTRAL supertree presented in Table 1. The recalculated distance shows that ASTRAL (not SPA as originally reported) has the best summed quartet distance. The trees originally presented are correct and this error had no effect on our conclusions, because all three supertree analyses recovered a clade of eukaryotes and Asgard archaea.

In Table 1, the ‘MSC (ASTRAL)’ summed quartet distance value was corrected from ‘17213379’ to ‘17145892’, and is now listed in bold. The SPA value was unbolded and the last sentence of the Table 1 footnote was corrected from ‘The SPA supertree had the lowest summed quartet distance to the input gene trees (denoted in bold text)’ to ‘The MSC ASTRAL tree had the lowest summed quartet distance to the input gene trees (denoted in bold text)’.

Additionally, in the last paragraph of the ‘Results and discussion’ subsection ‘Supertree and multispecies coalescent methods support the 2D tree’, the sentence ‘The tree with the best score by this metric was the SPA supertree which, like the model-based MSC ASTRAL analysis, recovered Heimdallarchaeota and eukaryotes as sister taxa’ was corrected to ‘The tree with the best score by this metric was the model-based MSC ASTRAL analysis which, like the SPA supertree, recovered Heimdallarchaeota and eukaryotes as sister taxa.’

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