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* You should state whether an appropriate sample size was computed when the study was being designed
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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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High-throughput sequence data: NCBI BioProject PRJNA419411 (19 choanoflagellate transcriptomes), PRJNA420352 (*S. rosetta* polyA selection test).

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* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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Data generated for analysis (assemblies, annotations, etc.) are available as Datasets 1-8 on FigShare: https://dx.doi.org/10.6084/m9.figshare.5686984