


CORRECTION

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# Correction to: SPEAQeasy: a scalable pipeline for expression analysis and quantification for R/bioconductor-powered RNA-seq analyses

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The original article can be found online at <https://doi.org/10.1186/s12859-021-04142-3>.

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## Correction to: BMC Bioinformatics (2021) 22:224

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Following the publication of the original article [1], the authors identified the incorrect published Additional file 4 and missing Additional file 1: figures S1 and Additional file 2: S2.

The original article [1] has been corrected.

## Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s12859-021-04283-5>.

**Additional file 1: Figure S1.** Expected vs. Actual ERCC concentration. SPEAQeasy produces plots for each sample, for easy visual comparison of expected ERCC transcript abundance with the kallisto-measured concentration.

**Additional file 2: Figure S2.** SPEAQeasy logs tracing computational steps by sample. To aid transparency and greatly simplify the source of execution errors, SPEAQeasy automatically generates logs with several pieces of information for every sample. In order of submission, the name of each Nextflow process is printed, along with (1) the working directory: where all relevant files are present, (2) the exit code: a standard indication of whether the process succeeded or how it failed, (3) a list of the specific commands run during the given process. Above is a snapshot of the top of an example log

**Additional file 4:** SNVs supplementary BED files. The common SNVs used for sample identification are stored in the BED files (A) `common_missense_SNVs_hg19.bed` and (B) `common_missense_SNVs_hg38.bed`.

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