

CORRECTION

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# Correction to: Optimization of library preparation based on SMART for ultralow RNA-seq in mice brain tissues

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**Correction to: BMC Genomics 22, 809 (2021)**  
<https://doi.org/10.1186/s12864-021-08132-w>

Following publication of the original article [1], it was reported that there were errors in the x- and y-axes of Figs. 4, 6 and 7.

In Fig. 4 the x axes of panels E and F were missing ‘2’ and the y axes contained a ‘\$’ and “#” symbol after the values respectively.

In Fig. 6, in panel H the y axis contained a ‘\$’ symbol after the reported values.

In Fig. 7, the x and y axis of panel C erroneously contained the ‘\$’ symbol and in panel D both axes contained the “#” symbol.

The correct figures are presented in this Correction and the original article [1] has been corrected.

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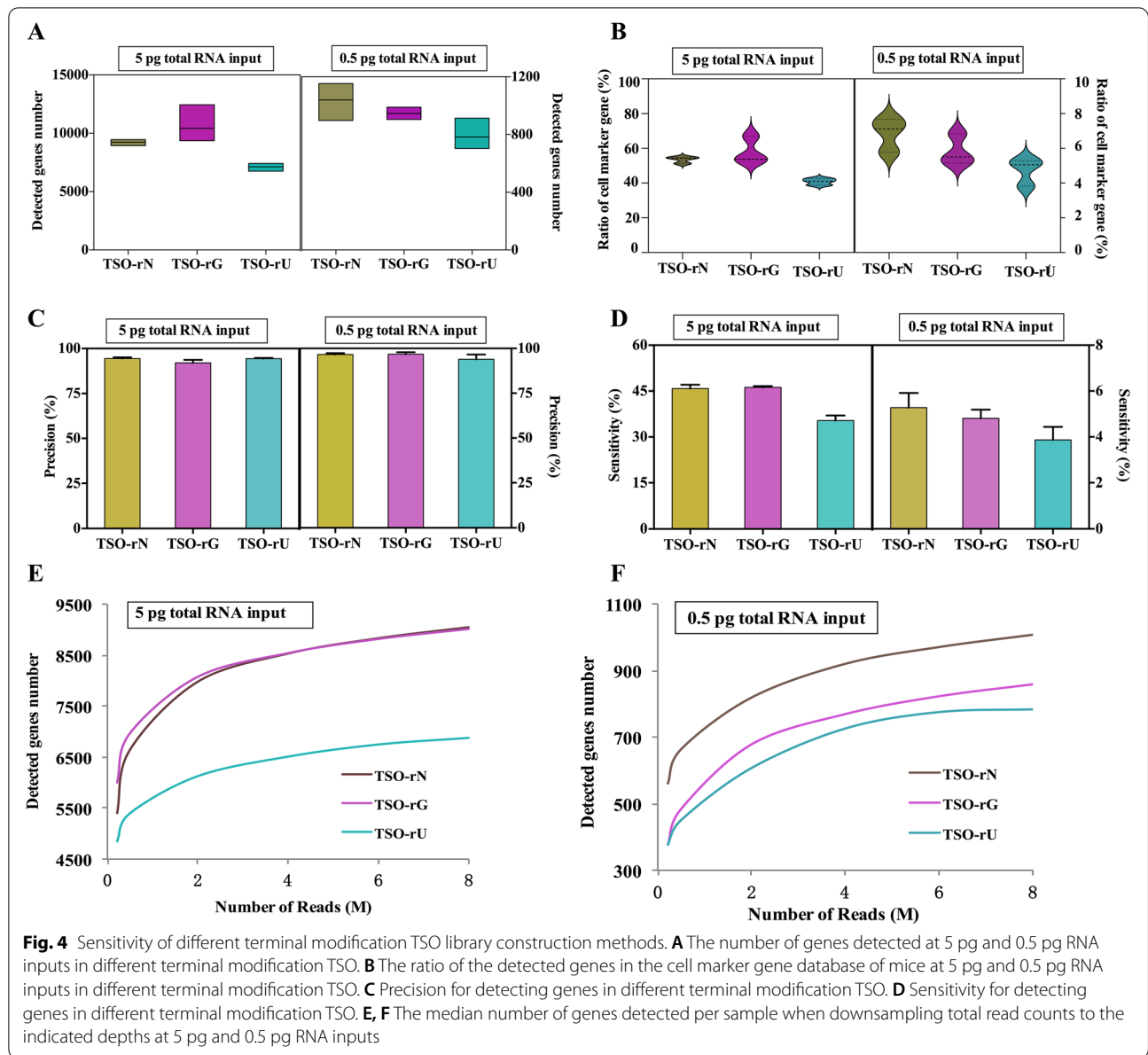
The original article can be found online at <https://doi.org/10.1186/s12864-021-08132-w>.

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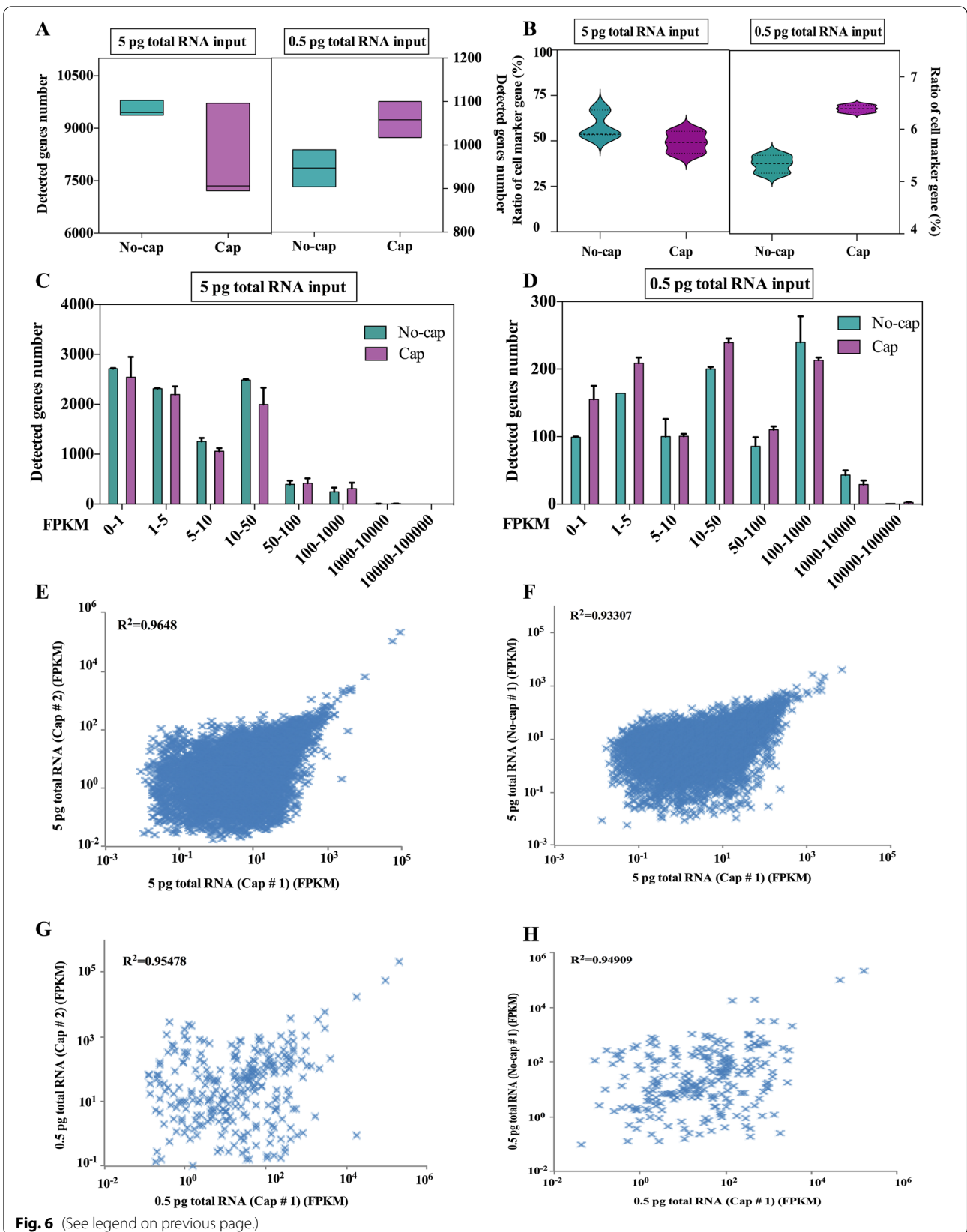


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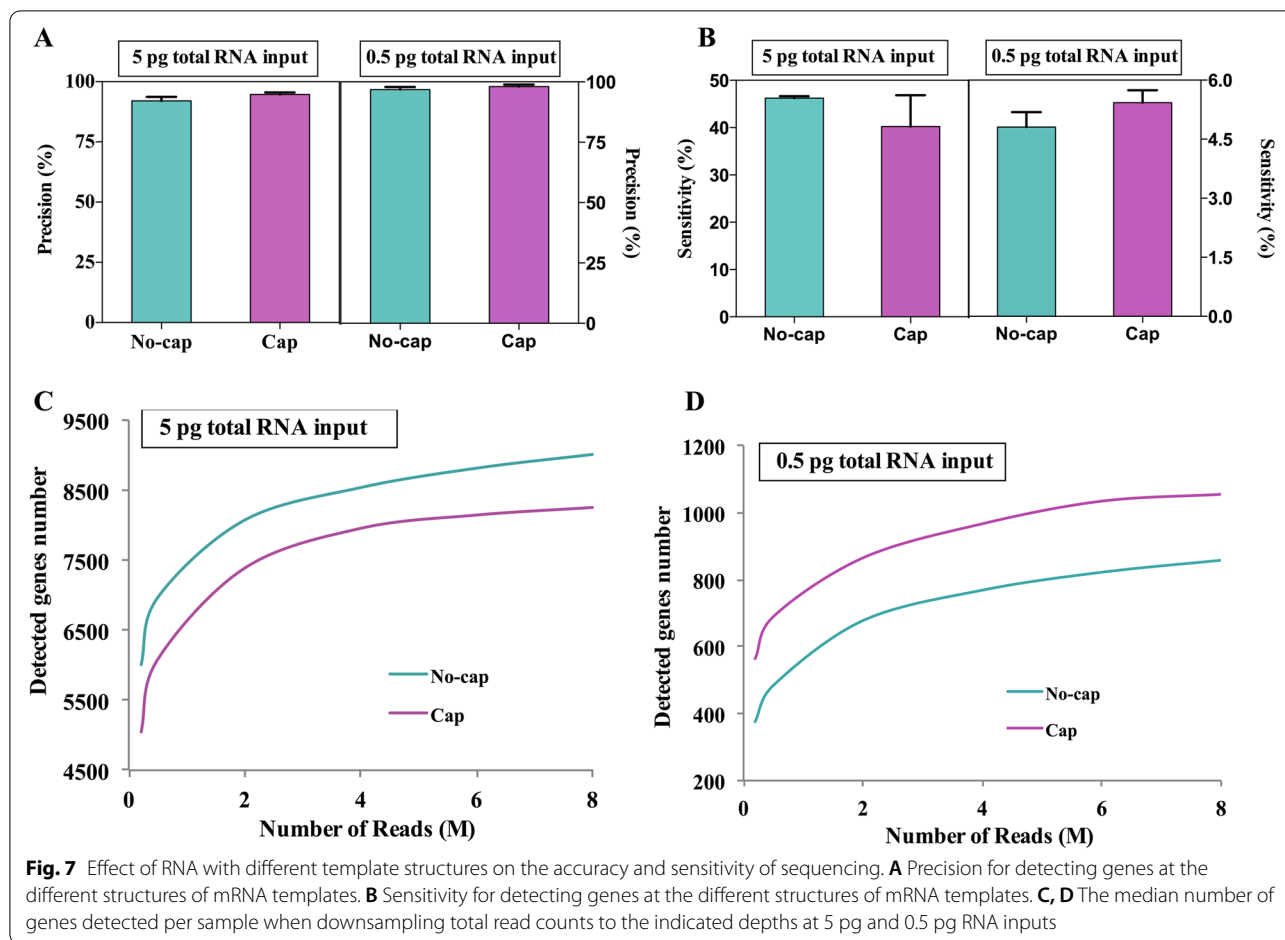


(See figure on next page.)

**Fig. 6** The effect of RNA with different template structures on gene detection. **A** The number of genes detected in the different structure of mRNA templates. **B** The ratio of the detected genes in the cell marker gene database of mice at the different structures of mRNA templates. **C, D** Number of genes detected in different expression levels binned by standardized expression FPKM at the different structures of mRNA templates. **E, F** Scatter plots show the correlation between different replicates and mRNA structure for 5 pg RNA inputs. **G, H** Scatter plots show the correlation between different replicates and mRNA structure for 0.5 pg RNA inputs



**Fig. 6** (See legend on previous page.)



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