

CORRECTION

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# Correction to: Post-diapause transcriptomic restarts: insight from a high-latitude copepod



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**Correction to: *BMC Genomics* 22, 409 (2021)**  
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Following publication of the original article [1], it was reported that due to a typesetting error the incorrect versions of Figs. 4, 7, 9 and 10 were published. The correct figures are given in this Correction article.

The original article has been updated.

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The original article can be found online at <https://doi.org/10.1186/s12864-021-07557-7>.

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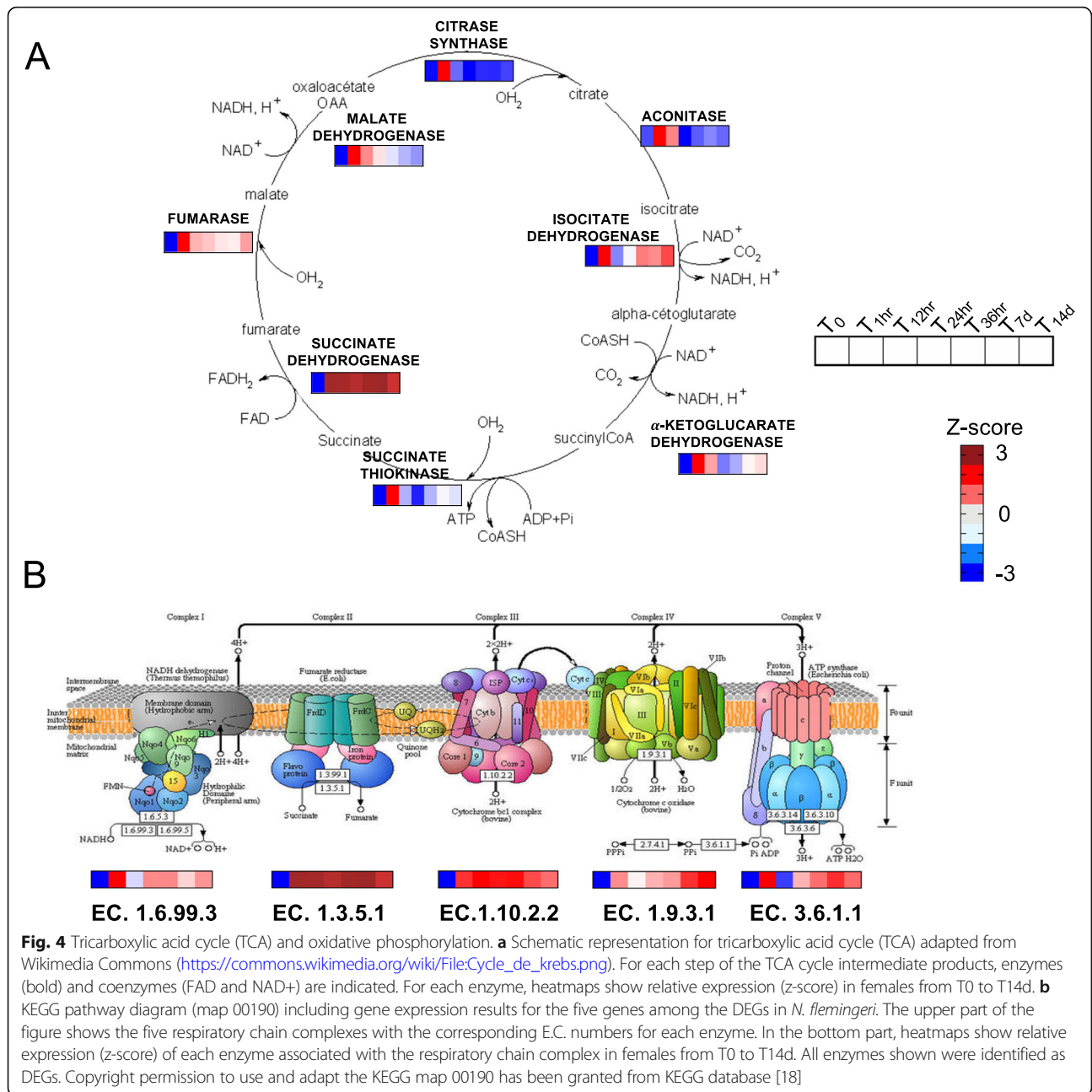
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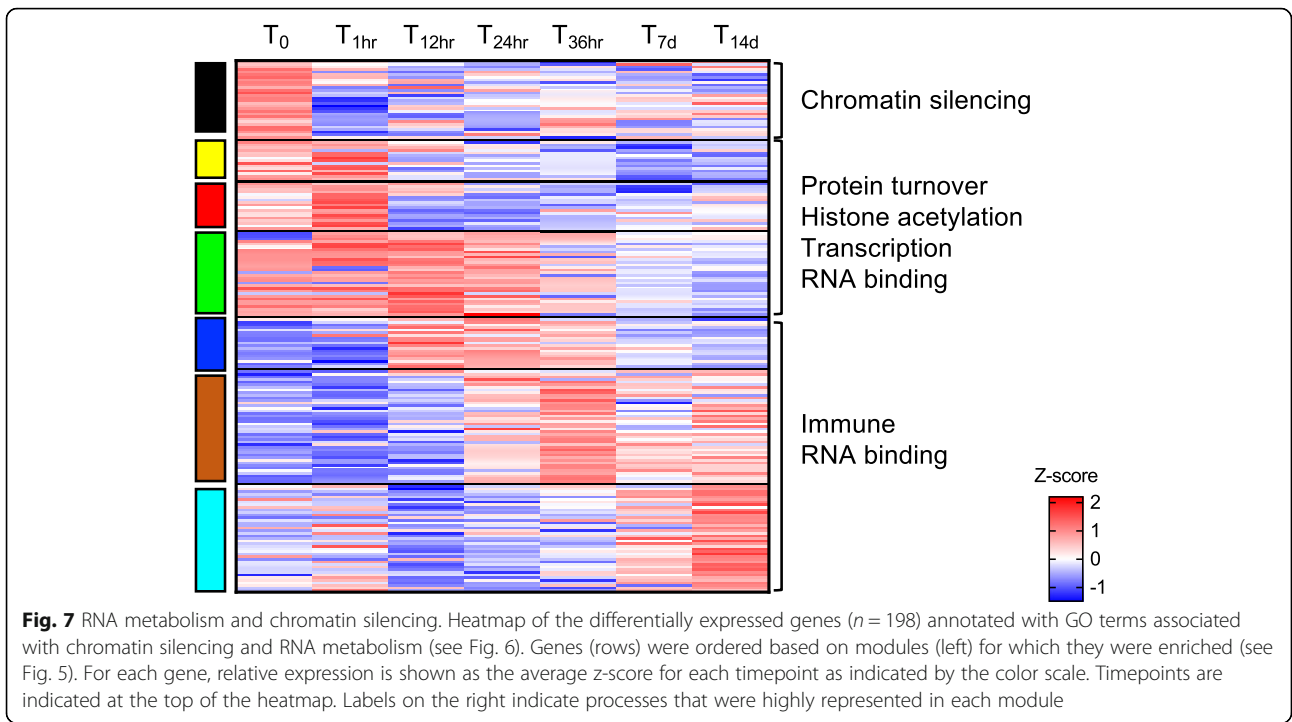
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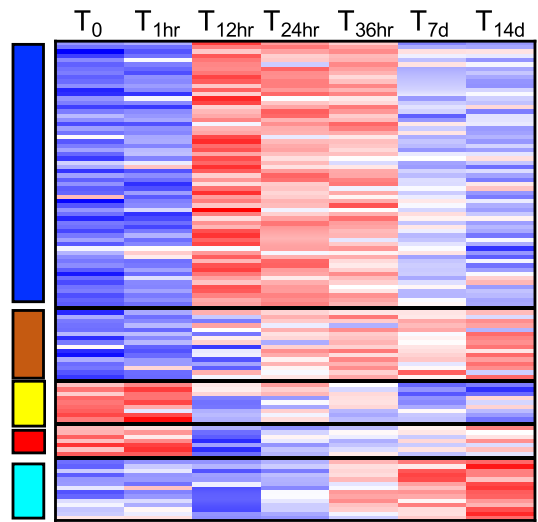


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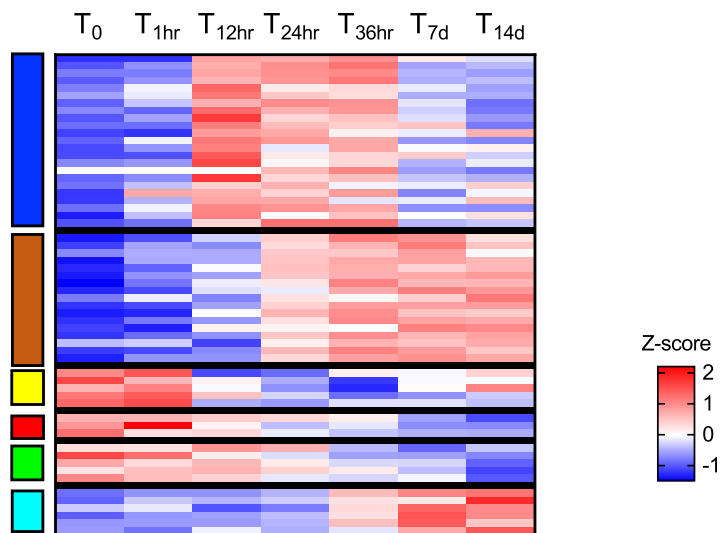




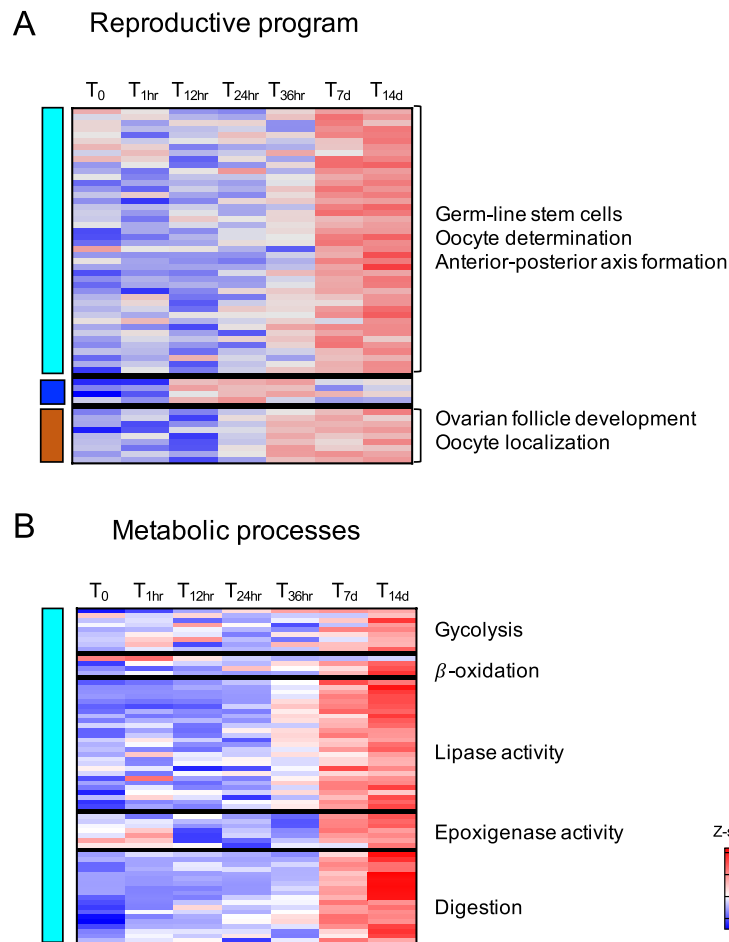
### A Multicellular organism development



### B Immune system process



**Fig. 9** Multicellular organism development and immune system process. Heatmap of the differentially expressed genes annotated with GO terms associated with: **a** multicellular organism development ( $n = 108$ ) and **b** immune system process ( $n = 61$ ) (see Fig. 6). Genes (rows) were ordered based on modules (left) for which they were enriched (see Fig. 5). For each gene, relative expression is shown as the average z-score for each timepoint as indicated by the color scale. Timepoints are indicated at the top of the heatmap



**Fig. 10** Reproductive program and metabolic processes. Heatmap of the differentially expressed genes annotated with GO terms associated with **a** oogenesis ( $n = 54$ ) and **b** metabolic processes: glycolysis ( $n = 9$ ),  $\beta$ -oxidation ( $n = 4$ ), lipase activity ( $n = 27$ ), epoxigenase activity ( $n = 9$ ) and digestion ( $n = 19$ ) (see Fig. 6). Genes (rows) were ordered based on modules (left) for which they were enriched (see Fig. 5). For each gene, relative expression is shown as the average z-score for each timepoint as indicated by the color scale. Timepoints are indicated at the top of the heatmap. Labels on the right indicate processes that were highly represented in each module

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