Proteomes of dormant and non-dormant embryos

LEGENDS TO SUPPLEMENTARY FIGURES

**Fig S1:** Signal distribution plots (A) and Principal component analysis (PCA, B) of all intensity values achieved in the study (three samples for each egg type AM, RE and E0).

**Fig S2:** Enriched GO biological process terms in amictic eggs (AM), resting eggs (RE) and resting eggs before hatching (E0).

**Fig S3:** Enriched KEGG pathways in AM (blue), RE (red) and E0 (green). For each pathway, the nominator in the bar labels shows the number of proteins displayed in each egg type and the denominator shows the total number of proteins (KOs) in the translated reference transcriptome that were associated with the pathway.

**Fig S4:** Enriched GO biological processes of the proteins with significant differences in their abundance in the comparisons of AM vs. RE (blue) and AM vs. E0 (red).

**Fig S5:** A heat-map showing the abundance level of proteins in Fatty acid degradation pathway after hierarchical clustering. Expand the figure x175 to view the text. White cells in the heat map denote missing values. Two vertical bars to the left of the heat map indicate whether the abundance of a protein significantly differed in the comparison of AM vs RE (left) or AM vs E0 (right). A red box indicates statistical significance in the 1-Way ANOVA test (FDR p-value <0.05, FC>3). An orange box indicates that the protein was identified in one egg type but not in the other. A while box indicates there were no statistically significant differences in the abundance of the protein, in the compared groups.

**Fig S6:** A KEGG map displaying the proteins in association with Valine, leucine and isoleucine degradation pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

**Fig S7:** A KEGG map displaying the proteins in association with the Glycolysis/Gluconeogenesis pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show
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proteins that were significantly more abundant in AM vs RE. Yellow boxes show the proteins that were detected only in AM eggs. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

**Fig S8:** A heat-map showing the abundance level of proteins in the Glycolysis/Gluconeogenesis pathway after hierarchical clustering. Expand the figure x175 to view the text. White cells in the heat map denote missing values. The two vertical bars to the left of the heat map indicate whether the protein showed differentially abundance in AM vs. RE (left) and in AM vs. E0 (right). A red box indicates statistical significance in the 1-Way ANOVA test (FDR p. 0.05, FC > 3). An orange box indicates that the protein was abundant in one egg type and not the other. A white box indicates that the protein did not display differentially abundance.

**Fig S9:** A heat-map showing the abundance level of proteins in the Citrate cycle (TCA) pathway after hierarchical clustering. Expand the figure x175 to view the text. White cells in the heat map denote missing values. The two vertical bars to the left of the heat map indicate whether the protein showed differentially abundance in AM vs. RE (left) and in AM vs. E0 (right). A red box indicates statistical significance in the 1-Way ANOVA test (FDR p. 0.05, FC > 3). An orange box indicates that the protein was abundant in one egg type and not the other. A white box indicates that the protein did not display differentially abundance.

**Fig S10:** A KEGG map displaying the proteins in association with the Pyruvate metabolism pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Yellow boxes show the proteins that were detected only in AM eggs. Boxes in blue show proteins with significantly higher abundance in RE vs AM. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

**Fig S11:** A heat-map showing the abundance level of proteins in the Pyruvate metabolism pathway after hierarchical clustering. Expand the figure x175 to view the text. White cells in the heat map denote missing values. The two vertical bars to the left of the heat map indicate whether the protein
Proteomes of dormant and non-dormant embryos showed differentially abundance in AM vs. RE (left) and in AM vs. E0 (right). A red box indicates statistical significance in the 1-Way ANOVA test (FDR p. 0.05, FC > 3). An orange box indicates that the protein was abundant in one egg type and not the other. A white box indicates that the protein did not display differentially abundance.

**Fig S12:** A KEGG map displaying the proteins in association with the Cell cycle pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Yellow boxes show the proteins that were detected only in AM eggs. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

**Fig S13:** A KEGG map displaying the proteins in association with the Spliceosome pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Yellow boxes show the proteins that were detected only in AM eggs. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

**Fig S14:** A KEGG map displaying the proteins in association with the mRNA surveillance pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Yellow boxes show the proteins that were detected only in AM eggs. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

**Fig S15:** A KEGG map displaying the proteins in association with the Proteasome pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Boxes in blue show proteins with significantly higher abundance in RE vs AM. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).
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**Fig S16:** A heat-map showing the abundance level of proteins in the Oxidative phosphorylation pathway after hierarchical clustering. Expand the figure x175 to view the text. White cells in the heat map denote missing values. The two vertical bars to the left of the heat map indicate whether the protein showed differentially abundance in AM vs. RE (left) and in AM vs. E0 (right). A red box indicates statistical significance in the 1-Way ANOVA test (FDR p. 0.05, FC > 3). An orange box indicates that the protein was abundant in one egg type and not the other. A white box indicates that the protein did not display differentially abundance.

**Fig S17:** A KEGG map displaying the proteins in association with the Pentose phosphate pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Boxes in blue show proteins with significantly higher abundance in RE vs AM. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).

**Fig S18:** A heat-map showing the abundance level of proteins in the Pentose phosphate pathway after hierarchical clustering. Expand the figure x175 to view the text. White cells in the heat map denote missing values. The two vertical bars to the left of the heat map indicate whether the protein showed differentially abundance in AM vs. RE (left) and in AM vs. E0 (right). A red box indicates statistical significance in the 1-Way ANOVA test (FDR p. 0.05, FC > 3). An orange box indicates that the protein was abundant in one egg type and not the other. A white box indicates that the protein did not display differentially abundance.

**Fig S19:** A KEGG map displaying the proteins in association with the Protein processing in endoplasmic reticulum pathway. Boxes in grey show the proteins that were identified in rotifer eggs. Boxes in red show proteins that were significantly more abundant in AM vs RE. Boxes in blue show proteins with significantly higher abundance in RE vs AM. Statistically significant differences were indicated by 1-Way ANOVA test (FDR p-value 0.05, FC>3).
Fig S1
Fig S3
negative regulation of sequence-specific DNA binding
transcription factor activity
hydrogen peroxide metabolic process
superoxide metabolic process
negative regulation of response to biotic stimulus
mitochondrial electron transport, NADH to ubiquinone
axoneme assembly
larval locomotory behavior
positive regulation of extrinsic apoptotic signaling
pathway in absence of ligand
negative regulation of mRNA splicing, via spliceosome
peptidyl-serine dephosphorylation
ADP biosynthetic process

Fig S4
Fig S5
Fig S6

**VALINE, LEUCINE AND ISOLEUCINE DEGRADATION**

- AM>RE
- AM< RE
- Only in AM
- Only in RE
- Grey- present

*Biocatalysts of type II polypeptide thioesters*

*Biocatalysts of 12-, 14- and 16-carboxylic acids*
AM > RE
AM < RE
Only in AM
Only in RE
Grey- present

Fig S7
Fig S9
Fig S10

PYRUVATE METABOLISM

AM>RE; AM< RE; Only in AM; Only in RE; Grey- present
Fig S11
AM > RE; AM < RE; Only in AM; Only in RE; Grey - present

Fig S15
AM > RE; AM < RE; Only in AM; Only in RE; Grey - present

Figure S17
Fig S18

Pentose phosphate pathway

AM | RE | EO

-2.00 | 0.00 | -2.00
Fig S19