

Supplementary Table S1 | Measured mRNA expression, mRNA fold-changes and protein fold changes at the OET. Table contains all merged datasets. After applying a threshold of 2 RPKM to filter out transcripts expressed at background level we were left with roughly 7,500 expressed genes in either oocytes or embryos. With proteomics we measure around 3,300 proteins, which, due to technical limitations of the mass spectrometry, only represent a fraction of the expressed proteins. Fold changes are given including confidence score.

Supplementary Table S2 | Genes used to normalize protein fold changes. We normalized our proteomics data under the assumption that a set of 100 structural, metabolic and translation machinery genes are constant at this transition.

Supplementary Table S3 | DNA oligos used in this study. Table lists all primers used in this study.