

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Identification of m⁶A peaks for single GV oocyte as determined by scm⁶A-seq, related to Figure 1.

File Name: Supplementary Data 2

Description: m⁶A peaks and modified RNAs in tens of GV oocytes, related to Figure 1.

File Name: Supplementary Data 3

Description: The expression of METTL3-dependent m⁶A modified RNAs in control and Mettl3 cKO GV oocytes, related to Figure 2.

File Name: Supplementary Data 4

Description: The m⁶A atlas during oocyte maturation, related Figure 4.

File Name: Supplementary Data 5

Description: Maternal decay and ZGA transcripts identification by DESeq2, related to Figure 5.

File Name: Supplementary Data 6

Description: The expression changes of m⁶A-modified RNAs during early embryonic development, related to Figure 5.

File Name: Supplementary Data 7

Description: The whole transcriptome of Mettl3 cKO MII oocytes and zygotes, related Figure 5.

File Name: Supplementary Data 8

Description: The m⁶A atlas during early embryonic development, related Figure 6.

File Name: Supplementary Data 9

Description: The adapters and primers used in scm⁶A-seq.

File Name: Supplementary Data 10

Description: The barcode sequences for single-cell labeling.