



Figure S1 Transcriptome analysis of *in vivo*-grown and *in vitro* grown (IVG) oocytes

Orange bars indicate the number of genes that substantially contributed to the PC1 axis variation (more than 2 S.D.). Gray bars indicate the number of genes that contributed less to the PC1 axis variation (within 2 S.D.). GO analysis of the 1,450 genes that contributed highly to PC1 axis variation. Several of these corresponded to the results of the GO analysis of 20%-IVG oocyte-specific DEGs (Figure 5B).