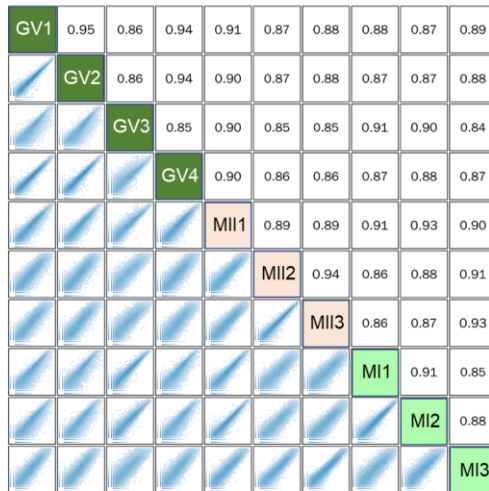


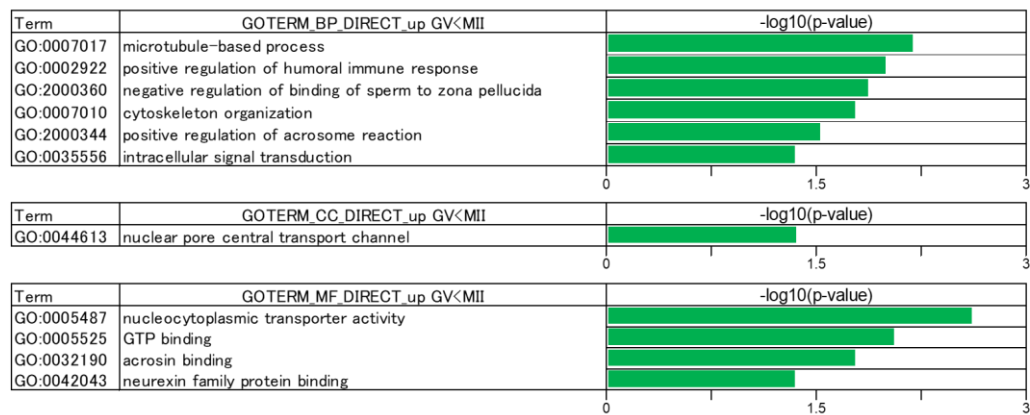
(A)



(B)

GO analysis (GV vs MII)

Up in MII



Down in MII

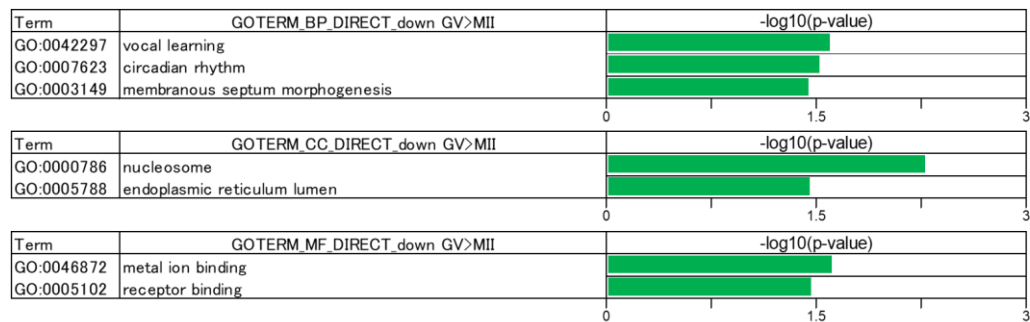


Figure S1 Global gene expression profiles of human oocytes at different maturation stages and GO analyses of DEGs found between GV and MII oocytes. (A) Scatterplot and Spearman correlation

coefficient comparing gene expression profiles among different oocyte samples. Biological replicates in each condition are shown such as (GV1-4), (MI1-3), and (MII1-3). (B) The enriched gene ontology (GO) terms within differentially expressed genes between GV and MII oocytes. GO analyses were performed using the DAVID tools. Significant GO terms are listed in each comparison ($P < 0.05$, Fisher's exact test).

GV; oocytes at the germinal vesicle stage, MI; maturing oocytes at the metaphase I stage, MII; oocytes at the metaphase II stage.

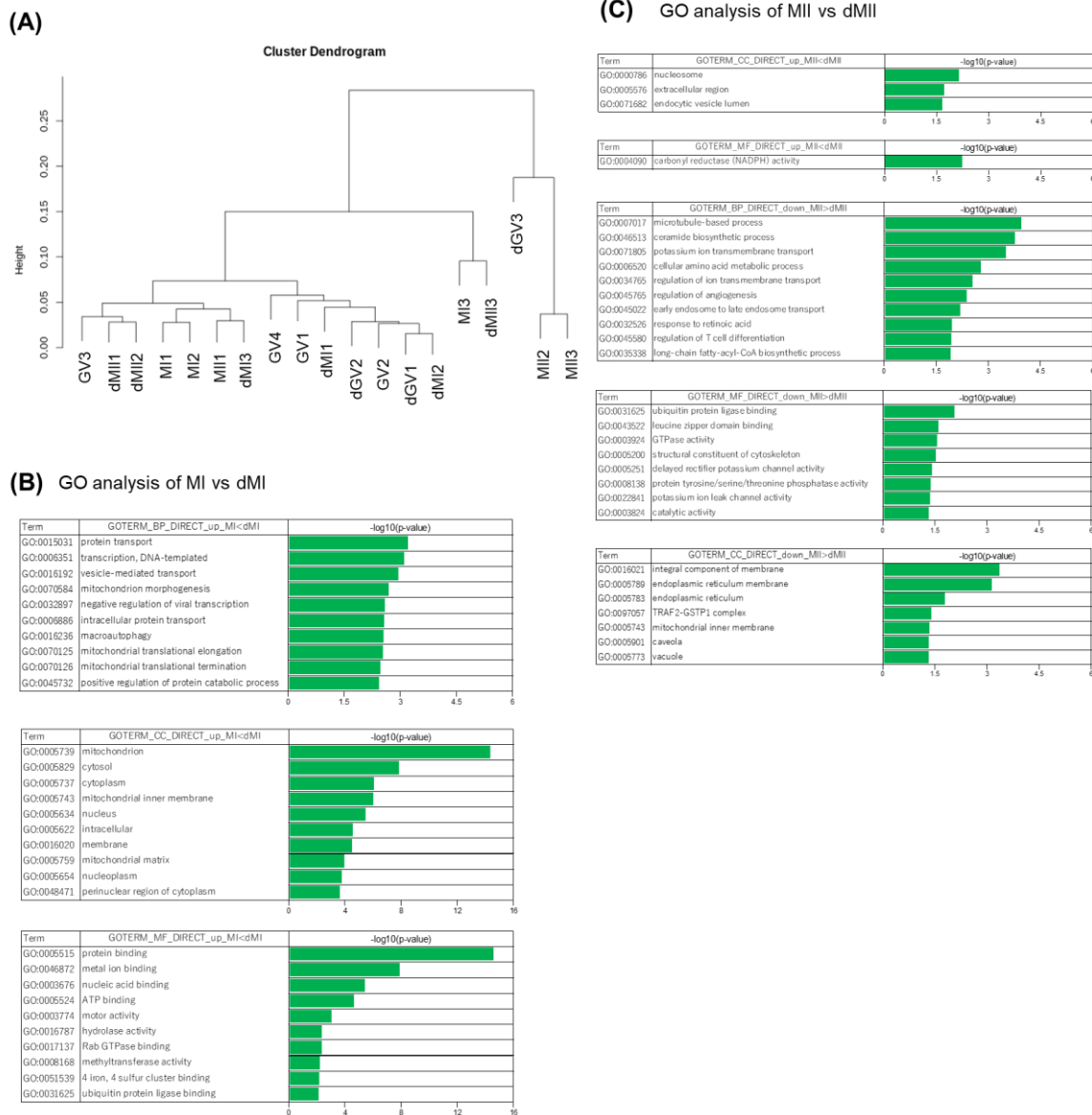


Figure S2 The effect of delayed maturation on oocyte transcriptomes. (A) Hierarchical clustering dendrogram generated using the gene expression profiles of all human oocyte samples including those delayed in their *in vitro* maturation. Pearson correlation was used. (B and C) The enriched GO terms within DEGs identified by comparing control oocytes and oocytes delayed in their maturation. GO analyses were performed using the DAVID tools. Top 10 significant GO terms are listed ($P < 0.05$, Fisher's exact test).

dGV; oocytes that were at the germinal vesicle stage the day after oocyte retrieval, dMI; oocytes that were at the metaphase I stage the day after oocyte retrieval, dMII; oocytes that were at the metaphase II stage the day after oocyte retrieval.

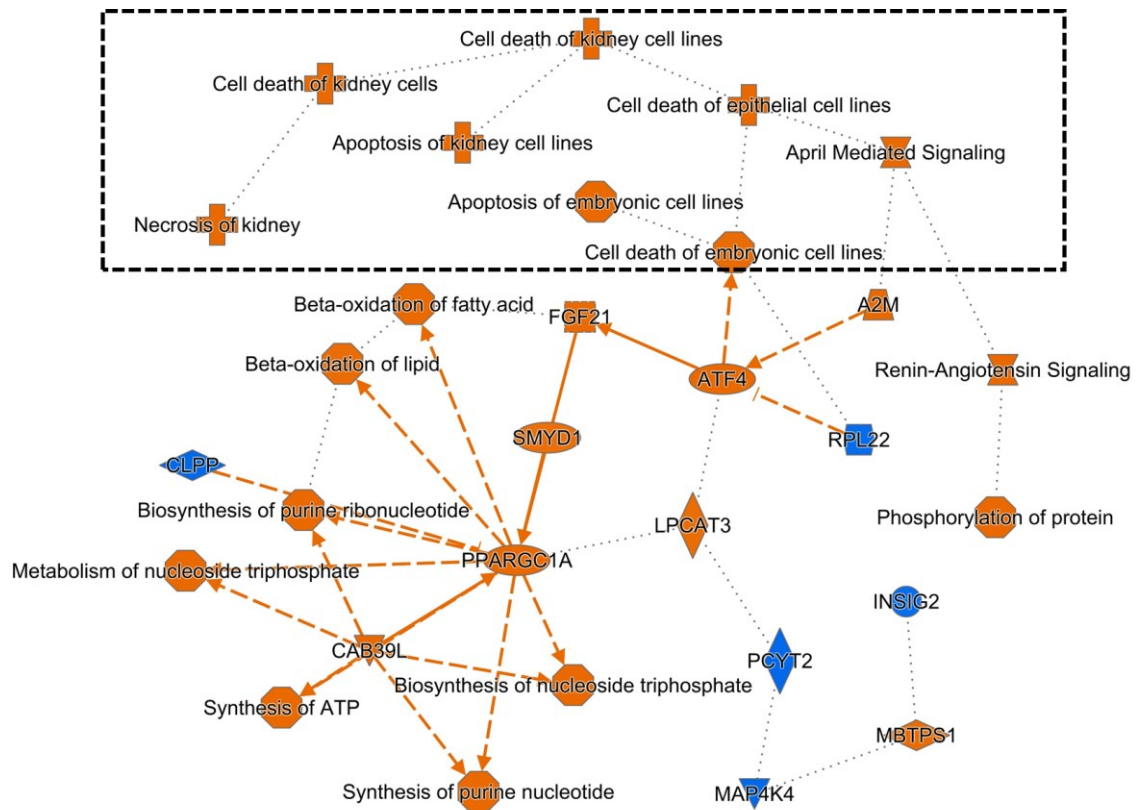


Figure S3 Regulatory networks predicted by Ingenuity Pathway Analysis (IPA) using the differentially expressed gene (DEG) list generated by the comparison between MI and dMI (delayed MI) oocytes. The dotted square indicates molecular pathways related to cell death. Molecules coloured orange indicate predicted activation, while those coloured blue show predicted inhibition.

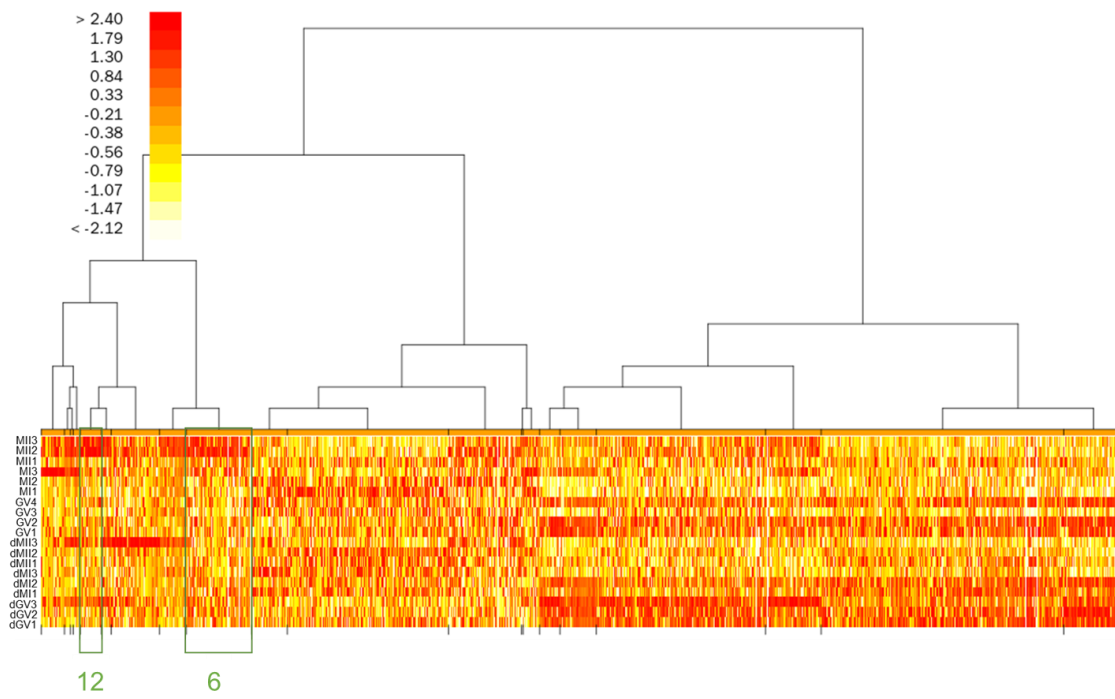


Figure S4 A heatmap of gene expression levels of all oocyte samples after clustering based on expression patterns. Twenty clusters were generated and clusters 6 and 12 are indicated.