(A)										
	GV1	0.95	0.86	0.94	0.91	0.87	0.88	0.88	0.87	0.89
	/	GV2	0.86	0.94	0.90	0.87	0.88	0.87	0.87	0.88
			GV3	0.85	0.90	0.85	0.85	0.91	0.90	0.84
	/	/		GV4	0.90	0.86	0.86	0.87	0.88	0.87
	/				MII1	0.89	0.89	0.91	0.93	0.90
					/	MII2	0.94	0.86	0.88	0.91
							МІІЗ	0.86	0.87	0.93
								MI1	0.91	0.85
			/					/	MI2	0.88
					/	/	/	1	/	MI3

(B)

GO analysis (GV vs MII) Up in MII

т		log10(p value)
Term		-log10(p-value)
GO:0007017	microtubule-based process	
GO:0002922	positive regulation of humoral immune response	
GO:2000360	negative regulation of binding of sperm to zona pellucida	
GO:0007010	cytoskeleton organization	
GO:2000344	positive regulation of acrosome reaction	
GO:0035556	intracellular signal transduction	
		0 1.5 3
Term	GOTERM_CC_DIRECT_up GV <mii< td=""><td>-log10(p-value)</td></mii<>	-log10(p-value)
GO:0044613	nuclear pore central transport channel	
		0 1.5 3
Term	GOTERM_MF_DIRECT_up_GV <mii< td=""><td>-log10(p-value)</td></mii<>	-log10(p-value)
GO:0005487	nucleocytoplasmic transporter activity	
GO:0005525	GTP binding	
GO:0032190	acrosin binding	
GO:0042043	neurexin family protein binding	
		0 1.5 3

Down in Mll

Term	GOTERM_BP_DIRECT_down GV>MII	-log10(p-value)				
GO:0042297	vocal learning					
GO:0007623	circadian rhythm					
GO:0003149	membranous septum morphogenesis					
		0 1.5				
Term	GOTERM_CC_DIRECT_down GV>MII	-log10(p-value)				
GO:0000786	nucleosome					
GO:0005788	endoplasmic reticulum lumen					
		0 1.5				
Term	GOTERM_MF_DIRECT_down GV>MII	-log10(p-value)				
GO:0046872	metal ion binding					
GO:0005102	receptor binding					
		0 1.5				

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; maturating oocytes at the metaphase I stage, MII; oocytes at the metaphase II stage.



(B) GO analysis of MI vs dMI

GOTERM BP DIRECT up MI<dM GO:0015031 GO:0006351 protein transport transcription, DNA-templated GO:0016192 vesicle-mediated transport GO-007058/ itochondrion m 60:0032897 negative regulation of viral trans GO:0006886 intracellular protein transport GO:0016236 GO:0070125 macroautophagy mitochondrial translational elongation GO:0070126 nitochondrial translational terminatio GO:0045732 ositive regulation of protein catab 4.5



(C) GO analysis of MII vs dMII



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 S4A heatmap of gene expression levels of all oocyte samples after clustering based onexpression patterns. Twenty clusters were generated and clusters 6 and 12 are indicated.