

Supplementary Table SVII Biological processes and cellular components for the transcripts enriched in AMA GV and MII oocytes, exclusively in the GV/II transition.

AMA MII only						
Category	Term	Count	%	P-value	Benjamini	FDR
BP	Positive regulation of transcription, DNA-templated	36	0.0	3.0E–5	6.9E–2	5.3E–2
BP	Positive regulation of transcription from RNA polymerase II promoter	56	0.1	4.8E–5	5.5E–2	8.5E–2
Category	Term	Count	%	P-value	Benjamini	FDR
CC	Nucleus	234	0.2	2.6E–9	1.2E–6	3.7E–6
CC	Nucleoplasm	138	0.1	1.2E–8	2.7E–6	1.7E–5
CC	Cytoplasm	218	0.2	2.9E–7	4.6E–5	4.1E–4
CC	Nuclear speck	20	0.0	1.7E–5	2.0E–3	2.5E–2
AMA GV only						
Category	Term	Count	%	P-value	Benjamini	FDR
BP	Mitochondrial electron transport, NADH to ubiquinone	17	0.0	2.8E–8	8.9E–5	5.1E–5
BP	Mitochondrial respiratory chain complex I assembly	18	0.0	2.4E–7	3.8E–4	4.4E–4
BP	Mitochondrial translational elongation	20	0.0	1.2E–6	1.2E–3	2.1E–3
BP	Mitochondrial translational termination	18	0.0	2.4E–5	1.9E–2	4.3E–2
Category	Term	Count	%	P-value	Benjamini	FDR
CC	Mitochondrion	148	0.1	2.6E–12	1.6E–9	3.9E–9
CC	Mitochondrial inner membrane	69	0.0	3.0E–12	9.0E–10	4.4E–9
CC	Mitochondrial respiratory chain complex I	16	0.0	1.6E–7	3.1E–5	2.3E–4
CC	Cytosol	260	0.1	2.5E–5	3.9E–3	3.8E–2
CC	Extracellular exosome	219	0.1	2.0E–4	2.4E–2	3.0E–1

AMA, advanced maternal age; BP, biological process; CC, cellular component; GV, germinal vesicle; MII, metaphase II.