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human reproduction

SUPPLEMENTARY DATA

Supplementary Table SV Biological processes and cellular components for the gene transcripts enriched in YMA GV and MII oocytes.

YMA GV up
Biological process

Term	*P*-value	Benjamini	FDR
Mitochondrial translational termination	5.2E−9	2.1E−5	9.6E−6
Mitochondrial translational elongation	1.6E−8	3.4E−5	3.1E−5
Transcription-coupled nucleotide-excision repair	8.0E−7	1.1E−3	1.5E−3
Proteasome-mediated ubiquitin-dependent protein catabolic process	1.9E−6	2.0E−3	3.6E−3
mRNA splicing, via spliceosome	2.0E−6	1.7E−3	3.7E−3
Mitochondrial translation	2.8E−6	1.9E−3	5.1E−3
RNA secondary structure unwinding	1.1E−5	6.3E−3	2.0E−2
Regulation of translational initiation	1.5E−5	8.0E−3	2.9E−2
tRNA processing	2.2E−5	1.0E−2	4.2E−2
Cell division	2.4E−5	9.8E−3	4.4E−2

YMA MII up
Biological process

Term	*P*-value	Benjamini	FDR
Viral transcription	3.3E−15	1.2E−11	5.9E−12
Cell division	1.2E−13	2.1E−10	2.1E−10
Nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	4.6E−12	5.5E−9	8.4E−9
Cell–cell adhesion	2.1E−10	1.9E−7	3.9E−7
Protein sumoylation	3.0E−10	2.2E−7	5.5E−7
Translational initiation	3.5E−10	2.1E−7	6.4E−7
rRNA processing	3.5E−10	1.8E−7	6.4E−7
SRP-dependent cotranslational protein targeting to membrane	4.5E−10	2.0E−7	8.2E−7
DNA repair	2.8E−9	1.1E−6	5.1E−6
RNA splicing	6.5E−9	2.4E−6	1.2E−5
mRNA export from nucleus	4.3E−8	1.4E−5	7.9E−5
Mitotic nuclear division	4.6E−8	1.4E−5	8.5E−5
mRNA splicing, via spliceosome	1.0E−7	2.8E−5	1.8E−4
Viral process	1.5E−7	3.8E−5	2.7E−4
Covalent chromatin modification	1.6E−7	3.8E−5	2.9E−4
G2/M transition of mitotic cell cycle	2.6E−7	5.9E−5	4.8E−4
Cilium assembly	3.3E−7	7.1E−5	6.1E−4
Cellular response to DNA damage stimulus	3.6E−7	7.3E−5	6.6E−4
tRNA export from nucleus	3.0E−6	5.7E−4	5.5E−3
RNA export from nucleus	3.4E−6	6.2E−4	6.3E−3
Sister chromatid cohesion	4.5E−6	7.7E−4	8.2E−3
Gene silencing by RNA	5.1E−6	8.4E−4	9.3E−3
Termination of RNA polymerase II transcription	6.7E−6	1.1E−3	1.2E−2
Mitotic cytokinesis	6.8E−6	1.0E−3	1.3E−2
Cilium morphogenesis	2.2E−5	3.1E−3	4.0E−2

YMA GV up
Cellular component

Term	*P*-value	Benjamini	FDR
Mitochondrion	1.8E−19	1.5E−16	2.8E−16
Nucleoplasm	6.8E−19	2.8E−16	1.0E−15
Mitochondrial inner membrane	3.7E−18	1.0E−15	5.7E−15
Cytosol	6.7E−14	1.4E−11	1.0E−10
Cytoplasm	1.5E−12	2.5E−10	2.3E−9
Nucleus	3.7E−10	5.0E−8	5.7E−7
Nucleolus	1.2E−8	1.4E−6	1.8E−5
Mitochondrial matrix	1.8E−7	1.8E−5	2.7E−4
Myelin sheath	1.9E−7	1.7E−5	3.0E−4
Mitochondrial large ribosomal subunit	2.1E−7	1.7E−5	3.3E−4
Membrane	4.0E−7	3.0E−5	6.1E−4
Mitochondrial intermembrane space	1.8E−6	1.2E−4	2.8E−3
Proteasome complex	2.5E−6	1.6E−4	3.9E−3
Eukaryotic 48S preinitiation complex	5.4E−6	3.2E−4	8.3E−3

(continued)

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SUPPLEMENTARY DATA

Supplementary Table SV Continued

YMA GV up **Cellular component** **Term**	***P*-value**	**Benjamini**	**FDR**
Eukaryotic translation initiation factor 3 complex	2.1E−5	1.2E−3	3.3E−2
Proteasome accessory complex	2.1E−5	1.2E−3	3.3E−2

YMA MII up **Cellular component** **Term**	***P*-value**	**Benjamini**	**FDR**
Nucleoplasm	2.0E−59	1.6E−56	3.1E−56
Nucleus	9.0E−27	3.5E−24	1.4E−23
Centrosome	6.2E−17	2.9E−14	1.7E−13
Cytoplasm	3.0E−15	5.8E−13	4.6E−12
Cytosol	5.0E−14	7.7E−12	7.6E−11
Cell–cell adherens junction	5.4E−11	7.1E−9	8.3E−8
Nucleolus	9.5E−11	1.1E−8	1.4E−7
Nuclear speck	7.3E−10	7.1E−8	1.1E−6
Cytosolic small ribosomal subunit	6.9E−9	5.9E−7	1.1E−5
Centriole	2.4E−8	1.9E−6	3.7E−5
Membrane	2.7E−7	1.9E−5	4.1E−4
Chromosome	3.1E−7	2.0E−5	4.7E−4
Ribosome	4.1E−7	2.5E−5	6.3E−4
Intracellular ribonucleoprotein complex	4.5E−7	2.5E−5	6.8E−4
Focal adhesion	1.2E−6	6.1E−5	1.8E−3
Ciliary basal body	4.4E−6	2.1E−4	6.7E−3
Catalytic step 2 spliceosome	5.5E−6	2.5E−4	8.3E−3
Microtubule organising centre	1.6E−5	6.8E−4	2.4E−2
Chromosome, telomeric region	3.1E−5	1.2E−3	4.7E−2

P-value, Benjamini and FDR are also reported.
FDR, false discovery rate; GV, germinal vesicle; MII, metaphase II; YMA, young maternal age.