Supplementary Table SII Paired-end reads mapping human (GRCh38.82) reference genome using CLC workbench.

	Day of library preparation	Total reads	Total aligned	% Aligned-total	Total gene aligned	% Aligned-total gene	Total exon aligned	% Aligned-total exon
AMA and young germinal vesicle oocyte samples								
AMA GV - 1	1	4,17,42,578	3,73,26,590	89.42%	3,33,47,581	79.89%	2,82,97,706	67.79%
AMA GV - 2	1	5,75,55,238	5,19,37,653	90.24%	4,71,86,330	81.98%	4,07,76,638	70.85%
AMA GV - 3	2	5,29,50,852	4,77,21,575	90.12%	4,29,26,902	81.07%	3,61,36,807	68.25%
AMA GV - 4	2	5,08,32,378	4,65,05,624	91.49%	4,19,68,497	82.56%	3,59,77,835	70.78%
AMA GV - 5	3	7,13,15,038	6,44,80,761	90.42%	5,84,29,169	81.93%	5,05,40,017	70.87%
AMA GV Avg.		5,48,79,217	4,95,94,441	90.37%	4,47,71,696	81.49%	3,83,45,801	69.71%
YNG GV - 1	3	5,51,13,088	4,94,36,344	89.70%	4,42,94,386	80.37%	3,79,15,697	68.80%
YNG GV - 2	2	4,72,77,162	4,24,29,443	89.75%	3,82,34,764	80.87%	3,28,81,264	69.55%
YNG GV - 3	1	5,72,46,446	5,30,09,182	92.60%	4,76,53,172	83.24%	4,04,80,767	70.71%
YNG GV - 4	1	4,87,81,212	4,43,62,937	90.94%	3,99,46,608	81.89%	3,41,69,277	70.05%
YNG GV - 5	2	5,95,71,138	5,37,69,810	90.26%	4,89,76,917	82.22%	4,25,18,761	71.37%
YNG GV Avg.		5,35,97,809	4,86,01,543	90.68%	4,38,21,169	81.72%	3,75,93,153	70.10%
AMA and young metaphase II oocyte samples								
AMA MII - 1	1	4,96,04,302	4,50,23,779	90.77%	4,11,67,882	82.99%	3,61,06,340	72.79%
AMA MII - 2	1	6,32,65,120	5,69,38,115	90.00%	5,23,04,233	82.67%	4,56,48,418	72.15%
AMA MII - 3	2	6,49,10,604	5,82,90,367	89.80%	5,31,59,889	81.90%	4,53,62,901	69.89%
AMA MII - 4	2	7,23,98,740	6,56,66,513	90.70%	5,99,24,497	82.77%	5,16,88,542	71.39%
AMA MII - 5	3	5,85,49,970	5,32,89,928	91.02%	4,86,79,948	83.14%	4,25,32,802	72.64%
AMA MII Avg.		6,17,45,747	5,58,41,740	90.44%	5,10,47,290	82.70%	4,42,67,801	71.77%
YNG MII - 1	3	6,21,07,664	5,62,65,737	90.59%	5,13,04,758	82.61%	4,46,04,654	71.82%
YNG MII - 2	2	5,73,26,998	5,20,73,000	90.84%	4,76,86,424	83.18%	4,13,53,495	72.14%
YNG MII - 3	1	5,15,56,260	4,69,25,330	91.02%	4,28,60,330	83.13%	3,70,01,419	71.77%
YNG MII - 4	1	6,00,45,336	5,49,83,881	91.57%	5,05,42,528	84.17%	4,40,68,682	73.39%
YNG MII - 5	2	6,28,84,082	5,55,58,306	88.35%	5,11,86,048	81.40%	4,47,32,752	71.14%
YNG MII Avg.		5,87,84,068	5,31,61,251	90.43%	4,87,16,018	82.90%	4,23,52,200	72.05%

AMA, advanced maternal age; GV, germinal vesicle; MII, metaphase II.

Each read pair counts as two unless only one read of a pair maps in which case it counts as one. AMA (donor age ≥ 40): AMA, Young (donor age < 30): YNG. Total exon reads used in subsequent data analysis.