

Table II. Gene Set Enrichment Analysis of the transcriptome of CRCs of individual oocytes developing into embryos selected for transfer. PCOS women compared controls (n=6 PCOS arrays vs n=6 control arrays). Enriched pathways with FDR <0.05 were listed. NES=normalized enrichment score. All enriched pathways were upregulated in PCOS CRC samples.

Pathway	No of genes enriched/ total number of genes in the pathway	FDR	NES
Reactome Cell Cycle	127/421	0.001	0.42
Reactome G2 M Checkpoints	17/45	0.001	0.61
KEGG DNA Replication	20/36	0.001	0.65
Reactome Meiotic Recombination	35/86	0.001	0.59
Reactome Packaging of Telomere Ends	25/48	0.001	0.63
Reactome Activation of the Pre Replicative Complex	14/31	0.001	0.60
Reactome RNA POL I RNA POL III and Mitochondrial Transcription	45/122	0.001	0.53
Reactome RNA POL I Transcription	35/89	0.001	0.55
Reactome RNA POL I Promotor Opening	32/62	0.001	0.64
Reactome Activation of ATR in Response to Replication Stress	15/38	0.001	0.63
Reactome Deposition of new CENPA containing Nucleosomes at the Centromere	34/64	0.001	0.60
Reactome DNA strand Elongation	20/30	0.001	0.69
Reactome Telomere Maintenance	39/75	0.001	0.61
Reactome Cell Cycle Mitotic	94/325	0.01	0.41
Reactome Meiosis	45/116	0.01	0.49
Reactome Amyloids	34/83	0.01	0.51
Reactome lagging strand synthesis	12/19	0.01	0.69
Reactome Mitotic M M G1 Phases	55/137	0.03	0.42
Reactome Mitotic Prometaphase	32/87	0.03	0.47
Reactome DNA replication	56/192	0.03	0.42
Reactome Meiotic Synapsis	34/73	0.03	0.50
Reactome Chromosome Maintenance	55/122	0.03	0.42
Reactome Extension of Telomeres	13/27	0.03	0.59
Reactome Transcription	61/210	0.04	0.41