

Table 1. Selected overrepresented Gene Ontology (GO) biological processes in oocytes identified by Expression Analysis Systematic Explorer (EASE) (EASE score < 0.05)

	GO Biological Process term	Representative genes expressed by the human oocyte
1	<p>Cell Cycle</p> <p>Mitotic cell cycle</p> <p>M phase</p> <p>Nuclear division</p> <p>Cytokinesis</p> <p>Meiosis</p> <p>Meiosis I</p> <p>Meiotic prophase I</p> <p>DNA recombination</p> <p>Sister chromatid cohesion</p> <p>Regulation of cell cycle</p> <p>Cell cycle checkpoint</p> <p>Regulation of mitosis</p>	<p>ANAPC1, ANLN, APC10, BIN3, BRCA2, BUB1, BUB1B, BUB3, C2orf6, CCNA2, CCNB1, CCNB2, CCNB3, CCND2, CCNE1, CCNE2, CCNG2, CCNI, CDC14A, CDC20, CDC23, CDC25B, CDC25C, CDC27, CDC45L, CDC5L, CDC7, CDK3, CDK7, CDK8, CENPE, CENPF, CENPH, CETN3, CHC1, CHEK1, CHFR, CKS2, NAP1, CSPG6, EML4, ESPL1, GAJ, GPR125, HCAP-G, HCAP-G, HSPC135, HT014, IDN3, KATNA1, KIF11, KIF23, KIF2C, KNSL7, KNTC1, LIG1, LIG4, MAD2L1, MAD2L2, MAD2L2, MPHOSPH1, MRE11A, MSH5, MVP, NEDD5, NEK1, NEK2, PAFAH1B1, PARD3, PCCB, PLK1, PPP1R9B, PRC1, PREI3, PTTG1, RAD1, RAD17, RAD51L1, RAD54B, RAN, RBM11, SAP30, SKB1, SMC2L1, SMC4L1, STAG3, STK6, SUGT1, SYCP2, TARDBP, TPX2, TTK, UBE2C, UBE2D3, UNG2, ZW10</p>
2	<p>Nucleic acid metabolism</p> <p>DNA metabolism</p> <p>DNA replication DNA replication and chromosome cycle</p> <p>DNA repair</p> <p>RNA metabolism</p> <p>mRNA metabolism</p> <p>mRNA processing</p> <p>mRNA catabolism</p> <p>tRNA metabolism</p>	<p>ACF, CDC45L, CENPE, CENPF, CENPH, CHAF1A, CHAF1B, CPEB1, CPEB4, CPSF2, DNA2L, ESPL1, FEN1, FNBP3, HCAP-G, HNRPA1, IDN3, LIG1, LIG4, MAD2L1, MSH2, MSH3, MSH5, NAP1L1, ORC1L, ORC4L, ORC5L, PABPN1, PCF11, PCNA, PLRG1, POLA, POLB, POLD3, POLE2, POLG2, POLQ, POLS, PRIM2A, PRPF3, PRPF4, PSEN2, RAD17, RBM17, RFC4, SF3B4, SFRS12, SIP1, SLBP, SMN1, SNRPD1, SNRPE, SNRPF, TFAM, TOP1, TOP2A, U2AF2, XRN2</p>

3	Response to DNA damage stimulus DNA repair	<p>ABL1, ALKBH, APEX2, , BLM, BRCA2, BRIP1, BTG2, CDK7, CHAF1A, CHAF1B, CHEK1, CHEK2, CRY1, CSNK1E, CSPG6, DC13, DCLRE1A, DDB1, DKC1, FANCF, FANCL, FEN1, GTF2H1, GTF2H2, GTSE1, HNRPD, KLC2L, LIG1, LIG4, MBD4, MPG, MRE11A, MSH2, MSH3, MSH5, NBS1, NCOA6, NTHL1, OGG1, PMS1, PMS2L9, POLB, POLD3, POLE2, POLG2, POLQ, POLS, POT1, PTTG1, RAD1, RAD17, RAD51C, RAD51L1, REV1L, RFC1, RPA1, RPS6KA5, SESN1, SRISNF2L, TDP1, TERF2, TNKS2, UBE2C, UBE2N, UNG, UNG2, WDR33, XRCC1, XRCC4</p>
4	<p>Transcription Transcription from Pol II promoter Regulation of transcription Regulation of transcription from Pol II promoter Regulation of transcription\ DNA-dependent Negative regulation of transcription Regulation of gene expression\ epigenetic Positive regulation of gene expression\ epigenetic</p>	<p>ASF1B, BRD1, CBF, CDK7, CHD4, CLOCK, CREB5, CRK, CUTL1, DHX30, DHX9, DNMT1, DNMT3A, DNMT3B, DR1, E2F1, ELF4, ELK3, FOS, FOXD3, FOXL2, FOXM1, FOXO1A, FOXO3A, GABPB2, GCN5L2, HBP1, HELSNF1, HEY2, HIPK2, HMG20A, HMG20B, HMG2L1, HMGA1, HMGB2, HMGN4, HOXA1, HOXA13, HOXA7, HOXD1, HOXD13, HSF2BP, HTATIP2, LEF1, LHX5, MAX, MLL4, MSX2, MTF1, MXD4, NCOA6, NFATC1, NFATC3, NFRKB, PAXIP1L, PBX3, POLR2J, POU2F1, POU3F2, POU4F1, POU5F1, PPAR, REL, RNF14, SIRT7, SMARCA5, SMARCA5, SMARCB1, SMARCC2, SOX13, SOX15, SOX30, SOX5, SP2, SREBF2, STAU2, SURB7, TAF1A, TAF2, TAF4, TBDN100, TBP, TBPL1, TBX3, TBX5, TCF15, TCF7, TCFL1, TFAP2B, TFDP1, TIEG2, TRIM33, UBN1, WDHD1, WNT6, YBX2, YY1, ZCCHC8, ZDHHC18, ZDHHC5, ZDHHC7, ZHX1, ZNF10, ZNF136, ZNF148, ZNF161, ZNF174, ZNF177, ZNF202, ZNF237, ZNF281, ZNF354A, ZNF558, ZNF559, ZNF574, ZNF586, ZNF76, ZNF77, ZNF85, ZNF9</p>

5	<p>Ubiquitin-dependent protein catabolism</p> <p>Protein modification</p> <p>Ubiquitin cycle</p>	<p>ARIH1, ARIH2, BTRC, CDC20, CDC34, CYLD, DD5, DKFZP564G092, FBXO11, FBXO8, FLN29, FTS, HACE1, HIP2, HSPC150, HSXIAPAF1, LMO7, PSMA2, PSMA5, PSMA7, PSMD9, RNF14, SAE1, SIAH1, SMURF1, STAU2, TSG101, UBE2C, UBE2D3, UBE2G1, UBE2I, UBE2L3, UBE2N, UBE2Q, UBE2R2, UBE2S, UBE3B, UBPH, UCHL1, USP1, USP10, USP13, USP15, USP16, USP2, USP21, USP26, USP30, USP34, USP35, USP36, USP37, USP44, USP49, USP52, USP9X, WWP2</p>
6	<p>Phosphate metabolism</p> <p>Protein amino acid phosphorylation</p> <p>Protein amino acid dephosphorylation</p>	<p>ACVR1, ACVR1B, ACYP1, AKT2, AURKB, AURKC, BMP2K, BMPR1A, BRAP, BUB1, CAMK1D, CAMK2G, CCRK, CDC14A, CDC25B, CDC25C, CDC42BPA, CDC42BPB, CDC7, CDK3, CDK7, CDK8, CDKL5, CHEK1, CHEK2, CLK1, CLK2, , CLK3, CRK7, CSF1R, CSNK1E, DAPK1, DUSP10, DUSP5, EPHA1, EPHB1, ERN1, FER, FGFR1, FGFR2, FYN, GPR125, GRK6, GSK3A, HMGA1L4, IGF1R, IKBKB, ILKAP, IMPA1, INHBA, INPP5D, KIT, MADH2, MADH5, MAP2K1, MAP4K3, MAPK6, MAPK7, MAPK8, MAPKAPK5, MARK2, MARK4, MASTL, MELK, MKNK1, MOS, MTM1, MTMR3, NEK1, NTRK2, PACE-1, PASK, PDPK1, PLK1, PLK3, PPM1E, PRKAR1A, PRKCG, PRKG1, PRKRA, PTEN, PTK2, PTK9, PTP4A3, PTPN2, PTPN3, PTPRG, PTPRH, PTPRN2, RIOK1, STK24, STK31, STK38, STK6, TEC, TEX14</p>
7	<p>Reproduction</p> <p>Sexual reproduction</p> <p>Gametogenesis</p> <p>Spermatogenesis</p>	<p>AXIN1, BCL2L10, BMP15, BRD2, CCNI, CHEK1, CUGBP1, D8S2298E, DAZ, DAZ2, DAZL, DNAH9, FLJ10511, FUT10, GDF9, GMCL, HIST1H1E, HMGCR, HSF2BP, HSPC039, KHDRBS3, MAGOH, NASP, NDRG3, NJMU-R1, NOC4, NR6A1, NY-REN-24, ODC-p, PIWIL1, PPP1R12A, PTTG1, RNF125, RNF138, SOX30, SPAG6, SPATA2, SPIN, STRBP, TDRD1, TEX15, TSGA10, TUBD1, USP9X, WFDC2, XRN2, ZP2</p>
8	<p>Chromatin remodeling</p> <p>Chromatin modification</p> <p>Non-covalent chromatin modification</p>	<p>ARID1A, ASF1A, ASF1B, BAF53A, BRCA2, CHD4, EHMT1, GCN5L2, HDAC9, HELSNF1, HMG20B, MLL3, MLL4, MSL3L1, SETDB2, SIRT7, SMARCA1, SMARCA5, SMARCD1, SMARCC2, SMARCD1</p>