## SUPPLEMENTARY TABLES

### Supplementary Table 1. DEGs analysis result.

| NO. | genesymbol | ID      | logFC  | AveExpr | t        | P.Value  | adj.P.Val | B         |
|-----|------------|---------|--------|---------|----------|----------|-----------|-----------|
| 2660| CDC7       | 7902913 | 1.20992275 | 5.37396213 | 2.78602574 | 0.02154565 | 0.1726192 | -3.2848305 |
| 2701| CDK1       | 7927710 | 1.1229915 | 6.12909975 | 2.94803956 | 0.01658302 | 0.16063097 | -3.0362356 |
| 2965| CHEK1      | 7945014 | 1.25384825 | 8.16880263 | 4.37013511 | 0.0018745 | 0.09430518 | -0.9544463 |

### Supplementary Table 2. Kegg pathway.

| Term                                      | Count | PValue | Genes                                                                 | Fold Enrichment | Bonferroni | Benjamini | FDR             |
|-------------------------------------------|-------|--------|----------------------------------------------------------------------|-----------------|------------|-----------|-----------------|
| hsa04110:Cell cycle                       | 27    | 1.01E-06 | YWHAZ, E2F5, ANAPC13, PRKDC, ANAPC10, CHEK1, CDC16, CCNE2, RAD21, STAG2, CDC7, CDC6, CDK1, RBL2, ANAPC4, RBL1, YWHAH, SMAD4, CDC23, CDC6, SMAD2, RB1, ATM, SMC3, MCM6, HDA2C, MAD2L1 | 2.898047493 | 1.71E-04 | 1.71E-04 | 0.001229924 |
| hsa03050:Proteasome                      | 13    | 1.15E-04 | PSMA2, PSMA1, PSMC6, PSMD14, PSMB1, PSMD12, PSMA5, PSMA4, PSMC2, PSMA3, PSMD1, POMP, PSMD6, CDK1, YWHAZ, ANAPC13, ANAPC4, YWHAH, PPP3R1, CDC23, ANAPC10, Cdc16, PPP1CC, PPP1CB, SMC3, CCNE2, MAPK1, MAD2L1, SLK, PPP2CA, PPP2CB, PPP3CB, FBXO5, PPP3CA | 3.711053725 | 0.019301519 | 0.009697783 | 0.139771344 |
| hsa04114:Oocyte meiosis                   | 21    | 1.38E-04 | XIAP, UBE3A, ANAPC13, VHL, UBE2G1, ANAPC4, CDC23, UBA6, HERC4, ANAPC10, CDC16, UBE2H, BIRC2, CUL3, CUL2, CUL5, FBXW7, UBE2K, UBA2, UBA3, UBE2W, RCHY1, UBE2D1, TRIP12 | 2.561405613 | 0.023147852 | 0.007776264 | 0.167929275 |
| hsa04120:Ubiquitin mediated proteolysis   | 24    | 1.57E-04 | DIS3, PAPOLA, EXOSC8, CNOT8, CNOT6L, LMS5, CNOT2, LMS3, CNOT7, MPHOSPH6, LMS1, HSPA9, C1D, DDX6 | 2.350403482 | 0.026260353 | 0.006630747 | 0.190790462 |
| hsa03018:RNA degradation                  | 14    | 2.07E-04 | DIS3, PAPOLA, EXOSC8, CNOT8, CNOT6L, LMS5, CNOT2, LMS3, CNOT7, MPHOSPH6, LMS1, HSPA9, C1D, DDX6 | 3.295375642 | 0.034576002 | 0.007012874 | 0.25220896 |
| hsa03022:Base transcription factors       | 10    | 7.81E-04 | TAF11, TAF2, TAF13, GTF2A1, GTF2A2, TAF9B, GTF2H3, GTF2B, TBPL1, GTF2H1 | 3.833396155 | 0.124452204 | 0.021907392 | 0.94245571 |
| hsa00563:Glycosylphosphatidylinositol(GPI)-anchor biosynthesis | 7  | 0.0085312 | PIGK, PIGF, PIGY, PIGX, PIGW, PIGB, PIGN | 3.756728232 | 0.766958304 | 0.18785372 | 9.92491482 |
| hsa00520:Ammonium sugar and nucleotide sugar metabolism | 9  | 0.0143405 | PGD2, PGM3, GPNPA2, GEPT1, GNPNAT1, HEXB, UGDH, FPTG, UGP2 | 2.744363157 | 0.914183677 | 0.264307654 | 16.15657625 |
| hsa00510:N-Glycan biosynthesis            | 9  | 0.0185504 | STT3B, MAN1A2, ALG10B, DPM1, ALG5, ALG6, MAN1A1, ALG11, ALG8 | 2.625043019 | 0.958547035 | 0.297906315 | 20.42243587 |
| hsa04914:Progesterone-mediated oocyte maturation | 13  | 0.0241788 | CDK1, GNAI3, PIK3CB, ANAPC13, ANAPC4, CDC23, ANAPC10, CDC16, PPP1CB, MAPK1, MAD2L1, MAPK14, MAPK9 | 2.028134012 | 0.984406552 | 0.340379394 | 25.81453929 |
| Pathway Name                                                        | ID | Gene Symbols                                                                 | KM Score | KMI Score | P Score | FDR | P Value |
|-------------------------------------------------------------------|----|------------------------------------------------------------------------------|----------|-----------|---------|-----|---------|
| hsa00620:Pyruvate metabolism                                      | 8  | ME1, LDHB, ME2, PDHA1, DLAT, ACAT1, ALDH9A1, MDH1                             | 2.68377309 | 0.988808972 | 0.335301738 | 27.55979969 |
| hsa04210:Apoptosis                                                 | 13 | CFLAR, XIAP, PIK3CB, PPP3R1, BIRC2, ATM, IRAK4, CASP6, CASP3, PRKAR1A, PPP3CB, PPP3CA, CHUK | 2.004822127 | 0.989116299 | 0.313883203 | 27.70441471 |
| hsa05100:Epithelial cell signaling in Helicobacter pylori infection | 11 | ATP6V1C1, ATP6V1A, CASP3, ADAM10, LYN, MAPK14, MAP2K4, MAPK9, ATP6V1B2, ATP6V1D, CHUK | 2.170378706 | 0.991060391 | 0.313883203 | 27.70441471 |
| hsa00970:Aminoacyl-tRNA biosynthesis                              | 8  | TARS, NARS, DARS, RARS, RARS2, GARS, SEPSECS, FARSB                          | 2.762300171 | 0.998318070 | 0.346788431 | 36.77138752 |
| hsa00280:Valine, leucine and isoleucine degradation               | 8  | ACADSB, ACADM, OXCT1, ACAT1, HIBADH, PCCA, ALDH9A1, HADHB                  | 2.43943917 | 0.999272578 | 0.346268819 | 40.46256723 |
| hsa04140:Regulation of autophagy                                   | 7  | GABARAPL2, ATG4C, ATG5, BECN1, ATG4A, PRKAA1, ATG3                          | 2.68337309 | 0.999299928 | 0.332071236 | 40.62608511 |
| hsa04211:SNARE interactions in vesicular transport                | 7  | VAMP7, STX16, BET1, VTI1B, VAMP3, GOSR1, SNAP23                             | 2.471531732 | 0.99968258 | 0.420246165 | 52.44675687 |
| hsa04720:Long-term potentiation                                   | 10 | MAPK1, NRAS, PPP3CB, PPP3R1, PPP1R12A, RAP1A, RAP1B, PPP3CA, PPP1CC, PPP1CB | 1.973071551 | 0.999983735 | 0.423814781 | 54.67467678 |
| hsa00071:Fatty acid metabolism                                     | 7  | ACADSB, ACADM, ACSL4, ACSL3, ACAT1, ALDH9A1, HADHB                          | 2.347955145 | 0.999997313 | 0.457092772 | 60.16896485 |
| hsa00640:Propionate metabolism                                    | 6  | LDHB, ACADM, SUCLG2, ACAT1, PCCA, ALDH9A1                                  | 2.515662277 | 0.99999709 | 0.49546768 | 66.0436841 |
| hsa00900:Terpenoid backbone biosynthesis                           | 4  | HMGCR, IDH1, ACAT1, PDSS2                                                  | 3.577836412 | 0.99999958 | 0.522323875 | 70.46147324 |