**Table S23. Ovarian cancer modules enriched with GO terms using a TANGO tool.**

| Module ID | x | Description | p-value | q-value | Frequency | Genes |
|---|---|---|---|---|---|---|
| 2 | 13 | Leukocyte Activation | 6.94E-10 | 0.001 | 0.22 | PSMB10, MEF2C, LYN, PTPN22, VAV1, CD74, BTK, DOCK2, LCK, CD4, BLNK, LCP2, TYROBP |
| 2 | 11 | Positive Regulation Of Leukocyte Activation | 3.75E-09 | 0.001 | 0.19 | MEF2C, LYN, FGR, IL18, ICOS, LCK, CD4, VAV1, CD27, CD74, BTK |
| 2 | 10 | Immune Response-Regulating Signaling Pathway | 3.11E-08 | 0.002 | 0.17 | MEF2C, LYN, FGR, HCK, LCK, PTPN22, CD4, CTSH, LCP2, BTK |
| 2 | 11 | Response To Bacterium | 9.03E-08 | 0.002 | 0.19 | MEF2C, LYN, FGR, CCR5, CXCL13, HCK, IL18, MMP9, ACP5, CD4, CXCL10 |
| 2 | 10 | Regulation Of Cell Adhesion | 1.70E-07 | 0.005 | 0.17 | LPXN, LYN, CD44, CCR5, CXCL13, IL18, CYTH4, VAV1, ARHGDIB, SPP1 |
| 2 | 9 | Leukocyte Differentiation | 3.14E-07 | 0.01 | 0.15 | MEF2C, DOCK2, LYN, MMP9, LCK, PTPN22, CD4, CD74, BLNK |
| 2 | 7 | Adaptive Immune Response | 5.67E-07 | 0.014 | 0.12 | MEF2C, CXCL13, IL18, CTSH, CD27, CD74, BTK |
| 2 | 5 | Regulation Of Leukocyte Apoptotic Process | 1.36E-06 | 0.025 | 0.085 | MEF2C, LYN, CCR5, CD74, BTK |
| 2 | 8 | Regulation Of Immune Effector Process | 2.59E-06 | 0.042 | 0.14 | DOCK2, LYN, FGR, HCK, LCK, CD4, CD74, BTK |
| 3 | 17 | Interphase Of Mitotic Cell Cycle | 1.26E-18 | 0.001 | 0.49 | E2F1, GINS1, CDC6, GINS2, POLA2, MCM2, MCM10, MCM4, CDK2, CEP70, CCNE2, CDC45, CCNB2, MCM7, PLK1, TFDP2, TUBG1 |
| 3 | 12 | Cell Cycle Checkpoint | 3.08E-13 | 0.001 | 0.34 | E2F1, CCNE2, CDC6, CDC45, MCM7, CCNB2, PLK1, BUB1, MCM2, MCM10, MCM4, CDK2 |
| 3 | 7 | Dna Strand Elongation Involved In Dna Replication | 2.83E-12 | 0.001 | 0.2 | GINS1, GINS2, CDC45, MCM7, MCM2, POLA2, MCM4 |
| 3 | 10 | Dna Replication | 2.75E-11 | 0.001 | 0.29 | GINS1, GINS2, CDC6, CDC45, MCM7, MCM2, POLA2, MCM10, MCM4, CDK2 |
| 3 | 8 | M/G1 Transition Of Mitotic Cell Cycle | 3.51E-11 | 0.001 | 0.23 | CDC6, CDC45, MCM7, MCM2, POLA2, MCM10, MCM4, CDK2 |
| 3 | 5 | Dna-Dependent Dna Replication Initiation | 2.65E-09 | 0.001 | 0.14 | CDC45, MCM7, MCM2, POLA2, MCM4 |
| 3 | 8 | Mitosis | 4.30E-07 | 0.013 | 0.23 | KIF22, CDC6, CCNB2, PLK1, BUB1, CEP55, ASPM, CDK2 |
| 4 | 5 | Cilium Morphogenesis | 2.93E-06 | 0.049 | 0.1 | TMEM231, FOXJ1, DNAAF1, TCTN1, DNAI2 |
| 6 | 12 | Dna Replication | 1.47E-14 | 0.001 | 0.35 | CDC7, PRIM1, RFC5, POLE2, PCNA, CHEK1, MCM2, MCM4, CDK2, CDC25A, FEN1, MCM6 |
| 6 | 14 | Interphase Of Mitotic Cell Cycle | 2.66E-14 | 0.001 | 0.41 | CDC7, PRIM1, RFC5, CCNE2, POLE2, PCNA, CHEK1, MCM2, CDKN3, MCM4, CDK2, CDC25A, FEN1, MCM6 |
| 6 | 11 | G1/S Transition Of Mitotic Cell Cycle | 1.71E-13 | 0.001 | 0.32 | CDC7, PRIM1, CCNE2, POLE2, PCNA, MCM2, CDKN3, MCM4, CDK2, CDC25A, MCM6 |
| 6 | 10 | S Phase Of Mitotic Cell Cycle | 2.62E-13 | 0.001 | 0.29 | PRIM1, RFC5, POLE2, PCNA, MCM2, MCM4, CDK2, CDC25A, FEN1, MCM6 |
| 6 | 7 | Dna Strand Elongation Involved In Dna Replication | 2.28E-12 | 0.001 | 0.21 | PRIM1, RFC5, PCNA, MCM2, MCM4, FEN1, MCM6 |
| 6 | 11 | Cell Cycle Checkpoint | 6.43E-12 | 0.001 | 0.32 | CDC7, RFC5, CCNE2, KNTC1, BUB1, CHEK1, MCM2, MCM4, CDK2, CDC25A, MCM6 |

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| 6 | 10 | Mitosis | 1.04E-09 | 0.001 | 0.29 | KIF23, TIMELESS, DSN1, KIF15, KNTC1, BUB1, CEP55, RACGAP1, CDK2, CDC25A |
| 6 | 5 | Dna-Dependent Dna Replication Initiation | 2.29E-09 | 0.001 | 0.15 | PRIM1, POLE2, MCM2, MCM4, MCM6 |
| 6 | 5 | Telomere Maintenance Via Semi-Conservative Replication | 2.99E-09 | 0.001 | 0.15 | PRIM1, RFC5, POLE2, PCNA, FEN1 |
| 6 | 9 | Dna Repair | 9.72E-08 | 0.002 | 0.26 | RFC5, MSH6, POLE2, PCNA, CHEK1, PARP2, CDK2, FEN1, BARD1 |
| 8 | 7 | Regulation Of Cell-Substrate Adhesion | 1.22E-08 | 0.001 | 0.18 | CCL21, LGALS1, SERPINE1, COL1A1, THBS1, ITGB1, PLAU |
| 8 | 9 | Blood Vessel Morphogenesis | 2.99E-07 | 0.009 | 0.23 | ITGA5, SERPINE1, MMP19, PDGFRB, THBS1, ITGB1, PLAU, MYLK, FN1 |
| 8 | 4 | Peptide Cross-Linking | 1.05E-06 | 0.02 | 0.1 | BGN, COL3A1, THBS1, FN1 |
| 8 | 5 | Response To Amino Acid Stimulus | 1.88E-06 | 0.031 | 0.13 | COL3A1, COL1A2, COL1A1, COL16A1, TIMP3 |
| 8 | 7 | Platelet Activation | 2.47E-06 | 0.041 | 0.18 | SERPINE1, COL3A1, COL1A2, TUBA4A, COL1A1, THBS1, FN1 |
| 8 | 4 | Collagen Metabolic Process | 2.68E-06 | 0.042 | 0.1 | MMP19, COL3A1, COL1A1, MMP11 |
| 12 | 10 | Interphase Of Mitotic Cell Cycle | 4.68E-09 | 0.001 | 0.3 | PRIM1, RFC5, E2F3, NBN, PSMA5, GMNN, TFDP2, MCM2, MCM10, FEN1 |
| 12 | 4 | Dna Strand Elongation Involved In Dna Replication | 1.54E-06 | 0.028 | 0.12 | PRIM1, RFC5, MCM2, FEN1 |
| 13 | 21 | Interphase Of Mitotic Cell Cycle | 1.41E-16 | 0.001 | 0.27 | CDC6, GINS2, DBF4, GMNN, CHEK1, BIRC5, MCM10, MCM6, CCNE2, PSMB4, EIF4EBP1, CDC45, MCM7, POLE2, PLK1, TFDP2, PCNA, ORC5, ORC1, MELK, ORC2 |
| 13 | 18 | Cell Cycle Checkpoint | 6.03E-16 | 0.001 | 0.23 | CDC6, DBF4, CHEK1, BIRC5, MCM10, MCM6, RAD1, CCNE2, PSMB4, CDC45, MCM7, PLK1, BUB1, ORC5, FANCG, ORC1, BUB3, ORC2 |
| 13 | 16 | Dna Replication | 6.02E-15 | 0.001 | 0.21 | POLL, CDC6, GINS2, DBF4, CHEK1, MCM10, MCM6, RAD1, TFAM, CDC45, MCM7, POLE2, PCNA, ORC5, ORC1, ORC2 |
| 13 | 12 | M/G1 Transition Of Mitotic Cell Cycle | 4.19E-14 | 0.001 | 0.16 | PSMB4, CDC6, CDC45, MCM7, POLE2, GMNN, DBF4, ORC5, MCM10, ORC1, ORC2, MCM6 |
| 13 | 14 | G1/S Transition Of Mitotic Cell Cycle | 4.81E-13 | 0.001 | 0.18 | CDC6, DBF4, MCM10, MCM6, CCNE2, PSMB4, EIF4EBP1, CDC45, MCM7, POLE2, PCNA, ORC5, ORC1, ORC2 |
| 13 | 10 | Dna-Dependent Dna Replication | 1.49E-11 | 0.001 | 0.13 | GINS2, TFAM, CDC45, MCM7, POLE2, PCNA, ORC5, ORC1, ORC2, MCM6 |
| 13 | 7 | Dna-Dependent Dna Replication Initiation | 2.89E-11 | 0.001 | 0.091 | CDC45, MCM7, POLE2, ORC5, ORC1, ORC2, MCM6 |
| 13 | 6 | Regulation Of Chromosome Segregation | 1.15E-09 | 0.001 | 0.078 | CDC42, CDC6, BUB1, AURKB, ECT2, BUB3 |
| 13 | 13 | Mitosis | 5.27E-09 | 0.001 | 0.17 | CDC6, HAUS6, NCAPH, CDCA8, TIMELESS, PLK1, DSN1, BUB1, BIRC5, AURKB, SMC2, BUB3, SMC4 |
| 13 | 8 | Regulation Of Nuclear Division | 1.98E-08 | 0.002 | 0.1 | CDC42, CDC6, AURKAIP1, PLK1, BUB1, RANBP1, CHEK1, BUB3 |
| 13 | 12 | Regulation Of Mitotic Cell Cycle | 1.12E-07 | 0.002 | 0.16 | CDC42, PSMB4, CDC6, CDC45, EIF4EBP1, AURKAIP1, PLK1, BUB1, RANBP1, BIRC5, CHEK1, BUB3 |
| 13 | 4 | Regulation Of Cell Cycle Cytokinesis | 1.16E-06 | 0.021 | 0.052 | CDC42, CDC6, AURKB, ECT2 |

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| 13 | 11 | Dna Repair | 2.68E-06 | 0.042 | 0.14 | EXO1, RAD1, POLL, POLE2, UCHL5, PCNA, FANCE, CHEK1, FANCG, SMC2, SMC4 |
| 18 | 12 | Regulation Of Cell Cycle Arrest | 1.72E-13 | 0.001 | 0.39 | CDC7, RFC5, CCNE2, MCM7, FOXM1, KNTC1, CHEK1, MCM2, FANCG, MCM3, MCM4, MCM6 |
| 18 | 11 | Dna Replication | 1.80E-13 | 0.001 | 0.35 | CDC7, RFC5, MCM7, NASP, CHEK1, MCM2, MCM3, MCM4, FEN1, MCM6, SLBP |
| 18 | 13 | Interphase | 2.05E-13 | 0.001 | 0.42 | CDC7, RFC5, CCNE2, MCM7, FOXM1, CHEK1, MCM2, MCM3, MCM4, FEN1, MELK, MCM6, SLBP |
| 18 | 7 | Dna Strand Elongation Involved In Dna Replication | 1.12E-12 | 0.001 | 0.23 | RFC5, MCM7, MCM2, MCM3, MCM4, FEN1, MCM6 |
| 18 | 8 | Dna Repair | 6.37E-07 | 0.016 | 0.26 | EXO1, RFC5, FOXM1, CHEK1, TOPBP1, FANCG, FEN1, SMC4 |
| 18 | 4 | Regulation Of S Phase | 6.66E-07 | 0.016 | 0.13 | CDC7, TIMELESS, CHEK1, SLBP |
| 18 | 7 | Mitosis | 2.52E-06 | 0.042 | 0.23 | KIF23, TIMELESS, DSN1, KNTC1, AURKB, RACGAP1, SMC4 |
| 20 | 26 | Mitosis | 3.82E-33 | 0.001 | 0.59 | KIF23, NEK2, AURKA, CEP55, AURKB, MYBL2, SPC25, NCAPH, CDCA8, CENPA, BUB1, CCNA2, ASPM, CDCA3, ERCC6L, KIF15, CENPE, BIRC5, CDC20, RACGAP1, CCNB1, MAD2L1, CCNB2, SPAG5, PLK1, BUB1B |
| 20 | 13 | Mitotic Prometaphase | 2.13E-19 | 0.001 | 0.3 | CCNB1, SPC25, CDCA8, MAD2L1, PLK1, CENPA, BUB1, BUB1B, CENPE, BIRC5, CDC20, AURKB, ERCC6L |
| 20 | 17 | Microtubule-Based Process | 2.22E-17 | 0.001 | 0.39 | KIF14, KIF23, KIF4A, NEK2, KIF15, CENPE, AURKA, AURKB, RACGAP1, MYBL2, GTSE1, SPC25, PLK4, PLK1, CENPA, SPAG5, BUB1B |
| 20 | 11 | Chromosome Segregation | 5.43E-14 | 0.001 | 0.25 | CCNB1, SPC25, NCAPH, MAD2L1, NEK2, SPAG5, BUB1, CENPE, BIRC5, AURKB, TOP2A |
| 20 | 9 | Spindle Organization | 1.28E-12 | 0.001 | 0.2 | KIF23, SPC25, NEK2, SPAG5, BUB1B, AURKA, AURKB, RACGAP1, MYBL2 |
| 20 | 10 | G2/M Transition Of Mitotic Cell Cycle | 1.47E-11 | 0.001 | 0.23 | CCNB1, PLK4, CCNB2, PLK1, NEK2, FOXM1, BIRC5, TOP2A, CCNA2, MELK |
| 20 | 12 | Regulation Of Cell Cycle Arrest | 2.03E-11 | 0.001 | 0.27 | CCNB1, MAD2L1, CCNB2, PLK1, FOXM1, BUB1, BUB1B, BIRC5, CDC20, TOP2A, CCNA2, GTSE1 |
| 20 | 6 | Regulation Of Chromosome Segregation | 3.56E-11 | 0.001 | 0.14 | CCNB1, NEK2, SPAG5, BUB1, AURKB, RACGAP1 |
| 20 | 12 | Regulation Of Mitotic Cell Cycle | 1.32E-10 | 0.001 | 0.27 | CCNB1, MAD2L1, PLK1, NEK2, BUB1, BUB1B, AURKA, BIRC5, CDC20, TOP2A, CCNA2, GTSE1 |
| 20 | 6 | Spindle Checkpoint | 7.04E-10 | 0.001 | 0.14 | CCNB1, MAD2L1, BUB1, BUB1B, BIRC5, CDC20 |
| 20 | 7 | Organelle Assembly | 7.72E-09 | 0.001 | 0.16 | KIF23, NEK2, CENPA, CENPE, AURKB, RACGAP1, MYBL2 |
| 20 | 7 | Anaphase-Promoting Complex-Dependent Proteasomal Ubiquitin-Dependent Protein Catabolic Process | 7.72E-09 | 0.001 | 0.16 | CCNB1, MAD2L1, PLK1, BUB1B, AURKA, CDC20, AURKB |
| 20 | 7 | Regulation Of Nuclear Division | 7.72E-09 | 0.001 | 0.16 | MAD2L1, PLK1, NEK2, BUB1, BUB1B, AURKA, CDC20 |

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| 20 | 8 | Positive Regulation Of Cell Cycle Process | 4.55E-08 | 0.002 | 0.18 | KIF23, PLK4, PLK1, AURKA, BIRC5, AURKB, RACGAP1, GTSE1 |
| 20 | 6 | Regulation Of Microtubule Cytoskeleton Organization | 1.50E-07 | 0.005 | 0.14 | CCNB1, PLK4, NEK2, SPAG5, AURKA, RACGAP1 |
| 20 | 4 | Protein Localization To Chromosome | 6.47E-07 | 0.016 | 0.091 | PLK1, CENPA, BUB1B, AURKB |
| 21 | 7 | Activation Of Immune Response | 8.41E-07 | 0.02 | 0.23 | C1QA, ITK, HCK, LCK, MNDA, LCP2, BTK |
| 22 | 10 | Extracellular Matrix Organization | 2.27E-13 | 0.001 | 0.37 | COL3A1, COL1A1, GREM1, LOXL2, COL5A3, MMP2, COL5A1, MMP1, MMP11, DPT |
| 22 | 7 | Collagen Metabolic Process | 2.91E-13 | 0.001 | 0.26 | MMP19, COL3A1, COL1A1, MMP2, COL5A1, MMP1, MMP11 |
| 22 | 7 | Collagen Fibril Organization | 3.79E-13 | 0.001 | 0.26 | COL3A1, COL1A1, GREM1, LOXL2, COL5A3, COL5A1, DPT |
| 22 | 8 | Angiogenesis | 2.24E-08 | 0.002 | 0.3 | ITGA5, MMP19, GREM1, LOXL2, ECM1, MMP2, PLAU, FN1 |
| 22 | 4 | Cellular Response To Amino Acid Stimulus | 8.64E-07 | 0.02 | 0.15 | COL3A1, COL6A1, COL1A1, MMP2 |
| 22 | 4 | Skin Development | 2.83E-06 | 0.045 | 0.15 | COL3A1, COL1A1, COL5A3, COL5A1 |
| 25 | 15 | Interphase Of Mitotic Cell Cycle | 4.14E-17 | 0.001 | 0.52 | CDC7, CHEK1, MCM2, MCM10, MCM4, MCM6, CCNE2, CCNB2, MCM7, POLE2, PCNA, FBXO5, KPNA2, FEN1, MELK |
| 25 | 11 | Dna Replication | 7.52E-14 | 0.001 | 0.38 | CDC7, MCM7, POLE2, PCNA, TIPIN, CHEK1, MCM2, MCM10, MCM4, FEN1, MCM6 |
| 25 | 8 | Dna-Dependent Dna Replication | 2.91E-12 | 0.001 | 0.28 | MCM7, POLE2, PCNA, TIPIN, MCM2, MCM4, FEN1, MCM6 |
| 25 | 11 | Mitosis | 6.26E-12 | 0.001 | 0.38 | KIF23, CCNB2, TIMELESS, DSN1, KIF15, TIPIN, FBXO5, NDC80, RACGAP1, MYBL2, SMC4 |
| 25 | 10 | Cell Cycle Checkpoint | 2.90E-11 | 0.001 | 0.34 | CDC7, CCNE2, MCM7, CCNB2, TIPIN, CHEK1, MCM2, MCM10, MCM4, MCM6 |
| 25 | 7 | M/G1 Transition Of Mitotic Cell Cycle | 4.20E-10 | 0.001 | 0.24 | CDC7, MCM7, POLE2, MCM2, MCM10, MCM4, MCM6 |
| 25 | 5 | Dna-Dependent Dna Replication Initiation | 9.79E-10 | 0.001 | 0.17 | MCM7, POLE2, MCM2, MCM4, MCM6 |
| 25 | 4 | Dna Unwinding Involved In Replication | 2.12E-09 | 0.001 | 0.14 | MCM7, MCM2, MCM4, MCM6 |
| 25 | 5 | Mitotic Spindle Organization | 5.01E-09 | 0.001 | 0.17 | KIF23, PRC1, NDC80, RACGAP1, MYBL2 |
| 25 | 9 | Microtubule-Based Process | 8.30E-09 | 0.001 | 0.31 | KIF23, KIF4A, PRC1, KIF15, FBXO5, NDC80, RACGAP1, MYBL2, KPNA2 |
| 25 | 4 | Regulation Of S Phase | 5.07E-07 | 0.013 | 0.14 | CDC7, TIMELESS, TIPIN, CHEK1 |
| 25 | 4 | Spindle Assembly | 1.02E-06 | 0.02 | 0.14 | KIF23, FBXO5, RACGAP1, MYBL2 |
| 26 | 19 | Interphase Of Mitotic Cell Cycle | 1.88E-19 | 0.001 | 0.43 | CDC7, GINS2, GMNN, CHEK1, BIRC5, PSMA7, MCM10, MCM4, RPA3, CCNB1, RFC5, PLK4, RFC4, PLK1, PCNA, FBXO5, CCNA2, KPNA2, FEN1 |
| 26 | 13 | Cell Cycle Checkpoint | 2.78E-13 | 0.001 | 0.3 | CDC7, CHEK1, BIRC5, PSMA7, MCM10, MCM4, RPA3, RFC5, CCNB1, MAD2L1, RFC4, PLK1, CCNA2 |
| 26 | 13 | Mitosis | 2.89E-12 | 0.001 | 0.3 | CENPN, DSN1, RAN, DYNLT1, BIRC5, CCNB1, SPC25, MAD2L1, TIMELESS, CENPA, PLK1, FBXO5, CCNA2 |
| 26 | 7 | Dna Strand Elongation Involved In Dna Replication | 1.59E-11 | 0.001 | 0.16 | RFC5, GINS2, RFC4, PCNA, MCM4, FEN1, RPA3 |

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| 26 | 10 | Dna Replication | 3.34E-10 | 0.001 | 0.23 | CDC7, RFC5, GINS2, RFC4, PCNA, CHEK1, MCM10, MCM4, FEN1, RPA3 |
| 26 | 8 | Microtubule Cytoskeleton Organization | 2.81E-07 | 0.009 | 0.18 | SPC25, PLK4, RAN, PLK1, CENPA, FBXO5, RANBP1, DYNLT1 |
| 26 | 9 | Regulation Of Mitotic Cell Cycle | 4.10E-07 | 0.013 | 0.2 | CCNB1, MAD2L1, PLK1, FBXO5, RANBP1, BIRC5, CHEK1, PSMA7, CCNA2 |
| 26 | 7 | Dna Recombination | 7.29E-07 | 0.017 | 0.16 | RFC5, XRCC4, RFC4, UCHL5, PCNA, FEN1, RPA3 |
| 26 | 6 | Regulation Of Ligase Activity | 8.29E-07 | 0.019 | 0.14 | CCNB1, XRCC4, MAD2L1, PLK1, FBXO5, PSMA7 |
| 27 | 9 | Collagen Fibril Organization | 1.05E-14 | 0.001 | 0.16 | COL3A1, COL1A2, LOX, COL1A1, GREM1, LOXL2, COL11A1, COL5A2, COL5A1 |
| 27 | 13 | Extracellular Matrix Organization | 3.68E-14 | 0.001 | 0.24 | COL3A1, COL1A2, LOX, COL1A1, MMP14, GREM1, LOXL2, ECM2, COL11A1, COL5A2, MMP2, COL5A1, MMP11 |
| 27 | 7 | Cellular Response To Amino Acid Stimulus | 1.31E-10 | 0.001 | 0.13 | COL4A1, COL3A1, COL1A2, COL1A1, COL16A1, COL5A2, MMP2 |
| 27 | 12 | Angiogenesis | 3.07E-10 | 0.001 | 0.22 | COL4A1, SRPX2, MMP19, PDGFRB, MMP14, THBS1, GREM1, LOXL2, ECM1, MMP2, PLAU, FN1 |
| 27 | 6 | Collagen Metabolic Process | 4.38E-09 | 0.001 | 0.11 | MMP19, COL3A1, COL1A1, MMP2, COL5A1, MMP11 |
| 27 | 5 | Peptide Cross-Linking | 7.38E-08 | 0.002 | 0.091 | BGN, COL3A1, DCN, THBS1, FN1 |
| 27 | 8 | Ossification | 5.07E-07 | 0.013 | 0.15 | CTSK, SPARC, COL1A1, MMP14, COL11A1, ECM1, MMP2, TWIST1 |
| 27 | 5 | Skin Development | 1.76E-06 | 0.031 | 0.091 | COL3A1, COL1A2, COL1A1, COL5A2, COL5A1 |
| 31 | 11 | Response To Type I Interferon | 8.04E-15 | 0.001 | 0.17 | IRF9, USP18, OASL, SP100, ISG15, OAS3, IRF1, IRF2, OAS1, OAS2, STAT1 |
| 31 | 11 | Cellular Response To Interferon-Gamma | 1.22E-13 | 0.001 | 0.17 | IRF9, OASL, SP100, OAS3, IRF1, IRF2, OAS1, OAS2, STAT1, CCL5, GBP1 |
| 31 | 16 | Cytokine-Mediated Signaling Pathway | 1.73E-12 | 0.001 | 0.25 | SP100, OAS3, HERC5, OAS1, OAS2, STAT1, CCL5, STAT3, IRF9, USP18, OASL, ISG15, IRF1, PYCARD, IRF2, GBP1 |
| 31 | 13 | Response To Virus | 6.69E-12 | 0.001 | 0.2 | OAS3, HERC5, CXCL9, OAS1, OAS2, STAT1, CCL5, TRIM22, CXCL10, IRF9, OASL, ISG15, IRF1 |
| 31 | 6 | Negative Regulation Of Reproductive Process | 1.64E-07 | 0.005 | 0.094 | OASL, SP100, SERPINF1, OAS3, OAS1, CCL5 |
| 31 | 9 | Immune Effector Process | 5.85E-07 | 0.015 | 0.14 | C1QA, LYN, OAS3, IRF1, CXCL9, OAS1, S100A13, CXCL10, RAB27A |
| 31 | 4 | Adenylyltransferase Activity | 1.41E-06 | 0.027 | 0.063 | OASL, OAS3, OAS1, OAS2 |
| 33 | 34 | M Phase Of Mitotic Cell Cycle | 2.04E-43 | 0.001 | 0.61 | KIF23, KIFC1, AURKA, AURKB, CEP55, SPC25, NCAPH, CDCA8, CENPA, OIP5, NCAPG, BUB1, FBXO5, CCNA2, ASPM, KIF11, DLGAP5, KIF15, TPX2, CENPF, NUSAP1, CDC20, ESPL1, NDC80, BIRC5, PBK, RACGAP1, UBE2C, SMC4, CCNB2, PLK1, SPAG5, BUB1B, KIF20A |
| 33 | 26 | Microtubule-Based Process | 1.45E-28 | 0.001 | 0.46 | KIF14, KIF23, KIFC1, KIF4A, KIF11, PRC1, DLGAP5, KIF15, TTK, NUSAP1, NDC80, AURKA, ESPL1, AURKB, UBE2C, TACC3, RACGAP1, SPC25, CENPA, SPAG5, PLK1, CKS2, FBXO5, BUB1B, KPNA2, KIF20A |

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| 33 | 16 | Spindle Organization | 2.25E-24 | 0.001 | 0.29 | KIF23, KIF11, PRC1, TTK, NDC80, ESPL1, AURKA, AURKB, TACC3, UBE2C, RACGAP1, SPC25, SPAG5, CKS2, BUB1B, FBXO5 |
| 33 | 15 | Chromosome Segregation | 3.29E-19 | 0.001 | 0.27 | KIFC1, DLGAP5, NUSAP1, CENPF, BIRC5, NDC80, ESPL1, AURKB, SMC4, SPC25, NCAPH, SPAG5, NCAPG, BUB1, TOP2A |
| 33 | 10 | Regulation Of Mitotic Metaphase/Anaphase Transition | 7.52E-17 | 0.001 | 0.18 | PLK1, DLGAP5, BUB1, FBXO5, TTK, CENPF, BUB1B, ESPL1, CDC20, UBE2C |
| 33 | 12 | Regulation Of Nuclear Division | 5.04E-16 | 0.001 | 0.21 | PLK1, DLGAP5, BUB1, FBXO5, TTK, CENPF, BUB1B, NUSAP1, ESPL1, AURKA, CDC20, UBE2C |
| 33 | 10 | Sister Chromatid Segregation | 3.54E-15 | 0.001 | 0.18 | KIFC1, NCAPH, SPAG5, NCAPG, DLGAP5, NUSAP1, ESPL1, NDC80, TOP2A, SMC4 |
| 33 | 11 | Cytokinesis | 7.74E-15 | 0.001 | 0.2 | KIF23, PRC1, PLK1, NUSAP1, ESPL1, BIRC5, CEP55, AURKB, RACGAP1, ECT2, KIF20A |
| 33 | 16 | Regulation Of Mitotic Cell Cycle | 4.53E-14 | 0.001 | 0.29 | DLGAP5, TPX2, TTK, NUSAP1, CENPF, BIRC5, ESPL1, AURKA, CDC20, UBE2C, PLK1, BUB1, BUB1B, FBXO5, CCNA2, TOP2A |
| 33 | 13 | Regulation Of Cell Cycle Arrest | 2.68E-11 | 0.001 | 0.23 | FOXM1, TTK, CENPF, CDC20, BIRC5, MCM10, UBE2C, CCNB2, PLK1, BUB1, BUB1B, CCNA2, TOP2A |
| 33 | 7 | Spindle Checkpoint | 4.26E-11 | 0.001 | 0.13 | BUB1, TTK, CENPF, BUB1B, BIRC5, CDC20, UBE2C |
| 33 | 11 | Positive Regulation Of Cell Cycle Process | 5.12E-11 | 0.001 | 0.2 | KIF23, PLK1, DLGAP5, NUSAP1, ESPL1, AURKA, BIRC5, AURKB, RACGAP1, UBE2C, ECT2 |
| 33 | 6 | Regulation Of Chromosome Segregation | 1.61E-10 | 0.001 | 0.11 | SPAG5, BUB1, ESPL1, AURKB, RACGAP1, ECT2 |
| 33 | 9 | Organelle Localization | 9.74E-09 | 0.001 | 0.16 | CENPA, DLGAP5, CENPF, NUSAP1, ESPL1, NDC80, BIRC5, TACC3, ASPM |
| 33 | 12 | Interphase Of Mitotic Cell Cycle | 1.01E-08 | 0.001 | 0.21 | CCNB2, PLK1, FOXM1, RRM2, FBXO5, CENPF, BIRC5, MCM10, TOP2A, KPNA2, CCNA2, MELK |
| 33 | 8 | Meiosis | 1.39E-08 | 0.001 | 0.14 | EXO1, MKI67, PLK1, CKS2, FBXO5, ESPL1, TOP2A, RAD54L |
| 33 | 7 | Anaphase-Promoting Complex-Dependent Proteasomal Ubiquitin-Dependent Protein Catabolic Process | 4.39E-08 | 0.002 | 0.13 | PLK1, FBXO5, BUB1B, AURKA, CDC20, AURKB, UBE2C |
| 33 | 4 | Mitotic Spindle | 5.85E-08 | 0.002 | 0.071 | KIF23, SPAG5, RACGAP1, ECT2 |
| 33 | 7 | Inositol Lipid-Mediated Signaling | 6.39E-08 | 0.002 | 0.13 | SPAG5, CKS2, BUB1B, AURKA, NDC80, UBE2C, TOP2A |
| 33 | 4 | Regulation Of Cell Cycle Cytokinesis | 3.24E-07 | 0.01 | 0.071 | KIF23, AURKB, RACGAP1, ECT2 |
| 33 | 7 | Dna Packaging | 5.14E-07 | 0.013 | 0.13 | NCAPH, NCAPG, CENPA, OIP5, NUSAP1, TOP2A, SMC4 |
| 33 | 4 | Establishment Of Mitotic Spindle Localization | 6.14E-07 | 0.015 | 0.071 | CENPA, NUSAP1, ESPL1, NDC80 |
| 33 | 4 | Protein Localization To Chromosome | 1.72E-06 | 0.029 | 0.071 | PLK1, CENPA, BUB1B, AURKB |
| 33 | 6 | Regulation Of Microtubule-Based Process | 1.73E-06 | 0.03 | 0.11 | SPAG5, TPX2, AURKA, RACGAP1, TACC3, ECT2 |