Over-represented GO biological process terms in 217 significantly up-regulated genes in ADSCs from diseased sides

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| GO:ID | GO term | Term P value | Term corrected–P value | Group P value | Group corrected P value | GO groups | % Associated genes | Nr. genes | Associated genes found |
| GO:0051225 | Spindle assembly | 2.9E–12 | 4.4E–11 | 2.6E–15 | 2.6E–15 | Group 0 | 14.28571415 | 13 | *ASPM, AURKB, BIRC5, CDC20, KIF11, KIF23, KIF4A, KIFC1, NEK2, PLK1, RACGAP1, TPX2, ZNF367* |
| GO:0007052 | Mitotic spindle organization | 3.8E–16 | 7.2E–15 | 2.6E–15 | 2.6E–15 | Group 0 | 17.20430183 | 16 | *AURKB, BIRC5, CCNB1, CDC20, KIF11, KIF23, KIF4A, KIFC1, NDC80, NEK2, PLK1, RACGAP1, TPX2, TTK, WDR62, ZNF367* |
| GO:0051256 | Mitotic spindle midzone assembly | 0.000000031 | 0.00000027 | 2.6E–15 | 2.6E–15 | Group 0 | 45.45454407 | 5 | *AURKB, KIF23, KIF4A, RACGAP1, ZNF367* |
| GO:0007088 | Regulation of mitotic nuclear division | 5E–17 | 1E–15 | 2.7E–16 | 5.4E–16 | Group 1 | 12.42236042 | 20 | *BIRC5, BUB1, BUB1B, CCNB1, CDCA5, CENPE, CENPF, DLGAP5, ESPL1, FBXO43, KIF11, MKI67, NDC80, NEK2, NUSAP1, PLK1, TPX2, TTK, UBE2C, ZNF367* |
| GO:0033045 | Regulation of sister chromatid segregation | 2.6E–12 | 4.2E–11 | 2.7E–16 | 5.4E–16 | Group 1 | 16.90140915 | 12 | *BUB1, BUB1B, CCNB1, CDCA5, CENPE, CENPF, DLGAP5, ESPL1, NDC80, PLK1, TTK, UBE2C* |
| GO:1901989 | Positive regulation of cell cycle phase transition | 0.0000038 | 0.000023 | 2.7E–16 | 5.4E–16 | Group 1 | 10.14492798 | 7 | *BIRC5, CDCA5, CDK1, DLGAP5, ESPL1, FAM83D, UBE2C* |
| GO:0045840 | Positive regulation of mitotic nuclear division | 0.0000072 | 0.000021 | 2.7E–16 | 5.4E–16 | Group 1 | 12 | 6 | *BIRC5, CDCA5, DLGAP5, ESPL1, NUSAP1, UBE2C* |
| GO:1904668 | Positive regulation of ubiquitin protein ligase activity | 0.000018 | 0.000036 | 1.5E–26 | 4.7E–26 | Group 2 | 8.045976639 | 7 | *BUB1B, CCNB1, CDC20, CDK1, PLK1, UBE2C, ZNF367* |
| GO:0007093 | Mitotic cell cycle checkpoint | 0.00000053 | 0.0000037 | 1.5E–26 | 4.7E–26 | Group 2 | 6.586826324 | 11 | *BLM, BUB1, BUB1B, CCNB1, CDK1, CENPF, GTSE1, NDC80, PLK1, TOP2A, TTK* |
| GO:0031577 | Spindle checkpoint | 1.2E–13 | 2.2E–12 | 1.5E–26 | 4.7E–26 | Group 2 | 26.19047546 | 11 | *AURKB, BIRC5, BUB1, BUB1B, CCNB1, CENPF, GSG2, KNL1, NDC80, PLK1, TTK* |
| GO:0000070 | Mitotic sister chromatid segregation | 1.2E–30 | 2.5E–29 | 1.5E–26 | 4.7E–26 | Group 2 | 20.13888931 | 29 | *AURKB, BUB1, BUB1B, CCNB1, CDC20, CDCA5, CDCA8, CENPE, CENPF, DLGAP5, ESPL1, GSG2, KIF14, KIF18A, KIF18B, KIF23, KIF2C, KIF4A, KIFC1, NCAPG, NCAPH, NDC80, NEK2, NUSAP1, PLK1, RACGAP1, TTK, UBE2C, ZNF367* |
| GO:0007088 | Regulation of mitotic nuclear division | 5E–17 | 1E–15 | 1.5E–26 | 4.7E–26 | Group 2 | 12.42236042 | 20 | *BIRC5, BUB1, BUB1B, CCNB1, CDCA5, CENPE, CENPF, DLGAP5, ESPL1, FBXO43, KIF11, MKI67, NDC80, NEK2, NUSAP1, PLK1, TPX2, TTK, UBE2C, ZNF367* |
| GO:0033045 | Regulation of sister chromatid segregation | 2.6E–12 | 4.2E–11 | 1.5E–26 | 4.7E–26 | Group 2 | 16.90140915 | 12 | *BUB1, BUB1B, CCNB1, CDCA5, CENPE, CENPF, DLGAP5, ESPL1, NDC80, PLK1, TTK, UBE2C* |
| GO:0033046 | Negative regulation of sister chromatid segregation | 2.5E–09 | 0.000000025 | 1.5E–26 | 4.7E–26 | Group 2 | 20.5128212 | 8 | *BUB1, BUB1B, CCNB1, CENPF, ESPL1, NDC80, PLK1, TTK* |
| GO:0045840 | Positive regulation of mitotic nuclear division | 0.0000072 | 0.000021 | 1.5E–26 | 4.7E–26 | Group 2 | 12 | 6 | *BIRC5, CDCA5, DLGAP5, ESPL1, NUSAP1, UBE2C* |
| GO:0051784 | Negative regulation of nuclear division | 0.00000011 | 0.00000093 | 1.5E–26 | 4.7E–26 | Group 2 | 12.9032259 | 8 | *BUB1, BUB1B, CCNB1, CENPF, FBXO43, NDC80, PLK1, TTK* |
| GO:1901990 | Regulation of mitotic cell cycle phase transition | 9.9E–12 | 1.2E–10 | 1.5E–26 | 4.7E–26 | Group 2 | 6.15835762 | 21 | *BIRC5, BLM, BUB1, BUB1B, CCNA2, CCNB1, CDC20, CDCA5, CDK1, CENPE, CENPF, DLGAP5, ESPL1, FHL1, GTSE1, KIF14, NDC80, PLK1, TTK, UBE2C, ZNF367* |
| GO:0071173 | Spindle assembly checkpoint | 7.8E–10 | 8.6E–09 | 1.5E–26 | 4.7E–26 | Group 2 | 23.52941132 | 8 | *BUB1, BUB1B, CCNB1, CENPF, KNL1, NDC80, PLK1, TTK* |
| GO:0071459 | Protein localization to chromosome, centromeric region | 3.6E–12 | 5.1E–11 | 1.5E–26 | 4.7E–26 | Group 2 | 42.10526276 | 8 | *AURKB, BUB1B, CDK1, CENPA, GSG2, KNL1, NDC80, TTK* |
| GO:0030071 | Regulation of mitotic metaphase/anaphase transition | 8E–13 | 1.3E–11 | 1.5E–26 | 4.7E–26 | Group 2 | 22.44898033 | 11 | *BUB1, BUB1B, CCNB1, CENPE, CENPF, DLGAP5, ESPL1, NDC80, PLK1, TTK, UBE2C* |
| GO:0051439 | Regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle | 0.0000062 | 0.000024 | 1.5E–26 | 4.7E–26 | Group 2 | 9.459459305 | 7 | *BUB1B, CCNB1, CDC20, CDK1, FBXO43, PLK1, UBE2C* |
| GO:0051438 | Regulation of ubiquitin-protein transferase activity | 0.0000039 | 0.000019 | 1.5E–26 | 4.7E–26 | Group 2 | 6.923077106 | 9 | *BUB1B, CCNB1, CDC20, CDK1, FBXO43, PLK1, UBE2C, ZNF367, ZYG11A* |
| GO:0000079 | Regulation of cyclin-dependent protein serine/threonine kinase activity | 0.00022 | 0.00022 | NA | NA | None | 6.593406677 | 6 | *BLM, CCNA2, CCNB1, CDKN2C, CKS2, PLK1* |
| GO:0007080 | Mitotic metaphase plate congression | 1.6E–10 | 1.9E–09 | NA | NA | None | 21.4285717 | 9 | *CCNB1, CDCA5, CDCA8, CENPE, KIF14, KIF18A, KIF2C, KIFC1, NDC80* |

GO:ID: gene ontology term ID (biological process); GO term: name of gene ontology term; term P value: P value of enrichment test of the term; term corrected-P value: corrected p-value of enrichment test of the term; group P value: P value of the group; group corrected P value: corrected P value of the group; GO groups: group ID of the term. “none” denotes unclustered terms; % associated genes: the percentage of genes in the gene list found to be associated with the term compared to all genes associated with the term; Nr. genes: the number of genes in the gene list found to be associated with the term; associated genes found: genes in the gene list found to be associated with the term. GO, gene ontology.