Two hundred and eleven up-regulated gene sets in ADSCs from diseased sides compared to normal sides revealed by gene set enrichment analysis

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Group | ID | Description | Set size | Enrichment score | NES | P value | p.adjust | leading\_edge | core\_enrichment |
| G1 | GO:0009314 | Response to radiation | 346 | 0.340629715 | 1.478238373 | 0.004694836 | 0.037949001 | tags =21%, list =16%, signal =18% | *CRIP1/CNGB1/AURKB/PBK/CXCL12/BLM/RAD54L/KIT/KIAA0101/GRIN2A/SFRP2/RAD51/FANCD2/CDC25A/EYS/TICRR/BRCA1/HRH1/KRT14/POLD1/BCL2/HRH2/RAD51AP1/H2AFX/ADIRF/CDKN2D/SAG/DMC1/FEN1/ECT2/XRCC2/SLC4A10/FANCG/DTL/TRPC3/USP1/FIGNL1/NMT2/PMAIP1/NFATC4/CHEK1/HYAL1/HMGA2/RHNO1/NLGN3/PARP1/IL12B/RRM1/DNMT3B/POLG/MSH2/SCARA3/ATR/DCLRE1C/BRCA2/CAMKMT/GRM6/IFI16/RAD51B/ASNS/TOPBP1/ICAM1/SMC1A/KMT2A/USP28/DUSP1/FAM175A/THBD/AQP1/ERCC6/RFWD3* |
| G1 | GO:0009411 | Response to UV | 117 | 0.380408546 | 1.468274732 | 0.006389776 | 0.045290946 | tags =21%, list =16%, signal =18% | *CRIP1/AURKB/PBK/KIAA0101/CDC25A/POLD1/BCL2/CDKN2D/FEN1/DTL/USP1/PMAIP1/NFATC4/CHEK1/HYAL1/RHNO1/IL12B/MSH2/SCARA3/ATR/BRCA2/USP28/AQP1/ERCC6/MAP2K7* |
| G1 | GO:0010212 | Response to ionizing radiation | 132 | 0.383275666 | 1.517055043 | 0.006430868 | 0.045354927 | tags =27%, list =16%, signal =23% | *BLM/RAD54L/SFRP2/RAD51/FANCD2/TICRR/BRCA1/KRT14/BCL2/RAD51AP1/H2AFX/DMC1/ECT2/XRCC2/FIGNL1/PMAIP1/HMGA2/RHNO1/PARP1/RRM1/DNMT3B/POLG/MSH2/ATR/DCLRE1C/BRCA2/IFI16/RAD51B/TOPBP1/ICAM1/USP28/FAM175A/THBD/ERCC6/RFWD3* |
| G10 | GO:0061641 | CENP-A containing chromatin organization | 31 | 0.723808745 | 2.171749988 | 0.0025 | 0.030326036 | tags =61%, list =12%, signal =54% | *CASC5/HJURP/CENPA/OIP5/CENPK/CENPI/CENPU/CENPH/CENPM/CENPO/CENPN/MIS18A/CENPQ/MIS18BP1/ITGB3BP/RBBP7/CENPW/CENPL/CENPP* |
| G11 | GO:0006890 | Retrograde vesicle-mediated transport, Golgi to ER | 74 | 0.521450502 | 1.864142674 | 0.002785515 | 0.030326036 | tags =12%, list =2%, signal =12% | *KIF2C/CENPE/KIF4A/KIF11/KIF15/KIF18A/KIF23/RACGAP1/KIF22* |
| G12 | GO:0019080 | Viral gene expression | 181 | 0.497945957 | 2.032873528 | 0.003496503 | 0.031944406 | tags =58%, list =32%, signal =40% | *POU2F3/ZFP36/RPL37/RPL9/RPL38/TFAP4/RPL31/RPS23/RPS21/RPS27/RPL37A/RPL10A/HMGA2/RPS17L/POLR2L/RPS16/RPS29/RPS25/RPL10/RPL39/NUP50/RPS13/NUP35/RPS8/RPS7/NUP155/RPL12/INPP5K/RPS9/RPS3/NUP205/RPL7A/RPL14/RPL30/RPL3/RPL36/NUCKS1/RPLP0/NUP160/NOTCH1/RPL15/PCBP2/NUP107/RPS18/NUP54/RPS6/RPS14/EIF3F/PTBP1/RPL11/NELFB/RPL32/TARBP2/RPS4X/RPS5/RPL36A/RPL4/RPL18/POLR2J/RPLP2/RPL27/RPS27A/RPL24/RPL27A/RPSA/RPS3A/RPL26/RPL19/RPS12/RPS15A/TPR/NUP43/RPL13A/RPS11/RPL22/NUP62/NDC1/RPL35A/SEH1L/NUP85/RPL8/RPL18A/IFITM3/RPL29/TRIM21/RPS24/RPL5/NUP37/RPL13/HDAC1/RPL17/RPL23/RPL6/RPL23A/RPL28/RPL34/RPL35/POLR2D/RPL7/NELFA/RPL41/UBA52/NELFCD/NUP88/EIF3L* |
| G12 | GO:0019083 | Viral transcription | 170 | 0.508812584 | 2.062653942 | 0.003558719 | 0.032115724 | tags =58%, list =31%, signal =40% | *POU2F3/ZFP36/RPL37/RPL9/RPL38/TFAP4/RPL31/RPS23/RPS21/RPS27/RPL37A/RPL10A/HMGA2/RPS17L/POLR2L/RPS16/RPS29/RPS25/RPL10/RPL39/NUP50/RPS13/NUP35/RPS8/RPS7/NUP155/RPL12/INPP5K/RPS9/RPS3/NUP205/RPL7A/RPL14/RPL30/RPL3/RPL36/NUCKS1/RPLP0/NUP160/NOTCH1/RPL15/NUP107/RPS18/NUP54/RPS6/RPS14/RPL11/NELFB/RPL32/TARBP2/RPS4X/RPS5/RPL36A/RPL4/RPL18/POLR2J/RPLP2/RPL27/RPS27A/RPL24/RPL27A/RPSA/RPS3A/RPL26/RPL19/RPS12/RPS15A/TPR/NUP43/RPL13A/RPS11/RPL22/NUP62/NDC1/RPL35A/SEH1L/NUP85/RPL8/RPL18A/IFITM3/RPL29/TRIM21/RPS24/RPL5/NUP37/RPL13/HDAC1/RPL17/RPL23/RPL6/RPL23A/RPL28/RPL34/RPL35/POLR2D/RPL7/NELFA/RPL41/UBA52* |
| G13 | GO:0002029 | Desensitization of G-protein coupled receptor protein signaling pathway | 12 | 0.773288068 | 1.809305222 | 0.004651163 | 0.037949001 | tags =33%, list =5%, signal =32% | *DNM1/ADRB2/ADM/HTR2B* |
| G13 | GO:0022401 | Negative adaptation of signaling pathway | 12 | 0.773288068 | 1.809305222 | 0.004651163 | 0.037949001 | tags =33%, list =5%, signal =32% | *DNM1/ADRB2/ADM/HTR2B* |
| G14 | GO:0072074 | Kidney mesenchyme development | 15 | 0.726615535 | 1.836148098 | 0.004587156 | 0.037949001 | tags =40%, list =13%, signal =35% | *SIX2/SIX1/TCF21/PDGFRB/OSR1/BASP1* |
| G14 | GO:0072075 | Metanephric mesenchyme development | 11 | 0.742019935 | 1.705005141 | 0.006696429 | 0.046379968 | tags =45%, list =13%, signal =40% | *SIX1/TCF21/PDGFRB/OSR1/BASP1* |
| G15 | GO:0006413 | Translational initiation | 182 | 0.460658446 | 1.880314874 | 0.003558719 | 0.032115724 | tags =54%, list =32%, signal =37% | *TICRR/C8orf88/PAIP2B/RPL37/EIF4EBP1/RPL9/RPL38/RPL31/RPS23/RPS21/RPS27/RPL37A/RPL10A/RPS17L/EIF4EBP3/RPS16/RPS29/RPS25/RPL10/RPL39/RPS13/RPS8/GLE1/RPS7/RPL12/RPS9/RPS3/RPL7A/RPL14/RPL30/RXRA/RPL3/RPL36/EIF1/RPLP0/EIF2S3/EIF4B/EIF1AX/RPL15/PCBP2/RPS18/RPS6/RPS14/EIF3F/PTBP1/RPL11/RPL32/RPS4X/RPS5/RPL36A/RPL4/RPL18/RPLP2/RPL27/RPS27A/RPL24/RPL27A/RPSA/RPS3A/RPL26/RPL19/RPS12/RPS15A/TPR/RPL13A/RPS11/PPP1CA/RPL22/RPL35A/PAIP2/RPL8/RPL18A/EIF2S2/RPL29/EIF3CL/RPS24/RPL5/RPL13/EIF3C/RPL17/RPL23/PPP1R15B/RPL6/RPL23A/ATF4/RPL28/RPL34/RPL35/POLR2D/EIF2S1/RPL7/RPL41/UBA52/RARA/AGO2/KLHL25/EIF3L/COPS5* |
| G16 | GO:0023058 | Adaptation of signaling pathway | 13 | 0.729896816 | 1.770137505 | 0.006960557 | 0.047759986 | tags =31%, list =5%, signal =29% | *DNM1/ADRB2/ADM/HTR2B* |
| G17 | GO:0007019 | Microtubule depolymerization | 25 | 0.804620282 | 2.262179818 | 0.002531646 | 0.030326036 | tags =32%, list =6%, signal =30% | *KIF18B/KIF2C/STMN3/KIF18A/STMN1/CKAP2/KIF24/STMN2* |
| G17 | GO:0046605 | Regulation of centrosome cycle | 39 | 0.651211352 | 2.036484212 | 0.002610966 | 0.030326036 | tags =36%, list =13%, signal =31% | *NEK2/PLK4/KIF11/AURKA/CCNF/BRCA1/STIL/CENPJ/GEN1/CHEK1/CEP85/CEP76/CDK5RAP2/ROCK2* |
| G17 | GO:0090307 | Mitotic spindle assembly | 45 | 0.716571652 | 2.327961081 | 0.002624672 | 0.030326036 | tags =24%, list =2%, signal =24% | *AURKB/NEK2/KIFC1/KIF4A/BIRC5/PLK1/KIF11/TPX2/KIF23/RACGAP1/MYBL2* |
| G17 | GO:0007052 | Mitotic spindle organization | 46 | 0.809837028 | 2.63601843 | 0.002645503 | 0.030326036 | tags =50%, list =8%, signal =46% | *AURKB/TTK/KIF4A/NDC80/CCNB1/KIF11/TPX2/KIF23/RACGAP1/WDR62/PSRC1/TACC3/AURKA/SPC25/STMN1/GPSM2/BORA/PRC1/STIL/ANKRD53/EML1/RCC1/PCNT* |
| G17 | GO:1902850 | Microtubule cytoskeleton organization involved in mitosis | 46 | 0.729846419 | 2.375649106 | 0.002645503 | 0.030326036 | tags =26%, list =2%, signal =26% | *AURKB/NEK2/KIFC1/KIF4A/BIRC5/PLK1/KIF11/TPX2/KIF23/RACGAP1/MYBL2/TACC3* |
| G17 | GO:0001578 | Microtubule bundle formation | 61 | 0.498571482 | 1.722649416 | 0.002747253 | 0.030326036 | tags =23%, list =12%, signal =20% | *PLK1/DNAH7/KIF20A/PSRC1/ARMC4/TPPP3/PRC1/ZMYND10/FES/SPEF2/LRRC6/SOGA2/CDK5RAP2/TTLL5* |
| G17 | GO:0051225 | Spindle assembly | 76 | 0.627518494 | 2.253488744 | 0.00280112 | 0.030326036 | tags =29%, list =11%, signal =26% | *AURKB/ASPM/NEK2/KIFC1/KIF4A/BIRC5/PLK1/KIF11/TPX2/KIF23/RACGAP1/MYBL2/AURKA/FBXO5/HAUS5/STARD9/RCC1/HAUS8/HAUS4/TUBB1/CEP97/MZT1* |
| G17 | GO:0031109 | Microtubule polymerization or depolymerization | 66 | 0.572045292 | 2.000069363 | 0.00280112 | 0.030326036 | tags =29%, list =9%, signal =26% | *SKA1/KIF18B/KIF2C/STMN3/KIF18A/SKA3/PSRC1/FBXO5/STMN1/TPPP3/CKAP2/KIF24/NDE1/MAP7D3/ANKRD53/STMN2/CENPJ/FES/CDKN1B* |
| G17 | GO:0051298 | Centrosome duplication | 55 | 0.534060356 | 1.801905356 | 0.002808989 | 0.030326036 | tags =31%, list =14%, signal =27% | *PLK4/WDR62/CCNF/BRCA1/CDK2/NDE1/STIL/SASS6/CEP72/CENPJ/GEN1/CEP76/CDK5RAP2/CEP192/BRCA2/ROCK2/ARHGEF10* |
| G17 | GO:0007098 | Centrosome cycle | 70 | 0.572614955 | 2.003776416 | 0.002816901 | 0.030326036 | tags =33%, list =14%, signal =28% | *NEK2/CDK1/PLK4/KIF11/WDR62/AURKA/CCNF/BRCA1/CDK2/NDE1/STIL/SASS6/CEP72/CENPJ/GEN1/CHEK1/CEP85/CEP76/CDK5RAP2/CEP192/BRCA2/ROCK2/ARHGEF10* |
| G17 | GO:0007051 | Spindle organization | 94 | 0.638856819 | 2.394549295 | 0.002849003 | 0.030380747 | tags =35%, list =15%, signal =30% | *AURKB/ASPM/NEK2/KIFC1/TTK/KIF4A/BIRC5/PLK1/KIF11/TPX2/KIF23/RACGAP1/MYBL2/SPAG5/AURKA/FBXO5/KNSTRN/PRC1/HAUS5/STARD9/RCC1/HAUS8/HAUS4/CEP72/PLK1S1/TUBB1/CEP97/MZT1/AUNIP/CEP192/ARHGEF10/HAUS1/EZR* |
| G17 | GO:0051297 | Centrosome organization | 98 | 0.5547157 | 2.07982563 | 0.002941176 | 0.030486975 | tags =45%, list =21%, signal =36% | *NEK2/CDK1/PLK4/PLK1/SGOL1/KIF11/WDR62/KIAA0101/AURKA/CCNF/BRCA1/CDK2/NDE1/STIL/HAUS5/XRCC2/SASS6/HAUS8/HAUS4/CEP72/CENPJ/FES/GEN1/CHEK1/CEP85/CEP76/CDK5RAP2/CEP192/BRCA2/ROCK2/ARHGEF10/CNTLN/HAUS1/ARL2/CEP68/CEP135/HAUS7/CROCC/TUBGCP6/HAUS2/TUBGCP3/CEP152/CNTROB/RANBP1* |
| G17 | GO:0070507 | Regulation of microtubule cytoskeleton organization | 99 | 0.545864379 | 2.048978171 | 0.003003003 | 0.030486975 | tags =27%, list =12%, signal =24% | *SKA1/NEK2/PLK4/PLK1/STMN3/KIF11/KIF18A/SKA3/EFNA5/PSRC1/AURKA/CCNF/STMN1/BRCA1/CKAP2/STIL/ANKRD53/STMN2/CENPJ/FES/GEN1/CDKN1B/CHEK1/CEP85/CEP97/CEP76/CDK5RAP2* |
| G17 | GO:0031023 | Microtubule organizing center organization | 107 | 0.543358616 | 2.061665298 | 0.003076923 | 0.030486975 | tags =41%, list =21%, signal =33% | *NEK2/CDK1/PLK4/PLK1/SGOL1/KIF11/WDR62/KIAA0101/AURKA/CCNF/BRCA1/CDK2/NDE1/STIL/HAUS5/XRCC2/SASS6/HAUS8/HAUS4/CEP72/CENPJ/FES/GEN1/CHEK1/CEP85/CEP76/CDK5RAP2/CEP192/BRCA2/ROCK2/ARHGEF10/CNTLN/HAUS1/ARL2/CEP68/CEP135/HAUS7/CROCC/TUBGCP6/HAUS2/TUBGCP3/CEP152/CNTROB/RANBP1* |
| G17 | GO:0051783 | Regulation of nuclear division | 136 | 0.542326889 | 2.156956062 | 0.003184713 | 0.030486975 | tags =32%, list =11%, signal =29% | *FBXO43/NEK2/CENPF/CDC20/UBE2C/CENPE/TTK/PLK1/MKI67/ESPL1/NDC80/DLGAP5/BUB1B/CCNB1/KIF11/BUB1/CDCA5/NUSAP1/CDC25C/MAD2L1/TACC3/AURKA/ANLN/KIF20B/FBXO5/BORA/PKMYT1/EDN1/CDC6/RPS6KA2/MAD1L1/IGF2/KNTC1/RCC1/MSX1/PDGFRB/GEN1/MTBP/MAD2L2/CHEK1/L3MBTL1/CEP85/CEP97/PCID2* |
| G17 | GO:0032886 | Regulation of microtubule-based process | 118 | 0.518765169 | 2.003255839 | 0.003205128 | 0.030486975 | tags =25%, list =12%, signal =22% | *SKA1/NEK2/PLK4/PLK1/STMN3/KIF11/KIF18A/SKA3/EFNA5/PSRC1/AURKA/CCNF/STMN1/ARMC4/BRCA1/CKAP2/STIL/ANKRD53/STMN2/CENPJ/FES/HAP1/GEN1/CDKN1B/CHEK1/CEP85/CEP97/CEP76/CDK5RAP2* |
| G17 | GO:0007018 | Microtubule-based movement | 198 | 0.395219122 | 1.630381932 | 0.003703704 | 0.033019352 | tags =11%, list =5%, signal =11% | *KIF18B/KIF2C/CENPE/KIFC1/KIF4A/KIF14/DLGAP5/KIF11/KIF15/KIF18A/DNAH7/KIF23/RACGAP1/KIF20A/KIF20B/KIF22/ARMC4/AP3B2/KLC3/KIF24/NDE1/ROPN1L* |
| G17 | GO:0051299 | Centrosome separation | 10 | 0.761404899 | 1.727968933 | 0.004357298 | 0.03701726 | tags =60%, list =10%, signal =54% | *NEK2/KIF11/AURKA/NDE1/CHEK1/CEP85* |
| G17 | GO:0000226 | Microtubule cytoskeleton organization | 363 | 0.500490873 | 2.188992483 | 0.004672897 | 0.037949001 | tags =25%, list =13%, signal =22% | *SKA1/AURKB/ASPM/NEK2/CENPA/KIF18B/KIF2C/CDK1/KIFC1/TTK/KIF4A/BIRC5/PLK4/PLK1/ESPL1/NDC80/STMN3/SGOL1/KIF11/KIF18A/DNAH7/NUSAP1/TPX2/KIF23/RACGAP1/SKA3/WDR62/KIF20A/EFNA5/KIAA0101/PSRC1/GAS2L3/MYBL2/TACC3/SPAG5/AURKA/CCNF/WEE1/FBXO5/STMN1/GPSM2/ARMC4/BRCA1/TPPP3/CKAP2/KNSTRN/CDK2/PRC1/KIF24/ZMYND10/NDE1/MAP7D3/STIL/HAUS5/XRCC2/ANKRD53/STMN2/CCDC13/EML1/STARD9/SASS6/RCC1/HAUS8/HAUS4/CEP72/PLK1S1/CENPJ/FES/PCNT/SPEF2/FIGNL1/TUBB1/GEN1/CDKN1B/LRRC6/SOGA2/FMN2/CHEK1/TACC2/CEP85/CEP97/MZT1/AUNIP/CEP76/CDK5RAP2/LMNA/CEP57/CEP192/TTLL5/BRCA2* |
| G17 | GO:0007067 | Mitotic nuclear division | 402 | 0.617248147 | 2.712936472 | 0.004975124 | 0.038667897 | tags =31%, list =11%, signal =28% | *SKA1/AURKB/NUF2/CASC5/FBXO43/ASPM/NEK2/CENPF/FAM83D/CDCA8/CENPA/NCAPG/KIF18B/PBK/CDC20/KIF2C/CDK1/CDCA2/UBE2C/CENPE/CIT/KIFC1/NCAPH/TTK/KIF4A/BIRC5/KIF14/ERCC6L/CCNA2/PLK1/CDCA3/MKI67/ESPL1/NDC80/DLGAP5/SGOL1/BUB1B/CCNB1/KIF11/KIF15/KIF18A/BUB1/CCNB2/CDCA5/NUSAP1/TPX2/KIF23/CDC25C/RACGAP1/SKA3/CDC25B/PSRC1/MAD2L1/GSG2/HELLS/MYBL2/TACC3/SPAG5/AURKA/OIP5/ANLN/CCNF/WEE1/KIF20B/FBXO5/SPC25/ZWINT/FAM64A/KIF22/NCAPD2/CDC25A/INCENP/BORA/SPC24/PKMYT1/NCAPG2/KNSTRN/CENPN/SMC4/CDK2/MIS18A/EDN1/PRC1/CDC6/NDE1/VRK1/TIMELESS/MAD1L1/IGF2/HAUS5/ANKRD53/DSN1/KNTC1/PTTG1/RCC1/HAUS8/MASTL/MIS18BP1/HAUS4/TEN1-CDK3/SAC3D1/REEP4/PDGFRB/GEN1/UBE2S/MTBP/MAD2L2/ITGB3BP/REC8/CHEK1/NCAPD3/SETDB2/HMGA2/L3MBTL1/SNX9/CEP85/CEP97/RAD21/PCID2/LRRCC1/MZT1/CENPW/PPP5C/TTN* |
| G17 | GO:0000280 | Nuclear division | 487 | 0.588344477 | 2.617324434 | 0.005813953 | 0.042799003 | tags =31%, list =12%, signal =28% | *SKA1/AURKB/NUF2/CASC5/FBXO43/ASPM/NEK2/CENPF/FAM83D/CDCA8/CENPA/NCAPG/KIF18B/PBK/CDC20/KIF2C/CDK1/CDCA2/UBE2C/CENPE/CIT/KIFC1/NCAPH/TTK/KIF4A/BIRC5/KIF14/ERCC6L/CCNA2/PLK1/CDCA3/MKI67/ESPL1/NDC80/DLGAP5/SGOL1/BUB1B/TOP2A/CCNB1/KIF11/CKS2/KIF15/KIF18A/MND1/BUB1/CCNB2/CDCA5/NUSAP1/TPX2/RAD54L/KIF23/CDC25C/RACGAP1/SKA3/CDC25B/PSRC1/MAD2L1/GSG2/HELLS/MYBL2/TACC3/SPAG5/AURKA/OIP5/ANLN/CCNF/WEE1/KIF20B/FBXO5/SPC25/ZWINT/FAM64A/KIF22/RAD51/FANCD2/SGOL2/NCAPD2/CDC25A/SYCE2/INCENP/BORA/SPDYA/SPC24/PKMYT1/NCAPG2/KNSTRN/CENPN/SMC4/CDK2/MIS18A/EDN1/PRC1/FANCA/CDC6/TRIP13/NDE1/VRK1/EME1/AGO4/RPS6KA2/TIMELESS/MAD1L1/DMC1/IGF2/HAUS5/XRCC2/ANKRD53/DSN1/KNTC1/PTTG1/RCC1/HAUS8/MASTL/MIS18BP1/HAUS4/TEN1-CDK3/MSX1/SAC3D1/SUN1/ZFP42/REEP4/PDGFRB/GEN1/UBE2S/MTBP/TDRKH/MAD2L2/FMN2/MRE11A/ITGB3BP/REC8/CHEK1/NCAPD3/SETDB2/HMGA2/L3MBTL1/SNX9/CEP85/CEP97/RAD21/MEI1/FANCM/PCID2/LRRCC1/MZT1/CENPW/PPP5C/TTN/SYCE1L/MSH2* |
| G18 | GO:0051640 | Organelle localization | 399 | 0.297993997 | 1.310682836 | 0.004901961 | 0.03838876 | tags =11%, list =8%, signal =11% | *P2RX7/ASPM/CENPF/FAM83D/CDCA8/CENPA/KIF2C/CENPE/KIFC1/KIF14/ESPL1/NDC80/DLGAP5/DNM1/CCNB1/KIF18A/CDCA5/NUSAP1/KIF23/KIT/PSRC1/SERPINA1/STON2/SPAG5/AURKA/KIF22/GPSM2/CTSC/PLIN5/AP3B2/LRRK2/SYT7/NDE1/RP11-599B13.6/MAD1L1/CENPQ/ANKRD53/PLXNA2/SLC4A5/GATA2/SYT17/FES/BIN1/DAB1/STX11* |
| G19 | GO:0000281 | Mitotic cytokinesis | 32 | 0.778877438 | 2.345954224 | 0.002538071 | 0.030326036 | tags =41%, list =5%, signal =39% | *CENPA/KIF4A/PLK1/NUSAP1/KIF23/RACGAP1/KIF20A/CEP55/ANLN/KIF20B/STMN1/CKAP2/ANKRD53* |
| G19 | GO:0032467 | Positive regulation of cytokinesis | 23 | 0.822380463 | 2.263543273 | 0.002557545 | 0.030326036 | tags =43%, list =5%, signal =41% | *AURKB/CIT/KIF14/KIF23/RACGAP1/CDC25B/KIF20B/CDC6/ECT2/SVIL* |
| G19 | GO:0061640 | Cytoskeleton-dependent cytokinesis | 40 | 0.749807335 | 2.368635373 | 0.002597403 | 0.030326036 | tags =35%, list =5%, signal =33% | *AURKB/CENPA/KIF4A/PLK1/NUSAP1/KIF23/RACGAP1/KIF20A/CEP55/ANLN/KIF20B/STMN1/CKAP2/ANKRD53* |
| G19 | GO:0032465 | Regulation of cytokinesis | 50 | 0.722593153 | 2.391372841 | 0.00273224 | 0.030326036 | tags =26%, list =5%, signal =25% | *AURKB/CIT/KIF14/KIF23/RACGAP1/CDC25B/AURKA/KIF20B/E2F8/CDC6/ECT2/ANKRD53/SVIL* |
| G19 | GO:0051302 | Regulation of cell division | 99 | 0.48820485 | 1.832545079 | 0.003003003 | 0.030486975 | tags =23%, list =5%, signal =22% | *FGF9/AURKB/ASPM/KIF18B/CIT/KIF14/BLM/KIF23/RACGAP1/CDC25B/AURKA/FIGF/SFRP2/KIF20B/E2F8/PDGFD/CDC6/HTR2B/SUSD2/IGF2/ECT2/ANKRD53/SVIL* |
| G19 | GO:0000910 | Cytokinesis | 117 | 0.641892488 | 2.477532457 | 0.003194888 | 0.030486975 | tags =22%, list =5%, signal =21% | *AURKB/CENPA/CIT/KIF4A/KIF14/PLK1/ESPL1/RAB11FIP4/NUSAP1/KIF23/RACGAP1/KIF20A/CDC25B/CEP55/AURKA/ANLN/KIF20B/STMN1/INCENP/E2F8/CKAP2/PRC1/CDC6/ECT2/ANKRD53/SVIL* |
| G19 | GO:0051782 | Negative regulation of cell division | 11 | 0.842484025 | 1.935850409 | 0.004464286 | 0.037712237 | tags =55%, list =9%, signal =50% | *AURKB/ASPM/BLM/E2F8/SUSD2/PTCH1* |
| G19 | GO:0032506 | Cytokinetic process | 14 | 0.753471008 | 1.856054088 | 0.004683841 | 0.037949001 | tags =50%, list =14%, signal =43% | *AURKB/KIF23/RACGAP1/KIF20B/SNX9/SNX18/ALKBH4* |
| G19 | GO:0051781 | Positive regulation of cell division | 57 | 0.494215924 | 1.676061615 | 0.005555556 | 0.04142949 | tags =26%, list =5%, signal =25% | *FGF9/AURKB/CIT/KIF14/KIF23/RACGAP1/CDC25B/FIGF/KIF20B/PDGFD/CDC6/HTR2B/IGF2/ECT2/SVIL* |
| G2 | GO:0071478 | Cellular response to radiation | 136 | 0.385012894 | 1.531282909 | 0.006369427 | 0.045290946 | tags =15%, list =10%, signal =14% | *CRIP1/CNGB1/AURKB/PBK/BLM/SFRP2/RAD51/CDC25A/POLD1/RAD51AP1/H2AFX/ADIRF/SAG/ECT2/FIGNL1/NMT2/NFATC4/CHEK1/HYAL1/HMGA2/RHNO1* |
| G20 | GO:0051310 | Metaphase plate congression | 45 | 0.791099327 | 2.570082755 | 0.002624672 | 0.030326036 | tags =36%, list =5%, signal =34% | *CENPF/FAM83D/CDCA8/KIF2C/CENPE/KIFC1/KIF14/NDC80/CCNB1/KIF18A/CDCA5/PSRC1/KIF22/MAD1L1/CENPQ/ANKRD53* |
| G20 | GO:0051653 | Spindle localization | 35 | 0.603584632 | 1.840371378 | 0.002659574 | 0.030326036 | tags =23%, list =4%, signal =22% | *ASPM/CENPA/ESPL1/NDC80/NUSAP1/SPAG5/GPSM2/NDE1* |
| G20 | GO:0007080 | Mitotic metaphase plate congression | 37 | 0.801846726 | 2.468782415 | 0.002659574 | 0.030326036 | tags =35%, list =5%, signal =33% | *CDCA8/KIF2C/CENPE/KIFC1/KIF14/NDC80/CCNB1/KIF18A/CDCA5/PSRC1/KIF22/MAD1L1/ANKRD53* |
| G20 | GO:0050000 | Chromosome localization | 57 | 0.746124169 | 2.530371884 | 0.002777778 | 0.030326036 | tags =32%, list =5%, signal =30% | *CENPF/FAM83D/CDCA8/KIF2C/CENPE/KIFC1/KIF14/NDC80/DLGAP5/CCNB1/KIF18A/CDCA5/PSRC1/KIF22/NDE1/MAD1L1/CENPQ/ANKRD53* |
| G20 | GO:0051303 | Establishment of chromosome localization | 56 | 0.747818157 | 2.526250451 | 0.002785515 | 0.030326036 | tags =32%, list =5%, signal =31% | *CENPF/FAM83D/CDCA8/KIF2C/CENPE/KIFC1/KIF14/NDC80/DLGAP5/CCNB1/KIF18A/CDCA5/PSRC1/KIF22/NDE1/MAD1L1/CENPQ/ANKRD53* |
| G20 | GO:0051642 | Centrosome localization | 17 | 0.698974584 | 1.833288436 | 0.004618938 | 0.037949001 | tags =41%, list =15%, signal =35% | *ASPM/AURKA/GPSM2/NDE1/PLXNA2/SYNE2/EZR* |
| G21 | GO:0001556 | Oocyte maturation | 19 | 0.750188061 | 2.005933384 | 0.002352941 | 0.030326036 | tags =53%, list =13%, signal =46% | *CCNB1/CDC25B/AURKA/FBXO5/TRIP13/RPS6KA2/DMC1/REC8/PTK2B/BRCA2* |
| G21 | GO:0048477 | Oogenesis | 54 | 0.503100983 | 1.690000569 | 0.00280112 | 0.030326036 | tags =30%, list =13%, signal =26% | *ASPM/CCNB1/CDC25B/AURKA/FBXO5/BCL2/TRIP13/RPS6KA2/DMC1/ZGLP1/FMN2/SOHLH2/REC8/H3F3B/PTK2B/BRCA2* |
| G21 | GO:0051321 | Meiotic cell cycle | 150 | 0.552337044 | 2.224338795 | 0.003267974 | 0.030673715 | tags =39%, list =14%, signal =33% | *FBXO43/ASPM/NEK2/CDC20/PLK1/MKI67/ESPL1/SGOL1/EXO1/TOP2A/CKS2/KIF18A/MND1/RAD54L/CDC25B/AURKA/FBXO5/RAD51/FANCD2/SGOL2/NCAPD2/SYCE2/SPDYA/SMC4/CDK2/H2AFX/FANCA/TRIP13/EME1/AGO4/RPS6KA2/DMC1/XRCC2/DSN1/PTTG1/MASTL/MSX1/SUN1/ZFP42/MNS1/TDRKH/FMN2/MRE11A/REC8/NCAPD3/RAD21/MEI1/FANCM/SYCE1L/MSH2/TDRD9/BRCA2/SMC2/BUB3/RAD51B/SMC1A/DUSP1/RAD54B* |
| G21 | GO:0007281 | Germ cell development | 142 | 0.431718209 | 1.72013667 | 0.003278689 | 0.030718331 | tags =22%, list =13%, signal =19% | *CASC5/ASPM/CCNB1/ACRBP/FAM9C/KIT/CDC25B/AURKA/FBXO5/HMGB2/BCL2/TRIP13/RPS6KA2/DMC1/PRDM14/ZGLP1/FANCG/CHD5/FMN2/SOHLH2/REC8/MEI1/STRBP/TTC26/MSH2/H3F3B/PTK2B/INSL6/CEP57/TTLL5/BRCA2* |
| G21 | GO:0044770 | Cell cycle phase transition | 442 | 0.504425681 | 2.226658076 | 0.005208333 | 0.039701985 | tags =27%, list =12%, signal =24% | *IQGAP3/NEK2/CENPF/FAM83D/CDK1/UBE2C/CENPE/CIT/TTK/KIF14/PLK4/CCNA2/PLK1/GTSE1/ESPL1/NDC80/DLGAP5/BLM/BUB1B/FHL1/CCNB1/CKS2/BUB1/CCNB2/CDCA5/CDKN2C/TPX2/CDC25C/MELK/HMMR/CDC25B/MAD2L1/PRIM1/MCM10/TACC3/AURKA/ANLN/FANCI/FOXM1/CDT1/WEE1/FBXO5/CDKN3/CDC25A/MCM5/CLSPN/ORC6/TICRR/BORA/SPDYA/PKMYT1/RRM2/POLE2/CDC45/DBF4B/ORC1/BCL2/PDPN/CDK2/CNTRL/CDC6/MCM2/CCNE2/CDKN2D/NDE1/SUSD2/POLE/MCM8/TIMELESS/MAD1L1/HAUS5/MCM4/CDC7/MCM6/KNTC1/RCC1/MCM7/HAUS8/PRIM2/MASTL/MCM3/HAUS4/SKP2/CEP72/SLFN11/PSME1/ID4/TEN1-CDK3/TYMS/CENPJ/PCNT/AJUBA/CTDSPL/EIF4EBP1/ZNF16/EZH2/DBF4/TNKS1BP1/GEN1/UBE2S/MTBP/CDKN1B/MUC1/MAD2L2/TUBB4B/MRE11A/POLA2/ZFP36L2/CHEK1/KDM8/HMGA2/PCID2/BACH1/RPA3/E2F1/CEP76/MIIP/CDK5RAP2/POLA1* |
| G21 | GO:0007286 | Spermatid development | 73 | 0.454048003 | 1.623973697 | 0.005509642 | 0.041266257 | tags =34%, list =21%, signal =27% | *CASC5/ACRBP/FAM9C/KIT/HMGB2/TRIP13/DMC1/FANCG/CHD5/REC8/MEI1/STRBP/TTC26/H3F3B/INSL6/CEP57/TTLL5/OSBP2/RFX2/TARBP2/CATSPER3/SIX5/TBPL1/ODF2/TPGS1* |
| G22 | GO:0000732 | Strand displacement | 27 | 0.770481953 | 2.229771652 | 0.00248139 | 0.030326036 | tags =59%, list =13%, signal =51% | *BLM/EXO1/RMI2/RAD51/BRCA1/BARD1/RAD51AP1/BRIP1/XRCC2/RTEL1-TNFRSF6B/MRE11A/DNA2/RMI1/BRCA2/RTEL1/RAD51B* |
| G22 | GO:0006312 | Mitotic recombination | 45 | 0.733103427 | 2.381668663 | 0.002624672 | 0.030326036 | tags =56%, list =14%, signal =48% | *TOP2A/PRIM1/RAD51/RFC3/POLE2/POLD1/POLE/DMC1/FEN1/XRCC2/RFC4/PRIM2/POLD3/RFC5/GEN1/MRE11A/POLA2/DNA2/RPA3/LIG1/RFC2/POLA1/BRCA2/RAD51B/RAD54B* |
| G22 | GO:0007131 | Reciprocal meiotic recombination | 37 | 0.590554069 | 1.818239636 | 0.002659574 | 0.030326036 | tags =38%, list =14%, signal =33% | *TOP2A/MND1/RAD51/TRIP13/EME1/DMC1/XRCC2/MRE11A/REC8/RAD21/FANCM/MSH2/RAD51B/RAD54B* |
| G22 | GO:0035825 | Reciprocal DNA recombination | 37 | 0.590554069 | 1.818239636 | 0.002659574 | 0.030326036 | tags =38%, list =14%, signal =33% | *TOP2A/MND1/RAD51/TRIP13/EME1/DMC1/XRCC2/MRE11A/REC8/RAD21/FANCM/MSH2/RAD51B/RAD54B* |
| G22 | GO:0045132 | Meiotic chromosome segregation | 50 | 0.642196392 | 2.125305235 | 0.00273224 | 0.030326036 | tags =46%, list =13%, signal =40% | *PLK1/ESPL1/SGOL1/TOP2A/FANCD2/SGOL2/SYCE2/SMC4/TRIP13/EME1/AGO4/DMC1/DSN1/PTTG1/SUN1/FMN2/MRE11A/REC8/RAD21/MEI1/FANCM/SYCE1L/SMC2* |
| G22 | GO:0070192 | Chromosome organization involved in meiotic cell cycle | 36 | 0.634751841 | 1.940962708 | 0.002739726 | 0.030326036 | tags =50%, list =13%, signal =44% | *RAD51/FANCD2/SGOL2/NCAPD2/SYCE2/SMC4/TRIP13/AGO4/DMC1/DSN1/SUN1/MRE11A/REC8/NCAPD3/RAD21/MEI1/SYCE1L/SMC2* |
| G22 | GO:0007127 | Meiosis I | 67 | 0.608677198 | 2.131920572 | 0.002770083 | 0.030326036 | tags =43%, list =14%, signal =37% | *PLK1/ESPL1/TOP2A/CKS2/MND1/CDC25B/AURKA/FBXO5/RAD51/FANCD2/SYCE2/TRIP13/EME1/AGO4/DMC1/XRCC2/PTTG1/SUN1/FMN2/MRE11A/REC8/RAD21/MEI1/FANCM/SYCE1L/MSH2/BRCA2/RAD51B/RAD54B* |
| G22 | GO:0000725 | Recombinational repair | 89 | 0.59777778 | 2.214374696 | 0.002923977 | 0.030486975 | tags =45%, list =17%, signal =37% | *BLM/RAD54L/GINS2/RAD51/BRCA1/SLX1B/CDC45/RAD51AP1/H2AFX/GINS4/MCM8/DMC1/FEN1/XRCC2/CDC7/TONSL/POLQ/PARPBP/RTEL1-TNFRSF6B/FIGNL1/MMS22L/GEN1/MRE11A/REC8/CHEK1/RHNO1/PARP1/RPA3/BRCA2/WDR48/RTEL1/RAD51B/SFR1/RAD54B/SHFM1/XRCC1/SIRT6/SWSAP1/RBBP8/NUCKS1* |
| G22 | GO:1903046 | Meiotic cell cycle process | 127 | 0.570241041 | 2.245308228 | 0.003225806 | 0.030486975 | tags =41%, list =14%, signal =35% | *FBXO43/ASPM/CDC20/PLK1/MKI67/ESPL1/SGOL1/TOP2A/CKS2/KIF18A/MND1/RAD54L/CDC25B/AURKA/FBXO5/RAD51/FANCD2/SGOL2/NCAPD2/SYCE2/SPDYA/SMC4/CDK2/FANCA/TRIP13/EME1/AGO4/RPS6KA2/DMC1/XRCC2/DSN1/PTTG1/MASTL/MSX1/SUN1/ZFP42/TDRKH/FMN2/MRE11A/REC8/NCAPD3/RAD21/MEI1/FANCM/SYCE1L/MSH2/TDRD9/BRCA2/SMC2/RAD51B/SMC1A/RAD54B* |
| G22 | GO:0007126 | Meiotic nuclear division | 121 | 0.570349585 | 2.211388417 | 0.003257329 | 0.030629592 | tags =41%, list =14%, signal =36% | *FBXO43/ASPM/CDC20/PLK1/MKI67/ESPL1/SGOL1/TOP2A/CKS2/KIF18A/MND1/RAD54L/CDC25B/AURKA/FBXO5/RAD51/FANCD2/SGOL2/SYCE2/SPDYA/SMC4/CDK2/FANCA/TRIP13/EME1/AGO4/RPS6KA2/DMC1/XRCC2/DSN1/PTTG1/MASTL/MSX1/SUN1/ZFP42/TDRKH/FMN2/MRE11A/REC8/RAD21/MEI1/FANCM/SYCE1L/MSH2/TDRD9/BRCA2/SMC2/RAD51B/SMC1A/RAD54B* |
| G22 | GO:0007143 | Female meiotic division | 20 | 0.684834281 | 1.83274932 | 0.004854369 | 0.038248567 | tags =35%, list =9%, signal =32% | *PLK1/CDC25B/AURKA/FBXO5/TRIP13/MASTL/FMN2* |
| G22 | GO:0045143 | Homologous chromosome segregation | 29 | 0.629053368 | 1.858661857 | 0.007334963 | 0.049685189 | tags =48%, list =11%, signal =43% | *PLK1/ESPL1/FANCD2/SYCE2/TRIP13/AGO4/DMC1/PTTG1/SUN1/FMN2/MRE11A/REC8/MEI1/SYCE1L* |
| G23 | GO:0071459 | Protein localization to chromosome, centromeric region | 16 | 0.826451795 | 2.135841351 | 0.002320186 | 0.030326036 | tags =50%, list =9%, signal =46% | *AURKB/CASC5/CENPA/CDK1/BUB1B/GSG2/CENPQ/MTBP* |
| G23 | GO:0006284 | Base-excision repair | 40 | 0.571721582 | 1.806063903 | 0.002597403 | 0.030326036 | tags =40%, list =16%, signal =34% | *NEIL3/POLD1/POLE/FEN1/POLQ/DNA2/HMGA2/RPA3/LIG1/POLG/RECQL4/XRCC1/ERCC6/SIRT6/RPS3/UNG* |
| G23 | GO:0036297 | Interstrand cross-link repair | 46 | 0.622627182 | 2.026650635 | 0.002645503 | 0.030326036 | tags =41%, list =12%, signal =36% | *FANCI/FANCD2/SLX1B/FANCC/RAD51AP1/FANCA/FANCB/EME1/UBE2T/FANCE/FANCG/USP1/FANCL/FANCM/RPA3/DCLRE1B/C19orf40/ATR/DCLRE1C* |
| G23 | GO:2000779 | Regulation of double-strand break repair | 37 | 0.558043565 | 1.718143999 | 0.002659574 | 0.030326036 | tags =54%, list =24%, signal =41% | *FOXM1/RAD51/RAD51AP1/WHSC1/POLQ/PARPBP/RTEL1-TNFRSF6B/DEK/FIGNL1/CHEK1/HMGA2/RTEL1/TWIST1/SIRT6/FAM178A/ANKRD32/MGMT/RIF1/RPA2/NUDT16* |
| G23 | GO:0000731 | DNA synthesis involved in DNA repair | 69 | 0.627518403 | 2.197556201 | 0.002816901 | 0.030326036 | tags =42%, list =13%, signal =37% | *BLM/EXO1/KIAA0101/RMI2/RAD51/RFC3/BRCA1/BARD1/POLE2/POLD1/RAD51AP1/CDKN2D/POLE/BRIP1/XRCC2/DTL/RFC4/POLD3/RFC5/REV3L/MAD2L2/MRE11A/DNA2/RMI1/RPA3/RFC2/BRCA2/TRIM25/RAD51B* |
| G23 | GO:0000724 | Double-strand break repair via homologous recombination | 88 | 0.594449618 | 2.200021917 | 0.002985075 | 0.030486975 | tags =44%, list =17%, signal =37% | *BLM/RAD54L/GINS2/RAD51/BRCA1/SLX1B/CDC45/RAD51AP1/H2AFX/GINS4/MCM8/DMC1/FEN1/XRCC2/CDC7/TONSL/POLQ/PARPBP/RTEL1-TNFRSF6B/FIGNL1/MMS22L/GEN1/MRE11A/REC8/CHEK1/PARP1/RPA3/BRCA2/WDR48/RTEL1/RAD51B/SFR1/RAD54B/SHFM1/XRCC1/SIRT6/SWSAP1/RBBP8/NUCKS1* |
| G23 | GO:0071168 | Protein localization to chromatin | 15 | 0.706672269 | 1.785751721 | 0.004587156 | 0.037949001 | tags =40%, list =11%, signal =36% | *PLK1/CDCA5/ESCO2/EZH2/CCDC101/RAD21* |
| G23 | GO:0034501 | Protein localization to kinetochore | 13 | 0.828695153 | 2.009742115 | 0.004640371 | 0.037949001 | tags =54%, list =9%, signal =49% | *AURKB/CASC5/CDK1/BUB1B/GSG2/CENPQ/MTBP* |
| G23 | GO:0051053 | Negative regulation of DNA metabolic process | 101 | 0.390217939 | 1.475184527 | 0.005934718 | 0.043501568 | tags =30%, list =19%, signal =24% | *BLM/PIF1/CDC6/POLQ/GMNN/PARPBP/RTEL1-TNFRSF6B/TEN1-CDK3/MRE11A/HMGA2/PARP1/HNRNPA1/ZNF93/ACVRL1/MSH2/ATR/BRCA2/TTF1/RTEL1/TWIST1/SMC1A/APOBEC3D/DUSP1/INPP5K/RPS3/SMC3/GPER1/TIPIN/STAG2/CDAN1* |
| G23 | GO:0006289 | Nucleotide-excision repair | 112 | 0.381822586 | 1.464628853 | 0.006289308 | 0.045145817 | tags =44%, list =33%, signal =29% | *NEIL3/RFC3/FANCC/POLD1/POLE/RFC4/POLD3/RFC5/PARP1/RPA3/LIG1/POLR2L/RFC2/BRCA2/COPS4/XRCC1/ERCC6/RBBP8/POLL/XPC/POLR2J/RPS27A/TCEA1/ATXN3/RPA1/CDK7/RPA2/UBE2I/SIRT1/PCNA/RAD52/SUMO2/PRPF19/XAB2/RBX1/ISY1/ERCC3/GTF2H5/POLR2D/GTF2H2C/NTHL1/PNKP/XPA/SUMO3/UBA52/BIVM/COPS5/COPS3/ERCC2* |
| G24 | GO:0044033 | Multi-organism metabolic process | 203 | 0.406667531 | 1.674744037 | 0.003759398 | 0.033400311 | tags =48%, list =28%, signal =35% | *TOP2A/POU2F3/ZFP36/RPL37/RPL9/RPL38/TFAP4/RPL31/RPS23/RPS21/RPS27/RPL37A/RPL10A/HMGA2/RPS17L/POLR2L/RPS16/RPS29/RPS25/RPL10/RPL39/ROCK2/NUP50/APOBEC3D/RPS13/NUP35/RPS8/RPS7/MAP2K2/NUP155/RPL12/INPP5K/RPS9/RPS3/NUP205/MAP2K7/RPL7A/RPL14/RPL30/RPL3/RPL36/NUCKS1/RPLP0/NUP160/NOTCH1/RPL15/PCBP2/NUP107/RPS18/NUP54/RPS6/RPS14/EIF3F/PTBP1/RPL11/NELFB/RPL32/TARBP2/RPS4X/RPS5/RPL36A/RPL4/RPL18/POLR2J/RPLP2/RPL27/RPS27A/RPL24/RPL27A/RPSA/RPS3A/RPL26/RPL19/RPS12/RPS15A/TPR/NUP43/RPL13A/RPS11/PCBP1/RPL22/NUP62/NDC1/RPL35A/SEH1L/NUP85/RPL8/RPL18A/IFITM3/RPL29/TRIM21/RPS24/RPL5/NUP37/RPL13/HDAC1/RPL17/RPL23* |
| G25 | GO:0043486 | Histone exchange | 42 | 0.644383197 | 2.04496136 | 0.002604167 | 0.030326036 | tags =57%, list =17%, signal =47% | *CASC5/HJURP/CENPA/OIP5/CENPK/CENPI/CENPU/CENPH/CENPM/CENPO/CENPN/MIS18A/CENPQ/MIS18BP1/CHD5/ITGB3BP/RBBP7/CENPW/CENPL/CENPP/ANP32B/NASP/PTMA/CENPC* |
| G25 | GO:0031055 | Chromatin remodeling at centromere | 35 | 0.731194532 | 2.229462809 | 0.002659574 | 0.030326036 | tags =60%, list =12%, signal =53% | *CASC5/HJURP/CENPA/HELLS/OIP5/CENPK/CENPI/CENPU/CENPH/CENPM/CENPO/CENPN/MIS18A/CENPQ/MIS18BP1/ITGB3BP/RBBP7/CENPW/H3F3B/CENPL/CENPP* |
| G25 | GO:0043044 | ATP-dependent chromatin remodeling | 62 | 0.583625196 | 2.018824096 | 0.002785515 | 0.030326036 | tags =40%, list =17%, signal =34% | *CASC5/HJURP/CENPA/OIP5/CENPK/CENPI/CENPU/CENPH/CENPM/CENPO/CENPN/MIS18A/CENPQ/MIS18BP1/CHD5/ITGB3BP/RBBP7/CENPW/CENPL/CENPP/ANP32B/NASP/PTMA/ACTL6A/CENPC* |
| G25 | GO:0006338 | Chromatin remodeling | 130 | 0.390148891 | 1.536724414 | 0.006622517 | 0.046053749 | tags =26%, list =17%, signal =22% | *CASC5/HJURP/CENPA/HELLS/OIP5/CENPK/CENPI/CENPU/CENPH/CENPM/CENPO/CENPN/MIS18A/CENPQ/MIS18BP1/DEK/CHD5/ITGB3BP/CHEK1/RBBP7/HMGA2/CENPW/KAT2B/H3F3B/CENPL/CENPP/TTF1/HDAC5/ANP32B/NASP/PTMA/ACTL6A/SUV39H2/CENPC* |
| G26 | GO:0051383 | Kinetochore organization | 16 | 0.752936577 | 1.945852239 | 0.004640371 | 0.037949001 | tags =44%, list =13%, signal =38% | *CENPF/CENPA/CENPE/CENPH/SMC4/CENPW/SMC2* |
| G27 | GO:0006271 | DNA strand elongation involved in DNA replication | 23 | 0.790002037 | 2.174423978 | 0.002557545 | 0.030326036 | tags =70%, list =12%, signal =62% | *GINS2/PRIM1/RFC3/POLD1/RNASEH2A/GINS4/FEN1/RFC4/PRIM2/POLD3/POLA2/GINS1/DNA2/PARP1/LIG1/POLA1* |
| G27 | GO:0044786 | Cell cycle DNA replication | 33 | 0.683129235 | 2.064673867 | 0.002564103 | 0.030326036 | tags =52%, list =19%, signal =42% | *GINS2/CDT1/E2F8/CDC45/DBF4B/CDC7/RTEL1-TNFRSF6B/MRE11A/GINS1/DONSON/DNA2/LIG1/RTEL1/SMC1A/SMC3/TIPIN/STAG2* |
| G27 | GO:0090329 | Regulation of DNA-dependent DNA replication | 40 | 0.624831451 | 1.973837553 | 0.002597403 | 0.030326036 | tags =48%, list =19%, signal =39% | *BLM/CDT1/RFC3/TICRR/E2F8/DBF4B/CDK2/CDC7/RFC4/RFC5/CHTF18/MRE11A/RFC2/BRCA2/BMP6/SMC1A/SMC3/TIPIN/STAG2* |
| G27 | GO:0006270 | DNA replication initiation | 37 | 0.807115947 | 2.485005665 | 0.002659574 | 0.030326036 | tags =59%, list =7%, signal =56% | *GINS2/PRIM1/MCM10/CDT1/MCM5/ORC6/TICRR/POLE2/CDC45/ORC1/CDK2/CDC6/MCM2/CCNE2/GINS4/POLE/MCM4/CDC7/MCM6/MCM7/PRIM2/MCM3* |
| G27 | GO:0006261 | DNA-dependent DNA replication | 132 | 0.640087325 | 2.533549062 | 0.003215434 | 0.030486975 | tags =45%, list =14%, signal =39% | *BLM/TOP2A/GINS2/PRIM1/MCM10/CDT1/RAD51/RFC3/MCM5/ORC6/TICRR/POLE2/E2F8/POLD1/CDC45/DBF4B/ORC1/RNASEH2A/CDK2/CDC6/MCM2/CCNE2/GINS4/EME1/POLE/FEN1/MCM4/CDC7/TONSL/POLQ/MCM6/RFC4/MCM7/PRIM2/MCM3/POLD3/RFC5/RTEL1-TNFRSF6B/REV3L/MMS22L/CHTF18/MRE11A/POLA2/GINS1/DONSON/DNA2/PARP1/FANCM/LIG1/POLG/TFAM/RFC2/POLA1/POLG2/BRCA2/BMP6/RTEL1/TOPBP1/SMC1A* |
| G27 | GO:0006302 | Double-strand break repair | 182 | 0.516941198 | 2.11004972 | 0.003558719 | 0.032115724 | tags =36%, list =17%, signal =31% | *BLM/MND1/CDCA5/RAD54L/GINS2/ESCO2/FOXM1/RAD51/BRCA1/BARD1/SLX1B/CDC45/RAD51AP1/H2AFX/GGN/TRIP13/GINS4/WHSC1/EME1/MCM8/BRIP1/DMC1/FEN1/XRCC6BP1/XRCC2/CDC7/TONSL/POLQ/PARPBP/RTEL1-TNFRSF6B/DEK/FIGNL1/MMS22L/GEN1/MAD2L2/MRE11A/DTX3L/REC8/CHEK1/DNA2/HMGA2/PARP1/RAD21/BACH1/RPA3/PARP9/DCLRE1B/MSH2/POLA1/DCLRE1C/BRCA2/RECQL4/C9orf142/WDR48/RTEL1/RAD51B/SFR1/TWIST1/RAD54B/FAM175A/SHFM1/XRCC1/SIRT6/SWSAP1/RBBP8/NHEJ1* |
| G27 | GO:0071897 | DNA biosynthetic process | 175 | 0.471734153 | 1.922588155 | 0.003584229 | 0.032289395 | tags =29%, list =13%, signal =25% | *AURKB/NEK2/CENPF/BLM/EXO1/KIAA0101/RMI2/TK1/RAD51/PIF1/KLF4/RFC3/BRCA1/BARD1/POLE2/POLD1/RAD51AP1/CDKN2D/POLE/BRIP1/XRCC2/POLQ/GREM1/DTL/RFC4/POLD3/RFC5/TEN1-CDK3/TYMS/TNKS1BP1/PDGFRB/REV3L/CHTF18/MAD2L2/MRE11A/POLA2/DNA2/RMI1/HNRNPA1/ACVRL1/RPA3/LIG1/POLG/RFC2/PTK2B/POLG2/LIN9/ATR/BRCA2/TRIM25/RAD51B* |
| G27 | GO:0006310 | DNA recombination | 224 | 0.537865205 | 2.239343017 | 0.003802281 | 0.033607472 | tags =37%, list =17%, signal =31% | *BLM/EXO1/TOP2A/MND1/RAD54L/IL7R/GINS2/PRIM1/RMI2/HMGB2/RAD51/PIF1/RFC3/KPNA2/BRCA1/BARD1/POLE2/SLX1B/POLD1/CDC45/RAD51AP1/H2AFX/TRIP13/GINS4/WHSC1/EME1/POLE/MCM8/BRIP1/DMC1/FEN1/XRCC2/CDC7/TONSL/POLQ/RFC4/BCL11B/PRIM2/POLD3/RFC5/PARPBP/RTEL1-TNFRSF6B/FIGNL1/TCF7/SWAP70/MMS22L/GEN1/EID3/IL27RA/MRE11A/POLA2/REC8/CHEK1/DNA2/RHNO1/PARP1/RAD21/RMI1/FANCM/BACH1/RPA3/LIG1/MSH2/RFC2/POLA1/DCLRE1C/BRCA2/RECQL4/WDR48/RTEL1/RAD51B/SFR1/HMGB3/RAD54B/HMGB1/SHFM1/XRCC1/SIRT6/UNG/SWSAP1/ACTL6A/RBBP8/NHEJ1* |
| G27 | GO:0006260 | DNA replication | 266 | 0.534272601 | 2.252958728 | 0.004065041 | 0.035205302 | tags =35%, list =14%, signal =31% | *CDK1/BLM/EXO1/TOP2A/CDC25C/KIAA0101/GINS2/PRIM1/MCM10/ESCO2/RMI2/CDT1/RAD51/CDC25A/RFC3/MCM5/CLSPN/ORC6/TICRR/BRCA1/BARD1/RRM2/POLE2/E2F8/POLD1/CDC45/DBF4B/ORC1/RNASEH2A/CDK2/CDC6/MCM2/CCNE2/GINS4/EME1/POLE/MCM8/BRIP1/TIMELESS/FEN1/MCM4/CDC7/TONSL/POLQ/MCM6/GMNN/DTL/RFC4/MCM7/CHAF1B/PRIM2/MCM3/POLD3/RFC5/RTEL1-TNFRSF6B/MCMDC2/FAM111A/DBF4/REV3L/MMS22L/CHTF18/CACYBP/MRE11A/POLA2/GINS1/CHEK1/DONSON/DNA2/RBBP7/RHNO1/PARP1/RMI1/FANCM/RRM1/ACVRL1/RPA3/LIG1/PTMS/POLG/TFAM/RFC2/POLA1/DUT/POLG2/ATR/BRCA2/TTF1/RECQL4/CHAF1A/BMP6/RTEL1/TOPBP1/SMC1A* |
| G27 | GO:0033260 | Nuclear DNA replication | 24 | 0.693607304 | 1.939233755 | 0.005025126 | 0.038706237 | tags =46%, list =13%, signal =40% | *GINS2/CDT1/CDC45/DBF4B/CDC7/RTEL1-TNFRSF6B/GINS1/DONSON/DNA2/LIG1/RTEL1* |
| G27 | GO:0006281 | DNA repair | 473 | 0.444294356 | 1.973580134 | 0.005494505 | 0.04121279 | tags =28%, list =17%, signal =24% | *NEIL3/CDK1/BLM/EXO1/MND1/CDCA5/RAD54L/KIAA0101/GINS2/FANCI/ESCO2/FOXM1/RMI2/HMGB2/KIF22/RAD51/FANCD2/PIF1/RFC3/CLSPN/TICRR/BRCA1/BARD1/POLE2/SLX1B/FANCC/POLD1/CDC45/RAD51AP1/RNASEH2A/CDK2/H2AFX/FANCA/GGN/TRIP13/GINS4/CDKN2D/WHSC1/FANCB/EME1/POLE/MCM8/BRIP1/DMC1/FEN1/XRCC6BP1/XRCC2/UBE2T/FANCE/CDC7/TONSL/POLQ/AXIN2/FANCG/DTL/PTTG1/RFC4/CHAF1B/NUDT1/POLD3/RFC5/PARPBP/RTEL1-TNFRSF6B/DEK/USP1/FIGNL1/FANCL/REV3L/MMS22L/GEN1/EID3/MAD2L2/MRE11A/DTX3L/REC8/CHEK1/DNA2/HMGA2/RHNO1/PARP1/RAD21/RMI1/FANCM/BACH1/RPA3/PARP9/PPP5C/LIG1/DCLRE1B/POLG/C19orf40/POLR2L/MSH2/RFC2/POLA1/CEBPG/POLG2/ATR/DCLRE1C/BRCA2/CDC14B/RECQL4/COPS4/C9orf142/CHAF1A/WDR48/TRIM25/RTEL1/RAD51B/SFR1/TWIST1/TOPBP1/SMC1A/USP28/RAD54B/SSRP1/HMGB1/FAM175A/SHFM1/XRCC1/ERCC6/SIRT6/RFWD3/RPS3/MGME1/SMC3/UNG/SWSAP1/ACTL6A/RBBP8/NHEJ1* |
| G27 | GO:2000105 | Positive regulation of DNA-dependent DNA replication | 11 | 0.746468351 | 1.715226662 | 0.006696429 | 0.046379968 | tags =45%, list =13%, signal =39% | *E2F8/DBF4B/CDK2/CDC7/BMP6* |
| G3 | GO:0022616 | DNA strand elongation | 29 | 0.761981268 | 2.251423473 | 0.002444988 | 0.030326036 | tags =62%, list =12%, signal =55% | *GINS2/PRIM1/RFC3/POLD1/RNASEH2A/GINS4/FEN1/RFC4/PRIM2/POLD3/MRE11A/POLA2/GINS1/DNA2/PARP1/LIG1/DCLRE1B/POLA1* |
| G4 | GO:0034502 | Protein localization to chromosome | 58 | 0.642906308 | 2.194565335 | 0.002724796 | 0.030326036 | tags =28%, list =13%, signal =24% | *AURKB/CASC5/CENPA/CDK1/PLK1/BUB1B/CDCA5/GSG2/ESCO2/CENPQ/EZH2/MTBP/CCDC101/RAD21/ATR/BRCA2* |
| G4 | GO:0006614 | SRP-dependent cotranslational protein targeting to membrane | 93 | 0.555100286 | 2.081680352 | 0.00286533 | 0.030380747 | tags =74%, list =31%, signal =51% | *RPL37/RPL9/RPL38/RPL31/RPS23/RPS21/RPS27/RPL37A/RPL10A/RPS17L/RPS16/RPS29/RPS25/RPL10/RPL39/RPS13/RPS8/RPS7/RPL12/RPS9/RPS3/RPL7A/RPL14/RPL30/RPL3/RPL36/RPLP0/RPL15/RPS18/RPS6/RPS14/RPL11/RPL32/RPS4X/RPS5/RPL36A/RPL4/RPL18/RPLP2/RPL27/RPS27A/RPL24/RPL27A/RPSA/RPS3A/RPL26/RPL19/RPS12/RPS15A/RPL13A/RPS11/RPL22/RPL35A/RPL8/RPL18A/RPL29/RPS24/RPL5/RPL13/RPL17/RPL23/RPL6/RPL23A/RPL28/RPL34/RPL35/RPL7/RPL41/UBA52* |
| G4 | GO:0006613 | Cotranslational protein targeting to membrane | 100 | 0.522765602 | 1.970213181 | 0.002967359 | 0.030486975 | tags =71%, list =31%, signal =49% | *RPL37/ARL6IP1/RPL9/RPL38/RPL31/RPS23/RPS21/RPS27/RPL37A/RPL10A/RPS17L/RPS16/RPS29/RPS25/RPL10/RPL39/RPS13/RPS8/RPS7/RPL12/RPS9/RPS3/RPL7A/RPL14/RPL30/RPL3/RPL36/RPLP0/RPL15/RPS18/RPS6/RPS14/RPL11/RPL32/RPS4X/RPS5/RPL36A/RPL4/RPL18/TRAM2/RPLP2/RPL27/RPS27A/RPL24/RPL27A/RPSA/RPS3A/RPL26/RPL19/RPS12/RPS15A/RPL13A/RPS11/RPL22/RPL35A/RPL8/RPL18A/RPL29/RPS24/RPL5/RPL13/RPL17/RPL23/RPL6/RPL23A/RPL28/RPL34/RPL35/RPL7/RPL41/UBA52* |
| G4 | GO:0072599 | Establishment of protein localization to endoplasmic reticulum | 102 | 0.512679094 | 1.938978985 | 0.002994012 | 0.030486975 | tags =68%, list =31%, signal =47% | *RPL37/RPL9/RPL38/RPL31/RPS23/RPS21/RPS27/RPL37A/RPL10A/RPS17L/RPS16/RPS29/RPS25/RPL10/RPL39/RPS13/RPS8/RPS7/RPL12/RPS9/RPS3/RPL7A/RPL14/RPL30/RPL3/RPL36/RPLP0/RPL15/RPS18/RPS6/RPS14/RPL11/RPL32/RPS4X/RPS5/RPL36A/RPL4/RPL18/RPLP2/RPL27/RPS27A/RPL24/RPL27A/RPSA/RPS3A/RPL26/RPL19/RPS12/RPS15A/RPL13A/RPS11/RPL22/RPL35A/RPL8/RPL18A/RPL29/RPS24/RPL5/RPL13/RPL17/RPL23/RPL6/RPL23A/RPL28/RPL34/RPL35/RPL7/RPL41/UBA52* |
| G4 | GO:0045047 | Protein targeting to ER | 99 | 0.522412803 | 1.960949408 | 0.003003003 | 0.030486975 | tags =70%, list =31%, signal =48% | *RPL37/RPL9/RPL38/RPL31/RPS23/RPS21/RPS27/RPL37A/RPL10A/RPS17L/RPS16/RPS29/RPS25/RPL10/RPL39/RPS13/RPS8/RPS7/RPL12/RPS9/RPS3/RPL7A/RPL14/RPL30/RPL3/RPL36/RPLP0/RPL15/RPS18/RPS6/RPS14/RPL11/RPL32/RPS4X/RPS5/RPL36A/RPL4/RPL18/RPLP2/RPL27/RPS27A/RPL24/RPL27A/RPSA/RPS3A/RPL26/RPL19/RPS12/RPS15A/RPL13A/RPS11/RPL22/RPL35A/RPL8/RPL18A/RPL29/RPS24/RPL5/RPL13/RPL17/RPL23/RPL6/RPL23A/RPL28/RPL34/RPL35/RPL7/RPL41/UBA52* |
| G4 | GO:0070972 | Protein localization to endoplasmic reticulum | 120 | 0.443309775 | 1.718213946 | 0.003236246 | 0.030486975 | tags =59%, list =31%, signal =41% | *RPL37/RPL9/RPL38/RPL31/RPS23/RPS21/RPS27/RPL37A/RPL10A/RPS17L/RPS16/RPS29/RPS25/RPL10/RPL39/RPS13/PEX16/RPS8/RPS7/RPL12/RPS9/RPS3/RPL7A/RPL14/RPL30/RPL3/RPL36/RPLP0/RPL15/RPS18/RPS6/RPS14/RPL11/RPL32/RPS4X/RPS5/RPL36A/RPL4/RPL18/RPLP2/RPL27/RPS27A/RPL24/RPL27A/RPSA/RPS3A/RPL26/RPL19/RPS12/RPS15A/RPL13A/RPS11/RPL22/RPL35A/RPL8/RPL18A/RPL29/RPS24/RPL5/RPL13/RPL17/RPL23/RPL6/RPL23A/RPL28/RPL34/RPL35/RPL7/ANKRD13C/RPL41/UBA52* |
| G5 | GO:0007059 | Chromosome segregation | 286 | 0.69439872 | 2.944575131 | 0.004310345 | 0.03701726 | tags =39%, list =13%, signal =35% | *SKA1/AURKB/NUF2/CASC5/HJURP/NEK2/CENPF/FAM83D/CDCA8/CENPA/NCAPG/KIF18B/CDC20/KIF2C/CDCA2/UBE2C/CENPE/KIFC1/NCAPH/TTK/KIF4A/BIRC5/KIF14/ERCC6L/PLK1/MKI67/ESPL1/NDC80/DLGAP5/SGOL1/BUB1B/TOP2A/CCNB1/KIF11/KIF18A/BUB1/CDCA5/NUSAP1/KIF23/RACGAP1/SKA3/PSRC1/MAD2L1/GSG2/TACC3/SPAG5/OIP5/ESCO2/CENPK/CENPI/SPC25/ZWINT/CENPU/KIF22/FANCD2/SGOL2/NCAPD2/CENPH/SYCE2/INCENP/BRCA1/CENPM/SPC24/CENPO/KNSTRN/CENPN/SMC4/MIS18A/PRC1/CDC6/TRIP13/NDE1/EME1/AGO4/MAD1L1/DMC1/CENPQ/ECT2/ANKRD53/DDX11/DSN1/AXIN2/KNTC1/PTTG1/RCC1/SUN1/GEN1/MAD2L2/RANGAP1/FMN2/RPS27/MRE11A/ITGB3BP/REC8/NCAPD3/SETDB2/CEP85/RAD21/MEI1/FANCM/PCID2/CENPW/TTN/SYCE1L/CDK5RAP2/B9D2/CENPL/CENPP/CEP57/SMC2/BUB3/ZWILCH* |
| G6 | GO:0060272 | Embryonic skeletal joint morphogenesis | 10 | 0.809789122 | 1.837774416 | 0.004357298 | 0.03701726 | tags =60%, list =10%, signal =54% | *HOXC11/SHOX2/OSR2/HOXA11/HYAL1/OSR1* |
| G6 | GO:0072498 | Embryonic skeletal joint development | 12 | 0.812547751 | 1.901163292 | 0.004651163 | 0.037949001 | tags =58%, list =10%, signal =52% | *HOXC11/SHOX2/OSR2/HOXA11/WNT9A/HYAL1/OSR1* |
| G7 | GO:1902100 | Negative regulation of metaphase/anaphase transition of cell cycle | 29 | 0.756242305 | 2.234466577 | 0.002444988 | 0.030326036 | tags =48%, list =14%, signal =42% | *CENPF/TTK/PLK1/NDC80/BUB1B/CCNB1/BUB1/MAD2L1/MAD1L1/GEN1/MAD2L2/PCID2/BUB3/DUSP1* |
| G7 | GO:0045841 | Negative regulation of mitotic metaphase/anaphase transition | 29 | 0.756242305 | 2.234466577 | 0.002444988 | 0.030326036 | tags =48%, list =14%, signal =42% | *CENPF/TTK/PLK1/NDC80/BUB1B/CCNB1/BUB1/MAD2L1/MAD1L1/GEN1/MAD2L2/PCID2/BUB3/DUSP1* |
| G7 | GO:0071174 | Mitotic spindle checkpoint | 29 | 0.756242305 | 2.234466577 | 0.002444988 | 0.030326036 | tags =48%, list =14%, signal =42% | *CENPF/TTK/PLK1/NDC80/BUB1B/CCNB1/BUB1/MAD2L1/MAD1L1/GEN1/MAD2L2/PCID2/BUB3/DUSP1* |
| G7 | GO:2000816 | Negative regulation of mitotic sister chromatid separation | 29 | 0.756242305 | 2.234466577 | 0.002444988 | 0.030326036 | tags =48%, list =14%, signal =42% | *CENPF/TTK/PLK1/NDC80/BUB1B/CCNB1/BUB1/MAD2L1/MAD1L1/GEN1/MAD2L2/PCID2/BUB3/DUSP1* |
| G7 | GO:0071173 | Spindle assembly checkpoint | 28 | 0.775868136 | 2.266509837 | 0.002475248 | 0.030326036 | tags =54%, list =14%, signal =46% | *CASC5/CENPF/TTK/PLK1/NDC80/BUB1B/CCNB1/BUB1/MAD2L1/MAD1L1/GEN1/MAD2L2/PCID2/BUB3/DUSP1* |
| G7 | GO:0030261 | Chromosome condensation | 28 | 0.791192431 | 2.311276033 | 0.002475248 | 0.030326036 | tags =57%, list =13%, signal =50% | *NCAPG/CDK1/NCAPH/TOP2A/CCNB1/CDCA5/NUSAP1/NCAPD2/NCAPG2/SMC4/NCAPH2/NCAPD3/HMGA2/TTN/H3F3B/SMC2* |
| G7 | GO:0007094 | Mitotic spindle assembly checkpoint | 27 | 0.766481691 | 2.21819491 | 0.00248139 | 0.030326036 | tags =52%, list =14%, signal =45% | *CENPF/TTK/PLK1/NDC80/BUB1B/CCNB1/BUB1/MAD2L1/MAD1L1/GEN1/MAD2L2/PCID2/BUB3/DUSP1* |
| G7 | GO:0033048 | Negative regulation of mitotic sister chromatid segregation | 31 | 0.743691593 | 2.231407426 | 0.0025 | 0.030326036 | tags =45%, list =14%, signal =39% | *CENPF/TTK/PLK1/NDC80/BUB1B/CCNB1/BUB1/MAD2L1/MAD1L1/GEN1/MAD2L2/PCID2/BUB3/DUSP1* |
| G7 | GO:0034080 | CENP-A containing nucleosome assembly | 31 | 0.723808745 | 2.171749988 | 0.0025 | 0.030326036 | tags =61%, list =12%, signal =54% | *CASC5/HJURP/CENPA/OIP5/CENPK/CENPI/CENPU/CENPH/CENPM/CENPO/CENPN/MIS18A/CENPQ/MIS18BP1/ITGB3BP/RBBP7/CENPW/CENPL/CENPP* |
| G7 | GO:0008608 | Attachment of spindle microtubules to kinetochore | 26 | 0.870824884 | 2.48105001 | 0.002512563 | 0.030326036 | tags =54%, list =5%, signal =51% | *AURKB/CASC5/NEK2/KIF2C/CENPE/NDC80/SGOL1/CCNB1/RACGAP1/SPAG5/KNSTRN/MAD1L1/ECT2/DSN1* |
| G7 | GO:0033046 | Negative regulation of sister chromatid segregation | 33 | 0.751458579 | 2.27119088 | 0.002564103 | 0.030326036 | tags =45%, list =14%, signal =39% | *CENPF/TTK/PLK1/ESPL1/NDC80/BUB1B/CCNB1/BUB1/MAD2L1/MAD1L1/GEN1/MAD2L2/PCID2/BUB3/DUSP1* |
| G7 | GO:0051985 | Negative regulation of chromosome segregation | 33 | 0.751458579 | 2.27119088 | 0.002564103 | 0.030326036 | tags =45%, list =14%, signal =39% | *CENPF/TTK/PLK1/ESPL1/NDC80/BUB1B/CCNB1/BUB1/MAD2L1/MAD1L1/GEN1/MAD2L2/PCID2/BUB3/DUSP1* |
| G7 | GO:0000722 | Telomere maintenance via recombination | 33 | 0.736255352 | 2.225241002 | 0.002564103 | 0.030326036 | tags =55%, list =13%, signal =48% | *PRIM1/RAD51/RFC3/POLE2/POLD1/POLE/FEN1/RFC4/PRIM2/POLD3/RFC5/POLA2/DNA2/RPA3/LIG1/RFC2/POLA1/BRCA2* |
| G7 | GO:0006336 | DNA replication-independent nucleosome assembly | 42 | 0.69373514 | 2.201580615 | 0.002604167 | 0.030326036 | tags =52%, list =13%, signal =46% | *CASC5/HJURP/CENPA/ASF1B/OIP5/CENPK/CENPI/CENPU/CENPH/CENPM/CENPO/CENPN/MIS18A/CENPQ/MIS18BP1/ITGB3BP/RBBP7/CENPW/H3F3B/CENPL/CENPP/CABIN1* |
| G7 | GO:0034724 | DNA replication-independent nucleosome organization | 42 | 0.69373514 | 2.201580615 | 0.002604167 | 0.030326036 | tags =52%, list =13%, signal =46% | *CASC5/HJURP/CENPA/ASF1B/OIP5/CENPK/CENPI/CENPU/CENPH/CENPM/CENPO/CENPN/MIS18A/CENPQ/MIS18BP1/ITGB3BP/RBBP7/CENPW/H3F3B/CENPL/CENPP/CABIN1* |
| G7 | GO:0045839 | Negative regulation of mitotic nuclear division | 39 | 0.676840013 | 2.116630794 | 0.002610966 | 0.030326036 | tags =41%, list =14%, signal =35% | *CENPF/TTK/PLK1/NDC80/BUB1B/CCNB1/BUB1/MAD2L1/MAD1L1/GEN1/MTBP/MAD2L2/CHEK1/PCID2/BUB3/DUSP1* |
| G7 | GO:0034508 | Centromere complex assembly | 43 | 0.735988408 | 2.3596482 | 0.002617801 | 0.030326036 | tags =53%, list =12%, signal =47% | *CASC5/HJURP/CENPF/CENPA/CENPE/HELLS/OIP5/CENPK/CENPI/CENPU/CENPH/CENPM/CENPO/CENPN/MIS18A/CENPQ/MIS18BP1/ITGB3BP/RBBP7/CENPW/H3F3B/CENPL/CENPP* |
| G7 | GO:1902099 | Regulation of metaphase/anaphase transition of cell cycle | 43 | 0.753744124 | 2.416574698 | 0.002617801 | 0.030326036 | tags =40%, list =11%, signal =35% | *CENPF/UBE2C/CENPE/TTK/PLK1/ESPL1/NDC80/DLGAP5/BUB1B/CCNB1/BUB1/MAD2L1/CDC6/MAD1L1/GEN1/MAD2L2/PCID2* |
| G7 | GO:0030071 | Regulation of mitotic metaphase/anaphase transition | 43 | 0.753744124 | 2.416574698 | 0.002617801 | 0.030326036 | tags =40%, list =11%, signal =35% | *CENPF/UBE2C/CENPE/TTK/PLK1/ESPL1/NDC80/DLGAP5/BUB1B/CCNB1/BUB1/MAD2L1/CDC6/MAD1L1/GEN1/MAD2L2/PCID2* |
| G7 | GO:0044784 | Metaphase/anaphase transition of cell cycle | 45 | 0.758139906 | 2.463005886 | 0.002624672 | 0.030326036 | tags =33%, list =5%, signal =32% | *CENPF/UBE2C/CENPE/TTK/PLK1/ESPL1/NDC80/DLGAP5/BUB1B/CCNB1/BUB1/MAD2L1/TACC3/CDC6/MAD1L1* |
| G7 | GO:0010965 | Regulation of mitotic sister chromatid separation | 45 | 0.758139906 | 2.463005886 | 0.002624672 | 0.030326036 | tags =33%, list =5%, signal =32% | *CENPF/UBE2C/CENPE/TTK/PLK1/ESPL1/NDC80/DLGAP5/BUB1B/CCNB1/BUB1/MAD2L1/TACC3/CDC6/MAD1L1* |
| G7 | GO:0007091 | Metaphase/anaphase transition of mitotic cell cycle | 45 | 0.758139906 | 2.463005886 | 0.002624672 | 0.030326036 | tags =33%, list =5%, signal =32% | *CENPF/UBE2C/CENPE/TTK/PLK1/ESPL1/NDC80/DLGAP5/BUB1B/CCNB1/BUB1/MAD2L1/TACC3/CDC6/MAD1L1* |
| G7 | GO:0051784 | Negative regulation of nuclear division | 46 | 0.631571635 | 2.055764816 | 0.002645503 | 0.030326036 | tags =43%, list =14%, signal =37% | *FBXO43/CENPF/TTK/PLK1/NDC80/BUB1B/CCNB1/BUB1/MAD2L1/FBXO5/RPS6KA2/MAD1L1/GEN1/MTBP/MAD2L2/CHEK1/PCID2/MSH2/BUB3/DUSP1* |
| G7 | GO:0010389 | Regulation of G2/M transition of mitotic cell cycle | 46 | 0.574629004 | 1.870416629 | 0.002645503 | 0.030326036 | tags =35%, list =14%, signal =30% | *CENPF/CDK1/KIF14/CCNA2/BLM/FHL1/FANCI/CLSPN/TICRR/DBF4B/CDC7/MRE11A/HMGA2/MIIP/RAD51B/TOPBP1* |
| G7 | GO:0031577 | Spindle checkpoint | 35 | 0.762320235 | 2.324367235 | 0.002659574 | 0.030326036 | tags =51%, list =14%, signal =44% | *AURKB/CASC5/CENPF/TTK/PLK1/NDC80/BUB1B/CCNB1/BUB1/MAD2L1/GSG2/MAD1L1/GEN1/MAD2L2/PCID2/CDK5RAP2/BUB3/DUSP1* |
| G7 | GO:0031572 | G2 DNA damage checkpoint | 35 | 0.666202351 | 2.031297144 | 0.002659574 | 0.030326036 | tags =40%, list =14%, signal =34% | *CDK1/CCNA2/PLK1/BLM/FANCI/CLSPN/BRCA1/DTL/MRE11A/CHEK1/HMGA2/CDC14B/TOPBP1/FAM175A* |
| G7 | GO:0051306 | Mitotic sister chromatid separation | 47 | 0.752980187 | 2.467109911 | 0.002680965 | 0.030326036 | tags =32%, list =5%, signal =30% | *CENPF/UBE2C/CENPE/TTK/PLK1/ESPL1/NDC80/DLGAP5/BUB1B/CCNB1/BUB1/MAD2L1/TACC3/CDC6/MAD1L1* |
| G7 | GO:2001251 | Negative regulation of chromosome organization | 59 | 0.693853726 | 2.377321272 | 0.002747253 | 0.030326036 | tags =36%, list =14%, signal =31% | *CENPF/TTK/PLK1/ESPL1/NDC80/BUB1B/CCNB1/BUB1/MAD2L1/PIF1/MAD1L1/RTEL1-TNFRSF6B/GEN1/MAD2L2/PARP1/PCID2/HNRNPA1/H3F3B/BUB3/RTEL1/DUSP1* |
| G7 | GO:0033047 | Regulation of mitotic sister chromatid segregation | 52 | 0.730097639 | 2.439926366 | 0.002747253 | 0.030326036 | tags =29%, list =5%, signal =28% | *CENPF/UBE2C/CENPE/TTK/PLK1/ESPL1/NDC80/DLGAP5/BUB1B/CCNB1/BUB1/MAD2L1/TACC3/CDC6/MAD1L1* |
| G7 | GO:0033045 | Regulation of sister chromatid segregation | 59 | 0.719260748 | 2.464372262 | 0.002747253 | 0.030326036 | tags =32%, list =9%, signal =29% | *CENPF/UBE2C/CENPE/TTK/PLK1/ESPL1/NDC80/DLGAP5/BUB1B/CCNB1/BUB1/CDCA5/MAD2L1/TACC3/CDC6/MAD1L1/AXIN2/GEN1/MAD2L2* |
| G7 | GO:0051304 | Chromosome separation | 62 | 0.722359733 | 2.498722203 | 0.002785515 | 0.030326036 | tags =37%, list =11%, signal =33% | *CENPF/UBE2C/CENPE/TTK/PLK1/ESPL1/NDC80/DLGAP5/BUB1B/TOP2A/CCNB1/BUB1/MAD2L1/TACC3/NCAPD2/CDC6/EME1/MAD1L1/GEN1/MAD2L2/NCAPD3/FANCM/PCID2* |
| G7 | GO:0051983 | Regulation of chromosome segregation | 74 | 0.756584419 | 2.704727097 | 0.002785515 | 0.030326036 | tags =34%, list =6%, signal =32% | *AURKB/NEK2/CENPF/KIF2C/UBE2C/CENPE/TTK/PLK1/MKI67/ESPL1/NDC80/DLGAP5/BUB1B/CCNB1/BUB1/CDCA5/RACGAP1/MAD2L1/TACC3/SPAG5/KNSTRN/CDC6/MAD1L1/ECT2/AXIN2* |
| G7 | GO:1902749 | Regulation of cell cycle G2/M phase transition | 54 | 0.596042545 | 2.002206859 | 0.00280112 | 0.030326036 | tags =24%, list =6%, signal =23% | *CENPF/CDK1/KIF14/CCNA2/PLK1/GTSE1/BLM/FHL1/FANCI/CLSPN/TICRR/DBF4B/CDC7* |
| G7 | GO:0032508 | DNA duplex unwinding | 76 | 0.601328752 | 2.159438467 | 0.00280112 | 0.030326036 | tags =30%, list =14%, signal =26% | *BLM/TOP2A/GINS2/RAD51/PIF1/MCM5/CDC45/MCM2/GINS4/BRIP1/DDX11/MCM4/MCM6/MCM7/MCM3/RTEL1-TNFRSF6B/MRE11A/GINS1/DNA2/PARP1/RECQL4/RTEL1/RAD54B* |
| G7 | GO:0032392 | DNA geometric change | 81 | 0.604300357 | 2.205654097 | 0.002824859 | 0.030326036 | tags =32%, list =14%, signal =28% | *BLM/TOP2A/GINS2/HMGB2/RAD51/PIF1/MCM5/CDC45/MCM2/GINS4/BRIP1/DDX11/MCM4/MCM6/MCM7/MCM3/RTEL1-TNFRSF6B/MRE11A/GINS1/DNA2/PARP1/RECQL4/RTEL1/HMGB3/RAD54B/HMGB1* |
| G7 | GO:1901991 | Negative regulation of mitotic cell cycle phase transition | 139 | 0.466153431 | 1.857452467 | 0.003184713 | 0.030486975 | tags =33%, list =17%, signal =28% | *CENPF/CDK1/TTK/CCNA2/PLK1/GTSE1/NDC80/BLM/BUB1B/FHL1/CCNB1/BUB1/CDC25C/MAD2L1/AURKA/FANCI/CLSPN/TICRR/BCL2/CDK2/MAD1L1/SLFN11/CENPJ/CTDSPL/EZH2/TNKS1BP1/GEN1/CDKN1B/MUC1/MAD2L2/MRE11A/ZFP36L2/HMGA2/PCID2/E2F1/MIIP/BUB3/TOPBP1/CNOT10/DUSP1/KANK2/RFWD3/CTDSP2/ZNF655/TFDP1/ZNF385A* |
| G7 | GO:0007062 | Sister chromatid cohesion | 117 | 0.730890515 | 2.82104092 | 0.003194888 | 0.030486975 | tags =45%, list =13%, signal =40% | *SKA1/AURKB/NUF2/CASC5/CENPF/CDCA8/CENPA/CDC20/KIF2C/CENPE/BIRC5/ERCC6L/PLK1/ESPL1/NDC80/SGOL1/BUB1B/KIF18A/BUB1/CDCA5/MAD2L1/GSG2/CENPK/CENPI/SPC25/ZWINT/CENPU/KIF22/SGOL2/CENPH/INCENP/CENPM/SPC24/CENPO/CENPN/NDE1/MAD1L1/CENPQ/DDX11/DSN1/AXIN2/KNTC1/RANGAP1/RPS27/MRE11A/ITGB3BP/REC8/RAD21/B9D2/CENPL/CENPP/BUB3/ZWILCH* |
| G7 | GO:0000723 | Telomere maintenance | 117 | 0.514290165 | 1.985021793 | 0.003194888 | 0.030486975 | tags =27%, list =13%, signal =24% | *AURKB/NEK2/PRIM1/RAD51/PIF1/RFC3/POLE2/SLX1B/POLD1/POLE/FEN1/RFC4/PRIM2/POLD3/RFC5/RTEL1-TNFRSF6B/TEN1-CDK3/TNKS1BP1/MRE11A/POLA2/DNA2/PARP1/HNRNPA1/RPA3/LIG1/DCLRE1B/RFC2/POLA1/ATR/DCLRE1C/BRCA2/RTEL1* |
| G7 | GO:0006323 | DNA packaging | 133 | 0.434703736 | 1.723559305 | 0.003205128 | 0.030486975 | tags =34%, list =13%, signal =30% | *CASC5/HJURP/CENPA/NCAPG/CDK1/NCAPH/TOP2A/CCNB1/ASF1B/CDCA5/NUSAP1/HELLS/OIP5/CENPK/CENPI/CENPU/HMGB2/NCAPD2/CENPH/CENPM/NCAPG2/CENPO/CENPN/SMC4/H2AFX/MIS18A/MCM2/CENPQ/CHAF1B/MIS18BP1/CHD5/H1FX/NCAPH2/ITGB3BP/NCAPD3/RBBP7/HMGA2/CENPW/TTN/H3F3B/CENPL/CENPP/SMC2/CHAF1A/CABIN1* |
| G7 | GO:0000070 | Mitotic sister chromatid segregation | 126 | 0.7485147 | 2.942454001 | 0.003225806 | 0.030486975 | tags =33%, list =5%, signal =32% | *AURKB/NEK2/CENPF/CDCA8/CENPA/NCAPG/KIF18B/KIF2C/UBE2C/CENPE/KIFC1/NCAPH/TTK/KIF4A/KIF14/PLK1/ESPL1/NDC80/DLGAP5/BUB1B/CCNB1/KIF18A/BUB1/CDCA5/NUSAP1/KIF23/RACGAP1/PSRC1/MAD2L1/GSG2/TACC3/SPAG5/ZWINT/KIF22/NCAPD2/KNSTRN/SMC4/PRC1/CDC6/MAD1L1/ANKRD53/DSN1* |
| G7 | GO:0007088 | Regulation of mitotic nuclear division | 120 | 0.589316161 | 2.284116671 | 0.003236246 | 0.030486975 | tags =34%, list =11%, signal =31% | *FBXO43/NEK2/CENPF/UBE2C/CENPE/TTK/PLK1/MKI67/ESPL1/NDC80/DLGAP5/BUB1B/CCNB1/KIF11/BUB1/CDCA5/NUSAP1/CDC25C/MAD2L1/TACC3/AURKA/ANLN/KIF20B/FBXO5/BORA/PKMYT1/EDN1/CDC6/MAD1L1/IGF2/KNTC1/RCC1/PDGFRB/GEN1/MTBP/MAD2L2/CHEK1/L3MBTL1/CEP85/CEP97/PCID2* |
| G7 | GO:0032200 | Telomere organization | 120 | 0.511966657 | 1.984319545 | 0.003236246 | 0.030486975 | tags =28%, list =13%, signal =24% | *AURKB/NEK2/PRIM1/RAD51/PIF1/RFC3/POLE2/SLX1B/POLD1/POLE/FEN1/RFC4/PRIM2/POLD3/RFC5/RTEL1-TNFRSF6B/TEN1-CDK3/TNKS1BP1/MRE11A/POLA2/DNA2/PARP1/HNRNPA1/RPA3/LIG1/DCLRE1B/RFC2/POLA1/H3F3B/ATR/DCLRE1C/BRCA2/RTEL1* |
| G7 | GO:0033044 | Regulation of chromosome organization | 128 | 0.613241624 | 2.408878836 | 0.003311258 | 0.03079065 | tags =26%, list =13%, signal =22% | *AURKB/NEK2/CENPF/UBE2C/CENPE/TTK/PLK1/ESPL1/NDC80/DLGAP5/BUB1B/CCNB1/BUB1/CDCA5/MAD2L1/TACC3/PIF1/SLX1B/CDC6/MAD1L1/AXIN2/RTEL1-TNFRSF6B/TEN1-CDK3/GEN1/MAD2L2/MRE11A/PARP1/PCID2/HNRNPA1/H3F3B/ATR/BUB3/RTEL1* |
| G7 | GO:1901988 | Negative regulation of cell cycle phase transition | 145 | 0.465500086 | 1.862829359 | 0.003322259 | 0.03079065 | tags =26%, list =12%, signal =23% | *CENPF/CDK1/TTK/CCNA2/PLK1/GTSE1/NDC80/BLM/BUB1B/FHL1/CCNB1/BUB1/CDC25C/MAD2L1/AURKA/FANCI/CLSPN/TICRR/BCL2/CDK2/SUSD2/MAD1L1/SLFN11/CENPJ/CTDSPL/EZH2/TNKS1BP1/GEN1/CDKN1B/MUC1/MAD2L2/MRE11A/ZFP36L2/HMGA2/PCID2/E2F1/MIIP* |
| G7 | GO:0007093 | Mitotic cell cycle checkpoint | 145 | 0.483158891 | 1.93349603 | 0.003322259 | 0.03079065 | tags =28%, list =14%, signal =24% | *CENPF/CDK1/TTK/CCNA2/PLK1/GTSE1/NDC80/BLM/BUB1B/TOP2A/CCNB1/BUB1/CDC25C/MAD2L1/AURKA/FANCI/ZWINT/CLSPN/TICRR/CDK2/EME1/MAD1L1/KNTC1/CENPJ/TNKS1BP1/WNT9A/GEN1/CDKN1B/MUC1/MAD2L2/MRE11A/HMGA2/PCID2/E2F1/MSH2/BUB3/ZWILCH/TOPBP1/CNOT10/SMC1A/DUSP1* |
| G7 | GO:0000077 | DNA damage checkpoint | 143 | 0.40595828 | 1.617084554 | 0.003322259 | 0.03079065 | tags =23%, list =14%, signal =20% | *CDK1/CCNA2/PLK1/GTSE1/BLM/CCNB1/CDC25C/AURKA/FANCI/CLSPN/BRCA1/CDK2/H2AFX/EME1/WDR76/BRIP1/DTL/CENPJ/TNKS1BP1/CDKN1B/MUC1/MRE11A/CHEK1/HMGA2/RHNO1/E2F1/MSH2/ATR/CDC14B/TOPBP1/CNOT10/USP28/FAM175A* |
| G7 | GO:0031570 | DNA integrity checkpoint | 152 | 0.448819588 | 1.803556212 | 0.003344482 | 0.030830257 | tags =26%, list =14%, signal =22% | *CDK1/CCNA2/PLK1/GTSE1/BLM/TOP2A/CCNB1/CDC25C/AURKA/FANCI/CDT1/CLSPN/TICRR/BRCA1/CDC45/CDK2/H2AFX/CDC6/EME1/WDR76/BRIP1/DTL/CENPJ/TNKS1BP1/CDKN1B/MUC1/MRE11A/CHEK1/DNA2/HMGA2/RHNO1/E2F1/MSH2/ATR/CDC14B/TOPBP1/CNOT10/USP28/FAM175A* |
| G7 | GO:0000086 | G2/M transition of mitotic cell cycle | 174 | 0.529289596 | 2.15798025 | 0.003533569 | 0.032057184 | tags =29%, list =12%, signal =26% | *NEK2/CENPF/CDK1/CIT/KIF14/PLK4/CCNA2/PLK1/BLM/FHL1/CCNB1/CCNB2/TPX2/CDC25C/MELK/HMMR/CDC25B/AURKA/FANCI/FOXM1/WEE1/CDC25A/CLSPN/TICRR/BORA/PKMYT1/DBF4B/CDK2/CNTRL/NDE1/HAUS5/CDC7/HAUS8/MASTL/HAUS4/SKP2/CEP72/CENPJ/PCNT/AJUBA/TUBB4B/MRE11A/CHEK1/KDM8/HMGA2/BACH1/CEP76/MIIP/CDK5RAP2/CEP57/CEP192* |
| G7 | GO:0044839 | Cell cycle G2/M phase transition | 183 | 0.529373483 | 2.166601983 | 0.003597122 | 0.03234899 | tags =28%, list =12%, signal =25% | *NEK2/CENPF/CDK1/CIT/KIF14/PLK4/CCNA2/PLK1/GTSE1/BLM/FHL1/CCNB1/CCNB2/TPX2/CDC25C/MELK/HMMR/CDC25B/AURKA/FANCI/FOXM1/WEE1/CDC25A/CLSPN/TICRR/BORA/PKMYT1/DBF4B/CDK2/CNTRL/NDE1/HAUS5/CDC7/HAUS8/MASTL/HAUS4/SKP2/CEP72/CENPJ/PCNT/AJUBA/TUBB4B/MRE11A/CHEK1/KDM8/HMGA2/BACH1/CEP76/MIIP/CDK5RAP2/CEP57/CEP192* |
| G7 | GO:0010948 | Negative regulation of cell cycle process | 196 | 0.473644932 | 1.95388209 | 0.003610108 | 0.032409213 | tags =26%, list =12%, signal =23% | *AURKB/FBXO43/CENPF/CDK1/TTK/CCNA2/PLK1/GTSE1/ESPL1/NDC80/BLM/BUB1B/FHL1/CCNB1/BUB1/CDC25C/MAD2L1/AURKA/FANCI/CCNF/FBXO5/CLSPN/TICRR/BRCA1/E2F8/BCL2/CDK2/SUSD2/RPS6KA2/MAD1L1/SLFN11/CENPJ/CTDSPL/EZH2/TNKS1BP1/GEN1/MTBP/CDKN1B/MUC1/TFAP4/MAD2L2/MRE11A/ZFP36L2/CHEK1/HMGA2/PCID2/E2F1/MSH2/MIIP/CDK5RAP2* |
| G7 | GO:0090068 | Positive regulation of cell cycle process | 198 | 0.41421128 | 1.708729536 | 0.003703704 | 0.033019352 | tags =22%, list =9%, signal =20% | *AURKB/FAM83D/CDK1/UBE2C/CIT/KIF14/PLK4/GTSE1/ESPL1/NDC80/DLGAP5/CCNB1/RAB11FIP4/CDCA5/NUSAP1/KIF23/CDC25C/RACGAP1/CDC25B/MAD2L1/AURKA/KIF20B/BRCA1/E2F8/CDC45/DBF4B/CDK2/EDN1/CDC6/IGF2/ECT2/SVIL/CDC7/SOX15/MSX1/CENPJ/ZNF16/TNKS1BP1/PDGFRB/GEN1/MTBP/CDKN1B/MUC1* |
| G7 | GO:0045930 | Negative regulation of mitotic cell cycle | 198 | 0.449645693 | 1.854905729 | 0.003703704 | 0.033019352 | tags =27%, list =14%, signal =23% | *CENPF/CDK1/TTK/CCNA2/PLK1/GTSE1/NDC80/BLM/BUB1B/TOP2A/FHL1/CCNB1/BUB1/CDC25C/MAD2L1/AURKA/FANCI/ZWINT/CLSPN/TICRR/BCL2/CDK2/EME1/MAD1L1/KNTC1/FOXC1/SLFN11/CENPJ/CTDSPL/EZH2/TNKS1BP1/WNT9A/GEN1/MTBP/CDKN1B/MUC1/MAD2L2/MRE11A/ZFP36L2/CHEK1/SMAD3/HMGA2/PCID2/E2F1/MSH2/MIIP/BUB3/ZWILCH/HECA/TOPBP1/CNOT10/SMC1A/DUSP1* |
| G7 | GO:0000819 | Sister chromatid segregation | 200 | 0.729454237 | 3.010425362 | 0.003731343 | 0.033208311 | tags =42%, list =13%, signal =37% | *SKA1/AURKB/NUF2/CASC5/NEK2/CENPF/CDCA8/CENPA/NCAPG/KIF18B/CDC20/KIF2C/UBE2C/CENPE/KIFC1/NCAPH/TTK/KIF4A/BIRC5/KIF14/ERCC6L/PLK1/ESPL1/NDC80/DLGAP5/SGOL1/BUB1B/TOP2A/CCNB1/KIF18A/BUB1/CDCA5/NUSAP1/KIF23/RACGAP1/PSRC1/MAD2L1/GSG2/TACC3/SPAG5/CENPK/CENPI/SPC25/ZWINT/CENPU/KIF22/SGOL2/NCAPD2/CENPH/INCENP/CENPM/SPC24/CENPO/KNSTRN/CENPN/SMC4/PRC1/CDC6/NDE1/MAD1L1/CENPQ/ANKRD53/DDX11/DSN1/AXIN2/KNTC1/GEN1/MAD2L2/RANGAP1/RPS27/MRE11A/ITGB3BP/REC8/NCAPD3/RAD21/PCID2/TTN/B9D2/CENPL/CENPP/CEP57/SMC2/BUB3/ZWILCH* |
| G7 | GO:0044843 | Cell cycle G1/S phase transition | 220 | 0.470207331 | 1.949824044 | 0.003816794 | 0.033677978 | tags =26%, list =9%, signal =24% | *IQGAP3/FAM83D/CDK1/KIF14/GTSE1/FHL1/CCNB1/CDCA5/CDKN2C/CDC25C/PRIM1/MCM10/AURKA/CDT1/FBXO5/CDKN3/CDC25A/MCM5/ORC6/SPDYA/PKMYT1/RRM2/POLE2/CDC45/ORC1/BCL2/PDPN/CDK2/CDC6/MCM2/CCNE2/CDKN2D/SUSD2/POLE/MCM8/MCM4/CDC7/MCM6/RCC1/MCM7/PRIM2/MCM3/SKP2/SLFN11/PSME1/ID4/TEN1-CDK3/TYMS/CENPJ/CTDSPL/EIF4EBP1/EZH2/DBF4/TNKS1BP1/MTBP/CDKN1B/MUC1/POLA2* |
| G7 | GO:0000075 | Cell cycle checkpoint | 210 | 0.514016755 | 2.125108743 | 0.003846154 | 0.033821213 | tags =30%, list =14%, signal =26% | *AURKB/CASC5/CENPF/CDK1/TTK/CCNA2/PLK1/GTSE1/NDC80/BLM/BUB1B/TOP2A/CCNB1/BUB1/CDC25C/MAD2L1/GSG2/AURKA/FANCI/CDT1/ZWINT/CLSPN/TICRR/BRCA1/CDC45/CDK2/H2AFX/CDC6/CCNE2/EME1/WDR76/BRIP1/MAD1L1/FANCG/KNTC1/DTL/CENPJ/TNKS1BP1/WNT9A/GEN1/CDKN1B/MUC1/MAD2L2/MRE11A/CHEK1/DNA2/HMGA2/RHNO1/PCID2/E2F1/DCLRE1B/MSH2/CDK5RAP2/ATR/CDC14B/BUB3/ZWILCH/TOPBP1/CNOT10/SMC1A/USP28/DUSP1/FAM175A* |
| G7 | GO:0000082 | G1/S transition of mitotic cell cycle | 213 | 0.461650304 | 1.907556751 | 0.003861004 | 0.033893957 | tags =26%, list =9%, signal =24% | *IQGAP3/CDK1/KIF14/GTSE1/FHL1/CCNB1/CDCA5/CDKN2C/CDC25C/PRIM1/MCM10/AURKA/CDT1/FBXO5/CDKN3/CDC25A/MCM5/ORC6/SPDYA/PKMYT1/RRM2/POLE2/CDC45/ORC1/BCL2/PDPN/CDK2/CDC6/MCM2/CCNE2/CDKN2D/POLE/MCM8/MCM4/CDC7/MCM6/RCC1/MCM7/PRIM2/MCM3/SKP2/SLFN11/PSME1/ID4/TEN1-CDK3/TYMS/CENPJ/CTDSPL/EIF4EBP1/EZH2/DBF4/TNKS1BP1/MTBP/CDKN1B/MUC1/POLA2* |
| G7 | GO:0071103 | DNA conformation change | 212 | 0.456863646 | 1.887936471 | 0.00390625 | 0.034232834 | tags =33%, list =15%, signal =28% | *CASC5/HJURP/CENPA/NCAPG/CDK1/NCAPH/BLM/TOP2A/CCNB1/ASF1B/CDCA5/NUSAP1/HELLS/GINS2/OIP5/CENPK/CENPI/CENPU/HMGB2/RAD51/PIF1/NCAPD2/CENPH/MCM5/CENPM/NCAPG2/CENPO/CDC45/CENPN/SMC4/H2AFX/MIS18A/MCM2/GINS4/BRIP1/CENPQ/DDX11/MCM4/MCM6/MCM7/CHAF1B/MIS18BP1/MCM3/RTEL1-TNFRSF6B/CHD5/H1FX/NCAPH2/MRE11A/ITGB3BP/GINS1/NCAPD3/DNA2/RBBP7/HMGA2/PARP1/CENPW/TTN/H3F3B/CENPL/CENPP/SMC2/RECQL4/CHAF1A/CABIN1/RTEL1/HMGB3/RAD54B/HMGB1/ANP32B/NASP* |
| G7 | GO:0098813 | Nuclear chromosome segregation | 240 | 0.704106186 | 2.936708613 | 0.004016064 | 0.034898447 | tags =41%, list =13%, signal =36% | *SKA1/AURKB/NUF2/CASC5/NEK2/CENPF/FAM83D/CDCA8/CENPA/NCAPG/KIF18B/CDC20/KIF2C/UBE2C/CENPE/KIFC1/NCAPH/TTK/KIF4A/BIRC5/KIF14/ERCC6L/PLK1/ESPL1/NDC80/DLGAP5/SGOL1/BUB1B/TOP2A/CCNB1/KIF18A/BUB1/CDCA5/NUSAP1/KIF23/RACGAP1/PSRC1/MAD2L1/GSG2/TACC3/SPAG5/CENPK/CENPI/SPC25/ZWINT/CENPU/KIF22/FANCD2/SGOL2/NCAPD2/CENPH/SYCE2/INCENP/CENPM/SPC24/CENPO/KNSTRN/CENPN/SMC4/PRC1/CDC6/TRIP13/NDE1/EME1/AGO4/MAD1L1/DMC1/CENPQ/ECT2/ANKRD53/DDX11/DSN1/AXIN2/KNTC1/PTTG1/SUN1/GEN1/MAD2L2/RANGAP1/FMN2/RPS27/MRE11A/ITGB3BP/REC8/NCAPD3/RAD21/MEI1/FANCM/PCID2/TTN/SYCE1L/B9D2/CENPL/CENPP/CEP57/SMC2/BUB3/ZWILCH* |
| G7 | GO:0010639 | Negative regulation of organelle organization | 234 | 0.369793434 | 1.532305407 | 0.004016064 | 0.034898447 | tags =20%, list =13%, signal =18% | *FBXO43/NEK2/CENPF/TTK/RLTPR/PLK1/ESPL1/NDC80/BUB1B/CCNB1/BUB1/MAD2L1/CCNF/FBXO5/STMN1/PIF1/MYOC/BRCA1/SPTBN5/CKAP2/ARHGAP6/LRRK2/TMSB15A/RPS6KA2/MAD1L1/PPARGC1A/STMN2/CAPG/RTEL1-TNFRSF6B/SWAP70/GEN1/MTBP/MAD2L2/CHEK1/SPTBN4/PARP1/CEP97/PCID2/HNRNPA1/MSH2/CDK5RAP2/H3F3B/LMNA/BUB3/ARHGAP28/RTEL1/SLC35F6* |
| G7 | GO:0045787 | Positive regulation of cell cycle | 267 | 0.392576813 | 1.654047101 | 0.004149378 | 0.035815314 | tags =19%, list =9%, signal =18% | *AURKB/FAM83D/CDK1/UBE2C/CIT/KIF14/PLK4/GTSE1/ESPL1/NDC80/DLGAP5/CCNB1/CKS2/RAB11FIP4/CDCA5/NUSAP1/KIF23/CDC25C/RACGAP1/CDC25B/PSRC1/MAD2L1/AURKA/KIF20B/FLT3LG/SPDYA/BRCA1/E2F8/CDC45/DBF4B/CDK2/EDN1/CDC6/IGF2/ECT2/CKS1B/SVIL/CDC7/SOX15/MSX1/CENPJ/EIF4EBP1/GDPD5/ZNF16/TNKS1BP1/PDGFRB/GEN1/MTBP/CDKN1B/MUC1/TFAP4* |
| G7 | GO:1901990 | Regulation of mitotic cell cycle phase transition | 275 | 0.434349189 | 1.830541723 | 0.004291845 | 0.036921335 | tags =18%, list =9%, signal =17% | *CENPF/CDC20/CDK1/UBE2C/CENPE/TTK/KIF14/CCNA2/PLK1/GTSE1/ESPL1/NDC80/DLGAP5/BLM/BUB1B/FHL1/CCNB1/BUB1/CDCA5/CDC25C/MAD2L1/PSMB9/AURKA/ANLN/FANCI/FBXO5/CLSPN/TICRR/CDC45/DBF4B/BCL2/PDPN/CDK2/CDC6/MAD1L1/CDC7/KNTC1/SLFN11/PSME1/CENPJ/CTDSPL/EZH2/TNKS1BP1/GEN1/MTBP/CDKN1B/MUC1/MAD2L2/MRE11A/ZFP36L2* |
| G7 | GO:1901987 | Regulation of cell cycle phase transition | 288 | 0.443355315 | 1.883198329 | 0.004329004 | 0.03701726 | tags =18%, list =9%, signal =17% | *CENPF/FAM83D/CDC20/CDK1/UBE2C/CENPE/TTK/KIF14/CCNA2/PLK1/GTSE1/ESPL1/NDC80/DLGAP5/BLM/BUB1B/FHL1/CCNB1/BUB1/CDCA5/CDC25C/MAD2L1/PSMB9/AURKA/ANLN/FANCI/FBXO5/CLSPN/TICRR/CDC45/DBF4B/BCL2/PDPN/CDK2/CDC6/SUSD2/MAD1L1/CDC7/KNTC1/SLFN11/PSME1/CENPJ/CTDSPL/ZNF16/EZH2/TNKS1BP1/GEN1/MTBP/CDKN1B/MUC1/MAD2L2/MRE11A/ZFP36L2* |
| G7 | GO:0006268 | DNA unwinding involved in DNA replication | 10 | 0.80535501 | 1.827711428 | 0.004357298 | 0.03701726 | tags =60%, list =6%, signal =56% | *TOP2A/RAD51/MCM2/MCM4/MCM6/MCM7* |
| G7 | GO:0051988 | Regulation of attachment of spindle microtubules to kinetochore | 11 | 0.882719309 | 2.028302597 | 0.004464286 | 0.037712237 | tags =55%, list =5%, signal =52% | *NEK2/CCNB1/RACGAP1/SPAG5/KNSTRN/ECT2* |
| G7 | GO:0000076 | DNA replication checkpoint | 15 | 0.711607982 | 1.798224205 | 0.004587156 | 0.037949001 | tags =67%, list =23%, signal =52% | *CDT1/CLSPN/TICRR/CDC45/CDC6/DNA2/TOPBP1/TIPIN/ANKRD32/RAD9B* |
| G7 | GO:0007095 | Mitotic G2 DNA damage checkpoint | 16 | 0.709699445 | 1.834112322 | 0.004640371 | 0.037949001 | tags =44%, list =14%, signal =38% | *CDK1/CCNA2/BLM/FANCI/MRE11A/HMGA2/TOPBP1* |
| G7 | GO:0090231 | Regulation of spindle checkpoint | 16 | 0.751634618 | 1.942487519 | 0.004640371 | 0.037949001 | tags =50%, list =14%, signal =43% | *NDC80/CCNB1/MAD2L1/GSG2/GEN1/PCID2/CDK5RAP2/DUSP1* |
| G7 | GO:0090266 | Regulation of mitotic cell cycle spindle assembly checkpoint | 13 | 0.744366347 | 1.805228849 | 0.004640371 | 0.037949001 | tags =46%, list =14%, signal =40% | *NDC80/CCNB1/MAD2L1/GEN1/PCID2/DUSP1* |
| G7 | GO:1903504 | Regulation of mitotic spindle checkpoint | 13 | 0.744366347 | 1.805228849 | 0.004640371 | 0.037949001 | tags =46%, list =14%, signal =40% | *NDC80/CCNB1/MAD2L1/GEN1/PCID2/DUSP1* |
| G7 | GO:0051382 | Kinetochore assembly | 14 | 0.778047438 | 1.916594153 | 0.004683841 | 0.037949001 | tags =29%, list =2%, signal =28% | *CENPF/CENPA/CENPE/CENPH* |
| G7 | GO:0007076 | Mitotic chromosome condensation | 14 | 0.812798499 | 2.002197778 | 0.004683841 | 0.037949001 | tags =64%, list =13%, signal =56% | *NCAPG/NCAPH/CDCA5/NUSAP1/NCAPD2/SMC4/NCAPD3/TTN/SMC2* |
| G7 | GO:0051984 | Positive regulation of chromosome segregation | 19 | 0.678901838 | 1.815320628 | 0.004705882 | 0.037949001 | tags =21%, list =4%, signal =20% | *ESPL1/DLGAP5/CCNB1/CDC6* |
| G7 | GO:0044818 | Mitotic G2/M transition checkpoint | 21 | 0.711294737 | 1.91816906 | 0.004889976 | 0.03838876 | tags =38%, list =10%, signal =34% | *CDK1/CCNA2/BLM/FANCI/CLSPN/TICRR/MRE11A/HMGA2* |
| G7 | GO:0045786 | Negative regulation of cell cycle | 400 | 0.347646916 | 1.527780259 | 0.004975124 | 0.038667897 | tags =20%, list =14%, signal =18% | *AURKB/FBXO43/CENPF/CDK1/TTK/CCNA2/PLK1/GTSE1/ESPL1/NDC80/BLM/BUB1B/TOP2A/FHL1/CCNB1/BUB1/CDKN2C/IRF6/CDC25C/MAD2L1/AURKA/FANCI/FOXM1/CCNF/KIF20B/FBXO5/ZWINT/CDKN3/CLSPN/TICRR/BRCA1/BARD1/E2F8/BCL2/CDK2/CDKN2D/EME1/SUSD2/RPS6KA2/MAD1L1/GMNN/KNTC1/PPP2R3B/FOXC1/C11orf82/SLFN11/CENPJ/BIN1/CTDSPL/EZH2/TNKS1BP1/WNT9A/GEN1/MTBP/CDKN1B/MUC1/TFAP4/MAD2L2/MRE11A/ZFP36L2/CHEK1/SMAD3/HMGA2/PCID2/IL12B/CDKN1C/E2F1/MSH2/MIIP/KAT2B/CDK5RAP2/IRF1/BUB3/ZWILCH/RNF112/SIPA1/DHCR24/HECA/TOPBP1/CNOT10/SMC1A* |
| G7 | GO:1902750 | Negative regulation of cell cycle G2/M phase transition | 26 | 0.710707451 | 2.024862589 | 0.005025126 | 0.038706237 | tags =42%, list =14%, signal =37% | *CDK1/CCNA2/BLM/FHL1/FANCI/CLSPN/TICRR/MRE11A/HMGA2/MIIP/TOPBP1* |
| G7 | GO:0010972 | Negative regulation of G2/M transition of mitotic cell cycle | 24 | 0.723224902 | 2.022040619 | 0.005025126 | 0.038706237 | tags =46%, list =14%, signal =40% | *CDK1/CCNA2/BLM/FHL1/FANCI/CLSPN/TICRR/MRE11A/HMGA2/MIIP/TOPBP1* |
| G7 | GO:0000083 | Regulation of transcription involved in G1/S transition of mitotic cell cycle | 24 | 0.731054405 | 2.043930868 | 0.005025126 | 0.038706237 | tags =50%, list =14%, signal =43% | *CDK1/CDT1/FBXO5/RRM2/CDC45/ORC1/CDC6/TYMS/BACH1/E2F1/POLA1/DHFR* |
| G7 | GO:1901976 | Regulation of cell cycle checkpoint | 32 | 0.597884832 | 1.800810216 | 0.005076142 | 0.038932682 | tags =59%, list =29%, signal =42% | *NDC80/CCNB1/MAD2L1/GSG2/WDR76/GEN1/PCID2/CDK5RAP2/DUSP1/RFWD3/FBXO4/XRCC3/TPR/RPA2/DYNC1LI1/DDX39B/CCAR2/NDRG1/CRY1* |
| G7 | GO:0007346 | Regulation of mitotic cell cycle | 424 | 0.428123454 | 1.879930065 | 0.005263158 | 0.039836829 | tags =23%, list =14%, signal =21% | *FBXO43/NEK2/CENPF/CDC20/CDK1/UBE2C/CENPE/TTK/KIF14/CCNA2/PLK1/GTSE1/MKI67/ESPL1/NDC80/DLGAP5/BLM/BUB1B/TOP2A/FHL1/CCNB1/KIF11/CKS2/BUB1/CDCA5/NUSAP1/TPX2/CDC25C/CDC25B/PSRC1/MAD2L1/PSMB9/TACC3/AURKA/ANLN/FANCI/KIF20B/FBXO5/ZWINT/CLSPN/TICRR/BORA/PKMYT1/CDC45/DBF4B/BCL2/PDPN/CDK2/EDN1/CDC6/EME1/MAD1L1/IGF2/ANKRD53/CKS1B/CDC7/KNTC1/RCC1/FOXC1/SLFN11/PSME1/PIM3/CENPJ/CTDSPL/EIF4EBP1/EZH2/TNKS1BP1/PDGFRB/WNT9A/GEN1/MTBP/CDKN1B/MUC1/MAD2L2/PTCH1/MRE11A/ZFP36L2/CHEK1/SMAD3/HMGA2/L3MBTL1/CEP85/CEP97/PCID2/CDKN1C/RPA3/E2F1/MSH2/MIIP/PSMB8/BRCA2/BUB3/ZWILCH/HECA/RAD51B/ASNS/TOPBP1/CNOT10/SMC1A* |
| G7 | GO:0044772 | Mitotic cell cycle phase transition | 423 | 0.507176997 | 2.224621709 | 0.005291005 | 0.039860454 | tags =27%, list =12%, signal =25% | *IQGAP3/NEK2/CENPF/CDK1/UBE2C/CENPE/CIT/TTK/KIF14/PLK4/CCNA2/PLK1/GTSE1/ESPL1/NDC80/DLGAP5/BLM/BUB1B/FHL1/CCNB1/CKS2/BUB1/CCNB2/CDCA5/CDKN2C/TPX2/CDC25C/MELK/HMMR/CDC25B/MAD2L1/PRIM1/MCM10/TACC3/AURKA/ANLN/FANCI/FOXM1/CDT1/WEE1/FBXO5/CDKN3/CDC25A/MCM5/CLSPN/ORC6/TICRR/BORA/SPDYA/PKMYT1/RRM2/POLE2/CDC45/DBF4B/ORC1/BCL2/PDPN/CDK2/CNTRL/CDC6/MCM2/CCNE2/CDKN2D/NDE1/POLE/MCM8/MAD1L1/HAUS5/MCM4/CDC7/MCM6/KNTC1/RCC1/MCM7/HAUS8/PRIM2/MASTL/MCM3/HAUS4/SKP2/CEP72/SLFN11/PSME1/ID4/TEN1-CDK3/TYMS/CENPJ/PCNT/AJUBA/CTDSPL/EIF4EBP1/EZH2/DBF4/TNKS1BP1/GEN1/UBE2S/MTBP/CDKN1B/MUC1/MAD2L2/TUBB4B/MRE11A/POLA2/ZFP36L2/CHEK1/KDM8/HMGA2/PCID2/BACH1/RPA3/E2F1/CEP76/MIIP/CDK5RAP2/POLA1* |
| G7 | GO:0010833 | Telomere maintenance via telomere lengthening | 57 | 0.484532314 | 1.643221056 | 0.005555556 | 0.04142949 | tags =21%, list =13%, signal =18% | *AURKB/NEK2/RAD51/PIF1/RTEL1-TNFRSF6B/TEN1-CDK3/TNKS1BP1/MRE11A/PARP1/HNRNPA1/ATR/RTEL1* |
| G7 | GO:0010564 | Regulation of cell cycle process | 489 | 0.440760364 | 1.961888743 | 0.005747126 | 0.042611428 | tags =22%, list =12%, signal =20% | *AURKB/FBXO43/NEK2/CENPF/FAM83D/CDC20/CDK1/UBE2C/CENPE/CIT/TTK/KIF14/PLK4/CCNA2/PLK1/GTSE1/MKI67/ESPL1/NDC80/DLGAP5/BLM/BUB1B/FHL1/CCNB1/KIF11/RAB11FIP4/BUB1/CDCA5/NUSAP1/TPX2/KIF23/CDC25C/RACGAP1/CDC25B/PSRC1/MAD2L1/GSG2/PSMB9/TACC3/SPAG5/AURKA/ANLN/FANCI/FOXM1/CDT1/CCNF/KIF20B/FBXO5/CLSPN/TICRR/BORA/BRCA1/PKMYT1/E2F8/CDC45/KNSTRN/DBF4B/BCL2/PDPN/CDK2/EDN1/CDC6/SUSD2/WDR76/RPS6KA2/MAD1L1/STIL/IGF2/ECT2/ANKRD53/SVIL/CDC7/AXIN2/KNTC1/RCC1/SOX15/SLFN11/PSME1/MSX1/CENPJ/BIN1/CTDSPL/ZNF16/EZH2/TNKS1BP1/PDGFRB/GEN1/MTBP/CDKN1B/MUC1/TFAP4/MAD2L2/MRE11A/ZFP36L2/CHEK1/HMGA2/L3MBTL1/RHNO1/CEP85/CEP97/PCID2/E2F1/CEP76/MSH2/MIIP/CDK5RAP2* |
| G7 | GO:0044774 | Mitotic DNA integrity checkpoint | 98 | 0.415153104 | 1.556556028 | 0.005882353 | 0.043240749 | tags =21%, list =12%, signal =19% | *CDK1/CCNA2/GTSE1/BLM/TOP2A/CCNB1/CDC25C/AURKA/FANCI/CLSPN/TICRR/CDK2/EME1/CENPJ/TNKS1BP1/CDKN1B/MUC1/MRE11A/HMGA2/E2F1/MSH2* |
| G7 | GO:0045931 | Positive regulation of mitotic cell cycle | 100 | 0.39006384 | 1.47008318 | 0.005934718 | 0.043501568 | tags =22%, list =9%, signal =20% | *CDK1/UBE2C/ESPL1/NDC80/DLGAP5/CCNB1/CDCA5/NUSAP1/CDC25B/MAD2L1/AURKA/KIF20B/CDC45/DBF4B/EDN1/CDC6/IGF2/CDC7/EIF4EBP1/PDGFRB/GEN1/MTBP* |
| G8 | GO:0051301 | Cell division | 495 | 0.554352361 | 2.475609689 | 0.005813953 | 0.042799003 | tags =25%, list =9%, signal =23% | *SKA1/FGF9/AURKB/NUF2/CASC5/ASPM/NEK2/CENPF/FAM83D/CDCA8/CENPA/NCAPG/KIF18B/CDC20/KIF2C/CDK1/CDCA2/UBE2C/CENPE/CIT/KIFC1/NCAPH/KIF4A/BIRC5/KIF14/ERCC6L/CCNA2/PLK1/CDCA3/ESPL1/NDC80/BLM/VANGL2/SGOL1/BUB1B/TOP2A/CCNB1/KIF11/CKS2/RAB11FIP4/BUB1/CCNB2/CDCA5/NUSAP1/TPX2/KIF23/CDC25C/KIT/RACGAP1/SKA3/KIF20A/CDC25B/PSRC1/MAD2L1/HELLS/CEP55/SPAG5/AURKA/OIP5/ANLN/PARD3B/FIGF/SFRP2/CCNF/WEE1/KIF20B/FBXO5/SPC25/ZWINT/FAM64A/STMN1/SGOL2/NCAPD2/CDC25A/SYCE2/INCENP/BORA/SPC24/E2F8/NCAPG2/CKAP2/KNSTRN/SMC4/PDGFD/CDK2/MIS18A/PRC1/CNTRL/CDC6/CCNE2/NDE1/VRK1/HTR2B/SUSD2/TIMELESS/MAD1L1/IGF2/ECT2/HAUS5/ANKRD53/CKS1B/DSN1/SVIL/CDC7/KNTC1/PTTG1/RCC1/HAUS8/MASTL/MIS18BP1/HAUS4/TEN1-CDK3/CENPJ/SOX5/SAC3D1/ZNF16/DLL1/REEP4/UBE2S/MAD2L2/PTCH1/FMN2/ITGB3BP/ZFP36L2* |
| G9 | GO:1904667 | Negative regulation of ubiquitin protein ligase activity | 73 | 0.60253145 | 2.155047965 | 0.002754821 | 0.030326036 | tags =14%, list =4%, signal =13% | *FBXO43/CDC20/CDK1/UBE2C/BUB1B/CCNB1/MAD2L1/PSMB9/FBXO5/CDK2* |
| G9 | GO:0051437 | Positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition | 74 | 0.59421888 | 2.124283642 | 0.002785515 | 0.030326036 | tags =12%, list =2%, signal =12% | *CDC20/CDK1/UBE2C/PLK1/BUB1B/CCNB1/MAD2L1/PSMB9/FBXO5* |
| G9 | GO:0031145 | Anaphase-promoting complex-dependent catabolic process | 76 | 0.62448382 | 2.242590894 | 0.00280112 | 0.030326036 | tags =18%, list =9%, signal =17% | *AURKB/CDC20/CDK1/UBE2C/PLK1/BUB1B/CCNB1/MAD2L1/PSMB9/AURKA/PTTG1/SKP2/PSME1/UBE2S* |
| G9 | GO:0051436 | Negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle | 71 | 0.618111873 | 2.179833505 | 0.00280112 | 0.030326036 | tags =14%, list =4%, signal =14% | *FBXO43/CDC20/CDK1/UBE2C/BUB1B/CCNB1/MAD2L1/PSMB9/FBXO5/CDK2* |
| G9 | GO:0051439 | Regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle | 72 | 0.640913608 | 2.269339352 | 0.002816901 | 0.030326036 | tags =15%, list =4%, signal =15% | *FBXO43/CDC20/CDK1/UBE2C/PLK1/BUB1B/CCNB1/MAD2L1/PSMB9/FBXO5/CDK2* |
| G9 | GO:1904668 | Positive regulation of ubiquitin protein ligase activity | 77 | 0.564884069 | 2.033552098 | 0.002824859 | 0.030326036 | tags =12%, list =2%, signal =11% | *CDC20/CDK1/UBE2C/PLK1/BUB1B/CCNB1/MAD2L1/PSMB9/FBXO5* |
| G9 | GO:1904666 | Regulation of ubiquitin protein ligase activity | 81 | 0.599468479 | 2.18801808 | 0.002824859 | 0.030326036 | tags =21%, list =13%, signal =18% | *FBXO43/CDC20/CDK1/UBE2C/PLK1/BUB1B/CCNB1/MAD2L1/PSMB9/FBXO5/CDK2/PSME1/UBE2S/MAD2L2/PSMB8/CDC14B/BUB3* |
| G9 | GO:0051443 | Positive regulation of ubiquitin-protein transferase activity | 94 | 0.510688453 | 1.914151402 | 0.002849003 | 0.030380747 | tags =10%, list =2%, signal =9% | *CDC20/CDK1/UBE2C/PLK1/BUB1B/CCNB1/MAD2L1/PSMB9/FBXO5* |
| G9 | GO:0051444 | Negative regulation of ubiquitin-protein transferase activity | 79 | 0.560090432 | 2.021114268 | 0.00286533 | 0.030380747 | tags =13%, list =4%, signal =12% | *FBXO43/CDC20/CDK1/UBE2C/BUB1B/CCNB1/MAD2L1/PSMB9/FBXO5/CDK2* |
| G9 | GO:2000058 | Regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process | 93 | 0.502346771 | 1.883849513 | 0.00286533 | 0.030380747 | tags =10%, list =2%, signal =10% | *CDC20/CDK1/UBE2C/PLK1/BUB1B/CCNB1/MAD2L1/PSMB9/FBXO5* |
| G9 | GO:2000060 | Positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process | 86 | 0.518929635 | 1.910615772 | 0.002985075 | 0.030486975 | tags =10%, list =2%, signal =10% | *CDC20/CDK1/UBE2C/PLK1/BUB1B/CCNB1/MAD2L1/PSMB9/FBXO5* |
| G9 | GO:0051438 | Regulation of ubiquitin-protein transferase activity | 109 | 0.508440822 | 1.928380348 | 0.003164557 | 0.030486975 | tags =17%, list =13%, signal =14% | *FBXO43/CDC20/CDK1/UBE2C/PLK1/BUB1B/CCNB1/MAD2L1/PSMB9/FBXO5/ZYG11A/CDK2/PSME1/UBE2S/MAD2L2/PSMB8/CDC14B/BUB3* |
| G9 | GO:0000184 | Nuclear-transcribed mrna catabolic process, nonsense-mediated decay | 118 | 0.530934598 | 2.050249126 | 0.003205128 | 0.030486975 | tags =63%, list =32%, signal =43% | *RPL37/RPL9/RPL38/RPL31/RPS23/RPS21/RPS27/RPL37A/RPL10A/RPS17L/RPS16/RPS29/RPS25/RPL10/RPL39/RPS13/RPS8/RPS7/MAGOH/RPL12/RPS9/RPS3/RPL7A/RPL14/RPL30/RPL3/RPL36/RPLP0/RPL15/RPS18/RPS6/RPS14/RPL11/RPL32/RPS4X/RPS5/RPL36A/RPL4/RPL18/RPLP2/RPL27/RPS27A/RPL24/RPL27A/DCP2/RPSA/RPS3A/RPL26/RPL19/RPS12/RPS15A/RPL13A/RPS11/RPL22/RPL35A/RPL8/PNRC2/RPL18A/RPL29/RPS24/RPL5/RPL13/RPL17/RPL23/RPL6/RPL23A/RPL28/RPL34/RPL35/RPL7/EIF4A3/RPL41/UBA52/EXOSC10* |
| G9 | GO:0000956 | Nuclear-transcribed mrna catabolic process | 193 | 0.439025263 | 1.812694387 | 0.003508772 | 0.031944406 | tags =53%, list =32%, signal =37% | *ZFP36/LSM6/RPL37/TNRC6B/RPL9/TNKS1BP1/RPL38/RPL31/RPS23/RPS21/RPS27/ZFP36L2/RPL37A/RPL10A/TNRC6C/RPS17L/EXOSC8/RPS16/RPS29/RPS25/RPL10/RPL39/EXOSC9/CNOT10/RPS13/RPS8/RPS7/LSM5/MAGOH/RPL12/RPS9/RPS3/RPL7A/RPL14/RPL30/RPL3/RPL36/RPLP0/EIF4B/RPL15/RPS18/RPS6/RPS14/PAN3/RPL11/RPL32/RPS4X/RPS5/RPL36A/RPL4/RPL18/LSM4/EXOSC3/RPLP2/RPL27/RPS27A/RPL24/RPL27A/DCP2/RPSA/RPS3A/RPL26/CNOT6L/RPL19/CPEB3/RPS12/RPS15A/RPL13A/LSM7/RPS11/RPL22/RPL35A/EXOSC2/SAMD4B/RPL8/PNRC2/RPL18A/LSM2/RPL29/RC3H1/RPS24/RPL5/EXOSC6/RPL13/RPL17/RPL23/PATL2/RPL6/RPL23A/AGO1/RPL28/DXO/RPL34/RPL35/POLR2D/RPL7/EIF4A3/PATL1/RPL41/UBA52/CNOT2/EXOSC10/AGO2* |
| G9 | GO:0006402 | Mrna catabolic process | 207 | 0.419215746 | 1.732506206 | 0.003802281 | 0.033607472 | tags =53%, list =32%, signal =36% | *ZFP36/LSM6/AGO4/RPL37/TNRC6B/RPL9/TNKS1BP1/RPL38/RPL31/RPS23/RPS21/RPS27/ZFP36L2/RPL37A/DIS3L/RPL10A/TNRC6C/RPS17L/EXOSC8/RPS16/RPS29/RPS25/RPL10/RPL39/EXOSC9/CNOT10/RPS13/RPS8/RPS7/LSM5/RNH1/MAGOH/RPL12/RPS9/RPS3/RPL7A/RPL14/RPL30/RPL3/RPL36/RPLP0/EIF4B/RPL15/RPS18/RPS6/RPS14/PAN3/RPL11/RPL32/RPS4X/RPS5/RPL36A/RPL4/RPL18/LSM4/EXOSC3/RPLP2/RPL27/RPS27A/RPL24/RPL27A/DCP2/RPSA/RPS3A/RPL26/CNOT6L/RPL19/CPEB3/RPS12/RPS15A/RPL13A/LSM7/RPS11/NUDT16/RPL22/RPL35A/EXOSC2/KHSRP/SAMD4B/RPL8/PNRC2/RPL18A/LSM2/RPL29/RC3H1/RPS24/RPL5/EXOSC6/RPL13/RPL17/RPL23/PATL2/RPL6/RPL23A/AGO1/RPL28/DXO/RPL34/RPL35/POLR2D/RPL7/EIF4A3/GTPBP1/PATL1/RPL41/UBA52/CNOT2/EXOSC10/AGO2* |
| G9 | GO:0006401 | RNA catabolic process | 233 | 0.3867136 | 1.607048205 | 0.004016064 | 0.034898447 | tags =50%, list =32%, signal =35% | *ZFP36/RNASEH2A/LSM6/AGO4/FEN1/RPL37/ISG20/TNRC6B/RPL9/TNKS1BP1/RPL38/RPL31/RPS23/RPS21/RPS27/ZFP36L2/RPL37A/DIS3L/DNA2/RPL10A/TNRC6C/RPS17L/EXOSC8/RPS16/RPS29/RPS25/RPL10/RPL39/EXOSC9/CNOT10/RPS13/RPS8/RPS7/OAS2/LSM5/RNH1/MAGOH/RPL12/LIN28A/RPS9/HNRNPD/RPS3/RPL7A/RPL14/RPL30/RPL3/RPL36/RPLP0/EIF4B/RPL15/RPS18/RPS6/RPS14/PAN3/RPL11/RPL32/RPS4X/RPS5/RPL36A/RPL4/RPL18/LSM4/EXOSC3/RPLP2/RPL27/RPS27A/RPL24/RPL27A/DCP2/RPSA/RPS3A/RPL26/CNOT6L/RPL19/CPEB3/RPS12/RPS15A/RPL13A/LSM7/RPS11/NUDT16/RPL22/RPL35A/EXOSC2/KHSRP/SAMD4B/RPL8/PNRC2/RPL18A/LSM2/RPL29/RC3H1/RPS24/RPL5/EXOSC6/RPL13/RPL17/RPL23/PATL2/RPL6/RPL23A/AGO1/RPL28/DXO/RPL34/RPL35/POLR2D/RPL7/EIF4A3/PABPC4/GTPBP1/PATL1/XRN2/RPL41/UBA52/CNOT2/EXOSC10* |
| G9 | GO:0031397 | Negative regulation of protein ubiquitination | 124 | 0.41273881 | 1.61348533 | 0.006369427 | 0.045290946 | tags =8%, list =4%, signal =8% | *FBXO43/CDC20/CDK1/UBE2C/BUB1B/CCNB1/MAD2L1/PSMB9/FBXO5/CDK2* |
| G9 | GO:1903321 | Negative regulation of protein modification by small protein conjugation or removal | 130 | 0.398650481 | 1.570210608 | 0.006622517 | 0.046053749 | tags =8%, list =4%, signal =7% | *FBXO43/CDC20/CDK1/UBE2C/BUB1B/CCNB1/MAD2L1/PSMB9/FBXO5/CDK2* |

Group: group ID; terms with the same group ID indicate high semantical similarities among them; ID: gene set id; description: description of the gene set; set size: the number of genes in the gene set; enrichment score: the degree to which a gene set is over-represented at the top (up-regulated) or bottom (down-regulated) of the list of genes ranked by expression fold change; NES: normalized enrichment score; P value: the P value of the enrichment score calculated using permutation test; P.adjust: adjusted P value for multiple hypothesis testing; leading\_edge: “tags” indicates the percentage of genes contributing to the enrichment score; “list” indicates where in the list the enrichment score is attained; “Signal” indicates enrichment signal strength; core\_enrichment: the core enriched genes that contribute to the enrichment.