**TABLE S10: Genes set enrichment analysis revealed a significant overrepresentation of the REACTOME_CELL_CYCLE set in high Combo score patients compared to low Combo score patients ($P< 0.01$).**

| PROBE | GENE SYMBOL | GENE_TITLE | RANK METRIC SCORE | RUNNING ES | CORE ENRICHMENT |
|---|---|---|---|---|---|
| CDT1 | CDT1 | chromatin licensing and DNA replication factor 1 | -0.127870694 | -0.5693202 | Yes |
| HIST1H2BC | HIST1H2BC | histone cluster 1, H2bc | -0.129817352 | -0.55808115 | Yes |
| PSMA8 | PSMA8 | proteasome (prosome, macropain) subunit, alpha type, 8 | -0.139692619 | -0.55166554 | Yes |
| HIST1H2AE | HIST1H2AE | histone cluster 1, H2ae | -0.145508602 | -0.5411239 | Yes |
| MCM4 | MCM4 | MCM4 minichromosome maintenance deficient 4 (S. cerevisiae) | -0.152304724 | -0.52887 | Yes |
| PLK4 | PLK4 | polo-like kinase 4 (Drosophila) | -0.152752295 | -0.51196724 | Yes |
| CDCA8 | CDCA8 | cell division cycle associated 8 | -0.154042289 | -0.49468413 | Yes |
| KIF23 | KIF23 | kinesin family member 23 | -0.157216638 | -0.4788693 | Yes |
| HIST1H2AD | HIST1H2AD | histone cluster 1, H2ad | -0.164881527 | -0.46468836 | Yes |
| HIST1H2BG | HIST1H2BG | histone cluster 1, H2bg | -0.167829394 | -0.44694582 | Yes |
| CCNB2 | CCNB2 | cyclin B2 | -0.168697953 | -0.42772296 | Yes |
| CCNB1 | CCNB1 | cyclin B1 | -0.170906231 | -0.40893194 | Yes |
| BUB1B | BUB1B | BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast) | -0.17234768 | -0.3890534 | Yes |
| AURKA | AURKA | aurora kinase A | -0.176049516 | -0.3696623 | Yes |
| CENPA | CENPA | centromere protein A | -0.176667497 | -0.34950963 | Yes |
| MCM10 | MCM10 | MCM10 minichromosome maintenance deficient 10 (S. cerevisiae) | -0.190355882 | -0.33626366 | Yes |
| KIF20A | KIF20A | kinesin family member 20A | -0.206273943 | -0.3179428 | Yes |
| HIST1H4H | HIST1H4H | histone cluster 1, H4h | -0.210105702 | -0.29526776 | Yes |
| OIP5 | OIP5 | Opa interacting protein 5 | -0.210215062 | -0.2707413 | Yes |
| BIRC5 | BIRC5 | baculoviral IAP repeat-containing 5 (survivin) | -0.215311497 | -0.24768871 | Yes |
| GINS1 | GINS1 | GINS complex subunit 1 (Psf1 homolog) | -0.225035444 | -0.22511041 | Yes |
| NEK2 | NEK2 | NIMA (never in mitosis gene a)-related kinase 2 | -0.227829218 | -0.19898851 | Yes |
| TYMS | TYMS | thymidylate synthetase | -0.23626557 | -0.17303148 | Yes |
| HIST1H4C | HIST1H4C | histone cluster 1, H4c | -0.240711197 | -0.1460961 | Yes |
| NUMA1 | NUMA1 | nuclear mitotic apparatus protein 1 | -0.241789743 | -0.11834538 | Yes |
| MCM2 | MCM2 | MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae) | -0.245723307 | -0.08990589 | Yes |
| HIST2H2BE | HIST2H2BE | histone cluster 2, H2be | -0.246814266 | -0.061109282 | Yes |
| RRM2 | RRM2 | ribonucleotide reductase M2 polypeptide | -0.280034333 | -0.030964933 | Yes |
| CHEK1 | CHEK1 | CHK1 checkpoint homolog (S. pombe) | -0.281156719 | 0.001838521 | Yes |