Supplement Table 2 Functional and pathway enrichment analysis of the module genes

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| Module | Term | Count | PValue | Genes | FDR |
| Module1 | GO:0007067~mitotic nuclear division | 10 | 6.34E-13 | CDC20, ASPM, ANLN, TPX2, NUF2, BUB1B, FAM64A, NDC80, SKA1, CEP55 | 9.89E-11 |
|  | GO:0051301~cell division | 7 | 8.01E-07 | CDC20, TPX2, NUF2, BUB1B, FAM64A, NDC80, SKA1 | 6.25E-05 |
|  | GO:0007062~sister chromatid cohesion | 5 | 2.99E-06 | CDC20, NUF2, BUB1B, NDC80, SKA1 | 0.000155385 |
|  | hsa04110:Cell cycle | 4 | 5.57E-05 | CDC20, ORC1, BUB1B, TTK | 0.000501195 |
|  | GO:0005819~spindle | 4 | 0.000181 | CDC20, TPX2, PRC1, TTK | 0.007255614 |
| Module2 | GO:0005198~structural molecule activity | 4 | 1.22E-05 | KRT81, KRT16, KRT23, KRT6A | 2.45E-05 |
|  | GO:0045095~keratin filament | 3 | 0.000178 | KRT81, KRT6B, KRT6A | 0.000793813 |
|  | GO:0005882~intermediate filament | 3 | 0.000227 | KRT16, KRT23, KRT6A | 0.000793813 |
|  | GO:0005200~structural constituent of cytoskeleton | 3 | 0.00025 | KRT16, KRT6B, KRT6A | 0.000250315 |
|  | GO:0002009~morphogenesis of an epithelium | 2 | 0.001667 | KRT16, KRT6A | 0.016072382 |
| Module3 | GO:0044212~transcription regulatory region DNA binding | 4 | 6.68E-05 | FOXA1, AR, FOXC1, GATA3 | 0.001494749 |
|  | GO:0001077~transcriptional activator activity | 4 | 9.06E-05 | FOXA1, AR, PGR, GATA3 | 0.001494749 |
|  | GO:0008134~transcription factor binding | 4 | 0.000157 | FOXA1, AR, FOXC1, GATA3 | 0.001725422 |
|  | GO:0003700~transcription factor activity, sequence-specific DNA binding | 5 | 0.000318 | FOXA1, AR, FOXC1, PGR, GATA3 | 0.002623593 |
|  | GO:0045944~positive regulation of transcription from RNA polymerase II promoter | 5 | 0.000351 | FOXA1, AR, FOXC1, PGR, GATA3 | 0.078369289 |