**Table S1. TFs potentially regulate the expression of DEGs in the key modules.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Module** | **TFs** | **NES(1)** | **Targets(2)** | **Motifs/Tracks(3)** |
| **Blue** | TCF12JAZF1BRCA1GATA1CHD2SMAD3STAT3SRFGATA5KLF13RAD21CEBPBSMC1ACTCFCCDC25MYBL2 | 4.7303.9273.8253.7723.7403.7123.6953.6493.5783.4953.2903.2173.1873.1833.0773.029 | 872434552945224621406816112030 | 16513151444121111 |
| **Turquoise** | ATF5E2F1BCL3SPIL1ELF1CREB1MTA3MEF2BCBFBKDM4EFOXN3STAT2TBPTCF12TGIF1SRFCTCF | 9.6215.2704.6404.5244.4654.4604.0323.7803.6393.5583.3733.2793.1833.0863.0163.0053.004 | 14890881215762191976105013221115511 | 14611737162161 21111 |
| **Yellow** | TCF12NFICDDX4CATEP300AVENMMS19ZBTB18TEAD4ADARB1CD59RXRAFOSL2DAB2JUNDGATA3RORCMAPK1NF1 | 7.3206.4125.3584.7284.6814.5664.2234.1314.1104.0643.8803.8713.7723.7503.5833.3503.3453.3103.055 | 6652628760924333437068361653355668548 | 226104131228221511321 |

Notes: TFs regulating genes of the key module are shown. (1) The highest enrichment score for a motif/track that is part of the current clustercode. (2) Number of unique target genes detected by the enriched motifs/tracks associated to the given TF. (3) Number of motifs/tracks that can be associated to the given TF.