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

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Module** | **TFs** | **NES(1)** | **Targets(2)** | **Motifs/Tracks(3)** |
| **Blue** | TCF12  JAZF1  BRCA1  GATA1  CHD2  SMAD3  STAT3  SRF  GATA5  KLF13  RAD21  CEBPB  SMC1A  CTCF  CCDC25  MYBL2 | 4.730  3.927  3.825  3.772  3.740  3.712  3.695  3.649  3.578  3.495  3.290  3.217  3.187  3.183  3.077  3.029 | 87  24  34  55  29  45  22  46  21  40  6  8  16  11  20  30 | 16  5  1  3  1  5  1  4  4  4  1  2  1  1  1  1 |
| **Turquoise** | ATF5  E2F1  BCL3  SPIL1  ELF1  CREB1  MTA3  MEF2B  CBFB  KDM4E  FOXN3  STAT2  TBP  TCF12  TGIF1  SRF  CTCF | 9.621  5.270  4.640  4.524  4.465  4.460  4.032  3.780  3.639  3.558  3.373  3.279  3.183  3.086  3.016  3.005  3.004 | 148  90  88  121  57  62  19  19  76  10  50  13  22  11  15  5  11 | 14  6  11  7  3  7  1  6  2  1  6  1  2  1  1  1  1 |
| **Yellow** | TCF12  NFIC  DDX4  CAT  EP300  AVEN  MMS19  ZBTB18  TEAD4  ADARB1  CD59  RXRA  FOSL2  DAB2  JUND  GATA3  RORC  MAPK1  NF1 | 7.320  6.412  5.358  4.728  4.681  4.566  4.223  4.131  4.110  4.064  3.880  3.871  3.772  3.750  3.583  3.350  3.345  3.310  3.055 | 66  52  62  87  60  92  43  33  43  70  68  36  16  53  35  56  68  54  8 | 2  2  6  10  4  13  1  2  2  8  2  2  1  5  1  1  3  2  1 |

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.