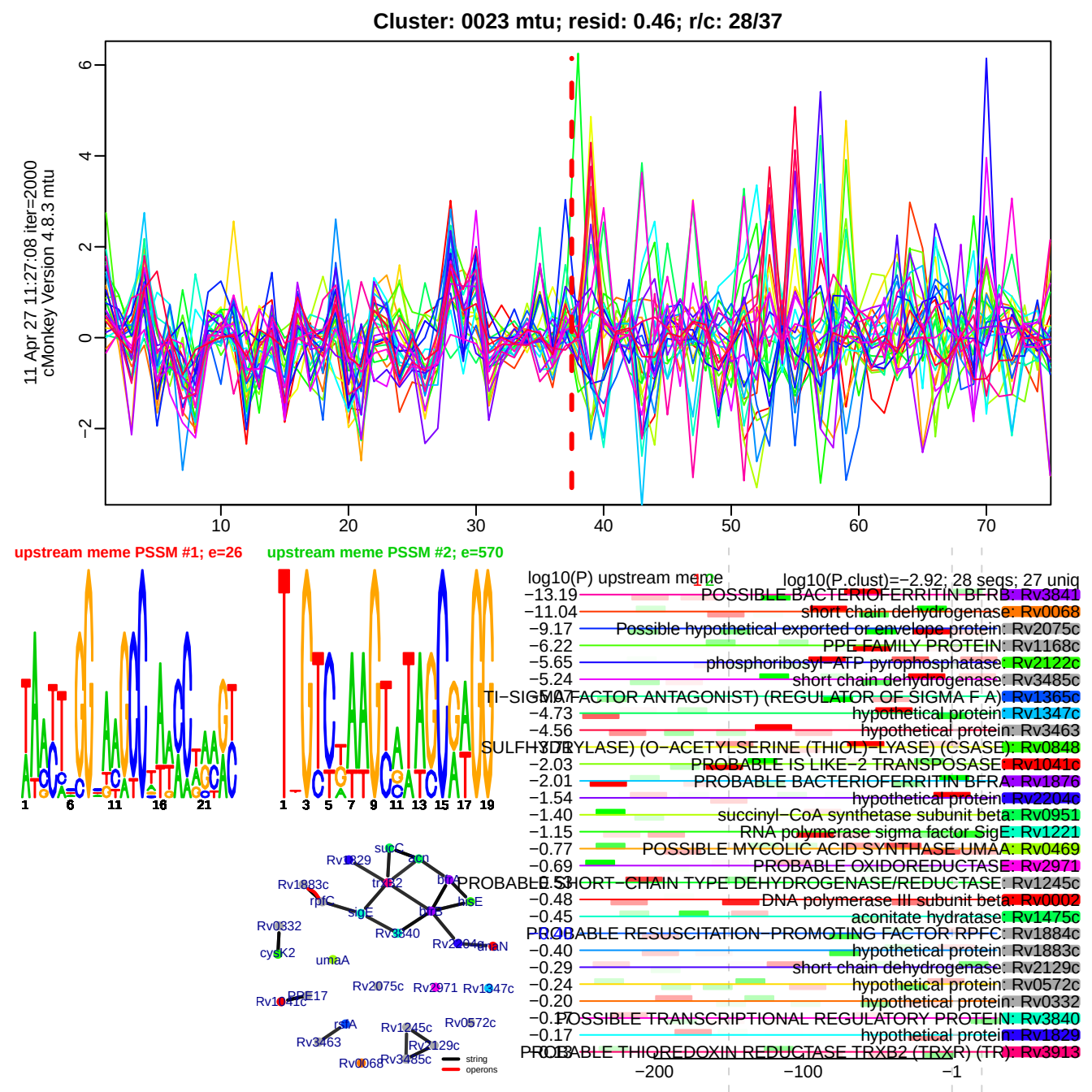
Cluster: 0023 mtu; resid: 0.46; r/c: 28/37
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=26
upstream meme PSSM #2; e=570
log10(P) upstream meme
log10(P.clust)=−2.92; 28 seqs; 27 uniq
−13.19 POSSIBLE BACTERIOFERRITIN BFRB: Rv3841
−11.04 short chain dehydrogenase: Rv0068
−9.17 Possible hypothetical exported or envelope protein: Rv2075c
−6.22 PPE FAMILY PROTEIN: Rv1168c
−5.65 phosphoribosyl−ATP pyrophosphatase: Rv2122c
−5.24 short chain dehydrogenase: Rv3485c
TI−SIGMA FACTOR ANTAGONIST) (REGULATOR OF SIGMA F A): Rv1365c
−4.73 hypothetical protein: Rv1347c
−4.56 hypothetical protein: Rv3463
SULFHYDRYLASE) (O−ACETYLSERINE (THIOL)−LYASE) (CSASE): Rv0848
−2.03 PROBABLE IS LIKE−2 TRANSPOSASE: Rv1041c
−2.01 PROBABLE BACTERIOFERRITIN BFRA: Rv1876
−1.54 hypothetical protein: Rv2204c
−1.40 succinyl−CoA synthetase subunit beta: Rv0951
−1.15 RNA polymerase sigma factor SigE: Rv1221
−0.77 POSSIBLE MYCOLIC ACID SYNTHASE UMAA: Rv0469
−0.69 PROBABLE OXIDOREDUCTASE: Rv2971
PROBABLE SHORT−CHAIN TYPE DEHYDROGENASE/REDUCTASE: Rv1245c
−0.48 DNA polymerase III subunit beta: Rv0002
−0.45 aconitate hydratase: Rv1475c
PROBABLE RESUSCITATION−PROMOTING FACTOR RPFC: Rv1884c
−0.40 hypothetical protein: Rv1883c
−0.29 short chain dehydrogenase: Rv2129c
−0.24 hypothetical protein: Rv0572c
−0.20 hypothetical protein: Rv0332
POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN: Rv3840
−0.17 hypothetical protein: Rv1829
PROBABLE THIOREDOXIN REDUCTASE TRXB2 (TRXR) (TR): Rv3913
−200
−100
−1
string
operons