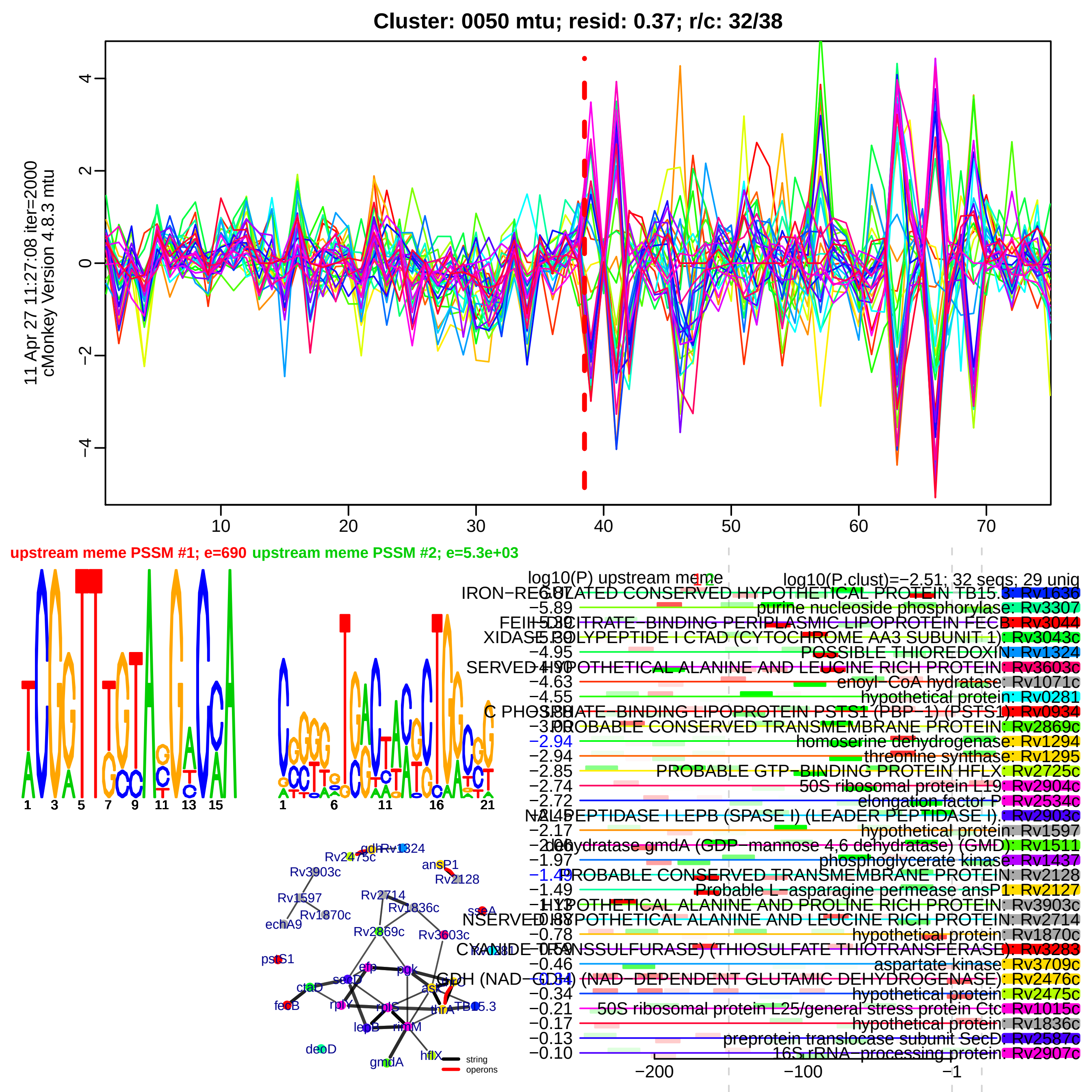
Cluster: 0050 mtu; resid: 0.37; r/c: 32/38
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=690
upstream meme PSSM #2; e=5.3e+03
log10(P) upstream meme
log10(P.clust)=−2.51; 32 seqs; 29 uniq
IRON−REGULATED CONSERVED HYPOTHETICAL PROTEIN TB15.3: Rv1636
purine nucleoside phosphorylase: Rv3307
FERRIC CITRATE−BINDING PERIPLASMIC LIPOPROTEIN FECB: Rv3044
OXIDASE POLYPEPTIDE I CTAD (CYTOCHROME AA3 SUBUNIT 1): Rv3043c
POSSIBLE THIOREDOXIN: Rv1324
CONSERVED HYPOTHETICAL ALANINE AND LEUCINE RICH PROTEIN: Rv3603c
enoyl−CoA hydratase: Rv1071c
hypothetical protein: Rv0281
PHOSPHATE−BINDING LIPOPROTEIN PSTS1 (PBP−1) (PSTS1): Rv0934
PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: Rv2869c
homoserine dehydrogenase: Rv1294
threonine synthase: Rv1295
PROBABLE GTP−BINDING PROTEIN HFLX: Rv2725c
50S ribosomal protein L19: Rv2904c
elongation factor P: Rv2534c
SIGNAL PEPTIDASE I LEPB (SPASE I) (LEADER PEPTIDASE I): Rv2903c
hypothetical protein: Rv1597
dehydratase gmdA (GDP−mannose 4,6 dehydratase) (GMD): Rv1511
phosphoglycerate kinase: Rv1437
PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: Rv2128
Probable L−asparagine permease ansP1: Rv2127
HYPOTHETICAL ALANINE AND PROLINE RICH PROTEIN: Rv3903c
CONSERVED HYPOTHETICAL ALANINE AND LEUCINE RICH PROTEIN: Rv2714
hypothetical protein: Rv1870c
CYANIDE TRANSSULFURASE) (THIOSULFATE THIOTRANSFERASE): Rv3283
aspartate kinase: Rv3709c
GDH (NAD−GDH) (NAD−DEPENDENT GLUTAMIC DEHYDROGENASE): Rv2476c
hypothetical protein: Rv2475c
50S ribosomal protein L25/general stress protein Ctc: Rv1015c
hypothetical protein: Rv1836c
preprotein translocase subunit SecD: Rv2587c
16S rRNA−processing protein: Rv2907c
string
operons