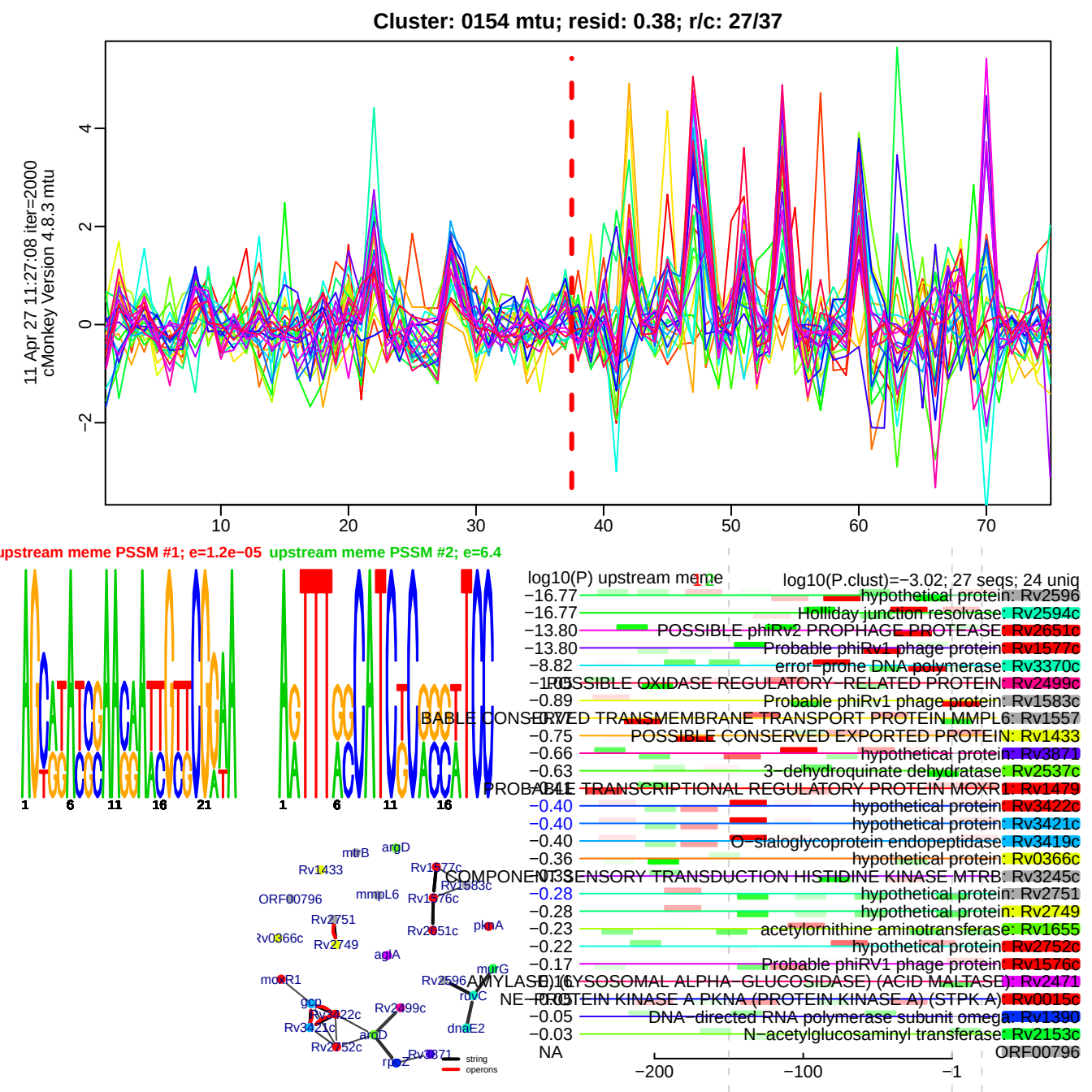
Cluster: 0154 mtu; resid: 0.38; r/c: 27/37
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=1.2e−05
upstream meme PSSM #2; e=6.4
log10(P) upstream meme
log10(P.clust)=−3.02; 27 seqs; 24 uniq
−16.77 hypothetical protein: Rv2596
−16.77 Holliday junction resolvase: Rv2594c
−13.80 POSSIBLE phiRv2 PROPHAGE PROTEASE: Rv2651c
−13.80 Probable phiRv1 phage protein: Rv1577c
−8.82 error−prone DNA polymerase: Rv3370c
−POSSIBLE OXIDASE REGULATORY−RELATED PROTEIN: Rv2499c
−0.89 Probable phiRv1 phage protein: Rv1583c
BABLE CONSERVED TRANSMEMBRANE TRANSPORT PROTEIN MMPL6: Rv1557
−0.75 POSSIBLE CONSERVED EXPORTED PROTEIN: Rv1433
−0.66 hypothetical protein: Rv3871
−0.63 3−dehydroquinate dehydratase: Rv2537c
PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN MOXR1: Rv1479
−0.40 hypothetical protein: Rv3422c
−0.40 hypothetical protein: Rv3421c
−0.40 O−slaloglycoprotein endopeptidase: Rv3419c
−0.36 hypothetical protein: Rv0366c
COMPONENT SENSORY TRANSDUCTION HISTIDINE KINASE MTRB: Rv3245c
−0.28 hypothetical protein: Rv2751
−0.28 hypothetical protein: Rv2749
−0.23 acetylornithine aminotransferase: Rv1655
−0.22 hypothetical protein: Rv2752c
−0.17 Probable phiRV1 phage protein: Rv1576c
AMYLASE)(LYSOSOMAL ALPHA−GLUCOSIDASE) (ACID MALTASE): Rv2471
NE−PROTEIN KINASE A PKNA (PROTEIN KINASE A) (STPK A): Rv0015c
−0.05 DNA−directed RNA polymerase subunit omega: Rv1390
−0.03 N−acetylglucosaminyl transferase: Rv2153c
NA
ORF00796
−200
−100
−1
mtrB
argD
Rv1433
Rv1577c
Rv1583c
ORF00796
mmpL6
Rv1576c
Rv2751
Rv2651c
phoA
Rv0366c
Rv2749
aglA
murG
moxR1
Rv2596
rpoC
gap
Rv2499c
Rv2422c
Rv3421c
dnaE2
argD
Rv2752c
Rv3871
rplZ
string
operons