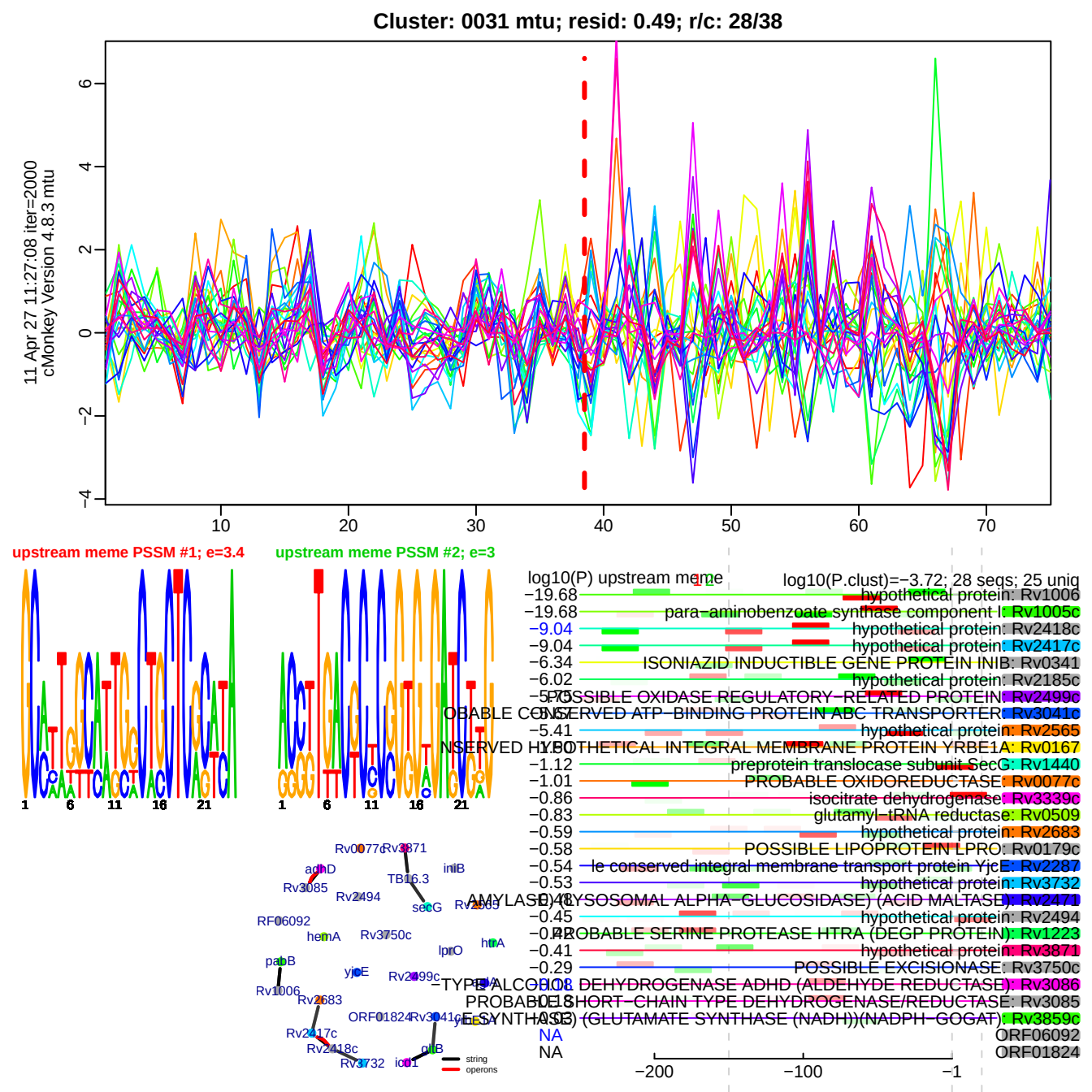
Cluster: 0031 mtu; resid: 0.49; r/c: 28/38
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=3.4
upstream meme PSSM #2; e=3
log10(P) upstream meme
log10(P.clust)=−3.72; 28 seqs; 25 uniq
−19.68 hypothetical protein: Rv1006
−19.68 para−aminobenzoate synthase component I: Rv1005c
−9.04 hypothetical protein: Rv2418c
−9.04 hypothetical protein: Rv2417c
−6.34 ISONIAZID INDUCTIBLE GENE PROTEIN INIB: Rv0341
−6.02 hypothetical protein: Rv2185c
−5.75 POSSIBLE OXIDASE REGULATORY−RELATED PROTEIN: Rv2499c
OBABLE CONSERVED ATP−BINDING PROTEIN ABC TRANSPORTER: Rv3041c
−5.41 hypothetical protein: Rv2565
NSERVED HYPOTHETICAL INTEGRAL MEMBRANE PROTEIN YRBE1A: Rv0167
−1.12 preprotein translocase subunit SecG: Rv1440
−1.01 PROBABLE OXIDOREDUCTASE: Rv0077c
−0.86 isocitrate dehydrogenase: Rv3339c
−0.83 glutamyl−tRNA reductase: Rv0509
−0.59 hypothetical protein: Rv2683
−0.58 POSSIBLE LIPOPROTEIN LPRO: Rv0179c
−0.54 le conserved integral membrane transport protein YjcE: Rv2287
−0.53 hypothetical protein: Rv3732
AMYLASE) (LYSOSOMAL ALPHA−GLUCOSIDASE) (ACID MALTASE): Rv2471
−0.45 hypothetical protein: Rv2494
−0.42 PROBABLE SERINE PROTEASE HTRA (DEGP PROTEIN): Rv1223
−0.41 hypothetical protein: Rv3871
−0.29 POSSIBLE EXCISIONASE: Rv3750c
−TYPE) ALCOHOL DEHYDROGENASE ADHD (ALDEHYDE REDUCTASE): Rv3086
PROBABLE SHORT−CHAIN TYPE DEHYDROGENASE/REDUCTASE: Rv3085
ASE) (GLUTAMATE SYNTHASE (NADH))(NADPH−GOGAT): Rv3859c
NA ORF06092
NA ORF01824
−200
−100
−1
Rv0077c
Rv3871
adhD
inlB
TB16.3
Rv3085
Rv2494
secG
Rv2565
RF06092
hemA
Rv3750c
lprO
htrA
pabB
yjcE
Rv2499c
Rv1006
Rv2683
ORF01824
Rv3041c
yjcE
Rv2417c
Rv2418c
Rv3732
inlB
string
operons