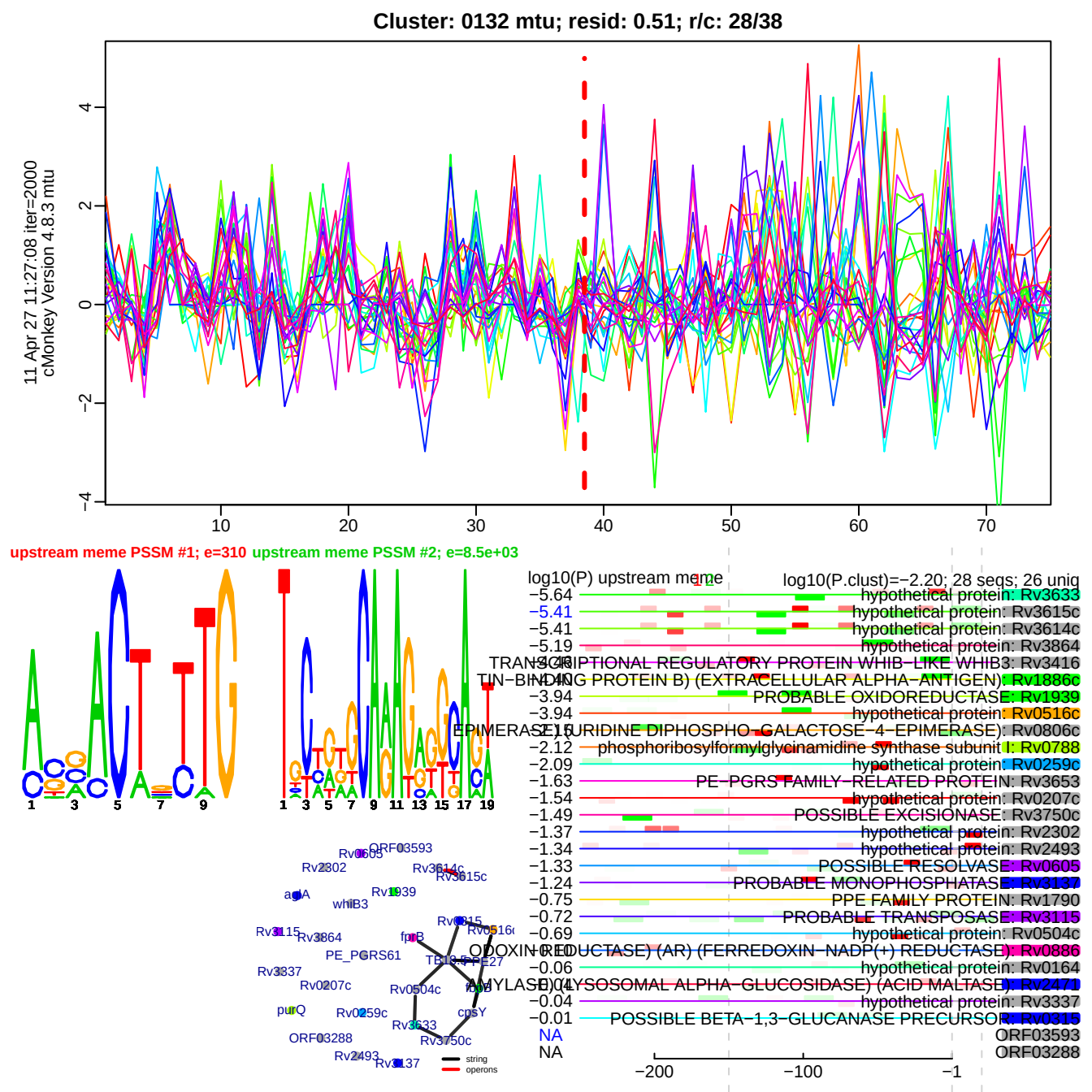
Cluster: 0132 mtu; resid: 0.51; r/c: 28/38
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=310
upstream meme PSSM #2; e=8.5e+03
log10(P) upstream meme
log10(P.clust)=−2.20; 28 seqs; 26 uniq
−5.64 hypothetical protein: Rv3633
−5.41 hypothetical protein: Rv3615c
−5.41 hypothetical protein: Rv3614c
−5.19 hypothetical protein: Rv3864
−4.48 TRANSCRIPTIONAL REGULATORY PROTEIN WHIB−LIKE WHIB3: Rv3416
−4.04 TIN−BINDING PROTEIN B) (EXTRACELLULAR ALPHA−ANTIGEN): Rv1886c
−3.94 PROBABLE OXIDOREDUCTASE: Rv1939
−3.94 hypothetical protein: Rv0516c
−2.15 EPIMERASE)/URIDINE DIPHOSPHO−GALACTOSE−4−EPIMERASE): Rv0806c
−2.12 phosphoribosylformylglycinamidine synthase subunit I: Rv0788
−2.09 hypothetical protein: Rv0259c
−1.63 PE−PGRS FAMILY−RELATED PROTEIN: Rv3653
−1.54 hypothetical protein: Rv0207c
−1.49 POSSIBLE EXCISIONASE: Rv3750c
−1.37 hypothetical protein: Rv2302
−1.34 hypothetical protein: Rv2493
−1.33 POSSIBLE RESOLVASE: Rv0605
−1.24 PROBABLE MONOPHOSPHATASE: Rv3137
−0.75 PPE FAMILY PROTEIN: Rv1790
−0.72 PROBABLE TRANSPOSASE: Rv3115
−0.69 hypothetical protein: Rv0504c
ODOXIN−REDUCTASE) (AR) (FERREDOXIN−NADP(+) REDUCTASE): Rv0886
−0.06 hypothetical protein: Rv0164
AMYLASE)/(LYSOSOMAL ALPHA−GLUCOSIDASE) (ACID MALTASE): Rv2471
−0.04 hypothetical protein: Rv3337
−0.01 POSSIBLE BETA−1,3−GLUCANASE PRECURSOR: Rv0315
NA ORF03593
NA ORF03288
−200
−100
−1
ORF03593
Rv0605
Rv2802
Rv3614c
Rv3615c
Rv1939
whiB3
Rv3115
Rv3864
fprB
Rv0516c
PE_PGRS61
Rv3337
Rv0207c
Rv0504c
purQ
Rv0259c
Rv3633
cpsY
ORF03288
Rv3750c
Rv2493
Rv3137
string
operons