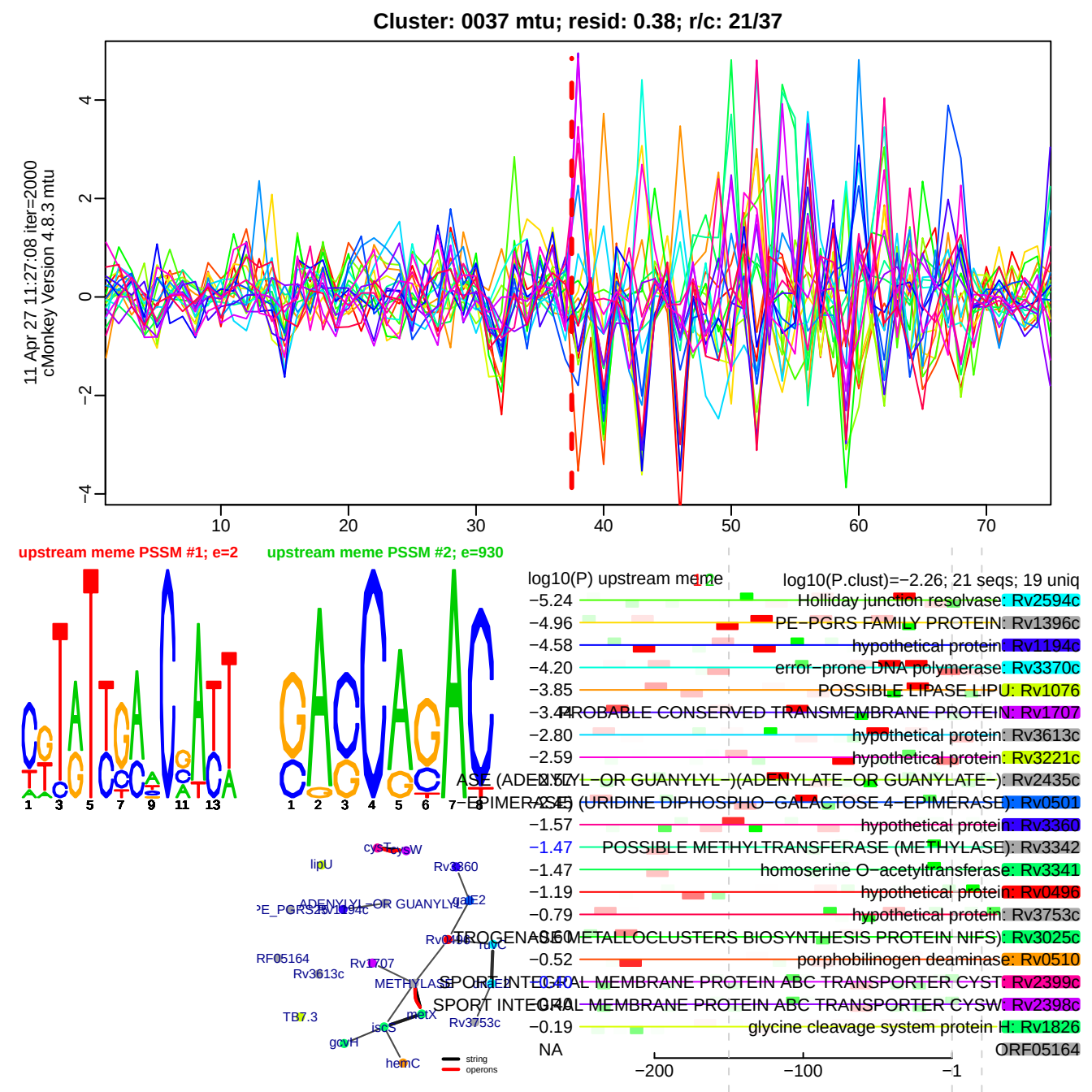
Cluster: 0037 mtu; resid: 0.38; r/c: 21/37
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=2
upstream meme PSSM #2; e=930
log10(P) upstream meme
log10(P.clust)=−2.26; 21 seqs; 19 uniq
−5.24 Holliday junction resolvase: Rv2594c
−4.96 PE−PGRS FAMILY PROTEIN: Rv1396c
−4.58 hypothetical protein: Rv1194c
−4.20 error−prone DNA polymerase: Rv3370c
−3.85 POSSIBLE LIPASE LIPU: Rv1076
−3.44 PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: Rv1707
−2.80 hypothetical protein: Rv3613c
−2.59 hypothetical protein: Rv3221c
−2.57 ASE (ADENYL−OR GUANYLYL−)(ADENYLATE−OR GUANYLATE−): Rv2435c
−1.57 ASE (URIDINE DIPHOSPHO−GALACTOSE 4−EPIMERASE): Rv0501
−1.47 hypothetical protein: Rv3360
−1.47 POSSIBLE METHYLTRANSFERASE (METHYLASE): Rv3342
−1.19 homoserine O−acetyltransferase: Rv3341
−0.79 hypothetical protein: Rv0496
−0.60 hypothetical protein: Rv3753c
−0.52 TROGENASE METALLOCLUSTERS BIOSYNTHESIS PROTEIN NIFS): Rv3025c
−0.40 porphobilinogen deaminase: Rv0510
−0.19 SPORT INTEGRAL MEMBRANE PROTEIN ABC TRANSPORTER CYST: Rv2399c
NA glycine cleavage system protein H: Rv1826
SPORT INTEGRAL MEMBRANE PROTEIN ABC TRANSPORTER CYSW: Rv2398c
ORF05164
−200
−100
−1
cysT
cysW
lipU
Rv3860
ADENYLYL−OR GUANYLYL−
PE_PGRS2
Rv1194c
glgE2
Rv0496
fdxC
RF05164
Rv1707
Rv3613c
METHYLASE
ORF05164
TB7.3
metX
Rv3753c
isoS
gcvH
hemC
string
operons