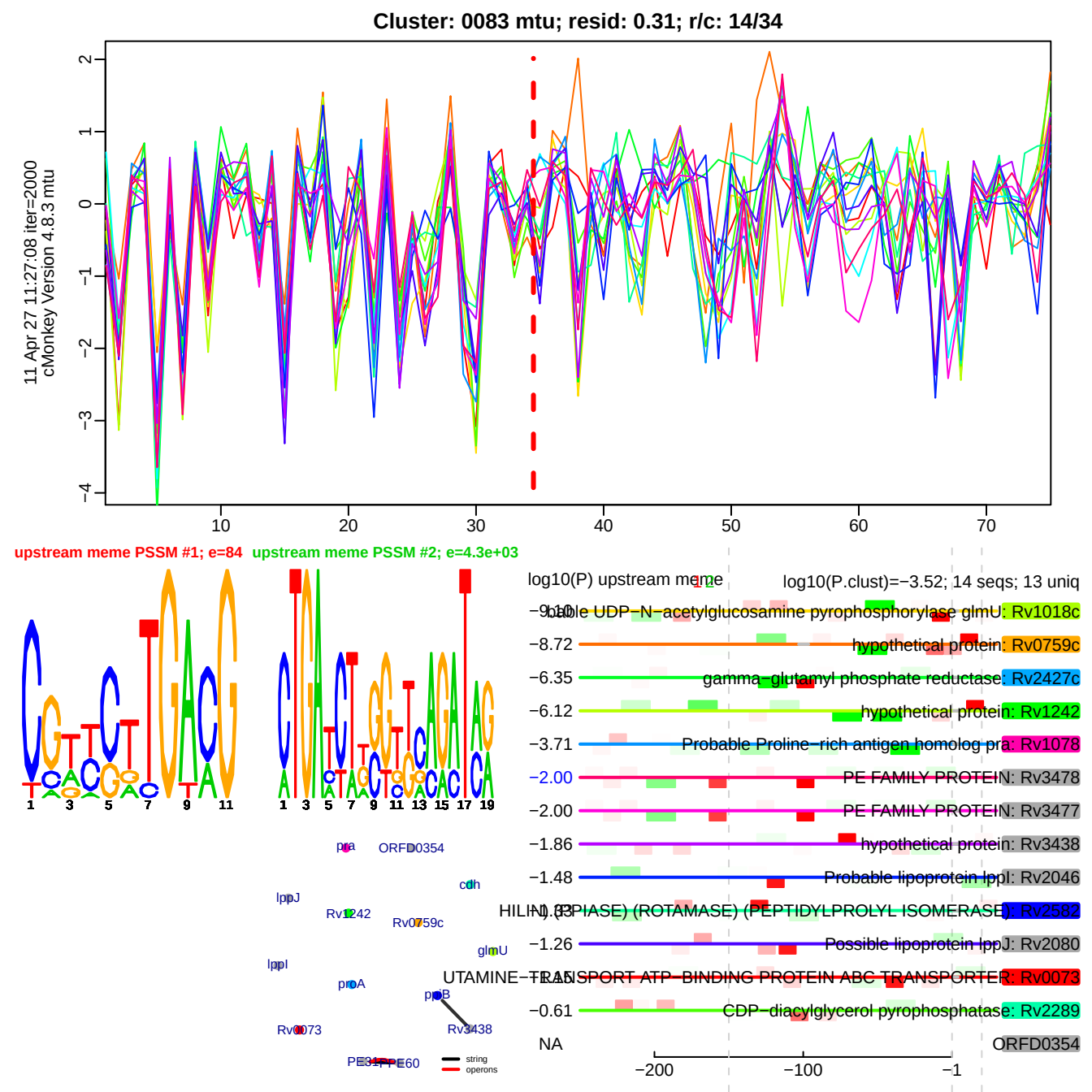
Cluster: 0083 mtu; resid: 0.31; r/c: 14/34
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=84
upstream meme PSSM #2; e=4.3e+03
log10(P) upstream meme
log10(P.clust)=−3.52; 14 seqs; 13 uniq
−9.10 Probable UDP−N−acetylglucosamine pyrophosphorylase glmU: Rv1018c
−8.72 hypothetical protein: Rv0759c
−6.35 gamma−glutamyl phosphate reductase: Rv2427c
−6.12 hypothetical protein: Rv1242
−3.71 Probable Proline−rich antigen homolog pra: Rv1078
−2.00 PE FAMILY PROTEIN: Rv3478
−2.00 PE FAMILY PROTEIN: Rv3477
−1.86 hypothetical protein: Rv3438
−1.48 Probable lipoprotein lppI: Rv2046
−1.33 HILINASE) (ROTAMASE) (PEPTIDYLPROLYL ISOMERASE): Rv2582
−1.26 Possible lipoprotein lppJ: Rv2080
−1.15 UTAMINE−TRANSPORT ATP−BINDING PROTEIN ABC TRANSPORTER: Rv0073
−0.61 CDP−diacylglycerol pyrophosphatase: Rv2289
NA ORFD0354
−200
−100
−1
pra
ORFD0354
cdh
lppJ
Rv1242
Rv0759c
glmU
lppI
proA
proB
Rv0073
Rv3438
PE34
PPE60
string
operons