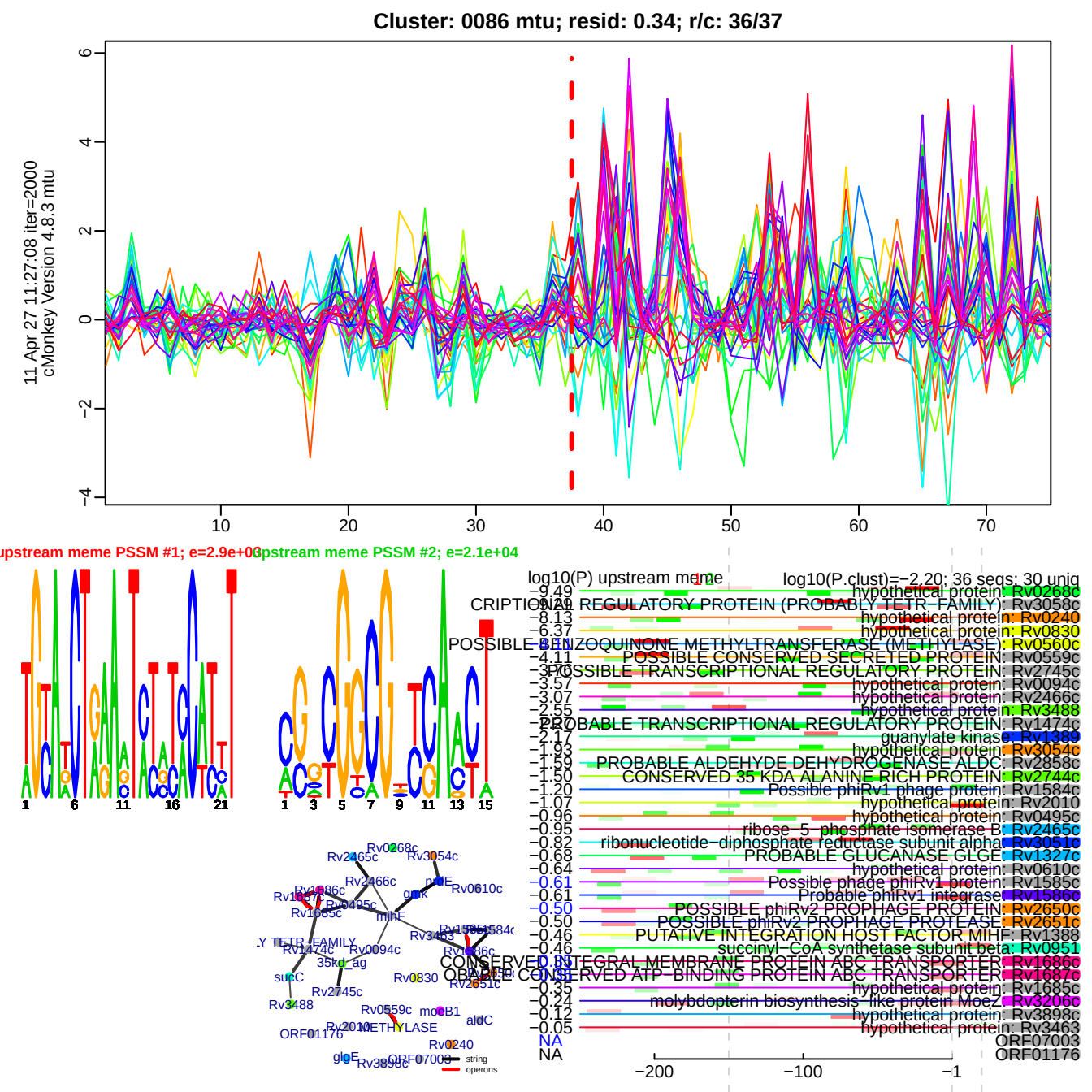
Cluster: 0086 mtu; resid: 0.34; r/c: 36/37
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=2.9e+03
upstream meme PSSM #2; e=2.1e+04
log10(P) upstream meme
log10(P.clust)=−2.20; 36 seqs; 30 uniq
−9.49 hypothetical protein: Rv0268c
CRIPTIONAL REGULATORY PROTEIN (PROBABLY TETR−FAMILY): Rv3058c
−8.13 hypothetical protein: Rv0240
−6.37 hypothetical protein: Rv0830
POSSIBLE BENZOQUINONE METHYLTRANSFERASE (METHYLASE): Rv0560c
−4.11 POSSIBLE CONSERVED SECRETED PROTEIN: Rv0559c
−3.76 POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN: Rv2745c
−3.57 hypothetical protein: Rv0094c
−3.07 hypothetical protein: Rv2466c
−2.55 hypothetical protein: Rv3488
−2.20 PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN: Rv1474c
−2.17 guanylate kinase: Rv1389
−1.93 hypothetical protein: Rv3054c
−1.59 PROBABLE ALDEHYDE DEHYDROGENASE ALDC: Rv2858c
−1.50 CONSERVED 35 KDA ALANINE RICH PROTEIN: Rv2744c
−1.20 Possible phiRv1 phage protein: Rv1584c
−1.07 hypothetical protein: Rv2010
−0.96 hypothetical protein: Rv0495c
−0.95 ribose−5−phosphate isomerase B: Rv2465c
−0.82 ribonucleotide−diphosphate reductase subunit alpha: Rv3051c
−0.68 PROBABLE GLUCANASE GLGE: Rv1327c
−0.64 hypothetical protein: Rv0610c
−0.61 Possible phage phiRv1 protein: Rv1585c
−0.61 Probable phiRv1 integrase: Rv1586c
−0.50 POSSIBLE phiRv2 PROPHAGE PROTEIN: Rv2650c
−0.50 POSSIBLE phiRv2 PROPHAGE PROTEASE: Rv2651c
−0.46 PUTATIVE INTEGRATION HOST FACTOR MIHF: Rv1388
−0.46 succinyl−CoA synthetase subunit beta: Rv0951
−0.41 INTEGRAL MEMBRANE PROTEIN ABC TRANSPORTER: Rv1686c
−0.39 CONSERVED ATP−BINDING PROTEIN ABC TRANSPORTER: Rv1687c
−0.35 hypothetical protein: Rv1685c
−0.24 molybdopterin biosynthesis−like protein MoeZ: Rv3206c
−0.12 hypothetical protein: Rv3898c
−0.05 hypothetical protein: Rv3463
NA ORF07003
NA ORF01176
−200
−100
−1
Rv0268c
Rv2465c
Rv3054c
Rv2466c
moaE
Rv0610c
Rv1586c
gmk
Rv0495c
mihF
Rv1585c
Rv3463
Rv1584c
Rv1474c
Rv0094c
35kd_ag
sucC
Rv0830
Rv2651c
Rv2745c
Rv3488
Rv0559c
moeB1
aldC
ORF01176
METHYLASE
Rv0240
glgE
ORF07003
Rv3898c
string
operons