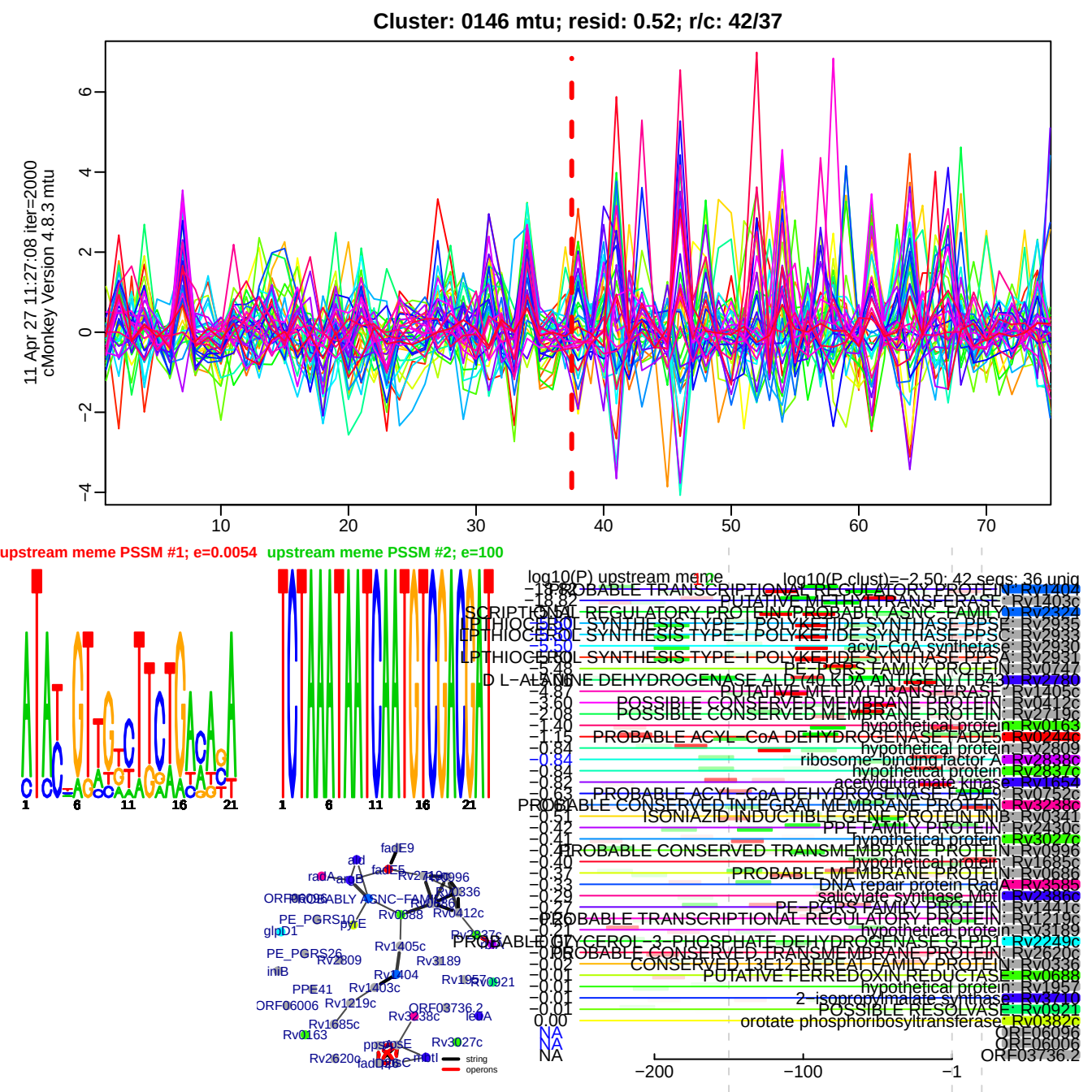
Cluster: 0146 mtu; resid: 0.52; r/c: 42/37
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=0.0054
upstream meme PSSM #2; e=100
log10(P) upstream meme
log10(P clust)=−2.50; 42 seqs; 36 uniq
PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN: Rv1404
PUTATIVE METHYLTRANSFERASE: Rv1403c
PROBABLY ASNC-FAMILY: Rv2324
POLYKETIDE SYNTHASE PPSE: Rv2935
POLYKETIDE SYNTHASE PPSC: Rv2933
acyl-CoA synthetase: Rv2930
POLYKETIDE SYNTHASE PPSA: Rv2931
PE-PGRS FAMILY PROTEIN: Rv0747
D L-ALANINE DEHYDROGENASE ALD (40 KDA ANTIGEN) (TB43): Rv2780
PUTATIVE METHYLTRANSFERASE: Rv1405c
POSSIBLE CONSERVED MEMBRANE PROTEIN: Rv0412c
POSSIBLE CONSERVED MEMBRANE PROTEIN: Rv2719c
hypothetical protein: Rv0163
PROBABLE ACYL−CoA DEHYDROGENASE FADE5: Rv0244c
hypothetical protein: Rv2809
ribosome−binding factor A: Rv2388c
hypothetical protein: Rv2837c
acetylglutamate kinase: Rv1654
PROBABLE ACYL−CoA DEHYDROGENASE FADE9: Rv0752c
PROBABLE CONSERVED INTEGRAL MEMBRANE PROTEIN: Rv3238c
ISONIAZID INDUCTIBLE GENE PROTEIN INIB: Rv0341
PPE FAMILY PROTEIN: Rv2430c
hypothetical protein: Rv3027c
PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: Rv0996
hypothetical protein: Rv1685c
PROBABLE MEMBRANE PROTEIN: Rv0686
DNA repair protein RadA: Rv3585
salicylate synthase MbtI: Rv2386c
PE-PGRS FAMILY PROTEIN: Rv1441c
PROBABLE TRANSCRIPTIONAL REGULATORY: Rv1219c
hypothetical protein: Rv3189
GLYCEROL−3−PHOSPHATE DEHYDROGENASE GLPD1: Rv2249c
PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: Rv2620c
CONSERVED 13E12 REPEAT FAMILY PROTEIN: Rv0336
PUTATIVE FERREDOXIN REDUCTASE: Rv0688
hypothetical protein: Rv1957
2−isopropylmalate synthase: Rv3710
POSSIBLE RESOLVASE: Rv0921
orotate phosphoribosyltransferase: Rv0382c
ORF06096
ORF06006
ORF03736.2
−200
−100
−1
string
operons