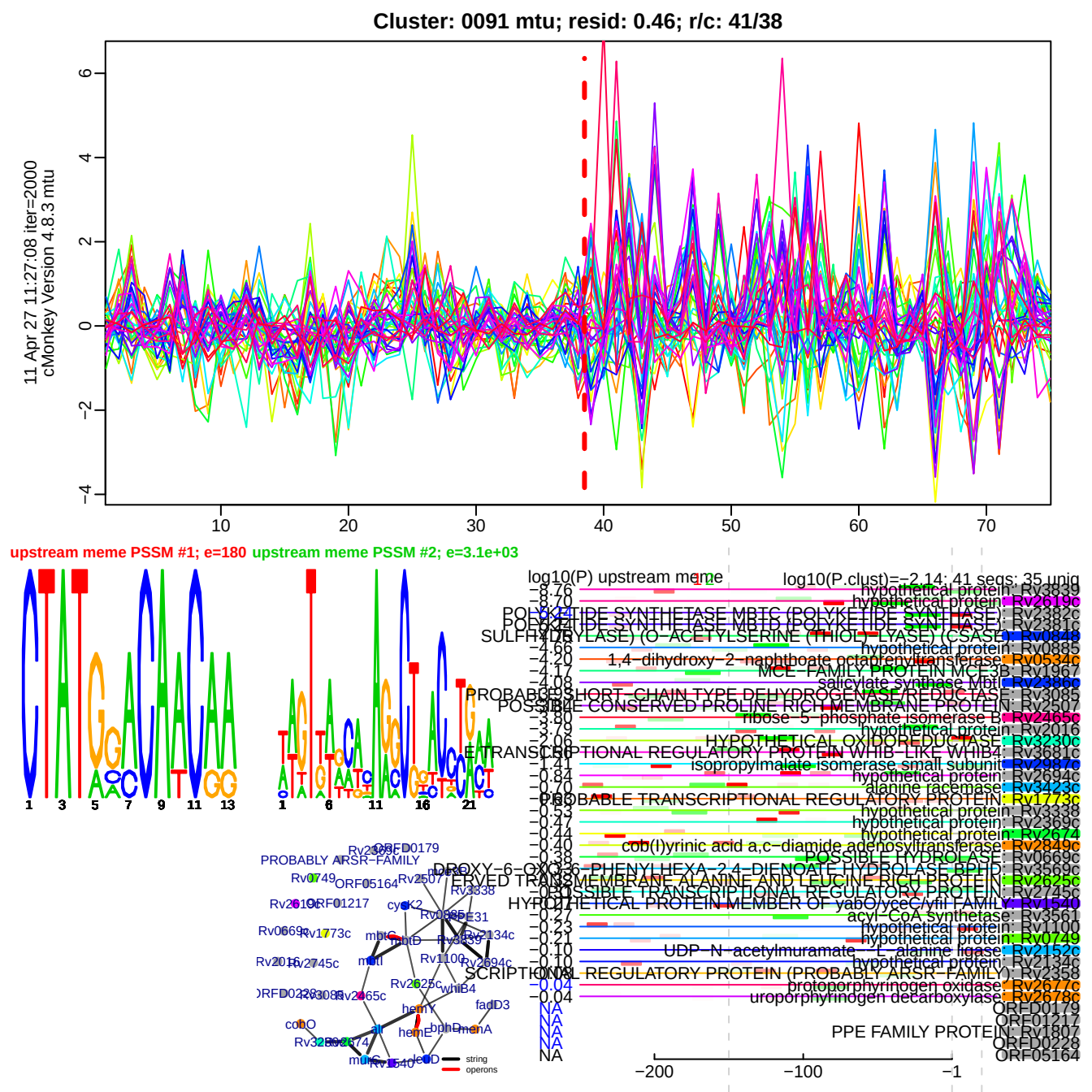
Cluster: 0091 mtu; resid: 0.46; r/c: 41/38
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=180
upstream meme PSSM #2; e=3.1e+03
log10(P) upstream meme
log10(P.clust)=−2.14; 41 seqs; 35 uniq
hypothetical protein; Rv3839
hypothetical protein; Rv2619c
POLYKETIDE SYNTHETASE MBTC (POLYKETIDE SYNTHASE); Rv2382c
POLYKETIDE SYNTHETASE MBTD (POLYKETIDE SYNTHASE); Rv2381c
SULFHYDRYLASE) (O−ACETYLSERINE (THIOL)−LYASE) (CSASE); Rv0848
hypothetical protein; Rv0885
1,4−dihydroxy−2−naphthoate octaprenyltransferase; Rv0534c
MCE−FAMILY PROTEIN MCE3B; Rv1967
salicylate synthase MbtI; Rv2386c
PROBABLE SHORT−CHAIN TYPE DEHYDROGENASE/REDUCTASE; Rv3085
POSSIBLE CONSERVED PROLINE RICH MEMBRANE PROTEIN; Rv2507
ribose−5−phosphate isomerase B; Rv2465c
hypothetical protein; Rv2016
HYPOTHETICAL OXIDOREDUCTASE; Rv3230c
ETRANSCRIPTIONAL REGULATORY PROTEIN WHIB−LIKE WHIB4; Rv3681c
isopropylmalate isomerase small subunit; Rv2987c
hypothetical protein; Rv2694c
alanine racemase; Rv3423c
PROBABLE TRANSCRIPTIONAL REGULATORY PROTEIN; Rv1773c
hypothetical protein; Rv3338
hypothetical protein; Rv2369c
hypothetical protein; Rv2674
cob(I)yrinic acid a,c−diamide adenosyltransferase; Rv2849c
POSSIBLE HYDROLASE; Rv0669c
DROXY−6−OXO−6−PHENYLHEXA−2,4−DIENOATE HYDROLASE BPHD; Rv3569c
ERVED TRANSMEMBRANE ALANINE AND LEUCINE RICH PROTEIN; Rv2625c
POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN; Rv2745c
HYPOTHETICAL PROTEIN MEMBER OF yabO/yceC/yfiI FAMILY; Rv1540
acyl−CoA synthetase; Rv3561
hypothetical protein; Rv1100
hypothetical protein; Rv0749
UDP−N−acetylmuramate−−L−alanine ligase; Rv2152c
hypothetical protein; Rv2134c
REGULATORY PROTEIN (PROBABLY ARSR−FAMILY); Rv2358
protoporphyrinogen oxidase; Rv2677c
uroporphyrinogen decarboxylase; Rv2678c
ORFD0179
ORF01217
PPE FAMILY PROTEIN; Rv1807
ORFD0228
ORF05164
−200
−100
−1
string
operons