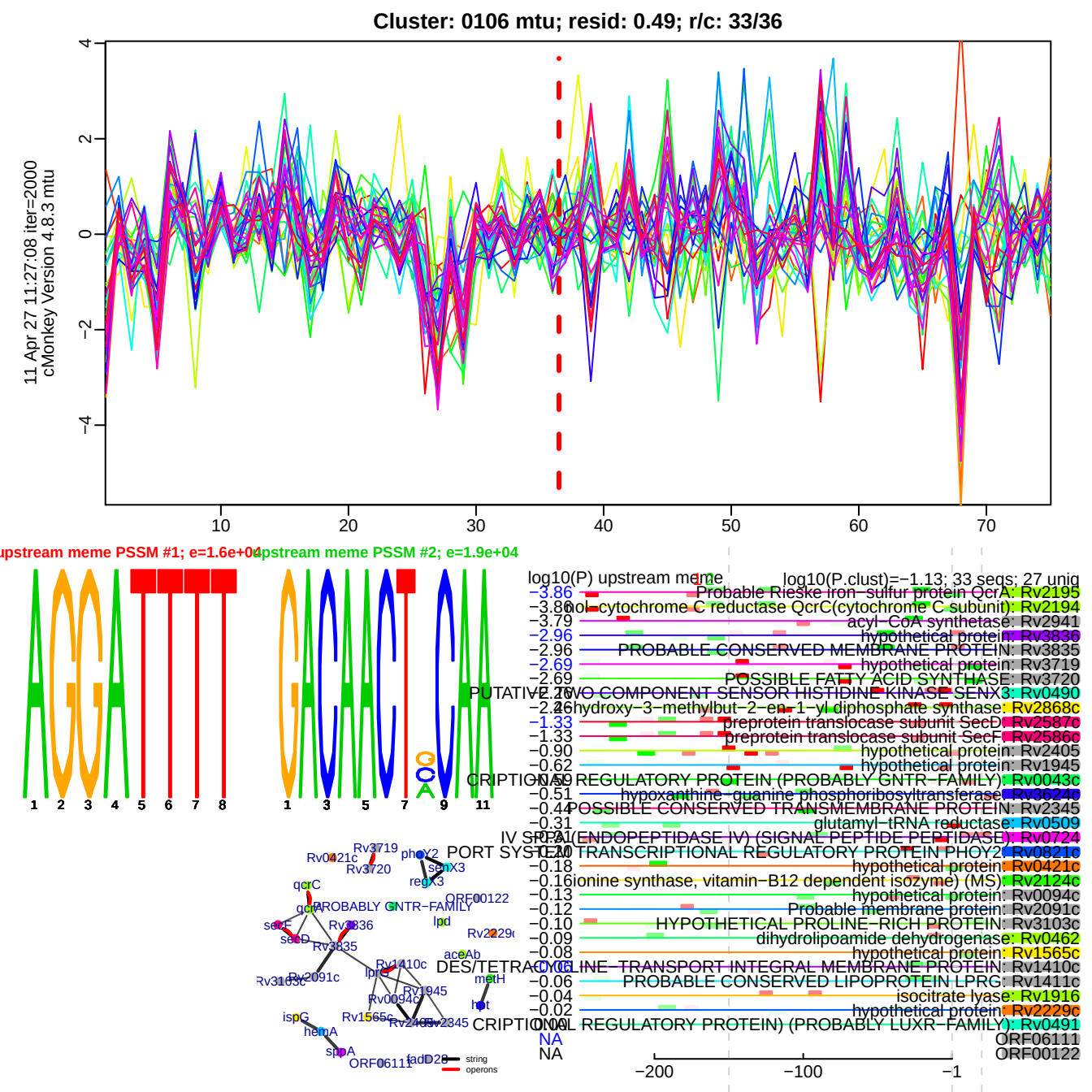
Cluster: 0106 mtu; resid: 0.49; r/c: 33/36
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=1.6e+04
upstream meme PSSM #2; e=1.9e+04
log10(P) upstream meme
log10(P.clust)=−1.13; 33 seqs; 27 uniq
−3.86 Probable Rieske iron−sulfur protein QcrA: Rv2195
−3.86 ol−cytochrome C reductase QcrC(cytochrome C subunit): Rv2194
−3.79 acyl−CoA synthetase: Rv2941
−2.96 hypothetical protein: Rv3836
−2.96 PROBABLE CONSERVED MEMBRANE PROTEIN: Rv3835
−2.69 hypothetical protein: Rv3719
−2.69 POSSIBLE FATTY ACID SYNTHASE: Rv3720
−2.26 PUTATIVE TWO COMPONENT SENSOR HISTIDINE KINASE SENX3: Rv0490
−2.26 hydroxy−3−methylbut−2−en−1−yl diphosphate synthase: Rv2868c
−1.33 preprotein translocase subunit SecD: Rv2587c
−1.33 preprotein translocase subunit SecF: Rv2586c
−0.90 hypothetical protein: Rv2405
−0.62 hypothetical protein: Rv1945
−0.51 CRIPTIONAL REGULATORY PROTEIN (PROBABLY GNTR−FAMILY): Rv0043c
−0.51 hypoxanthine−guanine phosphoribosyltransferase: Rv3624c
−0.44 POSSIBLE CONSERVED TRANSMEMBRANE PROTEIN: Rv2345
−0.31 glutamyl−tRNA reductase: Rv0509
IV SPA (ENDOPEPTIDASE IV) (SIGNAL PEPTIDE PEPTIDASE): Rv0724
−0.20 PORT SYSTEM TRANSCRIPTIONAL REGULATORY PROTEIN PHOY2: Rv0821c
−0.18 hypothetical protein: Rv0421c
−0.16 ionine synthase, vitamin−B12 dependent isozyme) (MS): Rv2124c
−0.13 hypothetical protein: Rv0094c
−0.12 Probable membrane protein: Rv2091c
−0.10 HYPOTHETICAL PROLINE−RICH PROTEIN: Rv3103c
−0.09 dihydrolipoamide dehydrogenase: Rv0462
−0.08 hypothetical protein: Rv1565c
−0.06 DES/TETRACYCLINE−TRANSPORT INTEGRAL MEMBRANE PROTEIN: Rv1410c
−0.06 PROBABLE CONSERVED LIPOPROTEIN LPRG: Rv1411c
−0.04 isocitrate lyase: Rv1916
−0.02 hypothetical protein: Rv2229c
0.00 CRIPTIONAL REGULATORY PROTEIN) (PROBABLY LUXR−FAMILY): Rv0491
NA ORF06111
NA ORF00122
−200
−100
−1
Rv3719
phoY2
Rv0421c
Rv3720
senX3
regX3
qcrC
qcrA
PROBABLY GNTR−FAMILY
ORF00122
Rv3836
lpd
Rv2229c
Rv3835
aceAb
Rv1410c
Rv2091c
lprG
metH
Rv1945
Rv0094c
hpt
ispG
Rv1565c
Rv2345
hemA
sppA
ORF06111
fadD28
string
operons