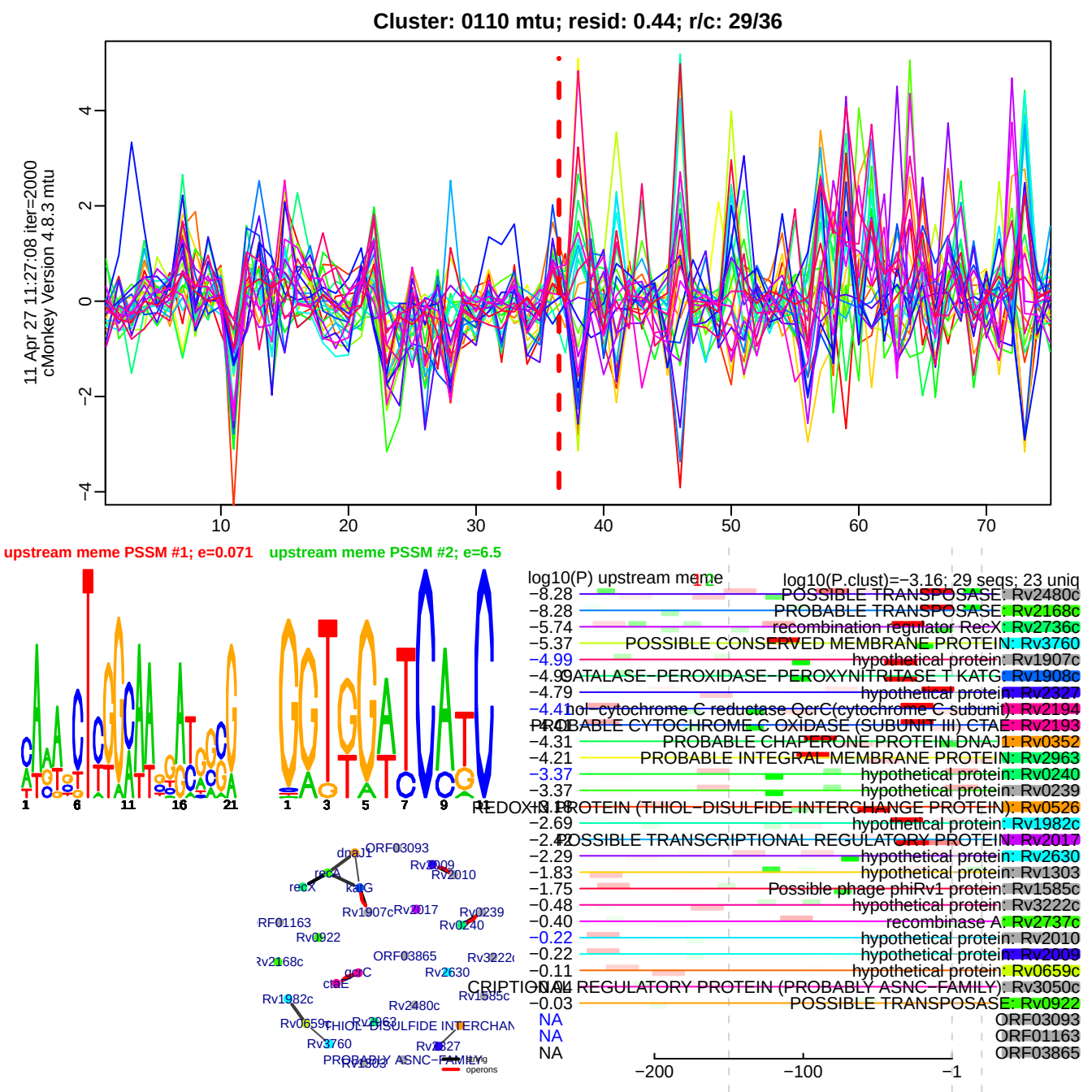
Cluster: 0110 mtu; resid: 0.44; r/c: 29/36
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=0.071
upstream meme PSSM #2; e=6.5
log10(P) upstream meme
log10(P.clust)=−3.16; 29 seqs; 23 uniq
−8.28 POSSIBLE TRANSPOSASE: Rv2480c
−8.28 PROBABLE TRANSPOSASE: Rv2168c
−5.74 recombination regulator RecX: Rv2736c
−5.37 POSSIBLE CONSERVED MEMBRANE PROTEIN: Rv3760
−4.99 hypothetical protein: Rv1907c
−4.9 CATALASE−PEROXIDASE−PEROXYNITRITASE T KATG: Rv1908c
−4.79 hypothetical protein: Rv2327
−4.41 ol−cytochrome C reductase QcrC(cytochrome C subunit): Rv2194
PROBABLE CYTOCHROME C OXIDASE (SUBUNIT III) CTAE: Rv2193
−4.31 PROBABLE CHAPERONE PROTEIN DNAJ1: Rv0352
−4.21 PROBABLE INTEGRAL MEMBRANE PROTEIN: Rv2963
−3.37 hypothetical protein: Rv0240
−3.37 hypothetical protein: Rv0239
REDOXIN PROTEIN (THIOL−DISULFIDE INTERCHANGE PROTEIN): Rv0526
−2.69 hypothetical protein: Rv1982c
POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN: Rv2017
−2.29 hypothetical protein: Rv2630
−1.83 hypothetical protein: Rv1303
−1.75 Possible phage phiRv1 protein: Rv1585c
−0.48 hypothetical protein: Rv3222c
−0.40 recombinase A: Rv2737c
−0.22 hypothetical protein: Rv2010
−0.22 hypothetical protein: Rv2009
−0.11 hypothetical protein: Rv0659c
CRIPTIONAL REGULATORY PROTEIN (PROBABLY ASNC−FAMILY): Rv3050c
−0.03 POSSIBLE TRANSPOSASE: Rv0922
NA ORF03093
NA ORF01163
NA ORF03865
−200
−100
−1
dnaJ1
ORF03093
Rv2009
Rv2010
recA
recX
katG
Rv1907c
Rv2017
Rv0239
Rv0240
RF01163
Rv0922
ORF03865
Rv2168c
qcrC
Rv2630
ctaE
Rv1982c
Rv2480c
Rv1585c
Rv0659c
THIOL−DISULFIDE INTERCHAN
Rv2963
Rv3760
Rv2327
PROBABLY ASNC−FAMILY
operons