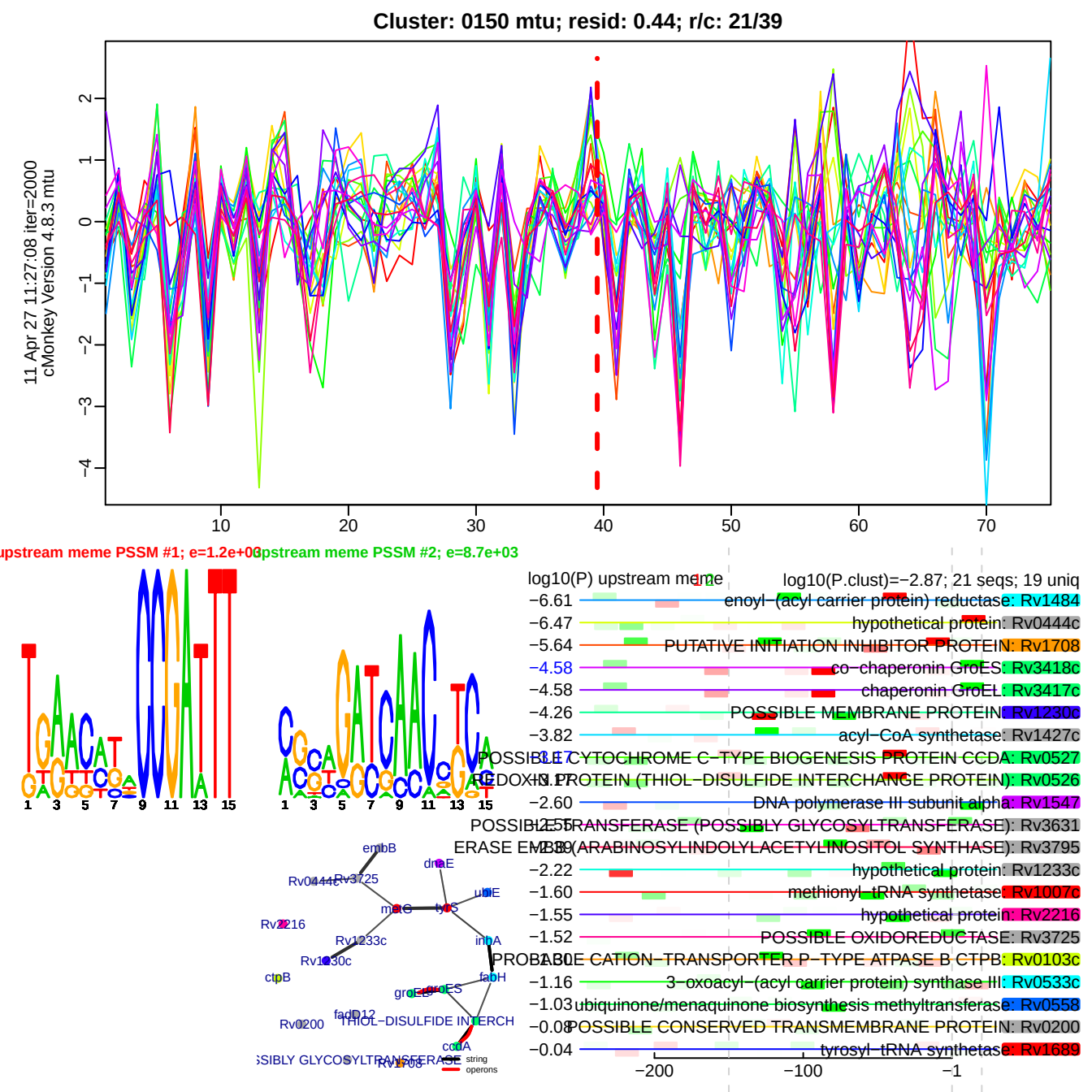
Cluster: 0150 mtu; resid: 0.44; r/c: 21/39
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=1.2e+03
upstream meme PSSM #2; e=8.7e+03
log10(P) upstream meme
log10(P.clust)=−2.87; 21 seqs; 19 uniq
−6.61 enoyl−(acyl carrier protein) reductase: Rv1484
−6.47 hypothetical protein: Rv0444c
−5.64 PUTATIVE INITIATION INHIBITOR PROTEIN: Rv1708
−4.58 co−chaperonin GroES: Rv3418c
−4.58 chaperonin GroEL: Rv3417c
−4.26 POSSIBLE MEMBRANE PROTEIN: Rv1230c
−3.82 acyl−CoA synthetase: Rv1427c
POSSIBLE CYTOCHROME C−TYPE BIOGENESIS PROTEIN CCDA: Rv0527
REDOXIN PROTEIN (THIOL−DISULFIDE INTERCHANGE PROTEIN): Rv0526
−2.60 DNA polymerase III subunit alpha: Rv1547
POSSIBLE TRANSFERASE (POSSIBLY GLYCOSYLTRANSFERASE): Rv3631
ERASE EMB(ARABINOSYLINDOLYLACETYLINOSITOL SYNTHASE): Rv3795
−2.22 hypothetical protein: Rv1233c
−1.60 methionyl−tRNA synthetase: Rv1007c
−1.55 hypothetical protein: Rv2216
−1.52 POSSIBLE OXIDOREDUCTASE: Rv3725
PROBABLE CATION−TRANSPORTER P−TYPE ATPASE B CTPB: Rv0103c
−1.16 3−oxoacyl−(acyl carrier protein) synthase III: Rv0533c
−1.03 ubiquinone/menaquinone biosynthesis methyltransferase: Rv0558
−0.08 POSSIBLE CONSERVED TRANSMEMBRANE PROTEIN: Rv0200
−0.04 tyrosyl−tRNA synthetase: Rv1689
embB
dnaE
Rv0444c
Rv3725
ubiE
metG
tyrS
Rv2216
Rv1233c
inhA
Rv1230c
ctpB
fabH
groES
fadD12
Rv0200
THIOL−DISULFIDE INTERCH
ccdA
SIBLY GLYCOSYLTRANSFERASE
Rv1708
string
operons