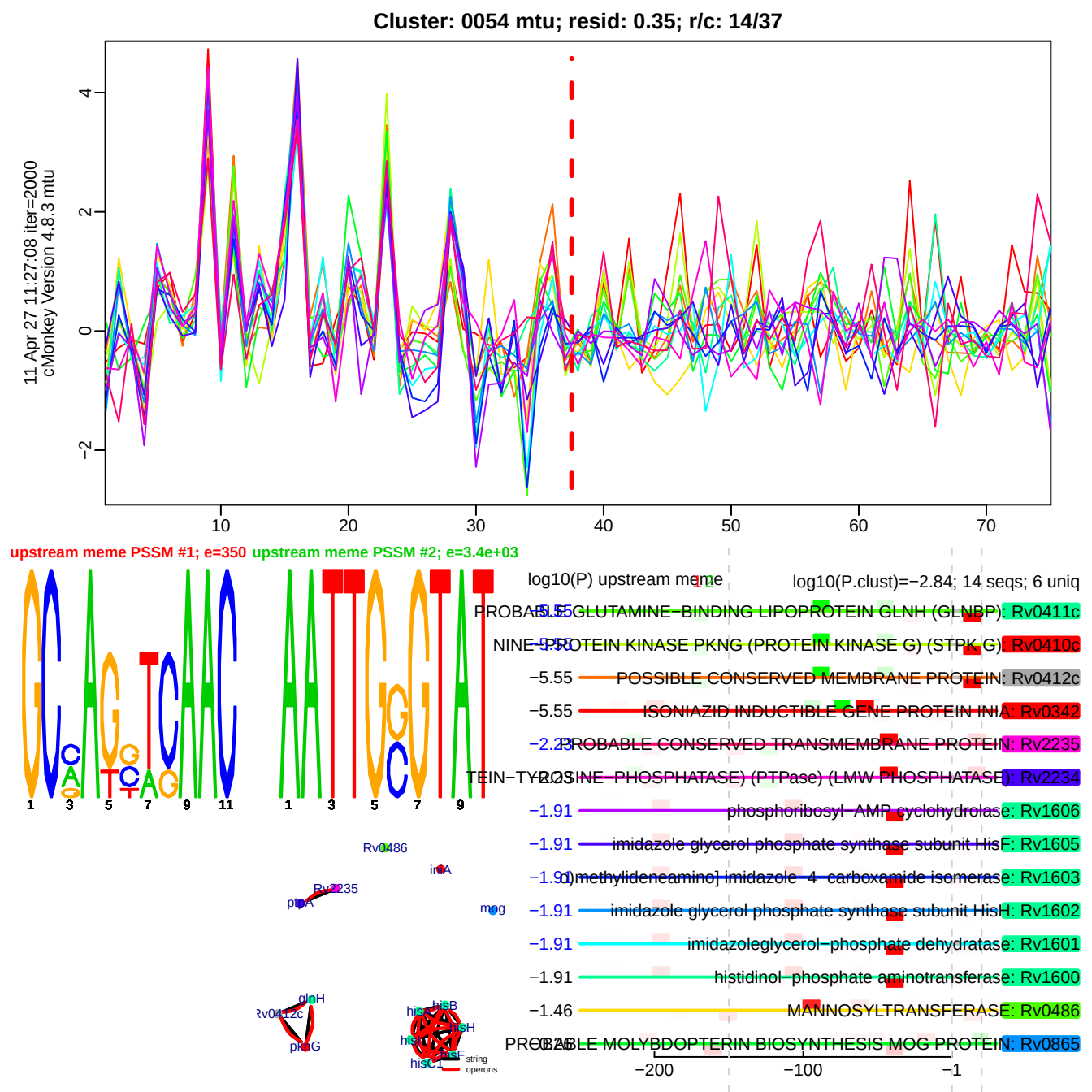
Cluster: 0054 mtu; resid: 0.35; r/c: 14/37
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=350
upstream meme PSSM #2; e=3.4e+03
log10(P) upstream meme
log10(P.clust)=−2.84; 14 seqs; 6 uniq
PROBABLE GLUTAMINE−BINDING LIPOPROTEIN GLNH (GLNBP): Rv0411c
NINE−PROTEIN KINASE PKNG (PROTEIN KINASE G) (STPK G): Rv0410c
−5.55 POSSIBLE CONSERVED MEMBRANE PROTEIN: Rv0412c
−5.55 ISONIAZID INDUCTIBLE GENE PROTEIN INIA: Rv0342
PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: Rv2235
TEIN−TYROSINE−PHOSPHATASE) (PTPase) (LMW PHOSPHATASE): Rv2234
−1.91 phosphoribosyl−AMP cyclohydrolase: Rv1606
−1.91 imidazole glycerol phosphate synthase subunit HisF: Rv1605
−1.91 methylideneamino] imidazole−4−carboxamide isomerase: Rv1603
−1.91 imidazole glycerol phosphate synthase subunit HisH: Rv1602
−1.91 imidazoleglycerol−phosphate dehydratase: Rv1601
−1.91 histidinol−phosphate aminotransferase: Rv1600
−1.46 MANNOSYLTRANSFERASE: Rv0486
PROBABLE MOLYBDOPTERIN BIOSYNTHESIS MOG PROTEIN: Rv0865
Rv0486
inhA
Rv2235
pknA
mog
glnH
Rv0412c
pknG
hisB
hisH
hisF
hisC1
string
operons