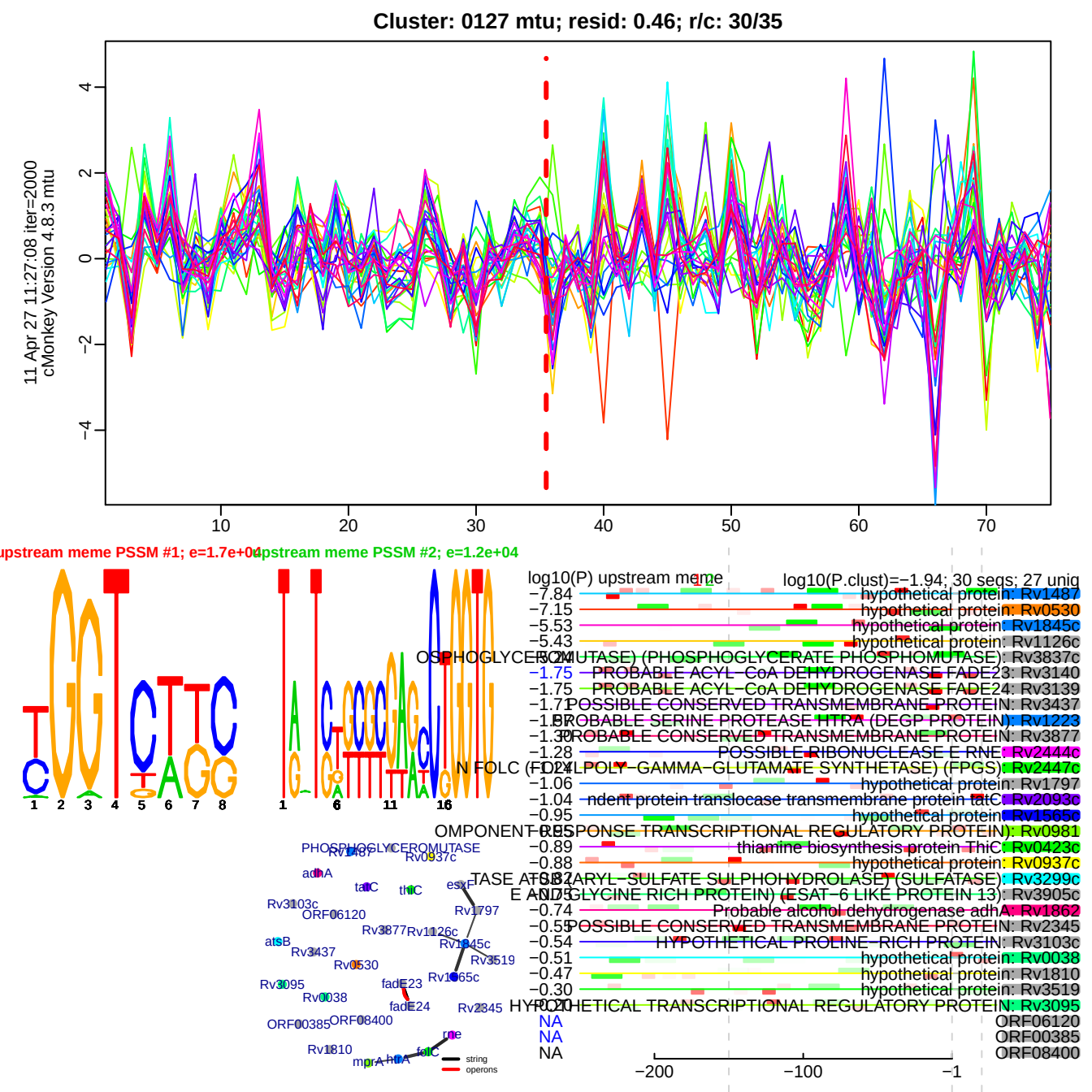
Cluster: 0127 mtu; resid: 0.46; r/c: 30/35
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=1.7e+04
upstream meme PSSM #2; e=1.2e+04
log10(P) upstream meme
log10(P.clust)=−1.94; 30 seqs; 27 uniq
hypothetical protein: Rv1487
hypothetical protein: Rv0530
hypothetical protein: Rv1845c
hypothetical protein: Rv1126c
OSPHOGLYCEROMUTASE) (PHOSPHOGLYCERATE PHOSPHOMUTASE): Rv3837c
PROBABLE ACYL−CoA DEHYDROGENASE FADE23: Rv3140
PROBABLE ACYL−CoA DEHYDROGENASE FADE24: Rv3139
POSSIBLE CONSERVED TRANSMEMBRANE PROTEIN: Rv3437
PROBABLE SERINE PROTEASE HTRA (DEGP PROTEIN): Rv1223
PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: Rv3877
POSSIBLE RIBONUCLEASE E RNE: Rv2444c
N FOLC (FOLYLPOLY−GAMMA−GLUTAMATE SYNTHETASE) (FPGS): Rv2447c
hypothetical protein: Rv1797
ndent protein translocase transmembrane protein tatC: Rv2093c
hypothetical protein: Rv1565c
OMPONENT RESPONSE TRANSCRIPTIONAL REGULATORY PROTEIN): Rv0981
thiamine biosynthesis protein ThiC: Rv0423c
hypothetical protein: Rv0937c
TASE ATSB (ARYL−SULFATE SULPHOHYDROLASE) (SULFATASE): Rv3299c
E AND GLYCINE RICH PROTEIN) (ESAT−6 LIKE PROTEIN 13): Rv3905c
Probable alcohol dehydrogenase adhA: Rv1862
POSSIBLE CONSERVED TRANSMEMBRANE PROTEIN: Rv2345
HYPOTHETICAL PROLINE−RICH PROTEIN: Rv3103c
hypothetical protein: Rv0038
hypothetical protein: Rv1810
hypothetical protein: Rv3519
HYPOTHETICAL TRANSCRIPTIONAL REGULATORY PROTEIN: Rv3095
ORF06120
ORF00385
ORF08400
string
operons