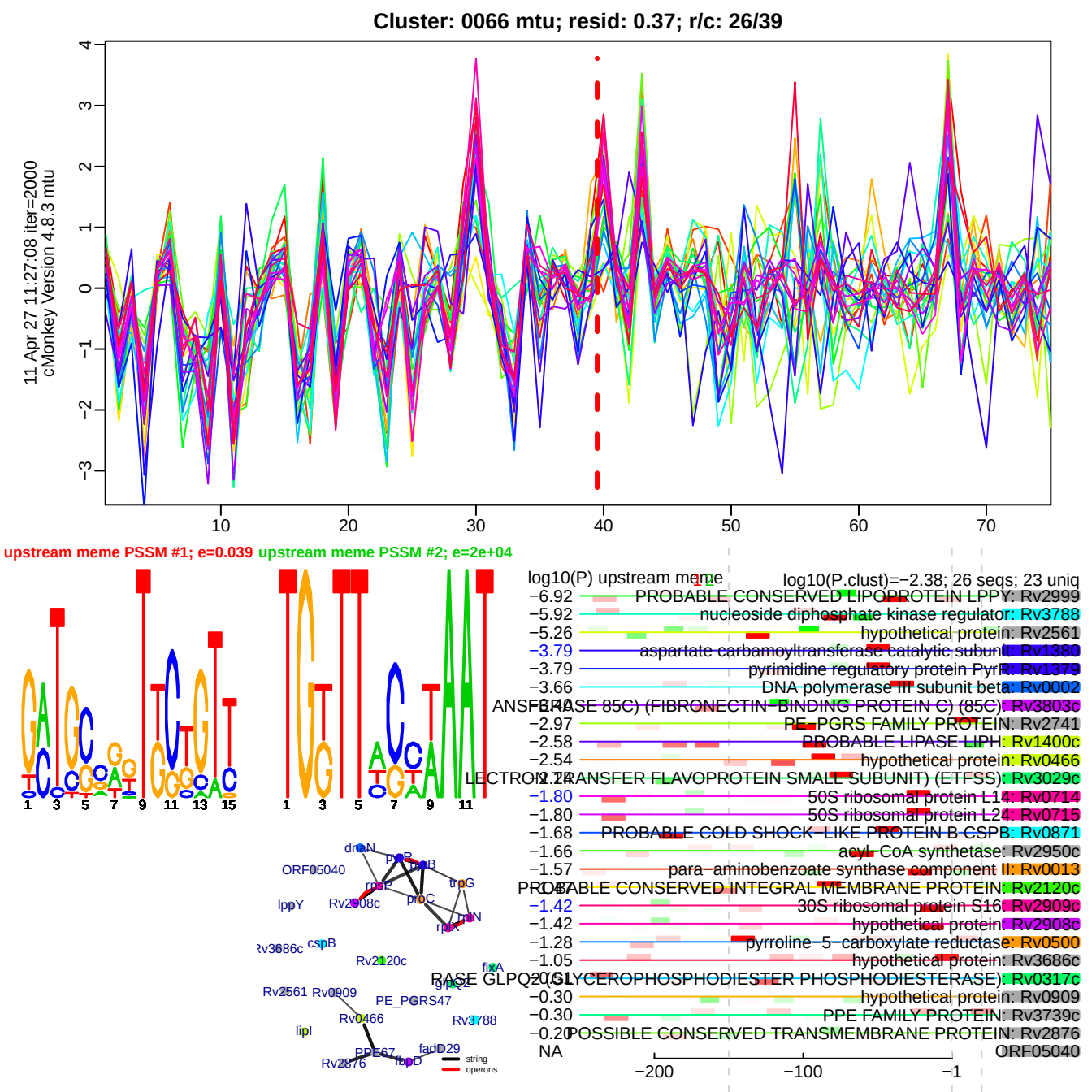
Cluster: 0066 mtu; resid: 0.37; r/c: 26/39
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=0.039
upstream meme PSSM #2; e=2e+04
log10(P) upstream meme
log10(P.clust)=−2.38; 26 seqs; 23 uniq
−6.92 PROBABLE CONSERVED LIPOPROTEIN LPPY: Rv2999
−5.92 nucleoside diphosphate kinase regulator: Rv3788
−5.26 hypothetical protein: Rv2561
−3.79 aspartate carbamoyltransferase catalytic subunit: Rv1380
−3.79 pyrimidine regulatory protein PyrR: Rv1379
−3.66 DNA polymerase III subunit beta: Rv0002
−3.40 ANSFERASE 85C) (FIBRONECTIN-BINDING PROTEIN C) (85C): Rv3803c
−2.97 PE-PGRS FAMILY PROTEIN: Rv2741
−2.58 PROBABLE LIPASE LIPH: Rv1400c
−2.54 hypothetical protein: Rv0466
−2.28 LECTRON TRANSFER FLAVOPROTEIN SMALL SUBUNIT) (ETFSS): Rv3029c
−1.80 50S ribosomal protein L14: Rv0714
−1.80 50S ribosomal protein L24: Rv0715
−1.68 PROBABLE COLD SHOCK-LIKE PROTEIN B-CSPB: Rv0871
−1.66 acyl-CoA synthetase: Rv2950c
−1.57 para-aminobenzoate synthase component II: Rv0013
−1.47 PROBABLE CONSERVED INTEGRAL MEMBRANE PROTEIN: Rv2120c
−1.42 30S ribosomal protein S16: Rv2909c
−1.42 hypothetical protein: Rv2908c
−1.28 pyrroline-5-carboxylate reductase: Rv0500
−1.05 hypothetical protein: Rv3686c
−0.91 RASE GLPQ2 (GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE): Rv0317c
−0.30 hypothetical protein: Rv0909
−0.30 PPE FAMILY PROTEIN: Rv3739c
−0.20 POSSIBLE CONSERVED TRANSMEMBRANE PROTEIN: Rv2876
NA ORF05040
−200
−100
−1
ORF05040
lppY
Rv2908c
Rv3686c
cspB
Rv2120c
Rv2561
Rv0909
PE_PGRS47
Rv0466
Rv3788
lipI
PPE67
Rv2876
fadD29
string
operons