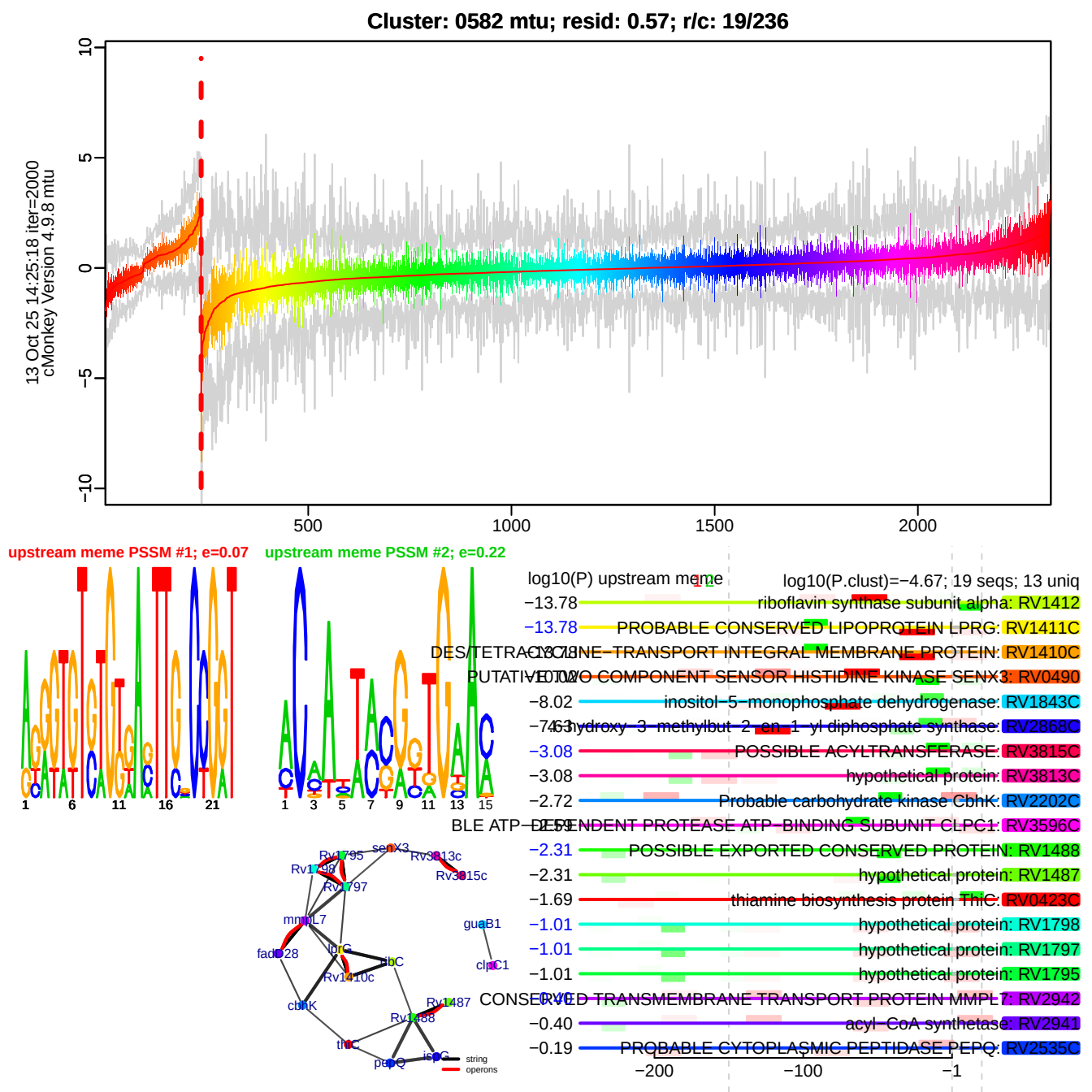
Cluster: 0582 mtu; resid: 0.57; r/c: 19/236
13 Oct 25 14:25:18 iter=2000
cMonkey Version 4.9.8 mtu
upstream meme PSSM #1; e=0.07
upstream meme PSSM #2; e=0.22
log10(P) upstream meme
log10(P.clust)=−4.67; 19 seqs; 13 uniq
−13.78 riboflavin synthase subunit alpha: RV1412
−13.78 PROBABLE CONSERVED LIPOPROTEIN LPRG: RV1411C
DES/TETRACYCLINE−TRANSPORT INTEGRAL MEMBRANE PROTEIN: RV1410C
PUTATIVE TWO COMPONENT SENSOR HISTIDINE KINASE SENX3: RV0490
−8.02 inositol−5−monophosphate dehydrogenase: RV1843C
−7.63 hydroxy−3−methylbut−2−en−1−yl diphosphate synthase: RV2868C
−3.08 POSSIBLE ACYLTRANSFERASE: RV3815C
−3.08 hypothetical protein: RV3813C
−2.72 Probable carbohydrate kinase CbhK: RV2202C
BLE ATP−DEPENDENT PROTEASE ATP−BINDING SUBUNIT CLPC1: RV3596C
−2.31 POSSIBLE EXPORTED CONSERVED PROTEIN: RV1488
−2.31 hypothetical protein: RV1487
−1.69 thiamine biosynthesis protein ThiC: RV0423C
−1.01 hypothetical protein: RV1798
−1.01 hypothetical protein: RV1797
−1.01 hypothetical protein: RV1795
CONSERVED TRANSMEMBRANE TRANSPORT PROTEIN MMPL7: RV2942
−0.40 acyl−CoA synthetase: RV2941
−0.19 PROBABLE CYTOPLASMIC PEPTIDASE PEPQ: RV2535C
−200
−100
−1
Rv1795
senX3
Rv3813c
Rv1796
Rv3815c
Rv1797
mmpL7
guaB1
fadD28
lprG
cbhC
clpC1
Rv1410c
cbhK
Rv1487
Rv1488
thiC
pepQ
isoG
string
operons