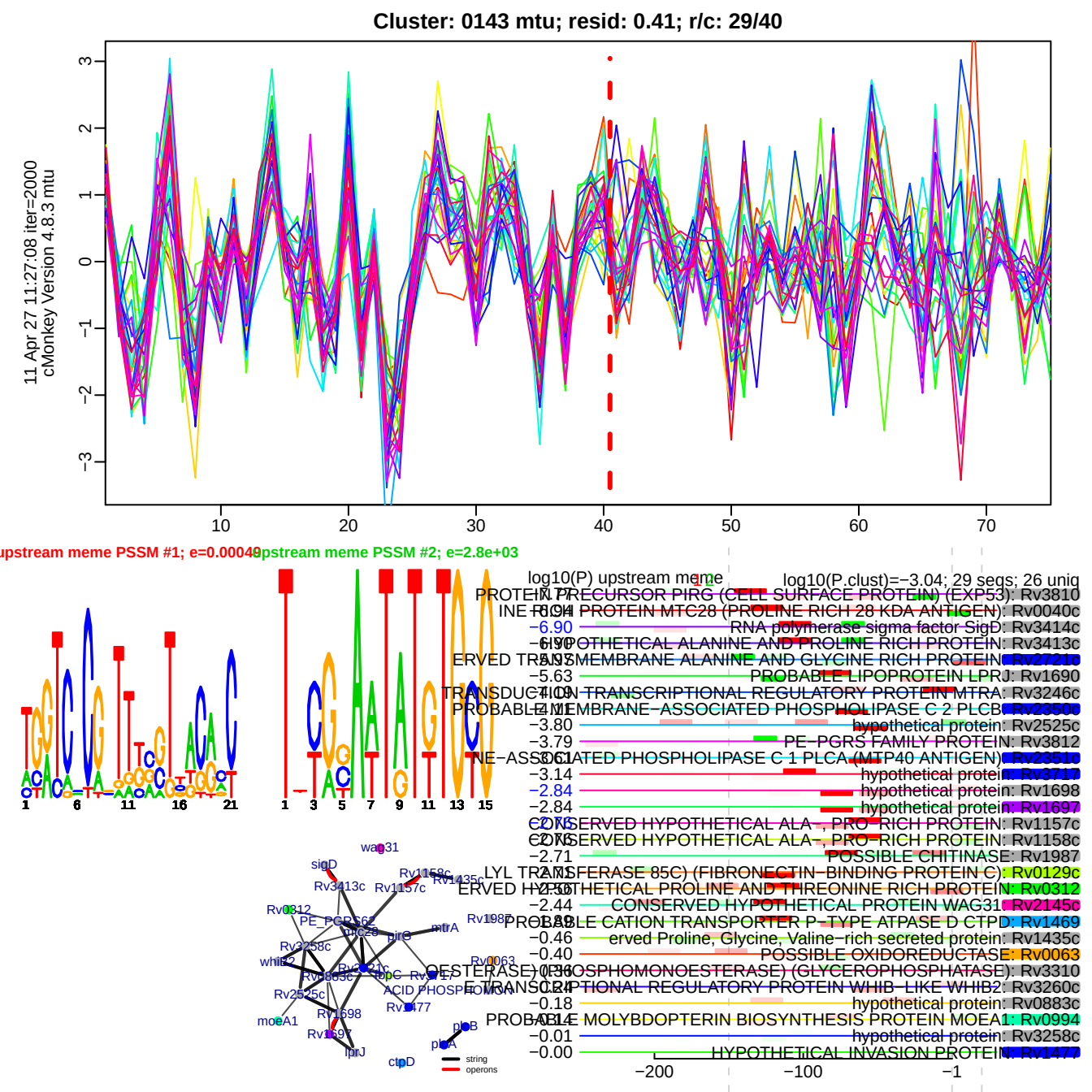
Cluster: 0143 mtu; resid: 0.41; r/c: 29/40
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=0.00049
upstream meme PSSM #2; e=2.8e+03
log10(P) upstream meme
log10(P.clust)=−3.04; 29 seqs; 26 uniq
PROTEIN: Rv3810
INE RICH PROTEIN MTC28 (PROLINE RICH 28 KDA ANTIGEN): Rv0040c
RNA polymerase sigma factor SigD: Rv3414c
HYPOTHETICAL ALANINE AND PROLINE RICH PROTEIN: Rv3413c
ERVED TRANSMEMBRANE ALANINE AND GLYCINE RICH PROTEIN: Rv2716c
PROBABLE LIPOPROTEIN LPRJ: Rv1690
TRANSDUCTION TRANSCRIPTIONAL REGULATORY PROTEIN MTRA: Rv3246c
PROBABLE MEMBRANE−ASSOCIATED PHOSPHOLIPASE C 2 PLCB: Rv2350c
hypothetical protein: Rv2525c
PE−PGRS FAMILY PROTEIN: Rv3812
NE−ASSOCIATED PHOSPHOLIPASE C 1 PLCA (MTP40 ANTIGEN): Rv2351c
hypothetical protein: Rv3717
hypothetical protein: Rv1698
hypothetical protein: Rv1697
CONSERVED HYPOTHETICAL ALA−, PRO−RICH PROTEIN: Rv1157c
CONSERVED HYPOTHETICAL ALA−, PRO−RICH PROTEIN: Rv1158c
POSSIBLE CHITINASE: Rv1987
LYL TRANSFERASE 85C) (FIBRONECTIN−BINDING PROTEIN C): Rv0129c
ERVED HYPOTHETICAL PROLINE AND THREONINE RICH PROTEIN: Rv0312
CONSERVED HYPOTHETICAL PROTEIN WAG31: Rv2145c
PROBABLE CATION TRANSPORTER P−TYPE ATPASE D CTPD: Rv1469
erved Proline, Glycine, Valine−rich secreted protein: Rv1435c
POSSIBLE OXIDOREDUCTASE: Rv0063
OESTERASE) (PHOSPHOMONOESTERASE) (GLYCEROPHOSPHATASE): Rv3310
E TRANSCRIPTIONAL REGULATORY PROTEIN WHIB−LIKE WHIB2: Rv3260c
hypothetical protein: Rv0883c
PROBABLE MOLYBDOPTERIN BIOSYNTHESIS PROTEIN MOEA1: Rv0994
hypothetical protein: Rv3258c
HYPOTHETICAL INVASION PROTEIN: Rv1477
wag31
sigD
Rv3413c
Rv1158c
Rv1157c
Rv1435c
Rv0312
PE_PGRS62
mtc28
pirG
mtrA
Rv1987
Rv3258c
whiB2
Rv0063
Rv2525c
ACID PHOSPHOMON
Rv1477
moeA1
Rv1698
Rv1697
lprJ
ctpD
plcB
plcA
string
operons