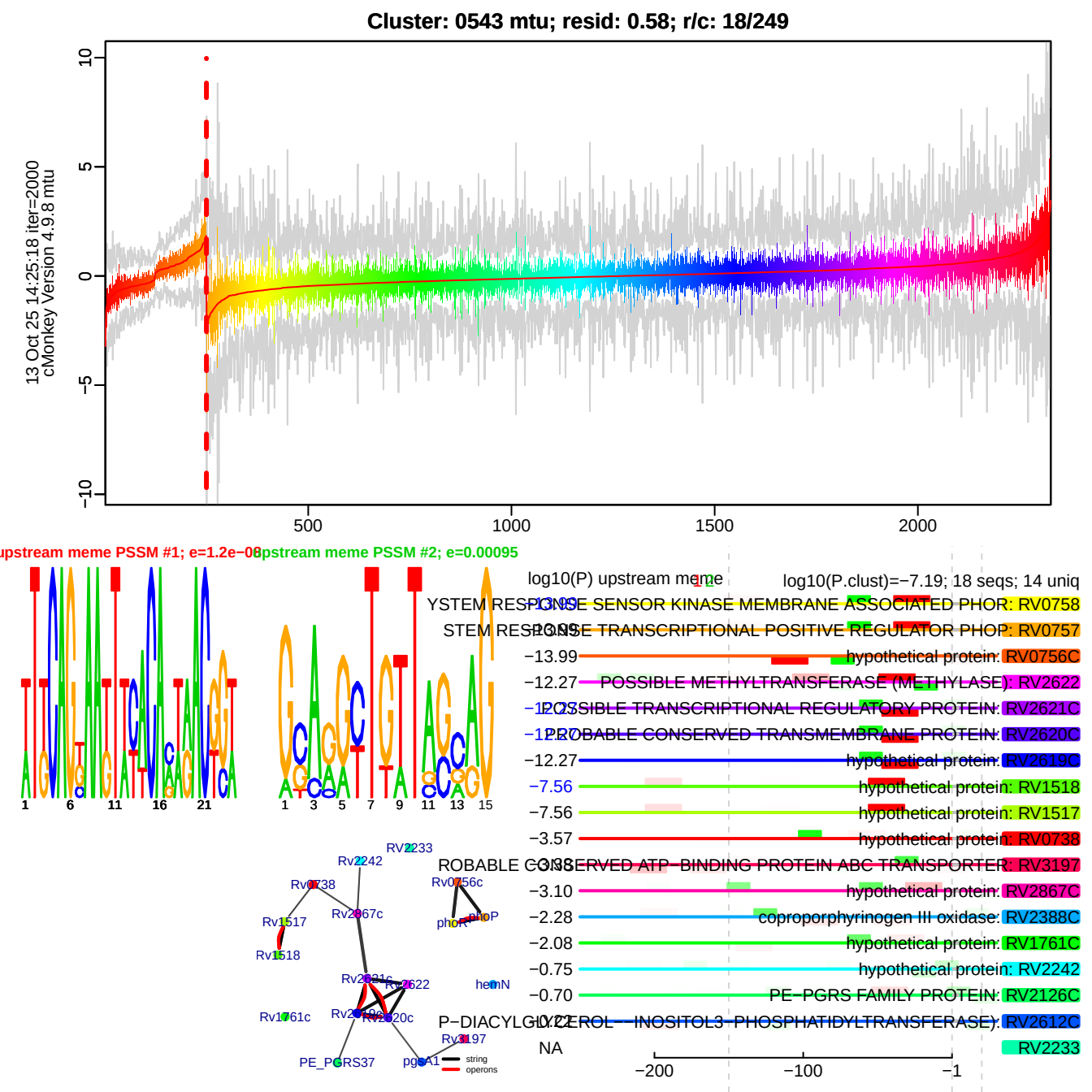
Cluster: 0543 mtu; resid: 0.58; r/c: 18/249
13 Oct 25 14:25:18 iter=2000
cMonkey Version 4.9.8 mtu
upstream meme PSSM #1; e=1.2e−08
upstream meme PSSM #2; e=0.00095
log10(P) upstream meme
log10(P.clust)=−7.19; 18 seqs; 14 uniq
YSTEM RESPONSE SENSOR KINASE MEMBRANE ASSOCIATED PHOR: RV0758
STEM RESPONSE TRANSCRIPTIONAL POSITIVE REGULATOR PHOP: RV0757
−13.99 hypothetical protein: RV0756C
−12.27 POSSIBLE METHYLTRANSFERASE (METHYLASE): RV2622
POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN: RV2621C
ROBABLE CONSERVED TRANSMEMBRANE PROTEIN: RV2620C
−12.27 hypothetical protein: RV2619C
−7.56 hypothetical protein: RV1518
−7.56 hypothetical protein: RV1517
−3.57 hypothetical protein: RV0738
ROBABLE CONSERVED ATP−BINDING PROTEIN ABC TRANSPORTER: RV3197
−3.10 hypothetical protein: RV2867C
−2.28 coproporphyrinogen III oxidase: RV2388C
−2.08 hypothetical protein: RV1761C
−0.75 hypothetical protein: RV2242
−0.70 PE−PGRS FAMILY PROTEIN: RV2126C
P−DIACYLGLYCEROL−INOSITOL3−PHOSPHATIDYLTRANSFERASE): RV2612C
RV2233
NA
Rv2242
Rv0738
Rv2867c
Rv1517
Rv1518
Rv2233c
Rv2622
Rv1761c
Rv2620c
PE_PGRS37
pgsA1
Rv3197
Rv0756c
phoR
phoP
hemN
string
operons
−200
−100
−1