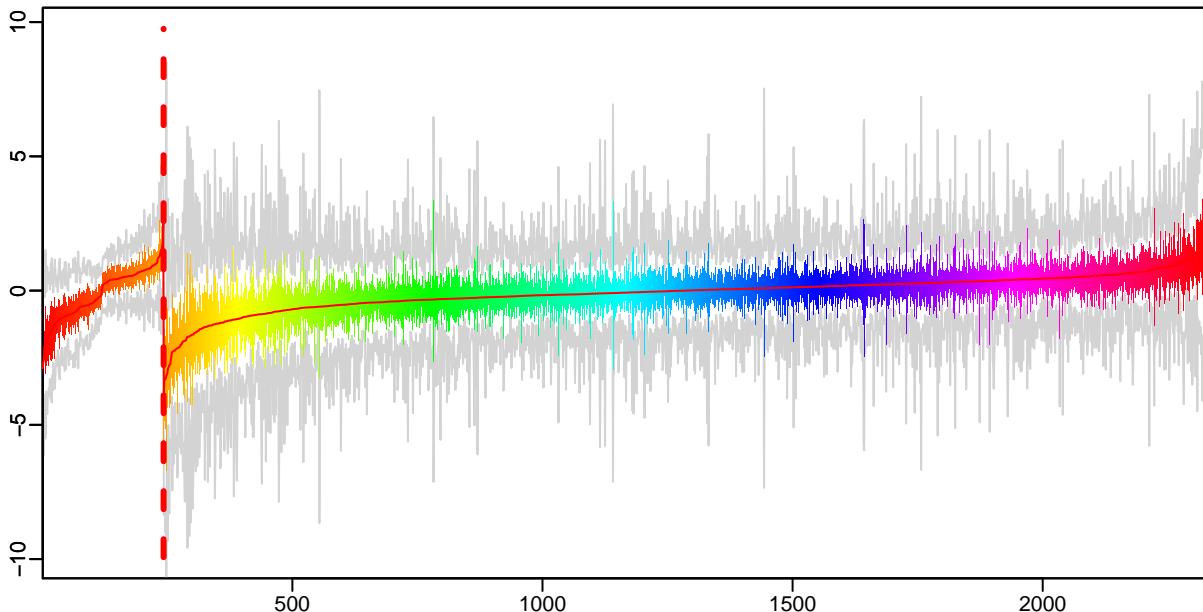**Cluster: 0407 mtu; resid: 0.55; r/c: 20/242**

13 Oct 25 14:25:18 iter=2000
cMonkey Version 4.9.8 mtu

upstream meme PSSM #1; e=0.096

upstream meme PSSM #2; e=1.7

log10(P) upstream meme

log10(P.clust)=−4.09; 20 seqs; 14 uniq

log10(P)	Description
−11.71	PROBABLE TRANSMEMBRANE PROTEIN: RV1234
−11.71	hypothetical protein: RV1233C
−7.11	hypothetical protein: RV0801
−7.11	putative aminopeptidase 2: RV0800
−7.10	29 KDa ANTIGEN CFP29: RV0798C
−7.10	hypothetical protein: RV0799C
−3.96	hypothetical protein: RV2771C
−3.59	PROBABLE BACTERIOFERRITIN COMIGRATORY PROTEIN BCP: RV2521
−3.44	hypothetical protein: RV0036C
−3.33	POSSIBLE CONSERVED MEMBRANE GLYCINE RICH PROTEIN: RV2575
−2.75	phosphatidylserine decarboxylase: RV0437C
−2.75	ASE PSSA (PS SYNTHASE) (PHOSPHATIDYLSERINE SYNTHASE): RV0436C
−2.75	PUTATIVE CONSERVED ATPASE: RV0435C
−2.26	hypothetical protein: RV0804
−2.26	phosphoribosylformylglycinamidine synthase II: RV0803
−1.04	BLUE DEHYDROGENASE FAD flavoprotein GMC oxidoreductase: RV1279
−0.72	Probable acyl−CoA thioesterase II tesB1: RV1618
−0.72	pyruvate kinase: RV1617
−0.18	POLIDE−TRANSPORT ATP−BINDING PROTEIN ABC TRANSPORTER: RV1667C
−0.18	hypothetical protein: RV0487

string
operons