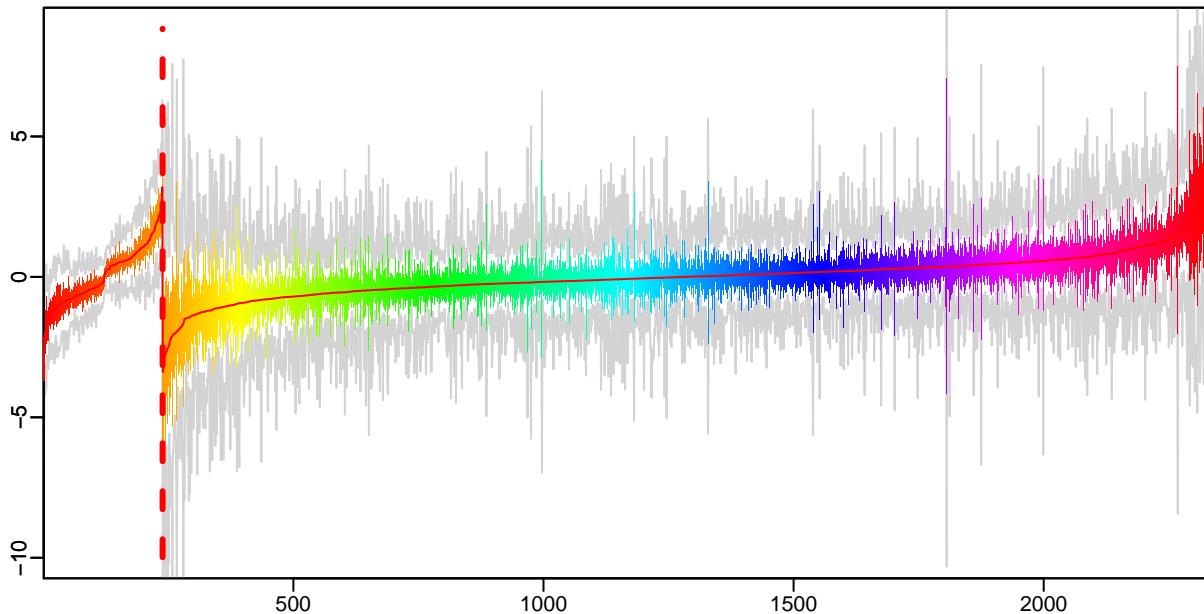**Cluster: 0195 mtu; resid: 0.47; r/c: 16/238**

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

upstream meme PSSM #1; e=1.6e−30   upstream meme PSSM #2; e=1.6e−29

log10(P) upstream meme   log10(P.clust)=−10.75; 16 seqs; 13 uniq

−21.55	PROBABLE TRANSPOSASE: RV1047
−21.55	PROBABLE TRANSPOSASE: RV3115
−21.55	PROBABLE TRANSPOSASE: RV3023C
−21.55	IS1081 transposase: RV2512C
−21.55	POSSIBLE TRANSPOSASE: RV1199C
−21.55	hypothetical protein: RV1046C
−5.80	50S ribosomal protein L1: RV0641
−5.80	50S ribosomal protein L11: RV0640
−5.80	transcription antitermination protein NusG: RV0639
−5.12	transcription elongation factor GreA: RV1080C
−4.81	POSSIBLE MYCOLIC ACID SYNTHASE UMAA: RV0469
−4.74	PE FAMILY PROTEIN: RV1195
−4.29	DNA−directed RNA polymerase subunit omega: RV1390
−4.29	guanylate kinase: RV1389
−1.38	PPE FAMILY PROTEIN: RV1196
−0.70	PE FAMILY PROTEIN: RV3478