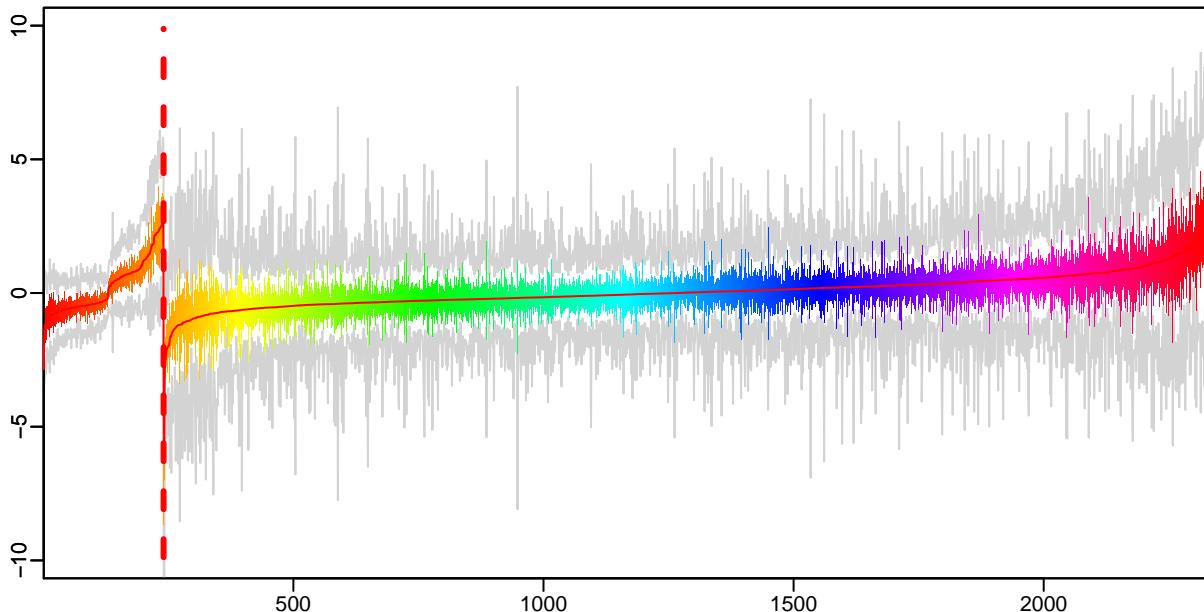**Cluster: 0158 mtu; resid: 0.52; r/c: 19/240**

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

upstream meme PSSM #1; e=2e+04 upstream meme PSSM #2; e=3.3e+04

log10(P) upstream meme   log10(P.clust)=−1.46; 19 seqs; 15 uniq

log10(P)	Description
−5.19	POSSIBLE TRANSMEMBRANE PROTEIN: RV0426C
−4.48	PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: RV0188
−4.20	hypothetical protein: RV3241C
−1.69	SERVED HYPOTHETICAL ALANINE AND ARGININE RICH PROTEIN: RV2731
−1.68	POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN: RV2745C
−1.67	hypothetical protein: RV2694C
−1.47	TRANSTRANSFERASE) (FARNESYL PYROPHOSPHATE SYNTHETASE): RV1086
−1.46	SE) (PYRUVATE DEHYDROGENASE) (PYRUVIC DEHYDROGENASE): RV2497C
−1.46	SE) (PYRUVATE DEHYDROGENASE) (PYRUVIC DEHYDROGENASE): RV2496C
−1.36	branched−chain alpha−keto acid dehydrogenase subunit E2: RV2495C
−1.09	BLE ATP−DEPENDENT PROTEASE ATP−BINDING SUBUNIT CLPC1: RV3596C
−0.70	inositol−5−monophosphate dehydrogenase: RV1843C
−0.41	POSSIBLE ACYLTRANSFERASE: RV3816C
−0.41	POSSIBLE ACYLTRANSFERASE: RV3814C
−0.17	1−acylglycerol−3−phosphate O−acyltransferase: RV2182C
−0.17	hypothetical protein: RV2342
−0.15	CONSERVED 35 KDA ALANINE RICH PROTEIN: RV2744C
−0.06	POSSIBLE CONSERVED TRANSMEMBRANE ALANINE RICH PROTEIN: RV2743C
−0.01	acyl−CoA synthetase: RV0270

string
operons