**Cluster: 0268 mtu; resid: 0.48; r/c: 16/236**

13 Oct 25 14:25:18 iter=2000
cMonkey Version 4.9.8 mtu
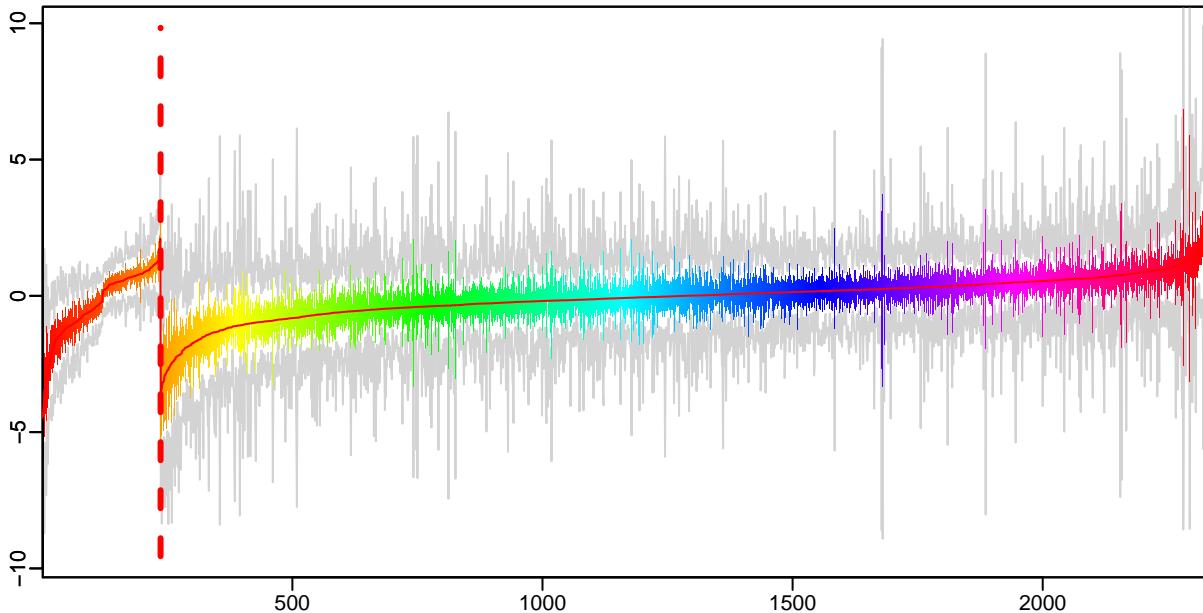
upstream meme PSSM #1; e=51
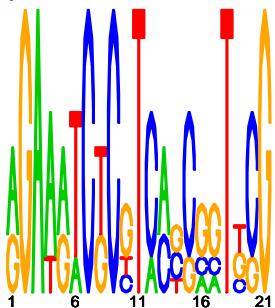
upstream meme PSSM #2; e=620
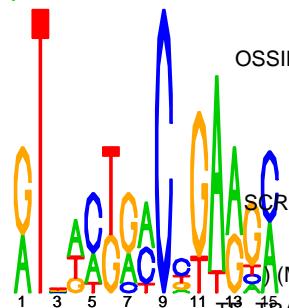
log10(P) upstream meme

log10(P.clust)=−4.70; 16 seqs; 10 uniq

log10(P)		
	POSSIBLE METAL CATION TRANSPORTING P−TYPE ATPASE CTPH:	RV0425C
−9.82	hypothetical protein:	RV0424C
−8.33	DNA polymerase III subunit alpha:	RV1547
−6.65	hypothetical protein:	RV3300C
	TRANSCRIPTIONAL REGULATORY PROTEIN (PROBABLY TETR−FAMILY):	RV3295
−6.34	molybdenum cofactor biosynthesis protein A:	RV0869C
−6.30	(MOLYBDOPTERIN [MPT] CONVERTING FACTOR, SUBUNIT 1):	RV0868C
	PHOSPHATE−TRANSPORT ATP−BINDING PROTEIN ABC TRANSPORTER PHOT:	RV0820
−2.37	NADH dehydrogenase subunit G:	RV3151
−2.37	NADH dehydrogenase subunit E:	RV3149
−2.37	NADH dehydrogenase subunit M:	RV3157
−2.37	NADH dehydrogenase subunit B:	RV3146
−2.14	PROBABLE ATP−DEPENDENT DNA HELICASE HELY:	RV2092C
−1.55	hypothetical protein:	RV2074
	TWO COMPONENT. SENSORY TRANSDUCTION HISTIDINE KINASE MTRB:	RV3245C
−1.12	PROBABLE CONSERVED LIPOPROTEIN LPQB:	RV3244C