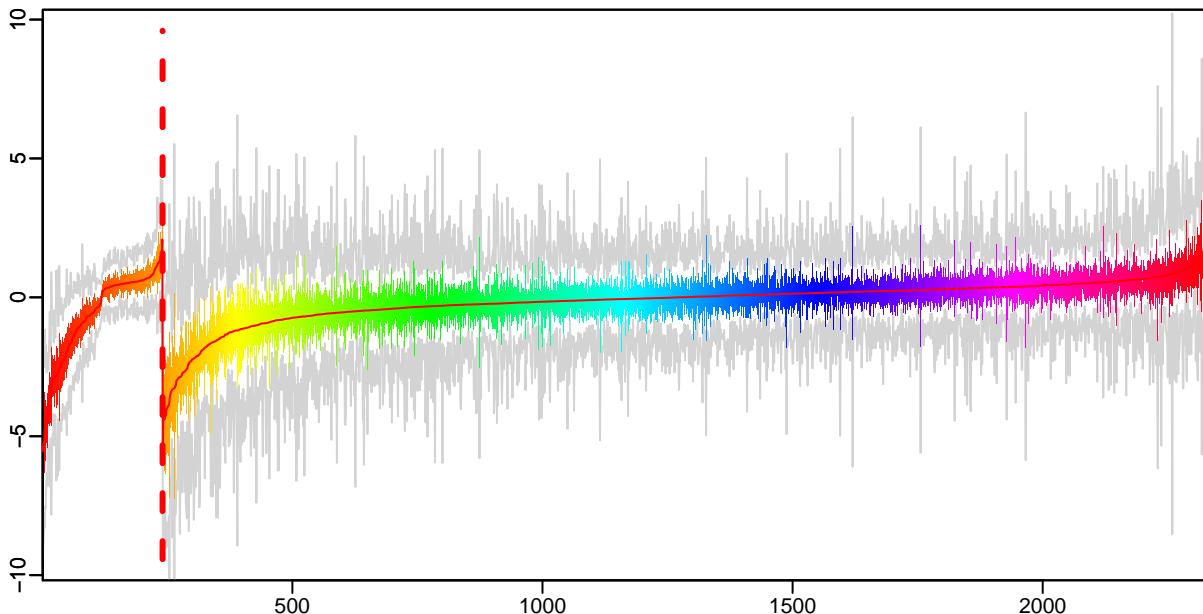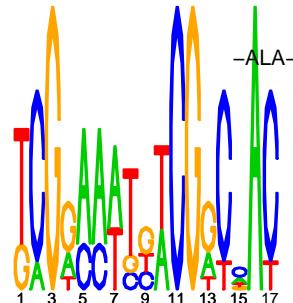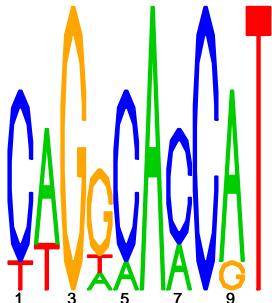**Cluster: 0208 mtu; resid: 0.56; r/c: 15/240**

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

upstream meme PSSM #1; e=2.2e+03   upstream meme PSSM #2; e=230

log10(P) upstream meme   log10(P.clust)=−3.46; 15 seqs; 13 uniq

	–ALA–D–ALA (CARBOXYPEPTIDASE) (D–AMINO ACID HYDROLASE):	RV2911
–5.56	hypothetical protein:	RV3228
–5.56	3–phoshoshikimate 1–carboxyvinyltransferase:	RV3227
–5.04	leucyl aminopeptidase:	RV2213
–4.82	POSSIBLE DEHYDROGENASE:	RV3726
–4.34	hypothetical protein:	RV2067C
–3.61	hypothetical protein:	RV3438
–3.52	prolipoprotein diacylglyceryl transferase:	RV1614
–3.52	indole–3–glycerol–phosphate synthase:	RV1611
–2.64	POSSIBLE CONSERVED LIPOPROTEIN LPQE:	RV3584
–2.45	hypothetical protein:	RV3686C
–1.76	hypothetical protein:	RV3718C
	ANSFERASE 85C) (FIBRONECTIN–BINDING PROTEIN C) (85C):	RV3803C
–1.34	hypothetical protein:	RV2102
–0.03	Probable transmembrane protein:	RV2144C