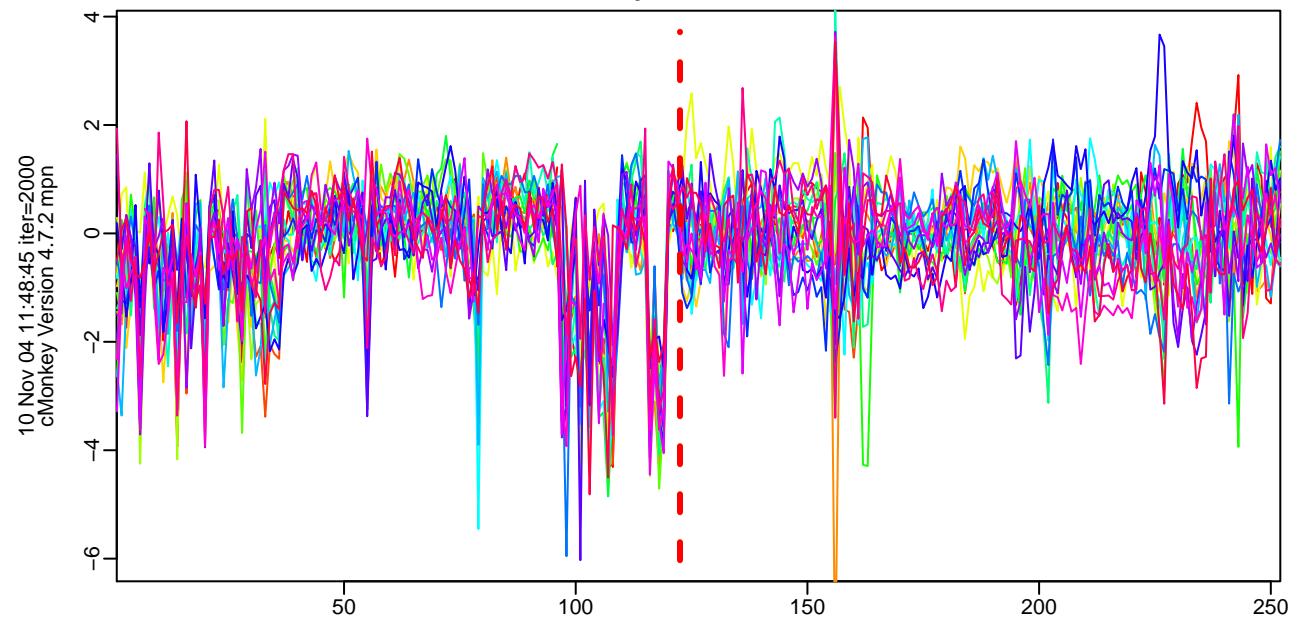
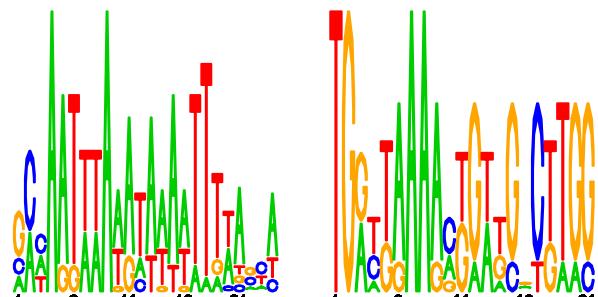


Cluster: 0050 mpn; resid: 0.51; r/c: 22/122



upstream meme PSSM #1; e=0.0021 upstream meme PSSM #2; e=18



$\log_{10}(P)$ upstream meme	$\log_{10}(P_{\text{clust}}) = -5.75$; 22 seqs; 15 uniq
-10.61	KtrA, K+ Na+ uptake: MPN461
-10.27	phosphoglyceromutase: MPN628
-10.27	elongation factor Ts: MPN631
-10.27	triosephosphate isomerase: MPN629
-10.27	tHPr protein kinase phosphoryltransferase (Enzyme I): MPN627
-8.45	hypothetical protein: MPN449
-8.45	hypothetical protein: MPN455
-7.72	membrane nuclease: MPN491
-6.70	hypothetical protein: MPN036
-6.26	Trk-type K+ transport systems, membrane components: MPN460
-4.48	hypothetical protein: MPN077
-4.34	methyltransferase GidB: MPN558
-4.85	carboxymethylaminomethyl modification enzyme GidA: MPN557
-4.24	pseudouridine synthase: MPN548
-4.24	ribonuclease III: MPN545
-4.24	fatty acid/phospholipid synthesis protein: MPN546
-2.81	hypothetical protein: MPN076
-2.71	cerol-3-phosphate transport system permease protein: MPN135
-2.17	chaperonin GroEL: MPN573
-1.48	hypothetical protein: MPN276
-1.10	predicted metalloenzyme interacting with hemolysin: MPN569
-1.10	A involved in regulating metabolism and cell division: MPN568

