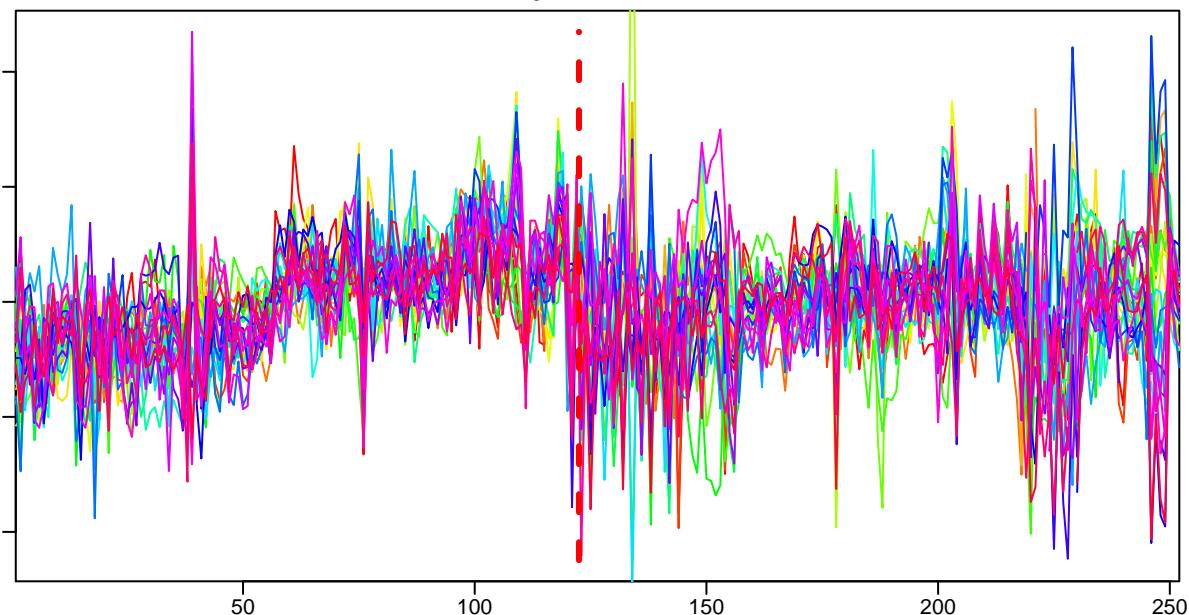
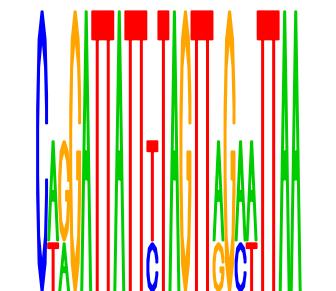
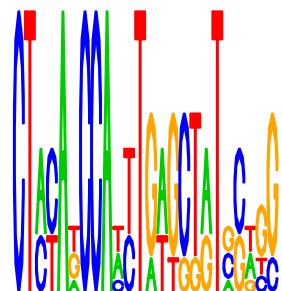


Cluster: 0068 mpn; resid: 0.47; r/c: 27/122

10 Nov 04 11:48:45 iter=2000
cMonkey Version 4.7.2 mpn



upstream meme PSSM #1; e=0.3 upstream meme PSSM #2; e=1.8e+03



log10(P) upstream meme	log10(P.clust)= -4.92; 27 seqs; 15 uniq
-18.87	DNA helicase II: MPN340
-18.87	icase II (with Mycoplasma specific C-terminal domain): MPN341
-18.87	hypothetical protein: MPN339
-18.87	putative nicotinate-nucleotide adenyltransferase: MPN336
-7.59	C family, chromosome/DNA binding/protection functions: MPN426
-7.59	cell division protein FtsY: MPN425
-7.59	hypothetical protein: MPN424
-7.08	5'-3' exonuclease (complete): MPN379
-5.84	methionyl tRNA synthetase: MPN023
-5.67	ical protein, similar to reticulocalbin binding protein: MPN262
-1.72	topoisomerase IV subunit A: MPN123
-1.72	topoisomerase IV subunit B: MPN122
-1.36	ribonuclease III: MPN545
-1.36	threonyl tRNA synthetase: MPN553
-1.36	hypothetical protein: MPN552
-1.36	hypothetical protein: MPN551
-1.36	Thiamin biosynthesis protein: MPN550
-1.36	dihydroacetone kinase: MPN547
-1.36	fatty acid/phospholipid synthesis protein: MPN546
-1.25	hypothetical protein: MPN312
-0.85	DNA primase: MPN353
-0.54	triacylglycerol lipase (lip) 3: MPN519
-0.14	glutamine transport ATP-binding protein: MPN081
-0.11	hypothetical protein: MPN270
-0.09	CDP-diglyceride synthetase: MPN637
-0.04	DNA gyrase subunit A: MPN004
-0.04	DNA gyrase subunit B: MPN003

