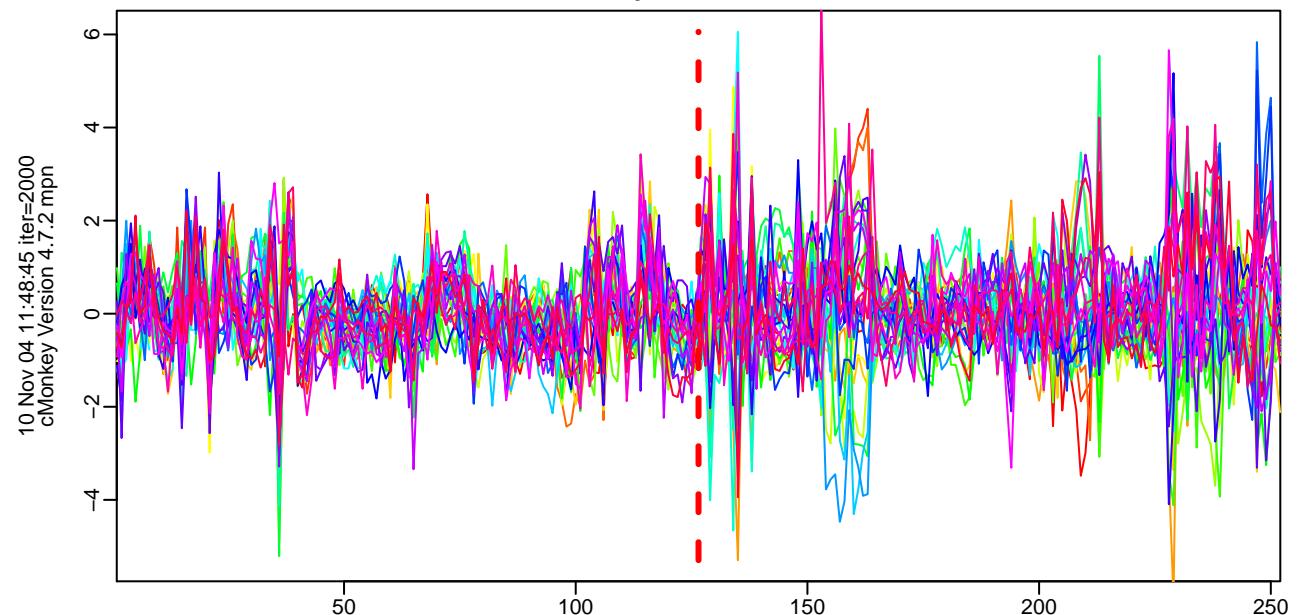
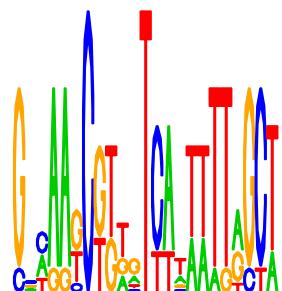


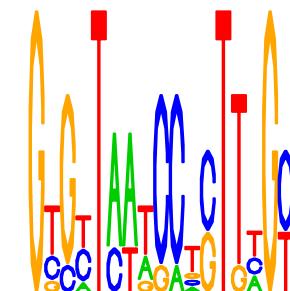
Cluster: 0032 mpn; resid: 0.51; r/c: 30/126



upstream meme PSSM #1; e=3.7



upstream meme PSSM #2; e=29



log10(P) upstream meme	log10(P.clust)= -3.47; 30 seqs; 19 uniq
-7.72	hypothetical protein: MPN419
-6.75	hypothetical protein: MPN673
-6.75	hypoxanthine-guanine phosphoribosyltransferase: MPN672
-5.64	hypothetical protein: MPN462
-5.14	threonine dehydrogenase; galactosyltransferase: MPN483
-4.98	PTS system, glucose-specific IIABC component: MPN207
-4.74	S-adenosylmethionine synthetases: MPN060
-4.72	triacylglycerol lipase (lip) 3: MPN445
-4.65	hypothetical protein: MPN469
-4.65	50S ribosomal protein L33: MPN471
-4.64	UV protection protein MucB: MPN537
-4.23	50S ribosomal protein L17: MPN192
-4.20	similar to cyto adherence proteins: MPN567
-4.20	q or Uplq glycerophosphoryl diester phosphodiesterase: MPN566
-3.95	DNA polymerase III alpha subunit: MPN378
-3.70	4'-phosphopantetheinyl transferase: MPN298
-3.70	hypothetical protein: MPN297
-3.70	30S ribosomal protein S21: MPN296
-3.70	hypothetical protein: MPN295
-2.68	hypothetical protein: MPN160
-2.68	ribosome binding factor A: MPN156
-2.68	translation initiation factor IF-2: MPN155
-1.23	hypothetical protein: MPN448
-0.56	GTPase ObgE: MPN663
-0.49	chromosomal replication initiation protein: MPN686
-0.49	inner membrane protein translocase component YidC: MPN680
-0.49	glutamyl-tRNA synthetase: MPN678
-0.49	similar to ATPase: MPN677
-0.47	similar to hemolysin ABC-type exporter: MPN571
-0.19	exonuclease ABC subunit A: MPN619