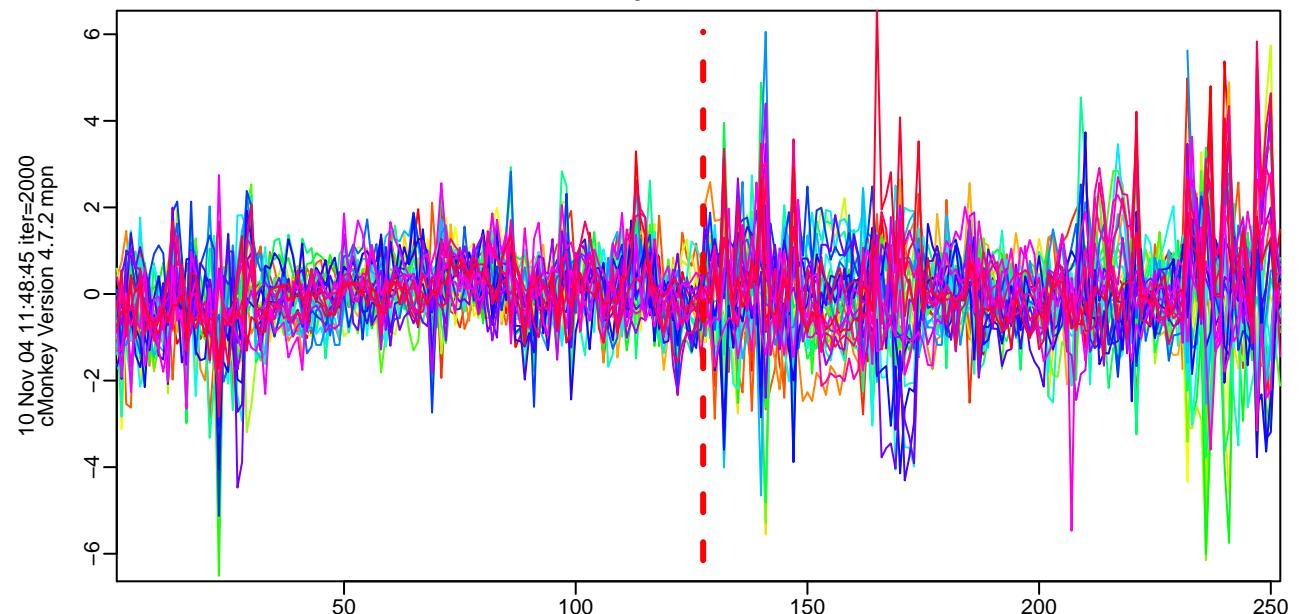
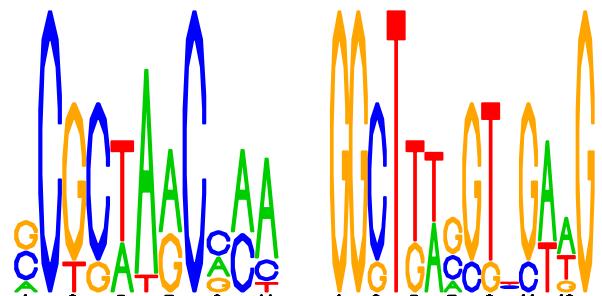


Cluster: 0067 mpn; resid: 0.51; r/c: 35/127



upstream meme PSSM #1; e=28 upstream meme PSSM #2; e=2.9e+03



$\log_{10}(P)$ upstream meme	$\log_{10}(P)$ clust= -2.55; 35 segs; 21 unig
-7.85	adenine-specific methyltransferase ECORI: MPN198
-7.85	30S ribosomal protein S14: MPN178
-6.57	150-end, similar to phosphate hydrolysing: MPN264
-6.57	thioredoxin: MPN263
-6.57	Ser/Thr/Tyr protein kinase: MPN248
-4.87	similar to helicases: MPN020
-4.67	methionine sulfoxide reductase B: MPN662
-4.67	hypothetical protein: MPN661
-3.84	30S ribosomal protein S4: MPN446
-3.33	hypothetical protein: MPN419
-2.86	segregation and condensation protein B: MPN201
-2.86	condensation protein A/unknown domain fusion protein: MPN300
-2.86	30S ribosomal protein S21: MPN296
-2.86	hypothetical protein: MPN295
-2.86	similar to intracellular protease: MPN294
-2.64	tyrosyl tRNA synthetase: MPN669
-2.44	aa permeases: MPN095
-2.35	hypothetical protein: MPN121
-1.91	similar to cytadherence proteins: MPN567
-1.91	g or Upf glycerophosphoryl diester phosphodiesterase: MPN566
-1.19	similar to PHOSPHOTRIESTERASE HOMOLOGY PROTEIN: MPN497
-1.19	similar to hemolysin ABC-type exporter: MPN571
-1.06	hypothetical protein: MPN582
-0.39	protein export, secD-like: MPN396
-0.29	large inner membrane protein translocase component YidC: MPN680
-0.29	similar to ATPase: MPN677
-0.29	ABC transporter subunit: MPN683
-0.29	dimethyladenosine transferase: MPN679
-0.29	glutamyl tRNA synthetase: MPN678
-0.28	hypothetical protein: MPN484
-0.25	hypoxanthine-guanine phosphoribosyltransferase: MPN672
-0.22	hypothetical protein: MPN290
-0.14	transcription elongation factor GreA: MPN401
-0.05	acetate kinase: MPN533