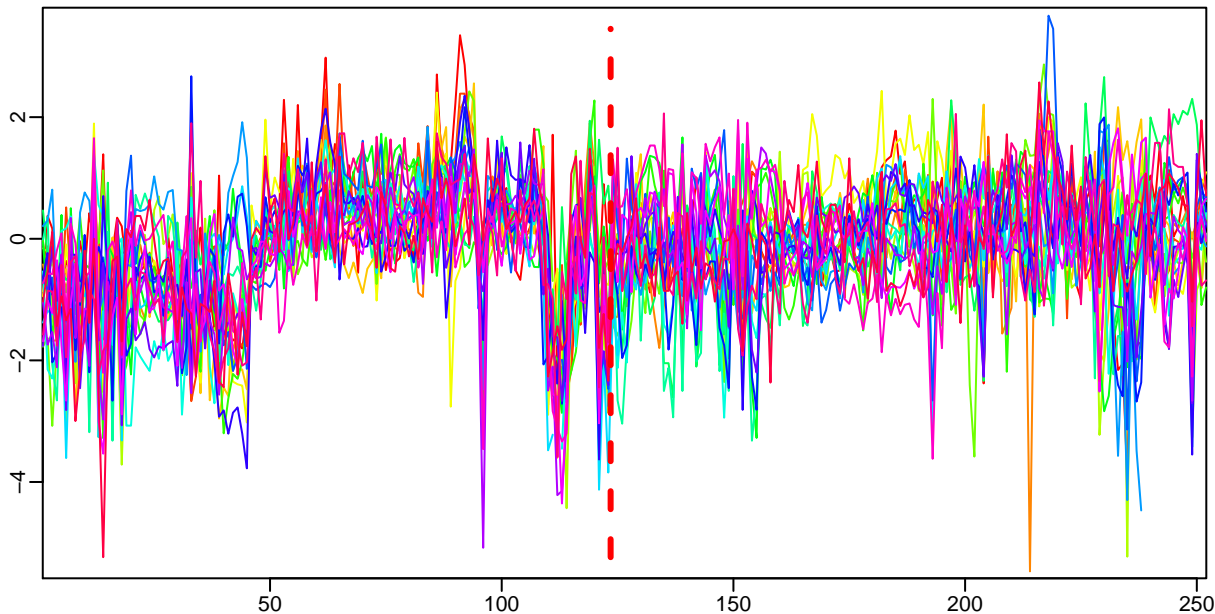# Cluster: 0010 mpn; resid: 0.53; r/c: 23/123

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

upstream meme PSSM #1; e=0.16 **upstream meme PSSM #2; e=7.6e+03**

log10(P) upstream meme | log10(P.clust)=−3.11; 23 seqs; 15 uniq

log10(P)	description	gene
−6.14	hypothetical protein:	MPN501
−5.40	hypothetical protein:	MPN121
−5.40	heat shock protein GrpE:	MPN120
−5.40	of DnaJ; and a domain common to cytadherence proteins:	MPN119
−4.09	arginyl−tRNA synthetase:	MPN556
−4.09	hypothetical protein:	MPN551
−4.09	pseudouridine synthase:	MPN548
−4.09	dihydroacetone kinase:	MPN547
−4.09	ribonuclease III:	MPN545
−4.01	peptide deformylase:	MPN245
−3.75	hypothetical protein:	MPN270
−3.45	hypothetical protein:	MPN363
−3.41	hypothetical protein:	MPN456
−2.54	thioredoxin reductase:	MPN240
−2.54	hypothetical protein:	MPN239
−2.51	similar to metallo hydrolase:	MPN621
−2.24	ribosome releasing factor:	MPN636
−0.75	hypothetical protein:	MPN408
−0.11	hypothetical protein:	MPN011
−0.11	abc transport ATP−binding protein:	MPN433
−0.11	permease:	MPN431
−0.02	trigger factor:	MPN331
NA		MPN012