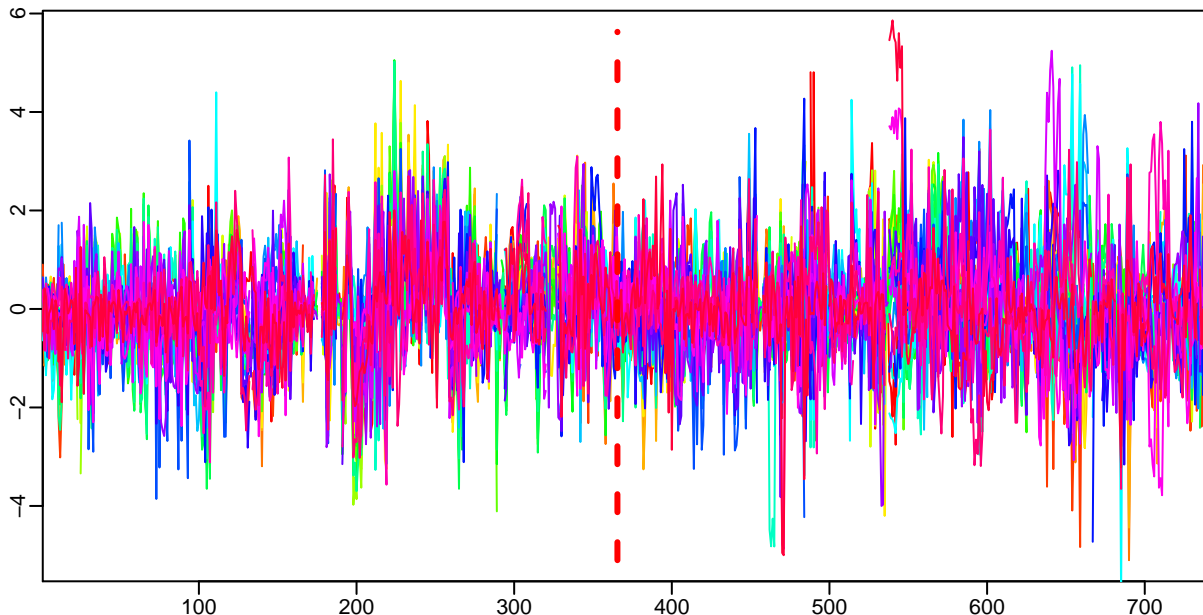
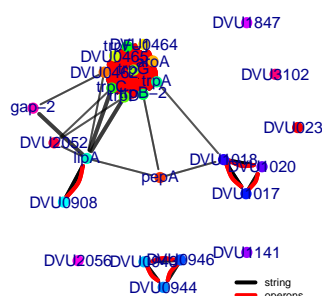
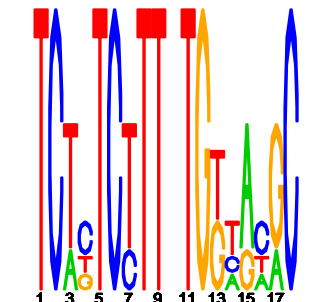
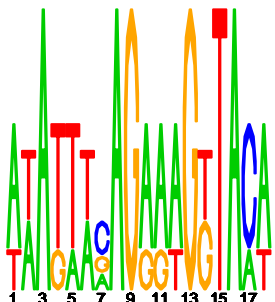


Cluster: 0054 dvu; resid: 0.57; r/c: 26/365

11 Mar 02 17:37:51 iter=1699
cMonkey Version 4.8.2 dvu



upstream meme PSSM #1; e=110 upstream meme PSSM #2; e=1e+03



log10(P) upstream meme	log10(P.clust)=-3.61; 26 seqs; 12 uniq
-11.16	site-specific recombinase, phage integrase family: DVU0236
-10.40	pendent transcriptional regulator/response regulator: DVU0946
-10.40	hypothetical protein: DVU0944
-10.40	hypothetical protein: DVU0943
-10.03	HD domain/sensory box protein: DVU1020
-10.03	type I secretion membrane fusion protein, HlyD family: DVU1018
-10.03	BC transporter, ATP-binding protein/permease protein: DVU1017
-6.74	iron-sulfur cluster-binding protein, putative: DVU0908
-6.74	lipoyl synthase: DVU0905
-4.90	hypothetical protein: DVU3102
-0.82	hypothetical protein: DVU1141
-0.61	glycosyl transferase, group 2 family protein: DVU2052
-0.54	hypothetical protein: DVU1847
-0.35	hypothetical protein: DVU2056
-0.10	glyceraldehyde 3-phosphate dehydrogenase: DVU2144
-0.06	tryptophan synthase subunit alpha: DVU0471
-0.06	tryptophan synthase subunit beta: DVU0470
-0.06	N-(5'-phosphoribosyl)anthranilate isomerase: DVU0469
-0.06	indole-3-glycerol phosphate synthase: DVU0468
-0.06	anthranilate phosphoribosyltransferase: DVU0467
-0.06	ilate synthase, glutamine amidotransferase component: DVU0466
-0.06	anthranilate synthase, component I: DVU0465
-0.06	prephenate dehydrogenase: DVU0464
-0.06	3-phosphoshikimate 1-carboxyvinyltransferase: DVU0463
-0.06	chorismate mutase/prephenate dehydratase: DVU0462
-0.00	cytosol aminopeptidase: DVU0415