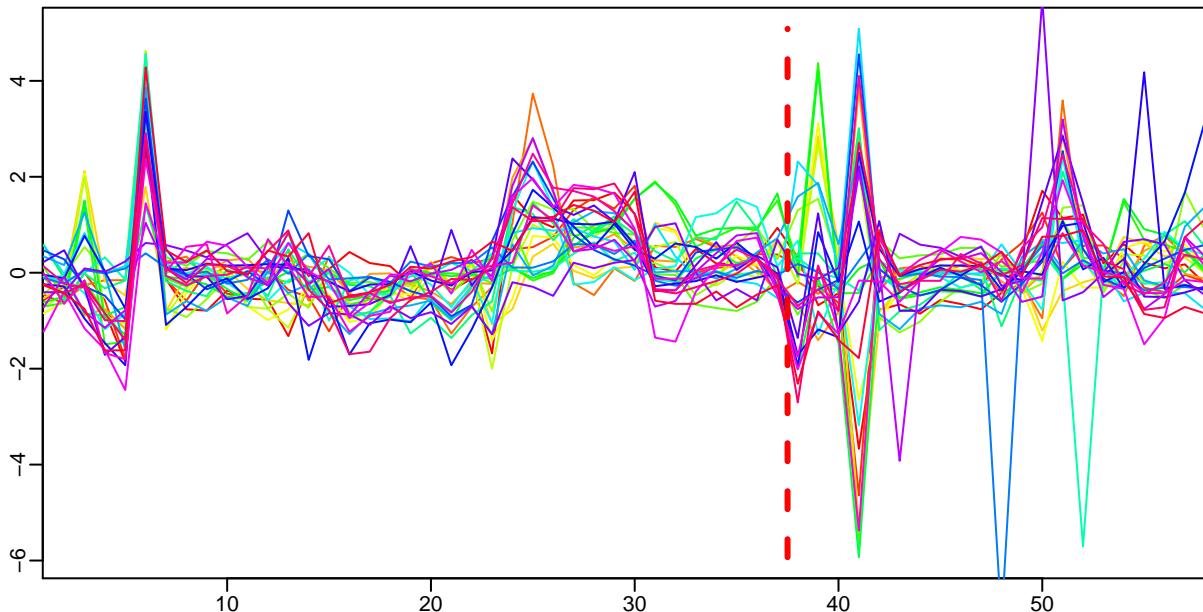**Cluster: 0001 mmp; resid: 0.42; r/c: 29/37**

upstream meme PSSM #1; e=30   upstream meme PSSM #2; e=7.6e+03

log10(P) upstream meme   log10(P.clust)=−1.55; 29 seqs; 19 uniq

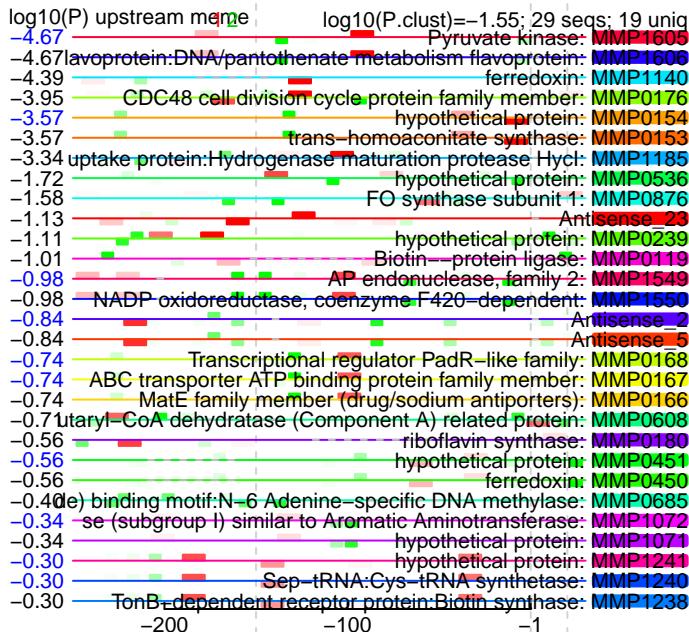|	
−4.67	Pyruvate kinase: MMP1605
−4.67	flavoprotein:DNA/pantothenate metabolism flavoprotein: MMP1606
−4.39	ferredoxin: MMP1140
−3.95	CDC48 cell division cycle protein family member: MMP0176
−3.57	hypothetical protein: MMP0154
−3.57	trans−homoaconitate synthase: MMP0153
−3.34	uptake protein:Hydrogenase maturation protease HycI: MMP1185
−1.72	hypothetical protein: MMP0536
−1.58	FO synthase subunit 1: MMP0876
−1.13	Antisense_23
−1.11	hypothetical protein: MMP0239
−1.01	Biotin−−protein ligase: MMP0119
−0.98	AP endonuclease, family 2: MMP1549
−0.98	NADP oxidoreductase, coenzyme F420−dependent: MMP1550
−0.84	Antisense_2
−0.84	Antisense_5
−0.74	Transcriptional regulator PadR−like family: MMP0168
−0.74	ABC transporter ATP binding protein family member: MMP0167
−0.74	MatE family member (drug/sodium antiporters): MMP0166
−0.71	Glutaryl−CoA dehydratase (Component A) related protein: MMP0608
−0.56	riboflavin synthase: MMP0180
−0.56	hypothetical protein: MMP0451
−0.56	ferredoxin: MMP0450
−0.40	(de) binding motif:N−6 Adenine−specific DNA methylase: MMP0685
−0.34	se (subgroup I) similar to Aromatic Aminotransferase: MMP1072
−0.34	hypothetical protein: MMP1071
−0.30	hypothetical protein: MMP1241
−0.30	Sep−tRNA:Cys−tRNA synthetase: MMP1240
−0.30	TonB−dependent receptor protein:Biotin synthase: MMP1238

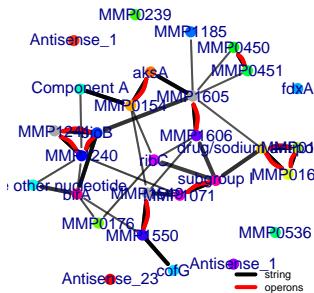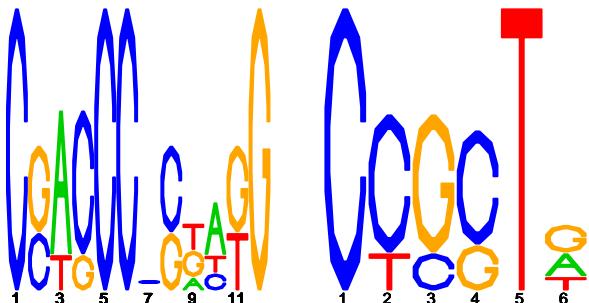−200   −100   −1

Cluster: 0002 mmp; resid: 0.20; r/c: 15/40

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cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=0.00077   upstream meme PSSM #2; e=1.8e+03

log10(P) upstream meme   log10(P.clust)=−2.82; 15 seqs; 13 uniq

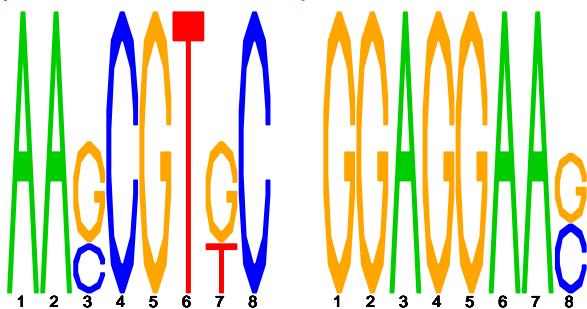| log10(P)	Description	Gene
−7.12	zein−L−isoaspartate(D−aspartate) O−methyltransferase:	MMP0102
−6.48	hypothetical protein:	MMP1059
−5.06	Antisense_10	
−3.23	hypothetical protein:	MMP0182
−2.90	Chymotrypsin serine protease, family S1:	MMP0785
−2.69	hypothetical protein:	MMP1338
−2.48	hypothetical protein:	MMP0115
−2.19	CBS domain:	MMP0863
−1.83	endent pyridine nucleotide−disulphide oxidoreductase:	MMP1332
−1.83	hypothetical protein:	MMP1331
−1.71	hypothetical protein:	MMP0600
−1.40	hydroxylamine reductase:	MMP0720
−1.32	oxidoreductase family member subunit alpha:	MMP0306
−1.32	2−oxoacid ferredoxin oxidoreductase subunit beta:	MMP0305
−0.80	exonuclease III:	MMP1012

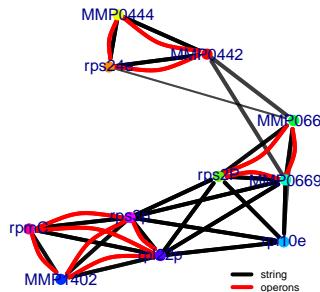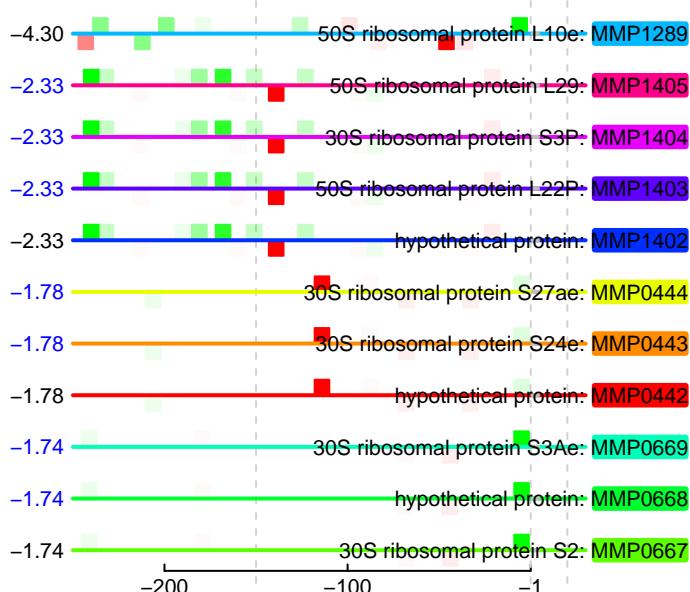**Cluster: 0003 mmp; resid: 0.13; r/c: 11/39**

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp
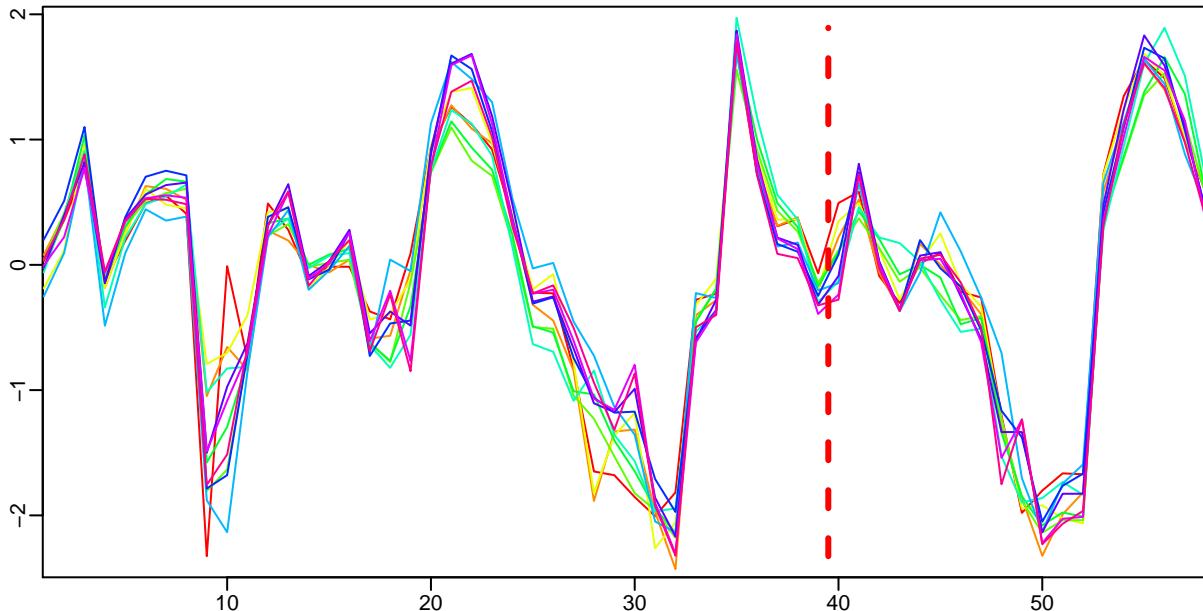
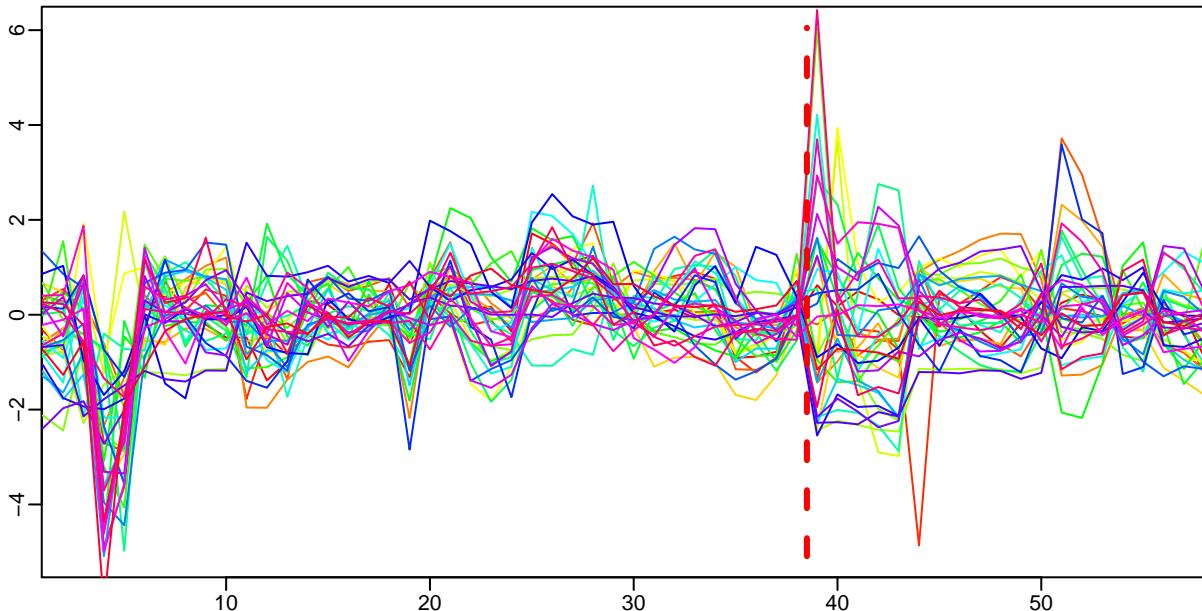upstream meme PSSM #1; e=390   upstream meme PSSM #2; e=1.1e+03

log10(P) upstream meme   log10(P.clust)=−2.20; 11 seqs; 4 uniq

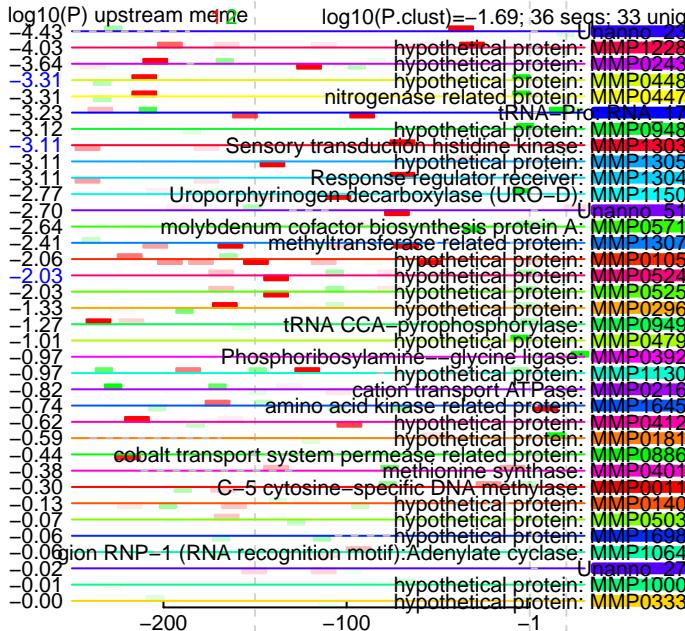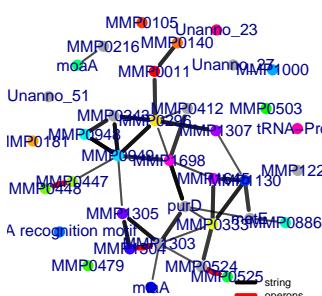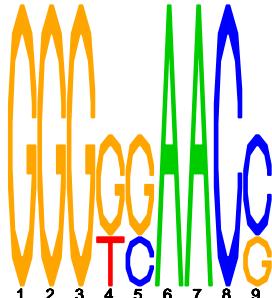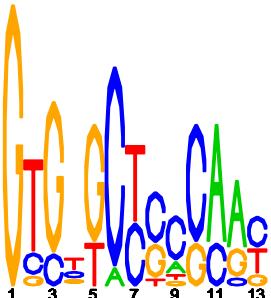| log10(P)	protein	gene
−4.30	50S ribosomal protein L10e:	MMP1289
−2.33	50S ribosomal protein L29:	MMP1405
−2.33	30S ribosomal protein S3P:	MMP1404
−2.33	50S ribosomal protein L22P:	MMP1403
−2.33	hypothetical protein:	MMP1402
−1.78	30S ribosomal protein S27ae:	MMP0444
−1.78	30S ribosomal protein S24e:	MMP0443
−1.78	hypothetical protein:	MMP0442
−1.74	30S ribosomal protein S3Ae:	MMP0669
−1.74	hypothetical protein:	MMP0668
−1.74	30S ribosomal protein S2:	MMP0667

string
operons

Cluster: 0004 mmp; resid: 0.53; r/c: 36/38

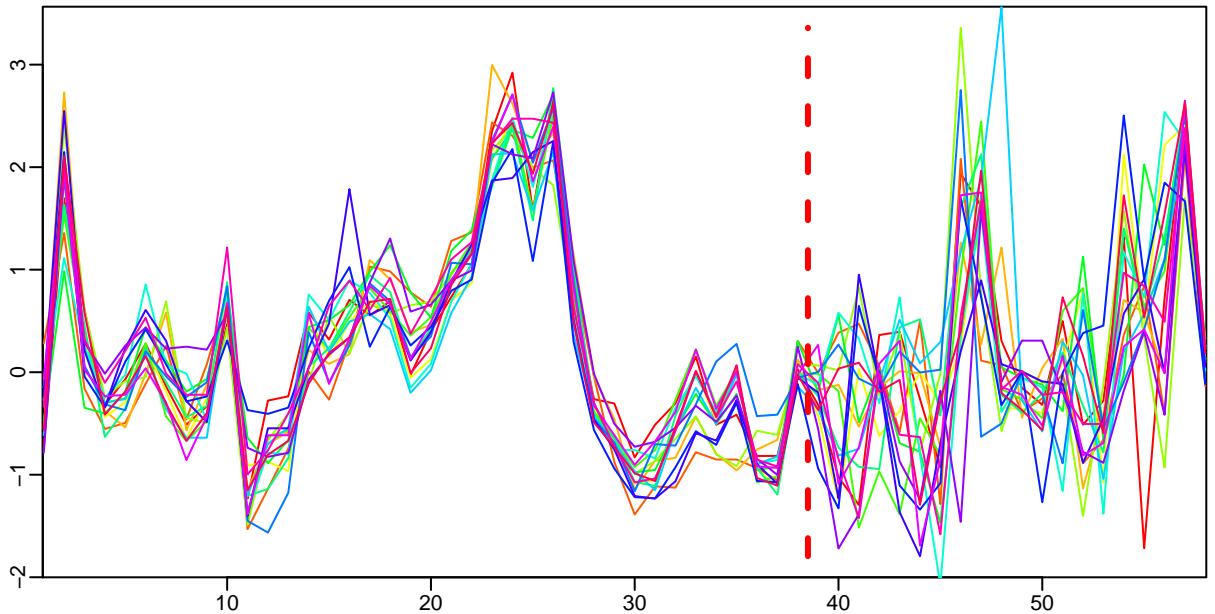11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

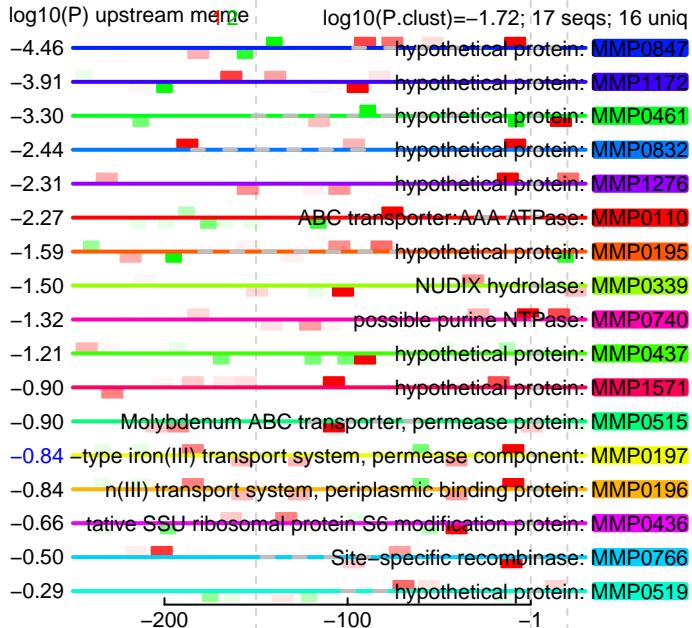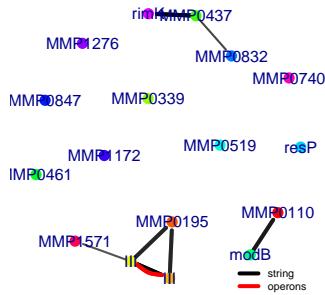upstream meme PSSM #1; e=0.023   upstream meme PSSM #2; e=1.1e+04

log10(P) upstream meme   log10(P.clust)=−1.69; 36 seqs: 33 uniq

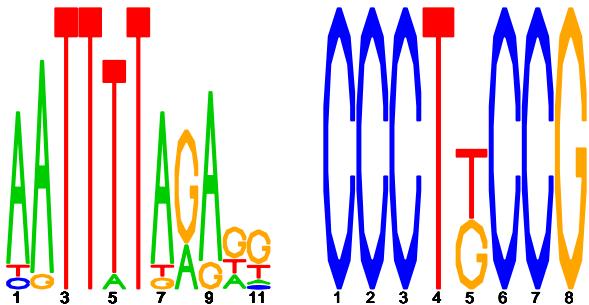| log10(P)	annotation	gene
−4.43		Unanno_23
−4.03	hypothetical protein:	MMP1228
−3.64	hypothetical protein:	MMP0243
−3.31	hypothetical protein:	MMP0448
−3.31	nitrogenase related protein:	MMP0447
−3.23	tRNA−Pro−RNA	17
−3.12	hypothetical protein:	MMP0948
−3.11	Sensory transduction histidine kinase:	MMP1303
−3.11	hypothetical protein:	MMP1305
−3.11	Response regulator receiver:	MMP1304
−2.77	Uroporphyrinogen−decarboxylase (URO−D):	MMP1150
−2.70		Unanno_51
−2.64	molybdenum cofactor biosynthesis protein A:	MMP0571
−2.41	methyltransferase related protein:	MMP1307
−2.06	hypothetical protein:	MMP0105
−2.03	hypothetical protein:	MMP0524
−2.03	hypothetical protein:	MMP0525
−1.33	hypothetical protein:	MMP0296
−1.27	tRNA CCA−pyrophosphorylase:	MMP0949
−1.01	hypothetical protein:	MMP0479
−0.97	Phosphoribosylamine−−glycine ligase:	MMP0392
−0.97	hypothetical protein:	MMP1130
−0.82	cation transport ATPase:	MMP0216
−0.74	amino acid kinase related protein:	MMP1645
−0.62	hypothetical protein:	MMP0412
−0.59	hypothetical protein:	MMP0181
−0.44	cobalt transport system permease related protein:	MMP0886
−0.38	methionine synthase:	MMP0401
−0.30	C−5 cytosine−specific DNA methylase:	MMP0011
−0.13	hypothetical protein:	MMP0140
−0.07	hypothetical protein:	MMP0503
−0.06	hypothetical protein:	MMP1698
−0.00	region RNP−1 (RNA recognition motif):Adenylate cyclase:	MMP1064
−0.02		Unanno_27
−0.01	hypothetical protein:	MMP1000
−0.00	hypothetical protein:	MMP0333

Cluster: 0005 mmp; resid: 0.38; r/c: 25/41

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cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=210   upstream meme PSSM #2; e=5.5e+03

log10(P) upstream meme   log10(P.clust)=−1.99; 25 seqs; 15 uniq

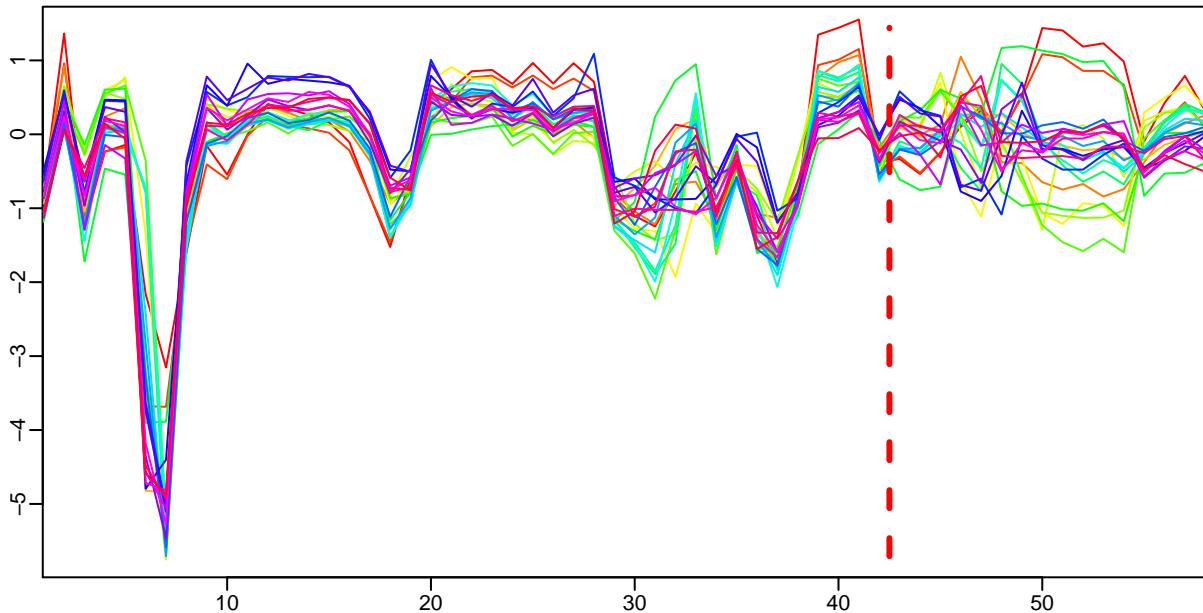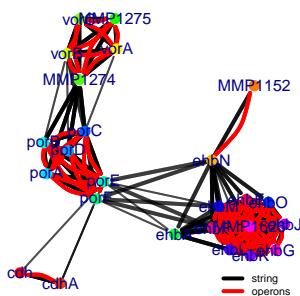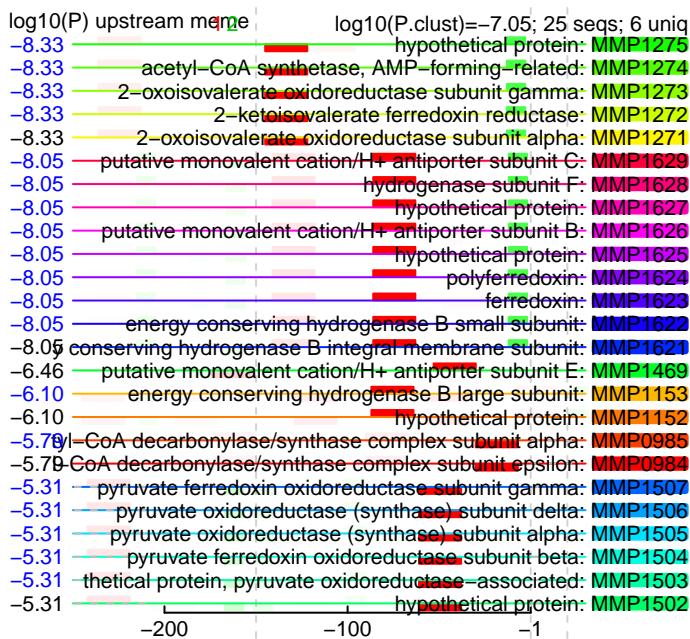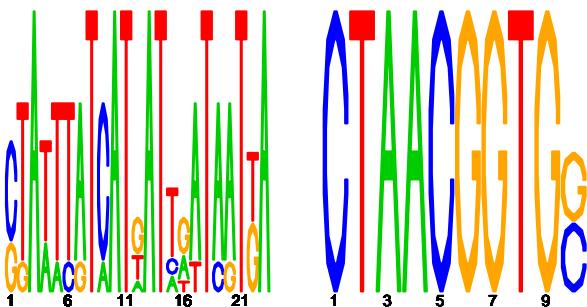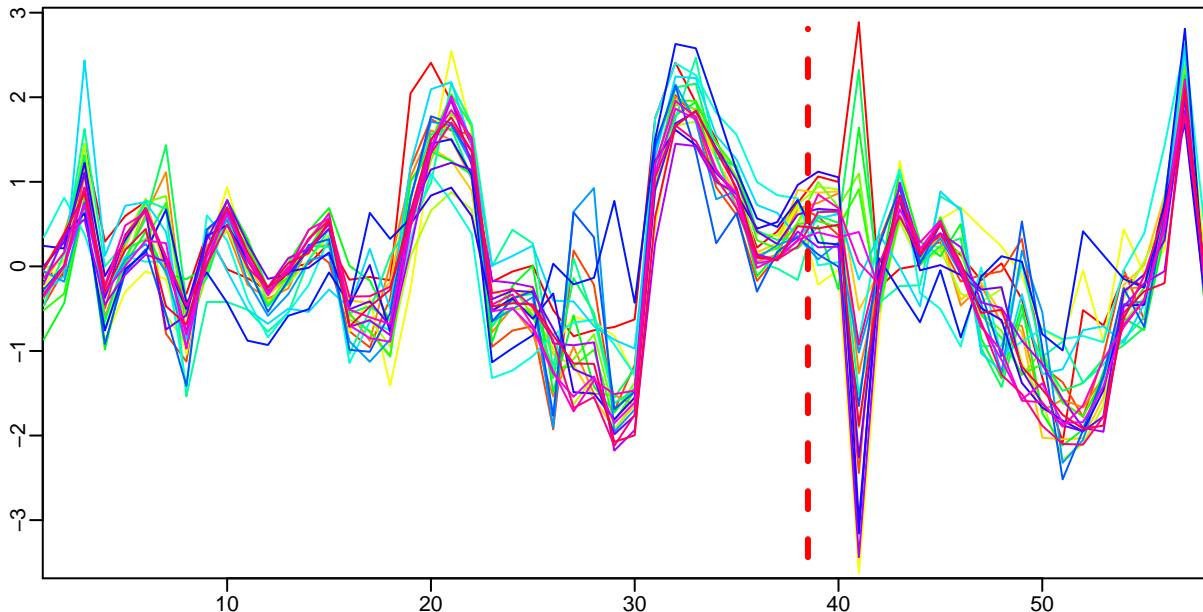|	
−7.8A (P−loop):ABC transporter:AAA ATPase:TOBE domain:	MMP1649
−6.66	hypothetical protein: MMP1055
−4.54	hypothetical protein: MMP0492
−4.54	MotA/TolQ/ExbB proton channel: MMP0491
−4.54	hypothetical protein: MMP0490
−4.03 containing formylmethanofuran dehydrogenase, subunit B:	MMP0511
−4.03 containing formylmethanofuran dehydrogenase, subunit E:	MMP0508
−3.90	hypothetical protein: MMP0552
−1.65	hypothetical protein: MMP0114
−1.37	TPR repeat: MMP0673
−1.29	transcriptional regulator PadR−like family: MMP0700
−1.17	hypothetical protein: MMP0752
−0.82	hypothetical protein: MMP0960
−0.57	hypothetical protein: MMP0675
−0.57	Helix−turn−helix DNA binding protein: MMP0674
−0.55	Antisense_24
−0.53	hypothetical protein: MMP0746
−0.53	hypothetical protein: MMP0745
−0.53	hypothetical protein: MMP0744
−0.53	Probable integrase/recombinase: MMP0743
−0.02	hypothetical protein: MMP0750
−0.02	hypothetical protein: MMP0749
−0.02	MCM family related protein: MMP0748
−0.02	hypothetical protein: MMP0747
0.00	hypothetical protein: MMP0478

Cluster: 0006 mmp; resid: 0.19; r/c: 17/38

upstream meme PSSM #1; e=3.9e+03 upstream meme PSSM #2; e=5.8e+03

log10(P) upstream meme   log10(P.clust)=−1.72; 17 seqs; 16 uniq

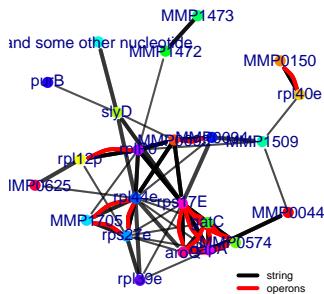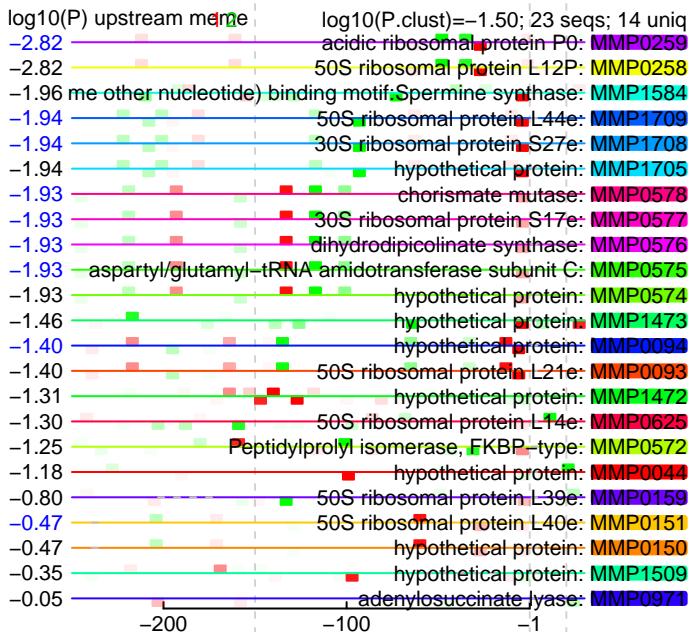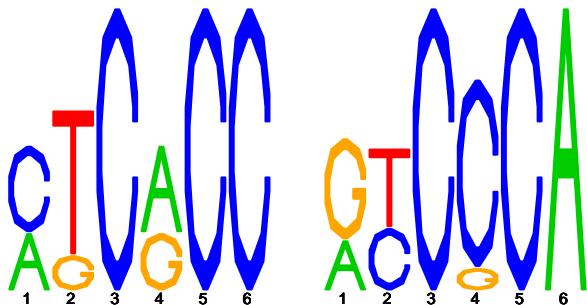|	
−4.46	hypothetical protein: MMP0847
−3.91	hypothetical protein: MMP1172
−3.30	hypothetical protein: MMP0461
−2.44	hypothetical protein: MMP0832
−2.31	hypothetical protein: MMP1276
−2.27	ABC transporter:AAA ATPase: MMP0110
−1.59	hypothetical protein: MMP0195
−1.50	NUDIX hydrolase: MMP0339
−1.32	possible purine NTPase: MMP0740
−1.21	hypothetical protein: MMP0437
−0.90	hypothetical protein: MMP1571
−0.90	Molybdenum ABC transporter, permease protein: MMP0515
−0.84	−type iron(III) transport system, permease component: MMP0197
−0.84	n(III) transport system, periplasmic binding protein: MMP0196
−0.66	tative SSU ribosomal protein S6 modification protein: MMP0436
−0.50	Site−specific recombinase: MMP0766
−0.29	hypothetical protein: MMP0519

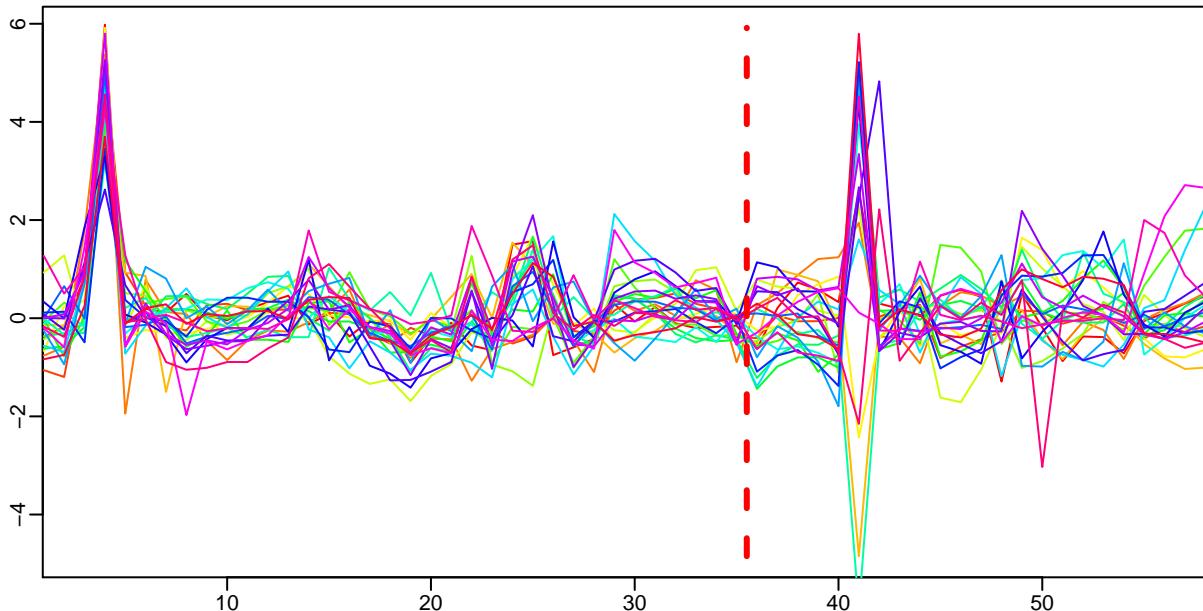# Cluster: 0007 mmp; resid: 0.32; r/c: 28/38

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cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=0.16 upstream meme PSSM #2; e=2.4e+03

log10(P) upstream meme   log10(P.clust)=−2.22; 28 seqs; 25 uniq

log10(P)	Annotation	Gene
−10.99	carbamoyl phosphate synthase small subunit	MMP1589
−10.99	D−3−phosphoglycerate dehydrogenase	MMP1588
−10.99	hypothetical protein	MMP1587
−8.23	glutamyl−tRNA(Gln) amidotransferase subunit D	MMP1266
−2.15	Glycosyl transferase, family 2	MMP0359
−1.70	3−isopropylmalate dehydrogenase	MMP0539
−1.41	(R)−citramalate synthase	MMP1018
−1.28	glutamate synthase; large subunit; archaeal subunit 1	MMP0080
−1.27	Na+/Pi−cotransporter related protein	MMP0666
−1.24	Dihydroxy−acid dehydratase	MMP0318
−1.14	hypothetical protein	MMP1615
−1.13	prolyl−tRNA synthetase	MMP0696
−1.02	oxoglutarate ferredoxin oxidoreductase subunit beta	MMP1316
−1.02	oxoglutarate ferredoxin oxidoreductase subunit gamma	MMP1315
−1.00	succinate−CoA ligase (ADP−forming), beta chain	MMP1105
−0.98	Phosphoserine phosphatase	MMP0541
−0.71	Prefoldin alpha subunit (GimC alpha subunit)	MMP1470
−0.70	hypothetical protein	MMP0708
−0.70	glutaryl−CoA dehydratase (Component D) related protein	MMP0346
−0.70	hypothetical protein	MMP0345
−0.62	CTP synthetase	MMP0893
−0.61	putative thiazole biosynthetic enzyme	MMP1352
−0.58	ATP phosphoribosyltransferase	MMP0947
−0.36	Amidophosphoribosyltransferase	MMP1146
−0.24	methionyl−tRNA synthetase	MMP0326
−0.19	phosphoribosylaminoimidazole carboxylase catalytic subunit	MMP0282
−0.13	hypothetical protein	MMP0308
−0.12	H+−transporting two−sector ATPase, A subunit	MMP0408

Cluster: 0008 mmp; resid: 0.54; r/c: 52/36

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cMonkey Version 4.8.8 mmp

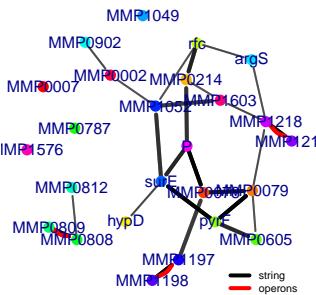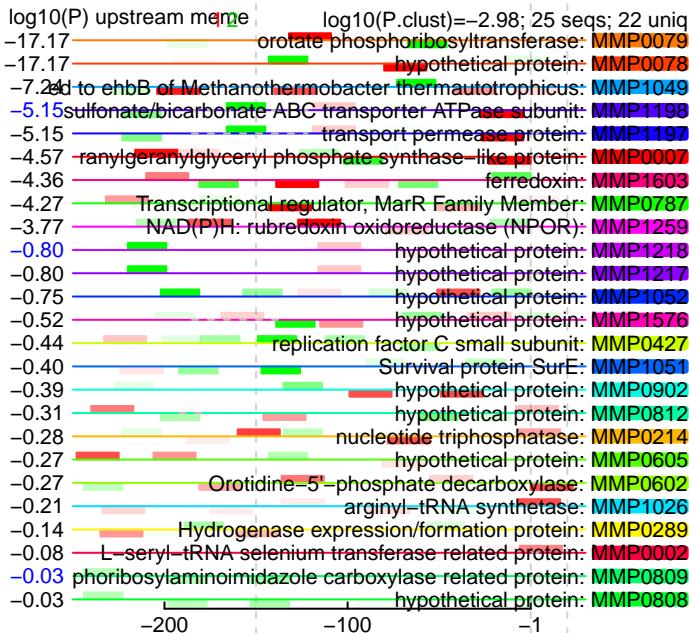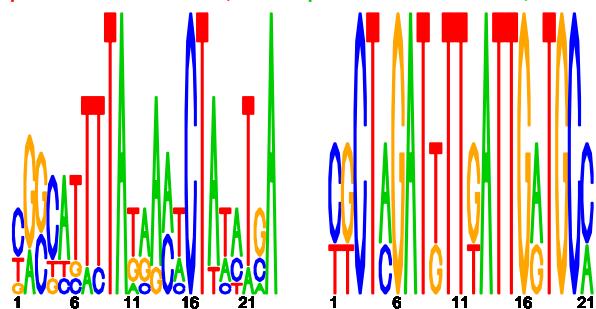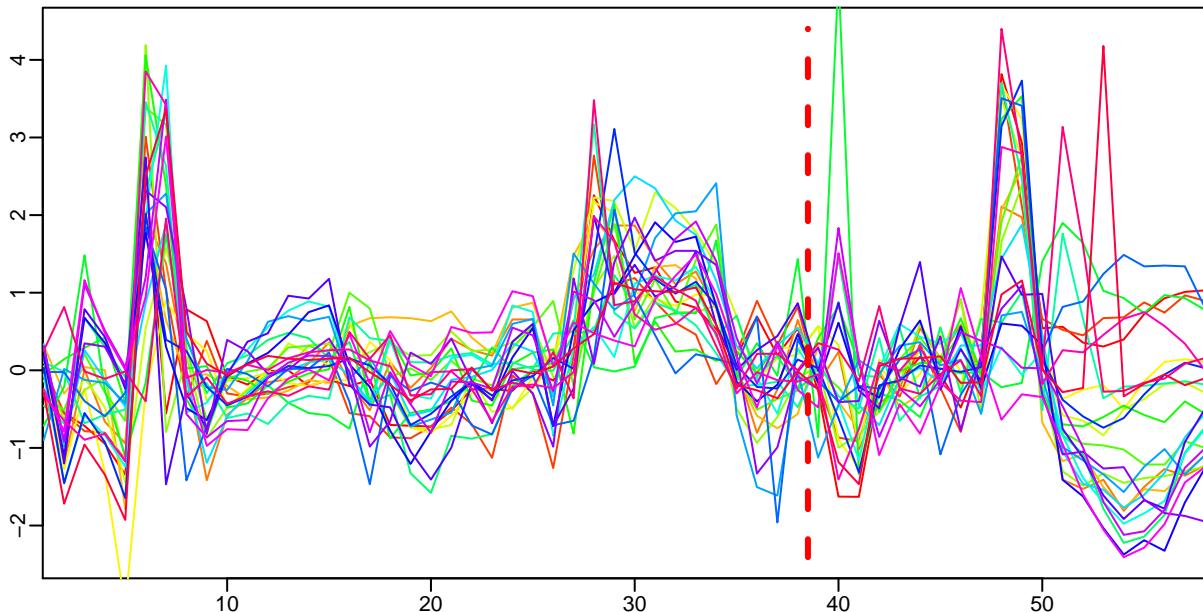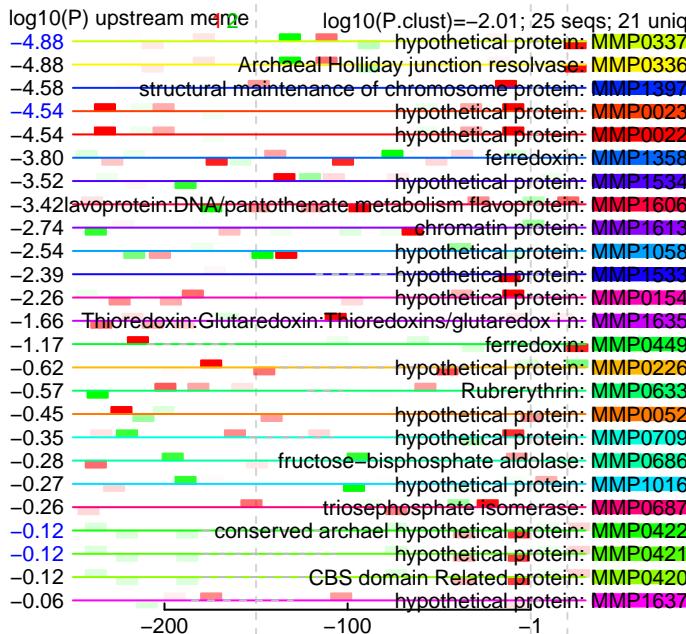upstream meme PSSM #1; e=0.063   upstream meme PSSM #2; e=0.83

log10(P) upstream meme   log10(P clust)=−1.56; 52 seqs; 47 uniq

30S ribosomal protein S11P
e pyridoxine biosynthetic glutamine amidotransferase
hypothetical protein
N−acetyl−gamma−glutamyl−phosphate reductase
hypothetical protein
hypothetical protein
fibrillarin
50S ribosomal protein L22e
hypothetical protein
3−isopropylmalate dehydrogenase
hypothetical protein
Cellulose−binding, bacterial type
putative ATPase, AFG1
hypothetical protein
hypothetical protein
aspartate aminotransferase
hypothetical protein
bacterial seryl−tRNA synthetase
hypothetical protein
D−3−phosphoglycerate dehydrogenase
hypothetical protein
triosephosphate isomerase
nascent polypeptide−associated complex protein
adenylosuccinate lyase
putative thiazole biosynthetic enzyme
hypothetical protein
phosphoribosylaminoimidazole−succinocarboxamide synthase
3,4−dihydroxy−2−butanone−4−phosphate synthase
alanine dehydrogenase
Alanine racemase
pyridoxine biosynthesis protein
L−aspartate oxidase
ParA−type ATPase
acetolactate synthase 3 regulatory subunit
acetolactate synthase catalytic subunit
translation initiation factor IF−6
hypothetical protein
hypothetical protein
threonyl−tRNA synthetase
gent methylenetetrahydromethanopterin dehydrogenase
intracellular sulfur reduction related protein
leucyl−tRNA synthetase
aspartyl/glutamyl−tRNA amidotransferase subunit B
malate dehydrogenase
methanofuran dehydrogenase subunit E−related protein
transcriptional regulator, TetR/AcrR family
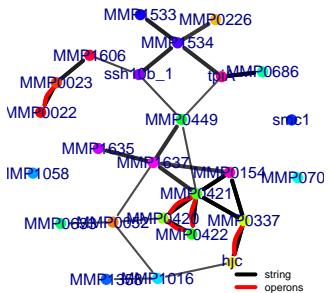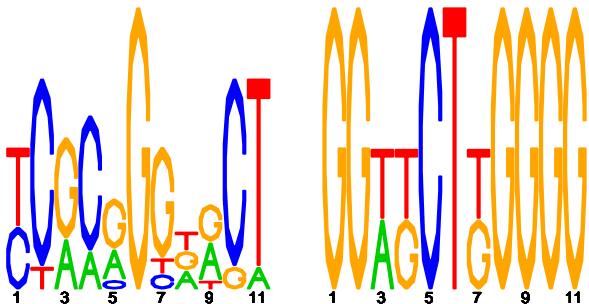hypothetical protein

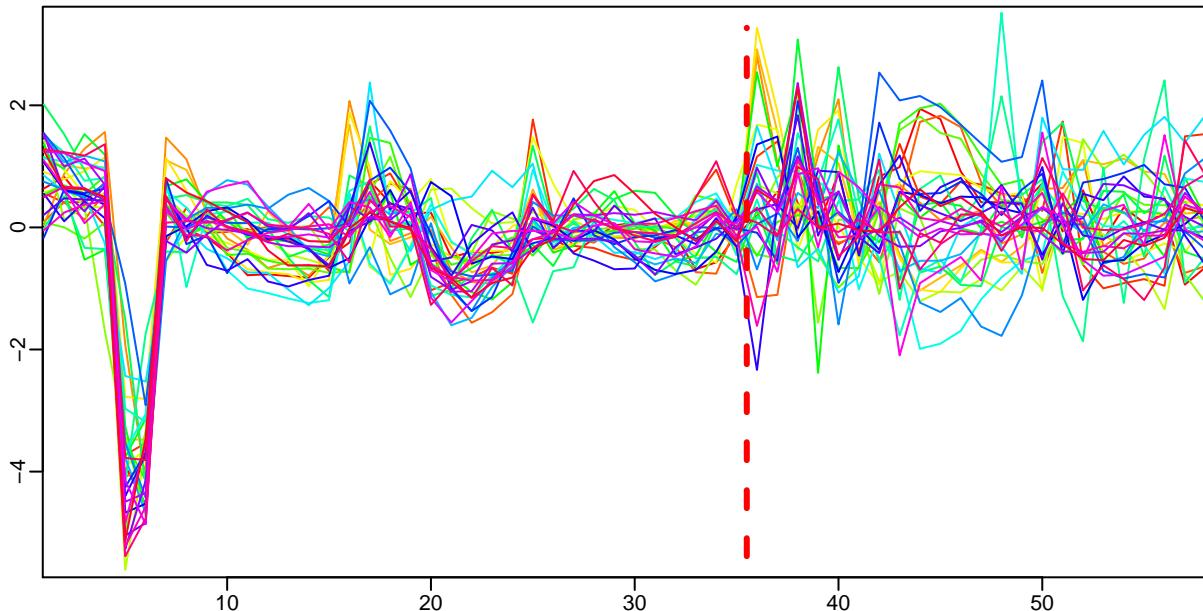**Cluster: 0009 mmp; resid: 0.44; r/c: 28/39**

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=0.21

upstream meme PSSM #2; e=5.2

log10(P) upstream meme

log10(P.clust)=−2.78; 28 seqs; 21 uniq

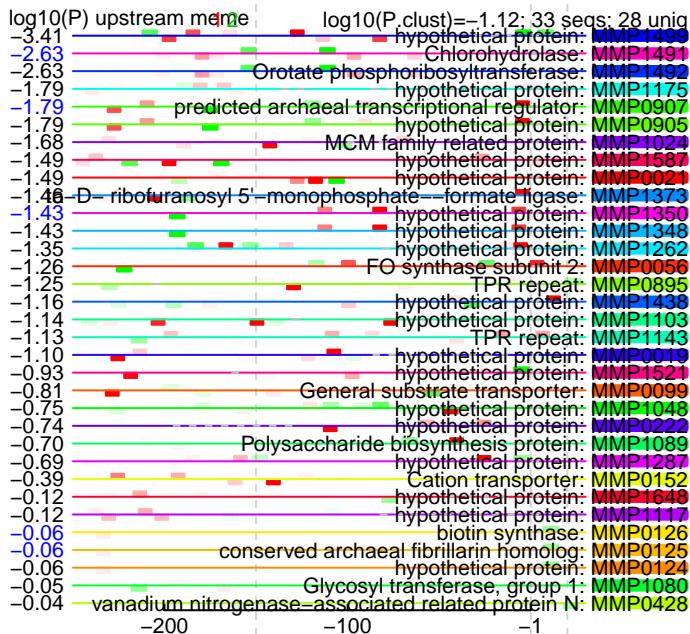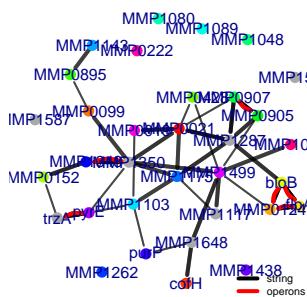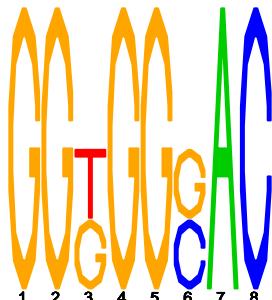| log10(P)	Description	Gene
−9.23	Transcriptional regulator, TetR Family Member:	MMP0799
−7.57	hypothetical protein:	MMP1302
−7.55	hypothetical protein:	MMP0793
−7.55	membrane protein:	MMP0792
−4.79	Transcriptional regulator, TetR Family Member:	MMP0791
−4.51	hypothetical protein:	MMP0486
−4.05	te motif A (P−loop).Small GTP−binding protein domain:	MMP1642
−3.87	FO synthase subunit 2:	MMP0057
−3.31		Antisense_22
−3.18	hypothetical protein:	MMP0347
−2.81		Unanno_45
−2.80	Formate transporter:	MMP1301
−2.80	hypothetical protein:	MMP1300
−2.80	carbonic anhydrase:	MMP1299
−2.61	coenzyme F420−non−reducing hydrogenase subunit beta:	MMP0824
−2.16	hypothetical protein:	MMP1378
−1.37	formate dehydrogenase beta subunit:	MMP0139
−1.37	formate dehydrogenase alpha subunit:	MMP0138
−0.56	coenzyme F420−reducing hydrogenase subunit delta:	MMP0819
−0.56	coenzyme F420−reducing hydrogenase subunit gamma:	MMP0818
−0.55		Unanno_18
−0.47	hypothetical protein:	MMP0172
−0.38	formate dehydrogenase alpha subunit:	MMP1298
−0.38	formate dehydrogenase beta subunit:	MMP1297
−0.28	heterodisulfide reductase; subunit C2:	MMP1054
−0.28	heterodisulfide reductase; subunit B2:	MMP1053
−0.05		Unanno_50
−0.05	coenzyme F420−non−reducing hydrogenase subunit gamma:	MMP0822

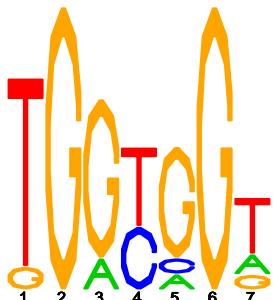**Cluster: 0010 mmp; resid: 0.23; r/c: 25/42**

upstream meme PSSM #1; e=0.0042 upstream meme PSSM #2; e=1.2e+03
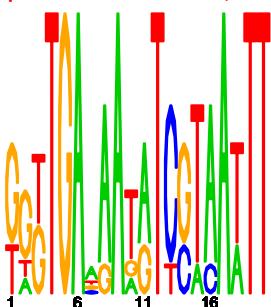
log10(P) upstream meme   log10(P.clust)=−7.05; 25 seqs; 6 uniq

log10(P)	annotation	gene
−8.33	hypothetical protein:	MMP1275
−8.33	acetyl−CoA synthetase, AMP−forming−related:	MMP1274
−8.33	2−oxoisovalerate oxidoreductase subunit gamma:	MMP1273
−8.33	2−ketoisovalerate ferredoxin reductase:	MMP1272
−8.33	2−oxoisovalerate oxidoreductase subunit alpha:	MMP1271
−8.05	putative monovalent cation/H+ antiporter subunit C:	MMP1629
−8.05	hydrogenase subunit F:	MMP1628
−8.05	hypothetical protein:	MMP1627
−8.05	putative monovalent cation/H+ antiporter subunit B:	MMP1626
−8.05	hypothetical protein:	MMP1625
−8.05	polyferredoxin:	MMP1624
−8.05	ferredoxin:	MMP1623
−8.05	energy conserving hydrogenase B small subunit:	MMP1622
−8.05	energy conserving hydrogenase B integral membrane subunit:	MMP1621
−6.46	putative monovalent cation/H+ antiporter subunit E:	MMP1469
−6.10	energy conserving hydrogenase B large subunit:	MMP1153
−6.10	hypothetical protein:	MMP1152
−5.79	yl−CoA decarbonylase/synthase complex subunit alpha:	MMP0985
−5.79	CoA decarbonylase/synthase complex subunit epsilon:	MMP0984
−5.31	pyruvate ferredoxin oxidoreductase subunit gamma:	MMP1507
−5.31	pyruvate oxidoreductase (synthase) subunit delta:	MMP1506
−5.31	pyruvate oxidoreductase (synthase) subunit alpha:	MMP1505
−5.31	pyruvate ferredoxin oxidoreductase subunit beta:	MMP1504
−5.31	thetical protein, pyruvate oxidoreductase−associated:	MMP1503
−5.31	hypothetical protein:	MMP1502

Cluster: 0011 mmp; resid: 0.26; r/c: 23/38
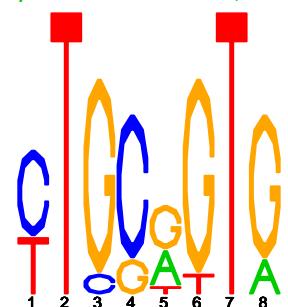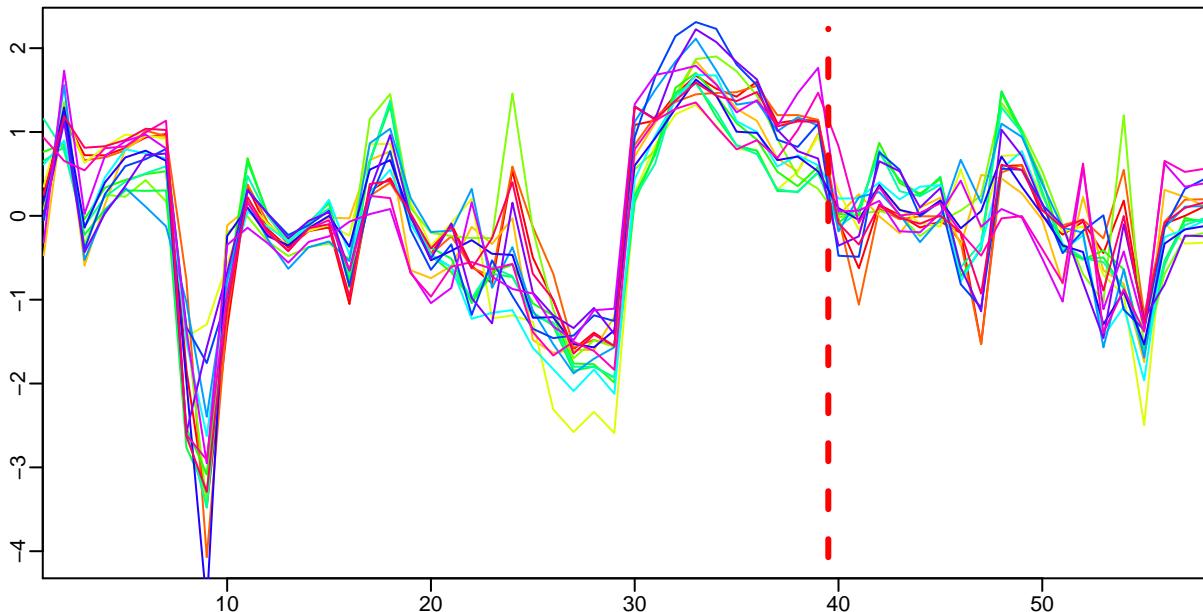
upstream meme PSSM #1; e=190

upstream meme PSSM #2; e=370

log10(P) upstream meme — log10(P.clust)=−1.50; 23 seqs; 14 uniq

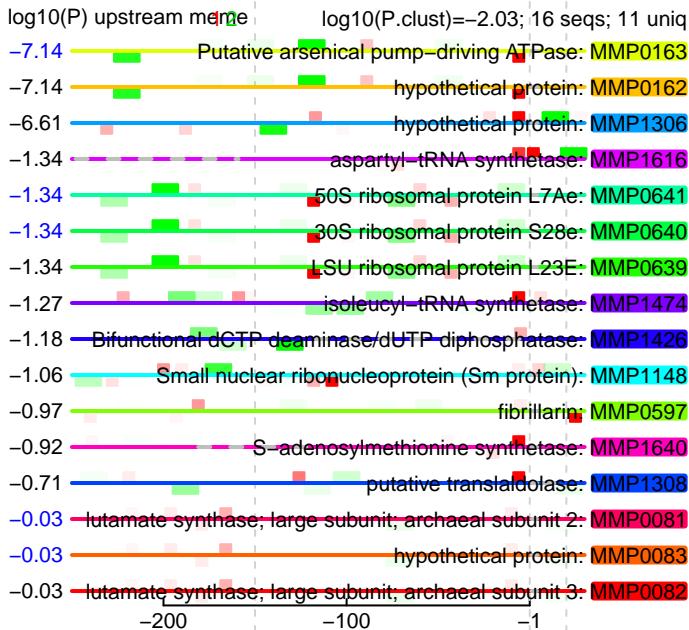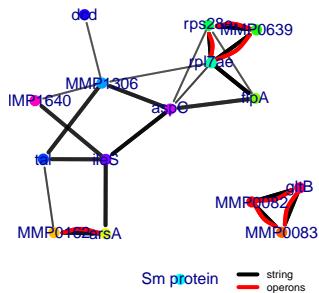| log10(P)	Description	Gene
−2.82	acidic ribosomal protein P0:	MMP0259
−2.82	50S ribosomal protein L12P:	MMP0258
−1.96	me other nucleotide) binding motif Spermine synthase:	MMP1584
−1.94	50S ribosomal protein L44e:	MMP1709
−1.94	30S ribosomal protein S27e:	MMP1708
−1.94	hypothetical protein:	MMP1705
−1.93	chorismate mutase:	MMP0578
−1.93	30S ribosomal protein S17e:	MMP0577
−1.93	dihydrodipicolinate synthase:	MMP0576
−1.93	aspartyl/glutamyl−tRNA amidotransferase subunit C:	MMP0575
−1.93	hypothetical protein:	MMP0574
−1.46	hypothetical protein:	MMP1473
−1.40	hypothetical protein:	MMP0094
−1.40	50S ribosomal protein L21e:	MMP0093
−1.31	hypothetical protein:	MMP1472
−1.30	50S ribosomal protein L14e:	MMP0625
−1.25	Peptidylprolyl isomerase, FKBP−type:	MMP0572
−1.18	hypothetical protein:	MMP0044
−0.80	50S ribosomal protein L39e:	MMP0159
−0.47	50S ribosomal protein L40e:	MMP0151
−0.47	hypothetical protein:	MMP0150
−0.35	hypothetical protein:	MMP1509
−0.05	adenylosuccinate lyase:	MMP0970

Cluster: 0012 mmp; resid: 0.37; r/c: 25/35

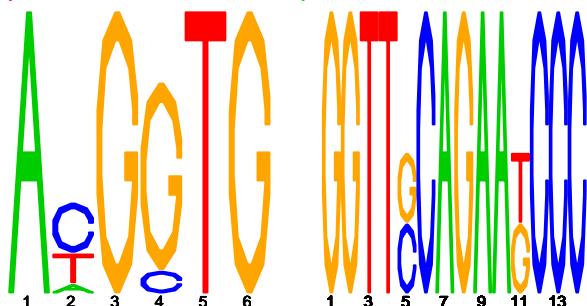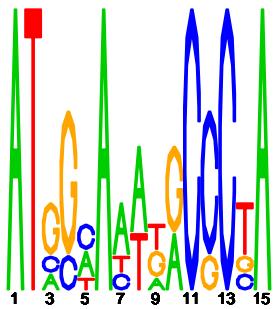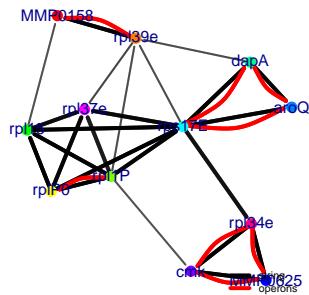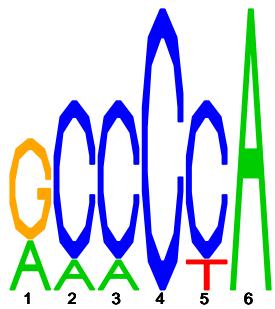11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=280   upstream meme PSSM #2; e=1.6e+03

log10(P) upstream meme   log10(P.clust)=−2.98; 25 seqs; 22 uniq

log10(P)	annotation	gene
−17.17	orotate phosphoribosyltransferase:	MMP0079
−17.17	hypothetical protein:	MMP0078
−7.24	...d to ehbB of Methanothermobacter thermautotrophicus:	MMP1049
−5.15	sulfonate/bicarbonate ABC transporter ATPase subunit:	MMP1198
−5.15	transport permease protein:	MMP1197
−4.57	...ranylgeranylglyceryl phosphate synthase–like protein:	MMP0007
−4.36	ferredoxin:	MMP1603
−4.27	Transcriptional regulator, MarR Family Member:	MMP0787
−3.77	NAD(P)H: rubredoxin oxidoreductase (NPOR):	MMP1259
−0.80	hypothetical protein:	MMP1218
−0.80	hypothetical protein:	MMP1217
−0.75	hypothetical protein:	MMP1052
−0.52	hypothetical protein:	MMP1576
−0.44	replication factor C small subunit:	MMP0427
−0.40	Survival protein SurE:	MMP1051
−0.39	hypothetical protein:	MMP0902
−0.31	hypothetical protein:	MMP0812
−0.28	nucleotide triphosphatase:	MMP0214
−0.27	hypothetical protein:	MMP0605
−0.27	Orotidine–5'–phosphate decarboxylase:	MMP0602
−0.21	arginyl–tRNA synthetase:	MMP1026
−0.14	Hydrogenase expression/formation protein:	MMP0289
−0.08	L–seryl–tRNA selenium transferase related protein:	MMP0002
−0.03	...phoribosylaminoimidazole carboxylase related protein:	MMP0809
−0.03	hypothetical protein:	MMP0808

−200   −100   −1

Cluster: 0013 mmp; resid: 0.42; r/c: 25/38
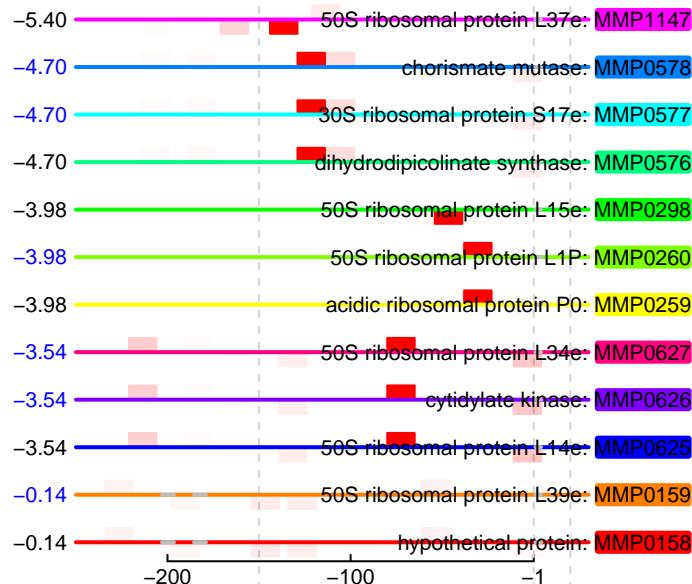
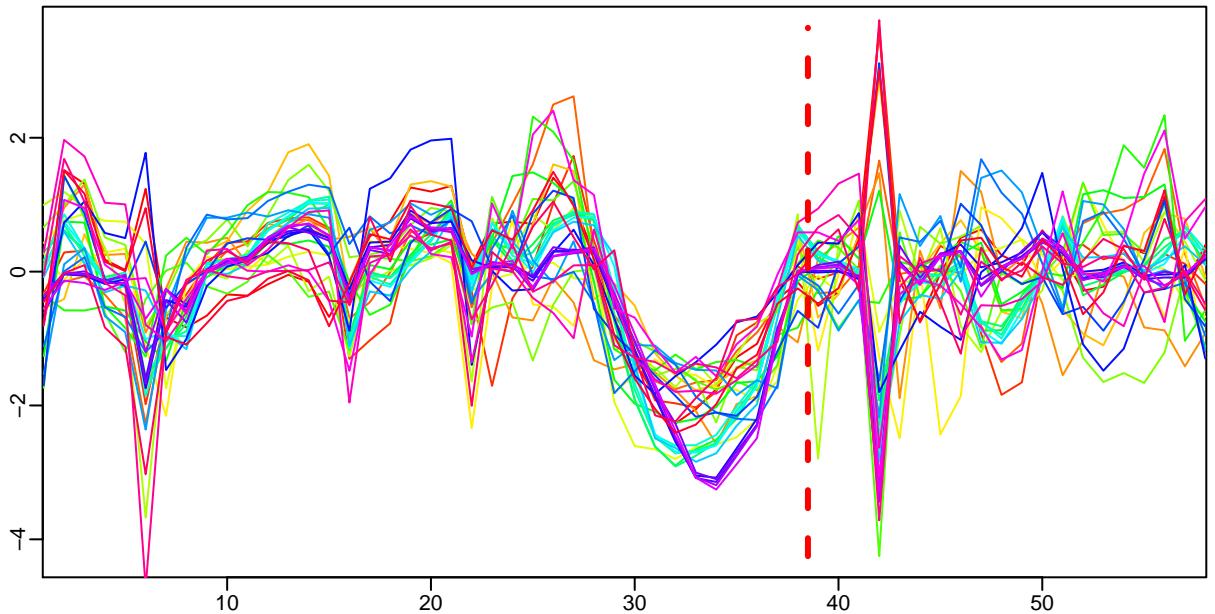upstream meme PSSM #1; e=9.7   upstream meme PSSM #2; e=1.9e+04

log10(P) upstream meme   log10(P.clust)=−2.01; 25 seqs; 21 uniq

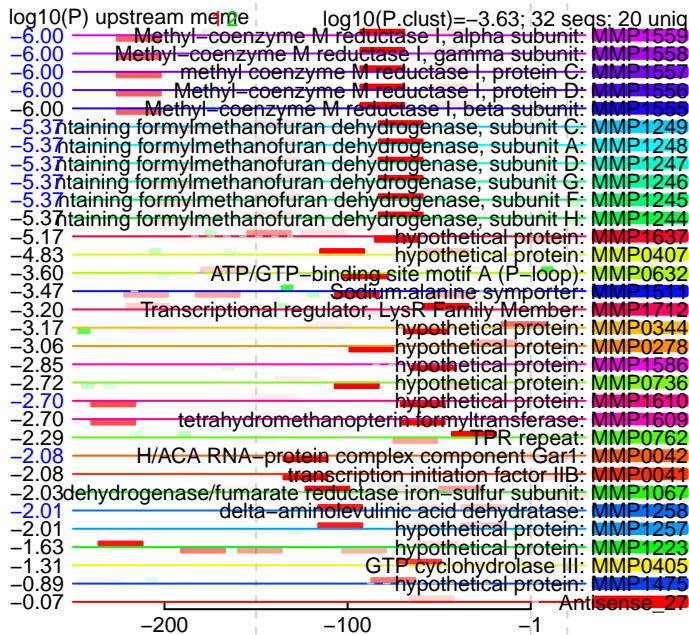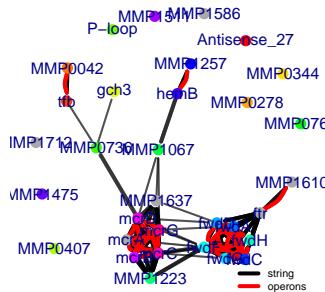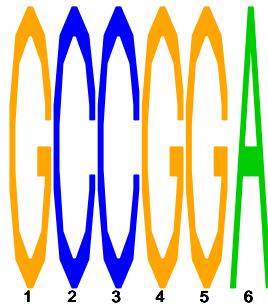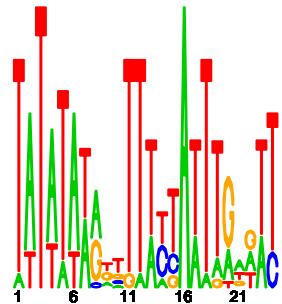| log10(P)	annotation	gene
−4.88	hypothetical protein	MMP0337
−4.88	Archaeal Holliday junction resolvase	MMP0336
−4.58	structural maintenance of chromosome protein	MMP1397
−4.54	hypothetical protein	MMP0023
−4.54	hypothetical protein	MMP0022
−3.80	ferredoxin	MMP1358
−3.52	hypothetical protein	MMP1534
−3.42	flavoprotein:DNA/pantothenate metabolism flavoprotein	MMP1606
−2.74	chromatin protein	MMP1613
−2.54	hypothetical protein	MMP1058
−2.39	hypothetical protein	MMP1533
−2.26	hypothetical protein	MMP0154
−1.66	Thioredoxin:Glutaredoxin:Thioredoxins/glutaredox i n	MMP1635
−1.17	ferredoxin	MMP0449
−0.62	hypothetical protein	MMP0226
−0.57	Rubrerythrin	MMP0633
−0.45	hypothetical protein	MMP0052
−0.35	hypothetical protein	MMP0709
−0.28	fructose−bisphosphate aldolase	MMP0686
−0.27	hypothetical protein	MMP1016
−0.26	triosephosphate isomerase	MMP0687
−0.12	conserved archael hypothetical protein	MMP0422
−0.12	hypothetical protein	MMP0421
−0.12	CBS domain Related protein	MMP0420
−0.06	hypothetical protein	MMP1637

Cluster: 0014 mmp; resid: 0.35; r/c: 33/35

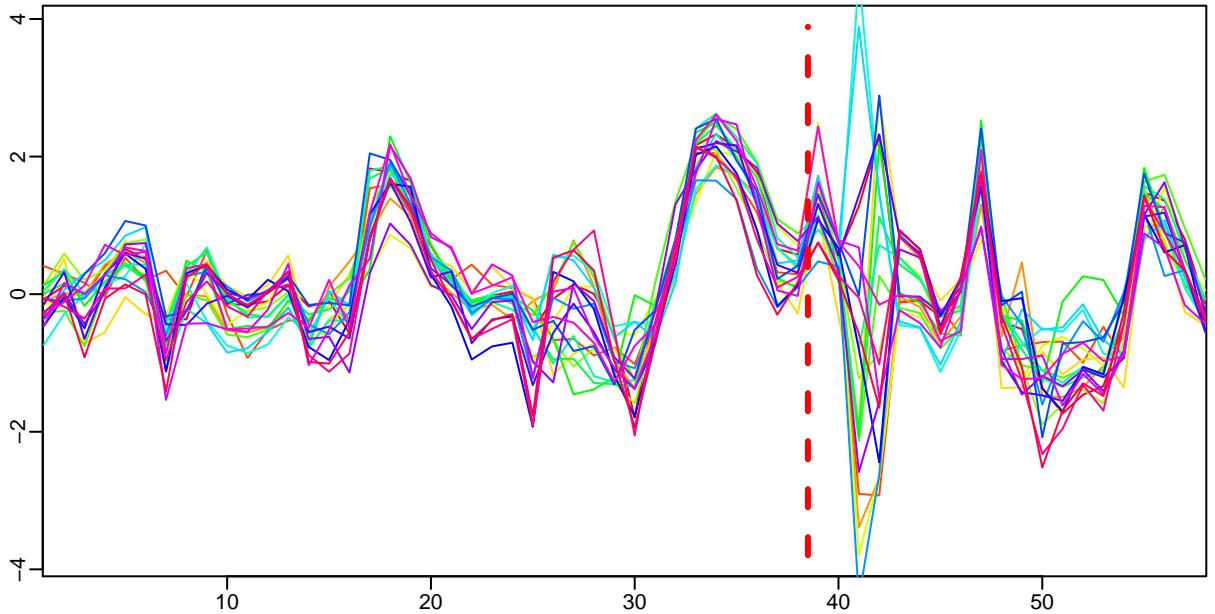11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=7.1   upstream meme PSSM #2; e=2.9e+04

log10(P) upstream meme   log10(P,clust)=−1.12: 33 seqs; 28 uniq

log10(P)	description	gene
−3.41	hypothetical protein:	MMP1493
−2.63	Chlorohydrolase:	MMP1491
−2.63	Orotate phosphoribosyltransferase:	MMP1492
−1.79	hypothetical protein:	MMP1175
−1.79	predicted archaeal transcriptional regulator:	MMP0907
−1.79	hypothetical protein:	MMP0905
−1.68	MCM family related protein:	MMP1024
−1.49	hypothetical protein:	MMP1587
−1.49	hypothetical protein:	MMP0021
−1.46	D−ribofuranosyl 5'−monophosphate−−formate ligase:	MMP1373
−1.43	hypothetical protein:	MMP1350
−1.43	hypothetical protein:	MMP1348
−1.35	hypothetical protein:	MMP1262
−1.26	FO synthase subunit 2:	MMP0056
−1.25	TPR repeat:	MMP0895
−1.16	hypothetical protein:	MMP1438
−1.14	hypothetical protein:	MMP1103
−1.13	TPR repeat:	MMP1143
−1.10	hypothetical protein:	MMP0019
−0.93	hypothetical protein:	MMP1521
−0.81	General substrate transporter:	MMP0099
−0.75	hypothetical protein:	MMP1048
−0.74	hypothetical protein:	MMP0222
−0.70	Polysaccharide biosynthesis protein:	MMP1089
−0.69	hypothetical protein:	MMP1287
−0.39	Cation transporter:	MMP0152
−0.12	hypothetical protein:	MMP1648
−0.12	hypothetical protein:	MMP1117
−0.06	biotin synthase:	MMP0126
−0.06	conserved archaeal fibrillarin homolog:	MMP0125
−0.06	hypothetical protein:	MMP0124
−0.05	Glycosyl transferase, group 1:	MMP1080
−0.04	vanadium nitrogenase−associated related protein N:	MMP0428

Cluster: 0015 mmp; resid: 0.36; r/c: 27/40

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp
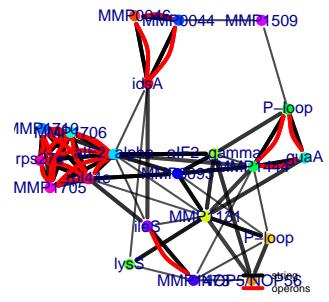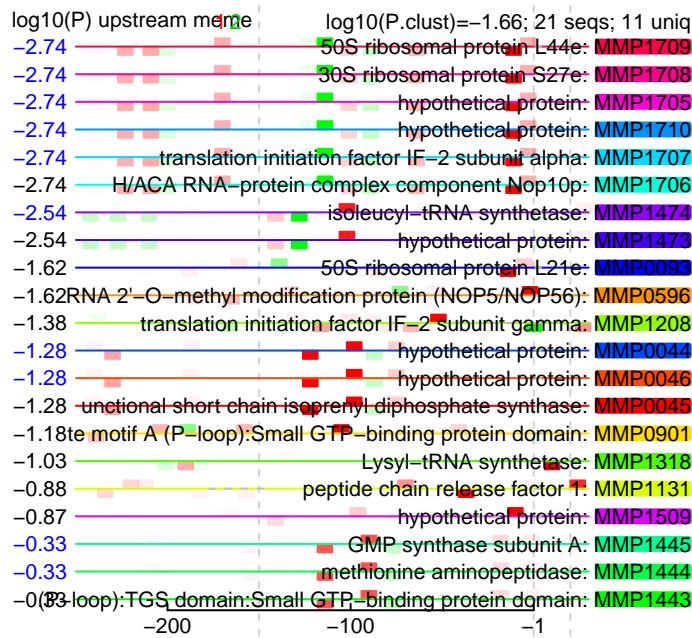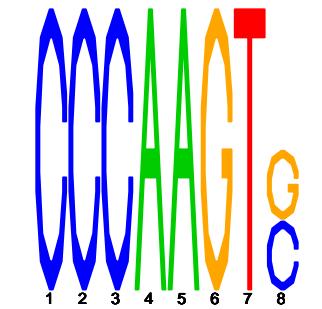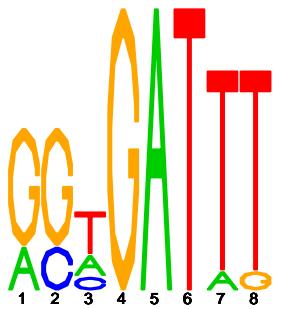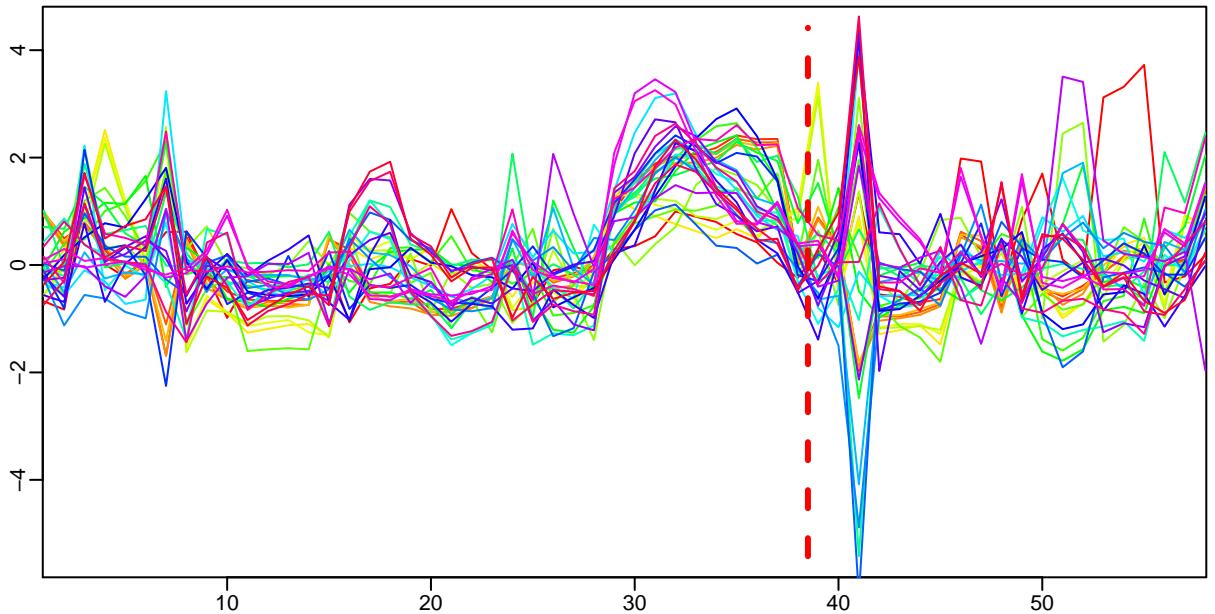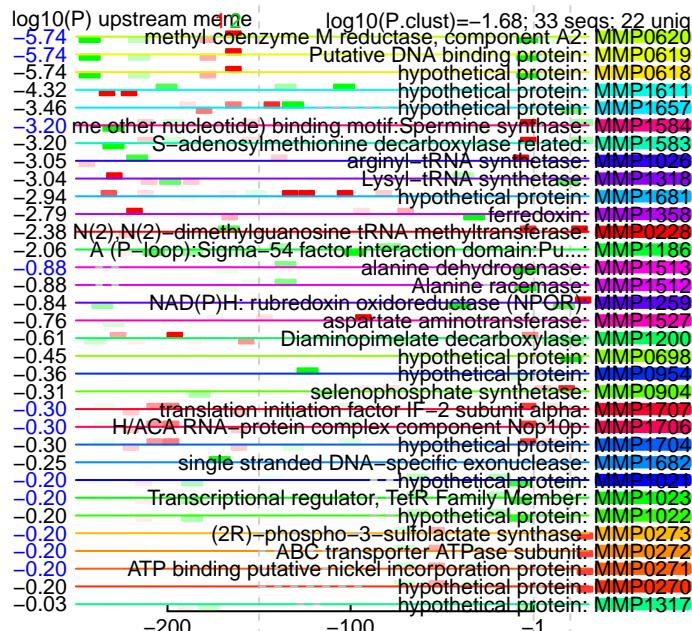
upstream meme PSSM #1; e=14

upstream meme PSSM #2; e=29

log10(P) upstream meme   log10(P.clust)=−3.19; 27 seqs; 19 uniq

log10(P)	annotation	gene
−7.36	nol dehydrogenase regulatory protein related protein:	MMP0363
−7.36	hypothetical protein:	MMP0362
−7.32	hypothetical protein:	MMP0367
−7.32	hypothetical protein:	MMP0366
−6.21	hypothetical protein:	MMP0252
−5.73	Sulfopyruvate decarboxylase subunit alpha:	MMP0411
−5.62	hypothetical protein:	MMP0218
−5.58	hypothetical protein:	MMP1169
−5.58	ABC transporter ATP−binding protein:	MMP1168
−5.58	flavoprotein related protein:	MMP1167
−5.58	on−sulfur flavoprotein of Methanosarcina thermophila:	MMP1166
−2.56	hypothetical protein:	MMP0328
−2.47	DNA polymerase family B:	MMP0380
−2.36	hypothetical protein:	MMP0374
−1.59	Anaerobic Ribonucleoside−triphosphate reductase:	MMP0227
−1.16	utaryl−CoA dehydratase (Component A) related protein:	MMP0349
−1am	ily M24:Xaa−Pro dipeptidase/Xaa−Pro aminopeptidase:	MMP1204
−1.06	Atrazine chlorohydrolase related protein:	MMP0378
−1.06	hypothetical protein:	MMP0376
−0.85	hypothetical protein:	MMP0390
−0.76	hypothetical protein:	MMP0409
−0.68	hypothetical protein:	MMP1070
−0.34	hypothetical protein:	MMP0402
−0.34	methionine synthase:	MMP0401
−0.24	hypothetical protein:	MMP0395
−0.24	Uroporphyrinogen III synthase:	MMP0394
−0.10	hypothetical protein:	MMP1554

Cluster: 0016 mmp; resid: 0.26; r/c: 16/39

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

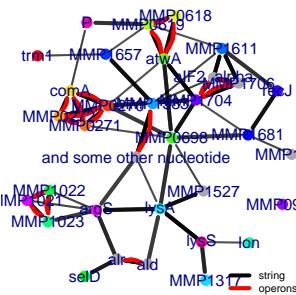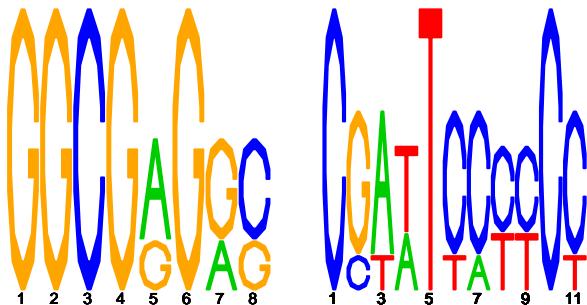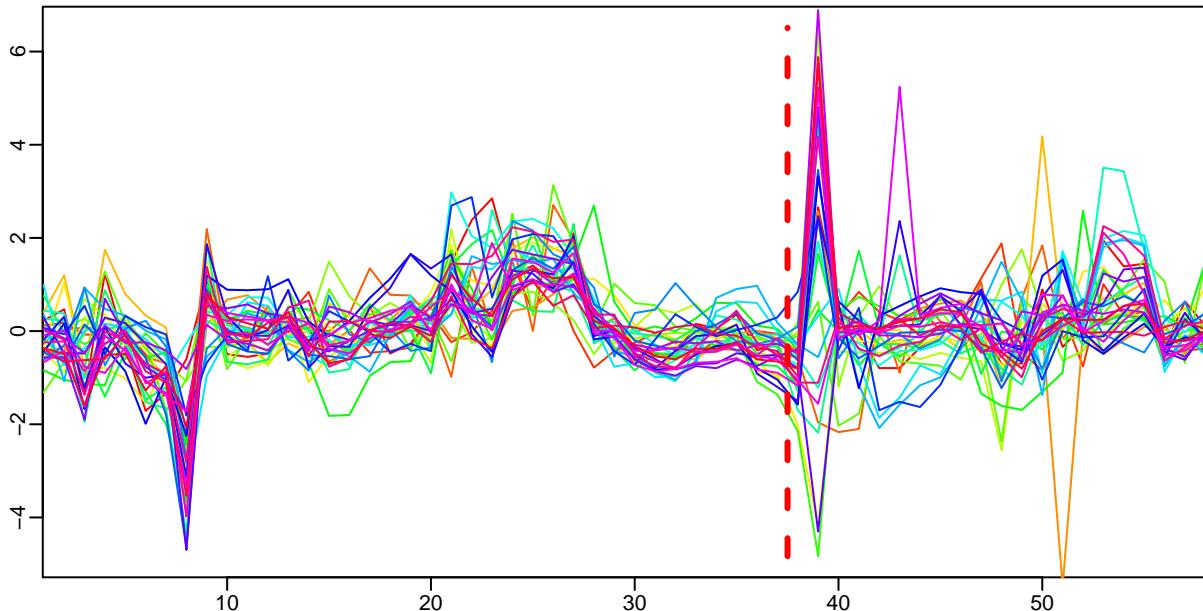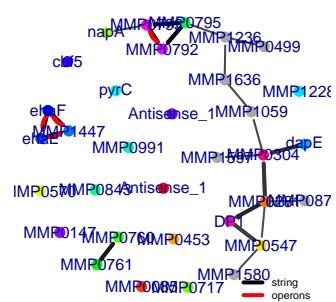**upstream meme PSSM #1; e=25**   **upstream meme PSSM #2; e=1.3e+03**

log10(P) upstream meme   log10(P.clust)=−2.03; 16 seqs; 11 uniq

log10(P)	Description	Gene
−7.14	Putative arsenical pump−driving ATPase:	MMP0163
−7.14	hypothetical protein:	MMP0162
−6.61	hypothetical protein:	MMP1306
−1.34	aspartyl−tRNA synthetase:	MMP1616
−1.34	50S ribosomal protein L7Ae:	MMP0641
−1.34	30S ribosomal protein S28e:	MMP0640
−1.34	LSU ribosomal protein L23E:	MMP0639
−1.27	isoleucyl−tRNA synthetase:	MMP1474
−1.18	Bifunctional dCTP deaminase/dUTP diphosphatase:	MMP1426
−1.06	Small nuclear ribonucleoprotein (Sm protein):	MMP1148
−0.97	fibrillarin:	MMP0597
−0.92	S−adenosylmethionine synthetase:	MMP1640
−0.71	putative translaldolase:	MMP1308
−0.03	glutamate synthase; large subunit; archaeal subunit 2:	MMP0081
−0.03	hypothetical protein:	MMP0083
−0.03	glutamate synthase; large subunit; archaeal subunit 3:	MMP0082

Sm protein — string / operons

−200   −100   −1

Cluster: 0017 mmp; resid: 0.36; r/c: 25/39

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp
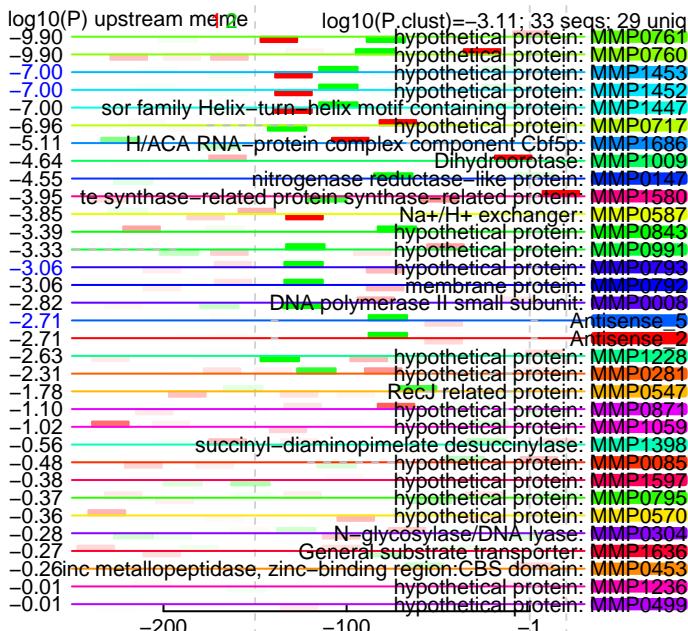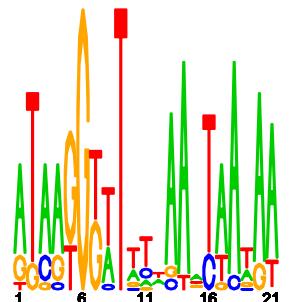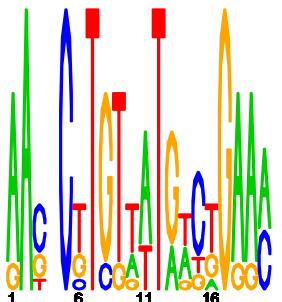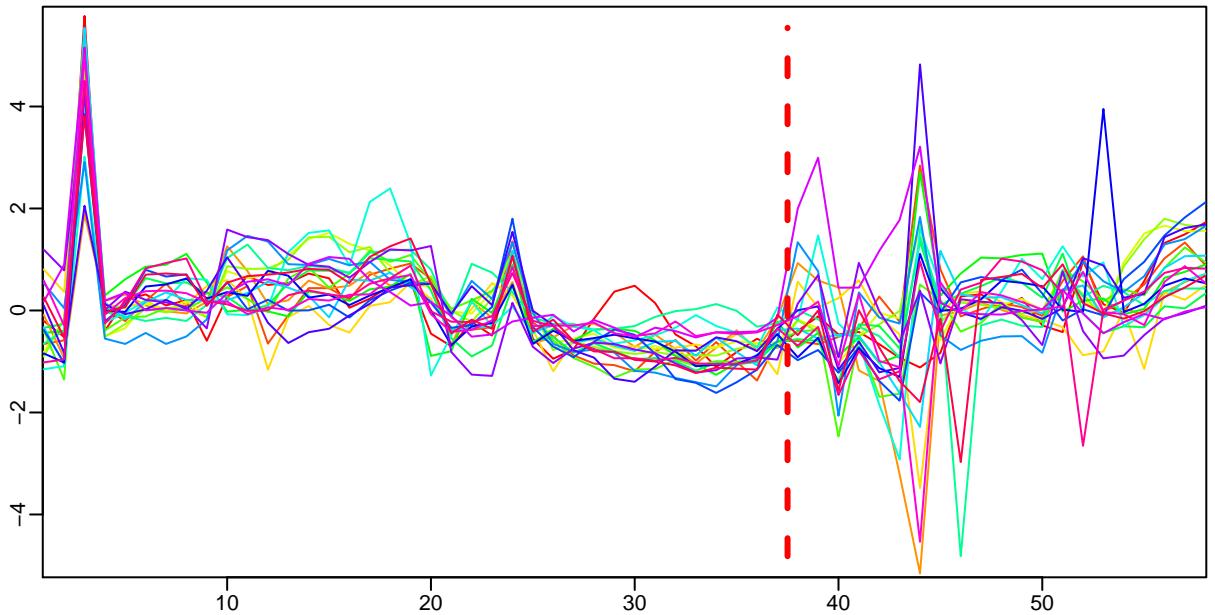
upstream meme PSSM #1; e=100   upstream meme PSSM #2; e=110

log10(P) upstream meme   log10(P.clust)=−9.10; 25 seqs; 10 uniq

log10(P)	description	gene
−13.04	acetyl−CoA synthetase, AMP−forming:	MMP0148
−13.04	nitrogenase reductase−like protein:	MMP0147
−13.04	hypothetical protein:	MMP0146
−13.04	5−oxopent−3−ene−1,2,5−tricarboxylate decarboxylase:	MMP0144
−13.04	te dependent enzyme related to acetolactate synthase:	MMP0142
−10.92	pyruvate ferredoxin oxidoreductase subunit gamma:	MMP1507
−10.92	pyruvate oxidoreductase (synthase) subunit delta:	MMP1506
−10.92	pyruvate oxidoreductase (synthase) subunit alpha:	MMP1505
−10.92	pyruvate ferredoxin oxidoreductase subunit beta:	MMP1504
−10.92	thetical protein, pyruvate oxidoreductase−associated:	MMP1503
−10.92	hypothetical protein:	MMP1502
−9.24	tyl−CoA decarbonylase/synthase complex subunit alpha:	MMP0985
−9.24	l−CoA decarbonylase/synthase complex subunit epsilon:	MMP0984
−9.24	etyl−CoA decarbonylase/synthase complex subunit beta:	MMP0983
−9.24	hypothetical protein:	MMP0982
−9.24	yl−CoA decarbonylase/synthase complex subunit delta:	MMP0981
−9.24	−CoA decarbonylase/synthase complex subunit gamma:	MMP0980
−9.24	hypothetical protein:	MMP0979
−8.71	acetyl−CoA synthetase, AMP−forming−related:	MMP1274
−8.71	2−oxoisovalerate oxidoreductase subunit alpha:	MMP1271
−6.39	hypothetical protein:	MMP0348
−3.85	hypothetical protein:	MMP0978
−3.73	hypothetical protein:	MMP1074
−0.61	CO dehydrogenase maturation factor:	MMP0977
−0.22	hypothetical protein:	MMP1468

Cluster: 0018 mmp; resid: 0.13; r/c: 12/38

Cluster: 0019 mmp; resid: 0.40; r/c: 32/38

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp
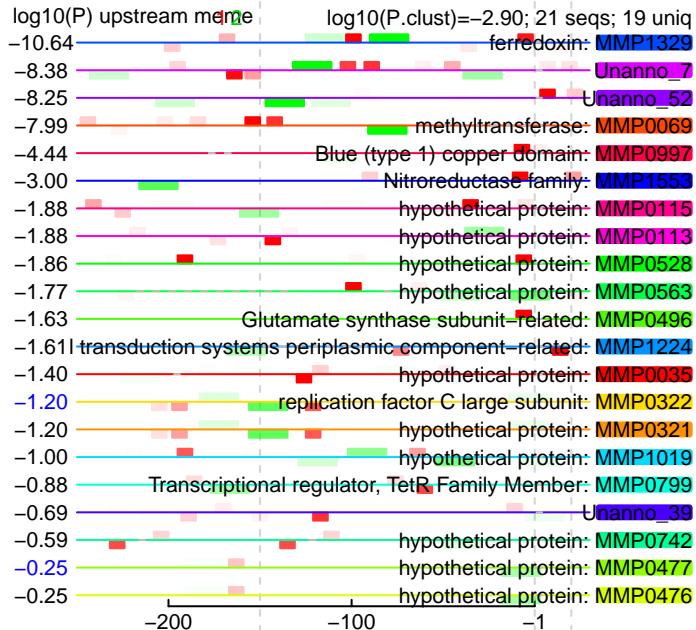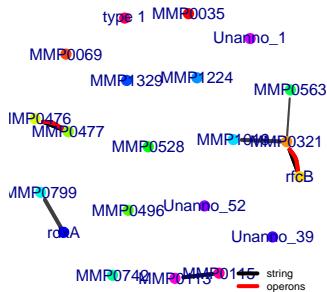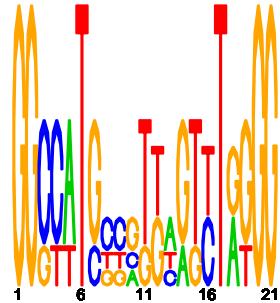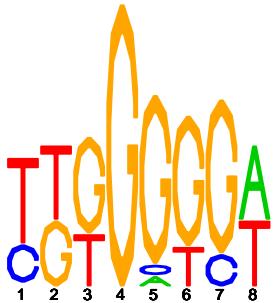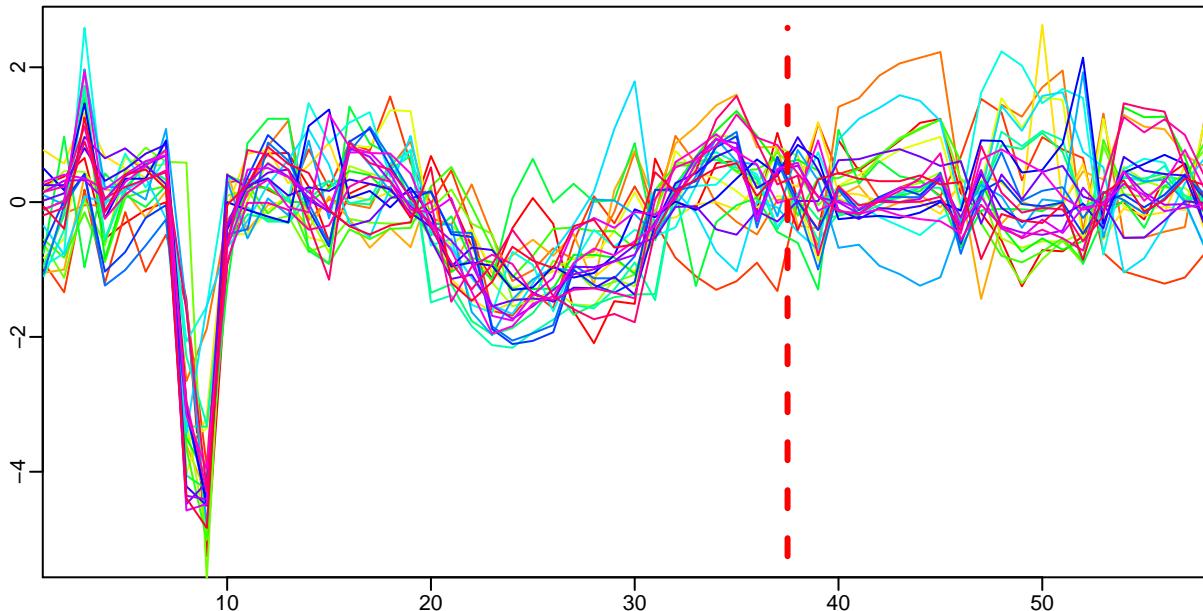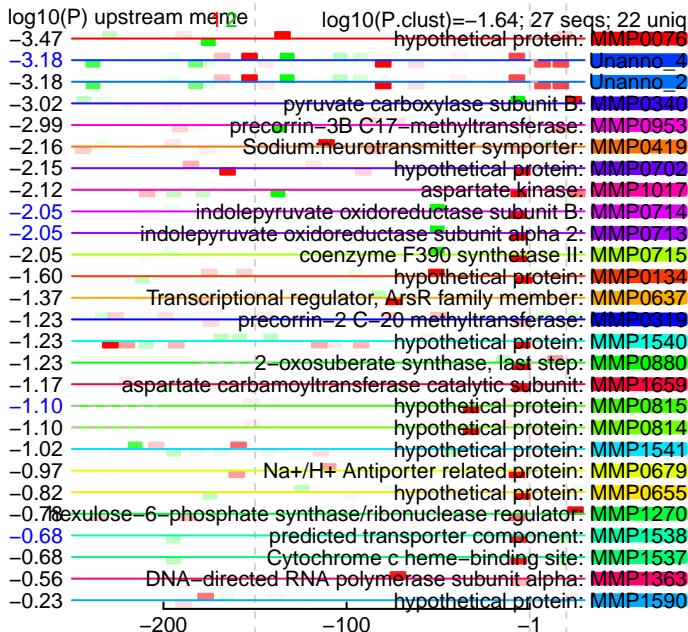
upstream meme PSSM #1; e=74   upstream meme PSSM #2; e=1.1e+04

log10(P) upstream meme   log10(P.clust)=−3.63; 32 seqs; 20 uniq

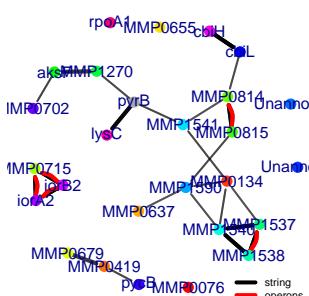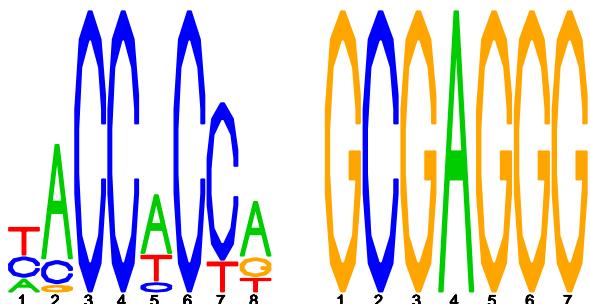| log10(P)		
−6.00	Methyl−coenzyme M reductase I, alpha subunit:	MMP1559
−6.00	Methyl−coenzyme M reductase I, gamma subunit:	MMP1558
−6.00	methyl coenzyme M reductase I, protein C:	MMP1557
−6.00	Methyl−coenzyme M reductase I, protein D:	MMP1556
−6.00	Methyl−coenzyme M reductase I, beta subunit:	MMP1555
−5.37	ntaining formylmethanofuran dehydrogenase, subunit C:	MMP1249
−5.37	ntaining formylmethanofuran dehydrogenase, subunit A:	MMP1248
−5.37	ntaining formylmethanofuran dehydrogenase, subunit D:	MMP1247
−5.37	ntaining formylmethanofuran dehydrogenase, subunit G:	MMP1246
−5.37	ntaining formylmethanofuran dehydrogenase, subunit F:	MMP1245
−5.37	ntaining formylmethanofuran dehydrogenase, subunit H:	MMP1244
−5.17	hypothetical protein:	MMP1637
−4.83	hypothetical protein:	MMP0407
−3.60	ATP/GTP−binding−site motif A (P−loop):	MMP0632
−3.47	Sodium:alanine symporter:	MMP1511
−3.20	Transcriptional regulator, LysR Family Member:	MMP1712
−3.17	hypothetical protein:	MMP0344
−3.06	hypothetical protein:	MMP0278
−2.85	hypothetical protein:	MMP1586
−2.72	hypothetical protein:	MMP0736
−2.70	hypothetical protein:	MMP1610
−2.70	tetrahydromethanopterin formyltransferase:	MMP1609
−2.29	TPR repeat:	MMP0762
−2.08	H/ACA RNA−protein complex component Gar1:	MMP0042
−2.08	transcription initiation factor IIB:	MMP0041
−2.03	dehydrogenase/fumarate reductase iron−sulfur subunit:	MMP1067
−2.01	delta−aminolevulinic acid dehydratase:	MMP1258
−2.01	hypothetical protein:	MMP1257
−1.63	hypothetical protein:	MMP1223
−1.31	GTP cyclohydrolase III:	MMP0405
−0.89	hypothetical protein:	MMP1475
−0.07	Antisense_27	

Cluster: 0020 mmp; resid: 0.26; r/c: 21/38

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upstream meme PSSM #1; e=17   upstream meme PSSM #2; e=1e+04
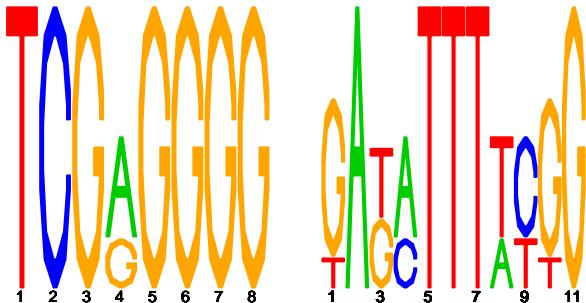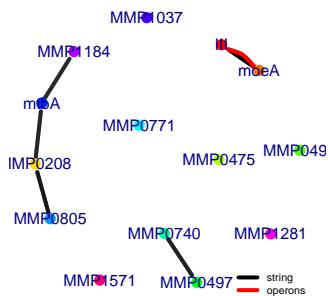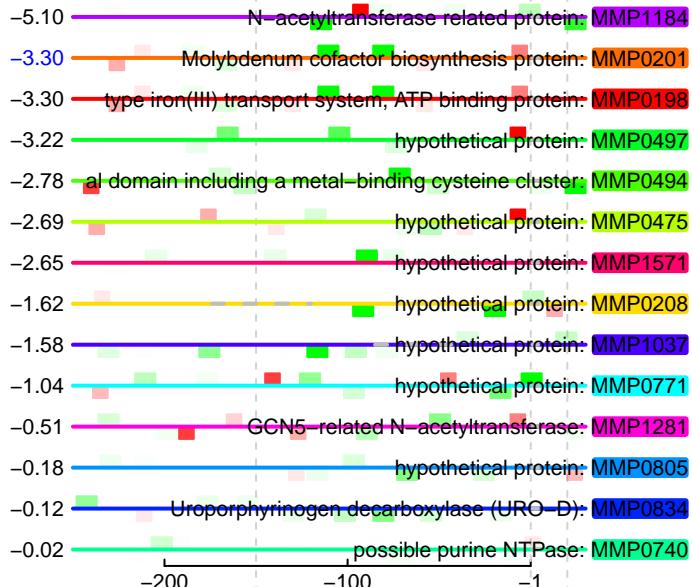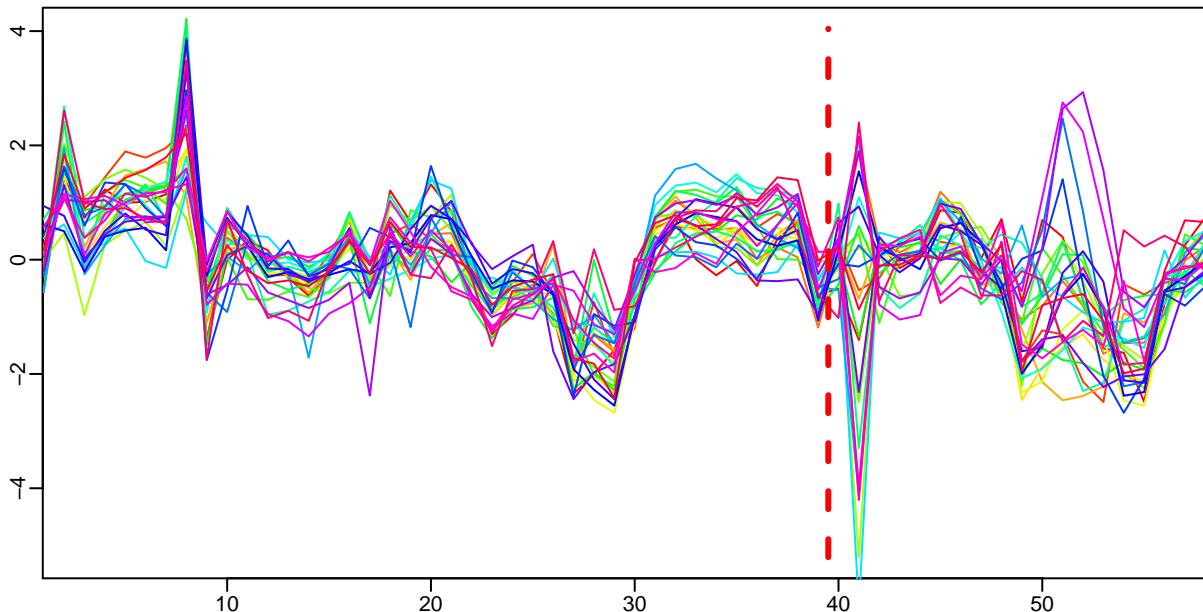
log10(P) upstream meme   log10(P.clust)=−1.66; 21 seqs; 11 uniq

log10(P)	Description	Gene
−2.74	50S ribosomal protein L44e:	MMP1709
−2.74	30S ribosomal protein S27e:	MMP1708
−2.74	hypothetical protein:	MMP1705
−2.74	hypothetical protein:	MMP1710
−2.74	translation initiation factor IF−2 subunit alpha:	MMP1707
−2.74	H/ACA RNA−protein complex component Nop10p:	MMP1706
−2.54	isoleucyl−tRNA synthetase:	MMP1474
−2.54	hypothetical protein:	MMP1473
−1.62	50S ribosomal protein L21e:	MMP0093
−1.62	RNA 2'−O−methyl modification protein (NOP5/NOP56):	MMP0596
−1.38	translation initiation factor IF−2 subunit gamma:	MMP1208
−1.28	hypothetical protein:	MMP0044
−1.28	hypothetical protein:	MMP0046
−1.28	unctional short chain isoprenyl diphosphate synthase:	MMP0045
−1.18	te motif A (P−loop):Small GTP−binding protein domain:	MMP0901
−1.03	Lysyl−tRNA synthetase:	MMP1318
−0.88	peptide chain release factor 1:	MMP1131
−0.87	hypothetical protein:	MMP1509
−0.33	GMP synthase subunit A:	MMP1445
−0.33	methionine aminopeptidase:	MMP1444
−0(P3−loop):TGS domain:Small GTP−binding protein domain:		MMP1443

Cluster: 0021 mmp; resid: 0.45; r/c: 33/38

upstream meme PSSM #1; e=3.8e+03   upstream meme PSSM #2; e=3.5e+03

log10(P) upstream meme   log10(P.clust)=−1.68; 33 seqs: 22 uniq

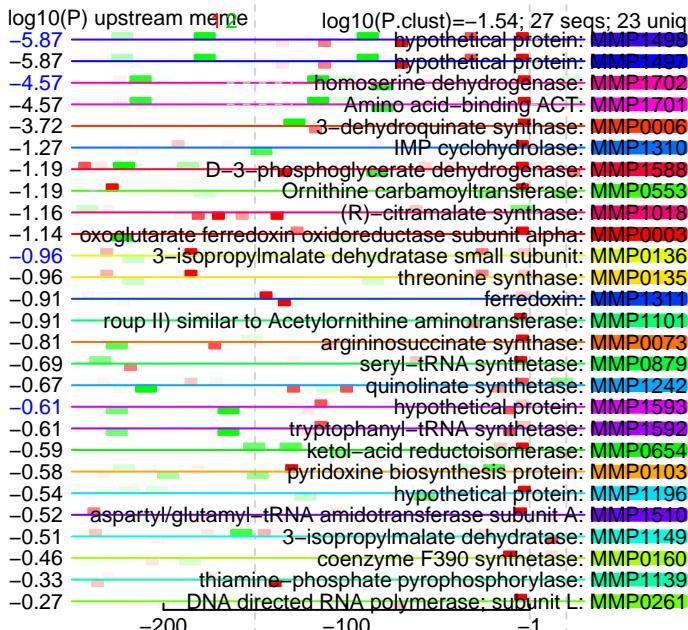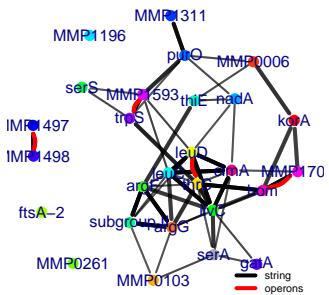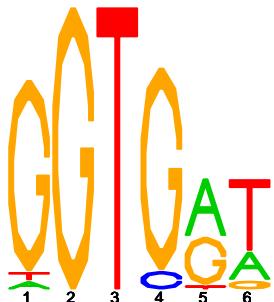| log10(P)	Description	Gene
−5.74	methyl coenzyme M reductase, component A2	MMP0620
−5.74	Putative DNA binding protein	MMP0619
−5.74	hypothetical protein	MMP0618
−4.32	hypothetical protein	MMP1611
−3.46	hypothetical protein	MMP1657
−3.20	me other nucleotide) binding motif:Spermine synthase	MMP1584
−3.20	S−adenosylmethionine decarboxylase related	MMP1583
−3.05	arginyl−tRNA synthetase	MMP1028
−3.04	Lysyl−tRNA synthetase	MMP1318
−2.94	hypothetical protein	MMP1681
−2.79	ferredoxin	MMP1358
−2.38	N(2),N(2)−dimethylguanosine tRNA methyltransferase	MMP0228
−2.06	A (P−loop):Sigma−54 factor interaction domain:Pu...	MMP1186
−0.88	alanine dehydrogenase	MMP1513
−0.88	Alanine racemase	MMP1512
−0.84	NAD(P)H: rubredoxin oxidoreductase (NPOR)	MMP1269
−0.76	aspartate aminotransferase	MMP1527
−0.61	Diaminopimelate decarboxylase	MMP1200
−0.45	hypothetical protein	MMP0698
−0.36	hypothetical protein	MMP0954
−0.31	selenophosphate synthetase	MMP0904
−0.30	translation initiation factor IF−2 subunit alpha	MMP1707
−0.30	H/ACA RNA−protein complex component Nop10p	MMP1706
−0.30	hypothetical protein	MMP1704
−0.25	single stranded DNA−specific exonuclease	MMP1682
−0.20	hypothetical protein	MMP1021
−0.20	Transcriptional regulator, TetR Family Member	MMP1023
−0.20	hypothetical protein	MMP1022
−0.20	(2R)−phospho−3−sulfolactate synthase	MMP0273
−0.20	ABC transporter ATPase subunit	MMP0272
−0.20	ATP binding putative nickel incorporation protein	MMP0271
−0.20	hypothetical protein	MMP0270
−0.03	hypothetical protein	MMP1317

Cluster: 0022 mmp; resid: 0.40; r/c: 33/37

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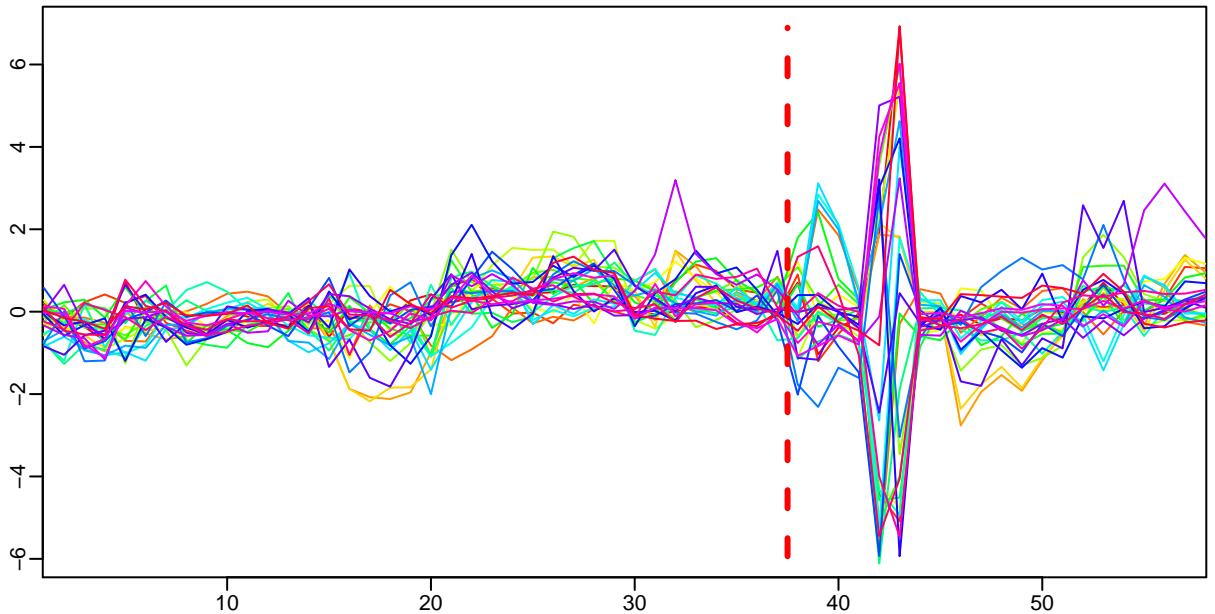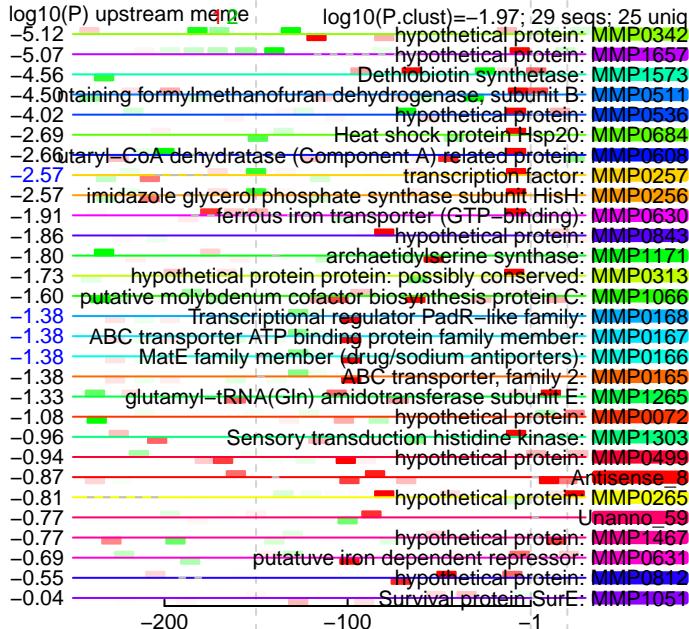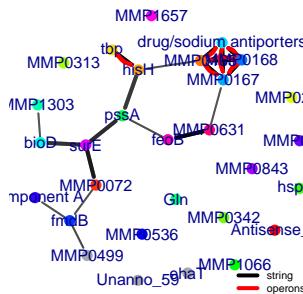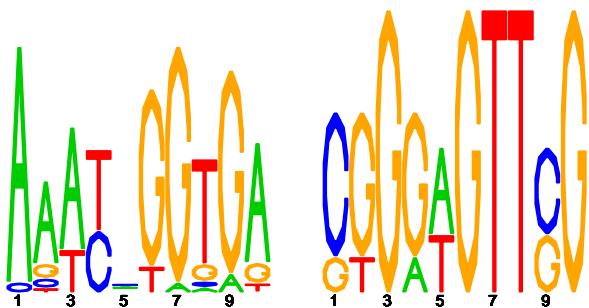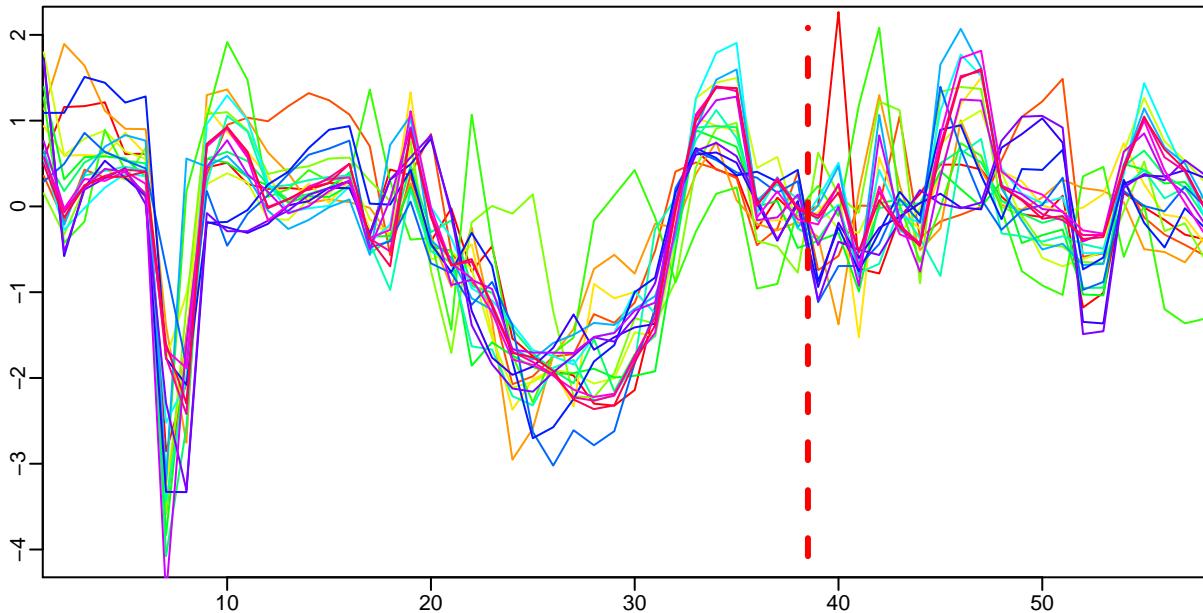
upstream meme PSSM #1; e=21

upstream meme PSSM #2; e=620

log10(P) upstream meme   log10(P.clust)=−3.11; 33 seqs: 29 uniq

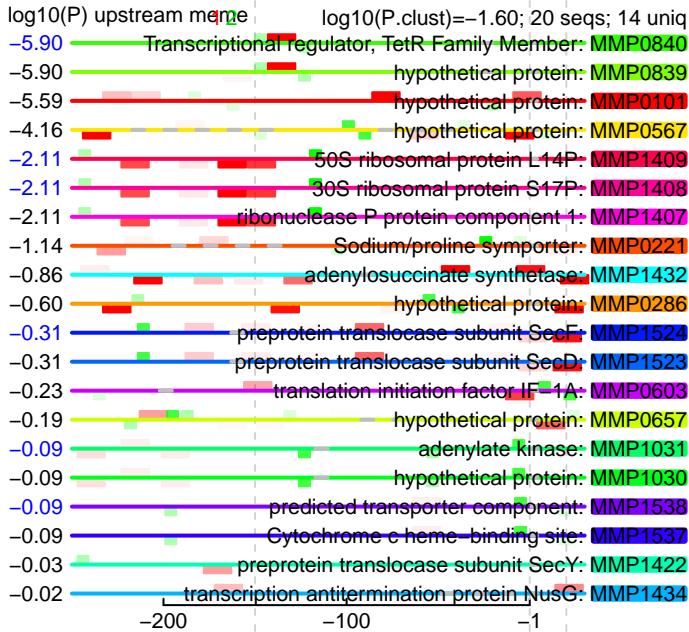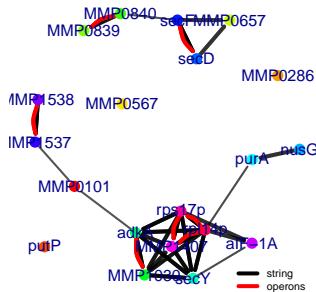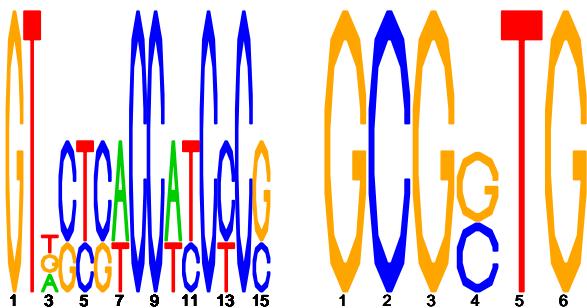| log10(P)	description	gene
−9.90	hypothetical protein:	MMP0761
−9.90	hypothetical protein:	MMP0760
−7.00	hypothetical protein:	MMP1453
−7.00	hypothetical protein:	MMP1452
−7.00	sor family Helix−turn−helix motif containing protein:	MMP1447
−6.96	hypothetical protein:	MMP0717
−5.11	H/ACA RNA−protein complex component Cbf5p:	MMP1686
−4.64	Dihydroorotase:	MMP1009
−4.55	nitrogenase reductase−like protein:	MMP0147
−3.95	te synthase−related protein synthase−related protein:	MMP1580
−3.85	Na+/H+ exchanger:	MMP0587
−3.39	hypothetical protein:	MMP0843
−3.33	hypothetical protein:	MMP0991
−3.06	hypothetical protein:	MMP0793
−3.06	membrane protein:	MMP0792
−2.82	DNA polymerase II small subunit:	MMP0008
−2.71		Antisense_5
−2.71		Antisense_2
−2.63	hypothetical protein:	MMP1228
−2.31	hypothetical protein:	MMP0281
−1.78	RecJ related protein:	MMP0547
−1.10	hypothetical protein:	MMP0871
−1.02	hypothetical protein:	MMP1059
−0.56	succinyl−diaminopimelate desuccinylase:	MMP1398
−0.48	hypothetical protein:	MMP0085
−0.38	hypothetical protein:	MMP1597
−0.37	hypothetical protein:	MMP0795
−0.36	hypothetical protein:	MMP0570
−0.28	N−glycosylase/DNA lyase:	MMP0304
−0.27	General substrate transporter:	MMP1636
−0.26	inc metallopeptidase, zinc−binding region:CBS domain:	MMP0453
−0.01	hypothetical protein:	MMP1236
−0.01	hypothetical protein:	MMP0499

Cluster: 0023 mmp; resid: 0.32; r/c: 21/37

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upstream meme PSSM #1; e=3.4e−06   upstream meme PSSM #2; e=37

log10(P) upstream meme   log10(P.clust)=−2.90; 21 seqs; 19 uniq

−10.64	ferredoxin: MMP1329
−8.38	Unanno_7
−8.25	Unanno_52
−7.99	methyltransferase: MMP0069
−4.44	Blue (type 1) copper domain: MMP0997
−3.00	Nitroreductase family: MMP1553
−1.88	hypothetical protein: MMP0115
−1.88	hypothetical protein: MMP0113
−1.86	hypothetical protein: MMP0528
−1.77	hypothetical protein: MMP0563
−1.63	Glutamate synthase subunit−related: MMP0496
−1.61	transduction systems periplasmic component−related: MMP1224
−1.40	hypothetical protein: MMP0035
−1.20	replication factor C large subunit: MMP0322
−1.20	hypothetical protein: MMP0321
−1.00	hypothetical protein: MMP1019
−0.88	Transcriptional regulator, TetR Family Member: MMP0799
−0.69	Unanno_39
−0.59	hypothetical protein: MMP0742
−0.25	hypothetical protein: MMP0477
−0.25	hypothetical protein: MMP0476

Cluster: 0024 mmp; resid: 0.43; r/c: 27/37
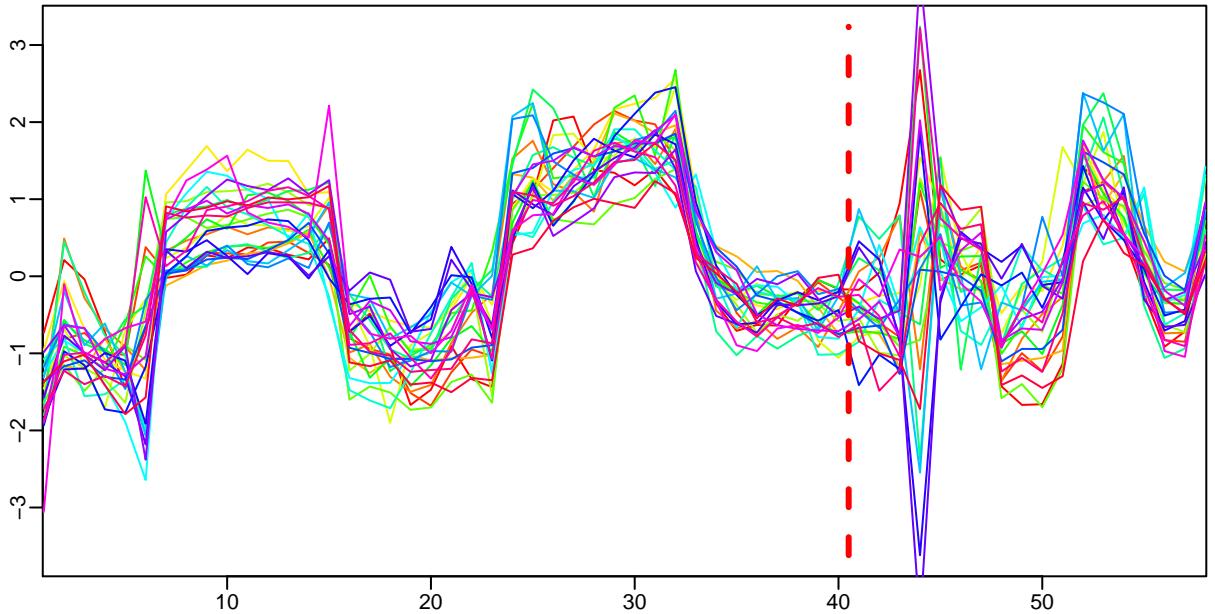
11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

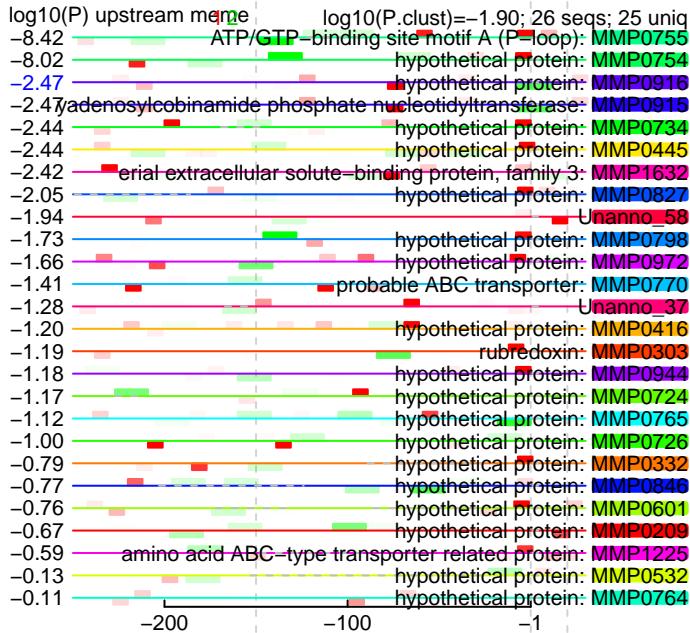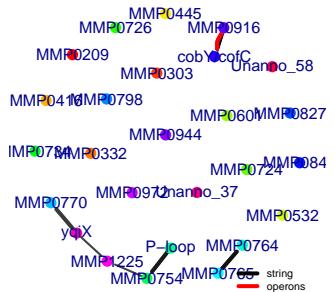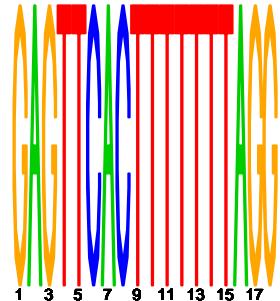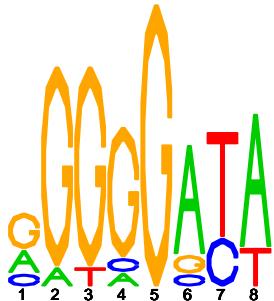upstream meme PSSM #1; e=0.00047 upstream meme PSSM #2; e=4.3e+03

log10(P) upstream meme   log10(P.clust)=−1.64; 27 seqs; 22 uniq

log10(P)	annotation
−3.47	hypothetical protein: MMP0076
−3.18	Unanno_4
−3.18	Unanno_2
−3.02	pyruvate carboxylase subunit B: MMP0340
−2.99	precorrin−3B C17−methyltransferase: MMP0953
−2.16	Sodium:neurotransmitter symporter: MMP0419
−2.15	hypothetical protein: MMP0702
−2.12	aspartate kinase: MMP1017
−2.05	indolepyruvate oxidoreductase subunit B: MMP0714
−2.05	indolepyruvate oxidoreductase subunit alpha 2: MMP0713
−2.05	coenzyme F390 synthetase II: MMP0715
−1.60	hypothetical protein: MMP0134
−1.37	Transcriptional regulator, ArsR family member: MMP0637
−1.23	precorrin−2 C−20 methyltransferase: MMP0319
−1.23	hypothetical protein: MMP1540
−1.23	2−oxosuberate synthase, last step: MMP0880
−1.17	aspartate carbamoyltransferase catalytic subunit: MMP1659
−1.10	hypothetical protein: MMP0815
−1.10	hypothetical protein: MMP0814
−1.02	hypothetical protein: MMP1541
−0.97	Na+/H+ Antiporter related protein: MMP0679
−0.82	hypothetical protein: MMP0655
−0.78	hexulose−6−phosphate synthase/ribonuclease regulator: MMP1270
−0.68	predicted transporter component: MMP1538
−0.68	Cytochrome c heme−binding site: MMP1537
−0.56	DNA−directed RNA polymerase subunit alpha: MMP1363
−0.23	hypothetical protein: MMP1590

−200   −100   −1

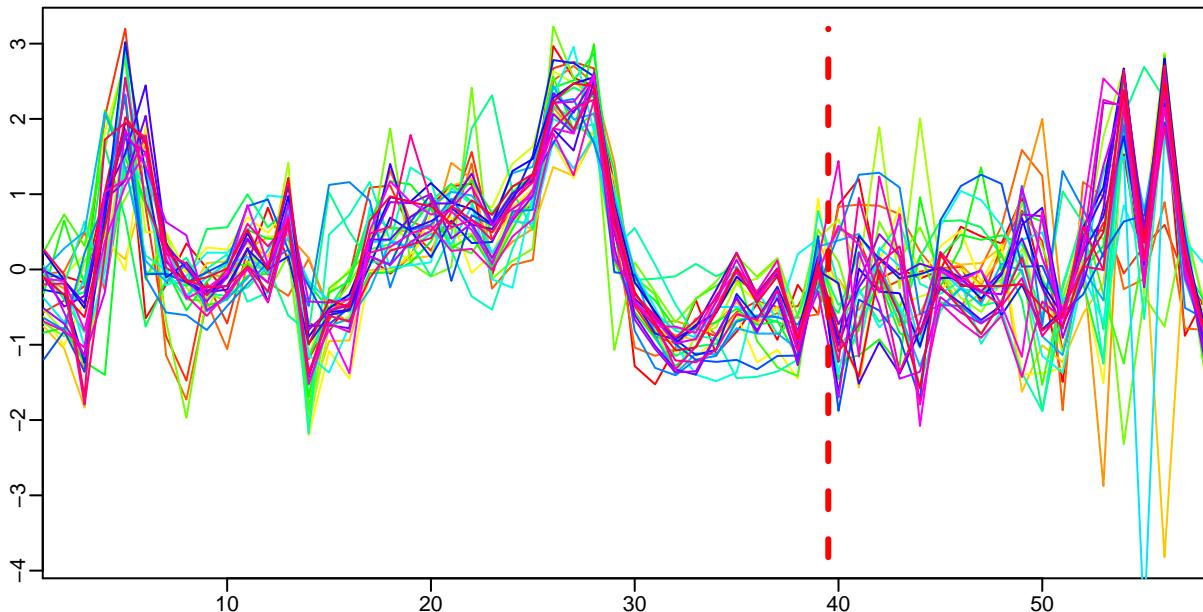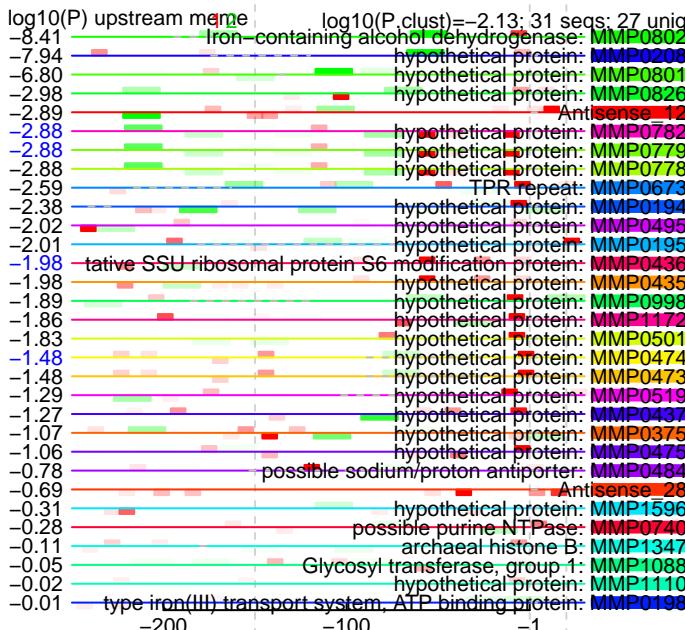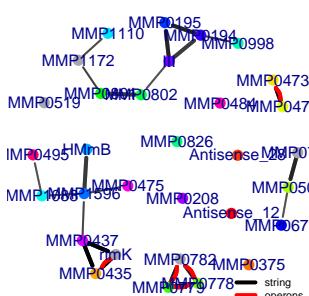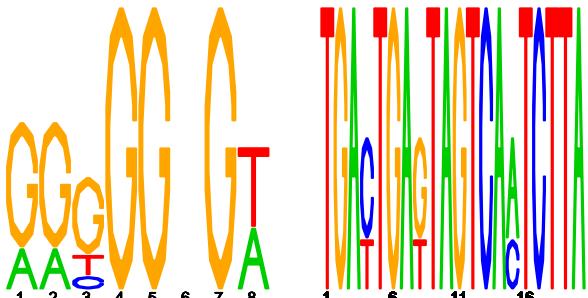**Cluster: 0025 mmp; resid: 0.31; r/c: 20/39**

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upstream meme PSSM #1; e=5.9

upstream meme PSSM #2; e=990

log10(P) upstream meme   log10(P.clust)=−2.71; 20 seqs; 19 uniq

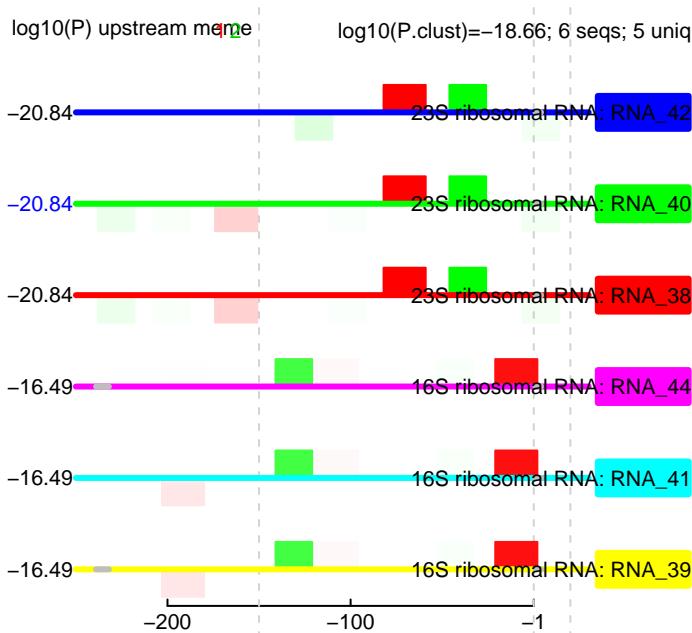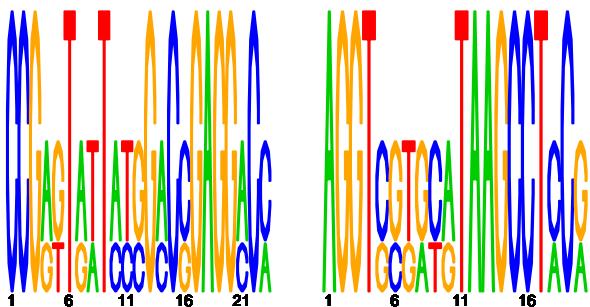| log10(P)	protein	gene
−8.55	hypothetical protein:	MMP1014
−7.42	erized domain 2:Archaeosine tRNA−ribosyltransferase:	MMP0610
−6.88	hypothetical protein:	MMP0412
−6.42	hypothetical protein:	MMP0243
−5.80	hypothetical protein:	MMP1048
−3.41	hypothetical protein:	MMP1356
−2.97	IMP dehydrogenase:	MMP0133
−2.66	diphthine synthase:	MMP0588
−2.25	glutamyl−tRNA synthetase:	MMP1011
−1.72	tRNA 2'−O−methylase:	MMP1425
−1.29	hypothetical protein:	MMP0921
−1.17	Ribonuclease P−related protein:	MMP0878
−1.04	DNA polymerase II large subunit:	MMP0026
−0.88	putative cytoplasmic protein:	MMP1195
−0.82	precorrin−3B C17−methyltransferase:	MMP0953
−0.26	translation initiation factor IF−2:	MMP0284
−0.19	indolepyruvate oxidoreductase subunit alpha 1:	MMP0316
−0.19	indolepyruvate oxidoreductase subunit B:	MMP0315
−0.16	DNA−directed RNA polymerase subunit beta'':	MMP1361
−0.06	putative deoxyhypusine synthase:	MMP0137

Cluster: 0026 mmp; resid: 0.18; r/c: 14/40

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upstream meme PSSM #1; e=180   upstream meme PSSM #2; e=4.1e+03

log10(P) upstream meme   log10(P.clust)=−2.01; 14 seqs; 13 uniq

−5.10	N−acetyltransferase related protein: MMP1184
−3.30	Molybdenum cofactor biosynthesis protein: MMP0201
−3.30	type iron(III) transport system, ATP binding protein: MMP0198
−3.22	hypothetical protein: MMP0497
−2.78	al domain including a metal−binding cysteine cluster: MMP0494
−2.69	hypothetical protein: MMP0475
−2.65	hypothetical protein: MMP1571
−1.62	hypothetical protein: MMP0208
−1.58	hypothetical protein: MMP1037
−1.04	hypothetical protein: MMP0771
−0.51	GCN5−related N−acetyltransferase: MMP1281
−0.18	hypothetical protein: MMP0805
−0.12	Uroporphyrinogen decarboxylase (URO−D): MMP0834
−0.02	possible purine NTPase: MMP0740

Cluster: 0027 mmp; resid: 0.34; r/c: 27/39

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

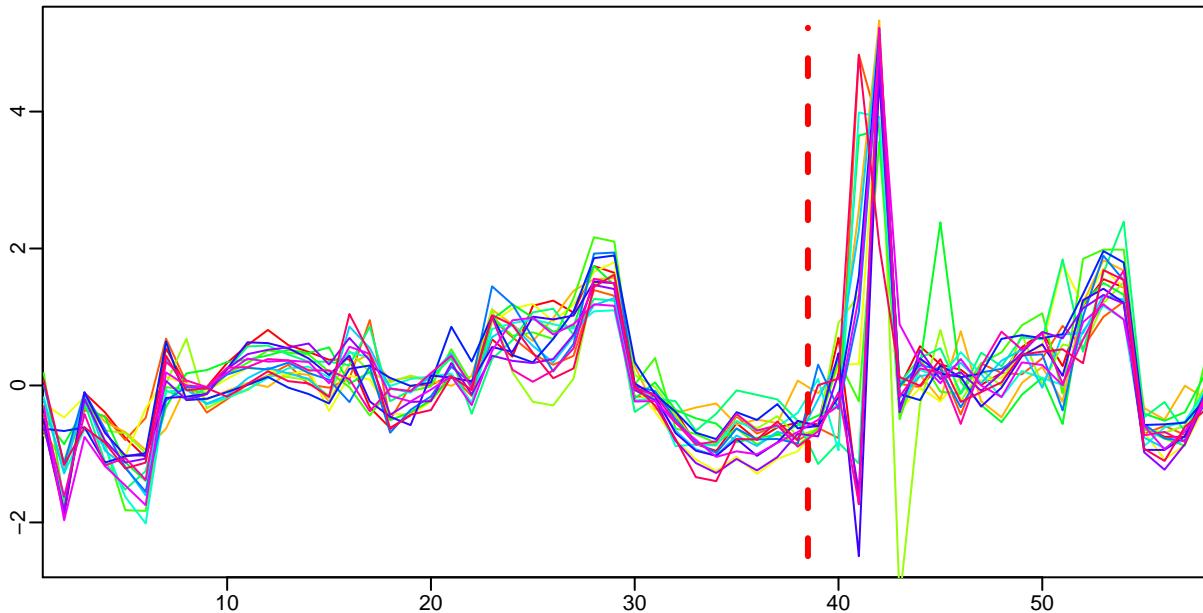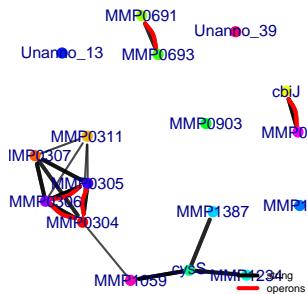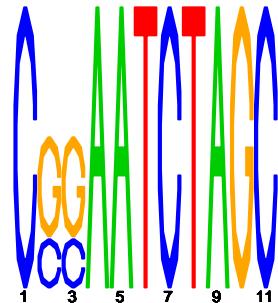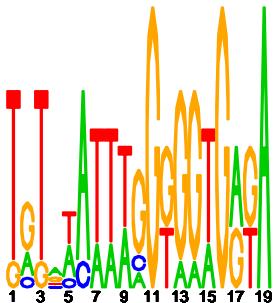upstream meme PSSM #1; e=0.034 upstream meme PSSM #2; e=2e+03

log10(P) upstream meme   log10(P.clust)=−1.54; 27 seqs; 23 uniq

log10(P)	Annotation	Gene
−5.87	hypothetical protein:	MMP1498
−5.87	hypothetical protein:	MMP1497
−4.57	homoserine dehydrogenase:	MMP1702
−4.57	Amino acid−binding ACT:	MMP1701
−3.72	3−dehydroquinate synthase:	MMP0006
−1.27	IMP cyclohydrolase:	MMP1310
−1.19	D−3−phosphoglycerate dehydrogenase:	MMP1588
−1.19	Ornithine carbamoyltransferase:	MMP0553
−1.16	(R)−citramalate synthase:	MMP1018
−1.14	oxoglutarate ferredoxin oxidoreductase subunit alpha:	MMP0003
−0.96	3−isopropylmalate dehydratase small subunit:	MMP0136
−0.96	threonine synthase:	MMP0135
−0.91	ferredoxin:	MMP1311
−0.91	roup II) similar to Acetylornithine aminotransferase:	MMP1101
−0.81	argininosuccinate synthase:	MMP0073
−0.69	seryl−tRNA synthetase:	MMP0879
−0.67	quinolinate synthetase:	MMP1242
−0.61	hypothetical protein:	MMP1593
−0.61	tryptophanyl−tRNA synthetase:	MMP1592
−0.59	ketol−acid reductoisomerase:	MMP0654
−0.58	pyridoxine biosynthesis protein:	MMP0103
−0.54	hypothetical protein:	MMP1196
−0.52	aspartyl/glutamyl−tRNA amidotransferase subunit A:	MMP1510
−0.51	3−isopropylmalate dehydratase:	MMP1149
−0.46	coenzyme F390 synthetase:	MMP0160
−0.33	thiamine−phosphate pyrophosphorylase:	MMP1139
−0.27	DNA directed RNA polymerase; subunit L:	MMP0261

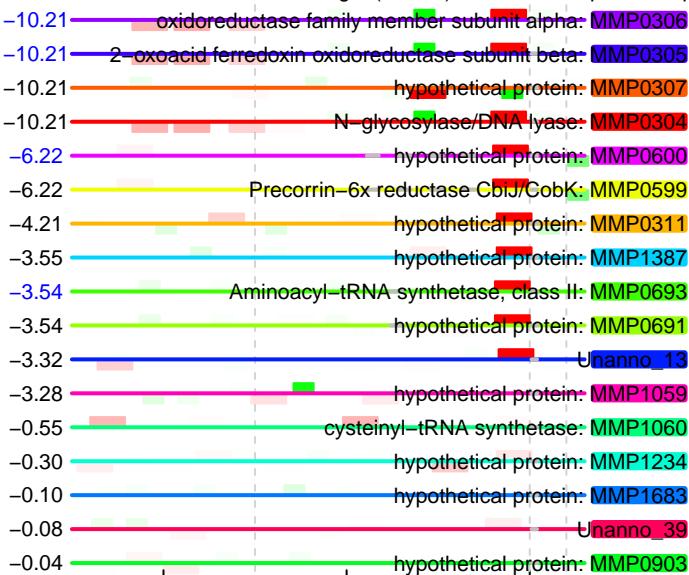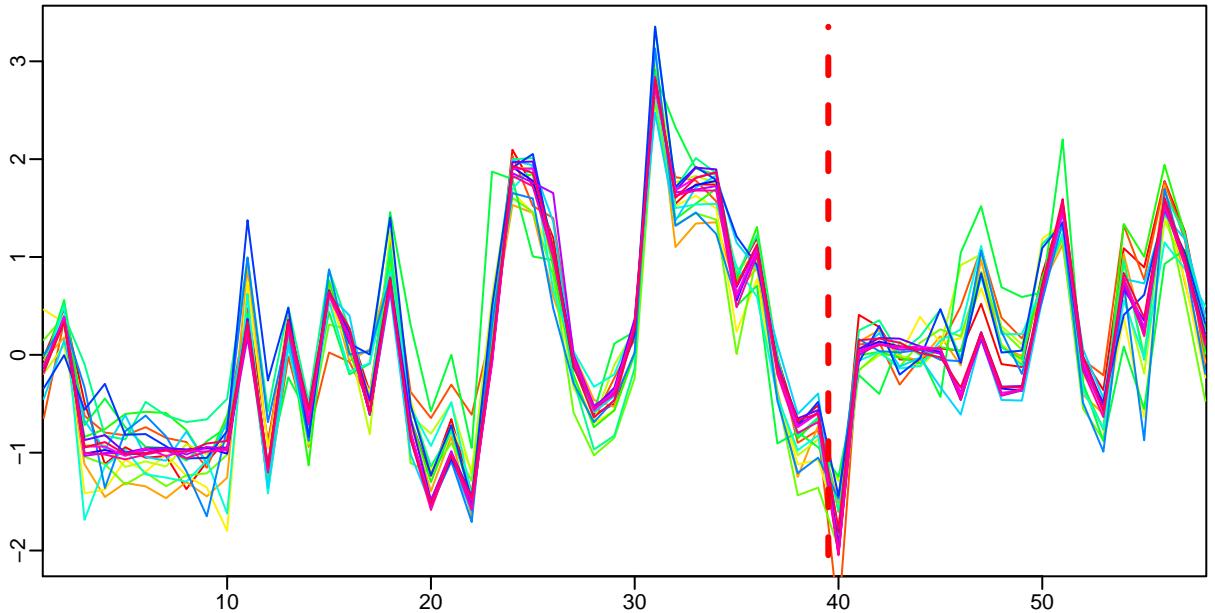**Cluster: 0028 mmp; resid: 0.35; r/c: 29/37**

upstream meme PSSM #1; e=0.00028   upstream meme PSSM #2; e=23

log10(P) upstream meme   log10(P.clust)=−1.97; 29 seqs: 25 uniq

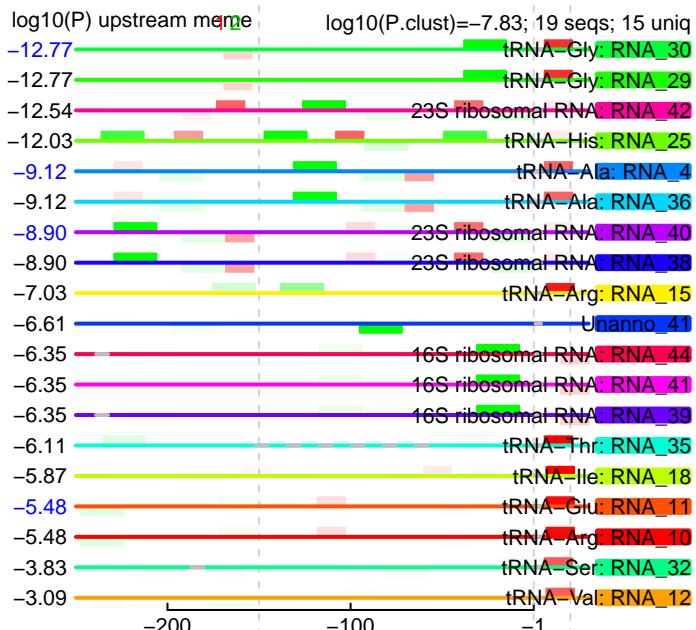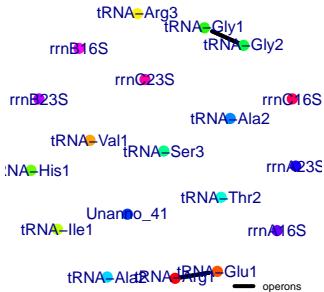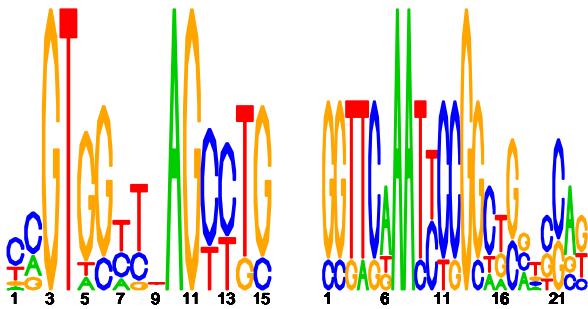| log10(P)	annotation	gene
−5.12	hypothetical protein:	MMP0342
−5.07	hypothetical protein:	MMP1657
−4.56	Dethiobiotin synthetase:	MMP1573
−4.50	ntaining formylmethanofuran dehydrogenase, subunit B:	MMP0511
−4.02	hypothetical protein:	MMP0536
−2.69	Heat shock protein Hsp20:	MMP0684
−2.66	utaryl−CoA dehydratase (Component A) related protein:	MMP0608
−2.57	transcription factor:	MMP0257
−2.57	imidazole glycerol phosphate synthase subunit HisH:	MMP0256
−1.91	ferrous iron transporter (GTP−binding):	MMP0630
−1.86	hypothetical protein:	MMP0843
−1.80	archaetidylserine synthase:	MMP1171
−1.73	hypothetical protein protein: possibly conserved:	MMP0313
−1.60	putative molybdenum cofactor biosynthesis protein C:	MMP1066
−1.38	Transcriptional regulator PadR−like family:	MMP0168
−1.38	ABC transporter ATP binding protein family member:	MMP0167
−1.38	MatE family member (drug/sodium antiporters):	MMP0166
−1.38	ABC transporter, family 2:	MMP0165
−1.33	glutamyl−tRNA(Gln) amidotransferase subunit E:	MMP1265
−1.08	hypothetical protein:	MMP0072
−0.96	Sensory transduction histidine kinase:	MMP1303
−0.94	hypothetical protein:	MMP0499
−0.87	Antisense_8	
−0.81	hypothetical protein:	MMP0265
−0.77	Unanno_59	
−0.77	hypothetical protein:	MMP1467
−0.69	putatuve iron dependent repressor:	MMP0631
−0.55	hypothetical protein:	MMP0812
−0.04	Survival protein SurE:	MMP1051

Cluster: 0029 mmp; resid: 0.34; r/c: 20/38
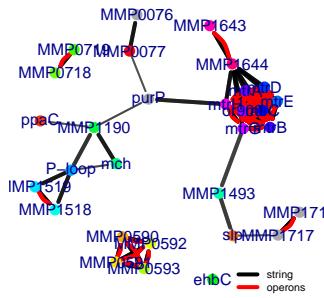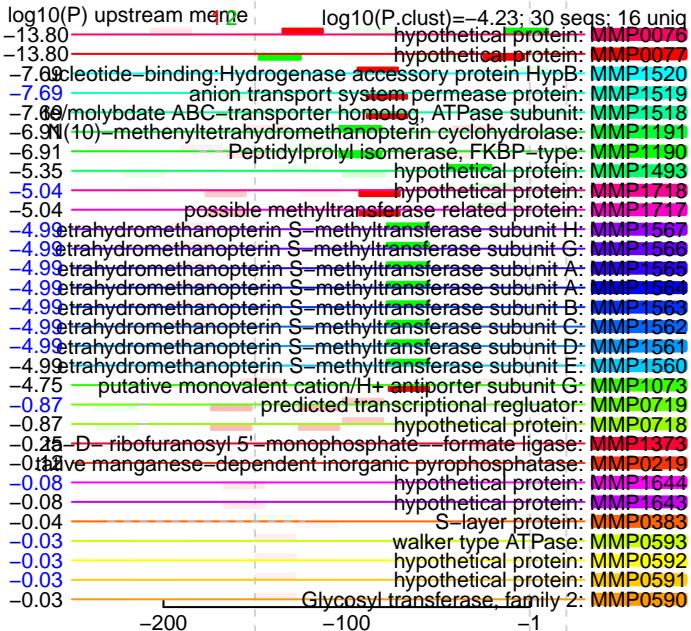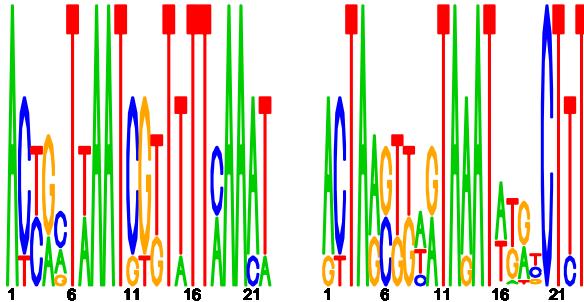
11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=1.7e+03 · upstream meme PSSM #2; e=9.3e+03

log10(P) upstream meme — log10(P.clust)=−1.60; 20 seqs; 14 uniq

log10(P)	Description	Gene
−5.90	Transcriptional regulator, TetR Family Member	MMP0840
−5.90	hypothetical protein	MMP0839
−5.59	hypothetical protein	MMP0101
−4.16	hypothetical protein	MMP0567
−2.11	50S ribosomal protein L14P	MMP1409
−2.11	30S ribosomal protein S17P	MMP1408
−2.11	ribonuclease P protein component 1	MMP1407
−1.14	Sodium/proline symporter	MMP0221
−0.86	adenylosuccinate synthetase	MMP1432
−0.60	hypothetical protein	MMP0286
−0.31	preprotein translocase subunit SecF	MMP1524
−0.31	preprotein translocase subunit SecD	MMP1523
−0.23	translation initiation factor IF−1A	MMP0603
−0.19	hypothetical protein	MMP0657
−0.09	adenylate kinase	MMP1031
−0.09	hypothetical protein	MMP1030
−0.09	predicted transporter component	MMP1538
−0.09	Cytochrome c heme−binding site	MMP1537
−0.03	preprotein translocase subunit SecY	MMP1422
−0.02	transcription antitermination protein NusG	MMP1434

Cluster: 0030 mmp; resid: 0.30; r/c: 26/40
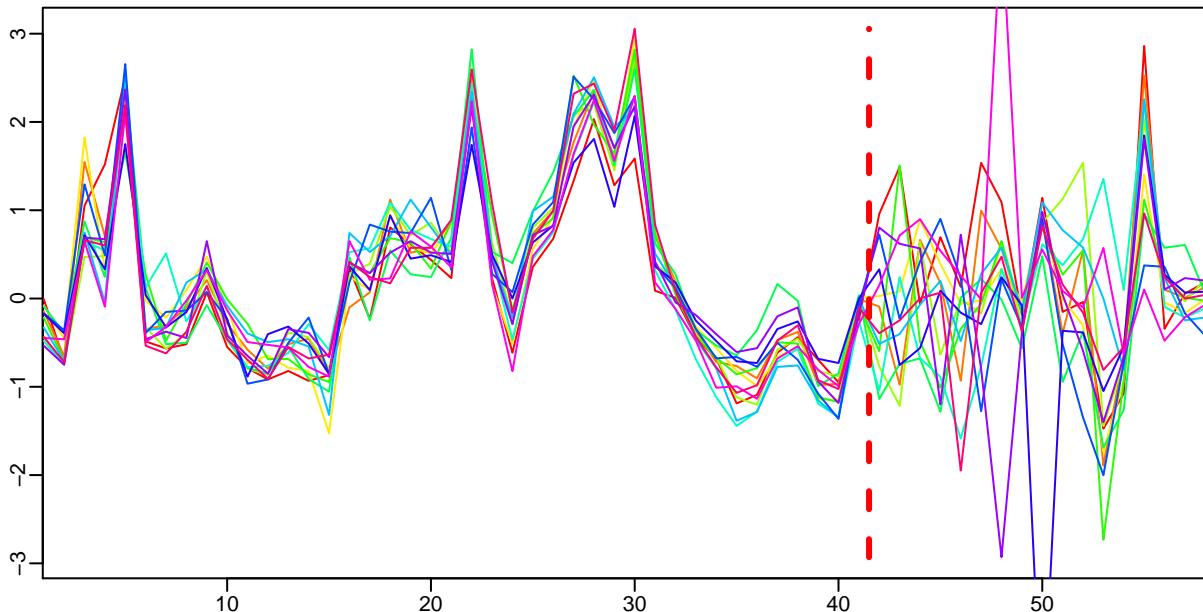
11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

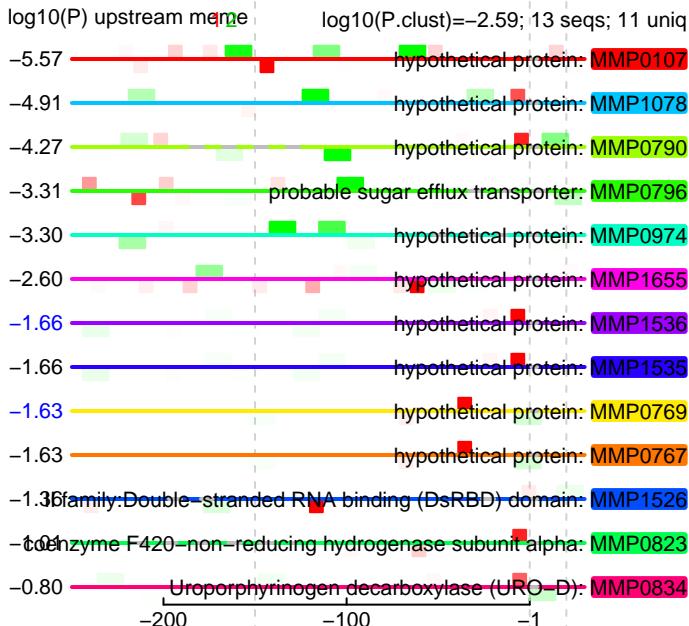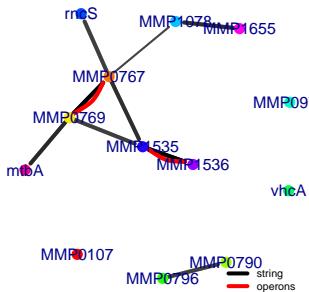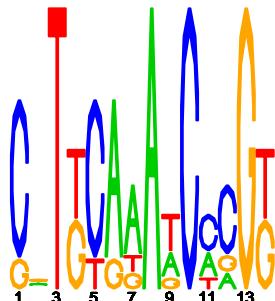upstream meme PSSM #1; e=1.2e−09   upstream meme PSSM #2; e=5.8e+04
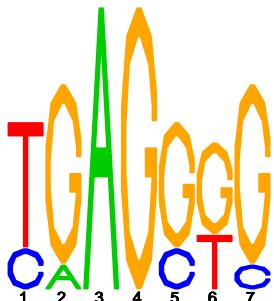
log10(P) upstream meme   log10(P.clust)=−1.90; 26 seqs; 25 uniq

log10(P)	annotation	gene
−8.42	ATP/GTP−binding site motif A (P−loop):	MMP0755
−8.02	hypothetical protein:	MMP0754
−2.47	hypothetical protein:	MMP0916
−2.47	adenosylcobinamide phosphate nucleotidyltransferase:	MMP0915
−2.44	hypothetical protein:	MMP0734
−2.44	hypothetical protein:	MMP0445
−2.42	erial extracellular solute−binding protein, family 3:	MMP1632
−2.05	hypothetical protein:	MMP0827
−1.94		Unanno_58
−1.73	hypothetical protein:	MMP0798
−1.66	hypothetical protein:	MMP0972
−1.41	probable ABC transporter:	MMP0770
−1.28		Unanno_37
−1.20	hypothetical protein:	MMP0416
−1.19	rubredoxin:	MMP0303
−1.18	hypothetical protein:	MMP0944
−1.17	hypothetical protein:	MMP0724
−1.12	hypothetical protein:	MMP0765
−1.00	hypothetical protein:	MMP0726
−0.79	hypothetical protein:	MMP0332
−0.77	hypothetical protein:	MMP0846
−0.76	hypothetical protein:	MMP0601
−0.67	hypothetical protein:	MMP0209
−0.59	amino acid ABC−type transporter related protein:	MMP1225
−0.13	hypothetical protein:	MMP0532
−0.11	hypothetical protein:	MMP0764

Cluster: 0031 mmp; resid: 0.33; r/c: 31/39

upstream meme PSSM #1; e=6.9e−06   upstream meme PSSM #2; e=510

log10(P) upstream meme   log10(P.clust)=−2.13; 31 seqs: 27 uniq

log10(P)	annotation	gene
−8.41	Iron−containing alcohol dehydrogenase:	MMP0802
−7.94	hypothetical protein:	MMP0208
−6.80	hypothetical protein:	MMP0801
−2.98	hypothetical protein:	MMP0826
−2.89	Antisense_12	
−2.88	hypothetical protein:	MMP0782
−2.88	hypothetical protein:	MMP0779
−2.88	hypothetical protein:	MMP0778
−2.59	TPR repeat:	MMP0673
−2.38	hypothetical protein:	MMP0194
−2.02	hypothetical protein:	MMP0495
−2.01	hypothetical protein:	MMP0195
−1.98	tative SSU ribosomal protein S6 modification protein:	MMP0436
−1.98	hypothetical protein:	MMP0435
−1.89	hypothetical protein:	MMP0998
−1.86	hypothetical protein:	MMP1172
−1.83	hypothetical protein:	MMP0501
−1.48	hypothetical protein:	MMP0474
−1.48	hypothetical protein:	MMP0473
−1.29	hypothetical protein:	MMP0519
−1.27	hypothetical protein:	MMP0437
−1.07	hypothetical protein:	MMP0375
−1.06	hypothetical protein:	MMP0475
−0.78	possible sodium/proton antiporter:	MMP0484
−0.69	Antisense_28	
−0.31	hypothetical protein:	MMP1596
−0.28	possible purine NTPase:	MMP0740
−0.11	archaeal histone B:	MMP1347
−0.05	Glycosyl transferase, group 1:	MMP1088
−0.02	hypothetical protein:	MMP1110
−0.01	type iron(III) transport system, ATP binding protein:	MMP0198

11 Oct 11 16:14:07 iter=2000
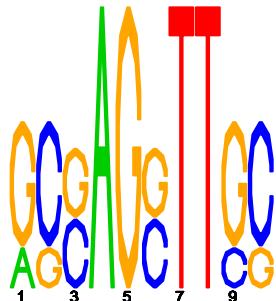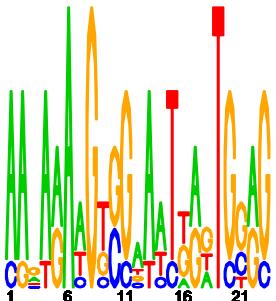cMonkey Version 4.8.8 mmp

Cluster: 0032 mmp; resid: 0.03; r/c: 6/39

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=0.00036 upstream meme PSSM #2; e=0.006
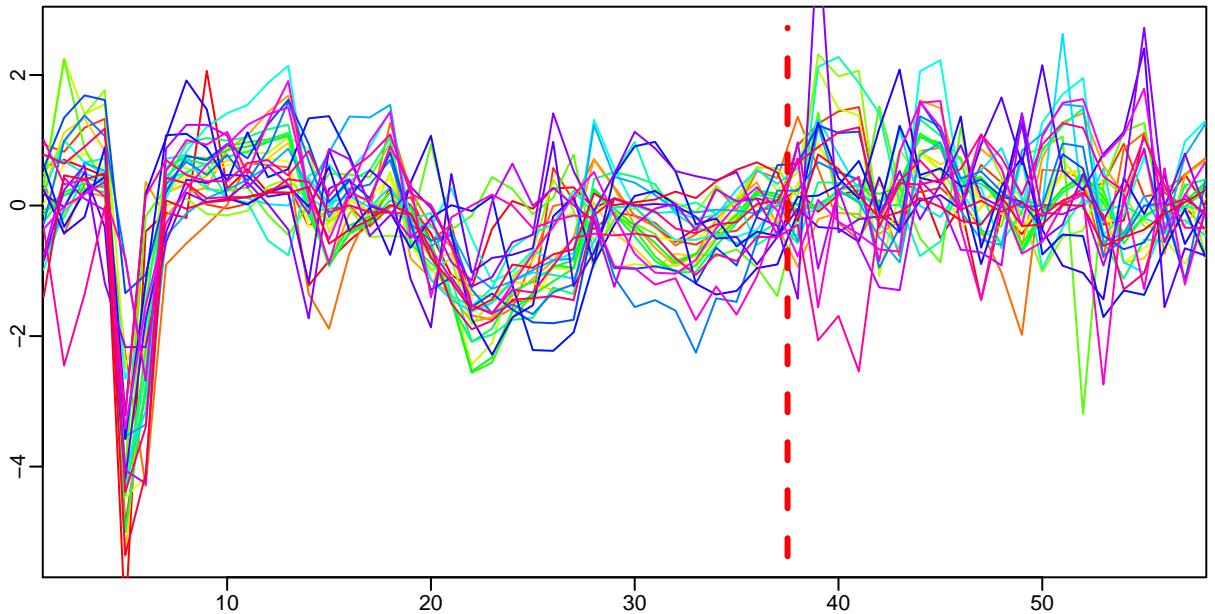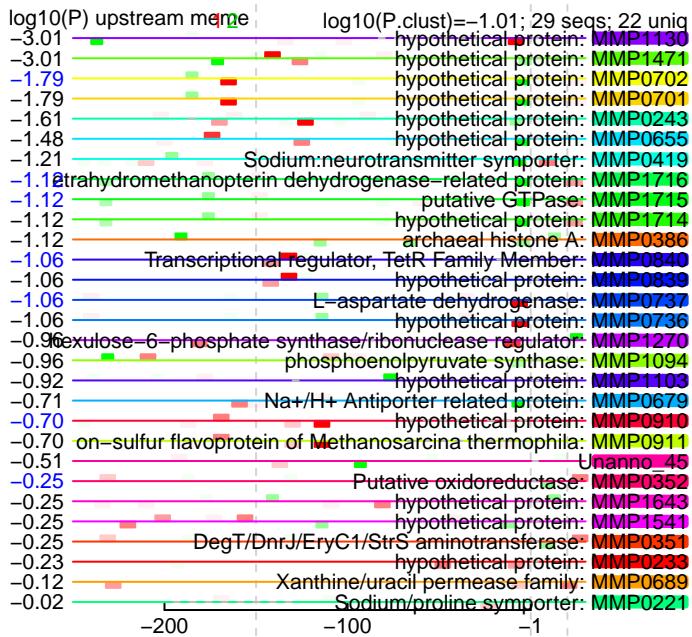
log10(P) upstream meme

log10(P.clust)=−18.66; 6 seqs; 5 uniq

−20.84 23S ribosomal RNA: RNA_42

−20.84 23S ribosomal RNA: RNA_40

−20.84 23S ribosomal RNA: RNA_38

−16.49 16S ribosomal RNA: RNA_44

−16.49 16S ribosomal RNA: RNA_41

−16.49 16S ribosomal RNA: RNA_39

rrnB 23S
rrnA 23S
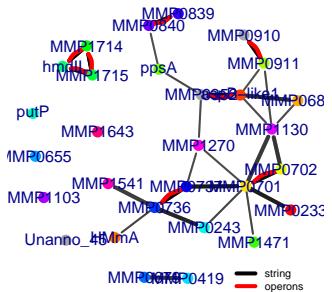rrnC 16S   rrnA 16S
rrnC 23S
rrnB 16S

−200   −100   −1
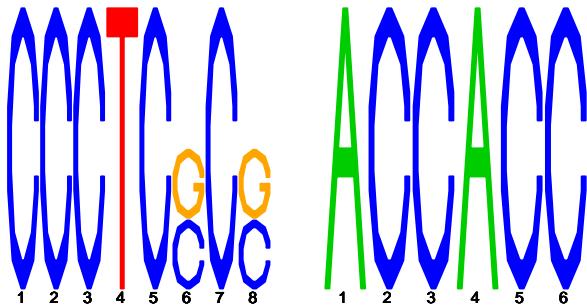
Cluster: 0033 mmp; resid: 0.21; r/c: 17/38

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=0.32   upstream meme PSSM #2; e=260

log10(P) upstream meme   log10(P.clust)=−4.46; 17 seqs; 13 uniq

log10(P)	Description	Gene
−10.21	oxidoreductase family member subunit alpha:	MMP0306
−10.21	2−oxoacid ferredoxin oxidoreductase subunit beta:	MMP0305
−10.21	hypothetical protein:	MMP0307
−10.21	N−glycosylase/DNA lyase:	MMP0304
−6.22	hypothetical protein:	MMP0600
−6.22	Precorrin−6x reductase CbiJ/CobK:	MMP0599
−4.21	hypothetical protein:	MMP0311
−3.55	hypothetical protein:	MMP1387
−3.54	Aminoacyl−tRNA synthetase, class II:	MMP0693
−3.54	hypothetical protein:	MMP0691
−3.32		Unanno_13
−3.28	hypothetical protein:	MMP1059
−0.55	cysteinyl−tRNA synthetase:	MMP1060
−0.30	hypothetical protein:	MMP1234
−0.10	hypothetical protein:	MMP1683
−0.08		Unanno_39
−0.04	hypothetical protein:	MMP0903

Cluster: 0034 mmp; resid: 0.16; r/c: 19/39
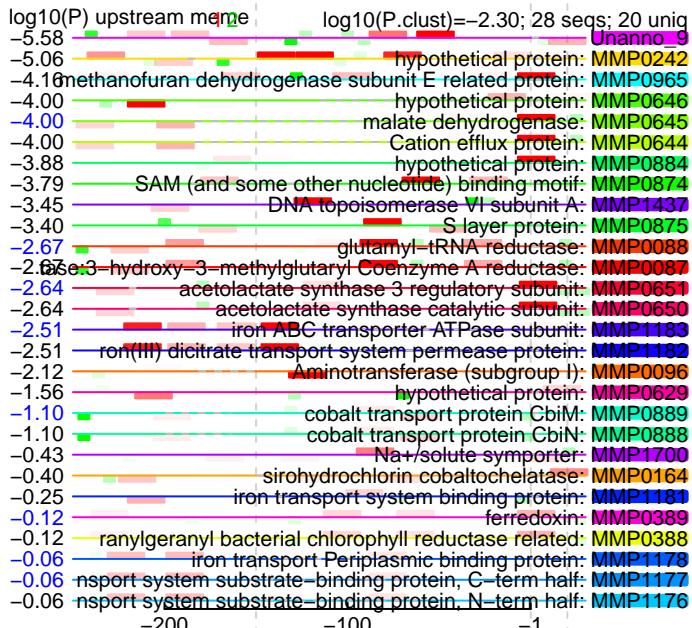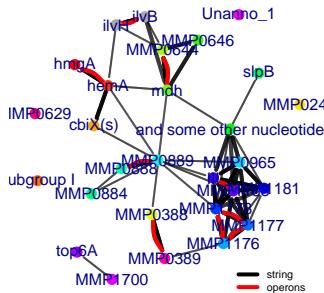
11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=6e−18   upstream meme PSSM #2; e=8.4e−09

log10(P) upstream meme   log10(P.clust)=−7.83; 19 seqs; 15 uniq

log10(P)		
−12.77	tRNA−Gly:	RNA_30
−12.77	tRNA−Gly:	RNA_29
−12.54	23S ribosomal RNA:	RNA_42
−12.03	tRNA−His:	RNA_25
−9.12	tRNA−Ala:	RNA_4
−9.12	tRNA−Ala:	RNA_36
−8.90	23S ribosomal RNA:	RNA_40
−8.90	23S ribosomal RNA:	RNA_38
−7.03	tRNA−Arg:	RNA_15
−6.61	Unanno_41	
−6.35	16S ribosomal RNA:	RNA_44
−6.35	16S ribosomal RNA:	RNA_41
−6.35	16S ribosomal RNA:	RNA_39
−6.11	tRNA−Thr:	RNA_35
−5.87	tRNA−Ile:	RNA_18
−5.48	tRNA−Glu:	RNA_11
−5.48	tRNA−Arg:	RNA_10
−3.83	tRNA−Ser:	RNA_32
−3.09	tRNA−Val:	RNA_12

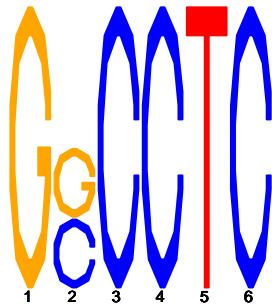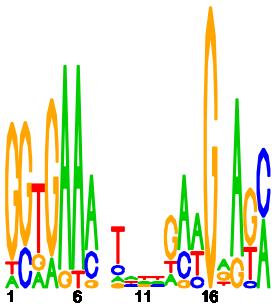**Cluster: 0035 mmp; resid: 0.43; r/c: 30/39**
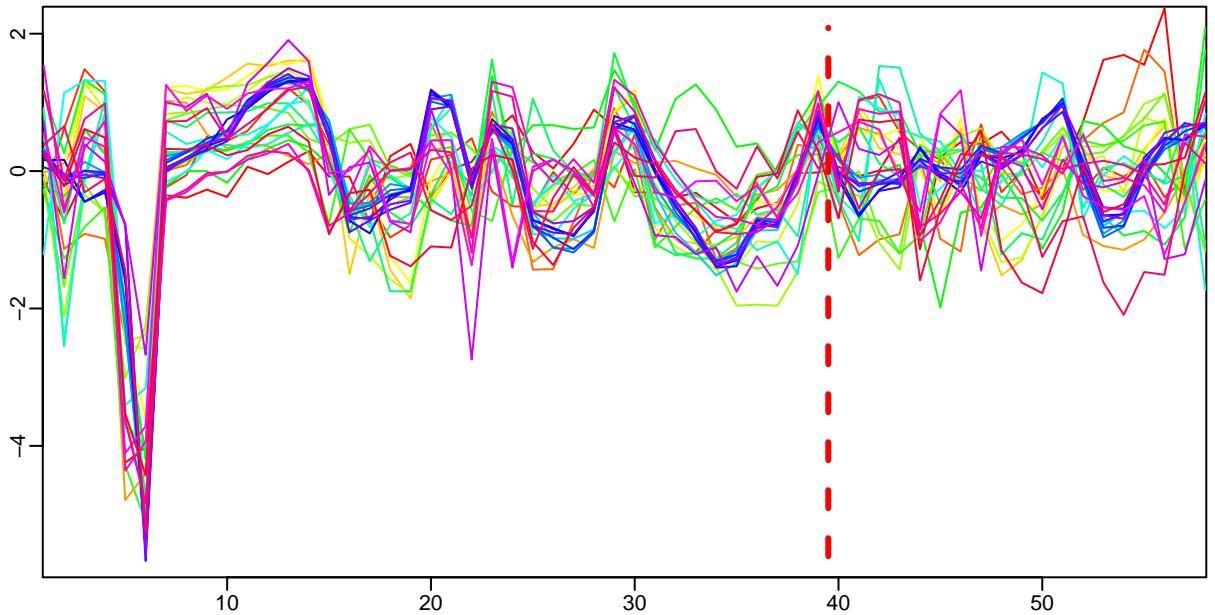
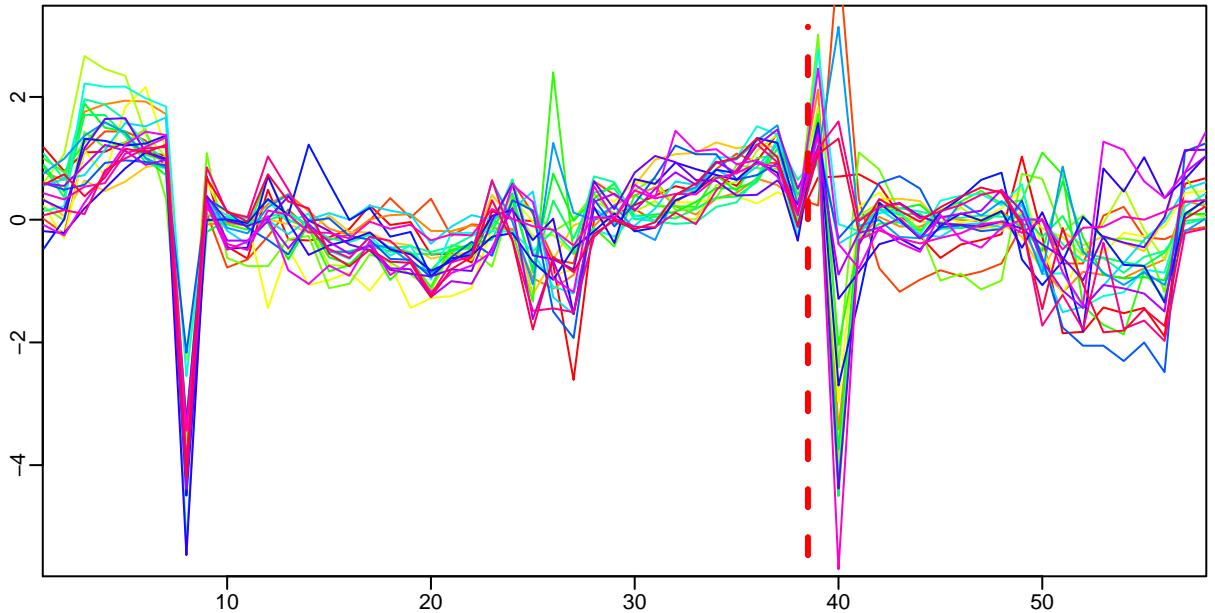**Cluster: 0036 mmp; resid: 0.18; r/c: 13/41**

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=23

upstream meme PSSM #2; e=390

log10(P) upstream meme

log10(P.clust)=−2.59; 13 seqs; 11 uniq

−5.57	hypothetical protein: MMP0107
−4.91	hypothetical protein: MMP1078
−4.27	hypothetical protein: MMP0790
−3.31	probable sugar efflux transporter: MMP0796
−3.30	hypothetical protein: MMP0974
−2.60	hypothetical protein: MMP1655
−1.66	hypothetical protein: MMP1536
−1.66	hypothetical protein: MMP1535
−1.63	hypothetical protein: MMP0769
−1.63	hypothetical protein: MMP0767
−1.36	family:Double−stranded RNA binding (DsRBD) domain: MMP1526
−1.09	coenzyme F420−non−reducing hydrogenase subunit alpha: MMP0823
−0.80	Uroporphyrinogen decarboxylase (URO−D): MMP0834

string
operons

Cluster: 0037 mmp; resid: 0.21; r/c: 18/41

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp
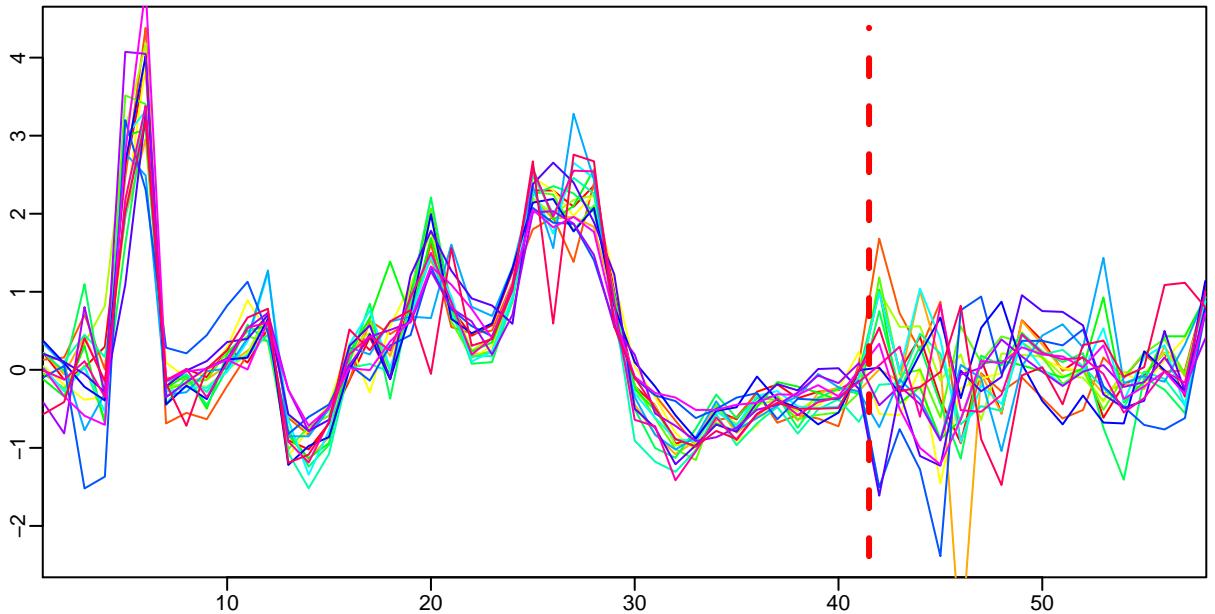
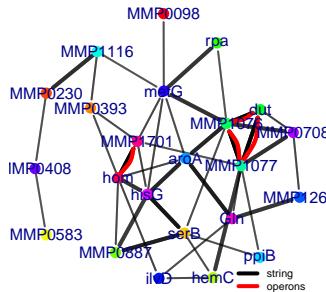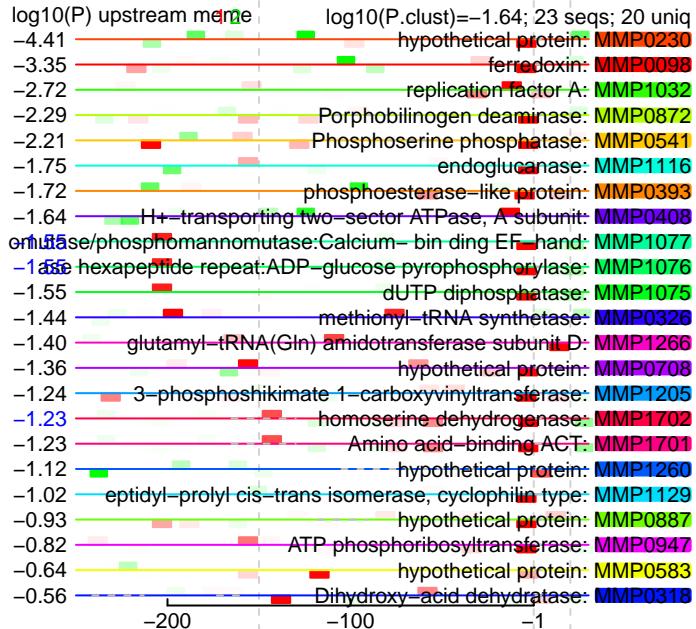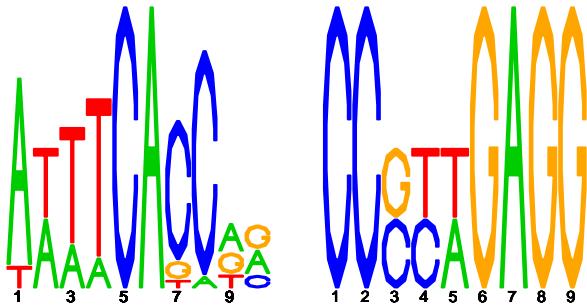upstream meme PSSM #1; e=0.071   upstream meme PSSM #2; e=730

log10(P) upstream meme   log10(P.clust)=−3.18; 18 seqs; 18 uniq

−8.10	prephenate dehydratase: MMP1528
−7.72	Antisense_15
−7.01	hypothetical protein: MMP0129
−6.33	Antisense_26
−5.20	Antisense_17
−5.02	de synthase:Cobyrinic acid a,c−diamide synthase CbiA: MMP1478
−4.72	Antisense_28
−3.96	membrane component:Ketopantoate reductase ApbA/PanE: MMP0672
−3.17	Antisense_20
−1.78	Antisense_7
−1.15	Unanno_46
−1.11	Antisense_25
−0.84	Antisense_14
−0.66	Antisense_21
−0.60	Unanno_30
−0.28	coenzyme F420−non−reducing hydrogenase subunit delta: MMP0821
−0.20	Antisense_19
−0.10	Antisense_11

Unanno_46
Antisense_14
Antisense_26
MMP0672
vhoD   cbbA
Antisense_15
:isense_17 Unanno_30 MMP0129   Antisense_
Antisense_11
Antisense_
Antisense_25 pheA
Antisense_28
Antisense_1
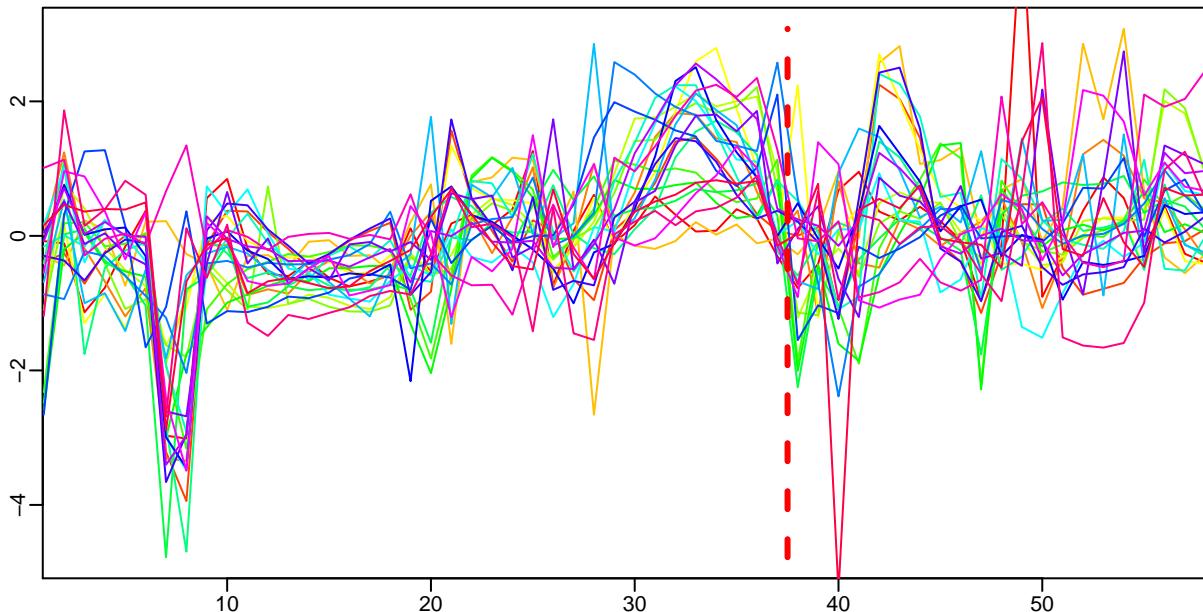Antisense_21

−200   −100   −1

Cluster: 0038 mmp; resid: 0.47; r/c: 29/37

upstream meme PSSM #1; e=3.9e+00   upstream meme PSSM #2; e=6.5e+03

log10(P) upstream meme   log10(P.clust)=−1.01; 29 seqs; 22 uniq

log10(P)	Annotation
−3.01	hypothetical protein: MMP1130
−3.01	hypothetical protein: MMP1471
−1.79	hypothetical protein: MMP0702
−1.79	hypothetical protein: MMP0701
−1.61	hypothetical protein: MMP0243
−1.48	hypothetical protein: MMP0655
−1.21	Sodium:neurotransmitter symporter: MMP0419
−1.12	tetrahydromethanopterin dehydrogenase−related protein: MMP1716
−1.12	putative GTPase: MMP1715
−1.12	hypothetical protein: MMP1714
−1.12	archaeal histone A: MMP0386
−1.06	Transcriptional regulator, TetR Family Member: MMP0840
−1.06	hypothetical protein: MMP0839
−1.06	L−aspartate dehydrogenase: MMP0737
−1.06	hypothetical protein: MMP0736
−0.96	hexulose−6−phosphate synthase/ribonuclease regulator: MMP1270
−0.96	phosphoenolpyruvate synthase: MMP1094
−0.92	hypothetical protein: MMP1103
−0.71	Na+/H+ Antiporter related protein: MMP0679
−0.70	hypothetical protein: MMP0910
−0.70	iron−sulfur flavoprotein of Methanosarcina thermophila: MMP0911
−0.51	Unanno_45
−0.25	Putative oxidoreductase: MMP0352
−0.25	hypothetical protein: MMP1643
−0.25	hypothetical protein: MMP1541
−0.25	DegT/DnrJ/EryC1/StrS aminotransferase: MMP0351
−0.23	hypothetical protein: MMP0233
−0.12	Xanthine/uracil permease family: MMP0689
−0.02	Sodium/proline symporter: MMP0221

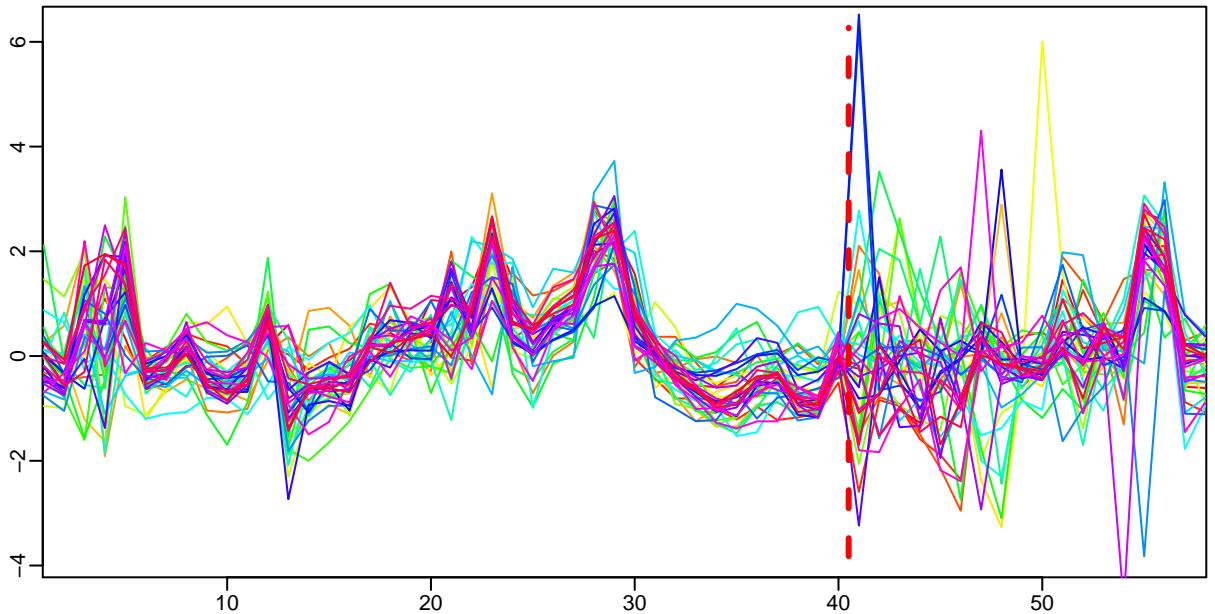**Cluster: 0039 mmp; resid: 0.44; r/c: 28/39**

upstream meme PSSM #1; e=4.2   upstream meme PSSM #2; e=4.9e+03

log10(P) upstream meme   log10(P.clust)=−2.30; 28 seqs; 20 uniq

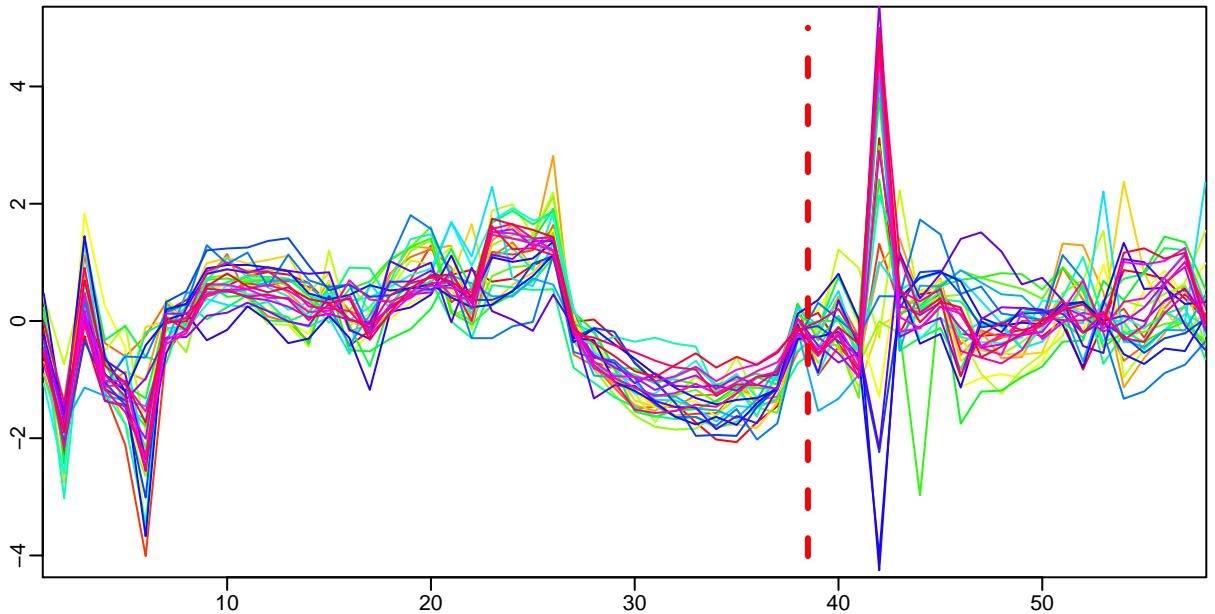| log10(P)	annotation	gene
−5.58		Unanno_9
−5.06	hypothetical protein:	MMP0242
−4.16	methanofuran dehydrogenase subunit E related protein:	MMP0965
−4.00	hypothetical protein:	MMP0646
−4.00	malate dehydrogenase:	MMP0645
−4.00	Cation efflux protein:	MMP0644
−3.88	hypothetical protein:	MMP0884
−3.79	SAM (and some other nucleotide) binding motif:	MMP0874
−3.45	DNA topoisomerase VI subunit A:	MMP1437
−3.40	S layer protein:	MMP0875
−2.67	glutamyl−tRNA reductase:	MMP0088
−2.65	3−hydroxy−3−methylglutaryl Coenzyme A reductase:	MMP0087
−2.64	acetolactate synthase 3 regulatory subunit:	MMP0651
−2.64	acetolactate synthase catalytic subunit:	MMP0650
−2.51	iron ABC transporter ATPase subunit:	MMP1183
−2.51	iron(III) dicitrate transport system permease protein:	MMP1182
−2.12	Aminotransferase (subgroup I):	MMP0096
−1.56	hypothetical protein:	MMP0629
−1.10	cobalt transport protein CbiM:	MMP0889
−1.10	cobalt transport protein CbiN:	MMP0888
−0.43	Na+/solute symporter:	MMP1700
−0.40	sirohydrochlorin cobaltochelatase:	MMP0164
−0.25	iron transport system binding protein:	MMP1181
−0.12	ferredoxin:	MMP0389
−0.12	geranylgeranyl bacterial chlorophyll reductase related:	MMP0388
−0.06	iron transport Periplasmic binding protein:	MMP1178
−0.06	transport system substrate−binding protein, C−term half:	MMP1177
−0.06	transport system substrate−binding protein, N−term half:	MMP1176

−200   −100   −1

Cluster: 0040 mmp; resid: 0.30; r/c: 23/38

upstream meme PSSM #1; e=0.0033 **upstream meme PSSM #2; e=4e+04**

log10(P) upstream meme   log10(P.clust)=−1.64; 23 seqs; 20 uniq

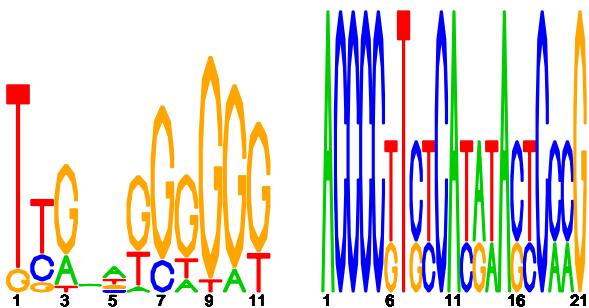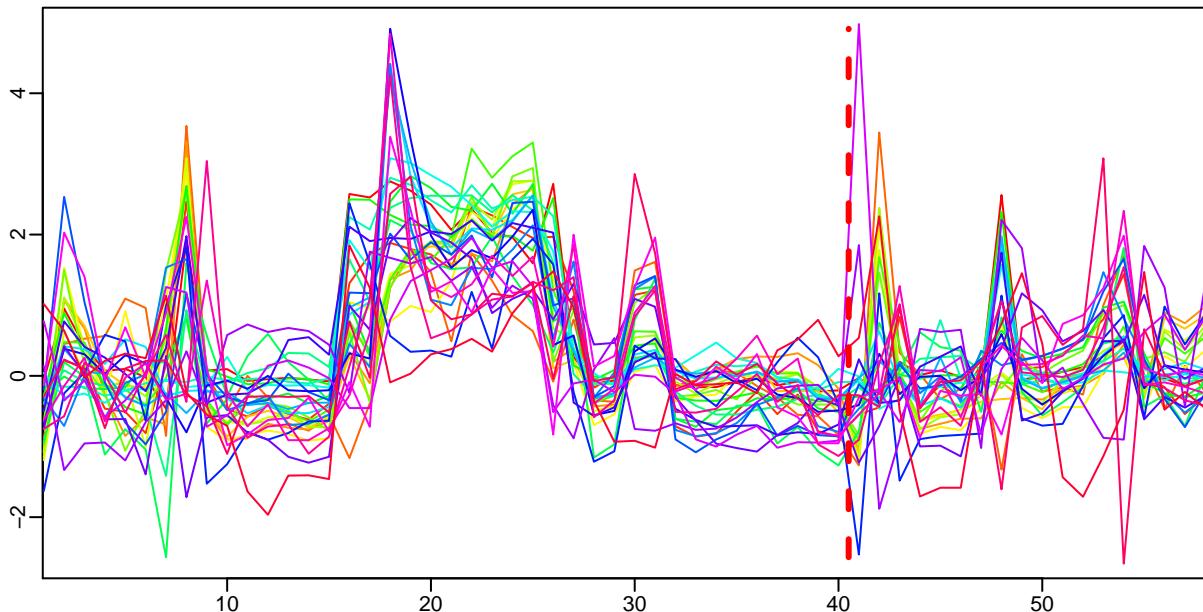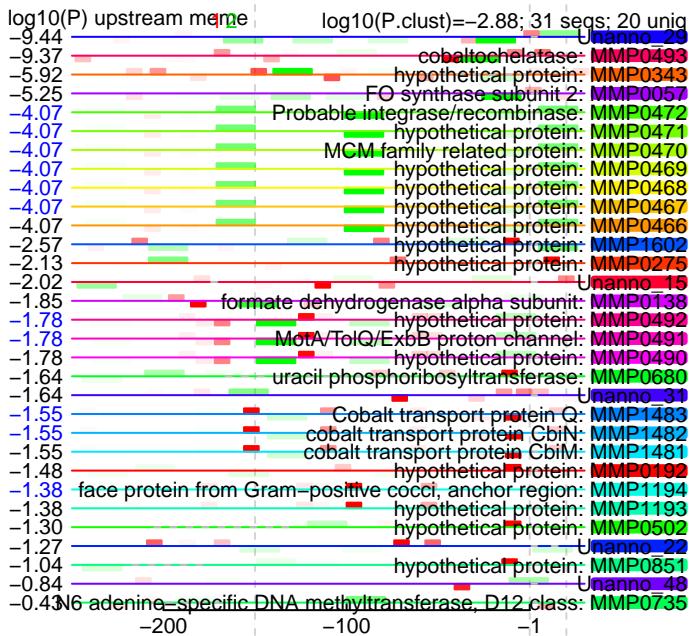| log10(P)	Description	Gene
−4.41	hypothetical protein:	MMP0230
−3.35	ferredoxin:	MMP0098
−2.72	replication factor A:	MMP1032
−2.29	Porphobilinogen deaminase:	MMP0872
−2.21	Phosphoserine phosphatase:	MMP0541
−1.75	endoglucanase:	MMP1116
−1.72	phosphoesterase−like protein:	MMP0393
−1.64	H+−transporting two−sector ATPase, A subunit:	MMP0408
−1.55	omutase/phosphomannomutase:Calcium− bin ding EF− hand:	MMP1077
−1.55	hexapeptide repeat:ADP−glucose pyrophosphorylase:	MMP1076
−1.55	dUTP diphosphatase:	MMP1075
−1.44	methionyl−tRNA synthetase:	MMP0326
−1.40	glutamyl−tRNA(Gln) amidotransferase subunit D:	MMP1266
−1.36	hypothetical protein:	MMP0708
−1.24	3−phosphoshikimate 1−carboxyvinyltransferase:	MMP1205
−1.23	homoserine dehydrogenase:	MMP1702
−1.23	Amino acid−binding ACT:	MMP1701
−1.12	hypothetical protein:	MMP1260
−1.02	eptidyl−prolyl cis−trans isomerase, cyclophilin type:	MMP1129
−0.93	hypothetical protein:	MMP0887
−0.82	ATP phosphoribosyltransferase:	MMP0947
−0.64	hypothetical protein:	MMP0583
−0.56	Dihydroxy−acid dehydratase:	MMP0318

Cluster: 0041 mmp; resid: 0.48; r/c: 24/37

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cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=160
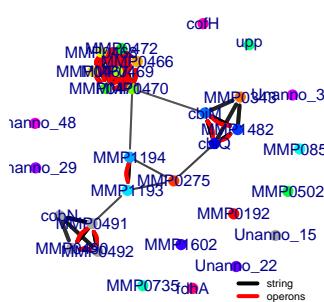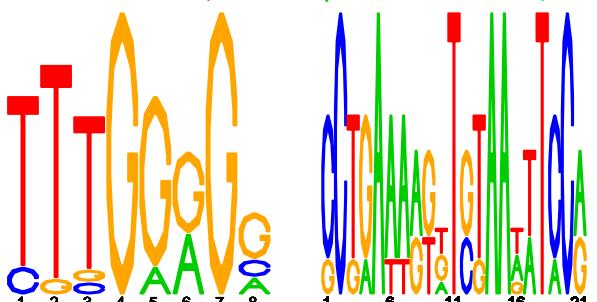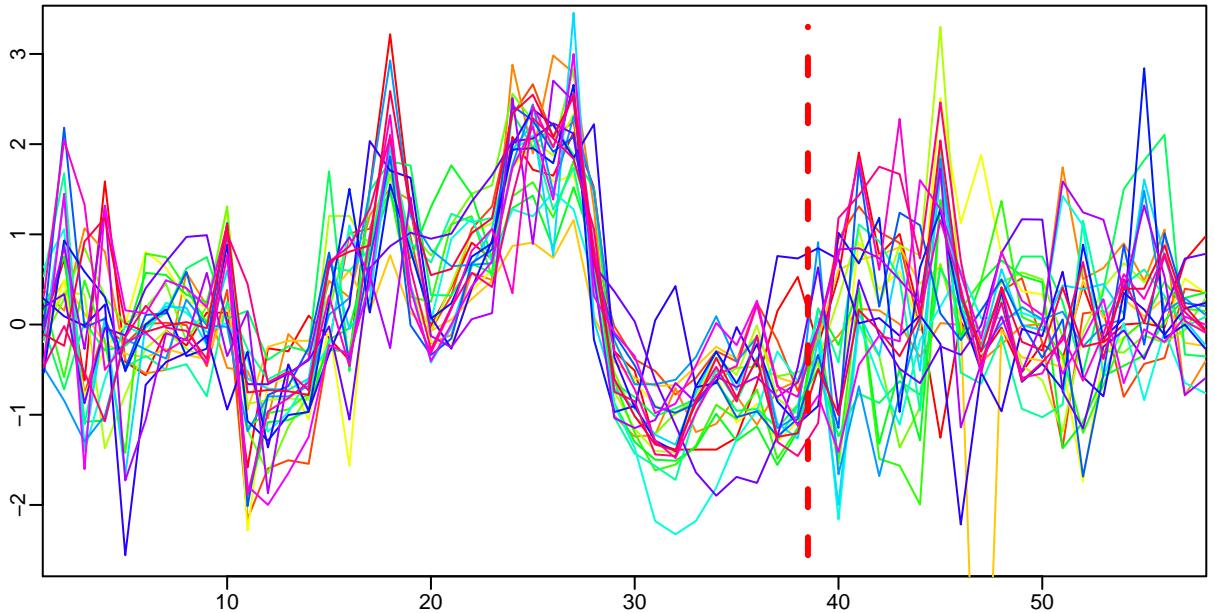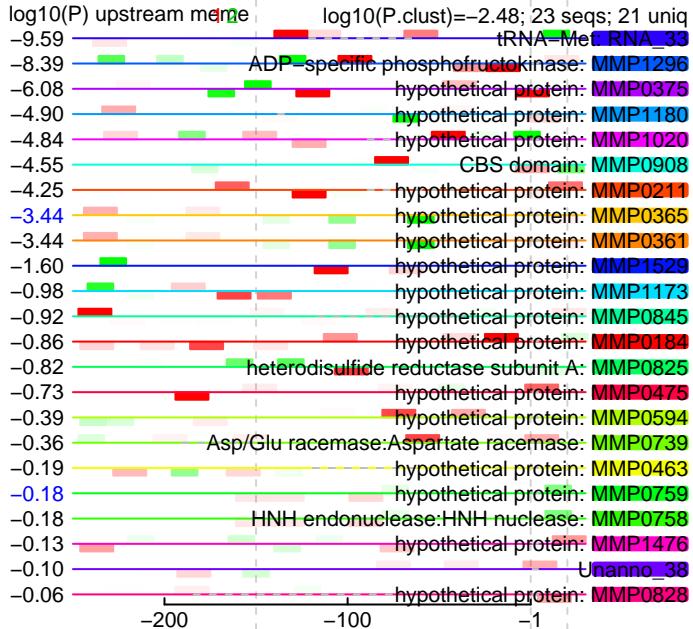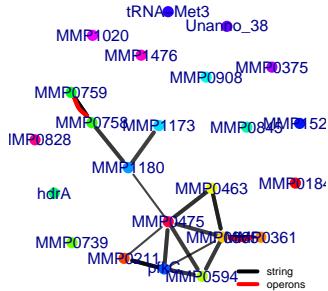
upstream meme PSSM #2; e=100

log10(P) upstream meme   log10(P.clust)=−2.96; 24 seqs; 18 uniq

−7.54	type Iron(III)−binding periplasmic protein precursor: MMP0108
−6.38	hypothetical protein: MMP0670
−5.30	ing site motif A (P−loop):ABC transporter:AAA ATPase: MMP0868
−5.30	transport system, permease component related protein: MMP0867
−5.30	ne/L−proline ABC transporter, solute−binding protein: MMP0866
−4.68	Uroporphyrinogen decarboxylase (URO−D): MMP1150
−4.60	cation transport ATPase: MMP0216
−3.46	periplasmic molybdate−binding protein: MMP1651
−3.01	ybdopterin−guanine dinucleotide biosynthesis protein: MMP1441
−2.95	terized domain 2:Archaeosine tRNA−ribosyltransferase: MMP0610
−2.66	p):GTP−binding protein, HSR1−related:GTP−binding...: MMP1334
−2.53	Unanno_28
−2.33	Arginase: MMP1585
−2.23	hypothetical protein: MMP1612
−2.06	DNA polymerase II large subunit: MMP0028
−2.02	hypothetical protein: MMP0146
−2.02	5−oxopent−3−ene−1,2,5−tricarboxylate decarboxylase..: MMP0144
−2.02	te dependent enzyme related to acetolactate synthase: MMP0142
−2.02	hypothetical protein: MMP0141
−1.72	cobaltochelatase: MMP0493
−0.65	Diaminopimelate decarboxylase: MMP1200
−0.15	GCN5−related N−acetyltransferase: MMP0862
−0.15	Lysine 2,3−aminomutase: MMP0861
−0.03	Na+/solute symporter: MMP1700

Cluster: 0042 mmp; resid: 0.38; r/c: 40/40

upstream meme PSSM #1; e=1.4e+03   upstream meme PSSM #2; e=240

log10(P) upstream meme   log10(P.clust)=−1.07; 40 seqs; 37 uniq

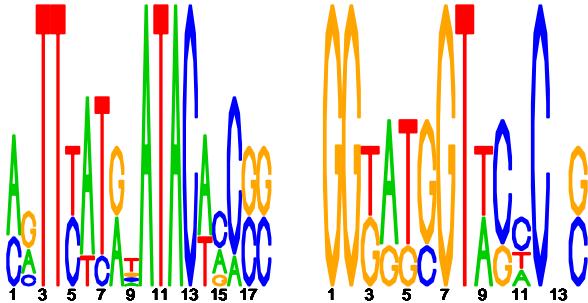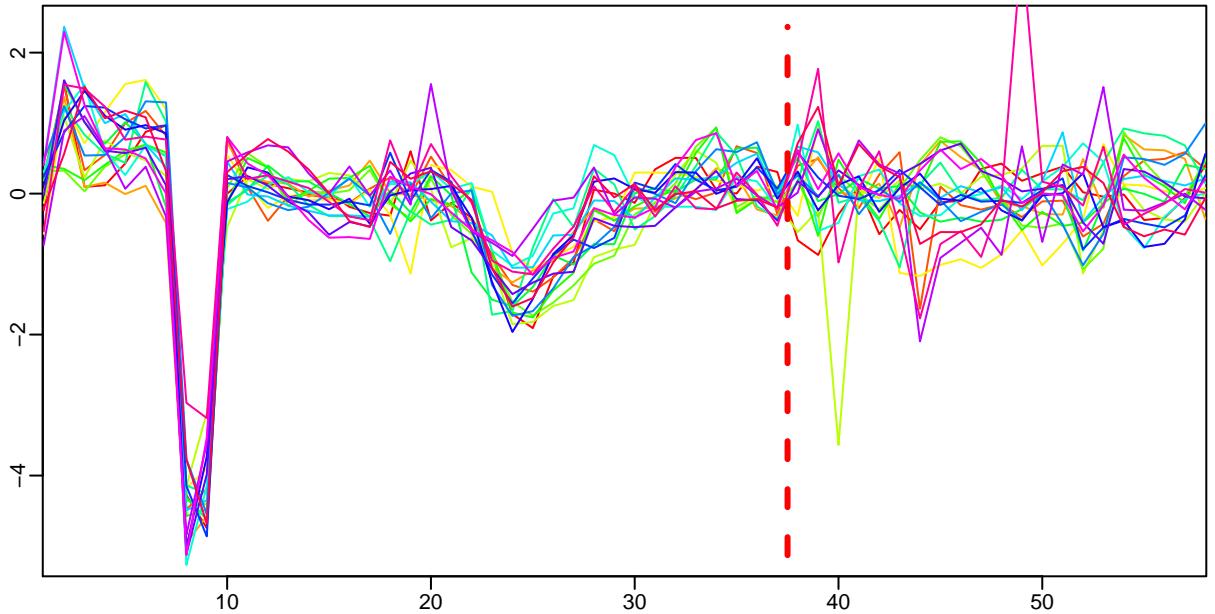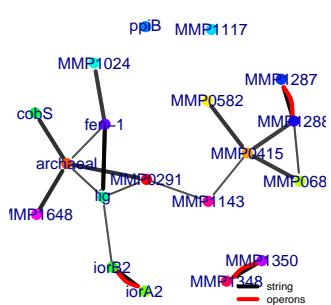| log10(P)	annotation	gene
−3.45	tRNA−Met	tRNA_34
−3.37	hypothetical protein	MMP1660
−3.09	hypothetical protein	MMP1664
−2.58	endonuclease IV	MMP1678
−2.31	hypothetical protein	MMP1620
−2.91	N(2),N(2)−dimethylguanosine tRNA methyltransferase	MMP0228
−2.15	hypothetical protein	MMP0437
−2.06	ABC transporter ATP−binding protein	MMP0523
−1.91	sodium−dependent transporter	MMP0653
−1.63	hypothetical protein	MMP1655
−1.47	ylate deaminase, zinc−binding region related protein	MMP0869
−1.41	Carboxymuconolactone decarboxylase Related Protein	MMP0807
−1.14		Unanno._16
−0.99	probable sugar efflux transporter	MMP0796
−0.93		Antisense_16
−0.85	hypothetical protein	MMP0361
−0.82	hypothetical protein	MMP0473
−0.82	methylcobalamin:coenzyme M methyltransferase	MMP0831
−0.80	acetyltransferase related protein	MMP0892
−0.74		Unanno._26
−0.74	hypothetical protein	MMP0777
−0.63	hypothetical protein	MMP0775
−0.83	hypothetical protein	MMP0772
−0.55	hypothetical protein	MMP0565
−0.51	hypothetical protein	MMP1389
−0.46	hypothetical protein	MMP1226
−0.39	hypothetical protein	MMP1536
−0.29		MMP0188
−0.25	tative SSU ribosomal protein S6 modification protein	MMP0436
−0.25		MMP0208
−0.18		MMP1476
−0.13		MMP1020
−0.10		MMP1280
−0.09	HD phosphohydrolase family member	MMP0174
−0.09		MMP0756
−0.08	Site−specific recombinase	MMP1047
−0.05	hypothetical protein	MMP0495
−0.01	Uroporphyrinogen decarboxylase (URO−D)	MMP0364

Cluster: 0043 mmp; resid: 0.30; r/c: 29/38

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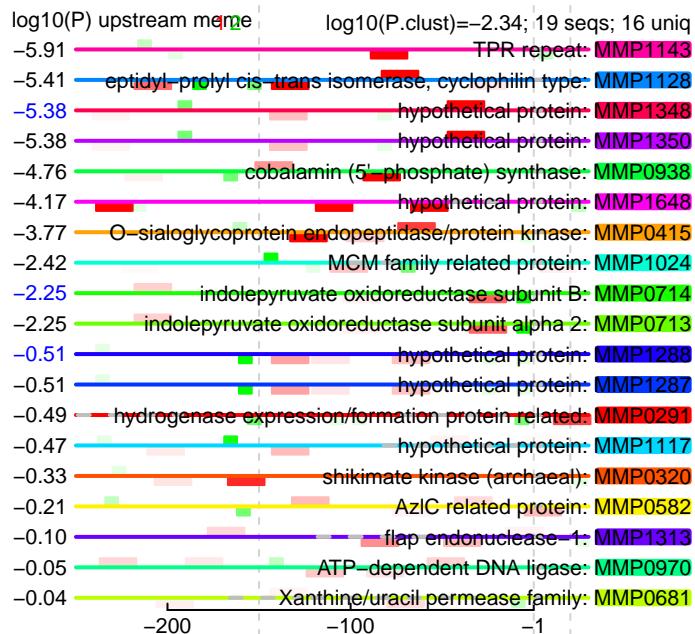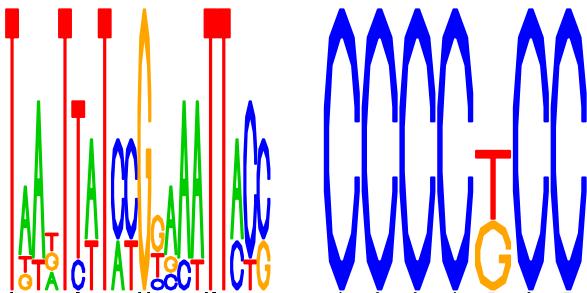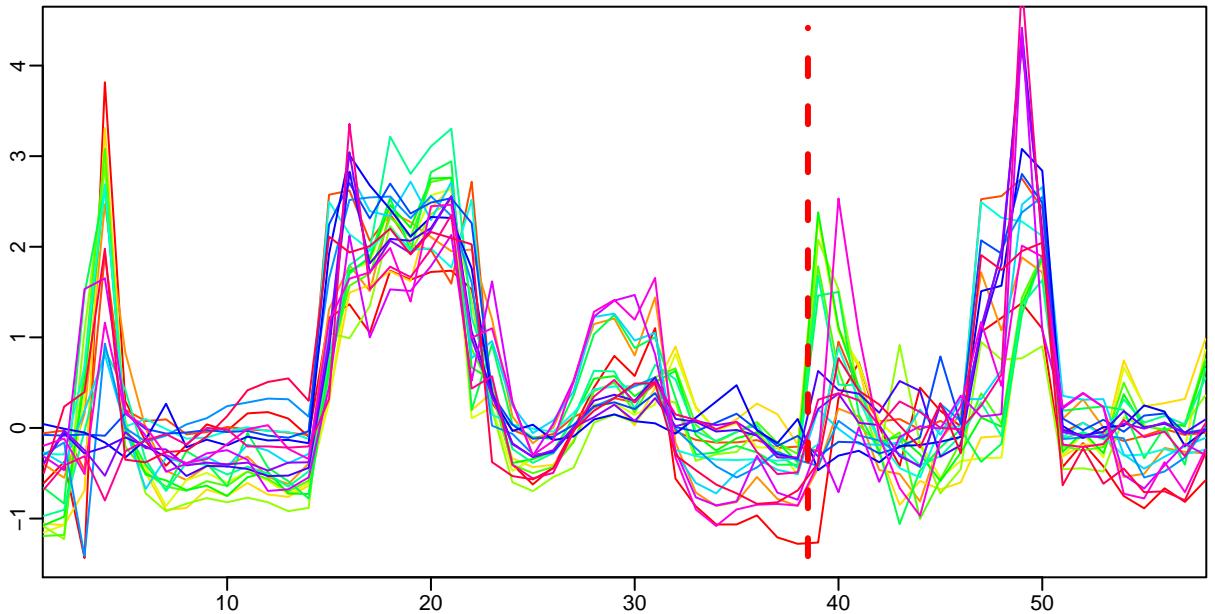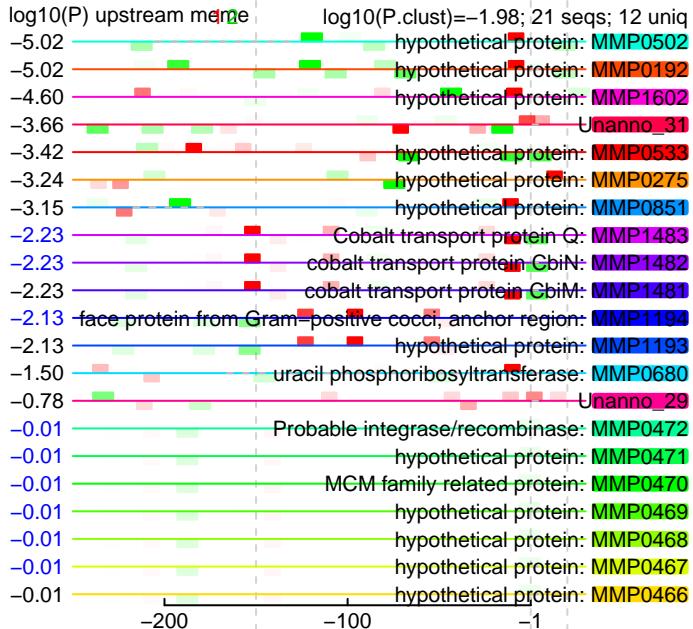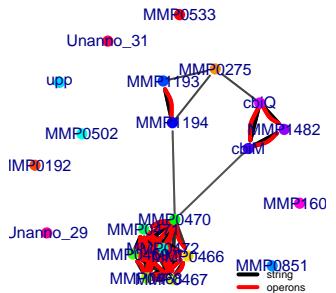upstream meme PSSM #1; e=1.8e−09   upstream meme PSSM #2; e=28

log10(P) upstream meme   log10(P.clust)=−4.09; 29 seqs: 20 uniq

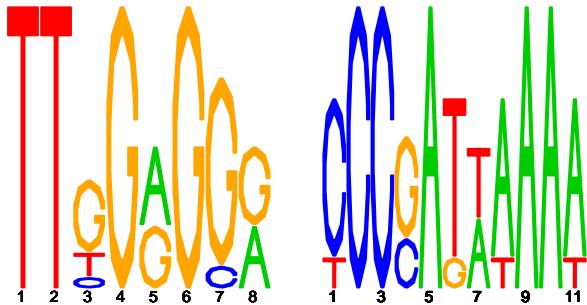|	
−11.56	hypothetical protein: MMP1703
−11.51	Glycosyl transferase, group 1: MMP1294
−11.51	glucose−6−phosphate isomerase: MMP1295
−11.51	Glycosyl transferase, group 1: MMP1293
−11.51	glucan 1,4−alpha−glucosidase (glucoamylase): MMP1292
−11.51	Glycoside hydrolase, family 57: MMP1291
−5.19	magnesium, nickel and cobalt transport protein: MMP0711
−5.19	cation−transporting ATPase: MMP0710
−3.98	predicted transcriptional regulator: MMP0719
−3.98	hypothetical protein: MMP0718
−3.16	Bacterial quinoprotein: MMP0294
−2.87	on−sulfur flavoprotein of Methanosarcina thermophila: MMP0614
−2.23	N−glycosylase/DNA lyase: MMP0304
−2.23	oxidoreductase family member subunit alpha: MMP0306
−2.23	2−oxoacid ferredoxin oxidoreductase subunit beta: MMP0305
−2.21	tein−L−isoaspartate(D−aspartate) O−methyltransferase: MMP0102
−2.00	hypothetical protein: MMP1604
−1.89	hypothetical protein: MMP0763
−1.68	Blue (type 1) copper domain: MMP0997
−1.68	hypothetical protein: MMP0996
−1.67	hypothetical protein: MMP0172
−1.39	Unanno_57
−1.38	TPR repeat: MMP0762
−1.37	hypothetical protein: MMP0784
−1.37	hypothetical protein: MMP0783
−1.00	hypothetical protein: MMP0964
−0.53	Antisense_10
−0.23	hypothetical protein: MMP1257
−0.08	hypothetical protein: MMP0634

Cluster: 0044 mmp; resid: 0.43; r/c: 31/40

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cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=0.0072   upstream meme PSSM #2; e=18
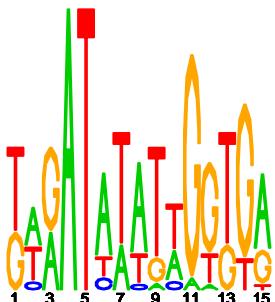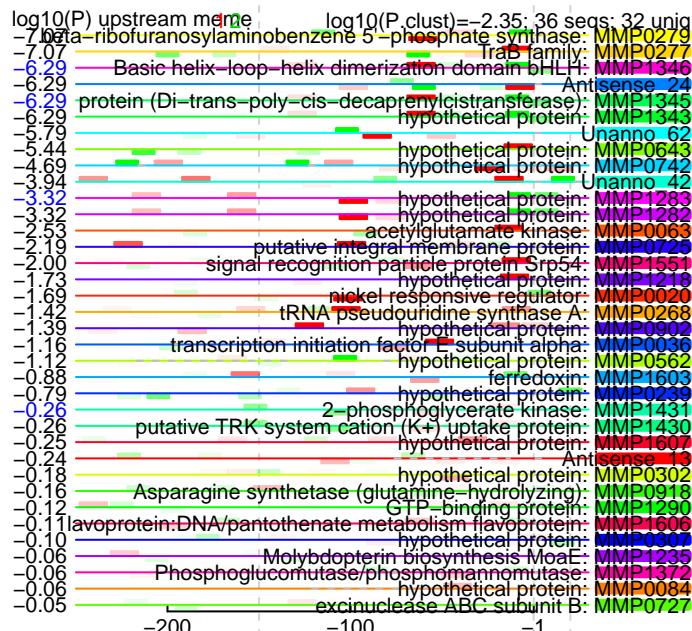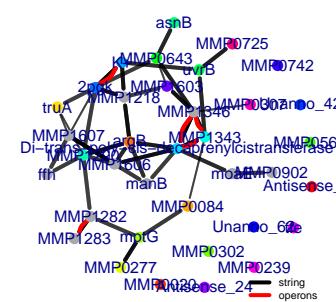
log10(P) upstream meme   log10(P.clust)=−2.88; 31 seqs; 20 uniq

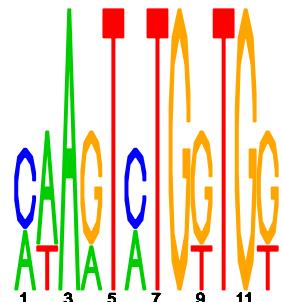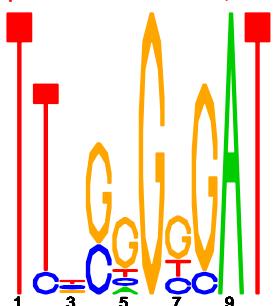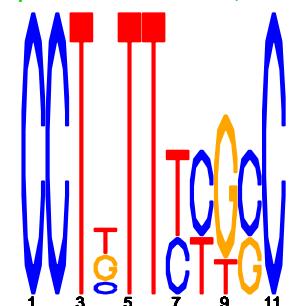| log10(P)	Annotation	ID
−9.44		Unanno_29
−9.37	cobaltochelatase:	MMP0493
−5.92	hypothetical protein:	MMP0343
−5.25	FO synthase subunit 2:	MMP0057
−4.07	Probable integrase/recombinase:	MMP0472
−4.07	hypothetical protein:	MMP0471
−4.07	MCM family related protein:	MMP0470
−4.07	hypothetical protein:	MMP0469
−4.07	hypothetical protein:	MMP0468
−4.07	hypothetical protein:	MMP0467
−4.07	hypothetical protein:	MMP0466
−2.57	hypothetical protein:	MMP1602
−2.13	hypothetical protein:	MMP0275
−2.02		Unanno_15
−1.85	formate dehydrogenase alpha subunit:	MMP0138
−1.78	hypothetical protein:	MMP0492
−1.78	MotA/TolQ/ExbB proton channel:	MMP0491
−1.78	hypothetical protein:	MMP0490
−1.64	uracil phosphoribosyltransferase:	MMP0680
−1.64		Unanno_31
−1.55	Cobalt transport protein Q:	MMP1483
−1.55	cobalt transport protein CbiN:	MMP1482
−1.55	cobalt transport protein CbiM:	MMP1481
−1.48	hypothetical protein:	MMP0192
−1.38	face protein from Gram−positive cocci, anchor region:	MMP1194
−1.38	hypothetical protein:	MMP1193
−1.30	hypothetical protein:	MMP0502
−1.27		Unanno_22
−1.04	hypothetical protein:	MMP0851
−0.84		Unanno_48
−0.43	N6 adenine−specific DNA methyltransferase, D12 class:	MMP0735

Cluster: 0045 mmp; resid: 0.40; r/c: 23/38

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cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=500   upstream meme PSSM #2; e=1.7e+03

log10(P) upstream meme   log10(P.clust)=−2.48; 23 seqs; 21 uniq

log10(P)	annotation	gene
−9.59	tRNA−Met	tRNA_33
−8.39	ADP−specific phosphofructokinase:	MMP1296
−6.08	hypothetical protein:	MMP0375
−4.90	hypothetical protein:	MMP1180
−4.84	hypothetical protein:	MMP1020
−4.55	CBS domain:	MMP0908
−4.25	hypothetical protein:	MMP0211
−3.44	hypothetical protein:	MMP0365
−3.44	hypothetical protein:	MMP0361
−1.60	hypothetical protein:	MMP1529
−0.98	hypothetical protein:	MMP1173
−0.92	hypothetical protein:	MMP0845
−0.86	hypothetical protein:	MMP0184
−0.82	heterodisulfide reductase subunit A:	MMP0825
−0.73	hypothetical protein:	MMP0475
−0.39	hypothetical protein:	MMP0594
−0.36	Asp/Glu racemase:Aspartate racemase:	MMP0739
−0.19	hypothetical protein:	MMP0463
−0.18	hypothetical protein:	MMP0759
−0.18	HNH endonuclease:HNH nuclease:	MMP0758
−0.13	hypothetical protein:	MMP1476
−0.10		Unanno_38
−0.06	hypothetical protein:	MMP0828

string
operons

Cluster: 0046 mmp; resid: 0.45; r/c: 31/38

Cluster: 0047 mmp; resid: 0.27; r/c: 19/37

11 Oct 11 16:14:07 iter=2000
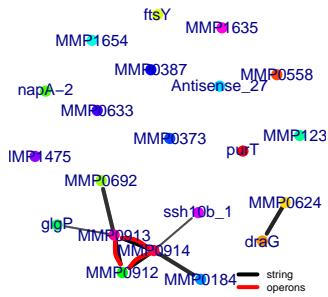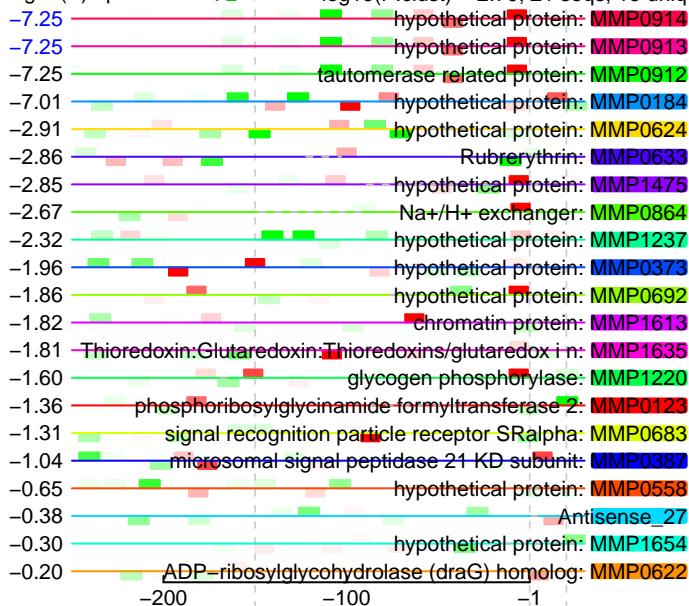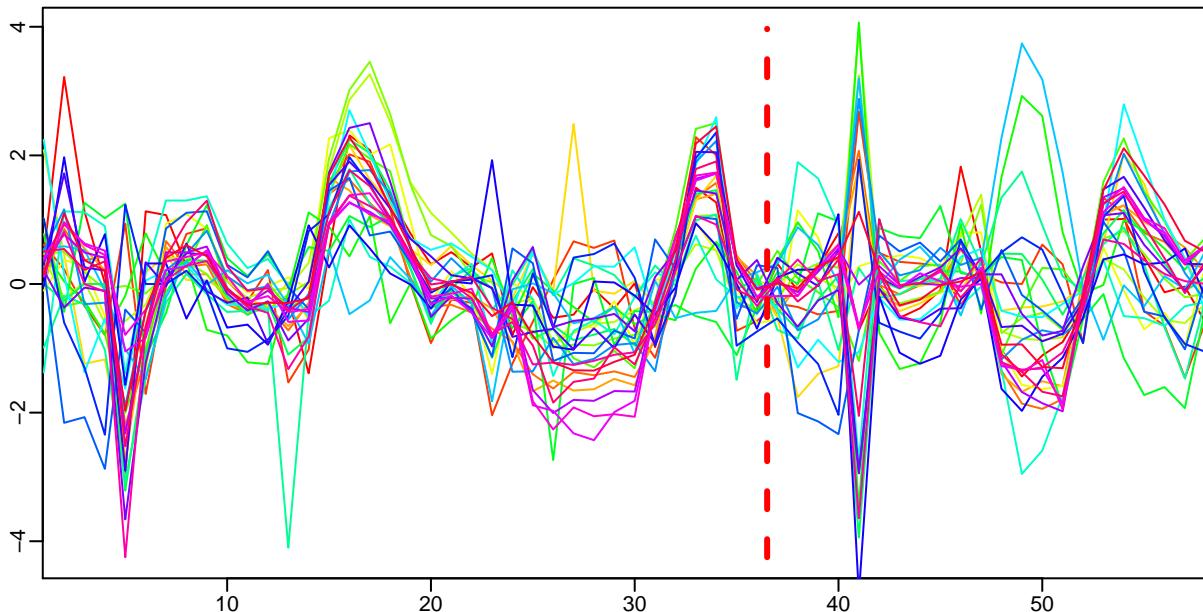cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=390   upstream meme PSSM #2; e=4e+03

log10(P) upstream meme   log10(P.clust)=−2.34; 19 seqs; 16 uniq

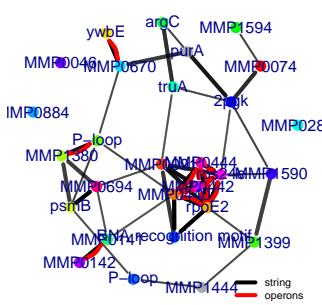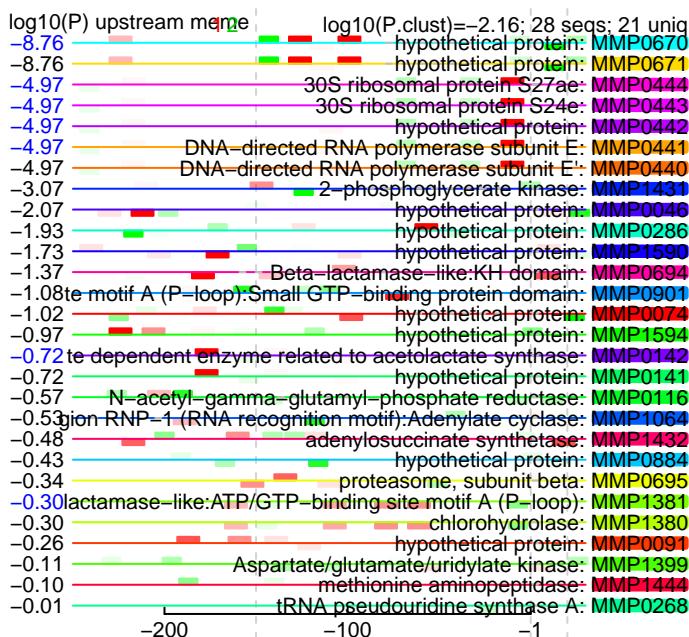| log10(P)	Annotation	Gene
−5.91	TPR repeat:	MMP1143
−5.41	eptidyl–prolyl cis–trans isomerase, cyclophilin type:	MMP1128
−5.38	hypothetical protein:	MMP1348
−5.38	hypothetical protein:	MMP1350
−4.76	cobalamin (5'–phosphate) synthase:	MMP0938
−4.17	hypothetical protein:	MMP1648
−3.77	O–sialoglycoprotein endopeptidase/protein kinase:	MMP0415
−2.42	MCM family related protein:	MMP1024
−2.25	indolepyruvate oxidoreductase subunit B:	MMP0714
−2.25	indolepyruvate oxidoreductase subunit alpha 2:	MMP0713
−0.51	hypothetical protein:	MMP1288
−0.51	hypothetical protein:	MMP1287
−0.49	hydrogenase expression/formation protein related:	MMP0291
−0.47	hypothetical protein:	MMP1117
−0.33	shikimate kinase (archaeal):	MMP0320
−0.21	AzlC related protein:	MMP0582
−0.10	flap endonuclease–1:	MMP1313
−0.05	ATP–dependent DNA ligase:	MMP0970
−0.04	Xanthine/uracil permease family:	MMP0681

Cluster: 0048 mmp; resid: 0.31; r/c: 21/38

11 Oct 11 16:14:07 iter=2000
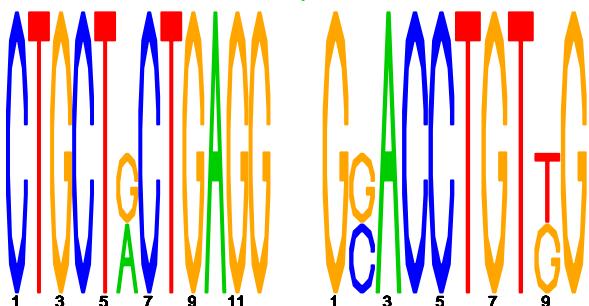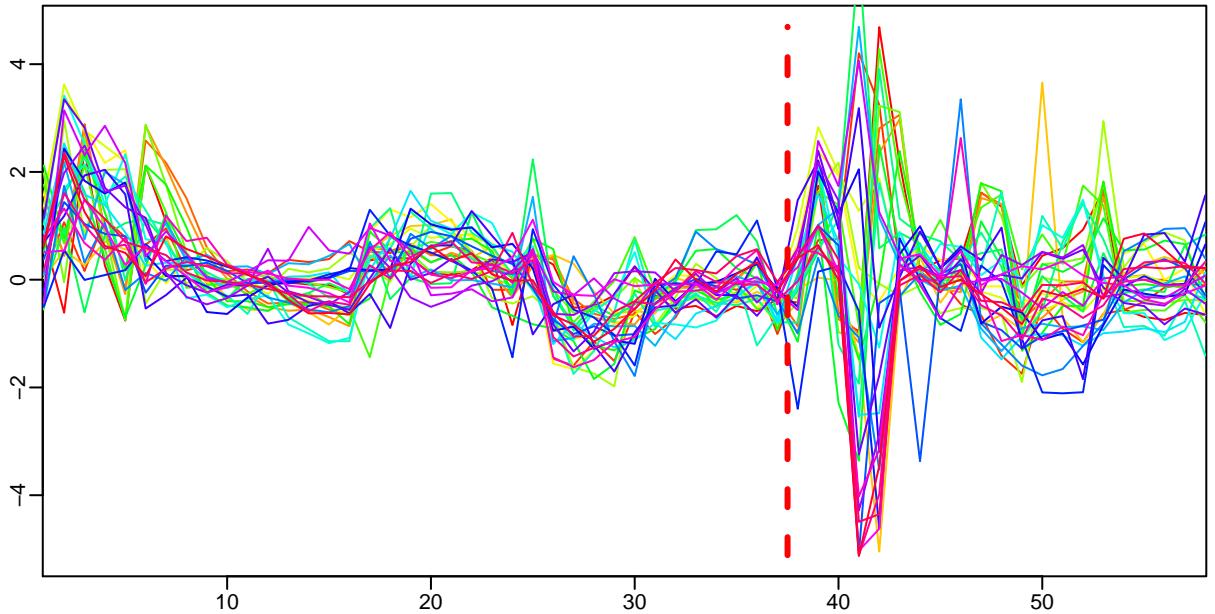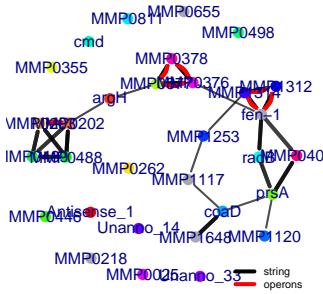cMonkey Version 4.8.8 mmp

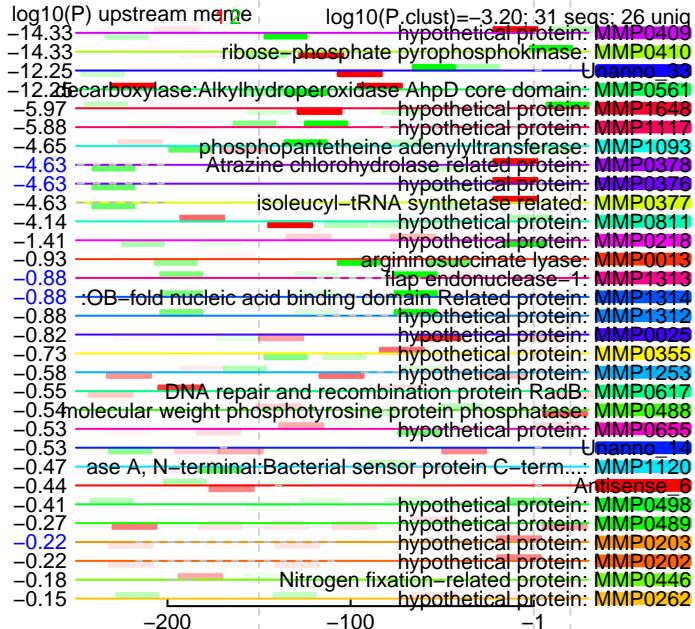upstream meme PSSM #1; e=0.0095   upstream meme PSSM #2; e=780

log10(P) upstream meme   log10(P.clust)=−1.98; 21 seqs; 12 uniq

log10(P)	Protein
−5.02	hypothetical protein: MMP0502
−5.02	hypothetical protein: MMP0192
−4.60	hypothetical protein: MMP1602
−3.66	Unanno_31
−3.42	hypothetical protein: MMP0533
−3.24	hypothetical protein: MMP0275
−3.15	hypothetical protein: MMP0851
−2.23	Cobalt transport protein Q: MMP1483
−2.23	cobalt transport protein CbiN: MMP1482
−2.23	cobalt transport protein CbiM: MMP1481
−2.13	face protein from Gram−positive cocci, anchor region: MMP1194
−2.13	hypothetical protein: MMP1193
−1.50	uracil phosphoribosyltransferase: MMP0680
−0.78	Unanno_29
−0.01	Probable integrase/recombinase: MMP0472
−0.01	hypothetical protein: MMP0471
−0.01	MCM family related protein: MMP0470
−0.01	hypothetical protein: MMP0469
−0.01	hypothetical protein: MMP0468
−0.01	hypothetical protein: MMP0467
−0.01	hypothetical protein: MMP0466

Cluster: 0049 mmp; resid: 0.49; r/c: 36/38

upstream meme PSSM #1; e=1.2

upstream meme PSSM #2; e=19

log10(P) upstream meme   log10(P.clust)=−2.35; 36 seqs; 32 uniq

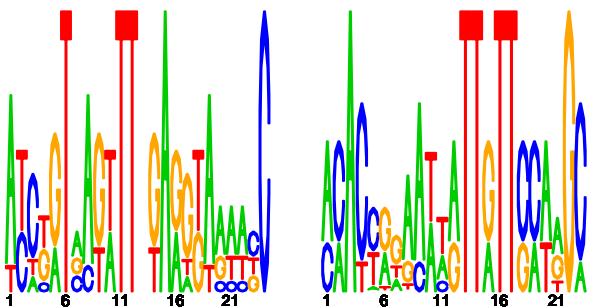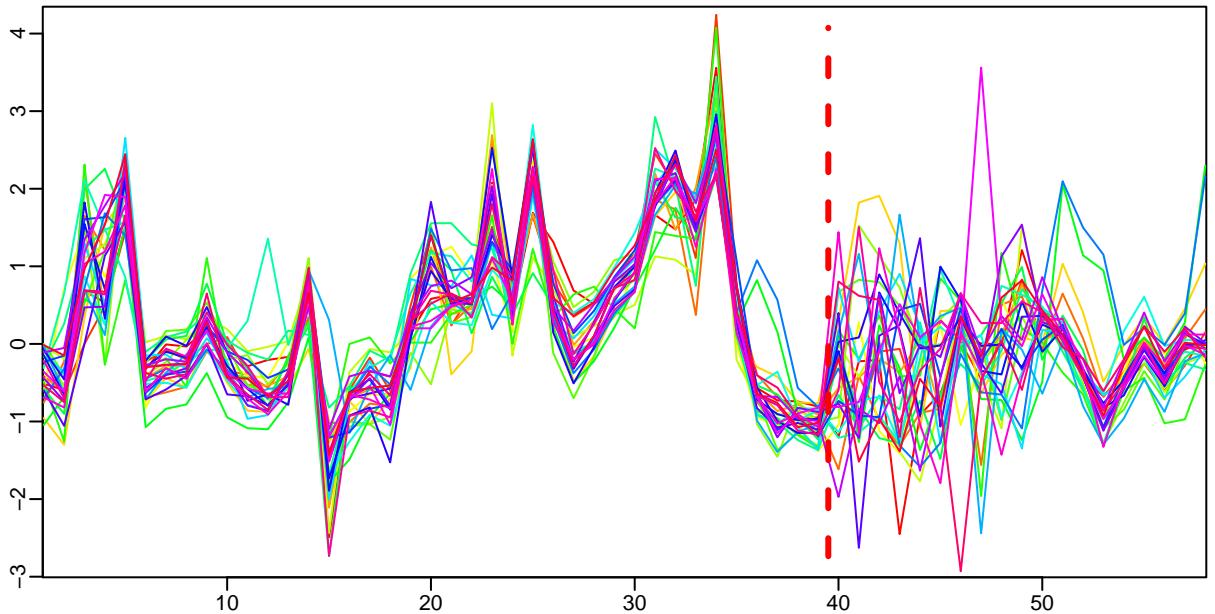| log10(P)	annotation	gene
−7.07	beta−ribofuranosylaminobenzene 5'−phosphate synthase:	MMP0279
−7.07	TraB family:	MMP0277
−6.29	Basic helix−loop−helix dimerization domain bHLH:	MMP1346
−6.29		Antisense_24
−6.29	protein (Di−trans−poly−cis−decaprenylcistransferase):	MMP1345
−6.29	hypothetical protein:	MMP1343
−5.79		Unanno_62
−5.44	hypothetical protein:	MMP0643
−4.69	hypothetical protein:	MMP0742
−3.94		Unanno_42
−3.32	hypothetical protein:	MMP1283
−3.32	hypothetical protein:	MMP1282
−2.53	acetylglutamate kinase:	MMP0063
−2.19	putative integral membrane protein:	MMP0728
−2.00	signal recognition particle protein Srp54:	MMP1551
−1.73	hypothetical protein:	MMP0902
−1.69	nickel responsive regulator:	MMP0020
−1.42	tRNA pseudouridine synthase A:	MMP0268
−1.39	hypothetical protein:	MMP1290
−1.16	transcription initiation factor E subunit alpha:	MMP0036
−1.12	hypothetical protein:	MMP0562
−0.88	ferredoxin:	MMP1603
−0.79	hypothetical protein:	MMP0239
−0.26	2−phosphoglycerate kinase:	MMP1431
−0.26	putative TRK system cation (K+) uptake protein:	MMP1430
−0.25	hypothetical protein:	MMP1607
−0.24		Antisense_13
−0.18	hypothetical protein:	MMP0302
−0.16	Asparagine synthetase (glutamine−hydrolyzing):	MMP0918
−0.12	GTP−binding protein:	MMP1290
−0.11	flavoprotein:DNA/pantothenate metabolism flavoprotein:	MMP1606
−0.10	hypothetical protein:	MMP0606
−0.06	Molybdopterin biosynthesis MoaE:	MMP1235
−0.06	Phosphoglucomutase/phosphomannomutase:	MMP1372
−0.06	hypothetical protein:	MMP0084
−0.05	excinuclease ABC subunit B:	MMP0727

Cluster: 0050 mmp; resid: 0.34; r/c: 21/37

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cMonkey Version 4.8.8 mmp

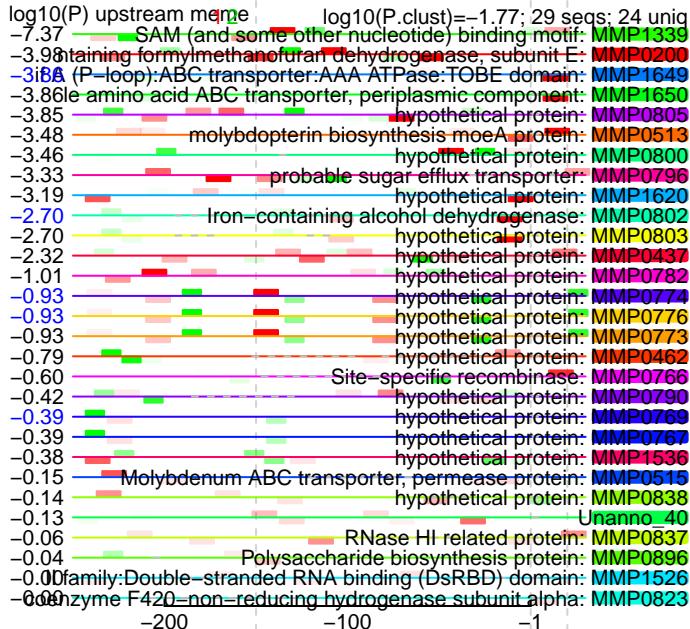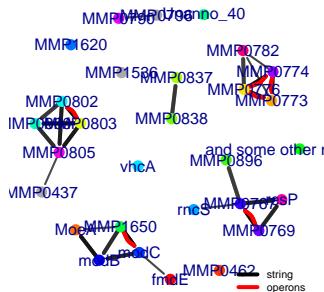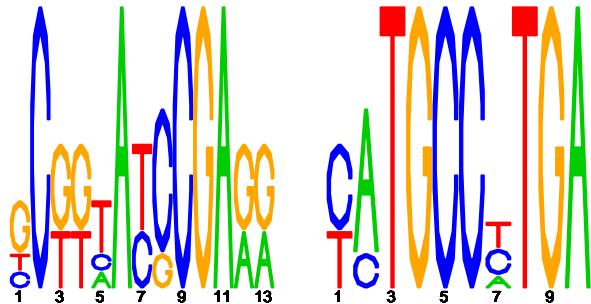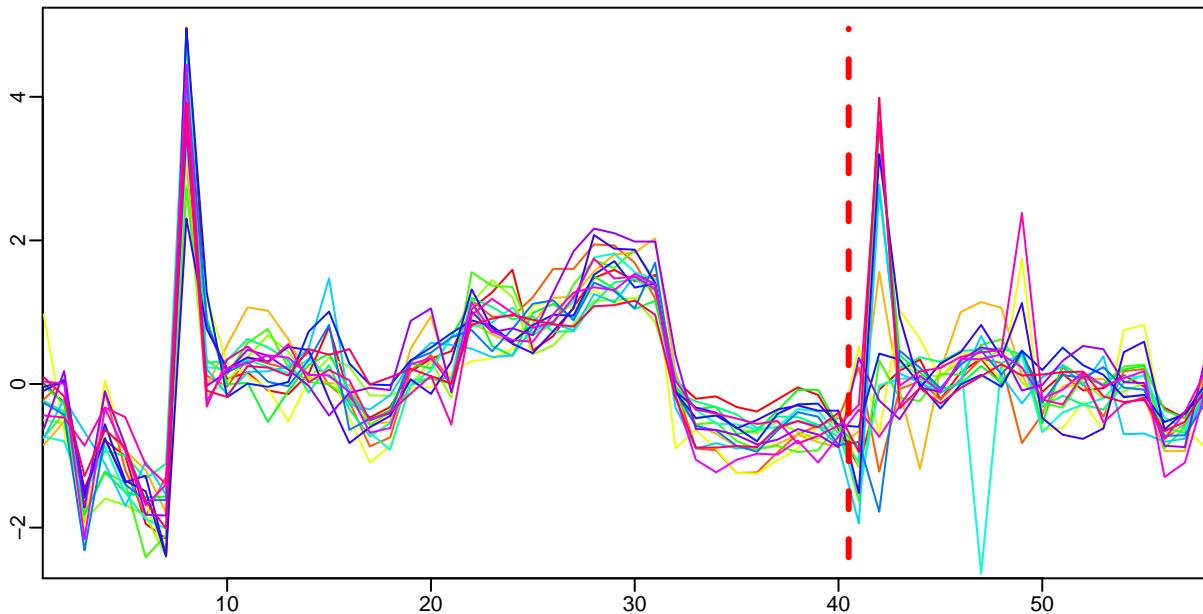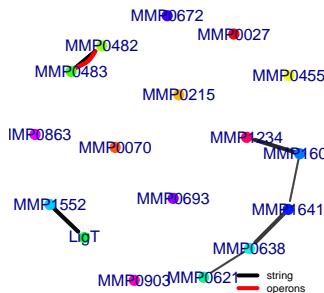upstream meme PSSM #1; e=65

upstream meme PSSM #2; e=130

log10(P) upstream meme

log10(P.clust)=−2.70; 21 seqs; 19 uniq

log10(P)	annotation	gene
−7.25	hypothetical protein:	MMP0914
−7.25	hypothetical protein:	MMP0913
−7.25	tautomerase related protein:	MMP0912
−7.01	hypothetical protein:	MMP0184
−2.91	hypothetical protein:	MMP0624
−2.86	Rubrerythrin:	MMP0633
−2.85	hypothetical protein:	MMP1475
−2.67	Na+/H+ exchanger:	MMP0864
−2.32	hypothetical protein:	MMP1237
−1.96	hypothetical protein:	MMP0373
−1.86	hypothetical protein:	MMP0692
−1.82	chromatin protein:	MMP1613
−1.81	Thioredoxin:Glutaredoxin:Thioredoxins/glutaredox i n:	MMP1635
−1.60	glycogen phosphorylase:	MMP1220
−1.36	phosphoribosylglycinamide formyltransferase 2:	MMP0123
−1.31	signal recognition particle receptor SRalpha:	MMP0683
−1.04	microsomal signal peptidase 21 KD subunit:	MMP0387
−0.65	hypothetical protein:	MMP0558
−0.38		Antisense_27
−0.30	hypothetical protein:	MMP1654
−0.20	ADP−ribosylglycohydrolase (draG) homolog:	MMP0622

Cluster: 0051 mmp; resid: 0.46; r/c: 28/36

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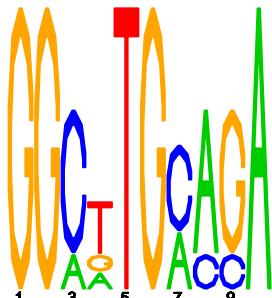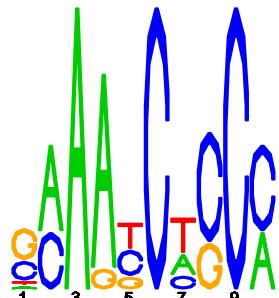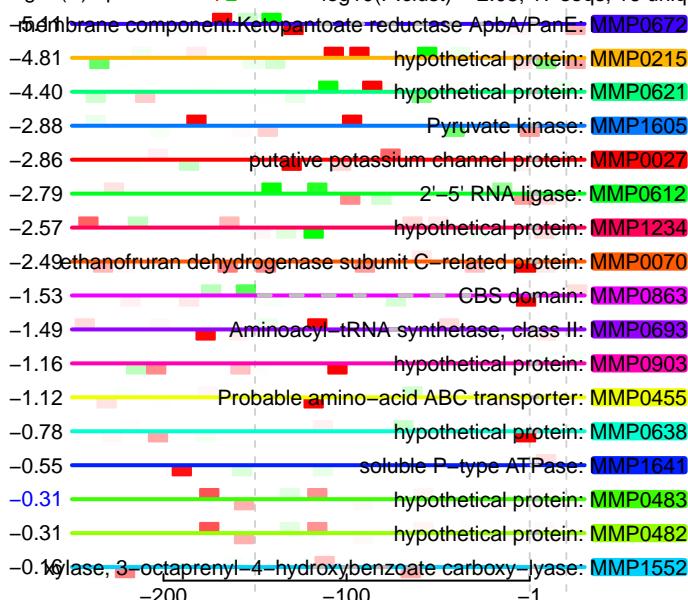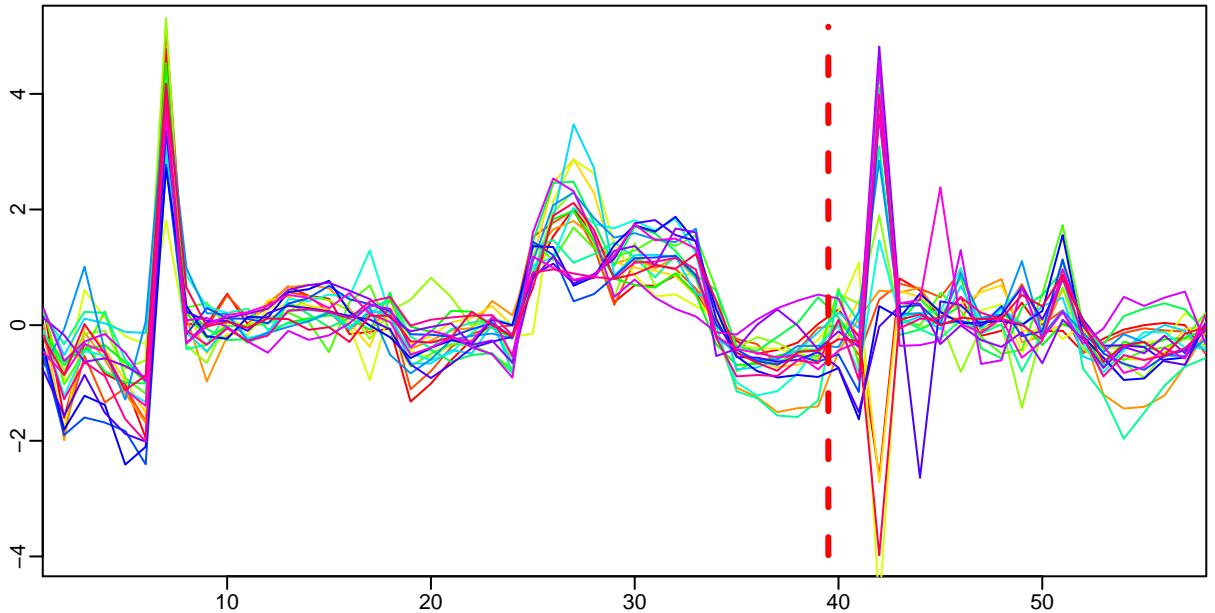upstream meme PSSM #1; e=7.3e+00   upstream meme PSSM #2; e=2.8e+04

log10(P) upstream meme   log10(P.clust)=−2.16; 28 seqs; 21 uniq

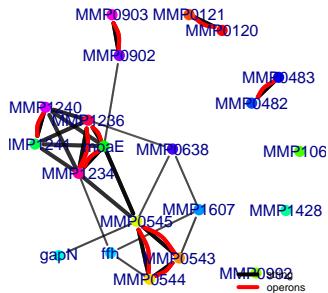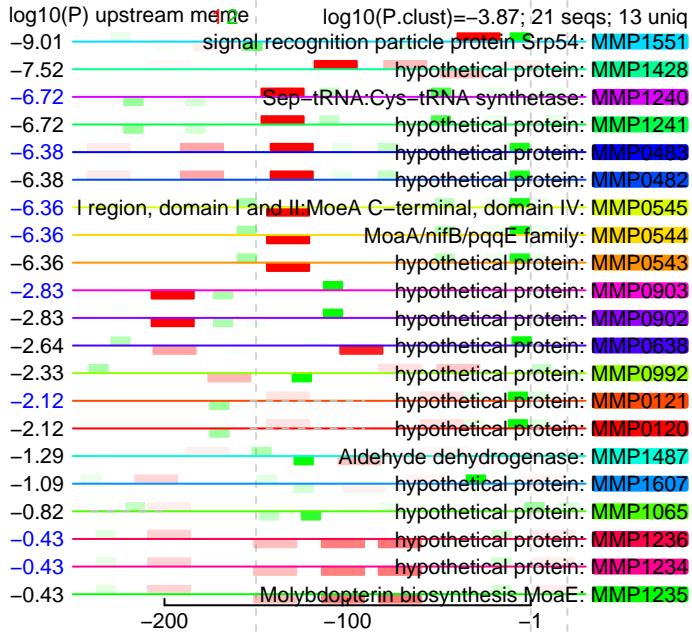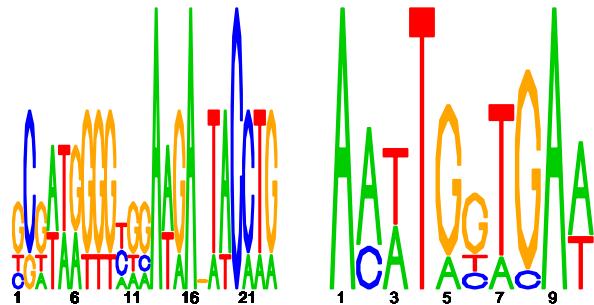| log10(P)	Description	Gene
−8.76	hypothetical protein:	MMP0670
−8.76	hypothetical protein:	MMP0671
−4.97	30S ribosomal protein S27ae:	MMP0444
−4.97	30S ribosomal protein S24e:	MMP0443
−4.97	hypothetical protein:	MMP0442
−4.97	DNA−directed RNA polymerase subunit E:	MMP0441
−4.97	DNA−directed RNA polymerase subunit E':	MMP0440
−3.07	2−phosphoglycerate kinase:	MMP1431
−2.07	hypothetical protein:	MMP0046
−1.93	hypothetical protein:	MMP0286
−1.73	hypothetical protein:	MMP1590
−1.37	Beta−lactamase−like:KH domain:	MMP0694
−1.08	te motif A (P−loop):Small GTP−binding protein domain:	MMP0901
−1.02	hypothetical protein:	MMP0074
−0.97	hypothetical protein:	MMP1594
−0.72	te dependent enzyme related to acetolactate synthase:	MMP0142
−0.72	hypothetical protein:	MMP0141
−0.57	N−acetyl−gamma−glutamyl−phosphate reductase:	MMP0116
−0.53	gion RNP−1 (RNA recognition motif):Adenylate cyclase:	MMP1064
−0.48	adenylosuccinate synthetase:	MMP1432
−0.43	hypothetical protein:	MMP0884
−0.34	proteasome, subunit beta:	MMP0695
−0.30	lactamase−like:ATP/GTP−binding site motif A (P−loop):	MMP1381
−0.30	chlorohydrolase:	MMP1380
−0.26	hypothetical protein:	MMP0091
−0.11	Aspartate/glutamate/uridylate kinase:	MMP1399
−0.10	methionine aminopeptidase:	MMP1444
−0.01	tRNA pseudouridine synthase A:	MMP0268

Cluster: 0052 mmp; resid: 0.39; r/c: 31/37

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cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=22

upstream meme PSSM #2; e=78

log10(P) upstream meme

log10(P.clust)=−3.20; 31 seqs: 26 uniq

log10(P)	annotation	gene
−14.33	hypothetical protein:	MMP0409
−14.33	ribose−phosphate pyrophosphokinase:	MMP0410
−12.25	Unanno_33	
−12.25	decarboxylase:Alkylhydroperoxidase AhpD core domain:	MMP0561
−5.97	hypothetical protein:	MMP1648
−5.88	hypothetical protein:	MMP1117
−4.65	phosphopantetheine adenylyltransferase:	MMP1093
−4.63	Atrazine chlorohydrolase related protein:	MMP0378
−4.63	hypothetical protein:	MMP0376
−4.63	isoleucyl−tRNA synthetase related:	MMP0377
−4.14	hypothetical protein:	MMP0811
−1.41	hypothetical protein:	MMP0218
−0.93	argininosuccinate lyase:	MMP0013
−0.88	flap endonuclease−1:	MMP1313
−0.88	:OB−fold nucleic acid binding domain Related protein:	MMP1314
−0.88	hypothetical protein:	MMP1312
−0.82	hypothetical protein:	MMP0025
−0.73	hypothetical protein:	MMP0355
−0.58	hypothetical protein:	MMP1253
−0.55	DNA repair and recombination protein RadB:	MMP0617
−0.54	molecular weight phosphotyrosine protein phosphatase:	MMP0488
−0.53	hypothetical protein:	MMP0655
−0.53	Unanno_14	
−0.47	ase A, N−terminal:Bacterial sensor protein C−term...:	MMP1120
−0.44	Antisense_6	
−0.41	hypothetical protein:	MMP0498
−0.27	hypothetical protein:	MMP0489
−0.22	hypothetical protein:	MMP0203
−0.22	hypothetical protein:	MMP0202
−0.18	Nitrogen fixation−related protein:	MMP0446
−0.15	hypothetical protein:	MMP0262

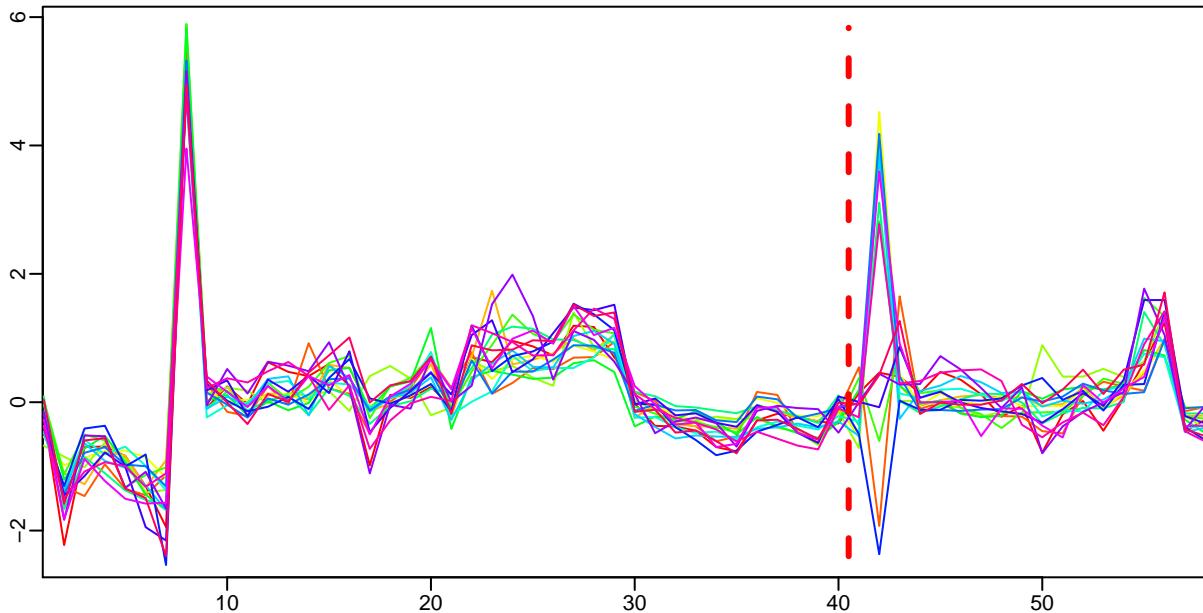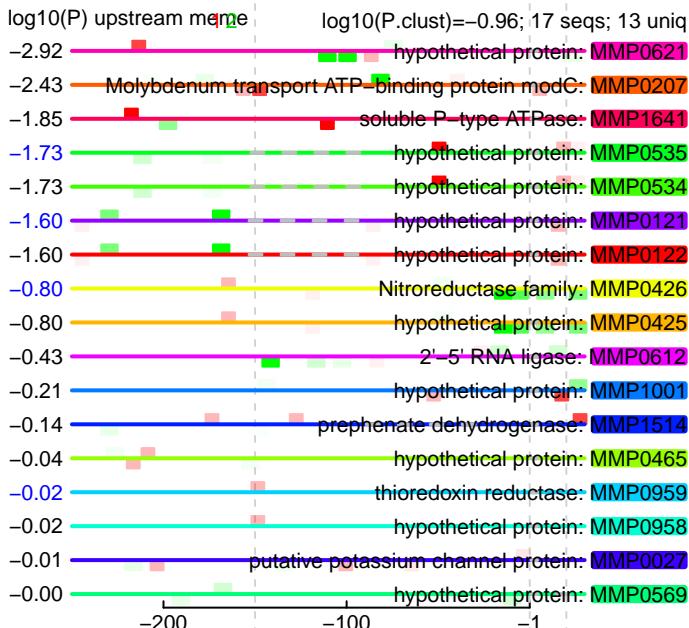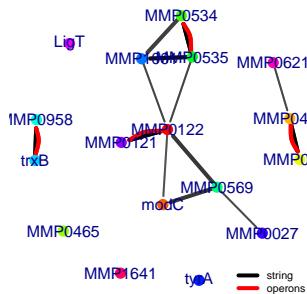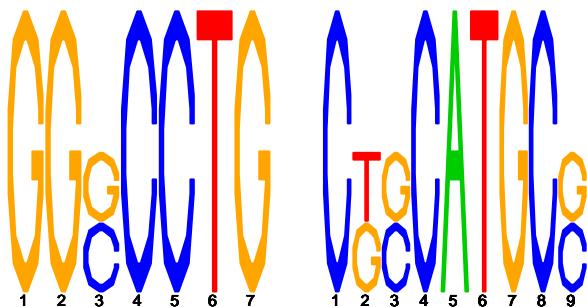string
operons

Cluster: 0053 mmp; resid: 0.26; r/c: 29/39
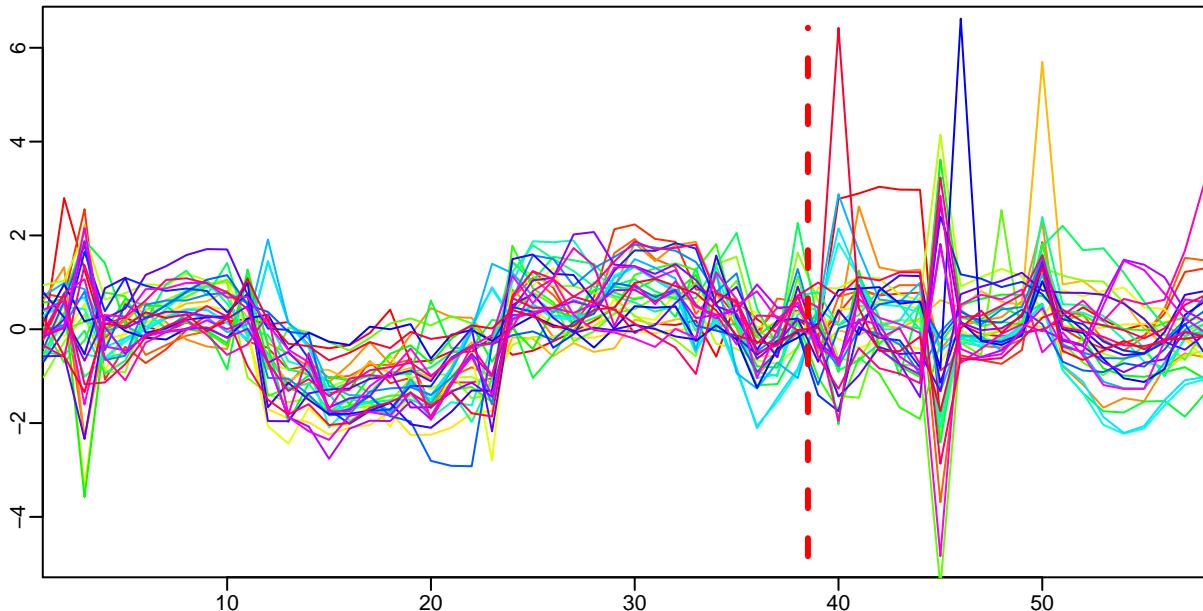
upstream meme PSSM #1; e=560   upstream meme PSSM #2; e=2.6e+03

log10(P) upstream meme   log10(P.clust)=−1.77; 29 seqs; 24 uniq

log10(P)	annotation	gene
−7.37	SAM (and some other nucleotide) binding motif:	MMP1339
−3.98	staining formylmethanofuran dehydrogenase, subunit E:	MMP0200
−3.86	ISA (P−loop):ABC transporter:AAA ATPase:TOBE domain:	MMP1649
−3.86	le amino acid ABC transporter, periplasmic component:	MMP1650
−3.85	hypothetical protein:	MMP0805
−3.48	molybdopterin biosynthesis moeA protein:	MMP0513
−3.46	hypothetical protein:	MMP0800
−3.33	probable sugar efflux transporter:	MMP0796
−3.19	hypothetical protein:	MMP1620
−2.70	Iron−containing alcohol dehydrogenase:	MMP0802
−2.70	hypothetical protein:	MMP0803
−2.32	hypothetical protein:	MMP0437
−1.01	hypothetical protein:	MMP0782
−0.93	hypothetical protein:	MMP0774
−0.93	hypothetical protein:	MMP0776
−0.93	hypothetical protein:	MMP0773
−0.79	hypothetical protein:	MMP0462
−0.60	Site−specific recombinase:	MMP0766
−0.42	hypothetical protein:	MMP0790
−0.39	hypothetical protein:	MMP0769
−0.39	hypothetical protein:	MMP0767
−0.38	hypothetical protein:	MMP1536
−0.15	Molybdenum ABC transporter, permease protein:	MMP0515
−0.14	hypothetical protein:	MMP0838
−0.13	Unanno_40	
−0.06	RNase HI related protein:	MMP0837
−0.04	Polysaccharide biosynthesis protein:	MMP0896
−0.00	family:Double−stranded RNA binding (DsRBD) domain:	MMP1526
−0.00	enzyme F420−non−reducing hydrogenase subunit alpha:	MMP0823

Cluster: 0054 mmp; resid: 0.25; r/c: 17/40

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cMonkey Version 4.8.8 mmp
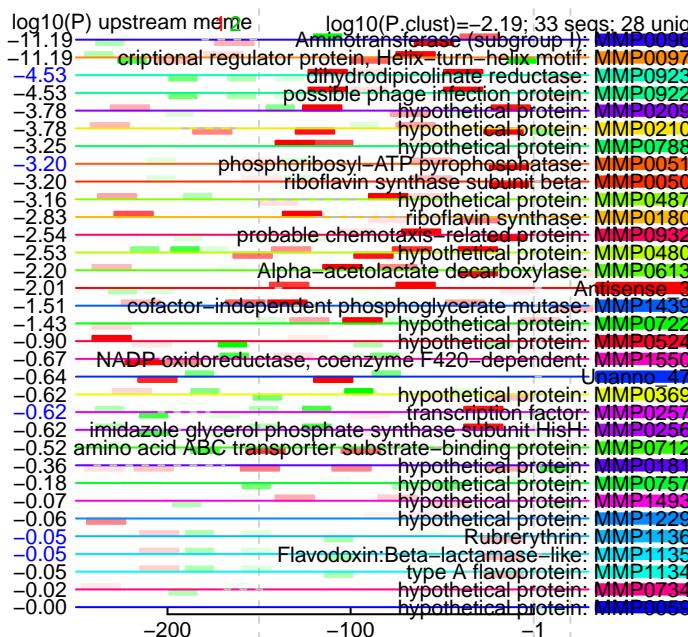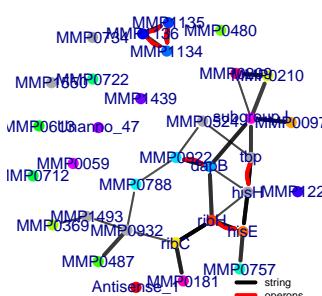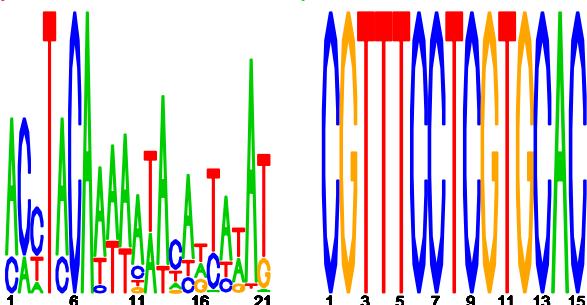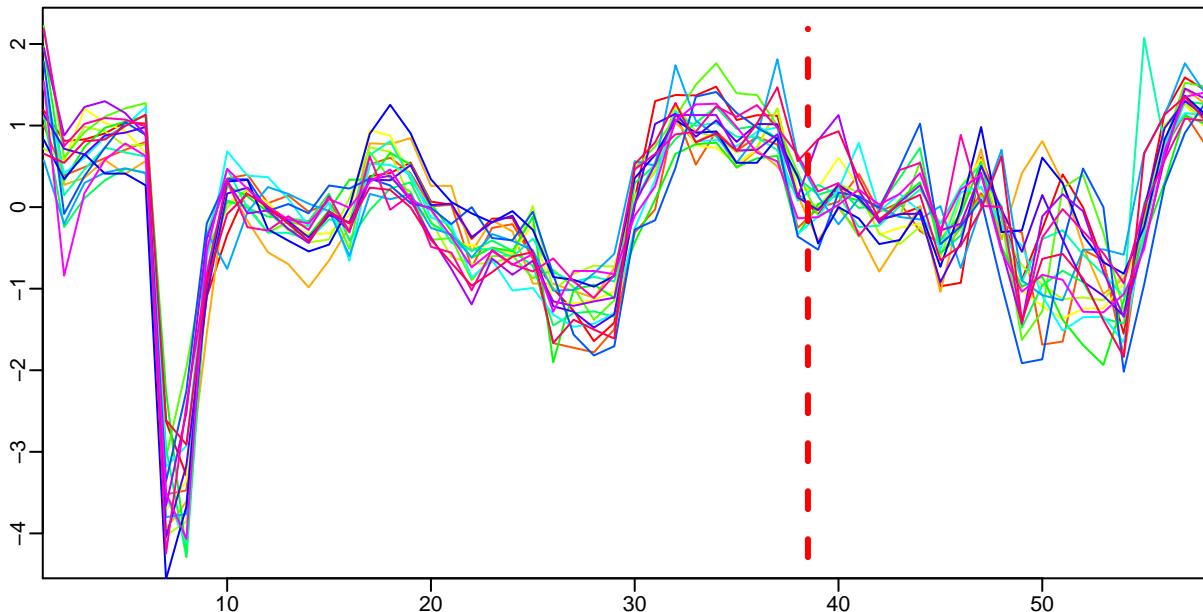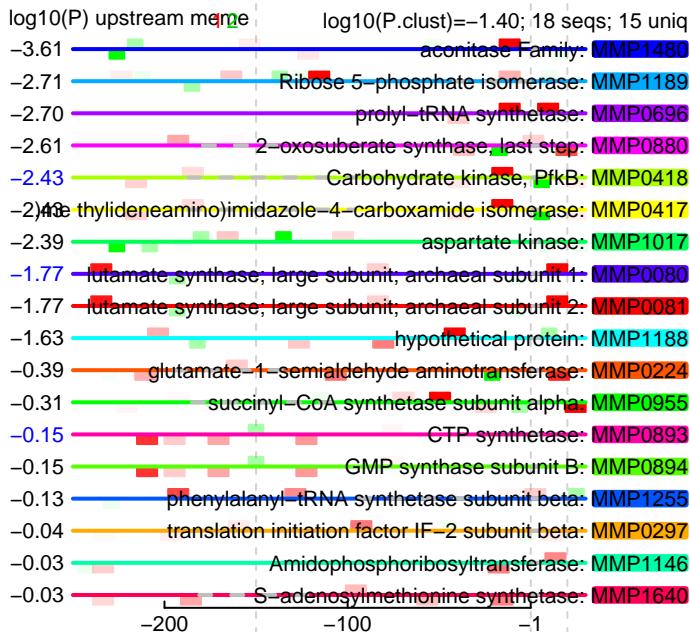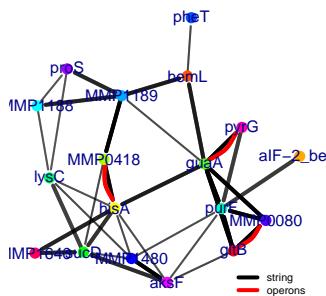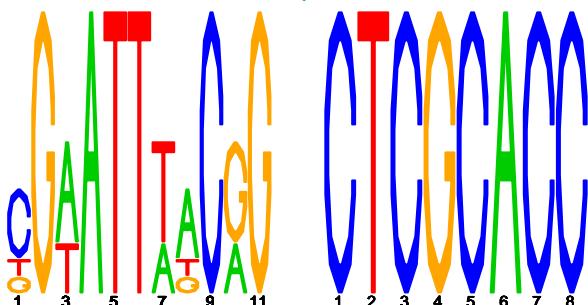
upstream meme PSSM #1; e=9.4

upstream meme PSSM #2; e=580

log10(P) upstream meme

log10(P.clust)=−2.08; 17 seqs; 16 uniq

−5.44	membrane component:Ketopantoate reductase ApbA/PanE: MMP0672
−4.81	hypothetical protein: MMP0215
−4.40	hypothetical protein: MMP0621
−2.88	Pyruvate kinase: MMP1605
−2.86	putative potassium channel protein: MMP0027
−2.79	2'−5' RNA ligase: MMP0612
−2.57	hypothetical protein: MMP1234
−2.49	methanofuran dehydrogenase subunit C−related protein: MMP0070
−1.53	CBS domain: MMP0863
−1.49	Aminoacyl−tRNA synthetase, class II: MMP0693
−1.16	hypothetical protein: MMP0903
−1.12	Probable amino−acid ABC transporter: MMP0455
−0.78	hypothetical protein: MMP0638
−0.55	soluble P−type ATPase: MMP1641
−0.31	hypothetical protein: MMP0483
−0.31	hypothetical protein: MMP0482
−0.16	lyase, 3 octaprenyl−4−hydroxybenzoate carboxy−lyase: MMP1552

string
operons

Cluster: 0055 mmp; resid: 0.31; r/c: 21/39
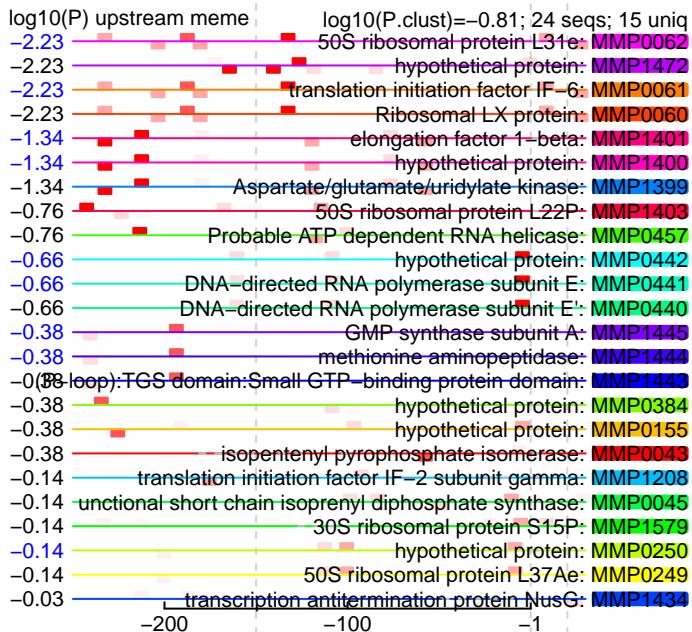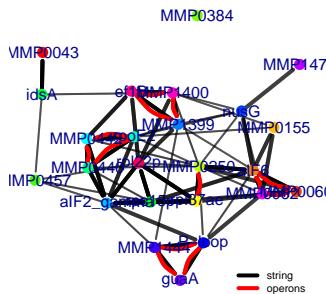
11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=24   **upstream meme PSSM #2; e=1.6e+03**

log10(P) upstream meme   log10(P.clust)=−3.87; 21 seqs; 13 uniq

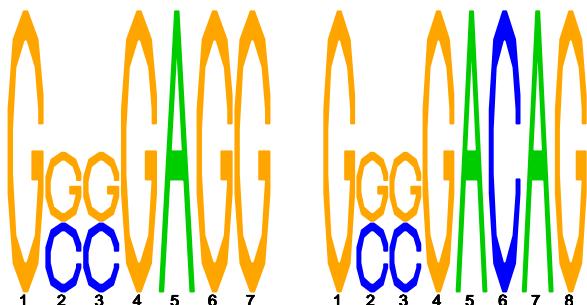| log10(P)	description	gene
−9.01	signal recognition particle protein Srp54:	MMP1551
−7.52	hypothetical protein:	MMP1428
−6.72	Sep−tRNA:Cys−tRNA synthetase:	MMP1240
−6.72	hypothetical protein:	MMP1241
−6.38	hypothetical protein:	MMP0483
−6.38	hypothetical protein:	MMP0482
−6.36	I region, domain I and II:MoeA C−terminal, domain IV:	MMP0545
−6.36	MoaA/nifB/pqqE family:	MMP0544
−6.36	hypothetical protein:	MMP0543
−2.83	hypothetical protein:	MMP0903
−2.83	hypothetical protein:	MMP0902
−2.64	hypothetical protein:	MMP0638
−2.33	hypothetical protein:	MMP0992
−2.12	hypothetical protein:	MMP0121
−2.12	hypothetical protein:	MMP0120
−1.29	Aldehyde dehydrogenase:	MMP1487
−1.09	hypothetical protein:	MMP1607
−0.82	hypothetical protein:	MMP1065
−0.43	hypothetical protein:	MMP1236
−0.43	hypothetical protein:	MMP1234
−0.43	Molybdopterin biosynthesis MoaE:	MMP1235

Cluster: 0056 mmp; resid: 0.13; r/c: 8/37

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=15

upstream meme PSSM #2; e=130

log10(P) upstream meme

log10(P.clust)=−2.76; 8 seqs; 3 uniq

−3.32	50S ribosomal protein L1P:	MMP0260
−3.32	acidic ribosomal protein P0:	MMP0259
−2.82	30S ribosomal protein S19P:	MMP1547
−2.82	50S ribosomal protein L2P:	MMP1546
−2.82	50S ribosomal protein L23:	MMP1545
−2.82	50S ribosomal protein L4P:	MMP1544
−2.07	cytidylate kinase:	MMP0626
−2.07	50S ribosomal protein L34e:	MMP0627

string
operons

Cluster: 0057 mmp; resid: 0.19; r/c: 17/40

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

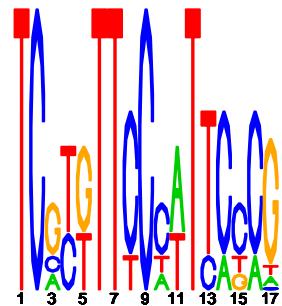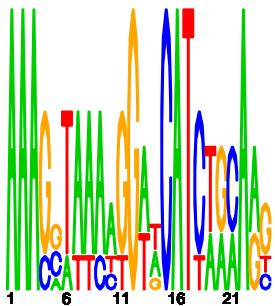upstream meme PSSM #1; e=2.5e+00 upstream meme PSSM #2; e=1.3e+04

log10(P) upstream meme   log10(P.clust)=−0.96; 17 seqs; 13 uniq

log10(P)	Description	ID
−2.92	hypothetical protein:	MMP0621
−2.43	Molybdenum transport ATP−binding protein modC:	MMP0207
−1.85	soluble P−type ATPase:	MMP1641
−1.73	hypothetical protein:	MMP0535
−1.73	hypothetical protein:	MMP0534
−1.60	hypothetical protein:	MMP0121
−1.60	hypothetical protein:	MMP0122
−0.80	Nitroreductase family:	MMP0426
−0.80	hypothetical protein:	MMP0425
−0.43	2'−5' RNA ligase:	MMP0612
−0.21	hypothetical protein:	MMP1001
−0.14	prephenate dehydrogenase:	MMP1514
−0.04	hypothetical protein:	MMP0465
−0.02	thioredoxin reductase:	MMP0959
−0.02	hypothetical protein:	MMP0958
−0.01	putative potassium channel protein:	MMP0027
−0.00	hypothetical protein:	MMP0569

Cluster: 0058 mmp; resid: 0.49; r/c: 33/38

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=0.39 upstream meme PSSM #2; e=1.2e+03
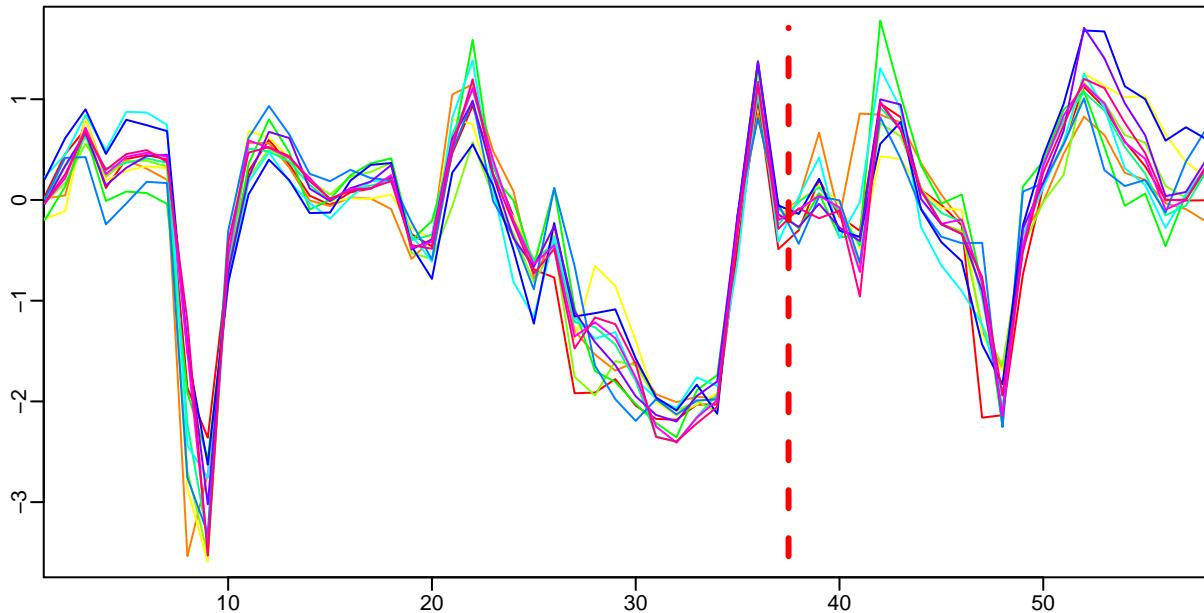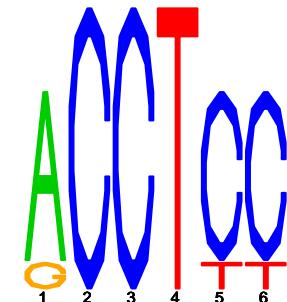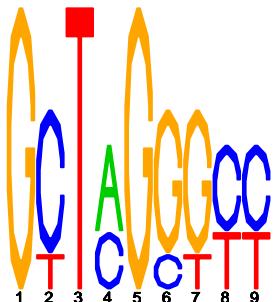
log10(P) upstream meme   log10(P.clust)=−2.19; 33 seqs; 28 uniq

log10(P)	Annotation	Gene
−11.19	Aminotransferase (subgroup I):	MMP0096
−11.19	criptional regulator protein, Helix−turn−helix motif:	MMP0097
−4.53	dihydrodipicolinate reductase:	MMP0923
−4.53	possible phage infection protein:	MMP0922
−3.78	hypothetical protein:	MMP0209
−3.78	hypothetical protein:	MMP0210
−3.25	hypothetical protein:	MMP0788
−3.20	phosphoribosyl−ATP pyrophosphatase:	MMP0051
−3.20	riboflavin synthase subunit beta:	MMP0050
−3.16	hypothetical protein:	MMP0487
−2.83	riboflavin synthase:	MMP0180
−2.54	probable chemotaxis−related protein:	MMP0932
−2.53	hypothetical protein:	MMP0480
−2.20	Alpha−acetolactate decarboxylase:	MMP0613
−2.01		Antisense_3
−1.51	cofactor−independent phosphoglycerate mutase:	MMP1439
−1.43	hypothetical protein:	MMP0722
−0.90	hypothetical protein:	MMP0524
−0.67	NADP oxidoreductase, coenzyme F420−dependent:	MMP1550
−0.64		Unanno_47
−0.62	hypothetical protein:	MMP0369
−0.62	transcription factor:	MMP0257
−0.62	imidazole glycerol phosphate synthase subunit HisH:	MMP0256
−0.52	amino acid ABC transporter substrate−binding protein:	MMP0712
−0.36	hypothetical protein:	MMP0181
−0.18	hypothetical protein:	MMP0757
−0.07	hypothetical protein:	MMP1493
−0.06	hypothetical protein:	MMP1229
−0.05	Rubrerythrin:	MMP1136
−0.05	Flavodoxin:Beta−lactamase−like:	MMP1135
−0.05	type A flavoprotein:	MMP1134
−0.02	hypothetical protein:	MMP0734
−0.00	hypothetical protein:	MMP0059

Cluster: 0059 mmp; resid: 0.19; r/c: 16/40

11 Oct 11 16:14:07 iter=2000
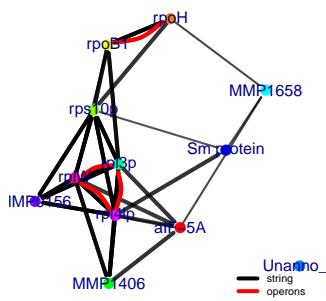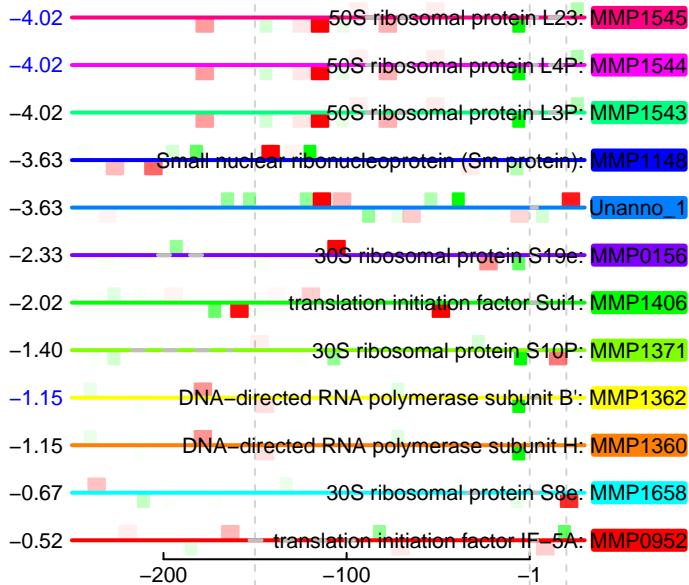cMonkey Version 4.8.8 mmp

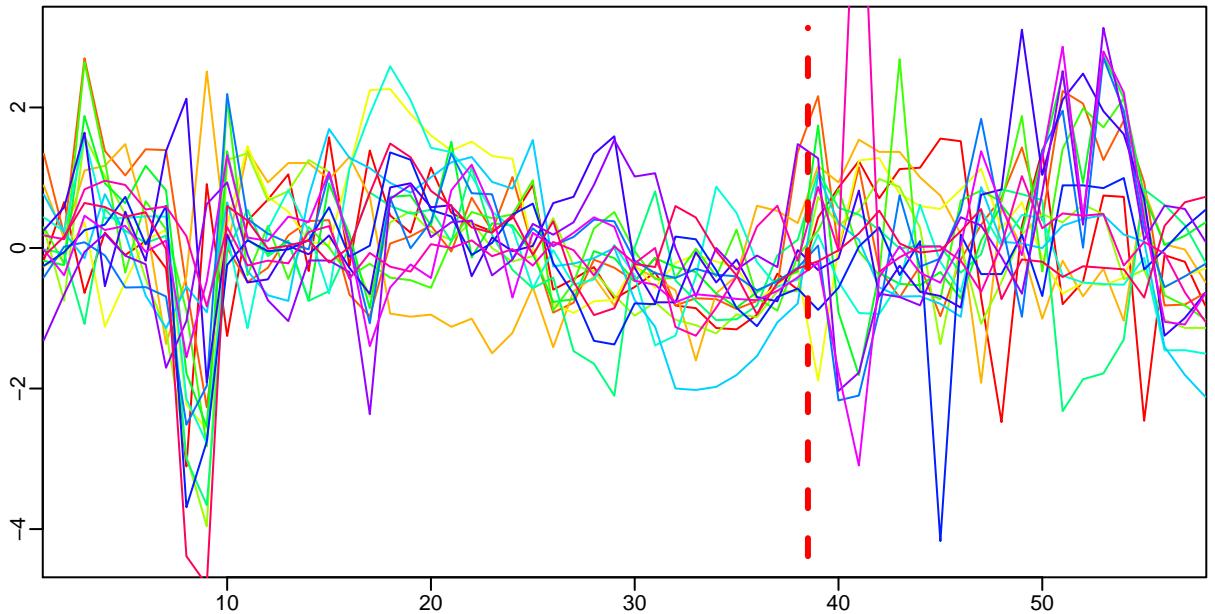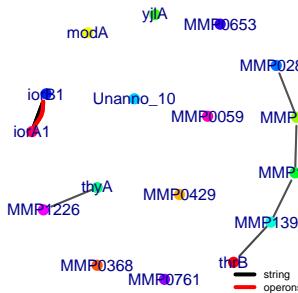upstream meme PSSM #1; e=0.00055   upstream meme PSSM #2; e=4.8e+03

log10(P) upstream meme   log10(P.clust)=−5.07; 16 seqs; 5 uniq

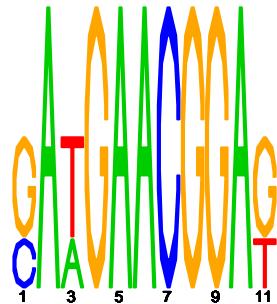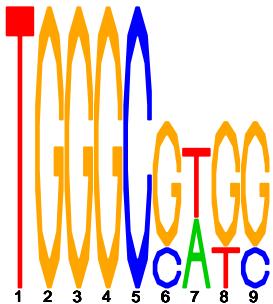| log10(P)	Annotation	ID
−6.01	Methyl−accepting chemotaxis protein (MCP):	MMP0929
−6.01	chemotaxis protein CheD:	MMP0928
−6.01	Chemotaxis protein CheA:	MMP0927
−5.23	flagella accessory protein G:	MMP1673
−5.23	flagella accessory protein F:	MMP1672
−5.23	flagella accessory protein E:	MMP1671
−5.23	flagella accessory protein D:	MMP1670
−5.23	flagella accessory protein C:	MMP1669
−5.23	flagellin:	MMP1668
−5.23	flagellin:	MMP1667
−5.23	flagellin:	MMP1666
−4.50	hypothetical protein:	MMP0413
−4.46	chemotaxis protein CheY:	MMP0933
−4.46	probable chemotaxis−related protein:	MMP0932
−4.46	probable chemotaxis−related protein:	MMP0931
−3.45	hypothetical protein:	MMP1719

Cluster: 0060 mmp; resid: 0.24; r/c: 18/38

11 Oct 11 16:14:07 iter=2000
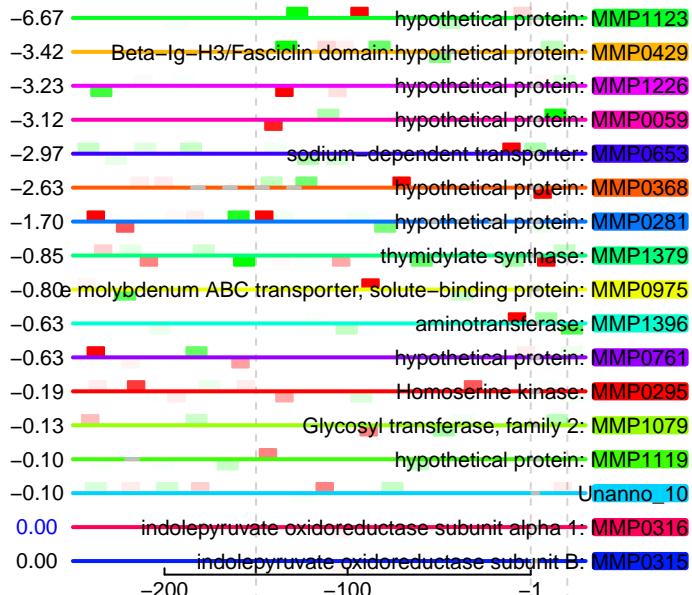cMonkey Version 4.8.8 mmp

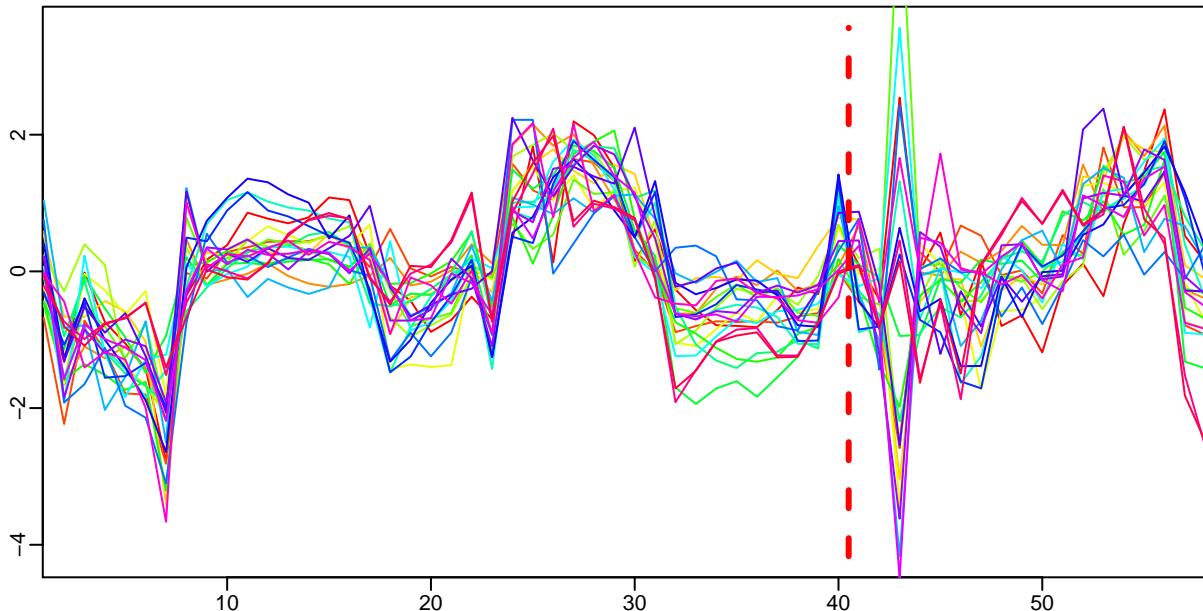upstream meme PSSM #1; e=1.8e+03   upstream meme PSSM #2; e=2.9e+03

log10(P) upstream meme   log10(P.clust)=−1.40; 18 seqs; 15 uniq

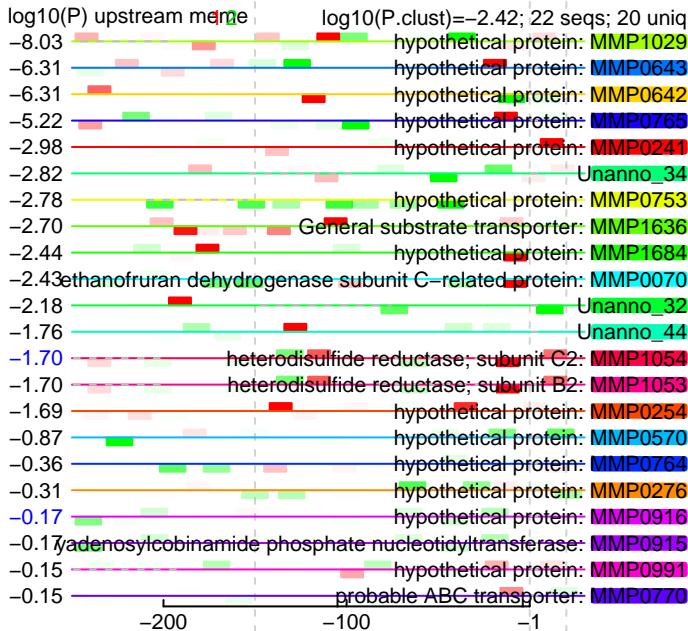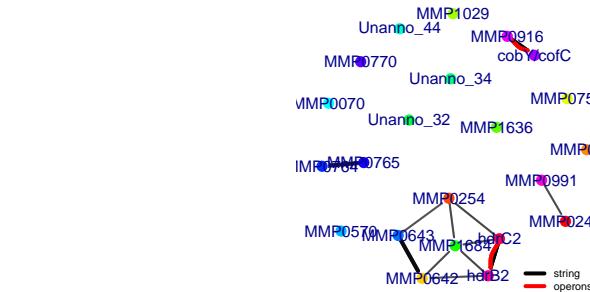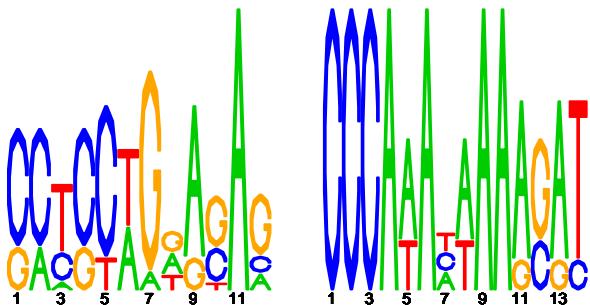| log10(P)	Annotation	ID
−3.61	aconitase Family	MMP1480
−2.71	Ribose 5−phosphate isomerase	MMP1189
−2.70	prolyl−tRNA synthetase	MMP0696
−2.61	2−oxosuberate synthase, last step	MMP0880
−2.43	Carbohydrate kinase, PfkB	MMP0418
−2.43	(methylideneamino)imidazole−4−carboxamide isomerase	MMP0417
−2.39	aspartate kinase	MMP1017
−1.77	glutamate synthase, large subunit, archaeal subunit 1	MMP0080
−1.77	glutamate synthase, large subunit, archaeal subunit 2	MMP0081
−1.63	hypothetical protein	MMP1188
−0.39	glutamate−1−semialdehyde aminotransferase	MMP0224
−0.31	succinyl−CoA synthetase subunit alpha	MMP0955
−0.15	CTP synthetase	MMP0893
−0.15	GMP synthase subunit B	MMP0894
−0.13	phenylalanyl−tRNA synthetase subunit beta	MMP1255
−0.04	translation initiation factor IF−2 subunit beta	MMP0297
−0.03	Amidophosphoribosyltransferase	MMP1146
−0.03	S−adenosylmethionine synthetase	MMP1640

Cluster: 0061 mmp; resid: 0.23; r/c: 24/37

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=5.6e+03 upstream meme PSSM #2; e=7.8e+03

log10(P) upstream meme   log10(P.clust)=−0.81; 24 seqs; 15 uniq

log10(P)	Annotation	ID
−2.23	50S ribosomal protein L31e:	MMP0062
−2.23	hypothetical protein:	MMP1472
−2.23	translation initiation factor IF−6:	MMP0061
−2.23	Ribosomal LX protein:	MMP0060
−1.34	elongation factor 1−beta:	MMP1401
−1.34	hypothetical protein:	MMP1400
−1.34	Aspartate/glutamate/uridylate kinase:	MMP1399
−0.76	50S ribosomal protein L22P:	MMP1403
−0.76	Probable ATP dependent RNA helicase:	MMP0457
−0.66	hypothetical protein:	MMP0442
−0.66	DNA−directed RNA polymerase subunit E:	MMP0441
−0.66	DNA−directed RNA polymerase subunit E':	MMP0440
−0.38	GMP synthase subunit A:	MMP1445
−0.38	methionine aminopeptidase:	MMP1444
−0.38	(P−loop):TGS domain:Small GTP−binding protein domain:	MMP1443
−0.38	hypothetical protein:	MMP0384
−0.38	hypothetical protein:	MMP0155
−0.38	isopentenyl pyrophosphate isomerase:	MMP0043
−0.14	translation initiation factor IF−2 subunit gamma:	MMP1208
−0.14	functional short chain isoprenyl diphosphate synthase:	MMP0045
−0.14	30S ribosomal protein S15P:	MMP1579
−0.14	hypothetical protein:	MMP0250
−0.14	50S ribosomal protein L37Ae:	MMP0249
−0.03	transcription antitermination protein NusG:	MMP1434

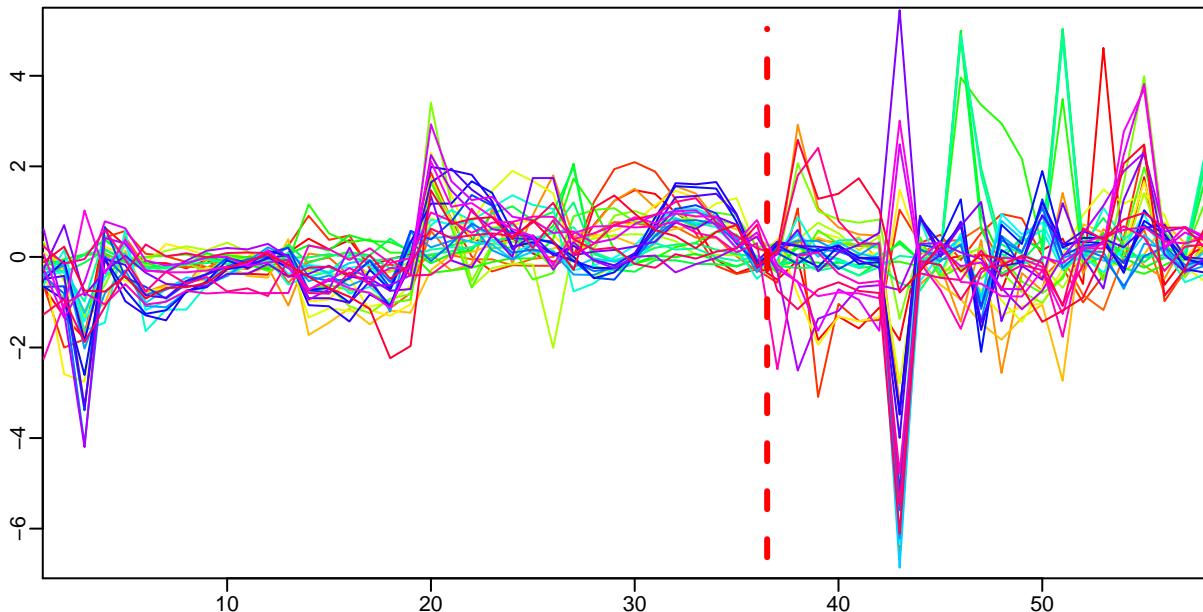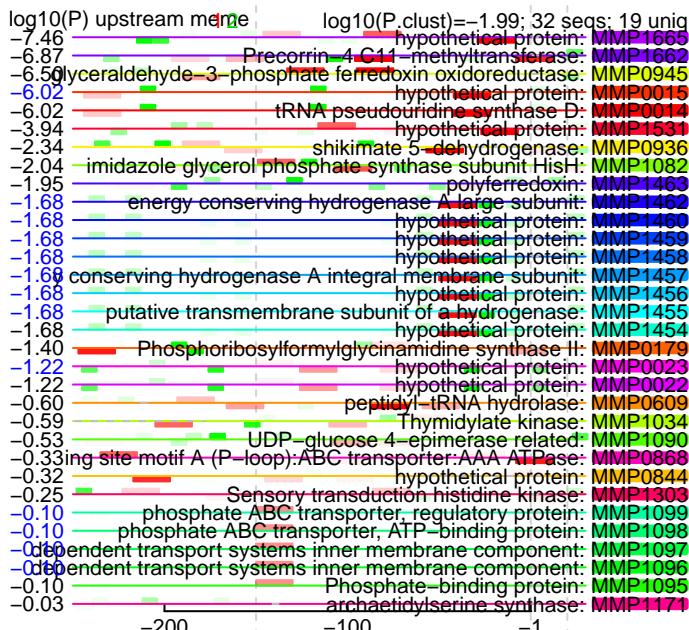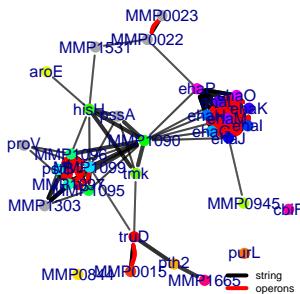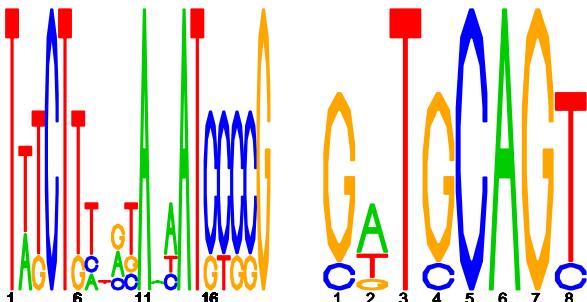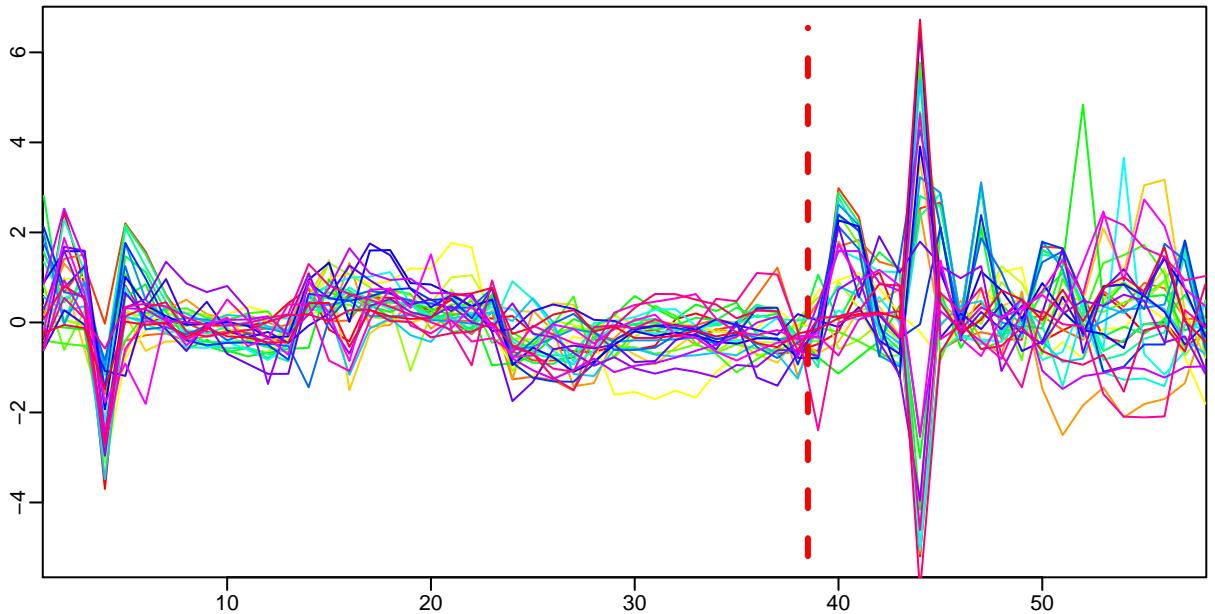**Cluster: 0062 mmp; resid: 0.46; r/c: 24/38**

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=11

upstream meme PSSM #2; e=3.8

log10(P) upstream meme

log10(P.clust)=−5.15; 24 seqs; 16 uniq

log10(P)	protein	gene
−16.46	hypothetical protein:	MMP0746
−16.46	hypothetical protein:	MMP0745
−16.46	hypothetical protein:	MMP0744
−16.46	Probable integrase/recombinase:	MMP0743
−16.46		Unanno_43
−6.82	hypothetical protein:	MMP0552
−6.12	hypothetical protein:	MMP1280
−5.15	containing formylmethanofuran dehydrogenase, subunit E:	MMP0508
−4.84		Unanno_22
−4.38	hypothetical protein:	MMP0777
−4.38	hypothetical protein:	MMP0776
−4.12	hypothetical protein:	MMP0324
−1.38	hypothetical protein:	MMP0960
−0.82	hypothetical protein:	MMP0343
−0.68	hypothetical protein:	MMP0665
−0.68	hypothetical protein:	MMP0662
−0.30	hypothetical protein:	MMP0750
−0.30	hypothetical protein:	MMP0749
−0.30	MCM family related protein:	MMP0748
−0.30	hypothetical protein:	MMP0747
−0.26	hypothetical protein:	MMP0486
−0.21	le amino acid ABC transporter, periplasmic component:	MMP1650
−0.13	transcriptional regulator PadR−like family:	MMP0700
−0.01	hypothetical protein:	MMP0485

Cluster: 0063 mmp; resid: 0.16; r/c: 12/37

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp
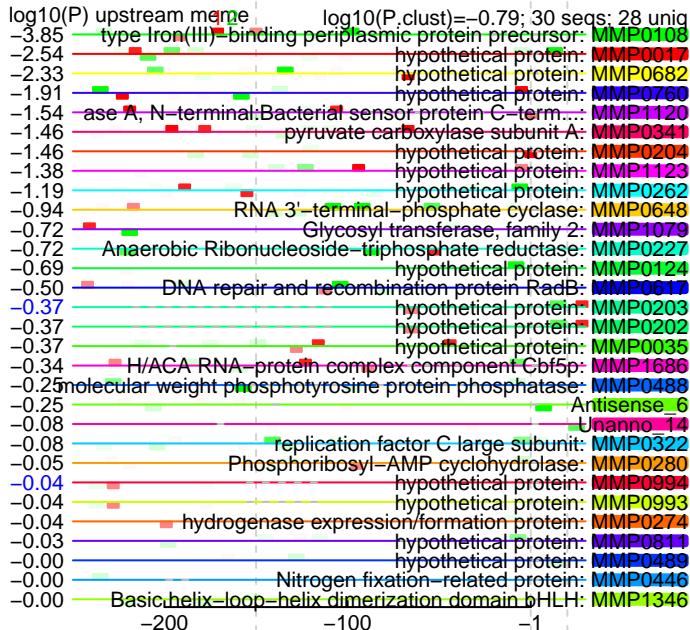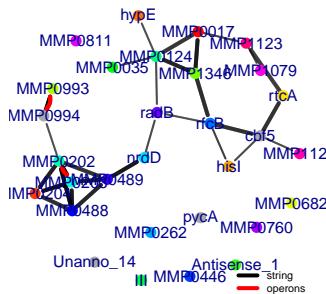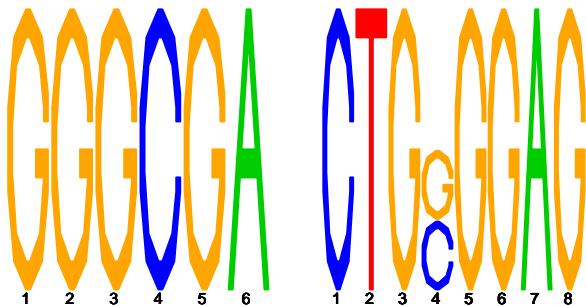
upstream meme PSSM #1; e=51

upstream meme PSSM #2; e=130

log10(P) upstream meme

log10(P.clust)=−2.38; 12 seqs; 9 uniq

−4.02	50S ribosomal protein L23	MMP1545
−4.02	50S ribosomal protein L4P	MMP1544
−4.02	50S ribosomal protein L3P	MMP1543
−3.63	Small nuclear ribonucleoprotein (Sm protein)	MMP1148
−3.63		Unanno_1
−2.33	30S ribosomal protein S19e	MMP0156
−2.02	translation initiation factor Sui1	MMP1406
−1.40	30S ribosomal protein S10P	MMP1371
−1.15	DNA−directed RNA polymerase subunit B'	MMP1362
−1.15	DNA−directed RNA polymerase subunit H	MMP1360
−0.67	30S ribosomal protein S8e	MMP1658
−0.52	translation initiation factor IF−5A	MMP0952

Cluster: 0064 mmp; resid: 0.55; r/c: 17/38

Cluster: 0065 mmp; resid: 0.34; r/c: 22/40

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=0.0046   upstream meme PSSM #2; e=140
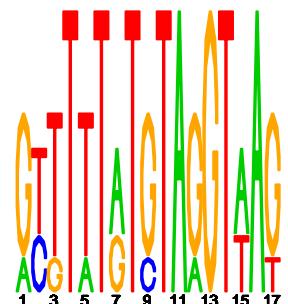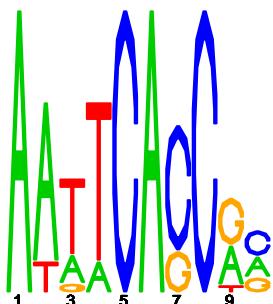
log10(P) upstream meme   log10(P.clust)=−2.42; 22 seqs; 20 uniq

log10(P)	annotation
−8.03	hypothetical protein: MMP1029
−6.31	hypothetical protein: MMP0643
−6.31	hypothetical protein: MMP0642
−5.22	hypothetical protein: MMP0765
−2.98	hypothetical protein: MMP0241
−2.82	Unanno_34
−2.78	hypothetical protein: MMP0753
−2.70	General substrate transporter: MMP1636
−2.44	hypothetical protein: MMP1684
−2.43	ethanofuran dehydrogenase subunit C−related protein: MMP0070
−2.18	Unanno_32
−1.76	Unanno_44
−1.70	heterodisulfide reductase; subunit C2: MMP1054
−1.70	heterodisulfide reductase; subunit B2: MMP1053
−1.69	hypothetical protein: MMP0254
−0.87	hypothetical protein: MMP0570
−0.36	hypothetical protein: MMP0764
−0.31	hypothetical protein: MMP0276
−0.17	hypothetical protein: MMP0916
−0.17	adenosylcobinamide phosphate nucleotidyltransferase: MMP0915
−0.15	hypothetical protein: MMP0991
−0.15	probable ABC transporter: MMP0770

Cluster: 0066 mmp; resid: 0.39; r/c: 32/36

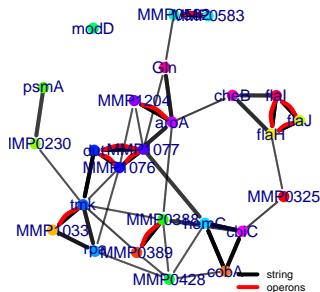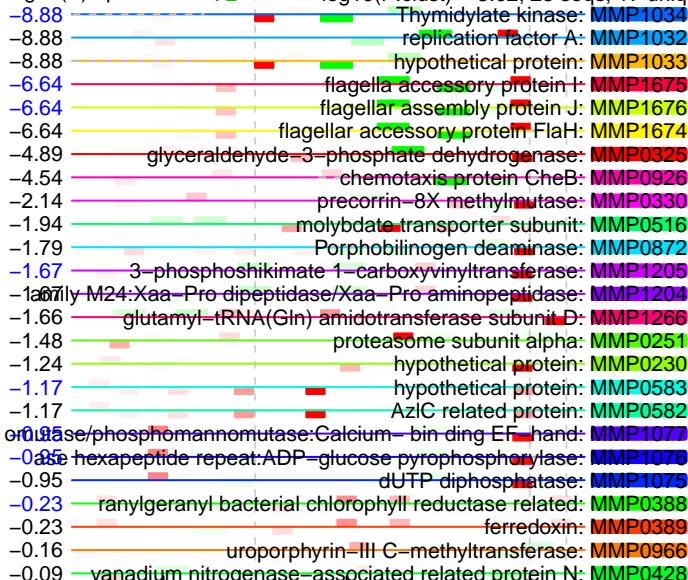11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp
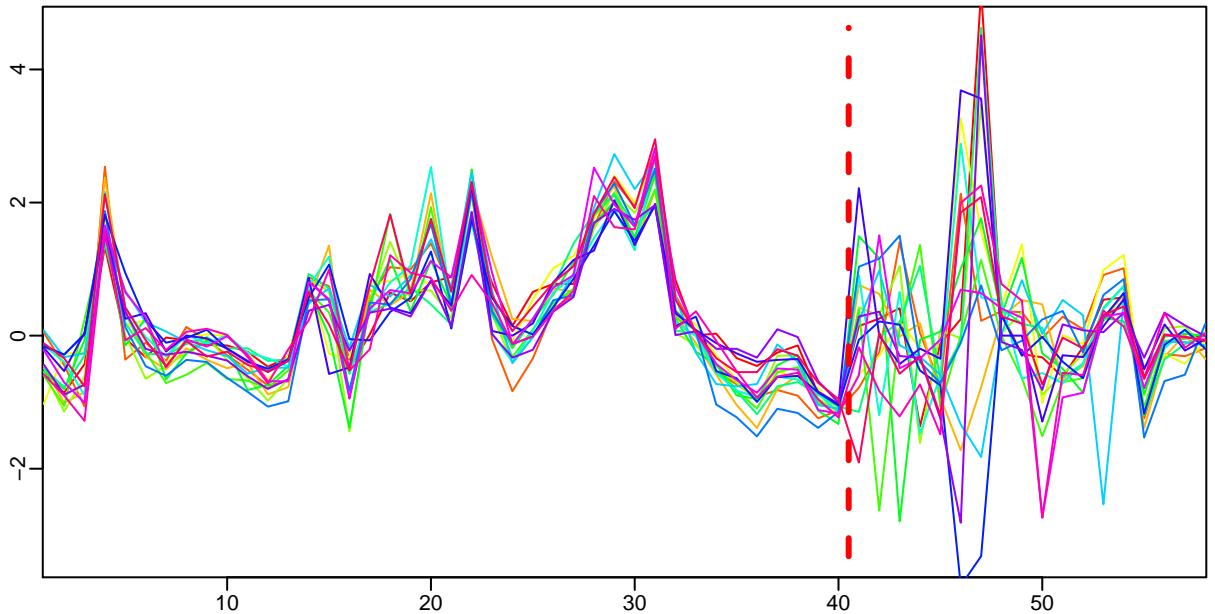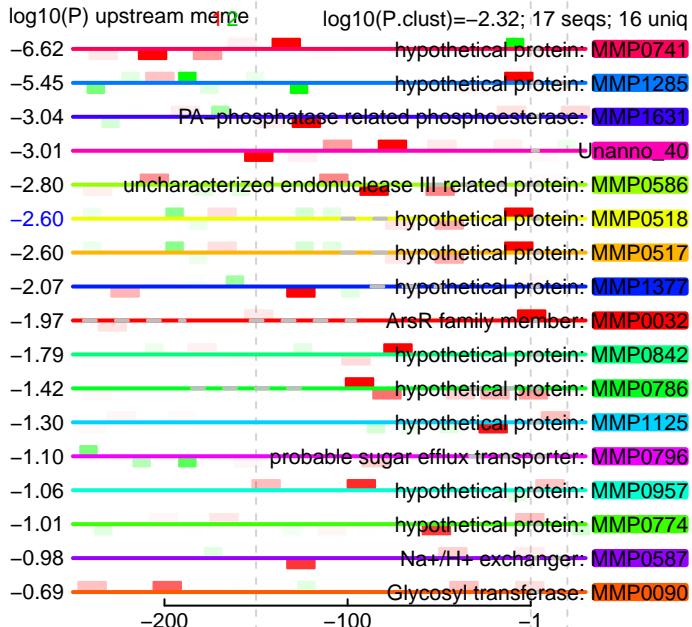
upstream meme PSSM #1; e=450   upstream meme PSSM #2; e=1.7e+03

log10(P) upstream meme   log10(P.clust)=−1.99; 32 seqs: 19 uniq

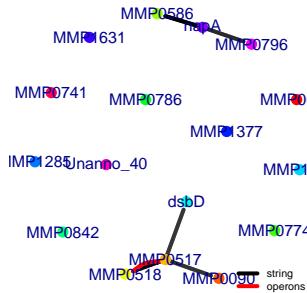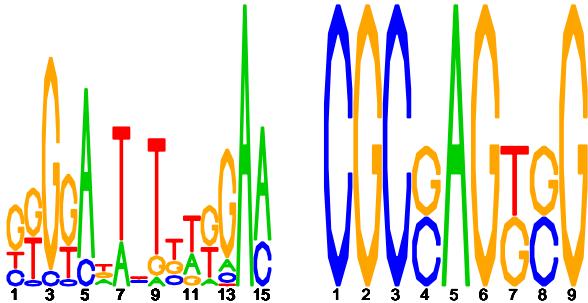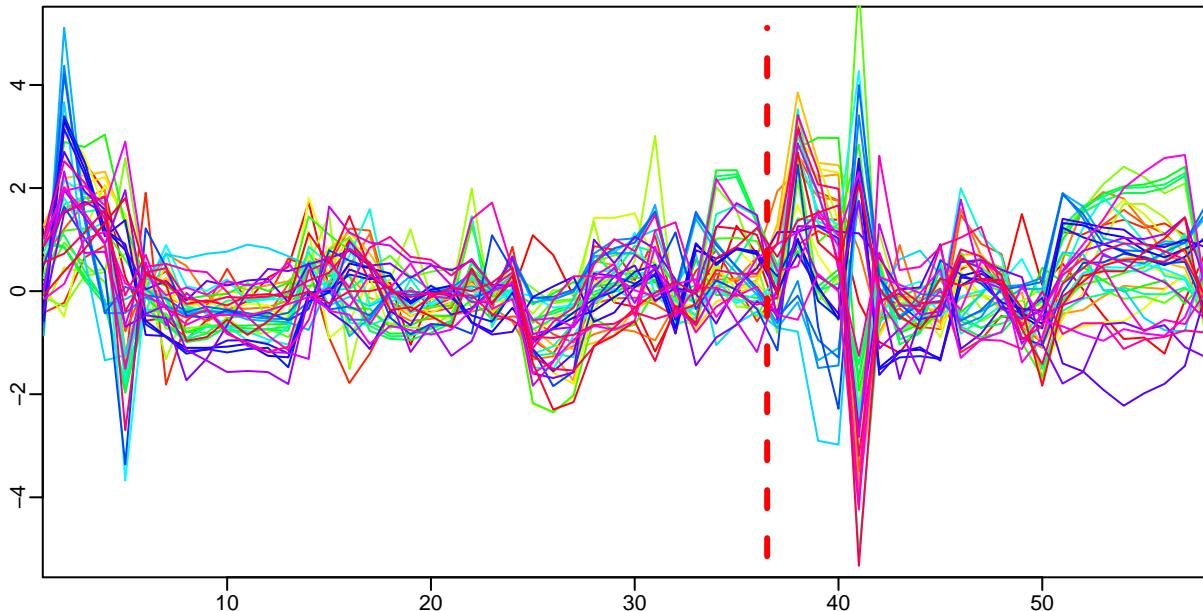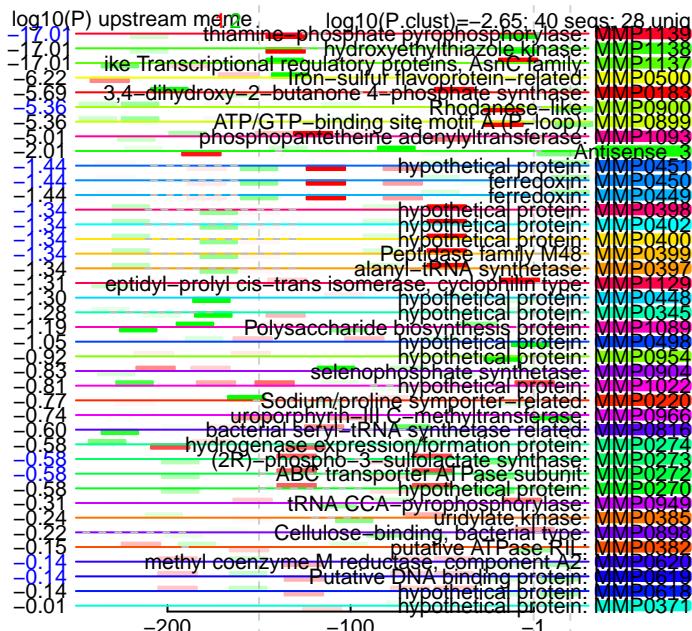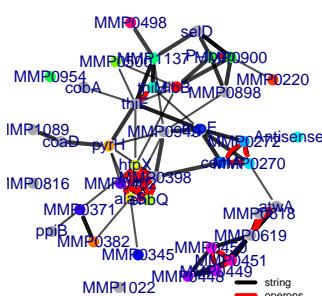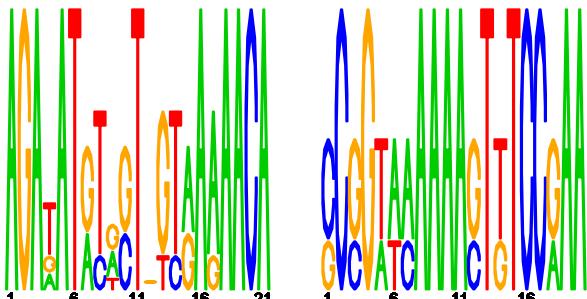| log10(P)	description	gene
−7.46	hypothetical protein:	MMP1665
−6.87	Precorrin−4 C11−methyltransferase:	MMP1662
−6.50	glyceraldehyde−3−phosphate ferredoxin oxidoreductase:	MMP0945
−6.02	hypothetical protein:	MMP0015
−6.02	tRNA pseudouridine synthase D:	MMP0014
−3.94	hypothetical protein:	MMP1531
−2.34	shikimate 5−dehydrogenase:	MMP0936
−2.04	imidazole glycerol phosphate synthase subunit HisH:	MMP1082
−1.95	polyferredoxin:	MMP1463
−1.68	energy conserving hydrogenase A large subunit:	MMP1462
−1.68	hypothetical protein:	MMP1460
−1.68	hypothetical protein:	MMP1459
−1.68	hypothetical protein:	MMP1458
−1.68	conserving hydrogenase A integral membrane subunit:	MMP1457
−1.68	hypothetical protein:	MMP1456
−1.68	putative transmembrane subunit of a hydrogenase:	MMP1455
−1.68	hypothetical protein:	MMP1454
−1.40	Phosphoribosylformylglycinamidine synthase II:	MMP0179
−1.22	hypothetical protein:	MMP0023
−1.22	hypothetical protein:	MMP0022
−0.60	peptidyl−tRNA hydrolase:	MMP0609
−0.59	Thymidylate kinase:	MMP1034
−0.53	UDP−glucose 4−epimerase related:	MMP1090
−0.33	ing site motif A (P−loop):ABC transporter:AAA ATPase:	MMP0868
−0.32	hypothetical protein:	MMP0844
−0.25	Sensory transduction histidine kinase:	MMP1303
−0.10	phosphate ABC transporter, regulatory protein:	MMP1099
−0.10	phosphate ABC transporter, ATP−binding protein:	MMP1098
−0.0	dependent transport systems inner membrane component:	MMP1097
−0.0	dependent transport systems inner membrane component:	MMP1096
−0.10	Phosphate−binding protein:	MMP1095
−0.03	archaetidylserine synthase:	MMP1171

Cluster: 0067 mmp; resid: 0.38; r/c: 30/38

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=3.1e+00   upstream meme PSSM #2; e=1.7e+04

log10(P) upstream meme   log10(P.clust)=−0.79; 30 seqs: 28 uniq

log10(P)	description
−3.85	type Iron(III)−binding periplasmic protein precursor: MMP0108
−2.54	hypothetical protein: MMP0017
−2.33	hypothetical protein: MMP0682
−1.91	hypothetical protein: MMP0760
−1.54	ase A, N−terminal:Bacterial sensor protein C−term...: MMP1120
−1.46	pyruvate carboxylase subunit A: MMP0341
−1.46	hypothetical protein: MMP0204
−1.38	hypothetical protein: MMP1123
−1.19	hypothetical protein: MMP0262
−0.94	RNA 3'−terminal−phosphate cyclase: MMP0648
−0.72	Glycosyl transferase, family 2: MMP1079
−0.72	Anaerobic Ribonucleoside−triphosphate reductase: MMP0227
−0.69	hypothetical protein: MMP0124
−0.50	DNA repair and recombination protein RadB: MMP0617
−0.37	hypothetical protein: MMP0203
−0.37	hypothetical protein: MMP0202
−0.37	hypothetical protein: MMP0035
−0.34	H/ACA RNA−protein complex component Cbf5p: MMP1686
−0.25	molecular weight phosphotyrosine protein phosphatase: MMP0488
−0.25	Antisense_6
−0.08	Unanno_14
−0.08	replication factor C large subunit: MMP0322
−0.05	Phosphoribosyl−AMP cyclohydrolase: MMP0280
−0.04	hypothetical protein: MMP0994
−0.04	hypothetical protein: MMP0993
−0.04	hydrogenase expression/formation protein: MMP0274
−0.03	hypothetical protein: MMP0811
−0.00	hypothetical protein: MMP0489
−0.00	Nitrogen fixation−related protein: MMP0446
−0.00	Basic helix−loop−helix dimerization domain bHLH: MMP1346

Cluster: 0068 mmp; resid: 0.37; r/c: 25/37
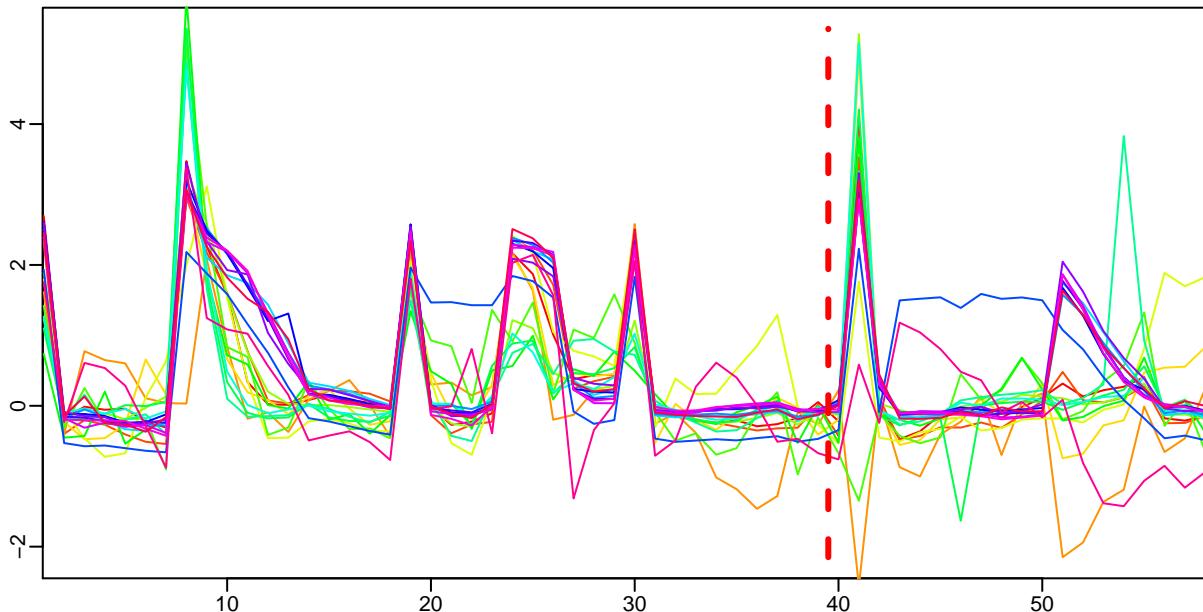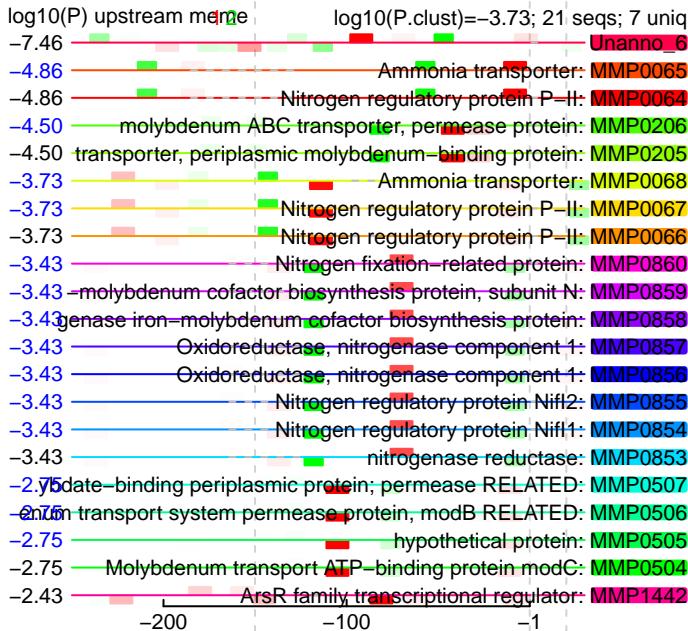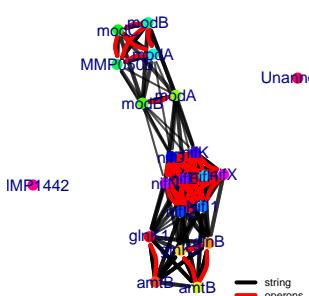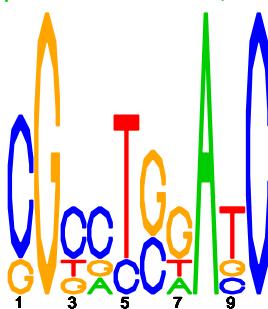

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=0.094

upstream meme PSSM #2; e=35

log10(P) upstream meme

log10(P.clust)=−3.02; 25 seqs; 17 uniq

log10(P)	Annotation	ID
−8.88	Thymidylate kinase:	MMP1034
−8.88	replication factor A:	MMP1032
−8.88	hypothetical protein:	MMP1033
−6.64	flagella accessory protein I:	MMP1675
−6.64	flagellar assembly protein J:	MMP1676
−6.64	flagellar accessory protein FlaH:	MMP1674
−4.89	glyceraldehyde-3-phosphate dehydrogenase:	MMP0325
−4.54	chemotaxis protein CheB:	MMP0926
−2.14	precorrin-8X methylmutase:	MMP0330
−1.94	molybdate transporter subunit:	MMP0516
−1.79	Porphobilinogen deaminase:	MMP0872
−1.67	3-phosphoshikimate 1-carboxyvinyltransferase:	MMP1205
−1.67	family M24:Xaa−Pro dipeptidase/Xaa−Pro aminopeptidase:	MMP1204
−1.66	glutamyl−tRNA(Gln) amidotransferase subunit D:	MMP1266
−1.48	proteasome subunit alpha:	MMP0251
−1.24	hypothetical protein:	MMP0230
−1.17	hypothetical protein:	MMP0583
−1.17	AzlC related protein:	MMP0582
−0.95	enolase/phosphomannomutase:Calcium−binding EF−hand:	MMP1077
−0.95	bacterial hexapeptide repeat:ADP−glucose pyrophosphorylase:	MMP1078
−0.95	dUTP diphosphatase:	MMP1075
−0.23	geranylgeranyl bacterial chlorophyll reductase related:	MMP0388
−0.23	ferredoxin:	MMP0389
−0.16	uroporphyrin−III C−methyltransferase:	MMP0966
−0.09	vanadium nitrogenase−associated related protein N:	MMP0428

Cluster: 0069 mmp; resid: 0.21; r/c: 17/40

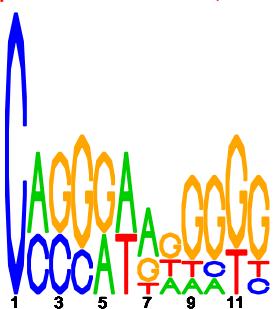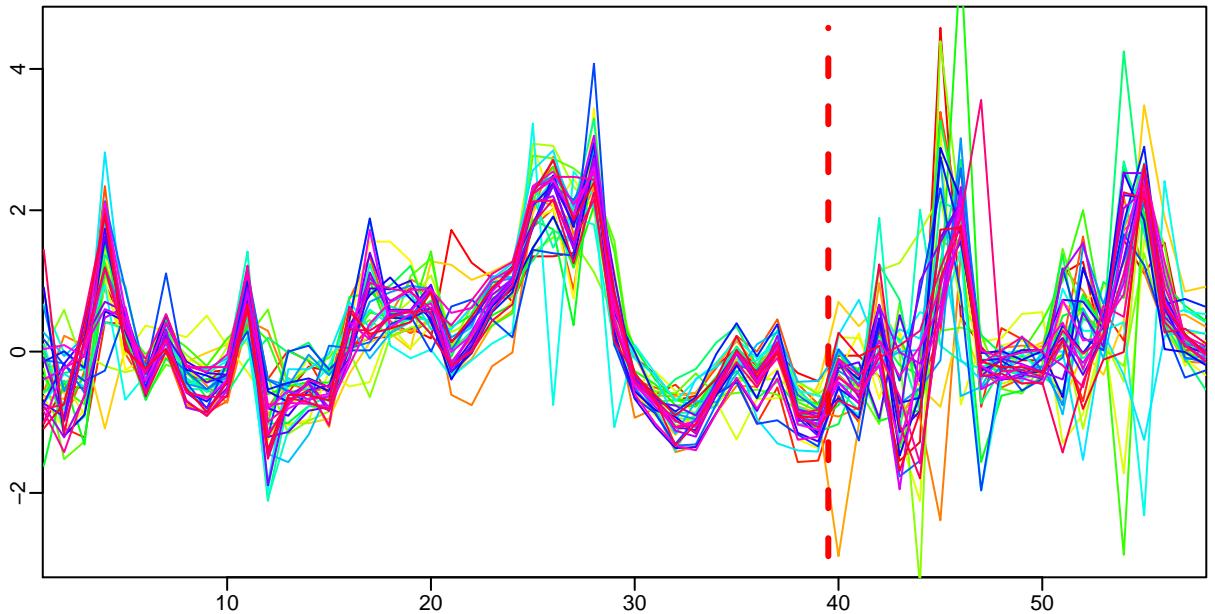11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp
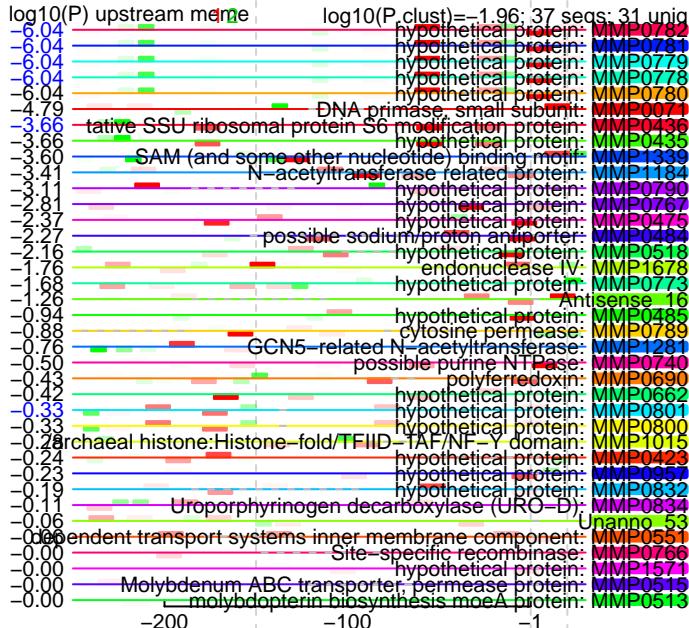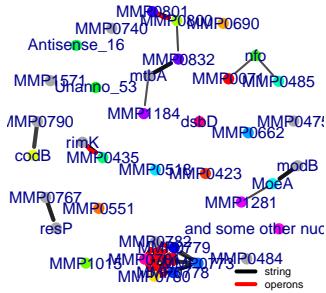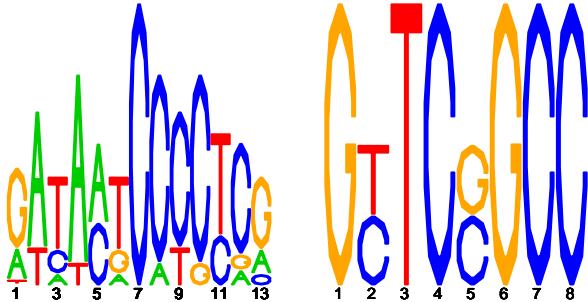
upstream meme PSSM #1; e=240   upstream meme PSSM #2; e=4.8e+03

log10(P) upstream meme   log10(P.clust)=−2.32; 17 seqs; 16 uniq

log10(P)	annotation	gene
−6.62	hypothetical protein	MMP0741
−5.45	hypothetical protein	MMP1285
−3.04	PA-phosphatase related phosphoesterase	MMP1631
−3.01		Unanno_40
−2.80	uncharacterized endonuclease III related protein	MMP0586
−2.60	hypothetical protein	MMP0518
−2.60	hypothetical protein	MMP0517
−2.07	hypothetical protein	MMP1377
−1.97	ArsR family member	MMP0032
−1.79	hypothetical protein	MMP0842
−1.42	hypothetical protein	MMP0786
−1.30	hypothetical protein	MMP1125
−1.10	probable sugar efflux transporter	MMP0796
−1.06	hypothetical protein	MMP0957
−1.01	hypothetical protein	MMP0774
−0.98	Na+/H+ exchanger	MMP0587
−0.69	Glycosyl transferase	MMP0090

Cluster: 0070 mmp; resid: 0.49; r/c: 40/36

upstream meme PSSM #1; e=150   upstream meme PSSM #2; e=4e+03

log10(P) upstream meme   log10(P.clust)=−2.65; 40 seqs; 28 uniq

−17.01	thiamine−phosphate pyrophosphorylase: MMP1139
−17.01	hydroxyethylthiazole kinase: MMP1138
−17.01	ike Transcriptional regulatory proteins, AsnC family: MMP1137
−6.22	iron−sulfur flavoprotein−related: MMP0500
−5.62	3,4−dihydroxy−2−butanone 4−phosphate synthase: MMP0900
−5.65	Rhodanese−like: MMP0900
−5.36	ATP/GTP−binding site motif A (P−loop): MMP0188
−5.01	phosphopantetheine adenylyltransferase: MMP1093
−2.01	Antisense_3
−1.44	hypothetical protein: MMP0451
−1.44	ferredoxin: MMP0450
−1.44	ferredoxin: MMP0449
−1.34	hypothetical protein: MMP0398
−1.34	hypothetical protein: MMP0402
−1.34	hypothetical protein: MMP0400
−1.34	Peptidase family M48: MMP0399
−1.31	alanyl−tRNA synthetase: MMP1129
−1.30	eptidyl−prolyl cis−trans isomerase, cyclophilin type: MMP1129
−1.28	hypothetical protein: MMP0448
−1.20	hypothetical protein: MMP0345
−1.19	Polysaccharide biosynthesis protein: MMP1089
−1.05	hypothetical protein: MMP0498
−0.92	hypothetical protein: MMP0954
−0.83	selenophosphate synthetase: MMP0904
−0.81	hypothetical protein: MMP1022
−0.77	Sodium/proline Symporter−related: MMP0866
−0.74	uroporphyrin−III C−methyltransferase: MMP0818
−0.60	bacterial seryl−tRNA synthetase related: MMP0274
−0.58	hydrogenase expression/formation protein: MMP0273
−0.58	(2R)−phospho−3−sulfolactate synthase: MMP0272
−0.58	ABC transporter ATPase subunit: MMP0270
−0.58	hypothetical protein: MMP0949
−0.31	tRNA CCA−pyrophosphorylase: MMP0385
−0.24	uridylate kinase: MMP0899
−0.22	Cellulose−binding, bacterial type: MMP0382
−0.15	putative ATPase RIL:
−0.14	methyl coenzyme M reductase, component A2:
−0.14	Putative DNA binding protein: MMP0619
−0.14	hypothetical protein:
−0.01	hypothetical protein: MMP0371

Cluster: 0071 mmp; resid: 0.31; r/c: 21/39

upstream meme PSSM #1; e=0.85   upstream meme PSSM #2; e=600

log10(P) upstream meme   log10(P.clust)=−3.73; 21 seqs; 7 uniq

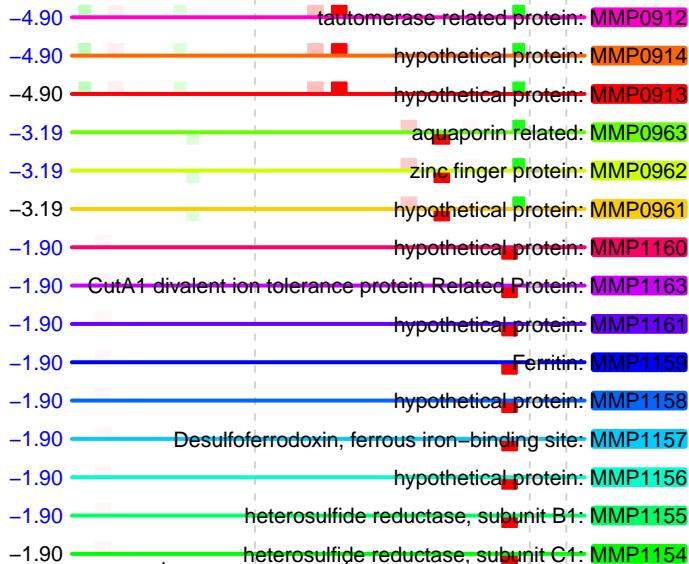| log10(P)	Annotation	Gene
−7.46		Unanno_6
−4.86	Ammonia transporter:	MMP0065
−4.86	Nitrogen regulatory protein P−II:	MMP0064
−4.50	molybdenum ABC transporter, permease protein:	MMP0206
−4.50	transporter, periplasmic molybdenum−binding protein:	MMP0205
−3.73	Ammonia transporter:	MMP0068
−3.73	Nitrogen regulatory protein P−II:	MMP0067
−3.73	Nitrogen regulatory protein P−II:	MMP0066
−3.43	Nitrogen fixation−related protein:	MMP0860
−3.43	molybdenum cofactor biosynthesis protein, subunit N:	MMP0859
−3.43	genase iron−molybdenum cofactor biosynthesis protein:	MMP0858
−3.43	Oxidoreductase, nitrogenase component 1:	MMP0857
−3.43	Oxidoreductase, nitrogenase component 1:	MMP0856
−3.43	Nitrogen regulatory protein NifI2:	MMP0855
−3.43	Nitrogen regulatory protein NifI1:	MMP0854
−3.43	nitrogenase reductase:	MMP0853
−2.75	date−binding periplasmic protein; permease RELATED:	MMP0507
−2.75	enum transport system permease protein, modB RELATED:	MMP0506
−2.75	hypothetical protein:	MMP0505
−2.75	Molybdenum transport ATP−binding protein modC:	MMP0504
−2.43	ArsR family transcriptional regulator:	MMP1442

Cluster: 0072 mmp; resid: 0.27; r/c: 37/39

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

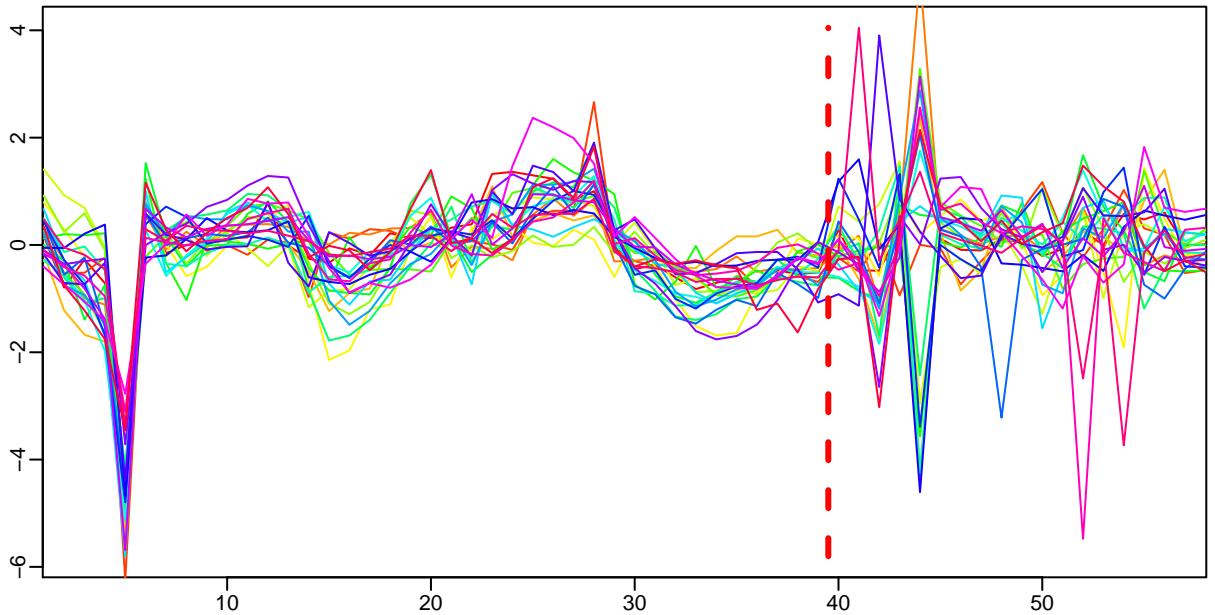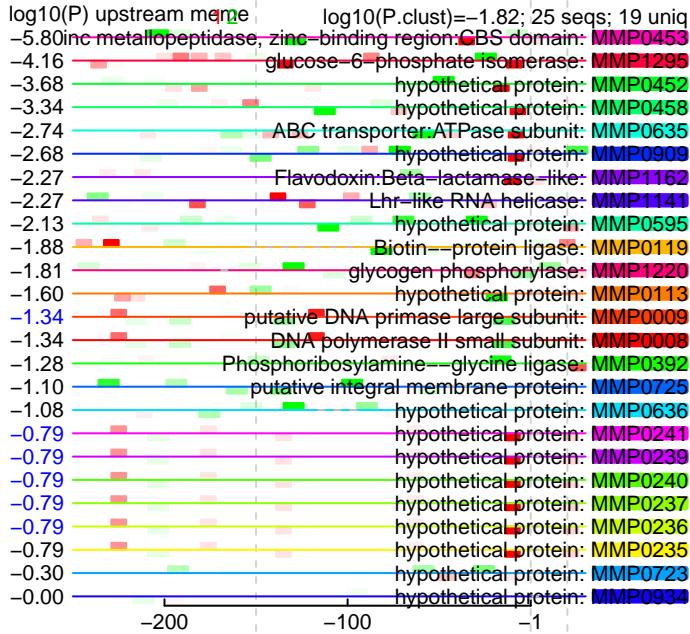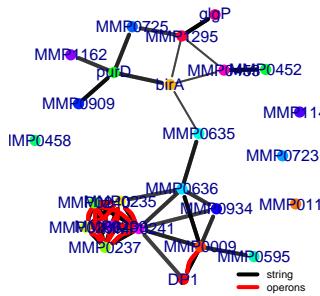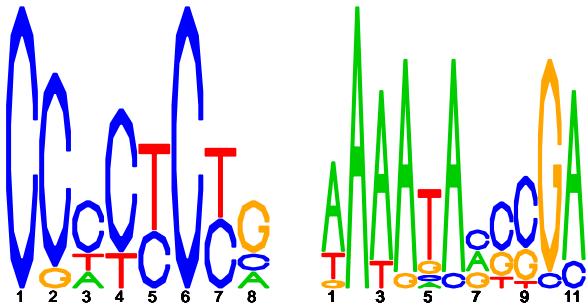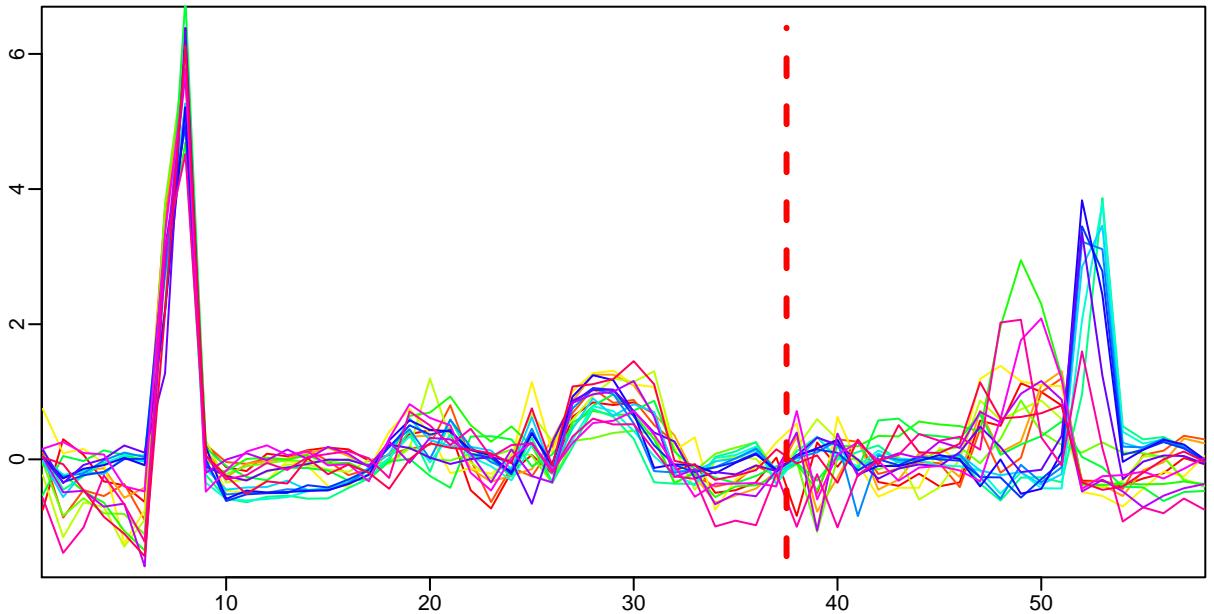upstream meme PSSM #1; e=11   upstream meme PSSM #2; e=3.7e+04

log10(P) upstream meme   log10(P,clust)=−1.96; 37 seqs; 31 uniq

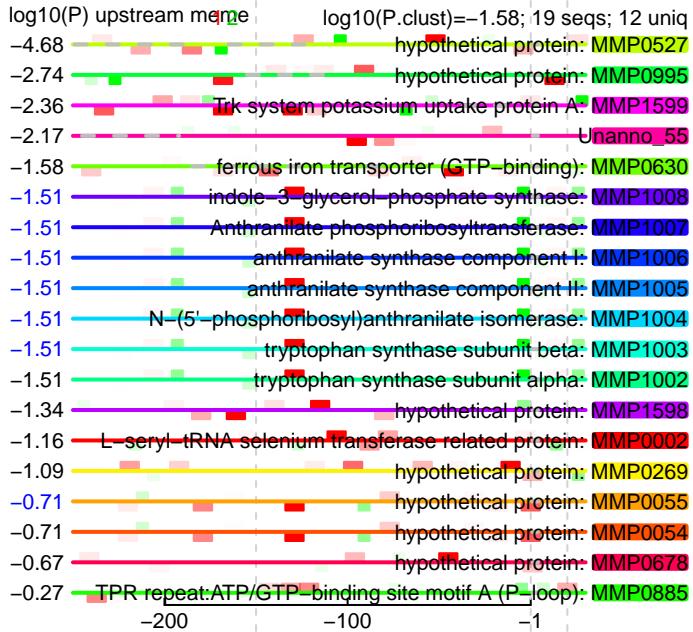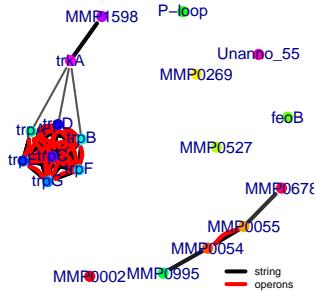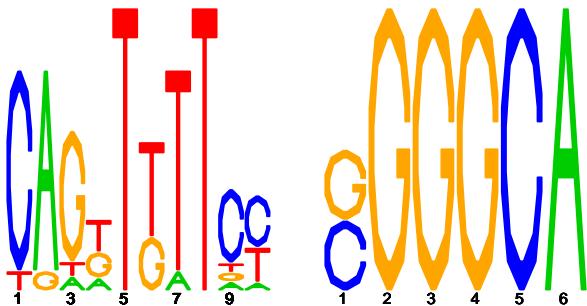| log10(P)	annotation	gene
−6.04	hypothetical protein:	MMP0782
−6.04	hypothetical protein:	MMP0781
−6.04	hypothetical protein:	MMP0779
−6.04	hypothetical protein:	MMP0778
−6.04	hypothetical protein:	MMP0780
−4.79	DNA primase, small subunit:	MMP0071
−3.66	tative SSU ribosomal protein S6 modification protein:	MMP0436
−3.66	hypothetical protein:	MMP0435
−3.60	SAM (and some other nucleotide) binding motif:	MMP1339
−3.41	N−acetyltransferase related protein:	MMP1184
−3.11	hypothetical protein:	MMP0790
−2.81	hypothetical protein:	MMP0767
−2.37	hypothetical protein:	MMP0475
−2.27	possible sodium/proton antiporter:	MMP0484
−2.16	hypothetical protein:	MMP0518
−1.76	endonuclease IV:	MMP1678
−1.68	hypothetical protein:	MMP0773
−1.26		Antisense_16
−0.94	hypothetical protein:	MMP0485
−0.88	cytosine permease:	MMP0789
−0.76	GCN5−related N−acetyltransferase:	MMP1281
−0.50	possible purine NTPase:	MMP0740
−0.43	polyferredoxin:	MMP0690
−0.42	hypothetical protein:	MMP0662
−0.33	hypothetical protein:	MMP0801
−0.33	hypothetical protein:	MMP0800
−0.28	archaeal histone:Histone−fold/TFIID−TAF/NF−Y domain:	MMP1015
−0.24	hypothetical protein:	MMP0423
−0.23	hypothetical protein:	MMP0957
−0.19	hypothetical protein:	MMP0832
−0.11	Uroporphyrinogen decarboxylase (URO−D):	MMP0834
−0.06		Unanno_53
−0.00	dependent transport systems inner membrane component:	MMP0551
−0.00	Site−specific recombinase:	MMP0766
−0.00	hypothetical protein:	MMP1571
−0.00	Molybdenum ABC transporter, permease protein:	MMP0513
−0.00	molybdopterin biosynthesis moeA protein:	MMP0513

Cluster: 0073 mmp; resid: 0.27; r/c: 17/39

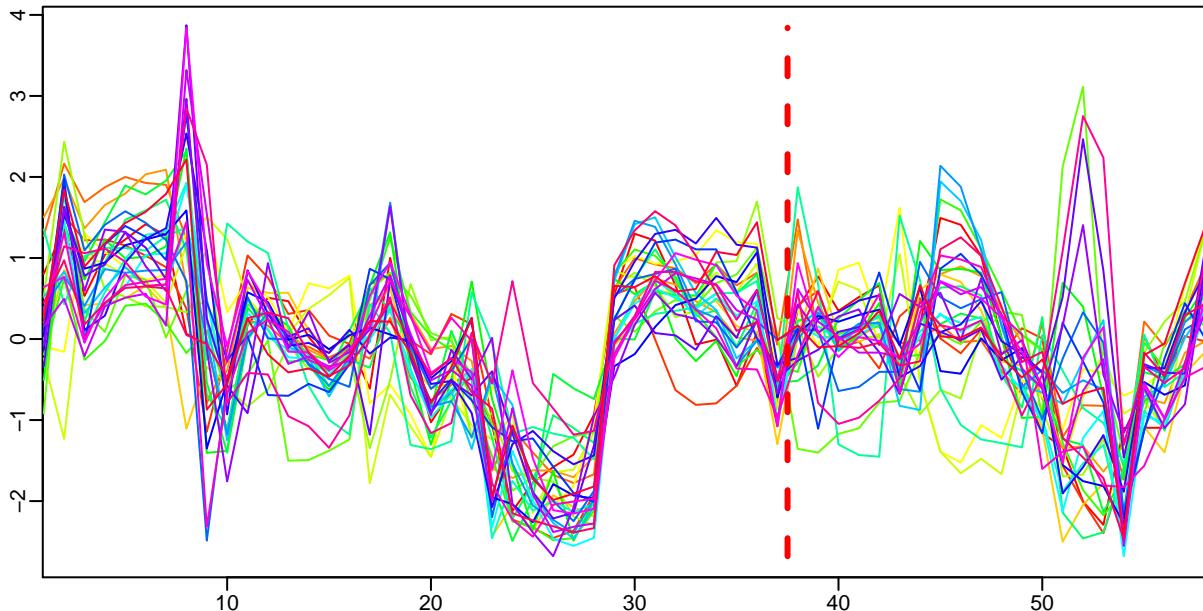11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

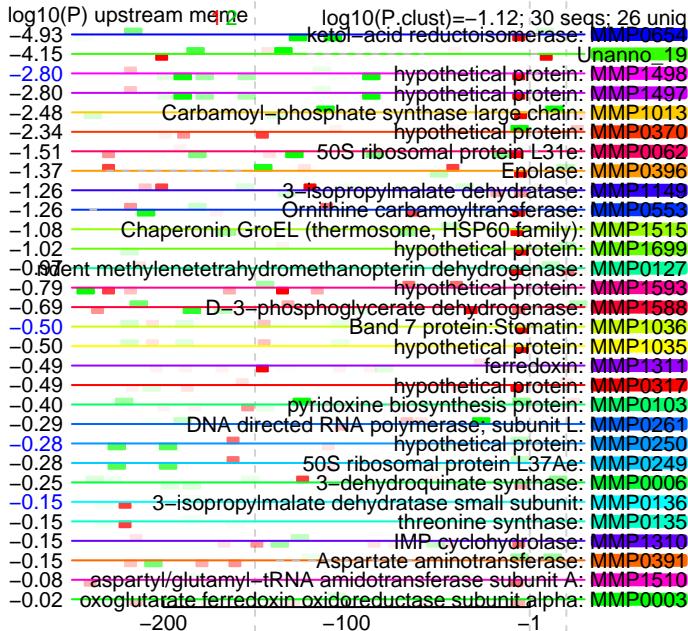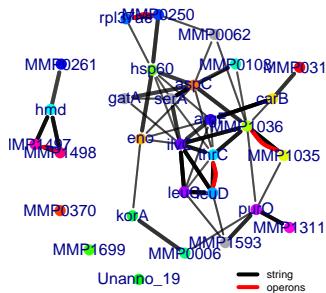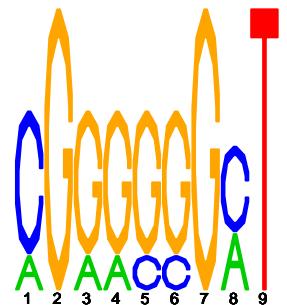upstream meme PSSM #1; e=350   upstream meme PSSM #2; e=1.4e+03

log10(P) upstream meme   log10(P.clust)=−2.44; 17 seqs; 15 uniq

−4.65	cation transport ATPase: MMP0520
−4.32	protein methionine−S−oxide reductase: MMP0848
−4.14	cobalt−precorrin−6Y C(5)−methyltransferase: MMP1227
−4.07	Phage integrase: MMP0456
−3.45	hypothetical protein: MMP0691
−3.18	Unanno_13
−2.97	hypothetical protein protein: possibly conserved: MMP0313
−2.97	hypothetical protein: MMP0311
−2.97	hypothetical protein: MMP0312
−2.93	hypothetical protein: MMP0678
−2.41	hypothetical protein: MMP1387
−1.83	hypothetical protein: MMP0128
−1.18	hypothetical protein: MMP0182
−0.18	hypothetical protein: MMP1683
−0.13	Unanno_30
−0.07	Family of unknown function ThiJ/PfpI: MMP0559
−0.06	hypothetical protein: MMP0976

Cluster: 0074 mmp; resid: 0.17; r/c: 15/40
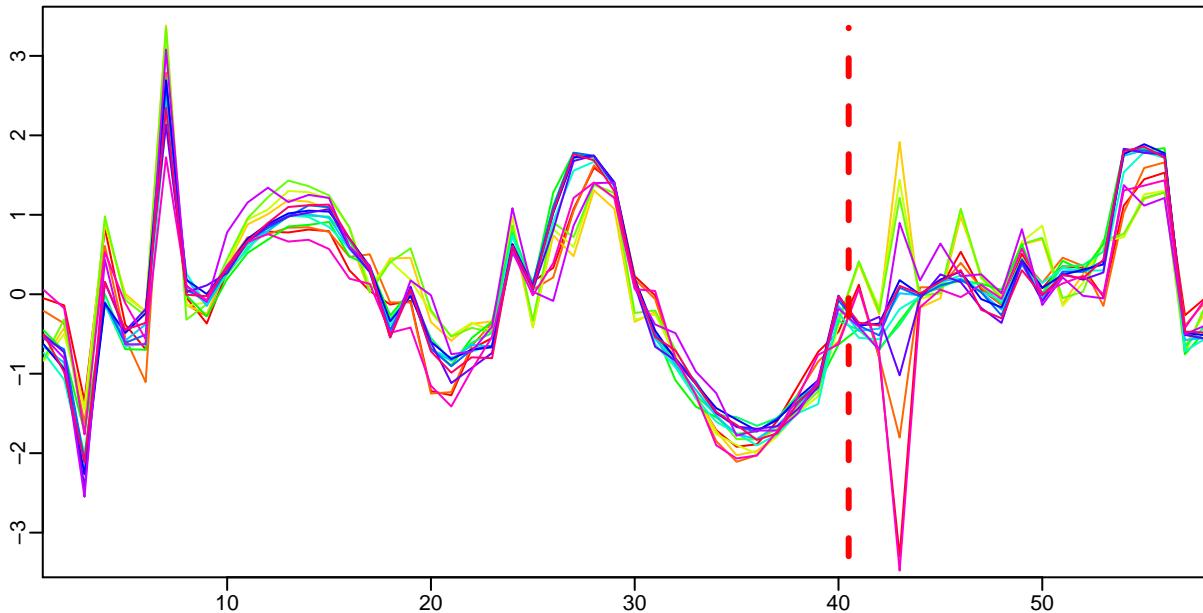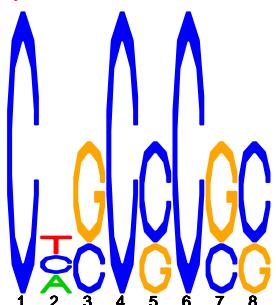
upstream meme PSSM #1; e=9   upstream meme PSSM #2; e=180
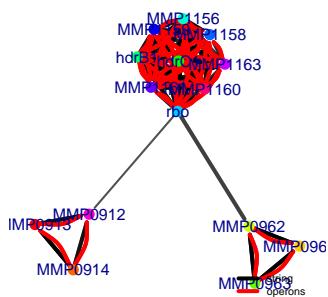
log10(P) upstream meme   log10(P.clust)=−2.76; 15 seqs; 3 uniq

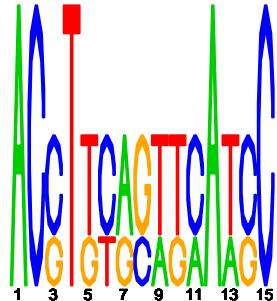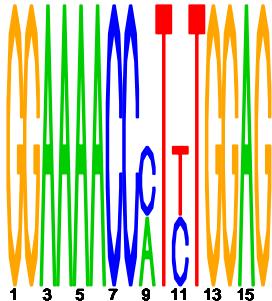| log10(P)	Protein	Gene
−4.90	tautomerase related protein:	MMP0912
−4.90	hypothetical protein:	MMP0914
−4.90	hypothetical protein:	MMP0913
−3.19	aquaporin related:	MMP0963
−3.19	zinc finger protein:	MMP0962
−3.19	hypothetical protein:	MMP0961
−1.90	hypothetical protein:	MMP1160
−1.90	CutA1 divalent ion tolerance protein Related Protein:	MMP1163
−1.90	hypothetical protein:	MMP1161
−1.90	Ferritin:	MMP1159
−1.90	hypothetical protein:	MMP1158
−1.90	Desulfoferrodoxin, ferrous iron−binding site:	MMP1157
−1.90	hypothetical protein:	MMP1156
−1.90	heterosulfide reductase, subunit B1:	MMP1155
−1.90	heterosulfide reductase, subunit C1:	MMP1154

Cluster: 0075 mmp; resid: 0.32; r/c: 25/39

11 Oct 11 16:14:07 iter=2000
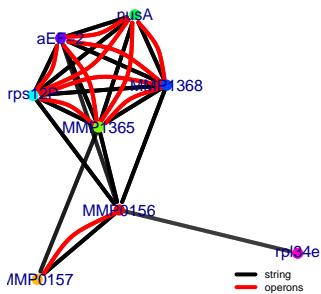cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=0.97 upstream meme PSSM #2; e=7.1e+03

log10(P) upstream meme   log10(P.clust)=−1.82; 25 seqs; 19 uniq

log10(P)	annotation	gene
−5.80	inc metallopeptidase, zinc−binding region:CBS domain:	MMP0453
−4.16	glucose−6−phosphate isomerase:	MMP1295
−3.68	hypothetical protein:	MMP0452
−3.34	hypothetical protein:	MMP0458
−2.74	ABC transporter:ATPase subunit:	MMP0635
−2.68	hypothetical protein:	MMP0909
−2.27	Flavodoxin:Beta−lactamase−like:	MMP1162
−2.27	Lhr−like RNA helicase:	MMP1141
−2.13	hypothetical protein:	MMP0595
−1.88	Biotin−−protein ligase:	MMP0119
−1.81	glycogen phosphorylase:	MMP1220
−1.60	hypothetical protein:	MMP0113
−1.34	putative DNA primase large subunit:	MMP0009
−1.34	DNA polymerase II small subunit:	MMP0008
−1.28	Phosphoribosylamine−−glycine ligase:	MMP0392
−1.10	putative integral membrane protein:	MMP0725
−1.08	hypothetical protein:	MMP0636
−0.79	hypothetical protein:	MMP0241
−0.79	hypothetical protein:	MMP0239
−0.79	hypothetical protein:	MMP0240
−0.79	hypothetical protein:	MMP0237
−0.79	hypothetical protein:	MMP0236
−0.79	hypothetical protein:	MMP0235
−0.30	hypothetical protein:	MMP0723
−0.00	hypothetical protein:	MMP0934

Cluster: 0076 mmp; resid: 0.23; r/c: 19/37

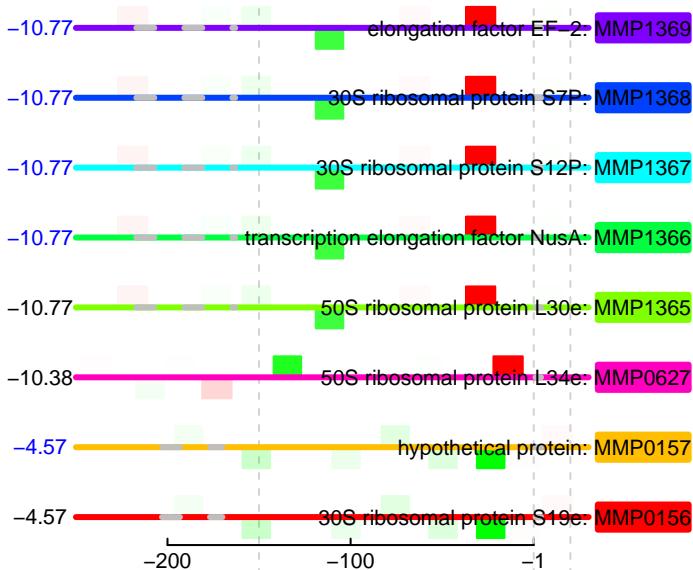11 Oct 11 16:14:07 iter=2000 cMonkey Version 4.8.8 mmp

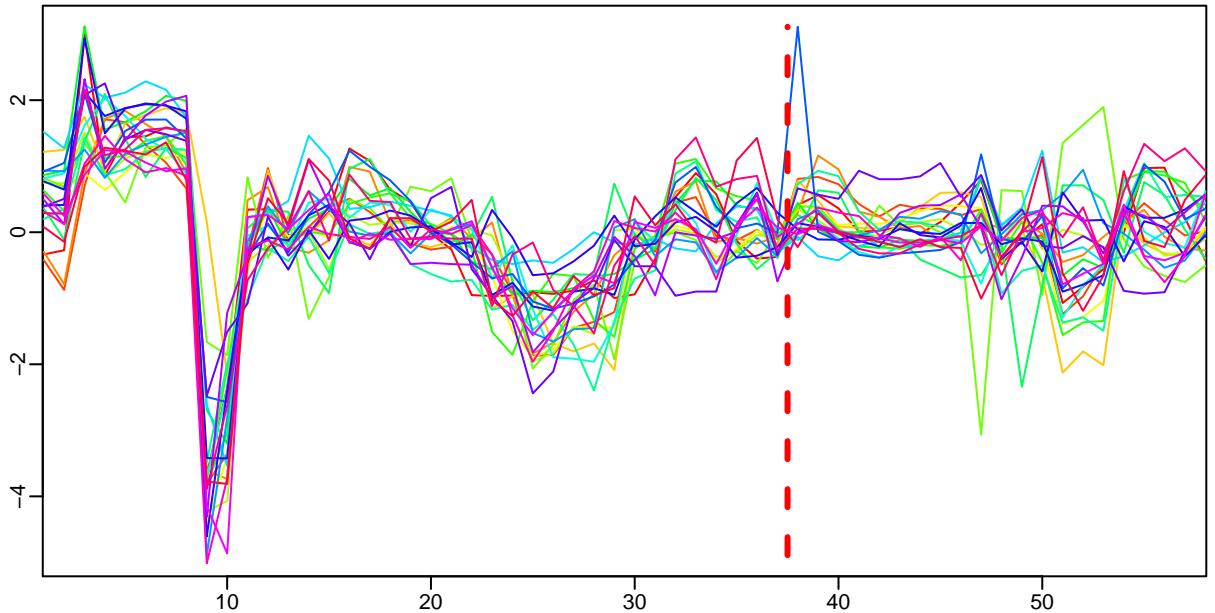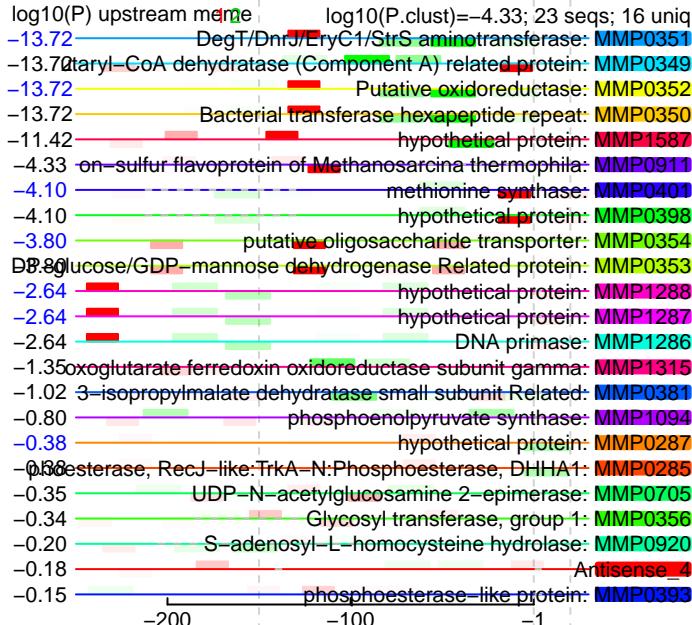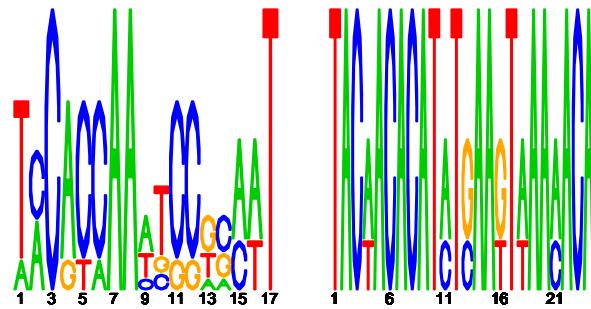upstream meme PSSM #1; e=440 upstream meme PSSM #2; e=6.8e+03

log10(P) upstream meme   log10(P.clust)=−1.58; 19 seqs; 12 uniq

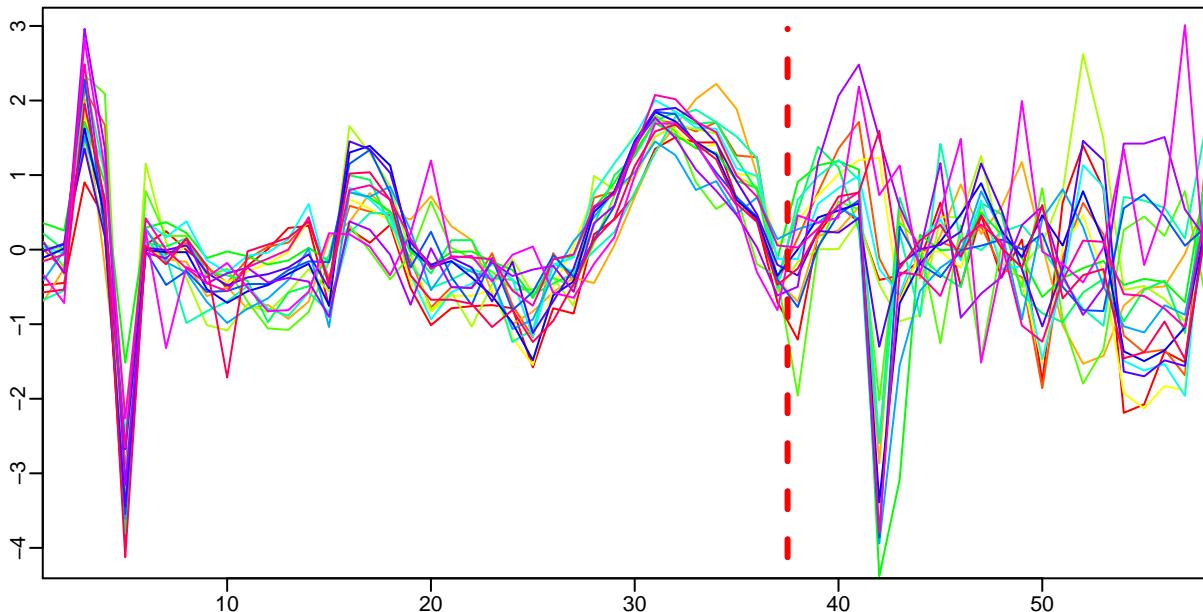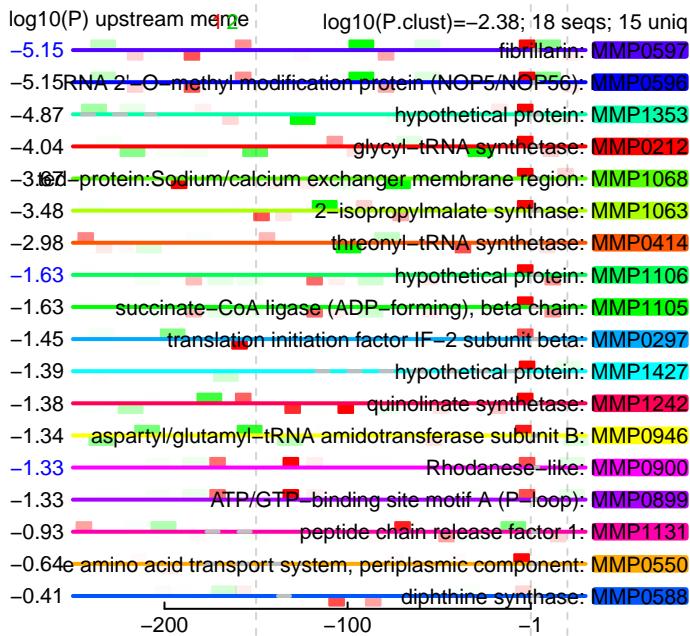| log10(P)	description	gene
−4.68	hypothetical protein:	MMP0527
−2.74	hypothetical protein:	MMP0995
−2.36	Trk system potassium uptake protein A:	MMP1599
−2.17		Unanno_55
−1.58	ferrous iron transporter (GTP−binding):	MMP0630
−1.51	indole−3−glycerol−phosphate synthase:	MMP1008
−1.51	Anthranilate phosphoribosyltransferase:	MMP1007
−1.51	anthranilate synthase component I:	MMP1006
−1.51	anthranilate synthase component II:	MMP1005
−1.51	N−(5'−phosphoribosyl)anthranilate isomerase:	MMP1004
−1.51	tryptophan synthase subunit beta:	MMP1003
−1.51	tryptophan synthase subunit alpha:	MMP1002
−1.34	hypothetical protein:	MMP1598
−1.16	L−seryl−tRNA selenium transferase related protein:	MMP0002
−1.09	hypothetical protein:	MMP0269
−0.71	hypothetical protein:	MMP0055
−0.71	hypothetical protein:	MMP0054
−0.67	hypothetical protein:	MMP0678
−0.27	TPR repeat:ATP/GTP−binding site motif A (P−loop):	MMP0885

Cluster: 0077 mmp; resid: 0.40; r/c: 30/37

upstream meme PSSM #1; e=87

upstream meme PSSM #2; e=69

log10(P) upstream meme   log10(P.clust)=−1.12; 30 seqs; 26 uniq

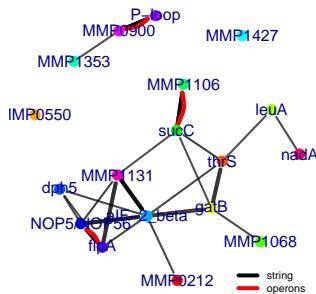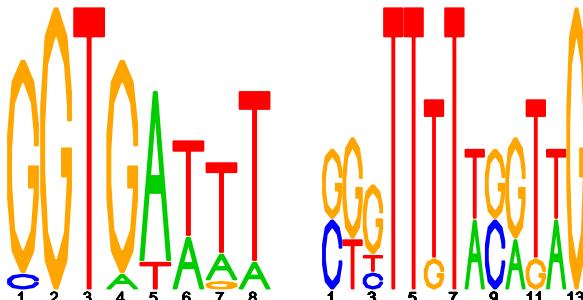| log10(P)	Annotation	Gene
−4.93	ketol−acid reductoisomerase:	MMP0654
−4.15	Unanno_19	
−2.80	hypothetical protein:	MMP1498
−2.80	hypothetical protein:	MMP1497
−2.48	Carbamoyl−phosphate synthase large chain:	MMP1013
−2.34	hypothetical protein:	MMP0370
−1.51	50S ribosomal protein L31e:	MMP0062
−1.37	Enolase:	MMP0396
−1.26	3−isopropylmalate dehydratase:	MMP1149
−1.26	Ornithine carbamoyltransferase:	MMP0553
−1.08	Chaperonin GroEL (thermosome, HSP60 family):	MMP1515
−1.02	hypothetical protein:	MMP1699
−0.97	dependent methylenetetrahydromethanopterin dehydrogenase:	MMP0127
−0.79	hypothetical protein:	MMP1593
−0.69	D−3−phosphoglycerate dehydrogenase:	MMP1588
−0.50	Band 7 protein:Stomatin:	MMP1036
−0.50	hypothetical protein:	MMP1035
−0.49	ferredoxin:	MMP1311
−0.49	hypothetical protein:	MMP0317
−0.40	pyridoxine biosynthesis protein:	MMP0103
−0.29	DNA directed RNA polymerase, subunit L:	MMP0261
−0.28	hypothetical protein:	MMP0250
−0.28	50S ribosomal protein L37Ae:	MMP0249
−0.25	3−dehydroquinate synthase:	MMP0006
−0.15	3−isopropylmalate dehydratase small subunit:	MMP0136
−0.15	threonine synthase:	MMP0135
−0.15	IMP cyclohydrolase:	MMP1310
−0.15	Aspartate aminotransferase:	MMP0391
−0.08	aspartyl/glutamyl−tRNA amidotransferase subunit A:	MMP1510
−0.02	oxoglutarate ferredoxin oxidoreductase subunit alpha:	MMP0003

Cluster: 0078 mmp; resid: 0.39; r/c: 27/38

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cMonkey Version 4.8.8 mmp
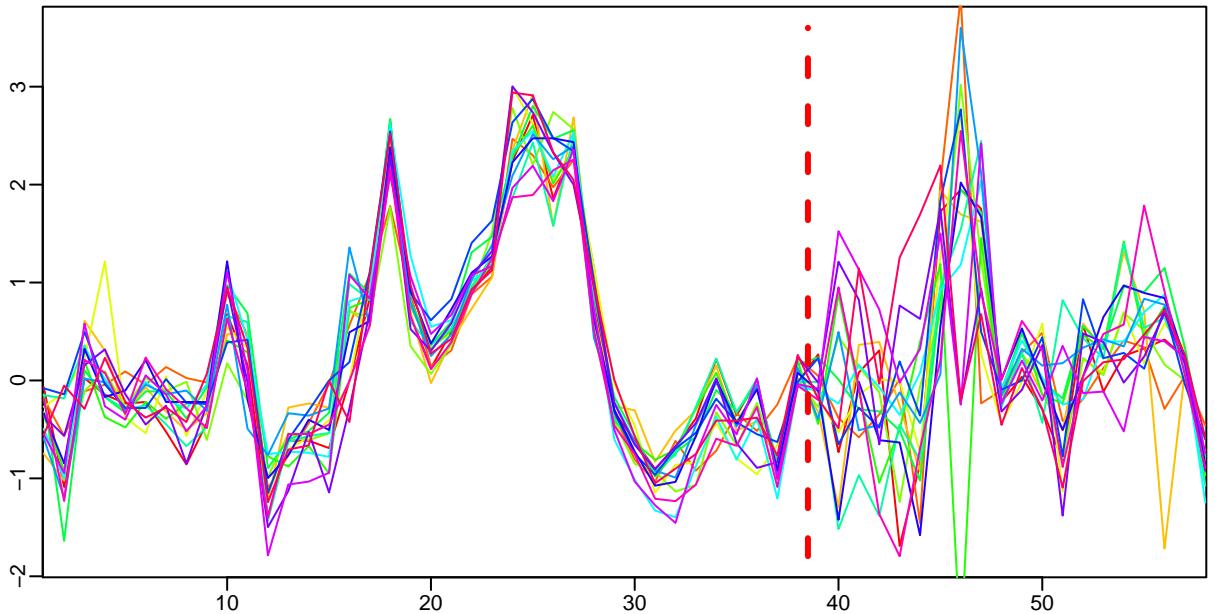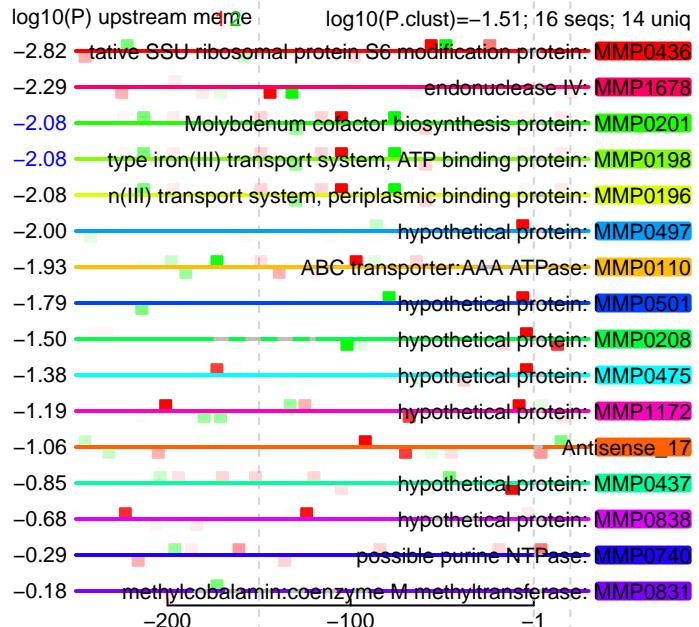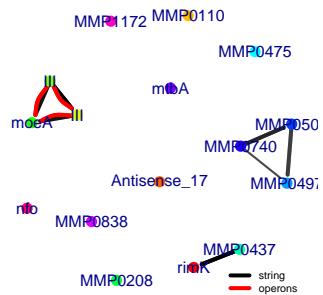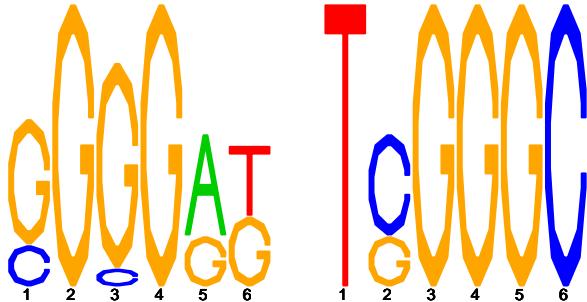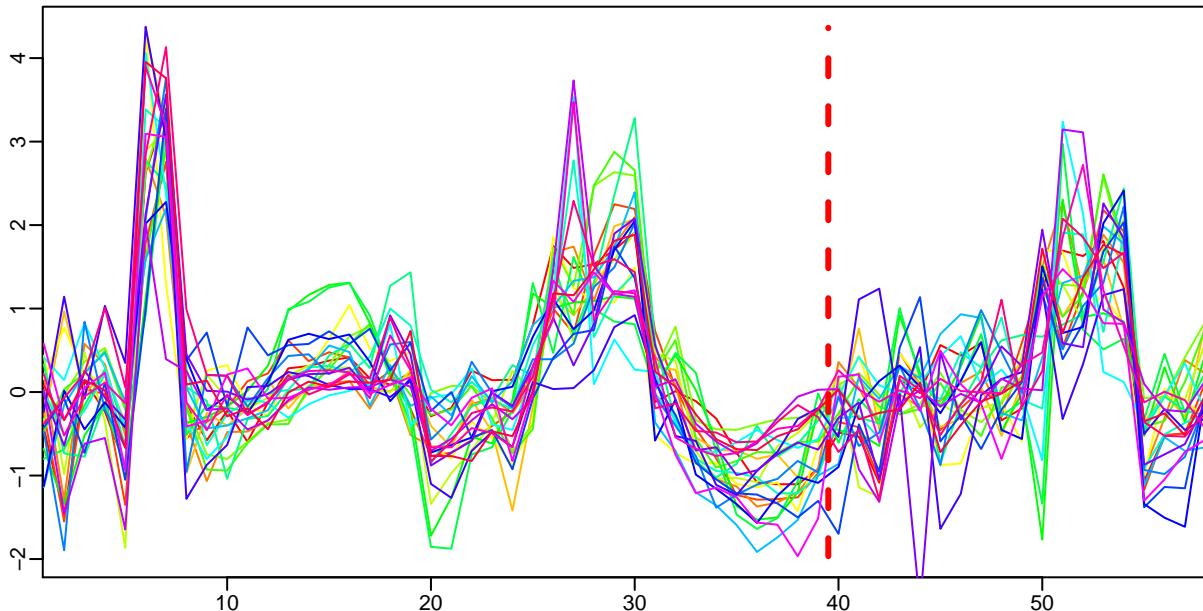
upstream meme PSSM #1; e=1.3   upstream meme PSSM #2; e=950

log10(P) upstream meme   log10(P.clust)=−3.27; 27 seqs; 23 uniq

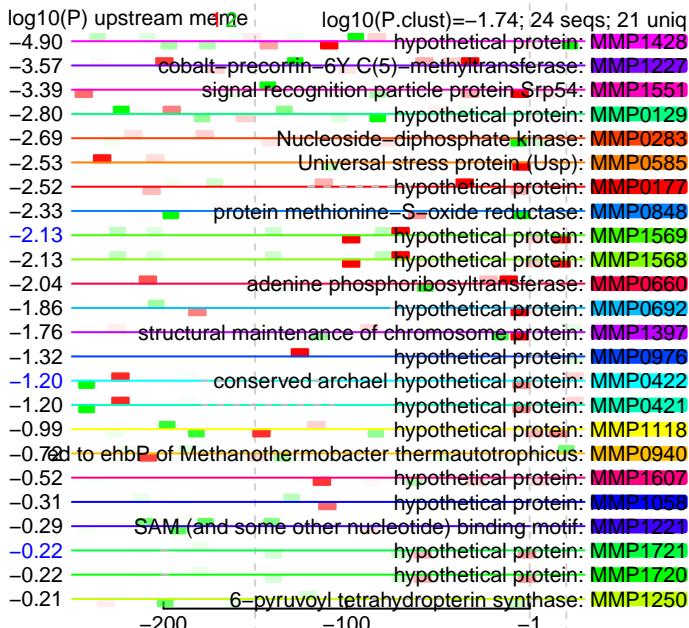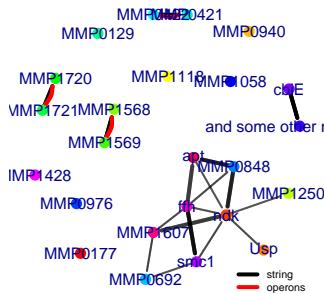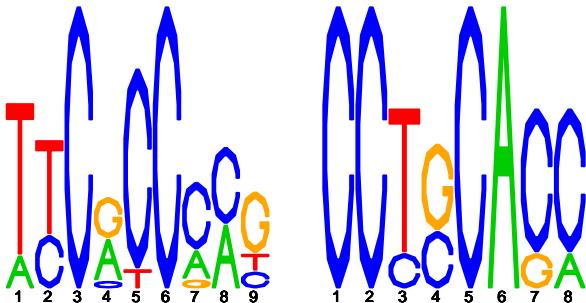| log10(P)	Annotation	Gene
−10.89	thiamine–phosphate pyrophosphorylase:	MMP1139
−10.89	hydroxyethylthiazole kinase:	MMP1138
−10.89	like Transcriptional regulatory proteins, AsnC family:	MMP1137
−5.23	intracellular sulfur reduction related protein:	MMP0309
−5.23	hypothetical protein:	MMP0308
−4.96	nascent polypeptide–associated complex protein:	MMP0290
−4.44	Transcriptional regulator, TetR Family Member:	MMP1023
−4.28	Iron–sulfur flavoprotein–related:	MMP0500
−4.02		Unanno_33
−3.89	hypothetical protein:	MMP0355
−3.72	Enolase:	MMP0396
−3.43	ribose–phosphate pyrophosphokinase:	MMP0410
−3.13		Unanno_8
−2.98	isoleucyl–tRNA synthetase related:	MMP0377
−1.73	ParA type ATPase:	MMP0704
−1.60	Glycosyl transferase, family 2:	MMP0359
−1.19	putative ATPase RIL:	MMP0382
−1.06	carbamoyl phosphate synthase small subunit:	MMP1589
−0.84	hypothetical protein:	MMP0400
−0.84	Peptidase family M48:	MMP0399
−0.84	alanyl–tRNA synthetase:	MMP0397
−0.83	peptidyl–prolyl cis–trans isomerase, cyclophilin type:	MMP1129
−0.46	endoglucanase:	MMP1116
−0.35	Aspartate aminotransferase:	MMP0391
−0.29	putative thiazole biosynthetic enzyme:	MMP1352
−0.25	3–isopropylmalate dehydratase small subunit Related:	MMP0381
−0.06	uridylate kinase:	MMP0385

Cluster: 0079 mmp; resid: 0.08; r/c: 8/39

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upstream meme PSSM #1; e=340   upstream meme PSSM #2; e=1.2e+03

log10(P) upstream meme

log10(P.clust)=−9.17; 8 seqs; 3 uniq

−10.77	elongation factor EF−2:	MMP1369
−10.77	30S ribosomal protein S7P:	MMP1368
−10.77	30S ribosomal protein S12P:	MMP1367
−10.77	transcription elongation factor NusA:	MMP1366
−10.77	50S ribosomal protein L30e:	MMP1365
−10.38	50S ribosomal protein L34e:	MMP0627
−4.57	hypothetical protein:	MMP0157
−4.57	30S ribosomal protein S19e:	MMP0156

string
operons

Cluster: 0080 mmp; resid: 0.35; r/c: 23/37

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=18   **upstream meme PSSM #2; e=1.1e+03**

log10(P) upstream meme   log10(P.clust)=−4.33; 23 seqs; 16 uniq

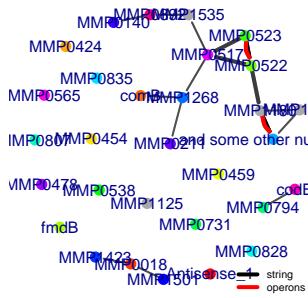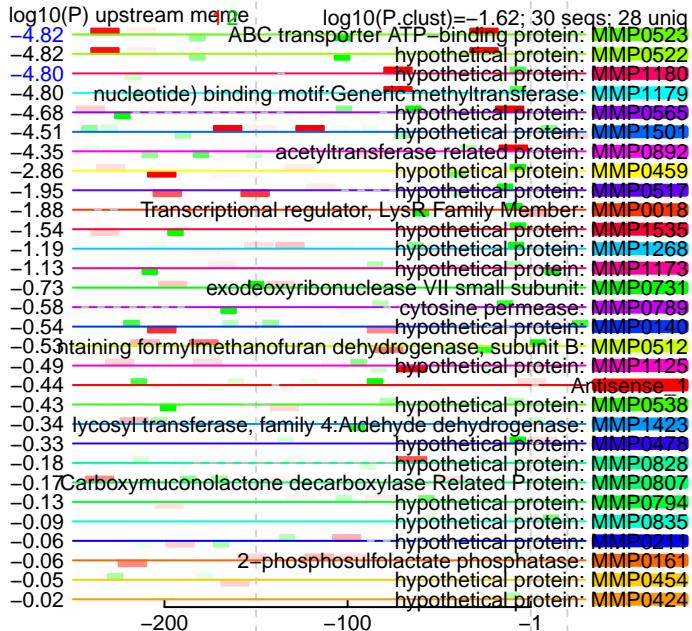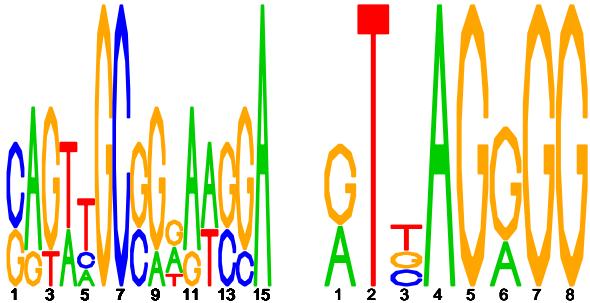| log10(P)	Protein
−13.72	DegT/DnrJ/EryC1/StrS aminotransferase: MMP0351
−13.72	Glutaryl−CoA dehydratase (Component A) related protein: MMP0349
−13.72	Putative oxidoreductase: MMP0352
−13.72	Bacterial transferase hexapeptide repeat: MMP0350
−11.42	hypothetical protein: MMP1587
−4.33	Iron−sulfur flavoprotein of Methanosarcina thermophila: MMP0911
−4.10	methionine synthase: MMP0401
−4.10	hypothetical protein: MMP0398
−3.80	putative oligosaccharide transporter: MMP0354
−3.80	UDP−glucose/GDP−mannose dehydrogenase Related protein: MMP0353
−2.64	hypothetical protein: MMP1288
−2.64	hypothetical protein: MMP1287
−2.64	DNA primase: MMP1286
−1.35	oxoglutarate ferredoxin oxidoreductase subunit gamma: MMP1315
−1.02	3−isopropylmalate dehydratase small subunit Related: MMP0381
−0.80	phosphoenolpyruvate synthase: MMP1094
−0.38	hypothetical protein: MMP0287
−0.38	phosphoesterase, RecJ−like:TrkA−N:Phosphoesterase, DHHA1: MMP0285
−0.35	UDP−N−acetylglucosamine 2−epimerase: MMP0705
−0.34	Glycosyl transferase, group 1: MMP0356
−0.20	S−adenosyl−L−homocysteine hydrolase: MMP0920
−0.18	Antisense_4
−0.15	phosphoesterase−like protein: MMP0393

Cluster: 0081 mmp; resid: 0.26; r/c: 18/37

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cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=0.64 **upstream meme PSSM #2; e=1.9e+04**

log10(P) upstream meme   log10(P.clust)=−2.38; 18 seqs; 15 uniq

−5.15	fibrillarin: MMP0597
−5.15	RNA 2'−O−methyl modification protein (NOP5/NOP56): MMP0596
−4.87	hypothetical protein: MMP1353
−4.04	glycyl−tRNA synthetase: MMP0212
−3.87	ted−protein:Sodium/calcium exchanger membrane region: MMP1068
−3.48	2−isopropylmalate synthase: MMP1063
−2.98	threonyl−tRNA synthetase: MMP0414
−1.63	hypothetical protein: MMP1106
−1.63	succinate−CoA ligase (ADP−forming), beta chain: MMP1105
−1.45	translation initiation factor IF−2 subunit beta: MMP0297
−1.39	hypothetical protein: MMP1427
−1.38	quinolinate synthetase: MMP1242
−1.34	aspartyl/glutamyl−tRNA amidotransferase subunit B: MMP0946
−1.33	Rhodanese−like: MMP0900
−1.33	ATP/GTP−binding site motif A (P−loop): MMP0899
−0.93	peptide chain release factor 1: MMP1131
−0.64	e amino acid transport system, periplasmic component: MMP0550
−0.41	diphthine synthase: MMP0588

Cluster: 0082 mmp; resid: 0.19; r/c: 16/38
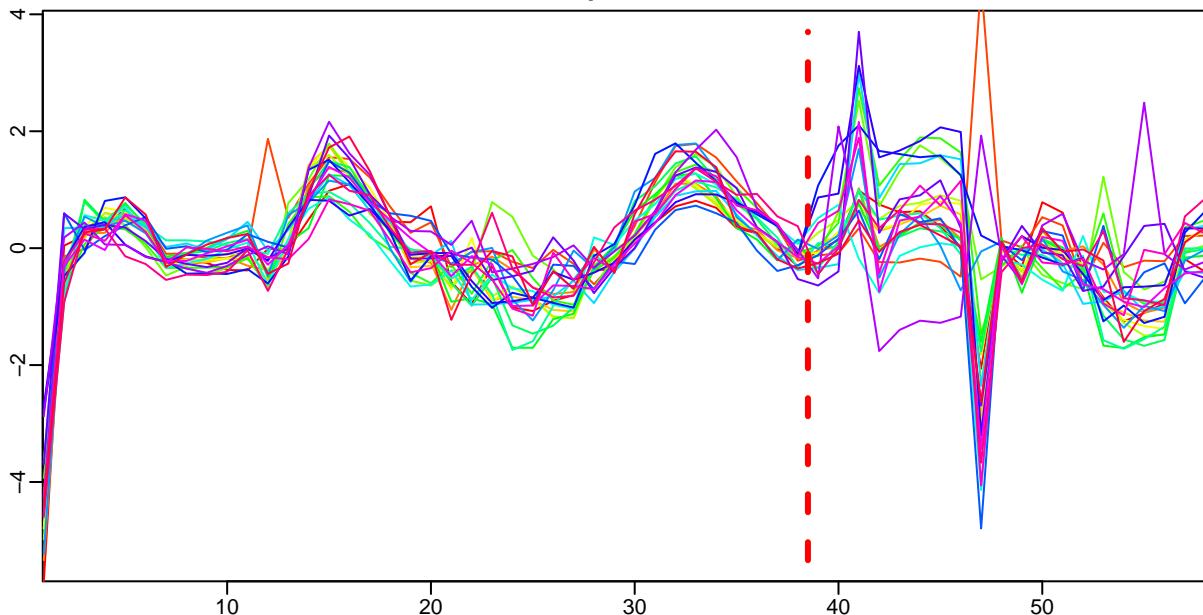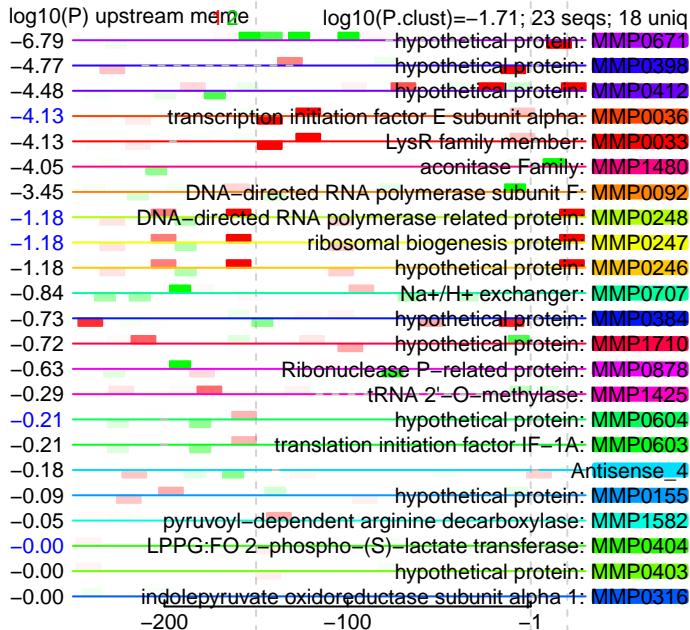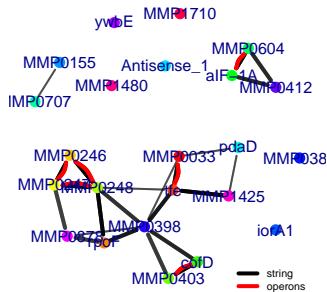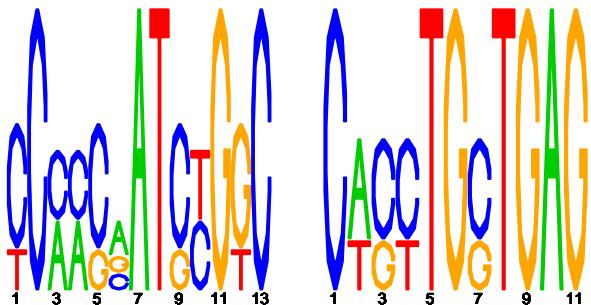
11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=0.0027   upstream meme PSSM #2; e=4.3e+03

log10(P) upstream meme   log10(P.clust)=−1.51; 16 seqs; 14 uniq

log10(P)	description	gene
−2.82	tative SSU ribosomal protein S6 modification protein:	MMP0436
−2.29	endonuclease IV:	MMP1678
−2.08	Molybdenum cofactor biosynthesis protein:	MMP0201
−2.08	type iron(III) transport system, ATP binding protein:	MMP0198
−2.08	n(III) transport system, periplasmic binding protein:	MMP0196
−2.00	hypothetical protein:	MMP0497
−1.93	ABC transporter:AAA ATPase:	MMP0110
−1.79	hypothetical protein:	MMP0501
−1.50	hypothetical protein:	MMP0208
−1.38	hypothetical protein:	MMP0475
−1.19	hypothetical protein:	MMP1172
−1.06		Antisense_17
−0.85	hypothetical protein:	MMP0437
−0.68	hypothetical protein:	MMP0838
−0.29	possible purine NTPase:	MMP0740
−0.18	methylcobalamin:coenzyme M methyltransferase:	MMP0831

Cluster: 0083 mmp; resid: 0.36; r/c: 24/39

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cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=6.9   **upstream meme PSSM #2; e=190**
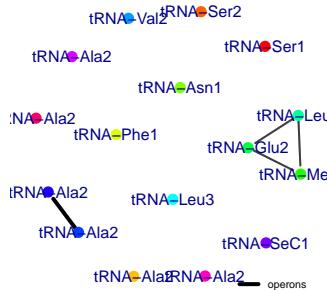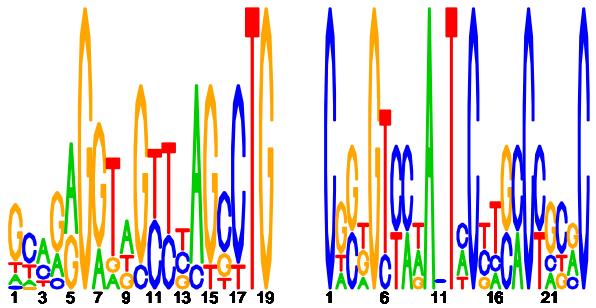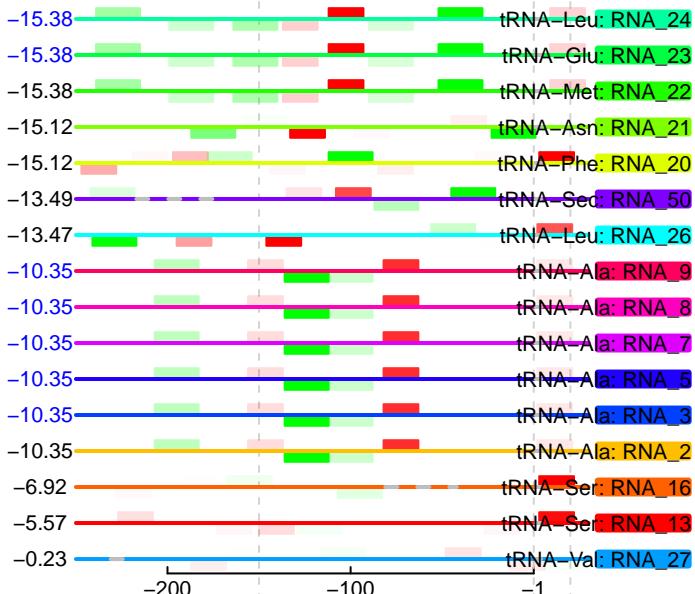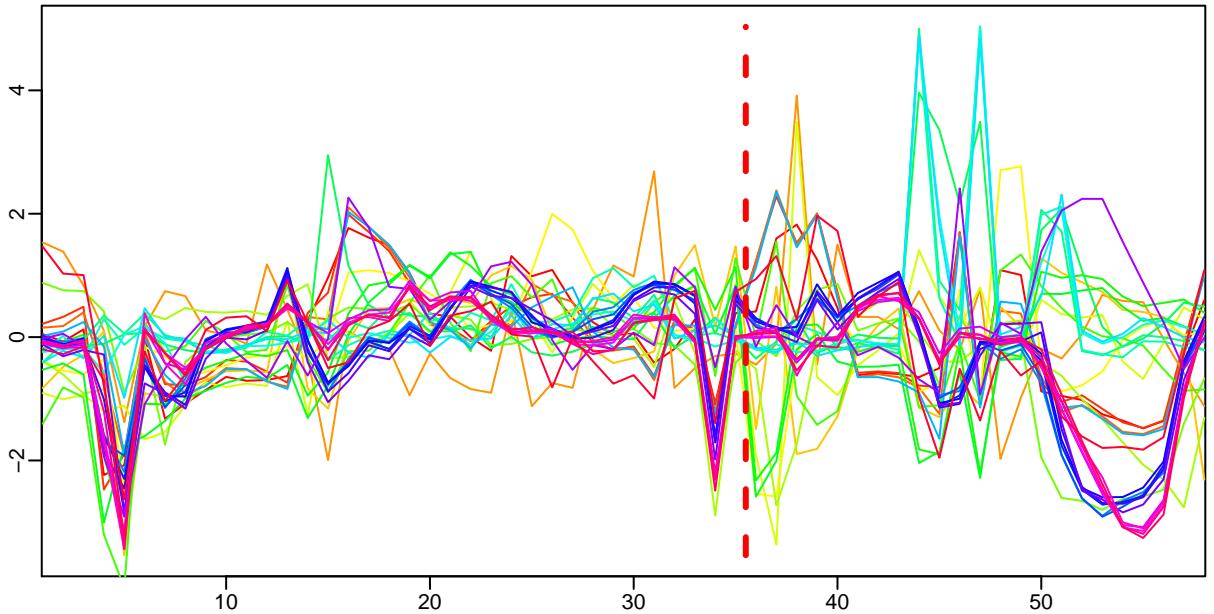
log10(P) upstream meme   log10(P.clust)=−1.74; 24 seqs; 21 uniq

log10(P)	Annotation
−4.90	hypothetical protein: MMP1428
−3.57	cobalt−precorrin−6Y C(5)−methyltransferase: MMP1227
−3.39	signal recognition particle protein Srp54: MMP1551
−2.80	hypothetical protein: MMP0129
−2.69	Nucleoside−diphosphate kinase: MMP0283
−2.53	Universal stress protein (Usp): MMP0585
−2.52	hypothetical protein: MMP0177
−2.33	protein methionine−S−oxide reductase: MMP0848
−2.13	hypothetical protein: MMP1569
−2.13	hypothetical protein: MMP1568
−2.04	adenine phosphoribosyltransferase: MMP0660
−1.86	hypothetical protein: MMP0692
−1.76	structural maintenance of chromosome protein: MMP1397
−1.32	hypothetical protein: MMP0976
−1.20	conserved archaeal hypothetical protein: MMP0422
−1.20	hypothetical protein: MMP0421
−0.99	hypothetical protein: MMP1118
−0.78	related to ehbP of Methanothermobacter thermautotrophicus: MMP0940
−0.52	hypothetical protein: MMP1607
−0.31	hypothetical protein: MMP1058
−0.29	SAM (and some other nucleotide) binding motif: MMP1227
−0.22	hypothetical protein: MMP1721
−0.22	hypothetical protein: MMP1720
−0.21	6−pyruvoyl tetrahydropterin synthase: MMP1250

Cluster: 0084 mmp; resid: 0.11; r/c: 10/39

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp
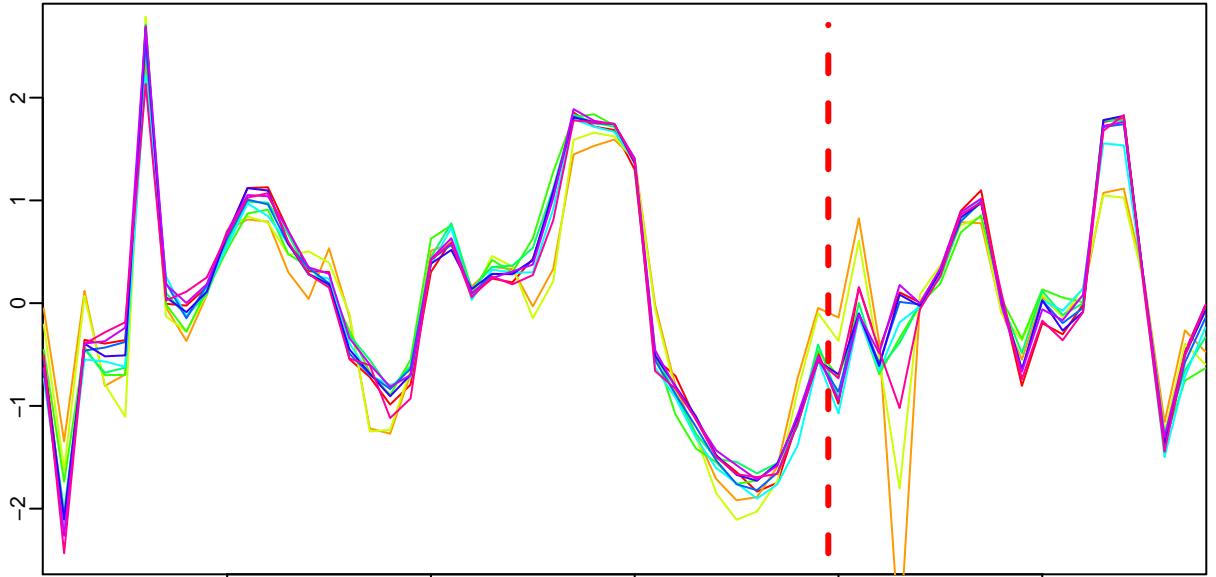
hypothetical protein: MMP0913

hypothetical protein: MMP0914

heterosulfide reductase, subunit C1: MMP1154

heterosulfide reductase, subunit B1: MMP1155

hypothetical protein: MMP1156

Desulfoferrodoxin, ferrous iron−binding site: MMP1157

hypothetical protein: MMP1158

Ferritin: MMP1159

hypothetical protein: MMP1160

hypothetical protein: MMP1161

−200   −100   −1

sequence position

string
operons

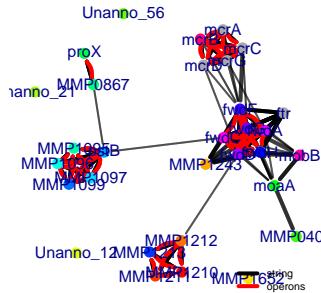**Cluster: 0085 mmp; resid: 0.38; r/c: 30/37**

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

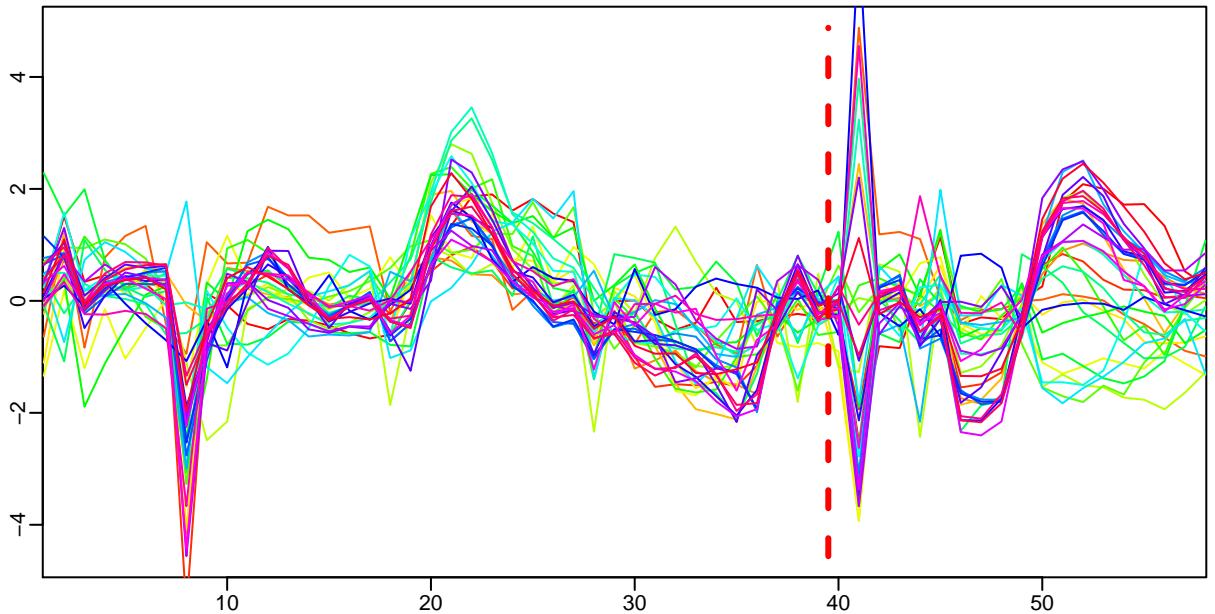upstream meme PSSM #1; e=1e+03   upstream meme PSSM #2; e=1.2e+04

log10(P) upstream meme   log10(P.clust)=−1.62; 30 seqs: 28 uniq

log10(P)	Description: Gene
−4.82	ABC transporter ATP−binding protein: MMP0523
−4.82	hypothetical protein: MMP0522
−4.80	hypothetical protein: MMP1180
−4.80	nucleotide) binding motif:Generic methyltransferase: MMP1179
−4.68	hypothetical protein: MMP0565
−4.51	hypothetical protein: MMP1501
−4.35	acetyltransferase related protein: MMP0892
−2.86	hypothetical protein: MMP0459
−1.95	hypothetical protein: MMP0517
−1.88	Transcriptional regulator, LysR Family Member: MMP0018
−1.54	hypothetical protein: MMP1535
−1.19	hypothetical protein: MMP1268
−1.13	hypothetical protein: MMP1173
−0.73	exodeoxyribonuclease VII small subunit: MMP0731
−0.58	cytosine permease: MMP0789
−0.54	hypothetical protein: MMP0140
−0.53	containing formylmethanofuran dehydrogenase, subunit B: MMP0512
−0.49	hypothetical protein: MMP1125
−0.44	Antisense 1
−0.43	hypothetical protein: MMP0538
−0.34	glycosyl transferase, family 4:Aldehyde dehydrogenase: MMP1423
−0.33	hypothetical protein: MMP0478
−0.18	hypothetical protein: MMP0828
−0.17	Carboxymuconolactone decarboxylase Related Protein: MMP0807
−0.13	hypothetical protein: MMP0794
−0.09	hypothetical protein: MMP0835
−0.06	hypothetical protein: MMP0211
−0.06	2−phosphosulfolactate phosphatase: MMP0161
−0.05	hypothetical protein: MMP0454
−0.02	hypothetical protein: MMP0424

Cluster: 0086 mmp; resid: 0.27; r/c: 19/38

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upstream meme PSSM #1; e=0.23   upstream meme PSSM #2; e=700

log10(P) upstream meme   log10(P.clust)=−2.64; 19 seqs; 14 uniq

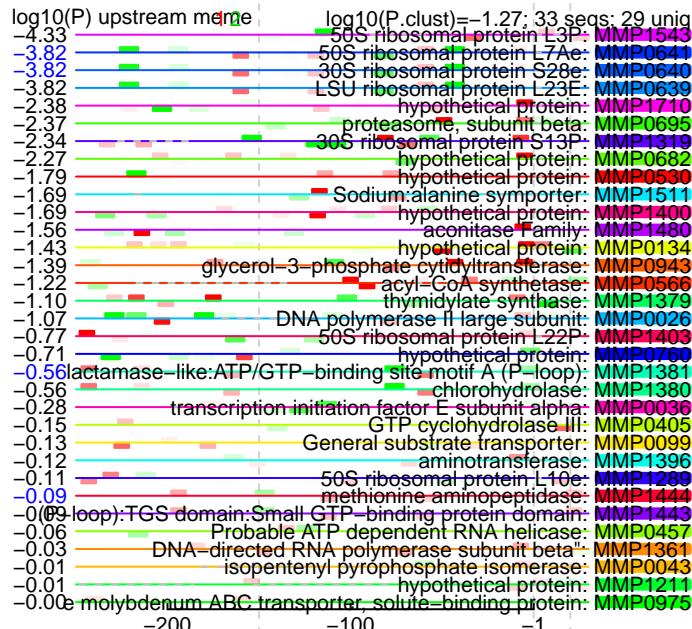| log10(P)	Annotation
−8.47	Unanno_4
−8.47	Unanno_2
−5.42	hypothetical protein: MMP0910
−2.90	hypothetical protein: MMP0815
−2.90	hypothetical protein: MMP0814
−2.47	pyruvate carboxylase subunit A: MMP0341
−2.42	coenzyme F390 synthetase: MMP0160
−2.41	pyruvate carboxylase subunit B: MMP0340
−2.39	hypothetical protein: MMP0287
−2.39	...esterase, RecJ−like:TrkA−N:Phosphoesterase, DHHA1: MMP0285
−2.19	Na+/H+ exchanger family: MMP0100
−1.75	coenzyme F390 synthetase II: MMP0715
−1.75	indolepyruvate oxidoreductase subunit B: MMP0714
−1.75	indolepyruvate oxidoreductase subunit alpha 2: MMP0713
−1.57	...eptidyl−prolyl cis−trans isomerase, cyclophilin type: MMP1128
−0.61	hydroorotate dehydrogenase electron transfer subunit: MMP0919
−0.20	Glycosyl transferase, family 2: MMP0590
−0.11	DNA repair and recombination protein RadA: MMP1222
−0.00	hypothetical protein: MMP1196

string
operons

Cluster: 0087 mmp; resid: 0.23; r/c: 23/38

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=360   upstream meme PSSM #2; e=3.8e+03

log10(P) upstream meme   log10(P.clust)=−1.71; 23 seqs; 18 uniq

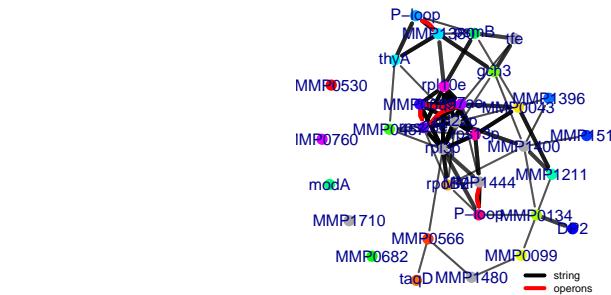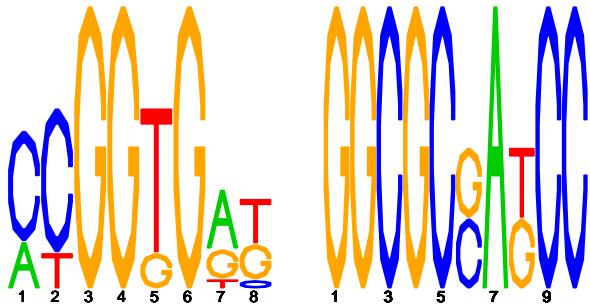| log10(P)	Annotation	Gene
−6.79	hypothetical protein:	MMP0671
−4.77	hypothetical protein:	MMP0398
−4.48	hypothetical protein:	MMP0412
−4.13	transcription initiation factor E subunit alpha:	MMP0036
−4.13	LysR family member:	MMP0033
−4.05	aconitase Family:	MMP1480
−3.45	DNA−directed RNA polymerase subunit F:	MMP0092
−1.18	DNA−directed RNA polymerase related protein:	MMP0248
−1.18	ribosomal biogenesis protein:	MMP0247
−1.18	hypothetical protein:	MMP0246
−0.84	Na+/H+ exchanger:	MMP0707
−0.73	hypothetical protein:	MMP0384
−0.72	hypothetical protein:	MMP1710
−0.63	Ribonuclease P−related protein:	MMP0878
−0.29	tRNA 2'−O−methylase:	MMP1425
−0.21	hypothetical protein:	MMP0604
−0.21	translation initiation factor IF−1A:	MMP0603
−0.18		Antisense_4
−0.09	hypothetical protein:	MMP0155
−0.05	pyruvoyl−dependent arginine decarboxylase:	MMP1582
−0.00	LPPG:FO 2−phospho−(S)−lactate transferase:	MMP0404
−0.00	hypothetical protein:	MMP0403
−0.00	indolepyruvate oxidoreductase subunit alpha 1:	MMP0316

Cluster: 0088 mmp; resid: 0.21; r/c: 16/39

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cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=9.9e-10   upstream meme PSSM #2; e=5.8e-05

log10(P) upstream meme

log10(P.clust)=-11.13; 16 seqs; 9 uniq

log10(P)	tRNA	RNA
-15.38	tRNA-Leu	RNA_24
-15.38	tRNA-Glu	RNA_23
-15.38	tRNA-Met	RNA_22
-15.12	tRNA-Asn	RNA_21
-15.12	tRNA-Phe	RNA_20
-13.49	tRNA-Sec	RNA_50
-13.47	tRNA-Leu	RNA_26
-10.35	tRNA-Ala	RNA_9
-10.35	tRNA-Ala	RNA_8
-10.35	tRNA-Ala	RNA_7
-10.35	tRNA-Ala	RNA_5
-10.35	tRNA-Ala	RNA_3
-10.35	tRNA-Ala	RNA_2
-6.92	tRNA-Ser	RNA_16
-5.57	tRNA-Ser	RNA_13
-0.23	tRNA-Val	RNA_27

tRNA-Val2 tRNA-Ser2
tRNA-Ala2   tRNA-Ser1
tRNA-Asn1
NA-Ala2 tRNA-Phe1 tRNA-Leu
tRNA-Glu2
tRNA-Me
tRNA-Ala2 tRNA-Leu3
tRNA-Ala2
tRNA-SeC1
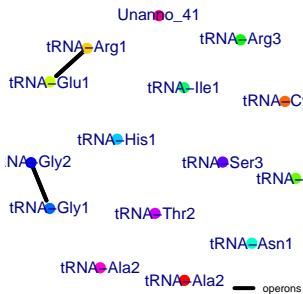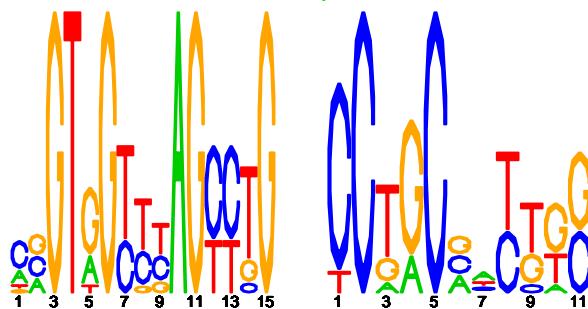tRNA-Ala2 tRNA-Ala2   operons

-200   -100   -1
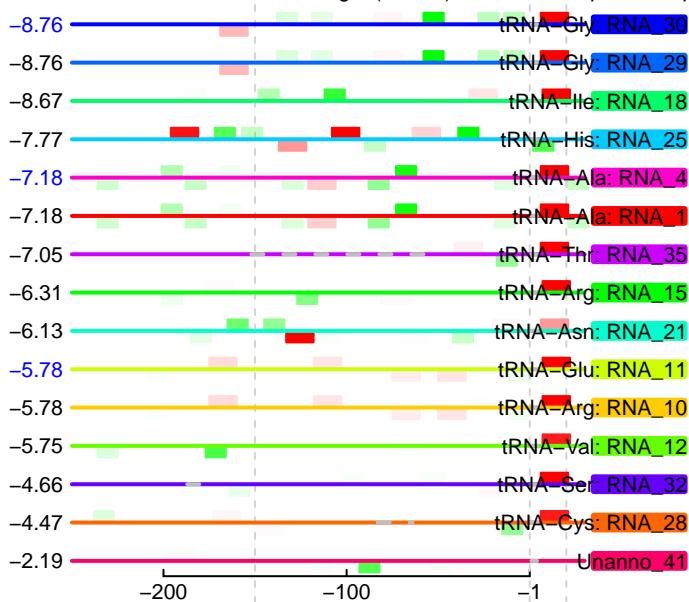
Cluster: 0089 mmp; resid: 0.42; r/c: 31/35

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cMonkey Version 4.8.8 mmp

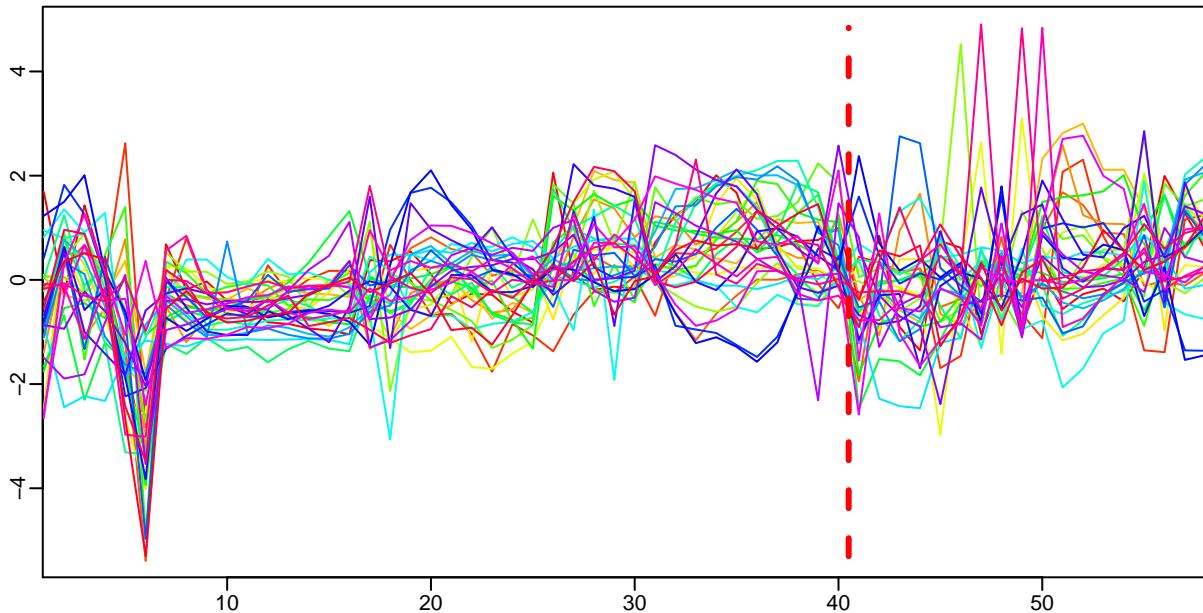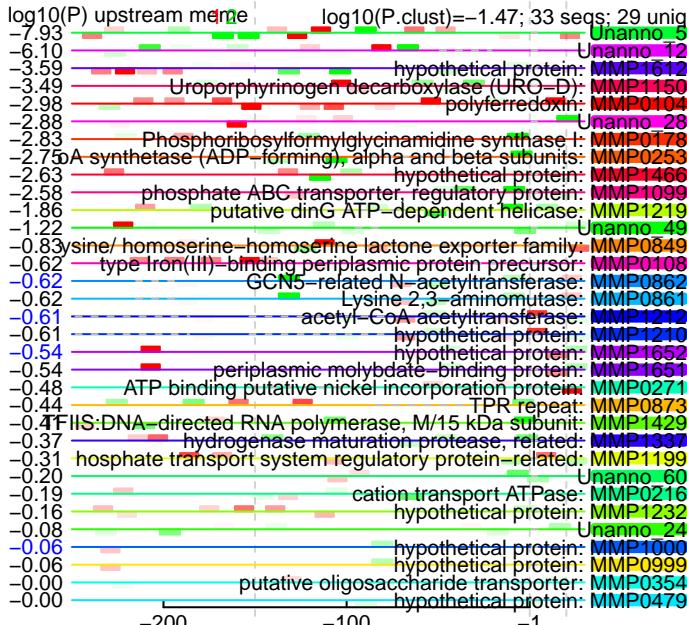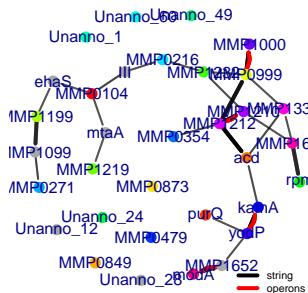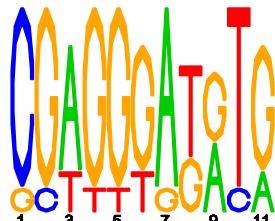upstream meme PSSM #1; e=2.3e−08   upstream meme PSSM #2; e=700
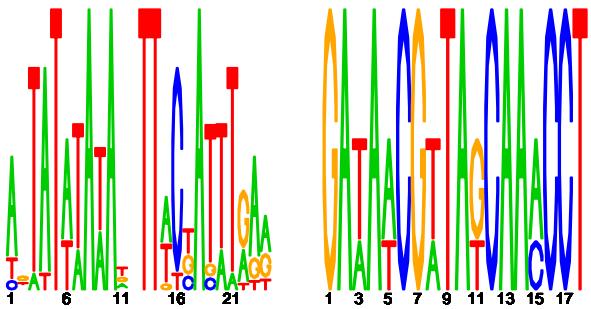
log10(P) upstream meme   log10(P.clust)=−6.97; 31 seqs: 14 uniq

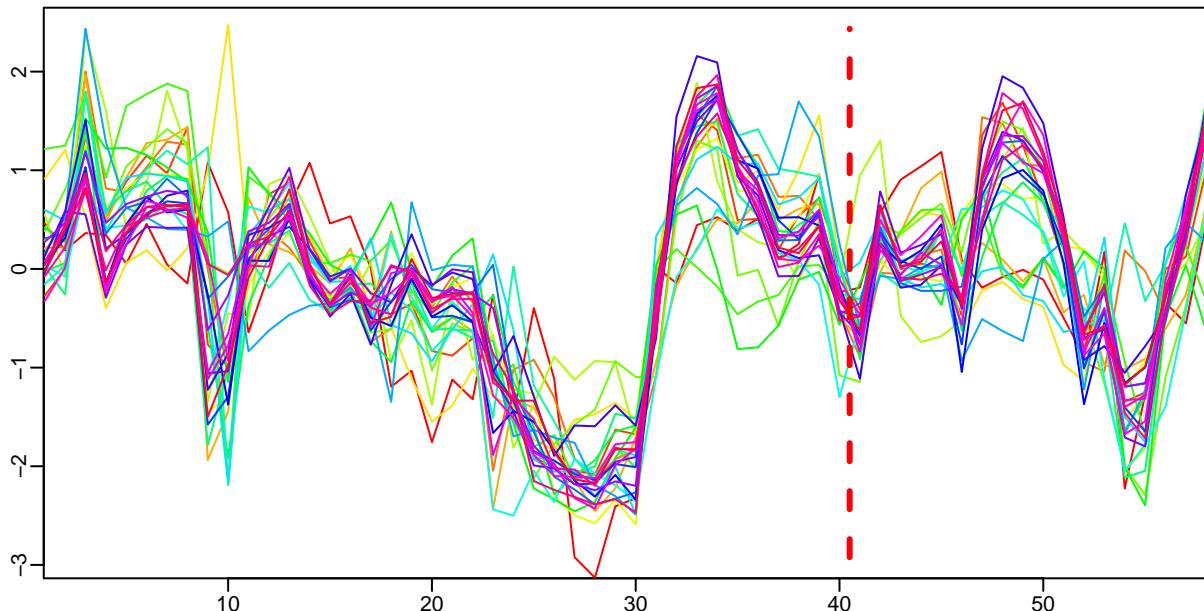| log10(P)	annotation	gene
−15.56	staining formylmethanofuran dehydrogenase, subunit C:	MMP1249
−15.56	staining formylmethanofuran dehydrogenase, subunit A:	MMP1248
−15.56	staining formylmethanofuran dehydrogenase, subunit D:	MMP1247
−15.56	staining formylmethanofuran dehydrogenase, subunit G:	MMP1246
−15.56	staining formylmethanofuran dehydrogenase, subunit F:	MMP1245
−15.56	staining formylmethanofuran dehydrogenase, subunit H:	MMP1244
−15.53	hypothetical protein:	MMP1243
−8.08	Methyl−coenzyme M reductase I, alpha subunit:	MMP1559
−8.08	Methyl−coenzyme M reductase I, gamma subunit:	MMP1558
−8.08	methyl coenzyme M reductase I, protein C:	MMP1557
−8.08	Methyl−coenzyme M reductase I, protein D:	MMP1556
−8.08	Methyl−coenzyme M reductase I, beta subunit:	MMP1555
−6.67	hypothetical protein:	MMP0407
−5.59		Unanno_12
−4.07	molybdenum cofactor biosynthesis protein A:	MMP0571
−4.00	phosphate ABC transporter, regulatory protein:	MMP1099
−4.00	phosphate ABC transporter, ATP−binding protein:	MMP1098
−4.00	dependent transport systems inner membrane component:	MMP1097
−4.00	dependent transport systems inner membrane component:	MMP1096
−4.00	Phosphate−binding protein:	MMP1095
−3.48		Unanno_56
−3.48	hypothetical protein:	MMP1213
−3.48	acetyl−CoA acetyltransferase:	MMP1212
−3.48	hypothetical protein:	MMP1211
−3.48	hypothetical protein:	MMP1210
−3.09	hypothetical protein:	MMP1652
−2.85		Unanno_21
−2.84	ybdopterin−guanine dinucleotide biosynthesis protein:	MMP1441
−2.40	tetrahydromethanopterin formyltransferase:	MMP1609
−0.97	transport system, permease component related protein:	MMP0867
−0.97	ne/L−proline ABC transporter, solute−binding protein:	MMP0866

Cluster: 0090 mmp; resid: 0.45; r/c: 33/37

upstream meme PSSM #1; e=3.5

upstream meme PSSM #2; e=340

log10(P) upstream meme

log10(P.clust)=−1.98; 33 seqs: 26 uniq

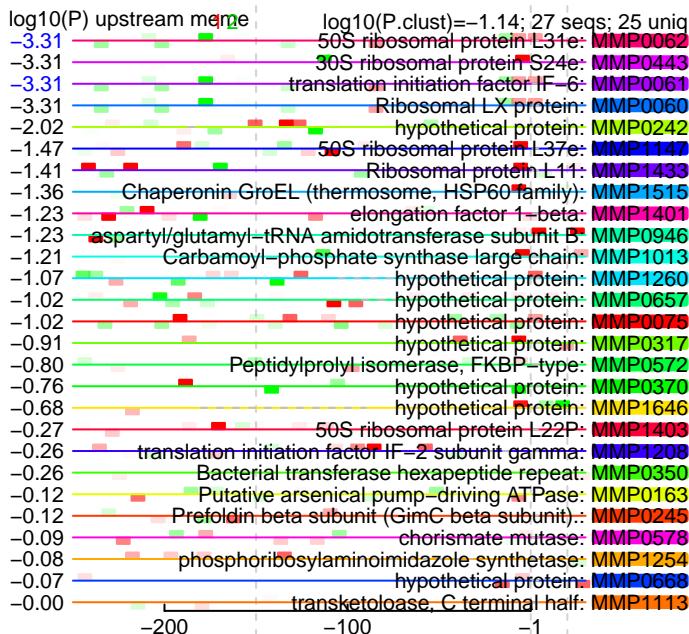| log10(P)	Annotation	Gene
−8.13	Phosphoribosyl−AMP cyclohydrolase:	MMP0280
−8.13	beta−ribofuranosylaminobenzene 5'−phosphate synthase:	MMP0279
−8.13	hypothetical protein:	MMP0278
−8.13	TraB family:	MMP0277
−6.50	N6 adenine−specific DNA methyltransferase, D12 class:	MMP0735
−3.25	Unanno_62	
−2.43	Blue (type 1) copper domain:	MMP0997
−2.43	hypothetical protein:	MMP0996
−2.35	Nitroreductase family:	MMP1553
−2.11	putative transcriptional regulator:	MMP1100
−2.01	hypothetical protein:	MMP0434
−1.94	hypothetical protein:	MMP0533
−1.79	signal transduction systems periplasmic component−related:	MMP1224
−1.67	Unanno_52	
−0.74	Homoserine kinase:	MMP0295
−0.69	putative integral membrane protein:	MMP0725
−0.64	Antisense_24	
−0.62	Unanno_42	
−0.55	MoaA/nifB/pqqE family:	MMP0658
−0.54	hypothetical protein:	MMP1633
−0.45	hypothetical protein:	MMP0321
−0.42	hypothetical protein:	MMP0344
−0.34	heavy−metal transport ATPase related protein:	MMP1164
−0.34	E2 type:Heavy metal transport/detoxification protein:	MMP1165
−0.26	Transcriptional regulator, TetR Family Member:	MMP0791
−0.19	ADP−ribosylglycohydrolase (draG) homolog:	MMP0622
−0.11	flavoprotein related protein:	MMP1167
−0.11	iron−sulfur flavoprotein of Methanosarcina thermophila:	MMP1166
−0.11	hypothetical protein:	MMP0477
−0.11	hypothetical protein:	MMP0476
−0.02	hypothetical protein:	MMP0302
−0.01	excinuclease ABC subunit A:	MMP0729
−0.01	excinuclease ABC subunit C:	MMP0728

Cluster: 0091 mmp; resid: 0.08; r/c: 8/36

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30S ribosomal protein S19e: MMP0156

hypothetical protein: MMP0157

hypothetical protein: MMP0158

50S ribosomal protein L30e: MMP1365

transcription elongation factor NusA: MMP1366

30S ribosomal protein S12P: MMP1367

30S ribosomal protein S7P: MMP1368

elongation factor EF-2: MMP1369

−200   −100   −1

sequence position

Cluster: 0092 mmp; resid: 0.41; r/c: 33/39
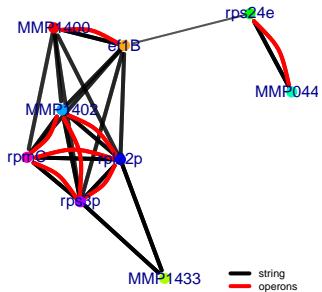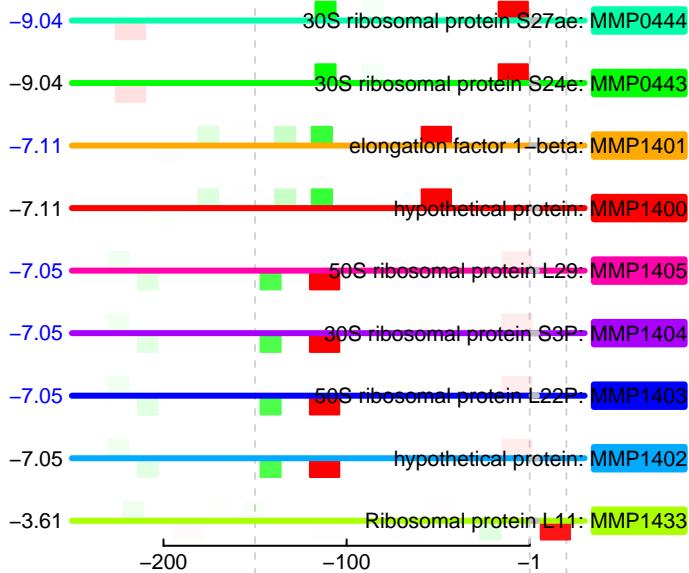
11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

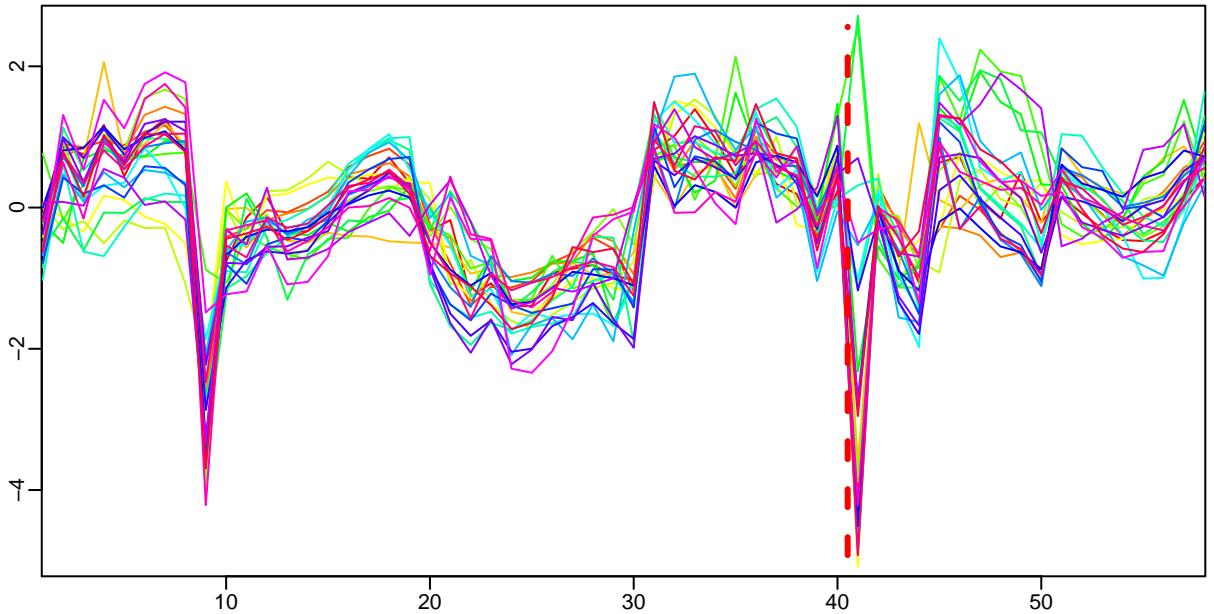upstream meme PSSM #1; e=390   upstream meme PSSM #2; e=3.3e+03

log10(P) upstream meme   log10(P.clust)=−1.27; 33 seqs; 29 uniq

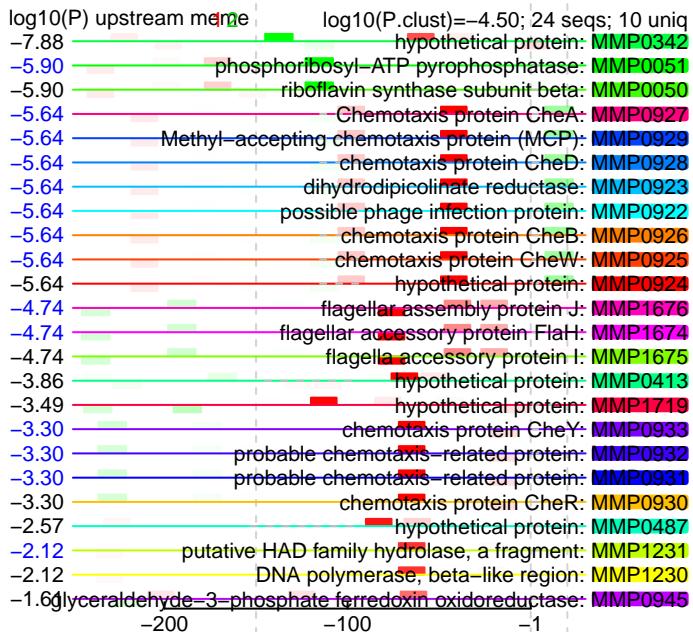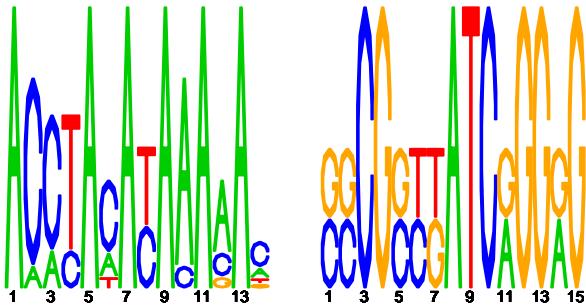| log10(P)	Annotation	Gene
−4.33	50S ribosomal protein L3P	MMP1543
−3.82	50S ribosomal protein L7Ae	MMP0641
−3.82	30S ribosomal protein S28e	MMP0640
−3.82	LSU ribosomal protein L23E	MMP0639
−2.38	hypothetical protein	MMP1710
−2.37	proteasome, subunit beta	MMP0695
−2.34	30S ribosomal protein S13P	MMP1319
−2.27	hypothetical protein	MMP0682
−1.79	hypothetical protein	MMP0530
−1.69	Sodium:alanine symporter	MMP1511
−1.69	hypothetical protein	MMP1400
−1.56	aconitase family	MMP1480
−1.43	hypothetical protein	MMP0134
−1.39	glycerol−3−phosphate cytidylyltransferase	MMP0760
−1.22	acyl−CoA synthetase	MMP0566
−1.10	thymidylate synthase	MMP1379
−1.07	DNA polymerase II large subunit	MMP0026
−0.77	50S ribosomal protein L22P	MMP1403
−0.71	hypothetical protein	MMP0760
−0.56	lactamase−like:ATP/GTP−binding site motif A (P−loop)	MMP1381
−0.56	chlorohydrolase	MMP1380
−0.28	transcription initiation factor E subunit alpha	MMP0036
−0.15	GTP cyclohydrolase III	MMP0405
−0.13	General substrate transporter	MMP0099
−0.12	aminotransferase	MMP1396
−0.11	50S ribosomal protein L10e	MMP1289
−0.09	methionine aminopeptidase	MMP1444
−0.09	(P−loop):TGS domain:Small GTP−binding protein domain	MMP1443
−0.06	Probable ATP dependent RNA helicase	MMP0457
−0.03	DNA−directed RNA polymerase subunit beta"	MMP1361
−0.01	isopentenyl pyrophosphate isomerase	MMP0043
−0.01	hypothetical protein	MMP1211
−0.00	molybdenum ABC transporter, solute−binding protein	MMP0975

Cluster: 0093 mmp; resid: 0.18; r/c: 15/38

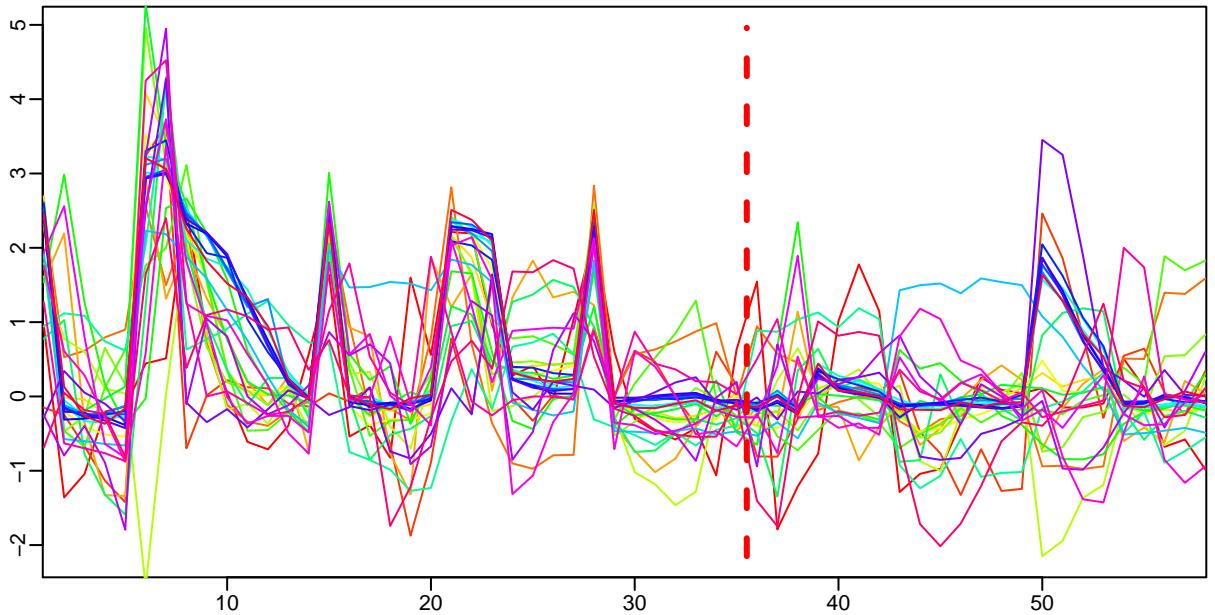**Cluster: 0094 mmp; resid: 0.25; r/c: 18/40**

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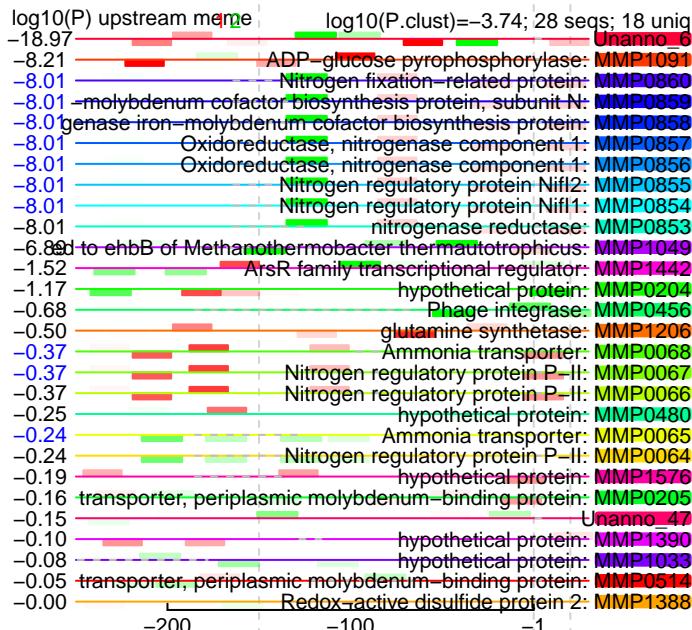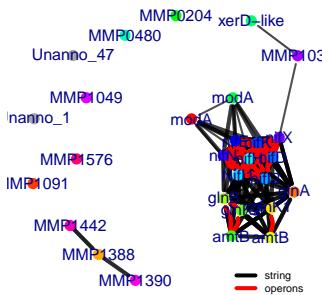
upstream meme PSSM #1; e=0.02

upstream meme PSSM #2; e=48

log10(P) upstream meme

log10(P.clust)=−4.61; 18 seqs; 15 uniq

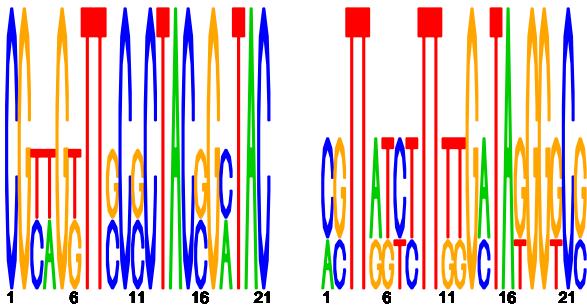| log10(P)	Annotation	Gene
−11.47	AP endonuclease, family 2:	MMP1549
−11.47	Fe−S type hydro−lyase tartrate/fumarate beta region:	MMP1548
−9.10	putative flavodoxin:	MMP0433
−9.10	hypothetical protein:	MMP0432
−9.10	Rhodopsin−like GPCR superfamily:Beta−lactamase−like:	MMP0431
−7.47	hypothetical protein:	MMP0117
−6.76	hypothetical protein:	MMP1241
−3.53	hypothetical protein:	MMP0276
−2.66	hypothetical protein:	MMP0337
−2.66	Archaeal Holliday junction resolvase:	MMP0336
−2.54	adenine phosphoribosyltransferase:	MMP0660
−2.40	hypothetical protein:	MMP0549
−2.40	Imidazoleglycerol−phosphate dehydratase:	MMP0548
−0.82	thymidine phosphorylase:	MMP0327
−0.69	hypothetical protein:	MMP0677
−0.36	Septum formation inhibitor−activating ATPase:	MMP1145
−0.20	Phosphoglucomutase/phosphomannomutase:	MMP1372
−0.19	hypothetical protein:	MMP0312

Cluster: 0095 mmp; resid: 0.56; r/c: 33/40

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upstream meme PSSM #1; e=32

upstream meme PSSM #2; e=50

log10(P) upstream meme   log10(P.clust)=−1.47; 33 seqs: 29 uniq

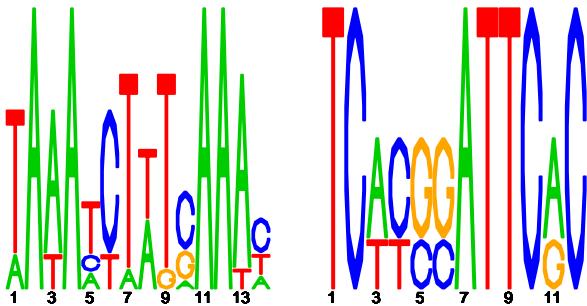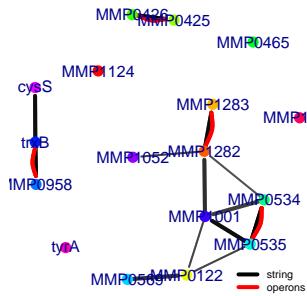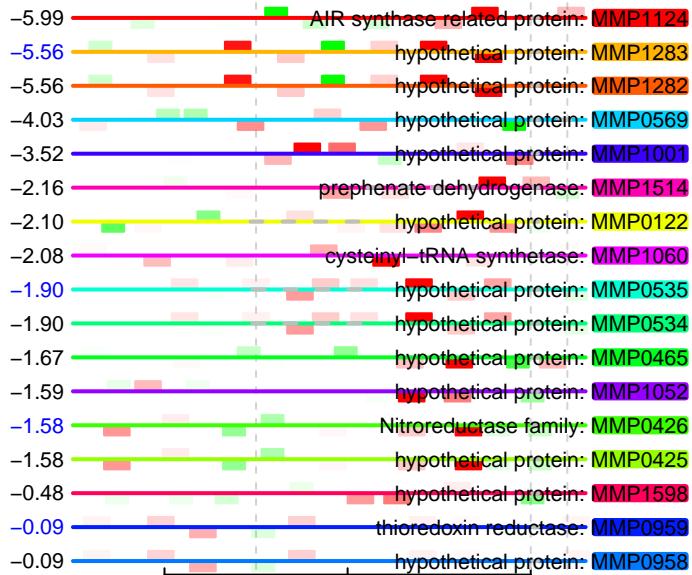| log10(P)	annotation
−7.93	Unanno_5
−6.10	Unanno_12
−3.59	hypothetical protein: MMP1612
−3.49	Uroporphyrinogen decarboxylase (URO−D): MMP1150
−2.98	polyferredoxin: MMP0104
−2.88	Unanno_28
−2.83	Phosphoribosylformylglycinamidine synthase I: MMP0178
−2.75	5A synthetase (ADP−forming), alpha and beta subunits: MMP0253
−2.63	hypothetical protein: MMP1466
−2.58	phosphate ABC transporter, regulatory protein: MMP1099
−1.86	putative dinG ATP−dependent helicase: MMP1219
−1.22	Unanno_49
−0.83	lysine/ homoserine−homoserine lactone exporter family: MMP0849
−0.62	type Iron(III)−binding periplasmic protein precursor: MMP0108
−0.62	GCN5−related N−acetyltransferase: MMP0862
−0.62	Lysine 2,3−aminomutase: MMP0861
−0.61	acetyl−CoA acetyltransferase: MMP1212
−0.61	hypothetical protein: MMP1210
−0.54	hypothetical protein: MMP1652
−0.54	periplasmic molybdate−binding protein: MMP1651
−0.48	ATP binding putative nickel incorporation protein: MMP0271
−0.44	TPR repeat: MMP0873
−0.4	TFIIS:DNA−directed RNA polymerase, M/15 kDa subunit: MMP1429
−0.37	hydrogenase maturation protease, related: MMP1337
−0.31	phosphate transport system regulatory protein−related: MMP1199
−0.20	Unanno_60
−0.19	cation transport ATPase: MMP0216
−0.16	hypothetical protein: MMP1232
−0.08	Unanno_24
−0.06	hypothetical protein: MMP1000
−0.06	hypothetical protein: MMP0999
−0.00	putative oligosaccharide transporter: MMP0354
−0.00	hypothetical protein: MMP0479

Cluster: 0096 mmp; resid: 0.31; r/c: 27/40

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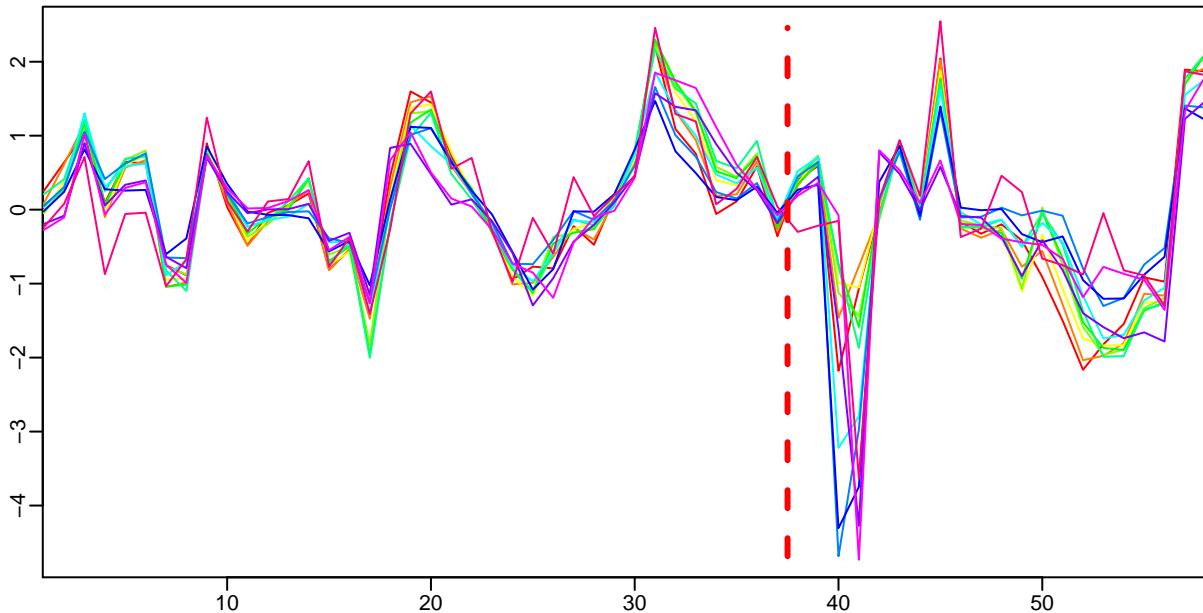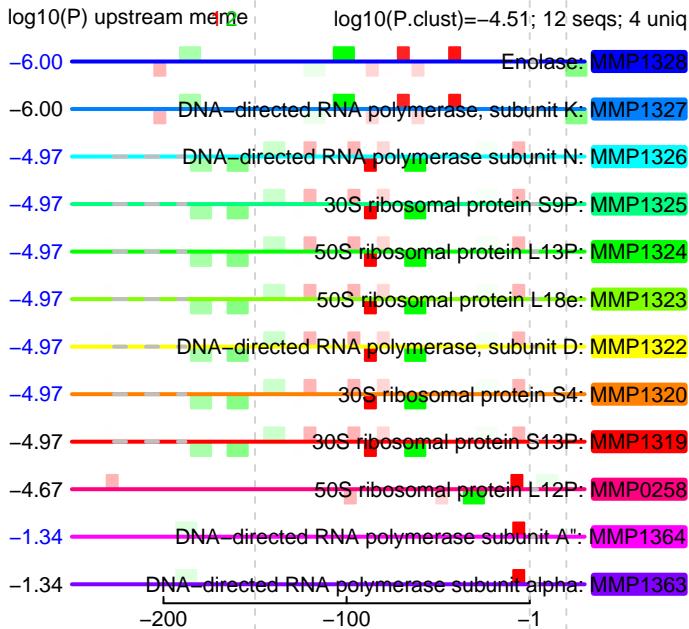upstream meme PSSM #1; e=170   upstream meme PSSM #2; e=1.6e+04

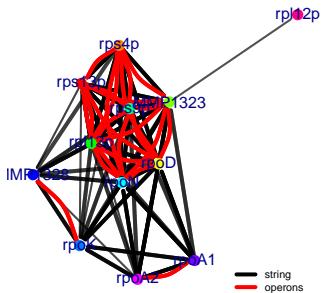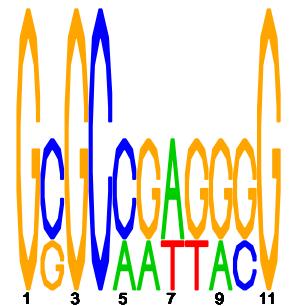log10(P) upstream meme   log10(P.clust)=−1.14; 27 seqs; 25 uniq

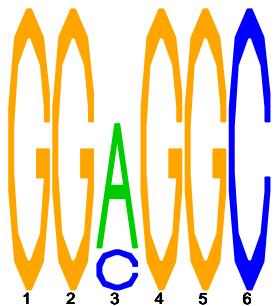| log10(P)	Description	Gene
−3.31	50S ribosomal protein L31e	MMP0062
−3.31	30S ribosomal protein S24e	MMP0443
−3.31	translation initiation factor IF−6	MMP0061
−3.31	Ribosomal LX protein	MMP0060
−2.02	hypothetical protein	MMP0242
−1.47	50S ribosomal protein L37e	MMP1147
−1.41	Ribosomal protein L11	MMP1433
−1.36	Chaperonin GroEL (thermosome, HSP60 family)	MMP1515
−1.23	elongation factor 1−beta	MMP1401
−1.23	aspartyl/glutamyl−tRNA amidotransferase subunit B	MMP0946
−1.21	Carbamoyl−phosphate synthase large chain	MMP1013
−1.07	hypothetical protein	MMP1260
−1.02	hypothetical protein	MMP0657
−1.02	hypothetical protein	MMP0075
−0.91	hypothetical protein	MMP0317
−0.80	Peptidylprolyl isomerase, FKBP−type	MMP0572
−0.76	hypothetical protein	MMP0370
−0.68	hypothetical protein	MMP1646
−0.27	50S ribosomal protein L22P	MMP1403
−0.26	translation initiation factor IF−2 subunit gamma	MMP1208
−0.26	Bacterial transferase hexapeptide repeat	MMP0350
−0.12	Putative arsenical pump−driving ATPase	MMP0163
−0.12	Prefoldin beta subunit (GimC beta subunit)	MMP0245
−0.09	chorismate mutase	MMP0578
−0.08	phosphoribosylaminoimidazole synthetase	MMP1254
−0.07	hypothetical protein	MMP0668
−0.00	transketolase, C terminal half	MMP1113

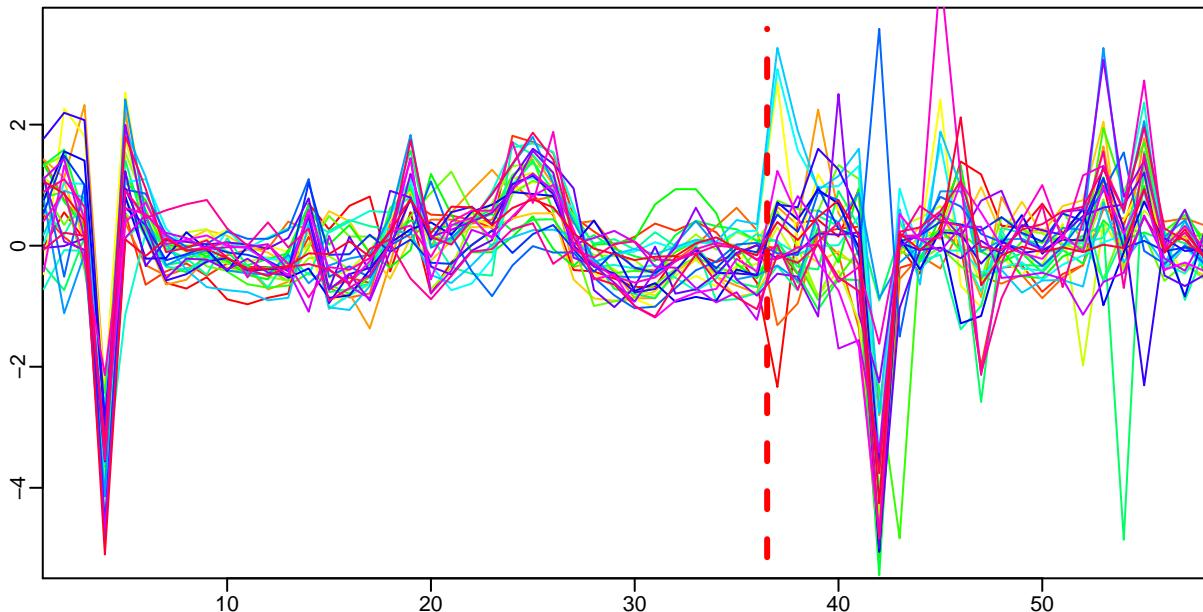**Cluster: 0097 mmp; resid: 0.10; r/c: 9/40**

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp
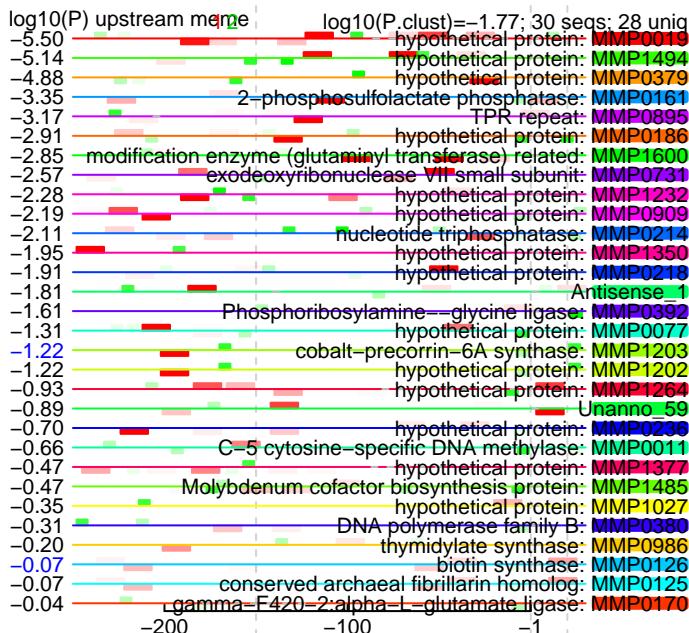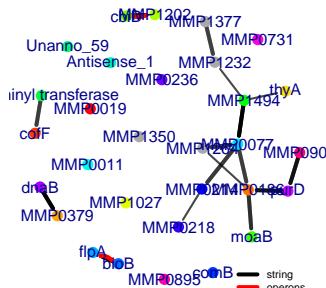
upstream meme PSSM #1; e=240   upstream meme PSSM #2; e=1.1e+03

log10(P) upstream meme

log10(P.clust)=−7.12; 9 seqs; 4 uniq

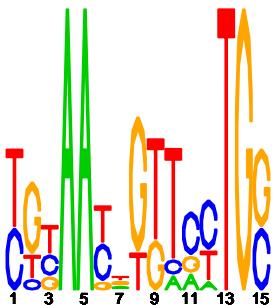| −9.04 | 30S ribosomal protein S27ae: | MMP0444 |
−9.04	30S ribosomal protein S24e:	MMP0443
−7.11	elongation factor 1−beta:	MMP1401
−7.11	hypothetical protein:	MMP1400
−7.05	50S ribosomal protein L29:	MMP1405
−7.05	30S ribosomal protein S3P:	MMP1404
−7.05	50S ribosomal protein L22P:	MMP1403
−7.05	hypothetical protein:	MMP1402
−3.61	Ribosomal protein L11:	MMP1433

string
operons

Cluster: 0098 mmp; resid: 0.32; r/c: 24/40

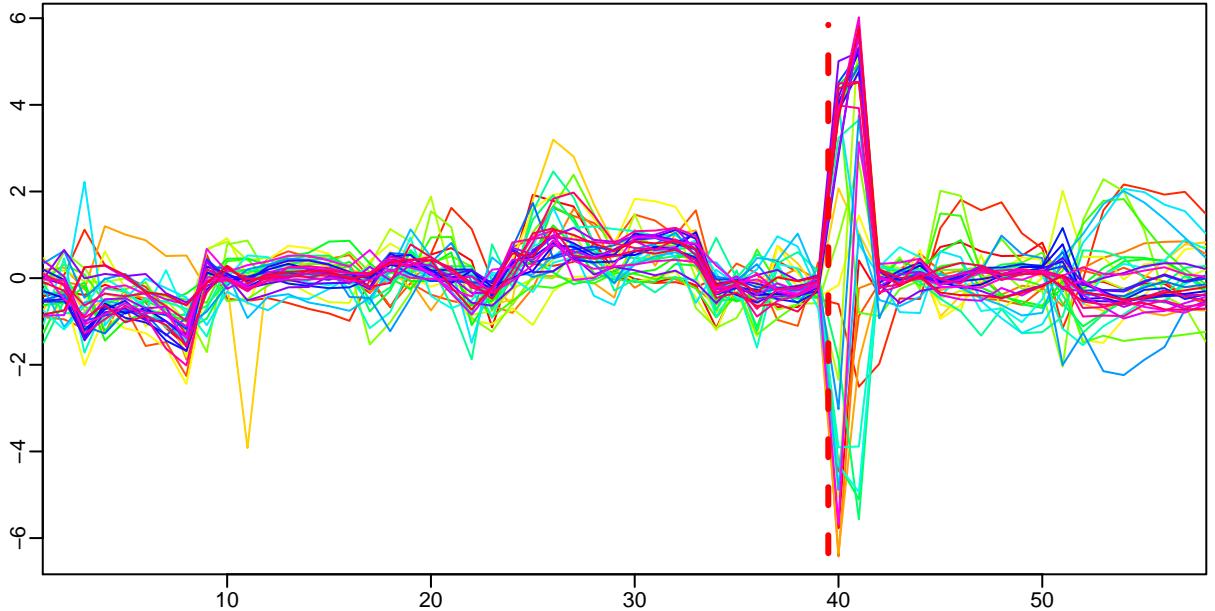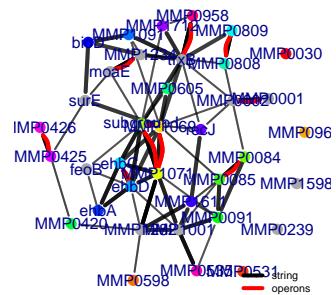11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=2.4e−05 upstream meme PSSM #2; e=3.3e+03

log10(P) upstream meme   log10(P.clust)=−4.50; 24 seqs; 10 uniq

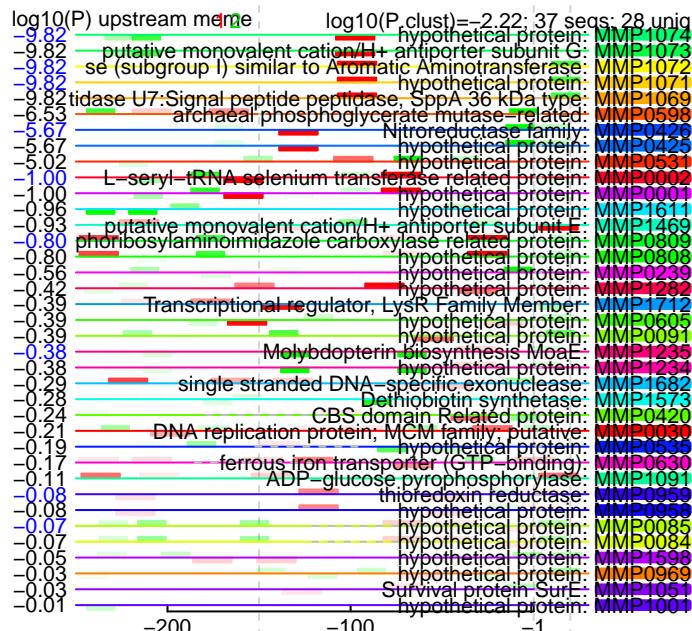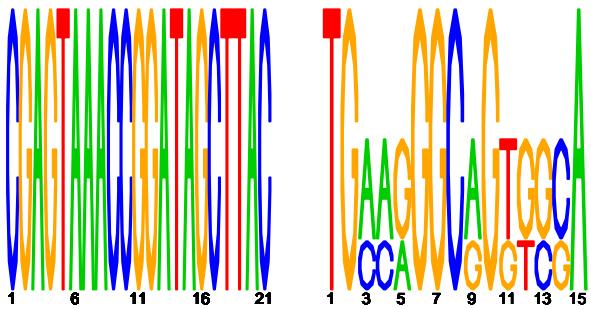| log10(P)	Description	Gene
−7.88	hypothetical protein:	MMP0342
−5.90	phosphoribosyl−ATP pyrophosphatase:	MMP0051
−5.90	riboflavin synthase subunit beta:	MMP0050
−5.64	Chemotaxis protein CheA:	MMP0927
−5.64	Methyl−accepting chemotaxis protein (MCP):	MMP0929
−5.64	chemotaxis protein CheD:	MMP0928
−5.64	dihydrodipicolinate reductase:	MMP0923
−5.64	possible phage infection protein:	MMP0922
−5.64	chemotaxis protein CheB:	MMP0926
−5.64	chemotaxis protein CheW:	MMP0925
−5.64	hypothetical protein:	MMP0924
−4.74	flagellar assembly protein J:	MMP1676
−4.74	flagellar accessory protein FlaH:	MMP1674
−4.74	flagella accessory protein I:	MMP1675
−3.86	hypothetical protein:	MMP0413
−3.49	hypothetical protein:	MMP1719
−3.30	chemotaxis protein CheY:	MMP0932
−3.30	probable chemotaxis−related protein:	MMP0932
−3.30	probable chemotaxis−related protein:	MMP0931
−3.30	chemotaxis protein CheR:	MMP0930
−2.57	hypothetical protein:	MMP0487
−2.12	putative HAD family hydrolase, a fragment:	MMP1231
−2.12	DNA polymerase, beta−like region:	MMP1230
−1.60	glyceraldehyde−3−phosphate ferredoxin oxidoreductase:	MMP0945

Cluster: 0099 mmp; resid: 0.48; r/c: 28/35
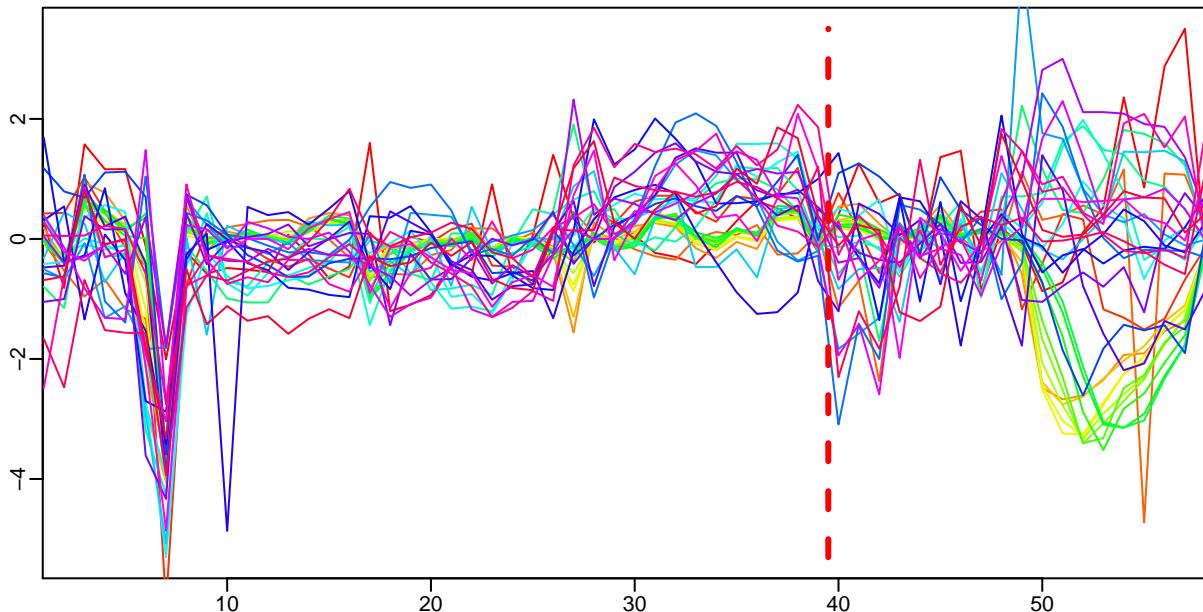
11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

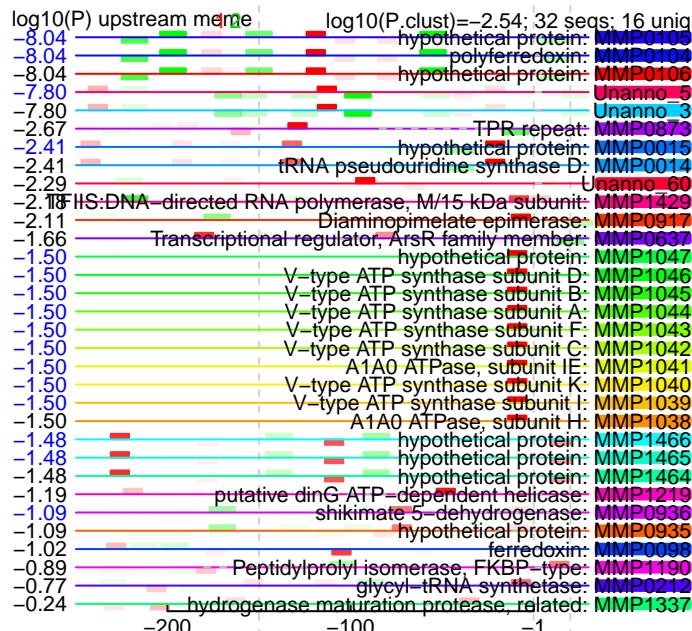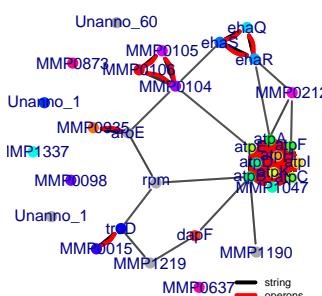upstream meme PSSM #1; e=3.1e+00   upstream meme PSSM #2; e=4.9e+03

log10(P) upstream meme   log10(P.clust)=−3.74; 28 seqs; 18 uniq

log10(P)	Description
−18.97	Unanno_6
−8.21	ADP−glucose pyrophosphorylase: MMP1091
−8.01	Nitrogen fixation−related protein: MMP0860
−8.01	molybdenum cofactor biosynthesis protein, subunit N: MMP0859
−8.01	genase iron−molybdenum cofactor biosynthesis protein: MMP0858
−8.01	Oxidoreductase, nitrogenase component 1: MMP0857
−8.01	Oxidoreductase, nitrogenase component 1: MMP0856
−8.01	Nitrogen regulatory protein NifI2: MMP0855
−8.01	Nitrogen regulatory protein NifI1: MMP0854
−8.01	nitrogenase reductase: MMP0853
−6.89	d to ehbB of Methanothermobacter thermautotrophicus: MMP1049
−1.52	ArsR family transcriptional regulator: MMP1442
−1.17	hypothetical protein: MMP0204
−0.68	Phage integrase: MMP0456
−0.50	glutamine synthetase: MMP1206
−0.37	Ammonia transporter: MMP0068
−0.37	Nitrogen regulatory protein P−II: MMP0067
−0.37	Nitrogen regulatory protein P−II: MMP0066
−0.25	hypothetical protein: MMP0480
−0.24	Ammonia transporter: MMP0065
−0.24	Nitrogen regulatory protein P−II: MMP0064
−0.19	hypothetical protein: MMP1576
−0.16	transporter, periplasmic molybdenum−binding protein: MMP0205
−0.15	Unanno_47
−0.10	hypothetical protein: MMP1390
−0.08	hypothetical protein: MMP1033
−0.05	transporter, periplasmic molybdenum−binding protein: MMP0514
−0.00	Redox−active disulfide protein 2: MMP1388

Cluster: 0100 mmp; resid: 0.38; r/c: 39/38

upstream meme PSSM #1; e=9e−29   upstream meme PSSM #2; e=7e−07

log10(P) upstream meme   log10(P.clust)=−5.16; 39 seqs: 27 uniq

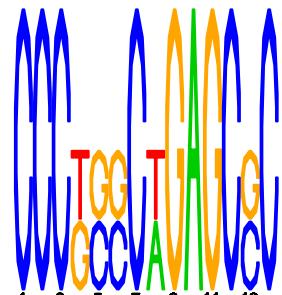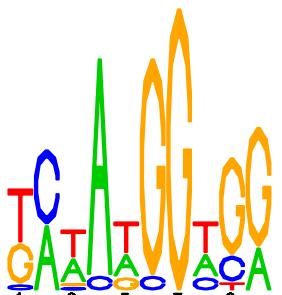**Cluster: 0101 mmp; resid: 0.35; r/c: 37/39**

Cluster: 0102 mmp; resid: 0.19; r/c: 17/41
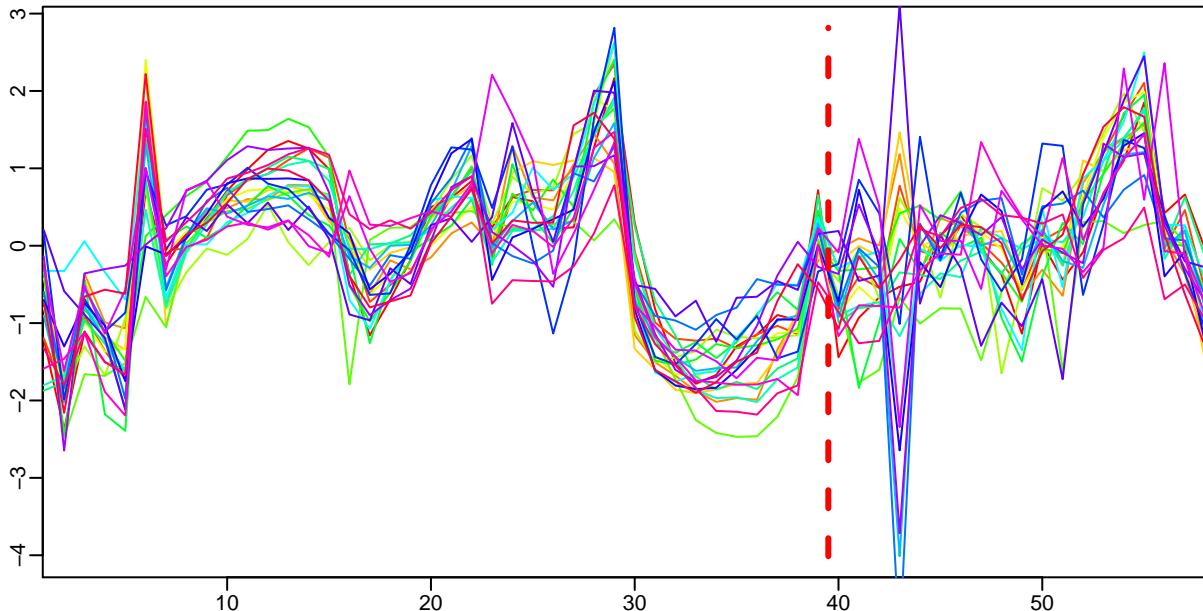
11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=1.6e+04   upstream meme PSSM #2; e=2.2e+04

log10(P) upstream meme   log10(P.clust)=−2.46; 17 seqs; 13 uniq

log10(P)	description	gene
−5.99	AIR synthase related protein	MMP1124
−5.56	hypothetical protein	MMP1283
−5.56	hypothetical protein	MMP1282
−4.03	hypothetical protein	MMP0569
−3.52	hypothetical protein	MMP1001
−2.16	prephenate dehydrogenase	MMP1514
−2.10	hypothetical protein	MMP0122
−2.08	cysteinyl−tRNA synthetase	MMP1060
−1.90	hypothetical protein	MMP0535
−1.90	hypothetical protein	MMP0534
−1.67	hypothetical protein	MMP0465
−1.59	hypothetical protein	MMP1052
−1.58	Nitroreductase family	MMP0426
−1.58	hypothetical protein	MMP0425
−0.48	hypothetical protein	MMP1598
−0.09	thioredoxin reductase	MMP0959
−0.09	hypothetical protein	MMP0958

Cluster: 0103 mmp; resid: 0.16; r/c: 12/37

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=0.61
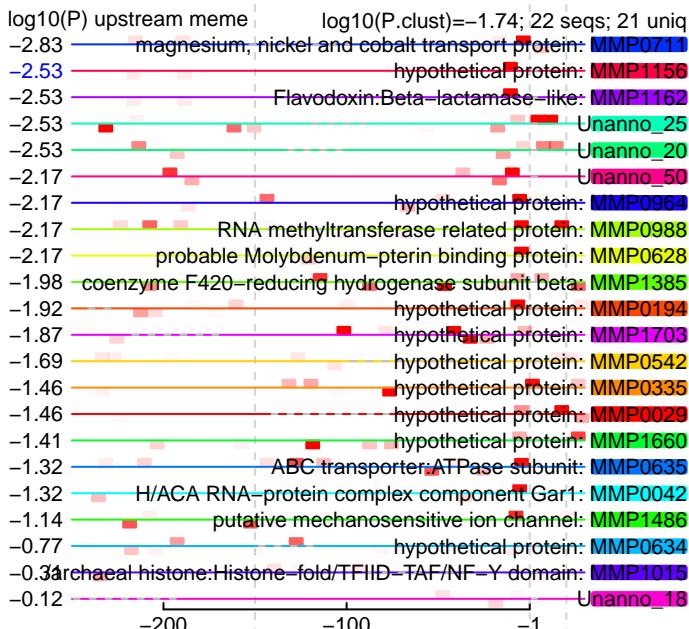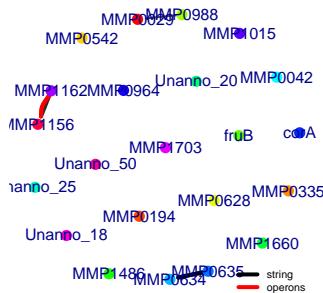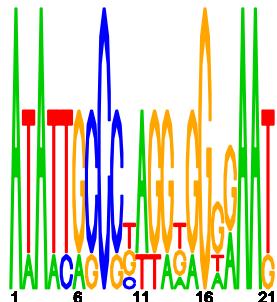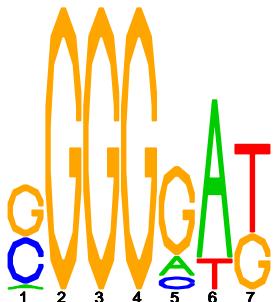
upstream meme PSSM #2; e=35

log10(P) upstream meme

log10(P.clust)=−4.51; 12 seqs; 4 uniq

−6.00	Enolase:	MMP1328
−6.00	DNA−directed RNA polymerase, subunit K:	MMP1327
−4.97	DNA−directed RNA polymerase subunit N:	MMP1326
−4.97	30S ribosomal protein S9P:	MMP1325
−4.97	50S ribosomal protein L13P:	MMP1324
−4.97	50S ribosomal protein L18e:	MMP1323
−4.97	DNA−directed RNA polymerase, subunit D:	MMP1322
−4.97	30S ribosomal protein S4:	MMP1320
−4.97	30S ribosomal protein S13P:	MMP1319
−4.67	50S ribosomal protein L12P:	MMP0258
−1.34	DNA−directed RNA polymerase subunit A":	MMP1364
−1.34	DNA−directed RNA polymerase subunit alpha:	MMP1363

string
operons

Cluster: 0104 mmp; resid: 0.35; r/c: 30/36
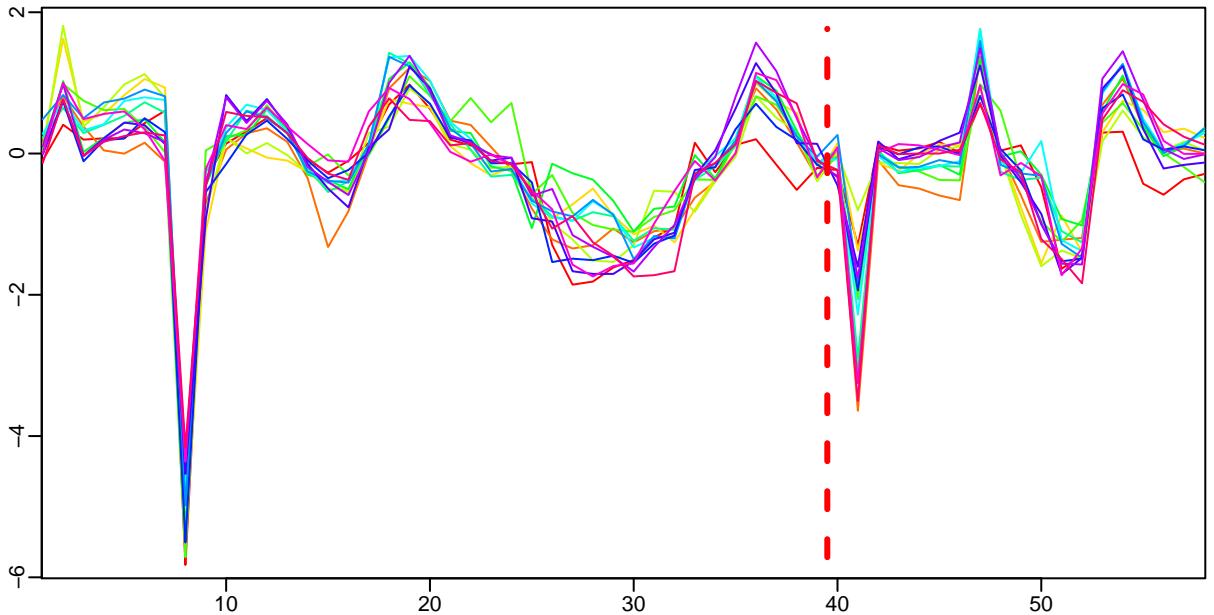
upstream meme PSSM #1; e=300   upstream meme PSSM #2; e=3.1e+03

log10(P) upstream meme   log10(P.clust)=−1.77; 30 seqs: 28 uniq

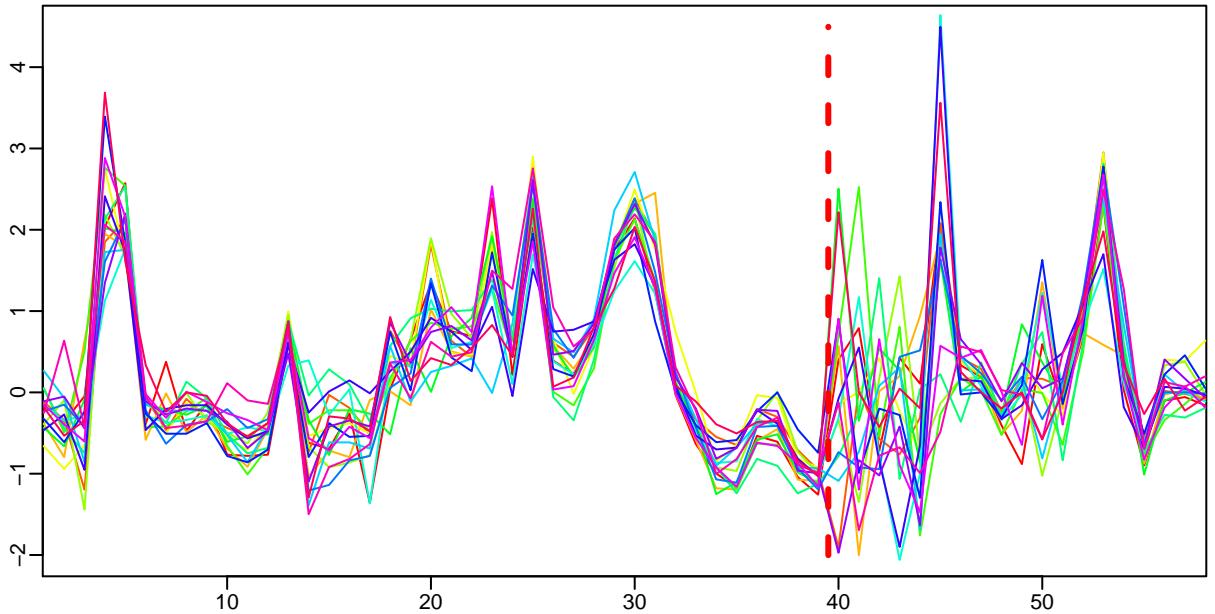| log10(P)	annotation	gene
−5.50	hypothetical protein:	MMP0019
−5.14	hypothetical protein:	MMP1494
−4.88	hypothetical protein:	MMP0379
−3.35	2−phosphosulfolactate phosphatase:	MMP0161
−3.17	TPR repeat:	MMP0895
−2.91	hypothetical protein:	MMP0186
−2.85	modification enzyme (glutaminyl transferase) related:	MMP1600
−2.57	exodeoxyribonuclease VII small subunit:	MMP0731
−2.28	hypothetical protein:	MMP1232
−2.19	hypothetical protein:	MMP0909
−2.11	nucleotide triphosphatase:	MMP0214
−1.95	hypothetical protein:	MMP1350
−1.91	hypothetical protein:	MMP0218
−1.81		Antisense_1
−1.61	Phosphoribosylamine−−glycine ligase:	MMP0392
−1.31	hypothetical protein:	MMP0077
−1.22	cobalt−precorrin−6A synthase:	MMP1203
−1.22	hypothetical protein:	MMP1202
−0.93	hypothetical protein:	MMP1264
−0.89		Unanno_59
−0.70	hypothetical protein:	MMP0236
−0.66	C−5 cytosine−specific DNA methylase:	MMP0011
−0.47	hypothetical protein:	MMP1377
−0.47	Molybdenum cofactor biosynthesis protein:	MMP1485
−0.35	hypothetical protein:	MMP1027
−0.31	DNA polymerase family B:	MMP0380
−0.20	thymidylate synthase:	MMP0986
−0.07	biotin synthase:	MMP0126
−0.07	conserved archaeal fibrillarin homolog:	MMP0125
−0.04	gamma−F420−2:alpha−L−glutamate ligase:	MMP0170

Cluster: 0105 mmp; resid: 0.15; r/c: 14/39

upstream meme PSSM #1; e=65

upstream meme PSSM #2; e=220

log10(P) upstream meme

log10(P.clust)=−3.44; 14 seqs; 9 uniq

log10(P)	Description	Gene
−9.18	30S ribosomal protein S11P:	MMP1321
−6.59	elongation factor 1- beta:	MMP1401
−6.59	hypothetical protein:	MMP1400
−5.83	50S ribosomal protein L10e:	MMP1289
−5.79	30S ribosomal protein S6e:	MMP1207
−4.83	50S ribosomal protein L39e:	MMP0159
−2.14	50S ribosomal protein L14e:	MMP0625
−1.97	30S ribosomal protein S3Ae:	MMP0669
−1.97	hypothetical protein:	MMP0668
−1.97	30S ribosomal protein S2:	MMP0667
−1.18	Ribosomal protein L11:	MMP1433
−0.04	50S ribosomal protein L22P:	MMP1403
−0.04	30S ribosomal protein S3P:	MMP1404
−0.04	hypothetical protein:	MMP1402

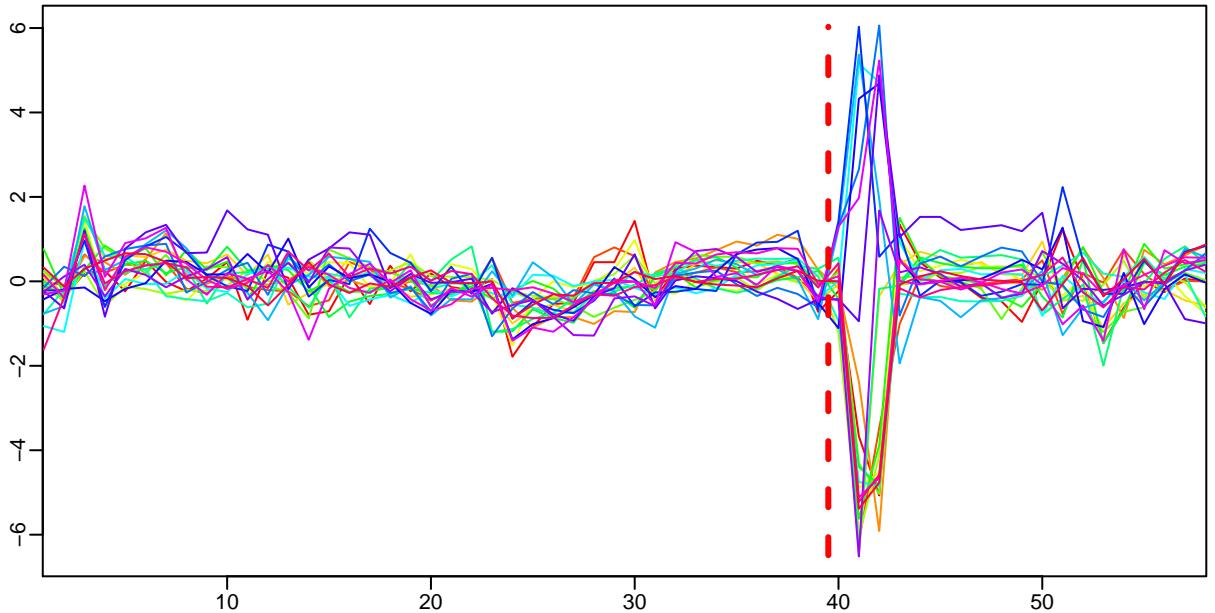**Cluster: 0106 mmp; resid: 0.34; r/c: 37/39**

upstream meme PSSM #1; e=1.1e+00   upstream meme PSSM #2; e=5.6e+03

log10(P) upstream meme   log10(P,clust)=−2.22; 37 seqs; 28 uniq

log10(P)	Protein	ID
−9.82	hypothetical protein:	MMP1074
−9.82	putative monovalent cation/H+ antiporter subunit G:	MMP1073
−9.82	se (subgroup I) similar to Aromatic Aminotransferase:	MMP1072
−9.82	hypothetical protein:	MMP1071
−9.82	tidase U7:Signal peptide peptidase, SppA 36 kDa type:	MMP1069
−6.53	archaeal phosphoglycerate mutase–related:	MMP0598
−5.67	Nitroreductase family:	MMP0426
−5.67	hypothetical protein:	MMP0425
−5.02	hypothetical protein:	MMP0531
−1.00	L–seryl–tRNA selenium transferase related protein:	MMP0002
−1.00	hypothetical protein:	MMP0001
−0.96	hypothetical protein:	MMP1611
−0.93	putative monovalent cation/H+ antiporter subunit E:	MMP1469
−0.80	phoribosylaminoimidazole carboxylase related protein:	MMP0809
−0.80	hypothetical protein:	MMP0808
−0.56	hypothetical protein:	MMP0239
−0.42	hypothetical protein:	MMP1282
−0.39	Transcriptional regulator, LysR Family Member:	MMP1712
−0.39	hypothetical protein:	MMP0605
−0.39	hypothetical protein:	MMP0091
−0.38	Molybdopterin biosynthesis MoaE:	MMP1235
−0.38	hypothetical protein:	MMP1234
−0.29	single stranded DNA–specific exonuclease:	MMP1682
−0.28	Dethiobiotin synthetase:	MMP1573
−0.24	CBS domain Related protein:	MMP0420
−0.21	DNA replication protein; MCM family–putative:	MMP0030
−0.19	hypothetical protein:	MMP0535
−0.17	ferrous iron transporter (GTP–binding):	MMP0630
−0.11	ADP–glucose pyrophosphorylase:	MMP1091
−0.08	thioredoxin reductase:	MMP0959
−0.08	hypothetical protein:	MMP0085
−0.07	hypothetical protein:	MMP0084
−0.05	hypothetical protein:	MMP1598
−0.03	hypothetical protein:	MMP0969
−0.03	Survival protein SurE:	MMP1051
−0.01	hypothetical protein:	MMP1001

Cluster: 0107 mmp; resid: 0.43; r/c: 32/39

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cMonkey Version 4.8.8 mmp
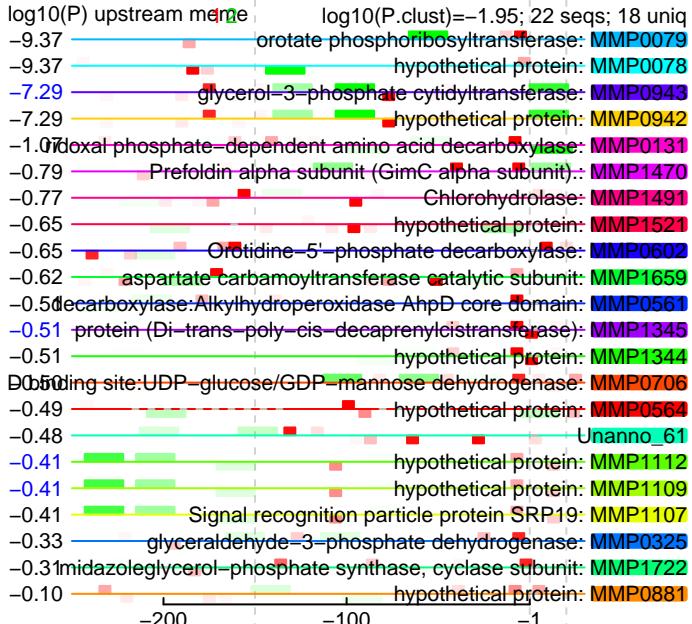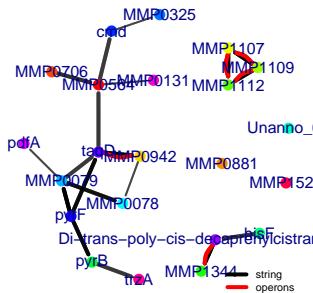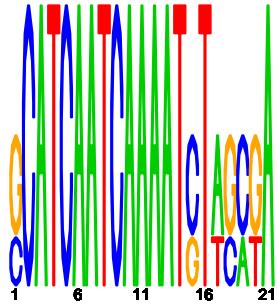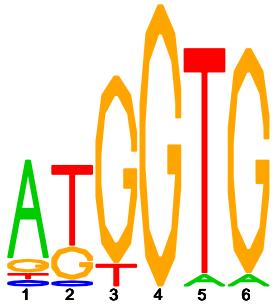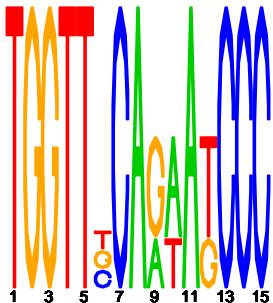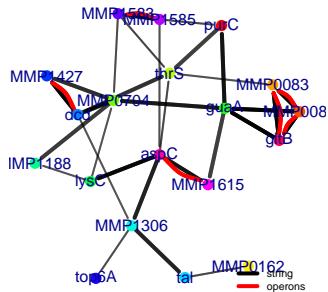
upstream meme PSSM #1; e=0.1

upstream meme PSSM #2; e=240

log10(P) upstream meme — log10(P.clust)=−2.54; 32 seqs: 16 uniq

log10(P)	annotation	gene
−8.04	hypothetical protein:	MMP0105
−8.04	polyferredoxin:	MMP0104
−8.04	hypothetical protein:	MMP0106
−7.80		Unanno_5
−7.80		Unanno_3
−2.67	TPR repeat:	MMP0873
−2.41	hypothetical protein:	MMP0015
−2.41	tRNA pseudouridine synthase D:	MMP0014
−2.29		Unanno_60
−2.18	TFIIS:DNA-directed RNA polymerase, M/15 kDa subunit:	MMP1429
−2.11	Diaminopimelate epimerase:	MMP0917
−1.66	Transcriptional regulator, ArsR family member:	MMP0637
−1.50	hypothetical protein:	MMP1047
−1.50	V-type ATP synthase subunit D:	MMP1046
−1.50	V-type ATP synthase subunit B:	MMP1045
−1.50	V-type ATP synthase subunit A:	MMP1044
−1.50	V-type ATP synthase subunit F:	MMP1043
−1.50	V-type ATP synthase subunit C:	MMP1042
−1.50	A1A0 ATPase, subunit IE:	MMP1041
−1.50	V-type ATP synthase subunit K:	MMP1040
−1.50	V-type ATP synthase subunit I:	MMP1039
−1.50	A1A0 ATPase, subunit H:	MMP1038
−1.48	hypothetical protein:	MMP1466
−1.48	hypothetical protein:	MMP1465
−1.48	hypothetical protein:	MMP1464
−1.19	putative dinG ATP-dependent helicase:	MMP1219
−1.09	shikimate 5-dehydrogenase:	MMP0936
−1.09	hypothetical protein:	MMP0935
−1.02	ferredoxin:	MMP0098
−0.89	Peptidylprolyl isomerase, FKBP-type:	MMP1190
−0.77	glycyl-tRNA synthetase:	MMP0212
−0.24	hydrogenase maturation protease, related:	MMP1337

Cluster: 0108 mmp; resid: 0.32; r/c: 22/39

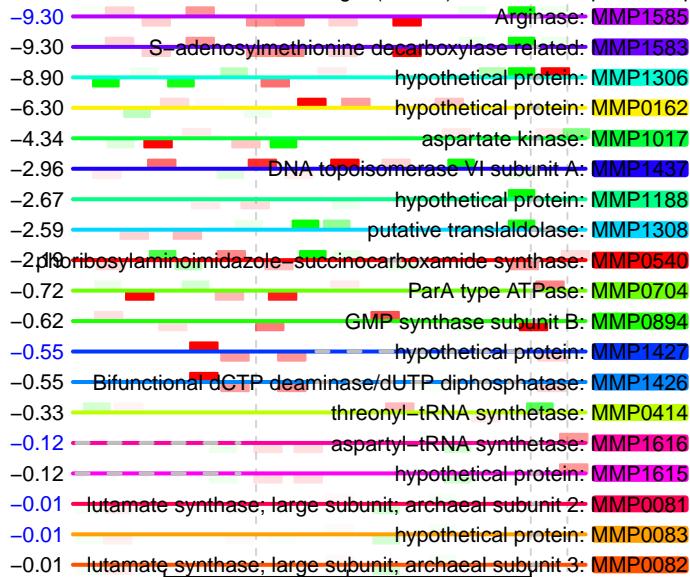11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

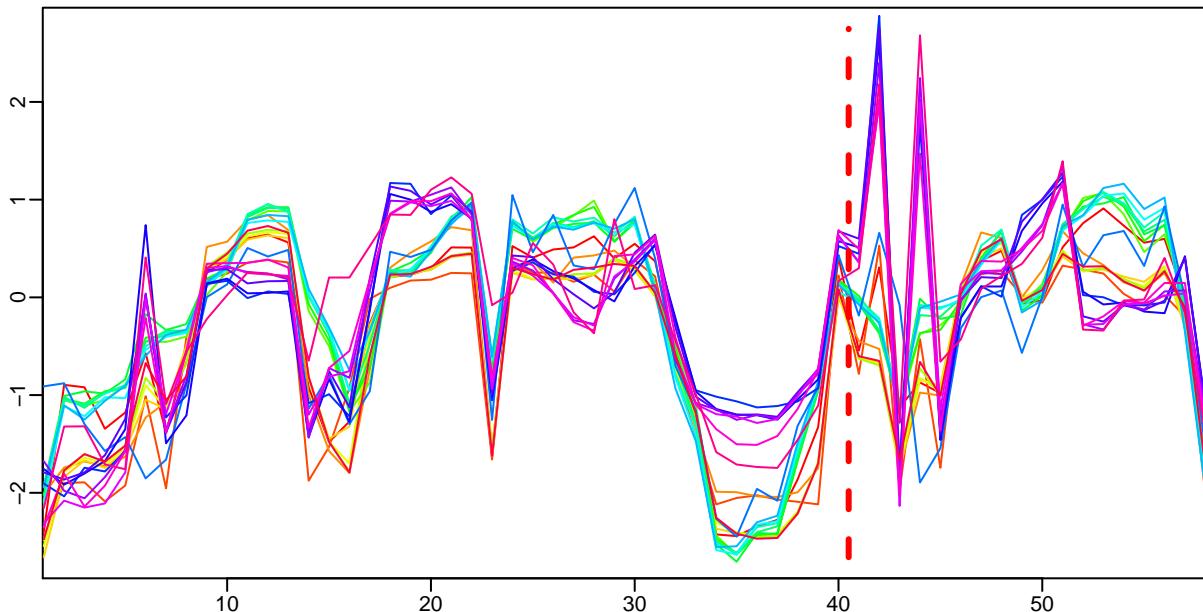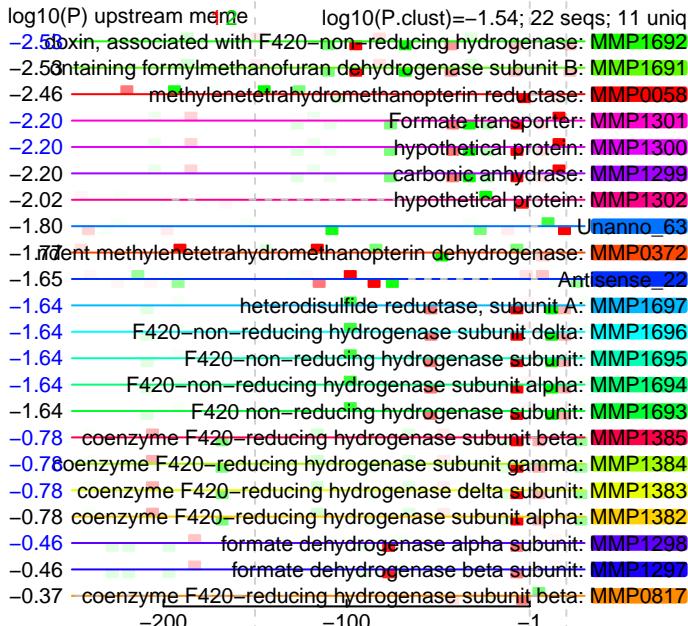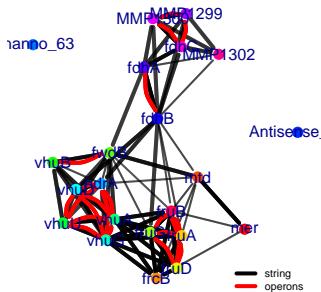upstream meme PSSM #1; e=1.2e−11 upstream meme PSSM #2; e=0.083

log10(P) upstream meme   log10(P.clust)=−1.74; 22 seqs; 21 uniq

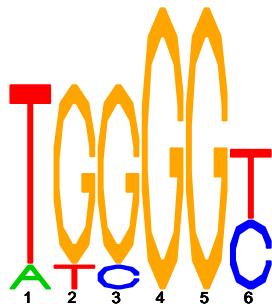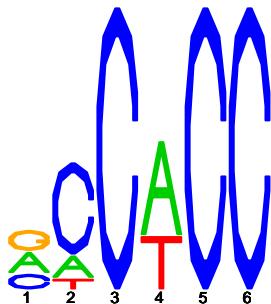| log10(P)	annotation
−2.83	magnesium, nickel and cobalt transport protein: MMP0711
−2.53	hypothetical protein: MMP1156
−2.53	Flavodoxin:Beta−lactamase−like: MMP1162
−2.53	Unanno_25
−2.53	Unanno_20
−2.17	Unanno_50
−2.17	hypothetical protein: MMP0964
−2.17	RNA methyltransferase related protein: MMP0988
−2.17	probable Molybdenum−pterin binding protein: MMP0628
−1.98	coenzyme F420−reducing hydrogenase subunit beta: MMP1385
−1.92	hypothetical protein: MMP0194
−1.87	hypothetical protein: MMP1703
−1.69	hypothetical protein: MMP0542
−1.46	hypothetical protein: MMP0335
−1.46	hypothetical protein: MMP0029
−1.41	hypothetical protein: MMP1660
−1.32	ABC transporter:ATPase subunit: MMP0635
−1.32	H/ACA RNA−protein complex component Gar1: MMP0042
−1.14	putative mechanosensitive ion channel: MMP1486
−0.77	hypothetical protein: MMP0634
−0.31	archaeal histone:Histone−fold/TFIID−TAF/NF−Y domain: MMP1015
−0.12	Unanno_18

−200   −100   −1

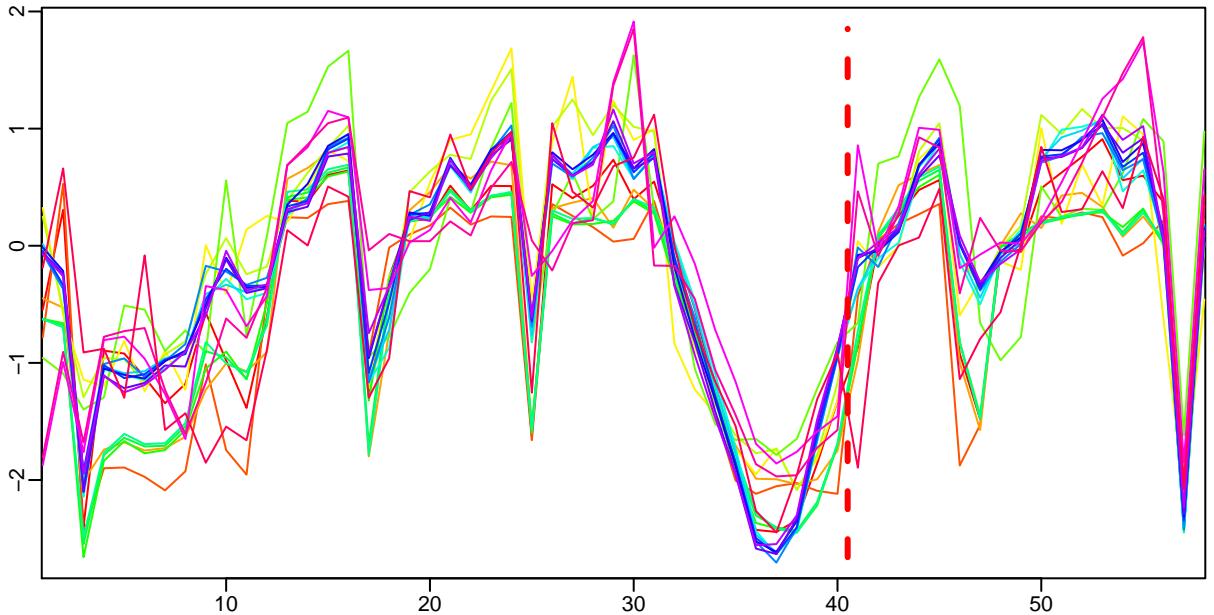**Cluster: 0109 mmp; resid: 0.20; r/c: 14/39**

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

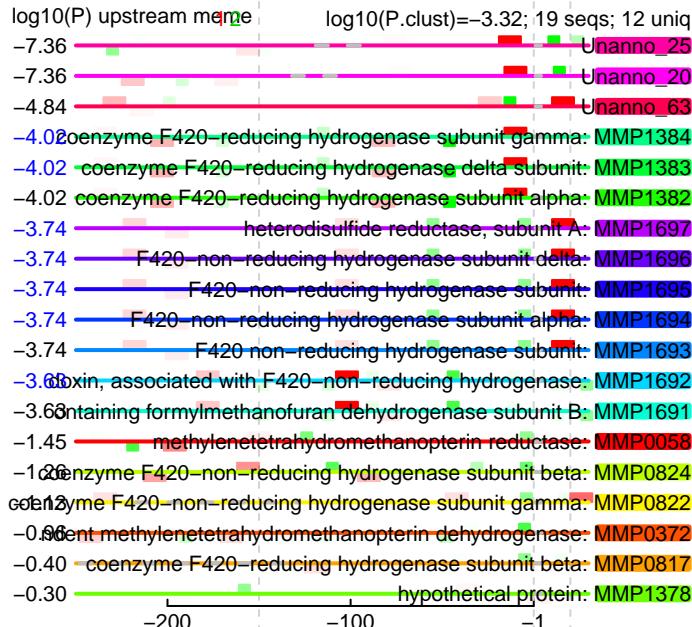upstream meme PSSM #1; e=220   upstream meme PSSM #2; e=8.7e+03

log10(P) upstream meme   log10(P.clust)=−1.28; 14 seqs; 9 uniq

log10(P)	Annotation	Gene
−3.35	LysR family member:	MMP0033
−2.11	DNA−directed RNA polymerase related protein:	MMP0248
−2.11	ribosomal biogenesis protein:	MMP0247
−2.11	hypothetical protein:	MMP0246
−1.94	acyl−CoA synthetase:	MMP0566
−1.94	transcriptional regulator−related protein:	MMP0568
−1.23	DNA−directed RNA polymerase subunit beta":	MMP1361
−1.02	Beta−lactamase−like:KH domain:	MMP0694
−1.01	DNA−directed RNA polymerase subunit F:	MMP0092
−0.40	hypothetical protein:	MMP0604
−0.40	translation initiation factor IF−1A:	MMP0603
−0.22	Na+/H+ exchanger:	MMP0707
−0.01	Transketolase, N terminal half:	MMP1115
−0.01	Pentose−5−phosphate 3−epimerase:	MMP1114

MMP0707
MMP1115
rpe
MMP0566
MMP0568 MMP0604
MMP0694

MMP0246 MMP0247
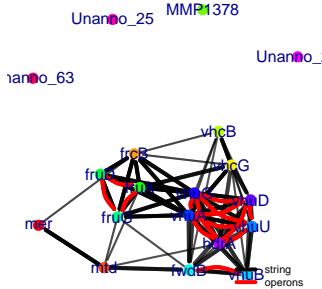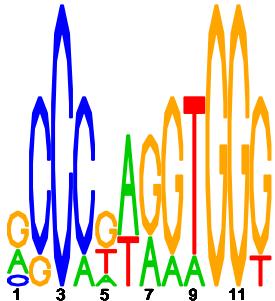MMP0248
rpoF
rpoB2
aIF1A
MMP003

string
operons

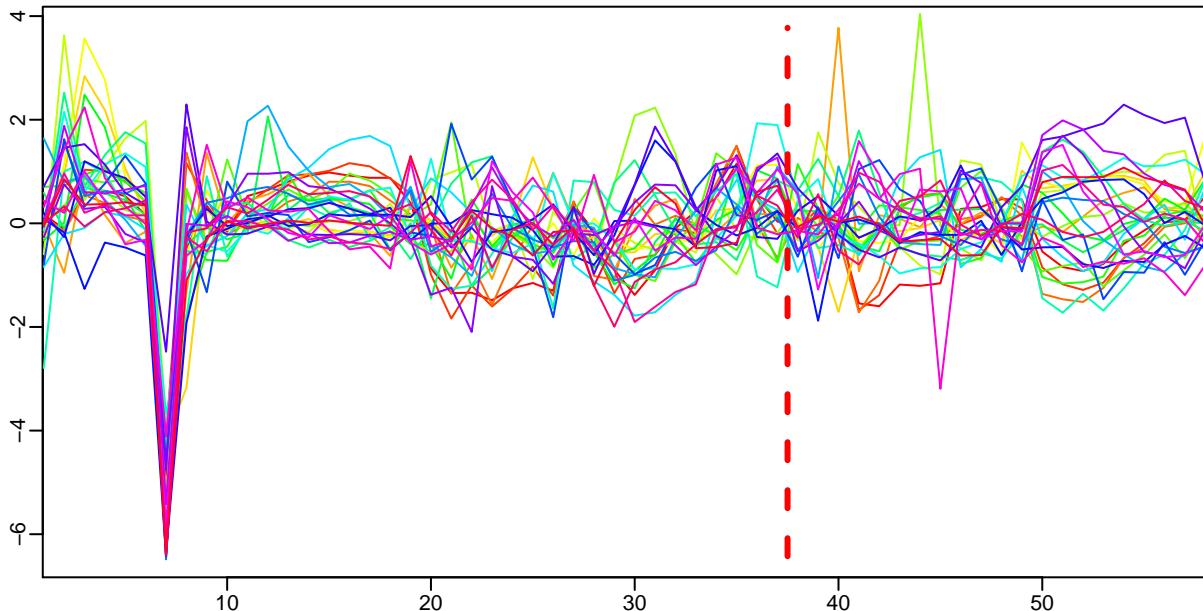**Cluster: 0110 mmp; resid: 0.22; r/c: 17/39**

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cMonkey Version 4.8.8 mmp
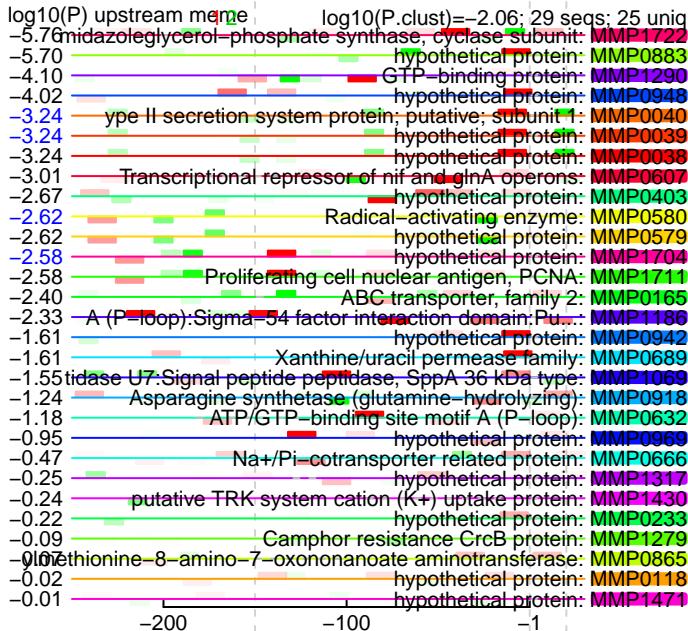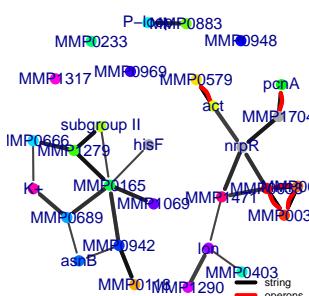
upstream meme PSSM #1; e=690   upstream meme PSSM #2; e=1.3e+03

log10(P) upstream meme   log10(P.clust)=−2.74; 17 seqs; 17 uniq

log10(P)	Annotation	Gene
−7.34	hypothetical protein:	MMP1572
−6.22	tide) binding motif:Family of unknown function Met10:	MMP0560
−4.23	PA-phosphatase related phosphoesterase:	MMP1631
−3.70	hypothetical protein:	MMP0781
−3.56	Glycosyl transferase:	MMP0090
−3.48	hypothetical protein:	MMP0957
−3.39	hypothetical protein:	MMP0741
−3.22	hypothetical protein:	MMP0752
−3.22	hypothetical protein:	MMP0751
−3.14	tative SSU ribosomal protein S6 modification protein:	MMP0436
−2.??	dependent transport systems inner membrane component:	MMP0551
−0.75	Molybdenum ABC transporter, permease protein:	MMP0515
−0.50	hypothetical protein:	MMP0805
−0.34	hypothetical protein:	MMP1309
−0.31	nucleotide) binding motif:Generic methyltransferase:	MMP1179
−0.29	hypothetical protein:	MMP0114
−0.20	hypothetical protein:	MMP0804

Cluster: 0111 mmp; resid: 0.30; r/c: 22/39

upstream meme PSSM #1; e=77

upstream meme PSSM #2; e=290

log10(P) upstream meme   log10(P.clust)=−1.95; 22 seqs; 18 uniq

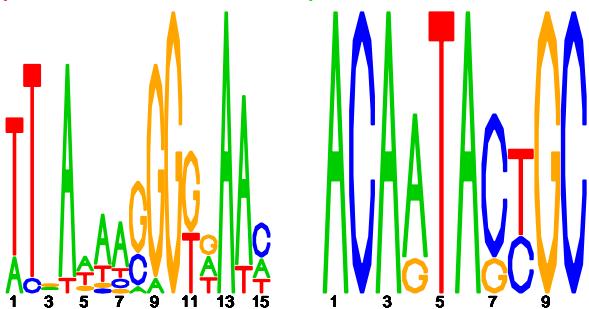| log10(P)	Annotation	Gene
−9.37	orotate phosphoribosyltransferase:	MMP0079
−9.37	hypothetical protein:	MMP0078
−7.29	glycerol−3−phosphate cytidyltransferase:	MMP0943
−7.29	hypothetical protein:	MMP0942
−1.07	Pyridoxal phosphate−dependent amino acid decarboxylase:	MMP0131
−0.79	Prefoldin alpha subunit (GimC alpha subunit):	MMP1470
−0.77	Chlorohydrolase:	MMP1491
−0.65	hypothetical protein:	MMP1521
−0.65	Orotidine−5'−phosphate decarboxylase:	MMP0602
−0.62	aspartate carbamoyltransferase catalytic subunit:	MMP1659
−0.54	decarboxylase:Alkylhydroperoxidase AhpD core domain:	MMP0561
−0.51	protein (Di−trans−poly−cis−decaprenylcistransferase):	MMP1345
−0.51	hypothetical protein:	MMP1344
−0.50	DNA binding site:UDP−glucose/GDP−mannose dehydrogenase:	MMP0706
−0.49	hypothetical protein:	MMP0564
−0.48		Unanno_61
−0.41	hypothetical protein:	MMP1112
−0.41	hypothetical protein:	MMP1109
−0.41	Signal recognition particle protein SRP19:	MMP1107
−0.33	glyceraldehyde−3−phosphate dehydrogenase:	MMP0325
−0.31	imidazoleglycerol−phosphate synthase, cyclase subunit:	MMP1722
−0.10	hypothetical protein:	MMP0881

Cluster: 0112 mmp; resid: 0.28; r/c: 19/38

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cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=420

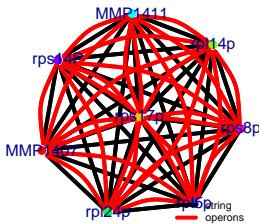upstream meme PSSM #2; e=370

log10(P) upstream meme

log10(P.clust)=−2.71; 19 seqs; 14 uniq

log10(P)	Description	Gene
−9.30	Arginase	MMP1585
−9.30	S−adenosylmethionine decarboxylase related	MMP1583
−8.90	hypothetical protein	MMP1306
−6.30	hypothetical protein	MMP0162
−4.34	aspartate kinase	MMP1017
−2.96	DNA topoisomerase VI subunit A	MMP1437
−2.67	hypothetical protein	MMP1188
−2.59	putative translaldolase	MMP1308
−2.pl9	phosphoribosylaminoimidazole−succinocarboxamide synthase	MMP0540
−0.72	ParA type ATPase	MMP0704
−0.62	GMP synthase subunit B	MMP0894
−0.55	hypothetical protein	MMP1427
−0.55	Bifunctional dCTP deaminase/dUTP diphosphatase	MMP1426
−0.33	threonyl−tRNA synthetase	MMP0414
−0.12	aspartyl−tRNA synthetase	MMP1616
−0.12	hypothetical protein	MMP1615
−0.01	lutamate synthase; large subunit; archaeal subunit 2	MMP0081
−0.01	hypothetical protein	MMP0083
−0.01	lutamate synthase; large subunit; archaeal subunit 3	MMP0082

−200   −100   −1

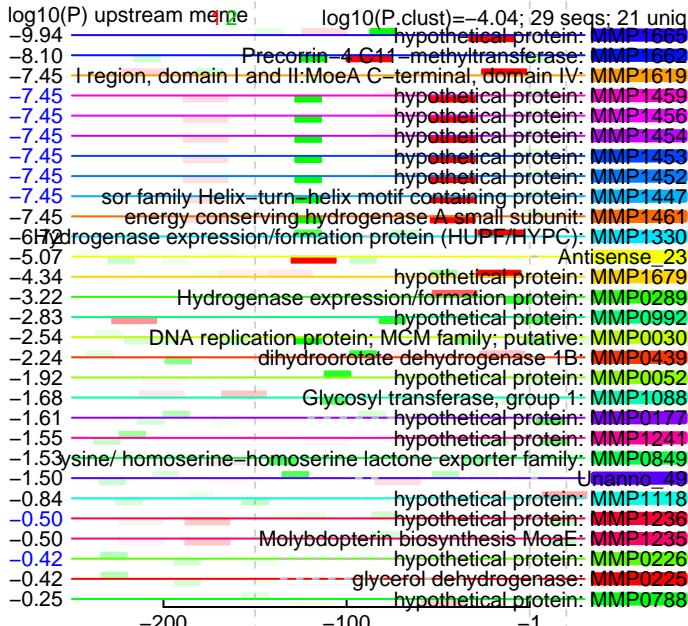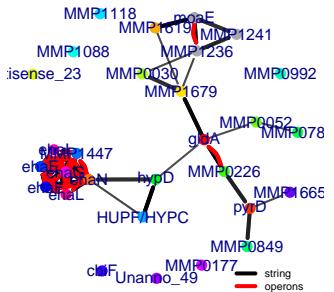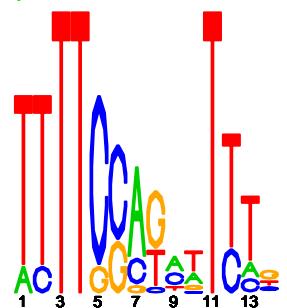# Cluster: 0113 mmp; resid: 0.27; r/c: 22/40

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=4

upstream meme PSSM #2; e=91

log10(P) upstream meme   log10(P.clust)=−1.54; 22 seqs; 11 uniq

log10(P)	Description	Gene
−2.56	toxin, associated with F420−non−reducing hydrogenase:	MMP1692
−2.53	containing formylmethanofuran dehydrogenase subunit B:	MMP1691
−2.46	methylenetetrahydromethanopterin reductase:	MMP0058
−2.20	Formate transporter:	MMP1301
−2.20	hypothetical protein:	MMP1300
−2.20	carbonic anhydrase:	MMP1299
−2.02	hypothetical protein:	MMP1302
−1.80		Unanno_63
−1.77	dent methylenetetrahydromethanopterin dehydrogenase:	MMP0372
−1.65		Antisense_22
−1.64	heterodisulfide reductase, subunit A:	MMP1697
−1.64	F420−non−reducing hydrogenase subunit delta:	MMP1696
−1.64	F420−non−reducing hydrogenase subunit:	MMP1695
−1.64	F420−non−reducing hydrogenase subunit alpha:	MMP1694
−1.64	F420 non−reducing hydrogenase subunit:	MMP1693
−0.78	coenzyme F420−reducing hydrogenase subunit beta:	MMP1385
−0.78	coenzyme F420−reducing hydrogenase subunit gamma:	MMP1384
−0.78	coenzyme F420−reducing hydrogenase delta subunit:	MMP1383
−0.78	coenzyme F420−reducing hydrogenase subunit alpha:	MMP1382
−0.46	formate dehydrogenase alpha subunit:	MMP1298
−0.46	formate dehydrogenase beta subunit:	MMP1297
−0.37	coenzyme F420−reducing hydrogenase subunit beta:	MMP0817

string
operons

Cluster: 0114 mmp; resid: 0.23; r/c: 19/40

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cMonkey Version 4.8.8 mmp

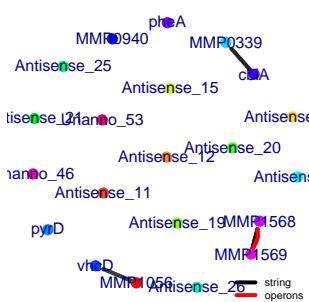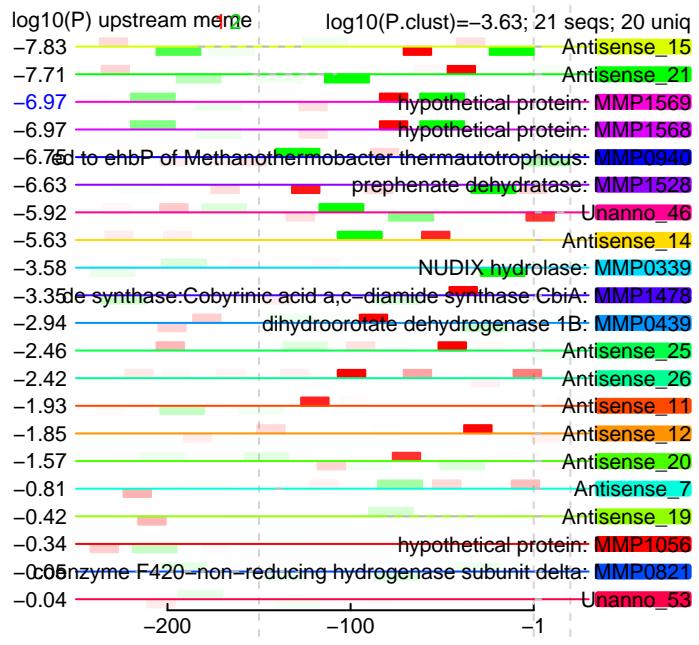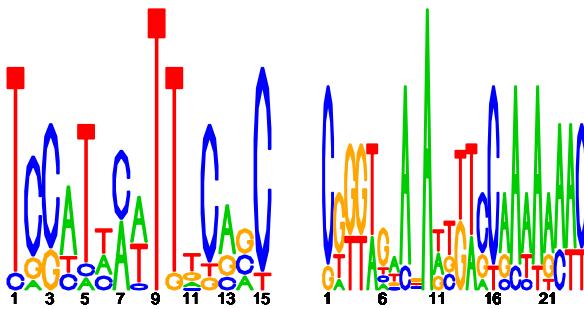upstream meme PSSM #1; e=0.0031   upstream meme PSSM #2; e=0.15

log10(P) upstream meme   log10(P.clust)=−3.32; 19 seqs; 12 uniq

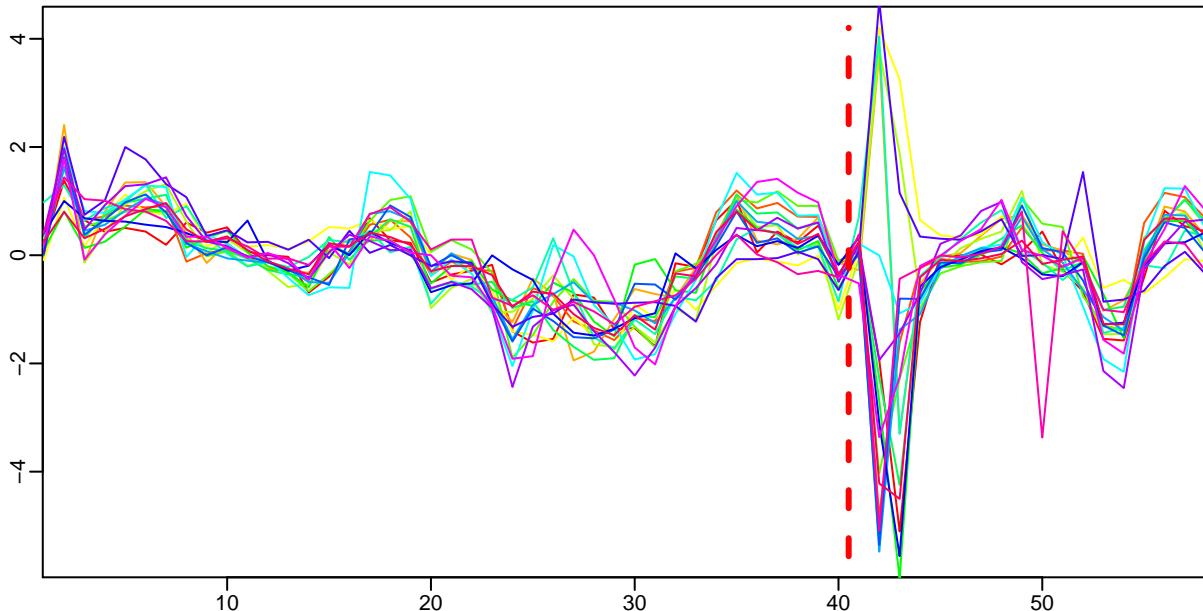| log10(P)	description	gene
−7.36		Unanno_25
−7.36		Unanno_20
−4.84		Unanno_63
−4.02	coenzyme F420−reducing hydrogenase subunit gamma	MMP1384
−4.02	coenzyme F420−reducing hydrogenase delta subunit	MMP1383
−4.02	coenzyme F420−reducing hydrogenase subunit alpha	MMP1382
−3.74	heterodisulfide reductase, subunit A	MMP1697
−3.74	F420−non−reducing hydrogenase subunit delta	MMP1696
−3.74	F420−non−reducing hydrogenase subunit	MMP1695
−3.74	F420−non−reducing hydrogenase subunit alpha	MMP1694
−3.74	F420 non−reducing hydrogenase subunit	MMP1693
−3.66	doxin, associated with F420−non−reducing hydrogenase	MMP1692
−3.63	containing formylmethanofuran dehydrogenase subunit B	MMP1691
−1.45	methylenetetrahydromethanopterin reductase	MMP0058
−1.26	coenzyme F420−non−reducing hydrogenase subunit beta	MMP0824
−1.12	coenzyme F420−non−reducing hydrogenase subunit gamma	MMP0822
−0.96	dent methylenetetrahydromethanopterin dehydrogenase	MMP0372
−0.40	coenzyme F420−reducing hydrogenase subunit beta	MMP0817
−0.30	hypothetical protein	MMP1378

Cluster: 0115 mmp; resid: 0.49; r/c: 29/37

upstream meme PSSM #1; e=320   upstream meme PSSM #2; e=2e+03

log10(P) upstream meme   log10(P.clust)=−2.06; 29 seqs; 25 uniq

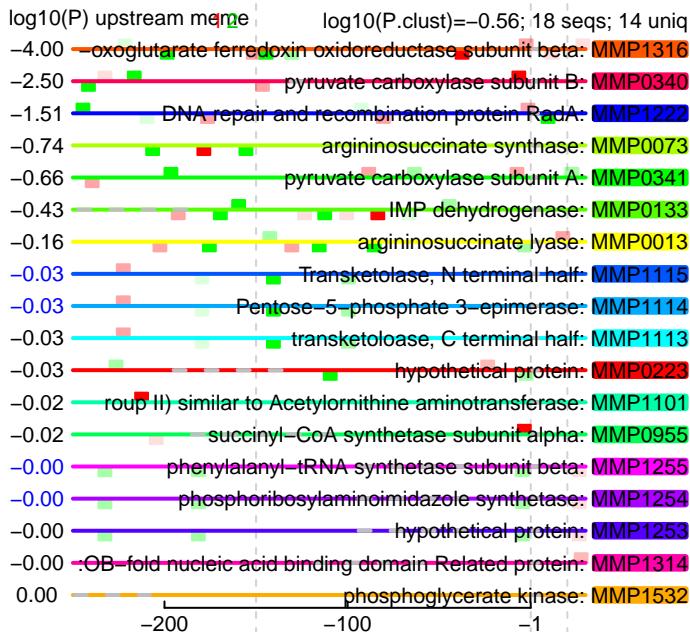| log10(P)	Description	Gene
−5.76	midazoleglycerol−phosphate synthase, cyclase subunit:	MMP1722
−5.70	hypothetical protein:	MMP0883
−4.10	GTP−binding protein:	MMP1290
−4.02	hypothetical protein:	MMP0948
−3.24	ype II secretion system protein; putative; subunit 1:	MMP0040
−3.24	hypothetical protein:	MMP0039
−3.24	hypothetical protein:	MMP0038
−3.01	Transcriptional repressor of nif and glnA operons:	MMP0607
−2.67	hypothetical protein:	MMP0403
−2.62	Radical−activating enzyme:	MMP0580
−2.62	hypothetical protein:	MMP0579
−2.58	hypothetical protein:	MMP1704
−2.58	Proliferating cell nuclear antigen, PCNA:	MMP1711
−2.40	ABC transporter, family 2:	MMP0165
−2.33	A (P−loop):Sigma−54 factor interaction domain:Pu...:	MMP1186
−1.61	hypothetical protein:	MMP0942
−1.61	Xanthine/uracil permease family:	MMP0689
−1.55	tidase U7:Signal peptide peptidase, SppA 36 kDa type:	MMP1069
−1.24	Asparagine synthetase (glutamine−hydrolyzing):	MMP0918
−1.18	ATP/GTP−binding site motif A (P−loop):	MMP0632
−0.95	hypothetical protein:	MMP0969
−0.47	Na+/Pi−cotransporter related protein:	MMP0666
−0.25	hypothetical protein:	MMP1317
−0.24	putative TRK system cation (K+) uptake protein:	MMP1430
−0.22	hypothetical protein:	MMP0233
−0.09	Camphor resistance CrcB protein:	MMP1279
−0.07	methionine−8−amino−7−oxononanoate aminotransferase:	MMP0865
−0.02	hypothetical protein:	MMP0118
−0.01	hypothetical protein:	MMP1471

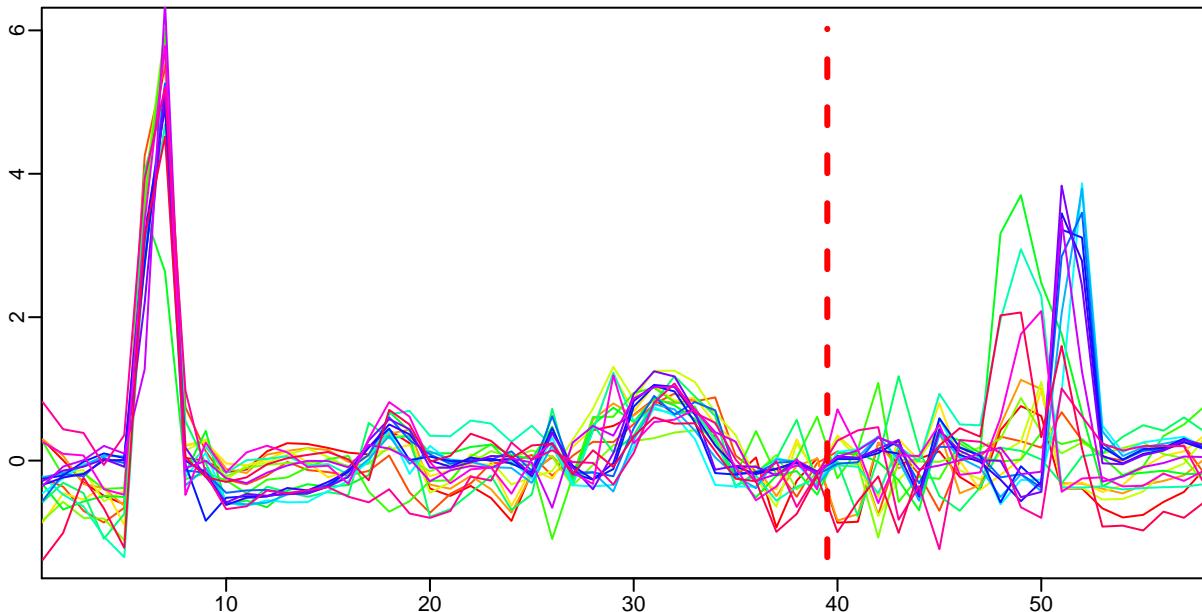**Cluster: 0116 mmp; resid: 0.07; r/c: 8/37**

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cMonkey Version 4.8.8 mmp

ribonuclease P protein component 1: MMP1407

30S ribosomal protein S17P: MMP1408

50S ribosomal protein L14P: MMP1409

50S ribosomal protein L24P: MMP1410

30S ribosomal protein S4e: MMP1411

50S ribosomal protein L5P: MMP1412

30S ribosomal protein S14P: MMP1413
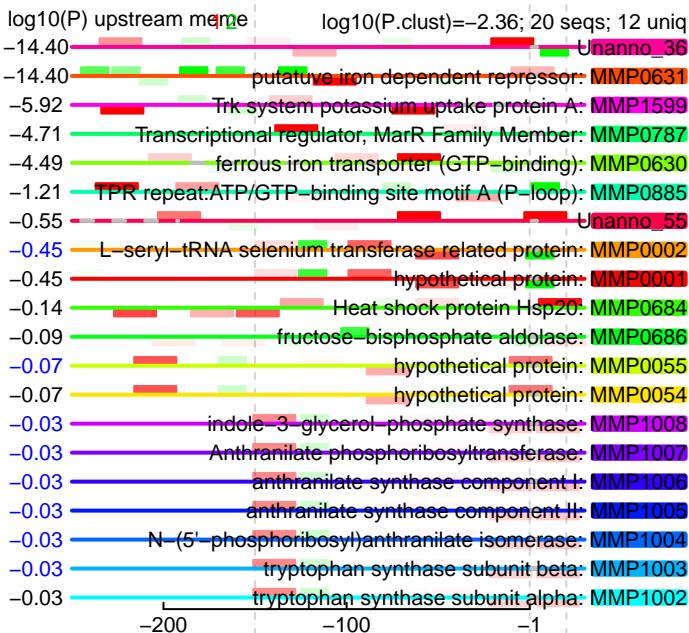
30S ribosomal protein S8P: MMP1414

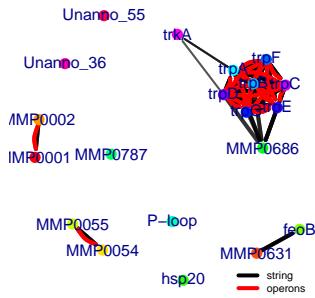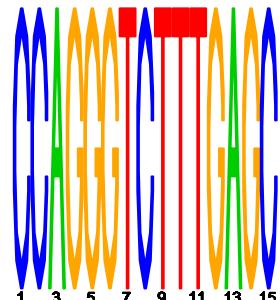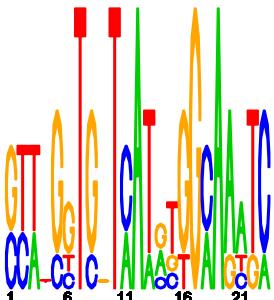−200   −100   −1

sequence position

Cluster: 0117 mmp; resid: 0.42; r/c: 29/37

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=21

upstream meme PSSM #2; e=34

log10(P) upstream meme   log10(P.clust)=−4.04; 29 seqs; 21 uniq

log10(P)	description	gene
−9.94	hypothetical protein:	MMP1665
−8.10	Precorrin−4 C11−methyltransferase:	MMP1662
−7.45	I region, domain I and II:MoeA C−terminal, domain IV:	MMP1619
−7.45	hypothetical protein:	MMP1459
−7.45	hypothetical protein:	MMP1456
−7.45	hypothetical protein:	MMP1454
−7.45	hypothetical protein:	MMP1453
−7.45	hypothetical protein:	MMP1452
−7.45	sor family Helix−turn−helix motif containing protein:	MMP1447
−7.45	energy conserving hydrogenase A small subunit:	MMP1461
−6.72	Hydrogenase expression/formation protein (HUPF/HYPC):	MMP1330
−5.07		Antisense_23
−4.34	hypothetical protein:	MMP1679
−3.22	Hydrogenase expression/formation protein:	MMP0289
−2.83	hypothetical protein:	MMP0992
−2.54	DNA replication protein; MCM family; putative:	MMP0030
−2.24	dihydroorotate dehydrogenase 1B:	MMP0439
−1.92	hypothetical protein:	MMP0052
−1.68	Glycosyl transferase, group 1:	MMP1088
−1.61	hypothetical protein:	MMP0177
−1.55	hypothetical protein:	MMP1241
−1.53	lysine/ homoserine−homoserine lactone exporter family:	MMP0849
−1.50		Unanno_49
−0.84	hypothetical protein:	MMP1118
−0.50	hypothetical protein:	MMP1236
−0.50	Molybdopterin biosynthesis MoaE:	MMP1235
−0.42	hypothetical protein:	MMP0226
−0.42	glycerol dehydrogenase:	MMP0225
−0.25	hypothetical protein:	MMP0788

Cluster: 0118 mmp; resid: 0.10; r/c: 8/38

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

30S ribosomal protein S13P: MMP1319
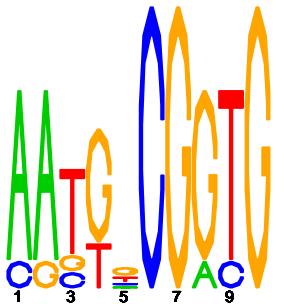30S ribosomal protein S4: MMP1320
30S ribosomal protein S11P: MMP1321
DNA−directed RNA polymerase, subunit D: MMP1322
50S ribosomal protein L18e: MMP1323
50S ribosomal protein L13P: MMP1324
30S ribosomal protein S9P: MMP1325
DNA−directed RNA polymerase subunit N: MMP1326
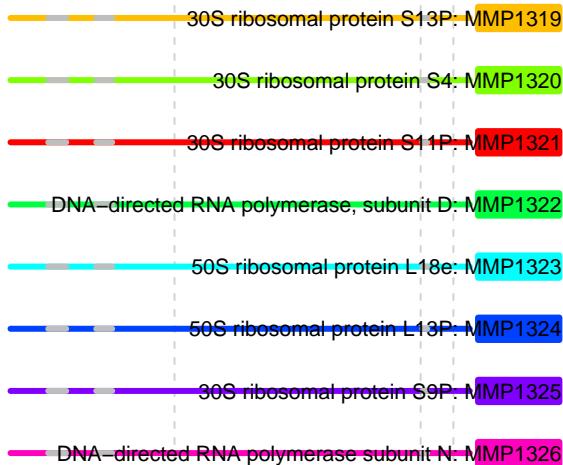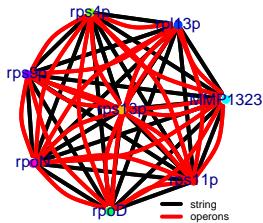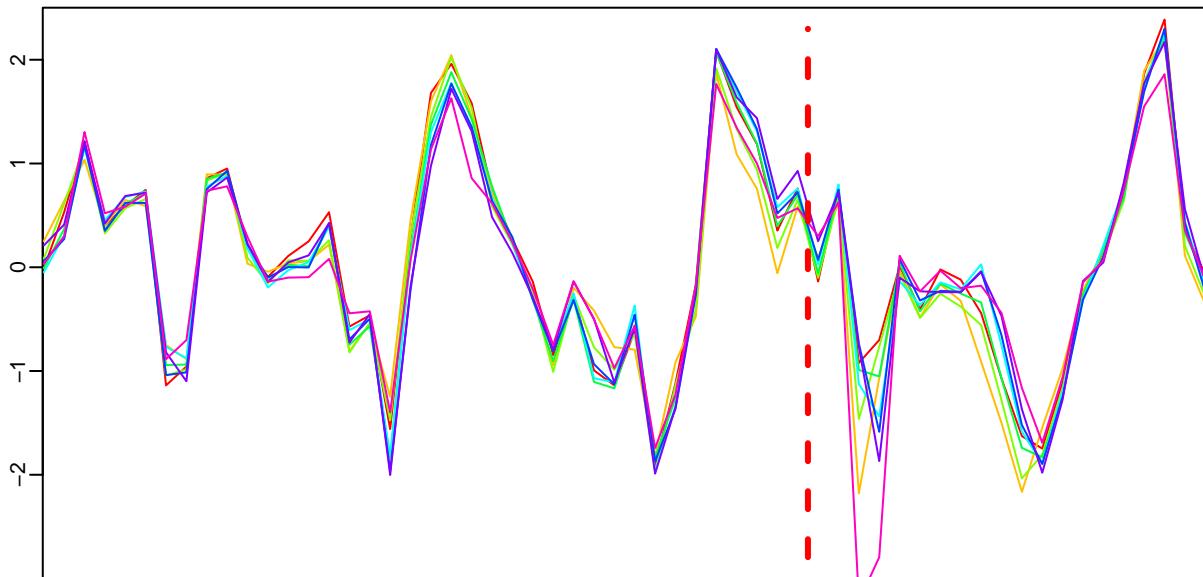
−200   −100   −1

string
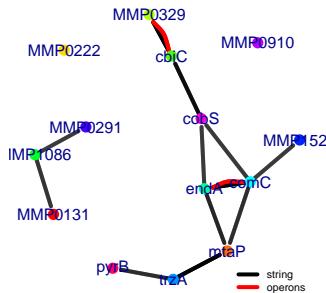operons

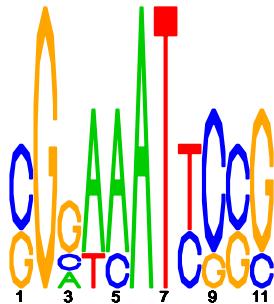**Cluster: 0119 mmp; resid: 0.25; r/c: 21/39**

11 Oct 11 16:14:07 iter=2000
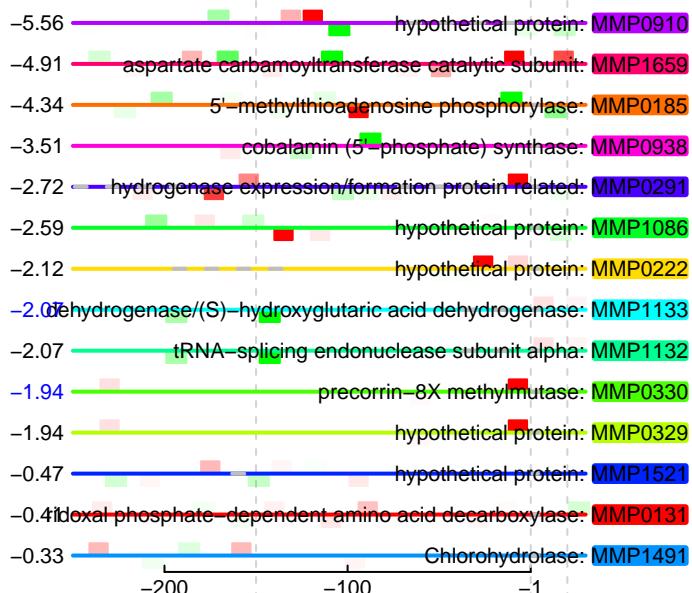cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=6.5   upstream meme PSSM #2; e=2.8e+03

log10(P) upstream meme   log10(P.clust)=−3.63; 21 seqs; 20 uniq

log10(P)	Annotation	Gene
−7.83		Antisense_15
−7.71		Antisense_21
−6.97	hypothetical protein:	MMP1569
−6.97	hypothetical protein:	MMP1568
−6.76	ed to ehbP of Methanothermobacter thermautotrophicus:	MMP0940
−6.63	prephenate dehydratase:	MMP1528
−5.92		Unanno_46
−5.63		Antisense_14
−3.58	NUDIX hydrolase:	MMP0339
−3.35	de synthase:Cobyrinic acid a,c−diamide synthase CbiA:	MMP1478
−2.94	dihydroorotate dehydrogenase 1B:	MMP0439
−2.46		Antisense_25
−2.42		Antisense_26
−1.93		Antisense_11
−1.85		Antisense_12
−1.57		Antisense_20
−0.81		Antisense_7
−0.42		Antisense_19
−0.34	hypothetical protein:	MMP1056
−0.05	coenzyme F420−non−reducing hydrogenase subunit delta:	MMP0821
−0.04		Unanno_53

Cluster: 0120 mmp; resid: 0.26; r/c: 18/40

11 Oct 11 16:14:07 iter=2000
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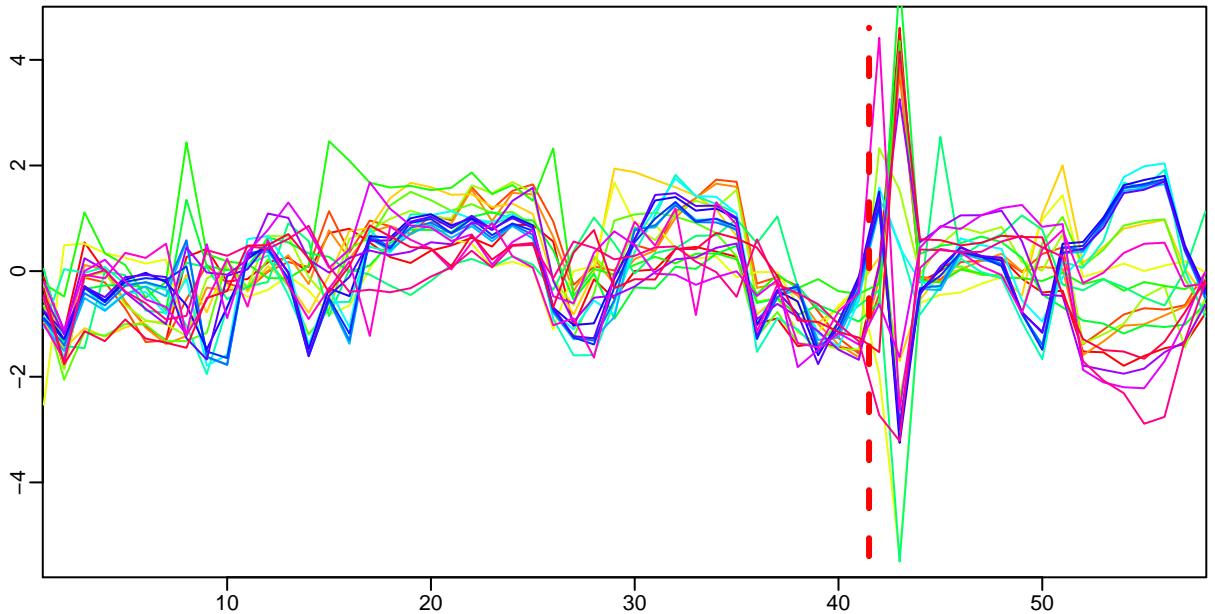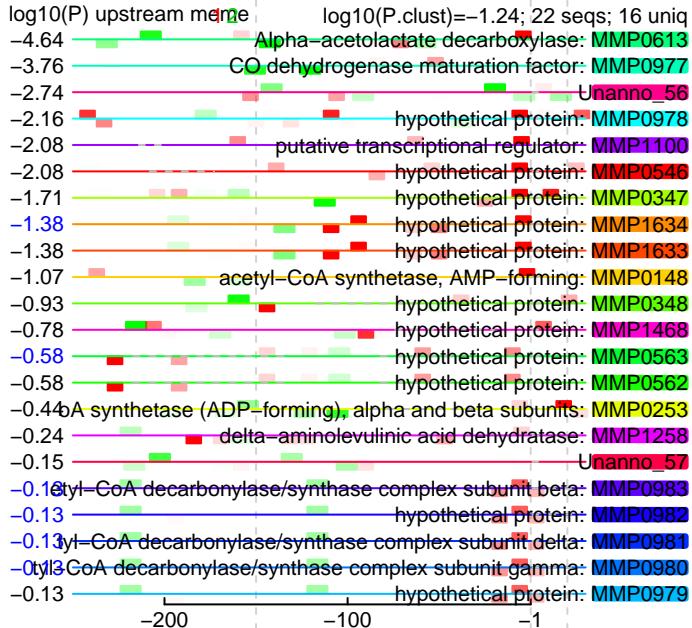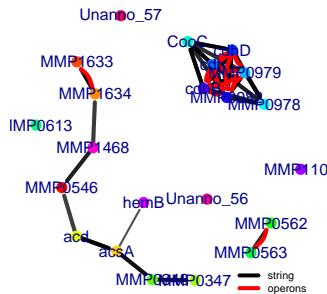upstream meme PSSM #1; e=1.4e+04   upstream meme PSSM #2; e=1.4e+04

log10(P) upstream meme   log10(P.clust)=−0.56; 18 seqs; 14 uniq

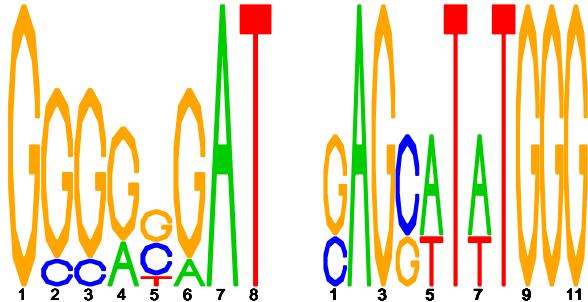| log10(P)	name	gene
−4.00	oxoglutarate ferredoxin oxidoreductase subunit beta:	MMP1316
−2.50	pyruvate carboxylase subunit B:	MMP0340
−1.51	DNA repair and recombination protein RadA:	MMP1222
−0.74	argininosuccinate synthase:	MMP0073
−0.66	pyruvate carboxylase subunit A:	MMP0341
−0.43	IMP dehydrogenase:	MMP0133
−0.16	argininosuccinate lyase:	MMP0013
−0.03	Transketolase, N terminal half:	MMP1115
−0.03	Pentose−5−phosphate 3−epimerase:	MMP1114
−0.03	transketoloase, C terminal half:	MMP1113
−0.03	hypothetical protein:	MMP0223
−0.02	group II) similar to Acetylornithine aminotransferase:	MMP1101
−0.02	succinyl−CoA synthetase subunit alpha:	MMP0955
−0.00	phenylalanyl−tRNA synthetase subunit beta:	MMP1255
−0.00	phosphoribosylaminoimidazole synthetase:	MMP1254
−0.00	hypothetical protein:	MMP1253
−0.00	:OB−fold nucleic acid binding domain Related protein:	MMP1314
0.00	phosphoglycerate kinase:	MMP1532

Cluster: 0121 mmp; resid: 0.24; r/c: 20/39

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=16

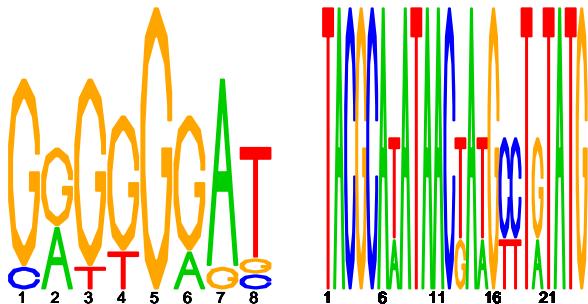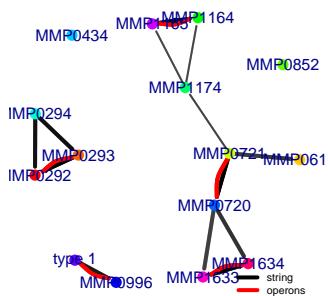upstream meme PSSM #2; e=200

log10(P) upstream meme

log10(P.clust)=−2.36; 20 seqs; 12 uniq

log10(P)	Description	ID
−14.40	Unanno_36	
−14.40	putatuve iron dependent repressor:	MMP0631
−5.92	Trk system potassium uptake protein A:	MMP1599
−4.71	Transcriptional regulator, MarR Family Member:	MMP0787
−4.49	ferrous iron transporter (GTP−binding):	MMP0630
−1.21	TPR repeat:ATP/GTP−binding site motif A (P−loop):	MMP0885
−0.55	Unanno_55	
−0.45	L−seryl−tRNA selenium transferase related protein:	MMP0002
−0.45	hypothetical protein:	MMP0001
−0.14	Heat shock protein Hsp20:	MMP0684
−0.09	fructose−bisphosphate aldolase:	MMP0686
−0.07	hypothetical protein:	MMP0055
−0.07	hypothetical protein:	MMP0054
−0.03	indole−3−glycerol−phosphate synthase:	MMP1008
−0.03	Anthranilate phosphoribosyltransferase:	MMP1007
−0.03	anthranilate synthase component I:	MMP1006
−0.03	anthranilate synthase component II:	MMP1005
−0.03	N−(5'−phosphoribosyl)anthranilate isomerase:	MMP1004
−0.03	tryptophan synthase subunit beta:	MMP1003
−0.03	tryptophan synthase subunit alpha:	MMP1002

string
operons

Cluster: 0122 mmp; resid: 0.23; r/c: 14/37
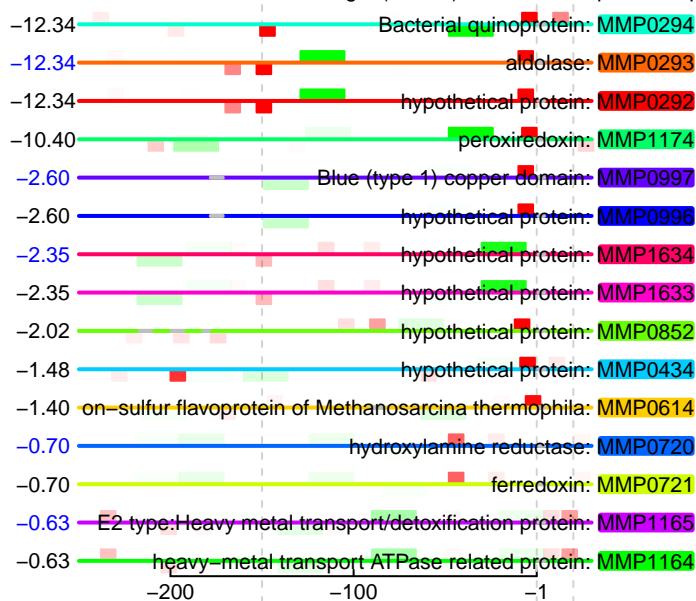
11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=7.5

upstream meme PSSM #2; e=710
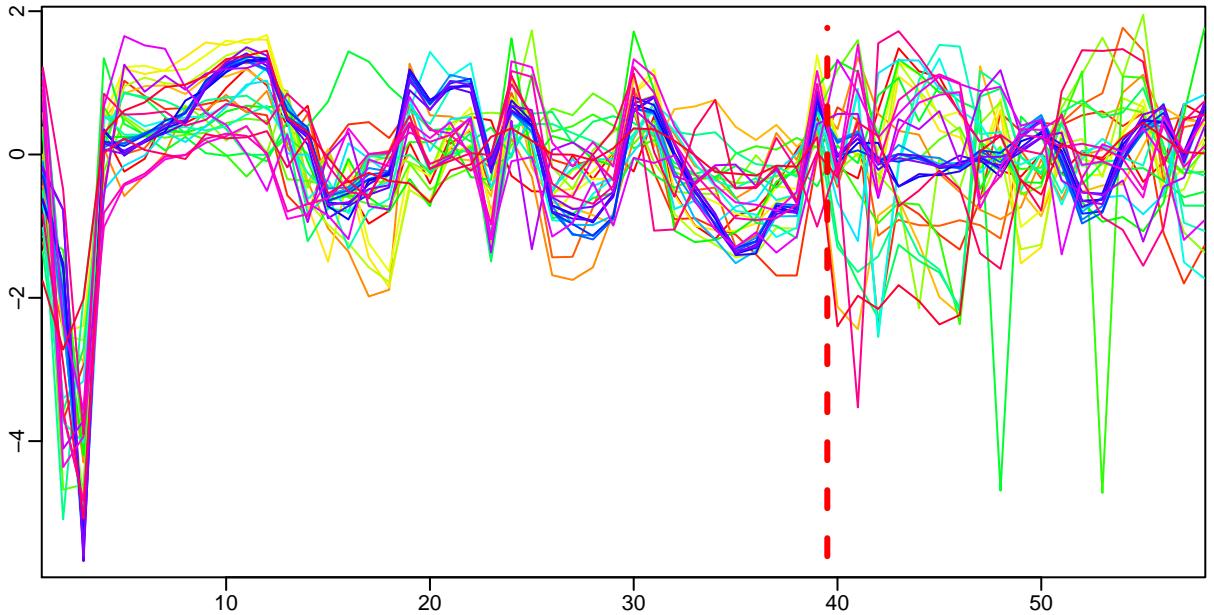
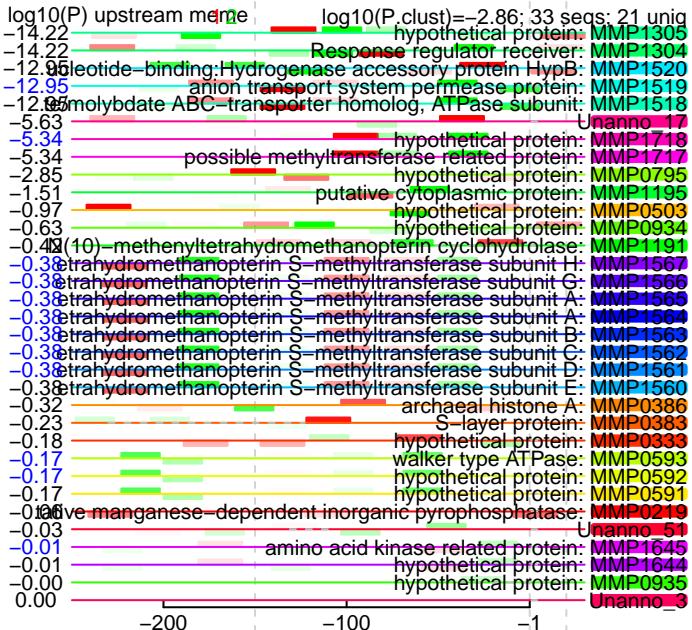log10(P) upstream meme

log10(P.clust)=−2.50; 14 seqs; 12 uniq

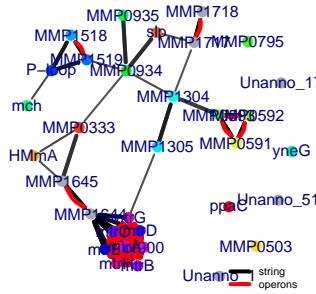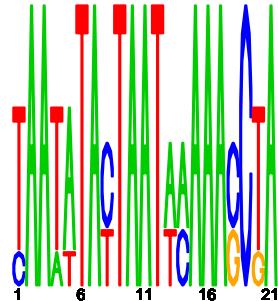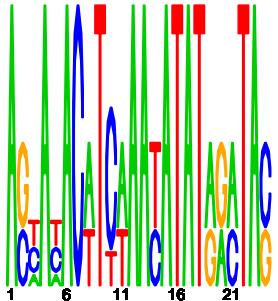| log10(P)	Annotation	Gene
−5.56	hypothetical protein:	MMP0910
−4.91	aspartate carbamoyltransferase catalytic subunit:	MMP1659
−4.34	5'−methylthioadenosine phosphorylase:	MMP0185
−3.51	cobalamin (5−phosphate) synthase:	MMP0938
−2.72	hydrogenase expression/formation protein related:	MMP0291
−2.59	hypothetical protein:	MMP1086
−2.12	hypothetical protein:	MMP0222
−2.08	dehydrogenase/(S)−hydroxyglutaric acid dehydrogenase:	MMP1133
−2.07	tRNA−splicing endonuclease subunit alpha:	MMP1132
−1.94	precorrin−8X methylmutase:	MMP0330
−1.94	hypothetical protein:	MMP0329
−0.47	hypothetical protein:	MMP1521
−0.41	pyridoxal phosphate−dependent amino acid decarboxylase:	MMP0131
−0.33	Chlorohydrolase:	MMP1491

Cluster: 0123 mmp; resid: 0.43; r/c: 33/38

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upstream meme PSSM #1; e=1.5e+03   upstream meme PSSM #2; e=4.6e+03

log10(P) upstream meme   log10(P,clust)=−1.77; 33 seqs: 27 uniq

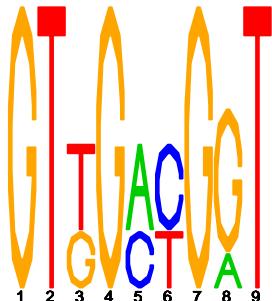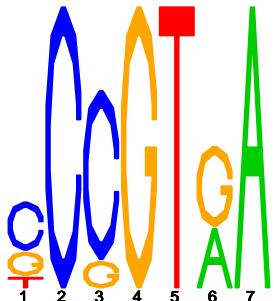| log10(P)	annotation
−6.29	hypothetical protein: MMP1660
−6.29	hypothetical protein: MMP1661
−5.95	hypothetical protein: MMP1533
−5.23	CBS domain: MMP0908
−3.24	Unanno_32
−3.08	dehydrogenase/fumarate reductase iron−sulfur subunit: MMP1067
−2.74	cofactor−independent phosphoglycerate mutase: MMP1439
−2.65	archaeal histone B: MMP1347
−2.43	hypothetical protein: MMP0763
−2.40	signal recognition particle receptor SRalpha: MMP0683
−2.00	hypothetical protein: MMP1534
−1.95	hypothetical protein: MMP1156
−1.95	hypothetical protein: MMP1158
−1.95	heterosulfide reductase, subunit C1: MMP1154
−1.73	hypothetical protein: MMP0624
−1.60	Unanno_38
−1.55	coenzyme F420−reducing hydrogenase subunit alpha: MMP0820
−0.95	hypothetical protein: MMP0772
−0.57	te motif A (P−loop):Small GTP−binding protein domain: MMP1642
−0.53	nickel responsive regulator: MMP0020
−0.46	hypothetical protein: MMP1223
−0.42	phosphoribosylglycinamide formyltransferase 2: MMP0123
−0.37	probable Molybdenum−pterin binding protein: MMP0628
−0.26	CBS domain: MMP1252
−0.26	hypothetical protein: MMP1251
−0.22	heterodisulfide reductase subunit A: MMP0825
−0.21	hypothetical protein: MMP1685
−0.20	Rubrerythrin: MMP1136
−0.20	Flavodoxin:Beta−lactamase−like: MMP1135
−0.20	type A flavoprotein: MMP1134
−0.16	heterodisulfide reductase, subunit A: MMP1697
−0.16	hypothetical protein: MMP1229
−0.14	hypothetical protein: MMP1016

Cluster: 0124 mmp; resid: 0.42; r/c: 22/41

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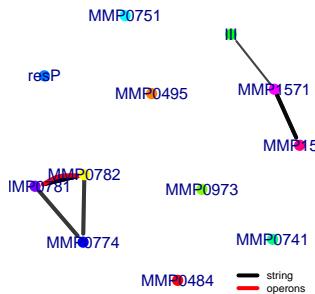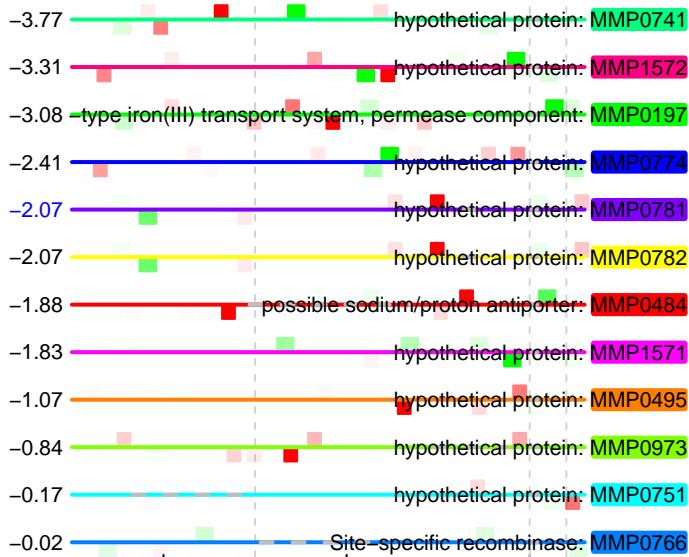cMonkey Version 4.8.8 mmp
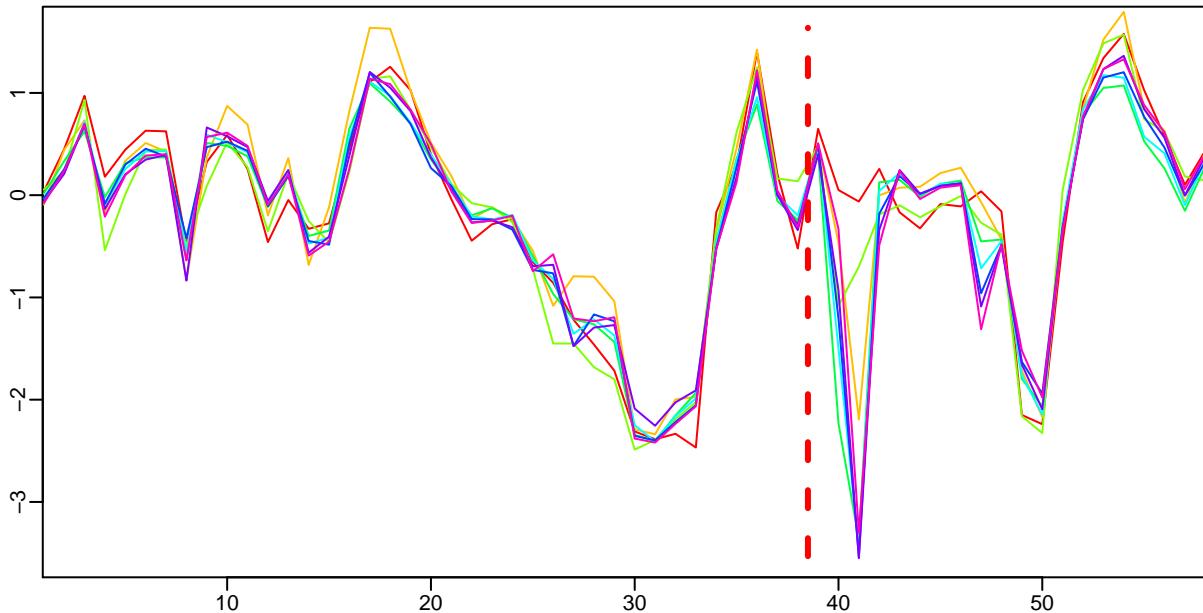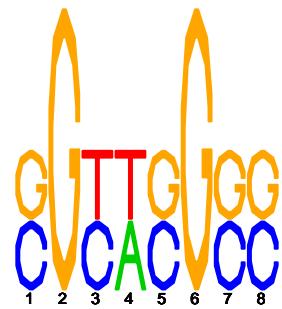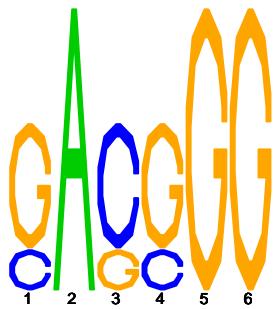
upstream meme PSSM #1; e=13   upstream meme PSSM #2; e=8.7e+03

log10(P) upstream meme   log10(P.clust)=−1.24; 22 seqs; 16 uniq

log10(P)	Annotation	Gene
−4.64	Alpha−acetolactate decarboxylase	MMP0613
−3.76	CO dehydrogenase maturation factor	MMP0977
−2.74		Unanno_56
−2.16	hypothetical protein	MMP0978
−2.08	putative transcriptional regulator	MMP1100
−2.08	hypothetical protein	MMP0546
−1.71	hypothetical protein	MMP0347
−1.38	hypothetical protein	MMP1634
−1.38	hypothetical protein	MMP1633
−1.07	acetyl−CoA synthetase, AMP−forming	MMP0148
−0.93	hypothetical protein	MMP0348
−0.78	hypothetical protein	MMP1468
−0.58	hypothetical protein	MMP0563
−0.58	hypothetical protein	MMP0562
−0.44	bA synthetase (ADP−forming), alpha and beta subunits	MMP0253
−0.24	delta−aminolevulinic acid dehydratase	MMP1258
−0.15		Unanno_57
−0.15	etyl−CoA decarbonylase/synthase complex subunit beta	MMP0983
−0.13	hypothetical protein	MMP0982
−0.13	tyl−CoA decarbonylase/synthase complex subunit delta	MMP0981
−0.13	tyl−CoA decarbonylase/synthase complex subunit gamma	MMP0980
−0.13	hypothetical protein	MMP0979

string
operons

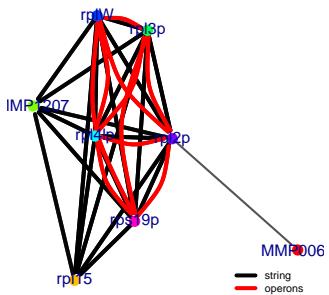**Cluster: 0125 mmp; resid: 0.24; r/c: 15/38**

upstream meme PSSM #1; e=0.0046   upstream meme PSSM #2; e=8.6

log10(P) upstream meme   log10(P.clust)=−4.33; 15 seqs; 10 uniq

−12.34	Bacterial quinoprotein: MMP0294
−12.34	aldolase: MMP0293
−12.34	hypothetical protein: MMP0292
−10.40	peroxiredoxin: MMP1174
−2.60	Blue (type 1) copper domain: MMP0997
−2.60	hypothetical protein: MMP0996
−2.35	hypothetical protein: MMP1634
−2.35	hypothetical protein: MMP1633
−2.02	hypothetical protein: MMP0852
−1.48	hypothetical protein: MMP0434
−1.40	on−sulfur flavoprotein of Methanosarcina thermophila: MMP0614
−0.70	hydroxylamine reductase: MMP0720
−0.70	ferredoxin: MMP0721
−0.63	E2 type:Heavy metal transport/detoxification protein: MMP1165
−0.63	heavy−metal transport ATPase related protein: MMP1164

−200   −100   −1
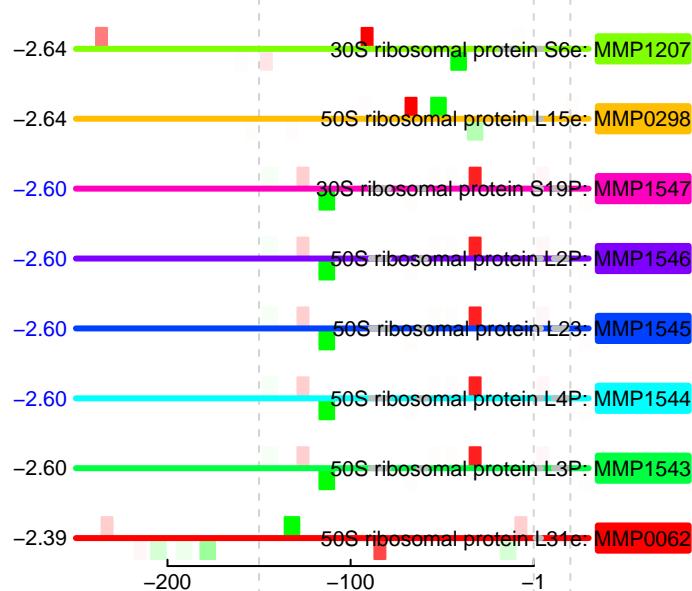
Cluster: 0126 mmp; resid: 0.41; r/c: 33/39

upstream meme PSSM #1; e=0.68   upstream meme PSSM #2; e=160

log10(P) upstream meme   log10(P.clust)=−2.86; 33 seqs: 21 unig

−14.22	hypothetical protein: MMP1305
−14.22	Response regulator receiver: MMP1304
−12.95	nucleotide−binding:Hydrogenase accessory protein HypB: MMP1520
−12.95	anion transport system permease protein: MMP1519
−12.95	molybdate ABC−transporter homolog, ATPase subunit: MMP1518
−5.63	Unanno_17
−5.34	hypothetical protein: MMP1718
−5.34	possible methyltransferase related protein: MMP1717
−2.85	hypothetical protein: MMP0795
−1.51	putative cytoplasmic protein: MMP1195
−0.97	hypothetical protein: MMP0503
−0.63	hypothetical protein: MMP0934
−0.41	12(10)−methenyltetrahydromethanopterin cyclohydrolase: MMP1191
−0.38	tetrahydromethanopterin S−methyltransferase subunit H: MMP1567
−0.38	tetrahydromethanopterin S−methyltransferase subunit G: MMP1566
−0.38	tetrahydromethanopterin S−methyltransferase subunit A: MMP1565
−0.38	tetrahydromethanopterin S−methyltransferase subunit A: MMP1564
−0.38	tetrahydromethanopterin S−methyltransferase subunit B: MMP1563
−0.38	tetrahydromethanopterin S−methyltransferase subunit C: MMP1562
−0.38	tetrahydromethanopterin S−methyltransferase subunit D: MMP1561
−0.38	tetrahydromethanopterin S−methyltransferase subunit E: MMP1560
−0.32	archaeal histone A: MMP0386
−0.23	S−layer protein: MMP0383
−0.18	hypothetical protein: MMP0333
−0.17	walker type ATPase: MMP0593
−0.17	hypothetical protein: MMP0592
−0.17	hypothetical protein: MMP0591
−0.10	putative manganese−dependent inorganic pyrophosphatase: MMP0219
−0.03	Unanno_51
−0.01	amino acid kinase related protein: MMP1645
−0.01	hypothetical protein: MMP1644
−0.00	hypothetical protein: MMP0935
0.00	Unanno_3

Cluster: 0127 mmp; resid: 0.14; r/c: 12/40

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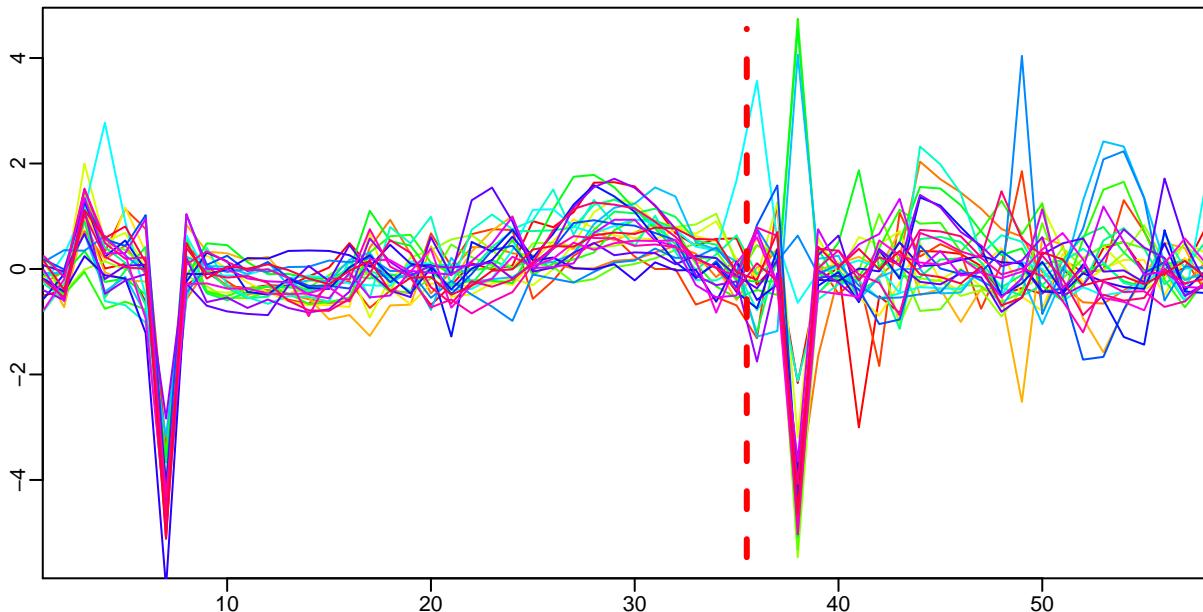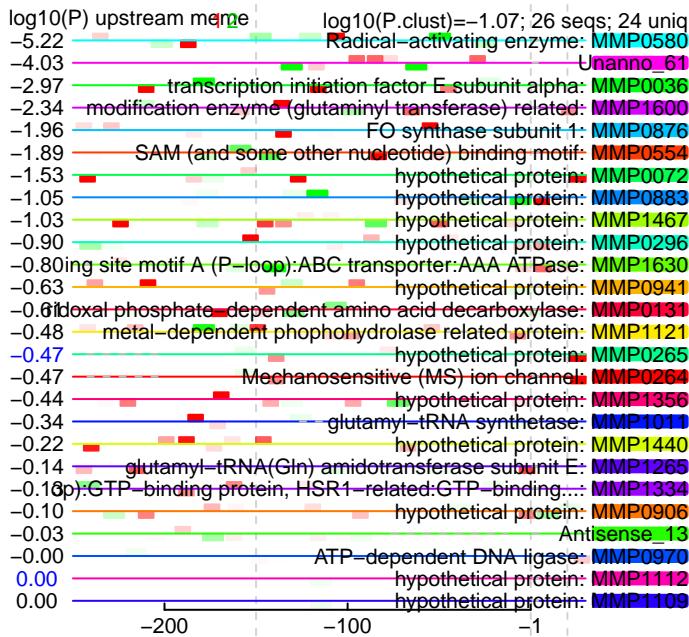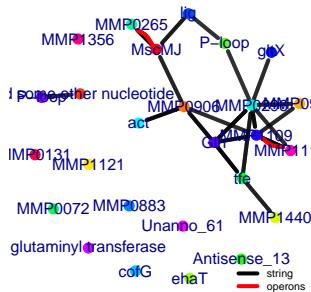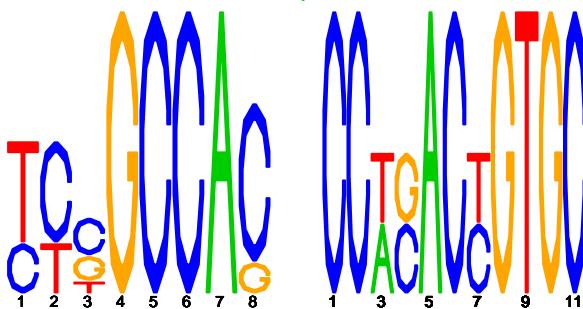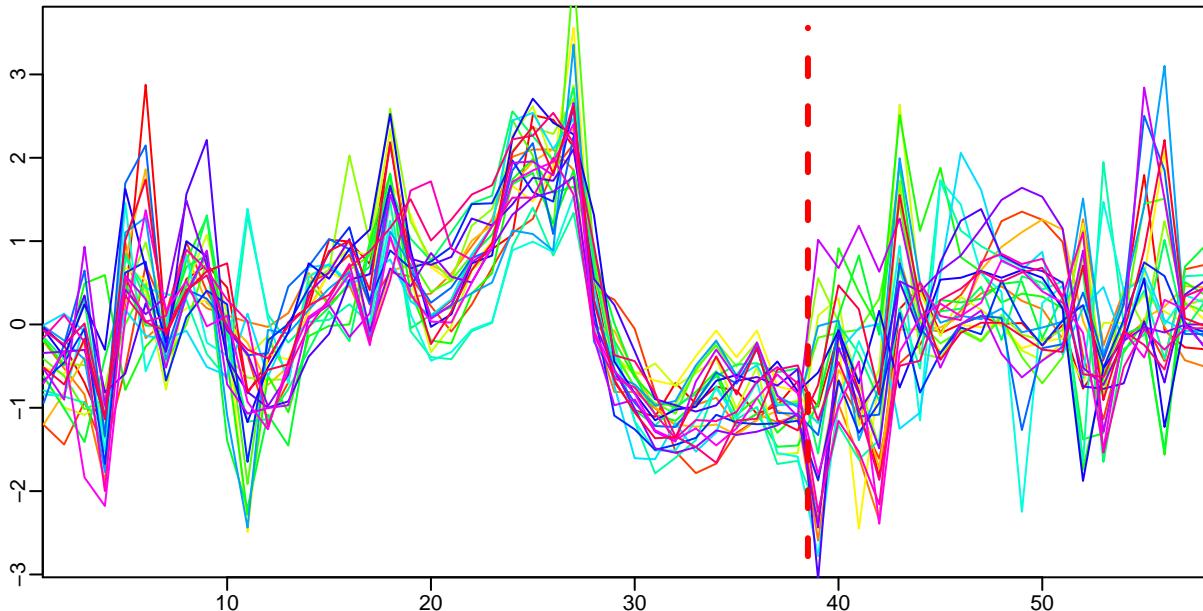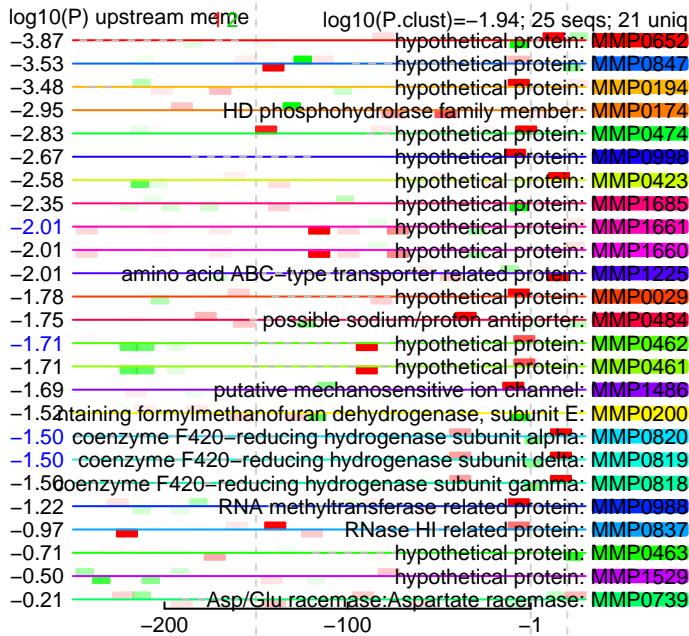upstream meme PSSM #1; e=150

upstream meme PSSM #2; e=420

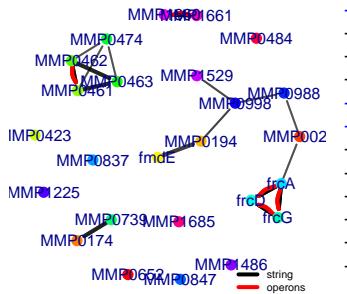log10(P) upstream meme

log10(P.clust)=−1.88; 12 seqs; 11 uniq

log10(P)	annotation	gene
−3.77	hypothetical protein:	MMP0741
−3.31	hypothetical protein:	MMP1572
−3.08	type iron(III) transport system, permease component:	MMP0197
−2.41	hypothetical protein:	MMP0774
−2.07	hypothetical protein:	MMP0781
−2.07	hypothetical protein:	MMP0782
−1.88	possible sodium/proton antiporter:	MMP0484
−1.83	hypothetical protein:	MMP1571
−1.07	hypothetical protein:	MMP0495
−0.84	hypothetical protein:	MMP0973
−0.17	hypothetical protein:	MMP0751
−0.02	Site−specific recombinase:	MMP0766

MMP0751
resP
MMP0495
MMP1571
MMP1572
MMP0782
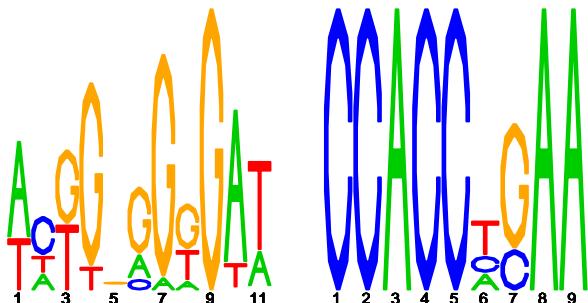IMP0781
MMP0973
MMP0774
MMP0741
MMP0484

string
operons

Cluster: 0128 mmp; resid: 0.10; r/c: 8/38

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upstream meme PSSM #1; e=10

upstream meme PSSM #2; e=21

log10(P) upstream meme

log10(P.clust)=−2.58; 8 seqs; 4 uniq

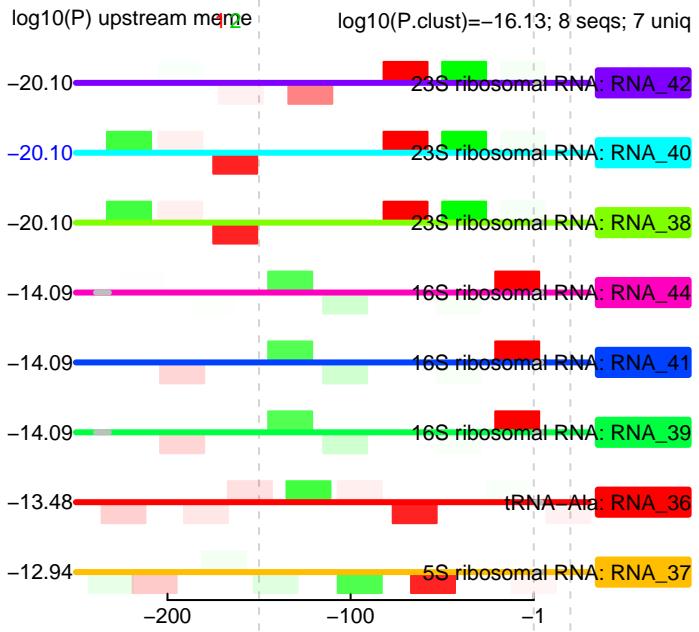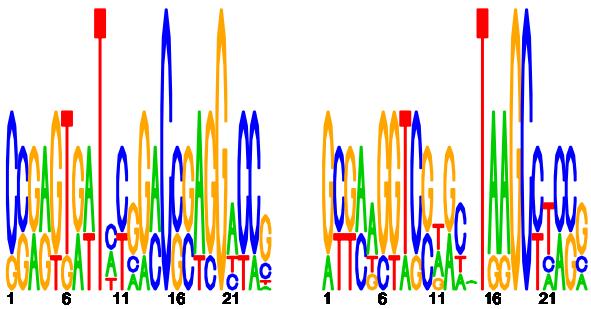|		
−2.64	30S ribosomal protein S6e:	MMP1207
−2.64	50S ribosomal protein L15e:	MMP0298
−2.60	30S ribosomal protein S19P:	MMP1547
−2.60	50S ribosomal protein L2P:	MMP1546
−2.60	50S ribosomal protein L23:	MMP1545
−2.60	50S ribosomal protein L4P:	MMP1544
−2.60	50S ribosomal protein L3P:	MMP1543
−2.39	50S ribosomal protein L31e:	MMP0062

Cluster: 0129 mmp; resid: 0.32; r/c: 26/35
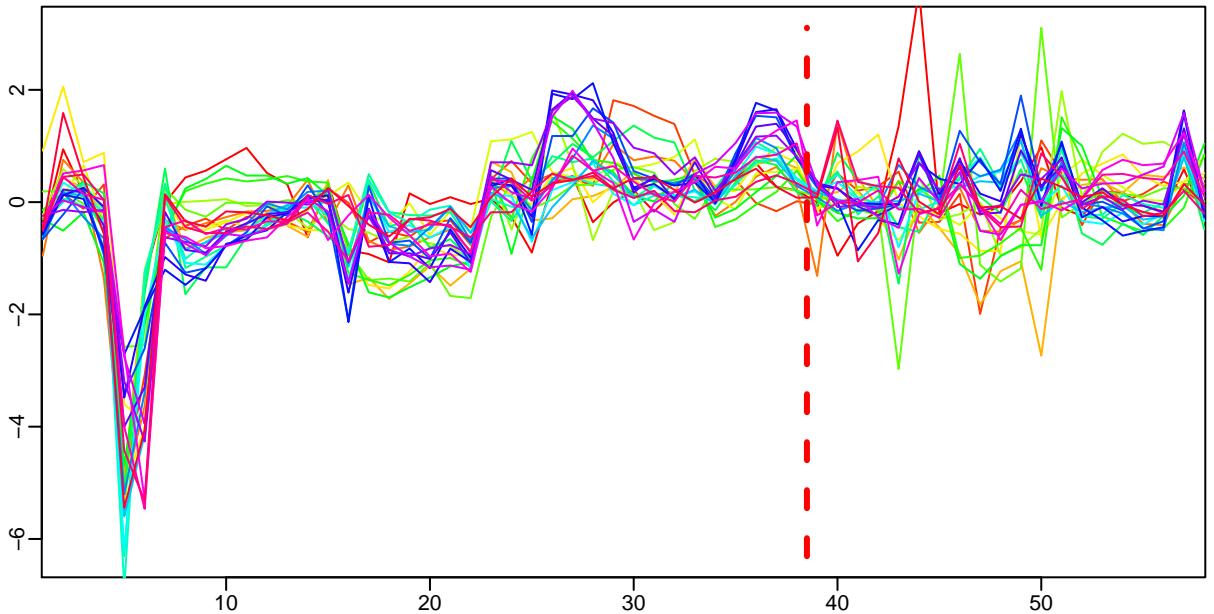

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cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=2.1e+00   upstream meme PSSM #2; e=2.4e+04

log10(P) upstream meme   log10(P.clust)=−1.07; 26 seqs; 24 uniq

log10(P)	annotation
−5.22	Radical–activating enzyme: MMP0580
−4.03	Unanno_61
−2.97	transcription initiation factor E subunit alpha: MMP0036
−2.34	modification enzyme (glutaminyl transferase) related: MMP1600
−1.96	FO synthase subunit 1: MMP0876
−1.89	SAM (and some other nucleotide) binding motif: MMP0554
−1.53	hypothetical protein: MMP0072
−1.05	hypothetical protein: MMP0883
−1.03	hypothetical protein: MMP1467
−0.90	hypothetical protein: MMP0296
−0.80	ing site motif A (P–loop):ABC transporter:AAA ATPase: MMP1630
−0.63	hypothetical protein: MMP0941
−0.61	idoxal phosphate–dependent amino acid decarboxylase: MMP0131
−0.48	metal–dependent phophohydrolase related protein: MMP1121
−0.47	hypothetical protein: MMP0265
−0.47	Mechanosensitive (MS) ion channel: MMP0264
−0.44	hypothetical protein: MMP1356
−0.34	glutamyl–tRNA synthetase: MMP1011
−0.22	hypothetical protein: MMP1440
−0.14	glutamyl–tRNA(Gln) amidotransferase subunit E: MMP1265
−0.10	op):GTP–binding protein, HSR1–related:GTP–binding...: MMP1334
−0.10	hypothetical protein: MMP0906
−0.03	Antisense_13
−0.00	ATP–dependent DNA ligase: MMP0970
0.00	hypothetical protein: MMP1112
0.00	hypothetical protein: MMP1109

Cluster: 0130 mmp; resid: 0.23; r/c: 14/39

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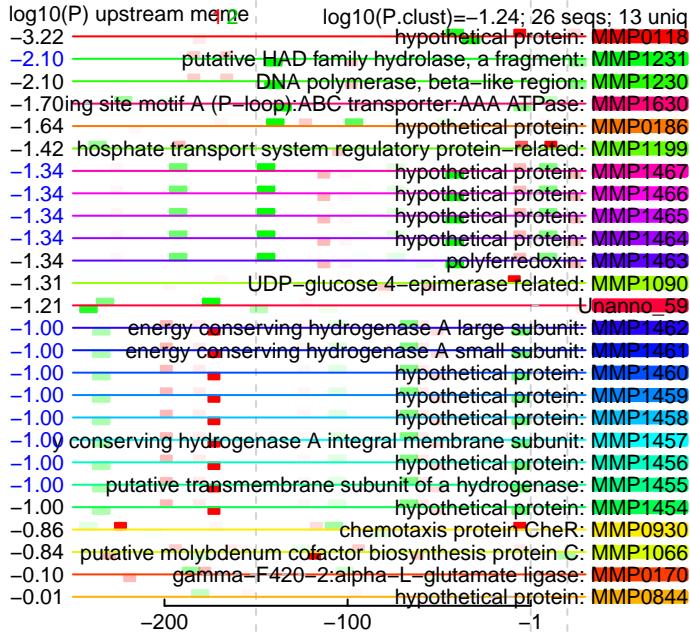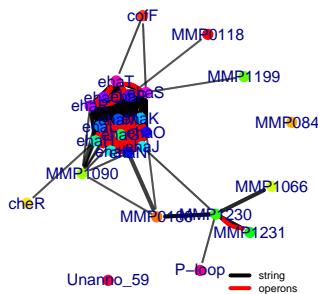**upstream meme PSSM #1; e=19** **upstream meme PSSM #2; e=1.9e+03**

log10(P) upstream meme   log10(P.clust)=−5.70; 14 seqs; 8 uniq

log10(P)	description	gene
−8.93	50S ribosomal protein L7Ae:	MMP0641
−8.93	30S ribosomal protein S28e:	MMP0640
−8.93	LSU ribosomal protein L23E:	MMP0639
−7.13	DNA−directed RNA polymerase subunit A'':	MMP1364
−7.13	DNA−directed RNA polymerase subunit alpha:	MMP1363
−7.13	DNA−directed RNA polymerase subunit B':	MMP1362
−6.61	hypothetical protein:	MMP0034
−6.17	glutamate−1−semialdehyde aminotransferase:	MMP0224
−6.17	hypothetical protein:	MMP0223
−5.20	adenylosuccinate synthetase:	MMP1432
−2.56	translation initiation factor IF−5A:	MMP0952
−2.33	30S ribosomal protein S10P:	MMP1371
−2.33	elongation factor 1−alpha:	MMP1370
−0.16	30S ribosomal protein S8e:	MMP1658

Cluster: 0131 mmp; resid: 0.33; r/c: 25/38

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upstream meme PSSM #1; e=0.0073   upstream meme PSSM #2; e=4.8e+03

log10(P) upstream meme   log10(P.clust)=−1.94; 25 seqs; 21 uniq

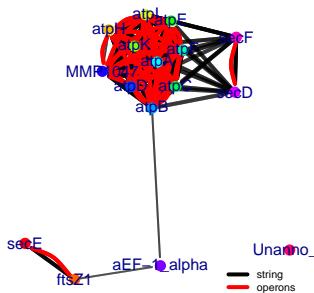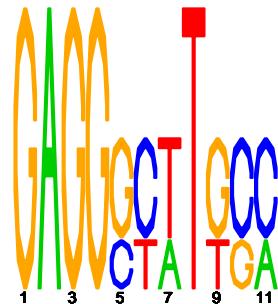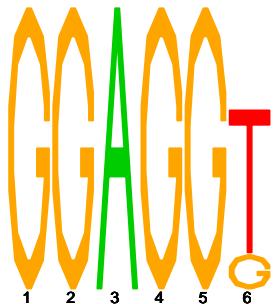| log10(P)	annotation	gene
−3.87	hypothetical protein:	MMP0652
−3.53	hypothetical protein:	MMP0847
−3.48	hypothetical protein:	MMP0194
−2.95	HD phosphohydrolase family member:	MMP0174
−2.83	hypothetical protein:	MMP0474
−2.67	hypothetical protein:	MMP0998
−2.58	hypothetical protein:	MMP0423
−2.35	hypothetical protein:	MMP1685
−2.01	hypothetical protein:	MMP1661
−2.01	hypothetical protein:	MMP1660
−2.01	amino acid ABC−type transporter related protein:	MMP1225
−1.78	hypothetical protein:	MMP0029
−1.75	possible sodium/proton antiporter:	MMP0484
−1.71	hypothetical protein:	MMP0462
−1.71	hypothetical protein:	MMP0461
−1.69	putative mechanosensitive ion channel:	MMP1486
−1.52	containing formylmethanofuran dehydrogenase, subunit E:	MMP0200
−1.50	coenzyme F420−reducing hydrogenase subunit alpha:	MMP0820
−1.50	coenzyme F420−reducing hydrogenase subunit delta:	MMP0819
−1.50	coenzyme F420−reducing hydrogenase subunit gamma:	MMP0818
−1.22	RNA methyltransferase related protein:	MMP0988
−0.97	RNase HI related protein:	MMP0837
−0.71	hypothetical protein:	MMP0463
−0.50	hypothetical protein:	MMP1529
−0.21	Asp/Glu racemase:Aspartate racemase:	MMP0739

Cluster: 0132 mmp; resid: 0.07; r/c: 8/38

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upstream meme PSSM #1; e=1e-09   upstream meme PSSM #2; e=2.3e-05

log10(P) upstream meme

log10(P.clust)=−16.13; 8 seqs; 7 uniq

−20.10	23S ribosomal RNA: RNA_42
−20.10	23S ribosomal RNA: RNA_40
−20.10	23S ribosomal RNA: RNA_38
−14.09	16S ribosomal RNA: RNA_44
−14.09	16S ribosomal RNA: RNA_41
−14.09	16S ribosomal RNA: RNA_39
−13.48	tRNA−Ala: RNA_36
−12.94	5S ribosomal RNA: RNA_37

rrnB 23S
rrnC 23S
:NA−Ala2
rrnC 16S   rrnB 16S
rrnA 16S
rrnA 23S
rrnD 5S

−200   −100   −1

Cluster: 0133 mmp; resid: 0.37; r/c: 26/38

11 Oct 11 16:14:07 iter=2000
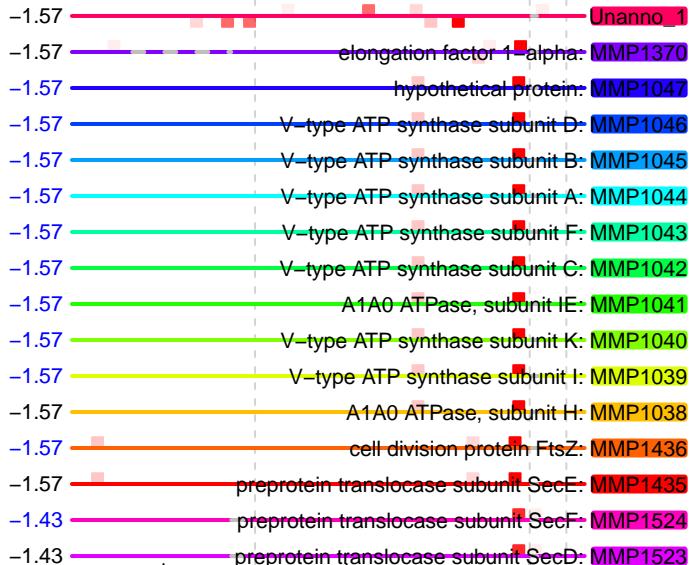cMonkey Version 4.8.8 mmp

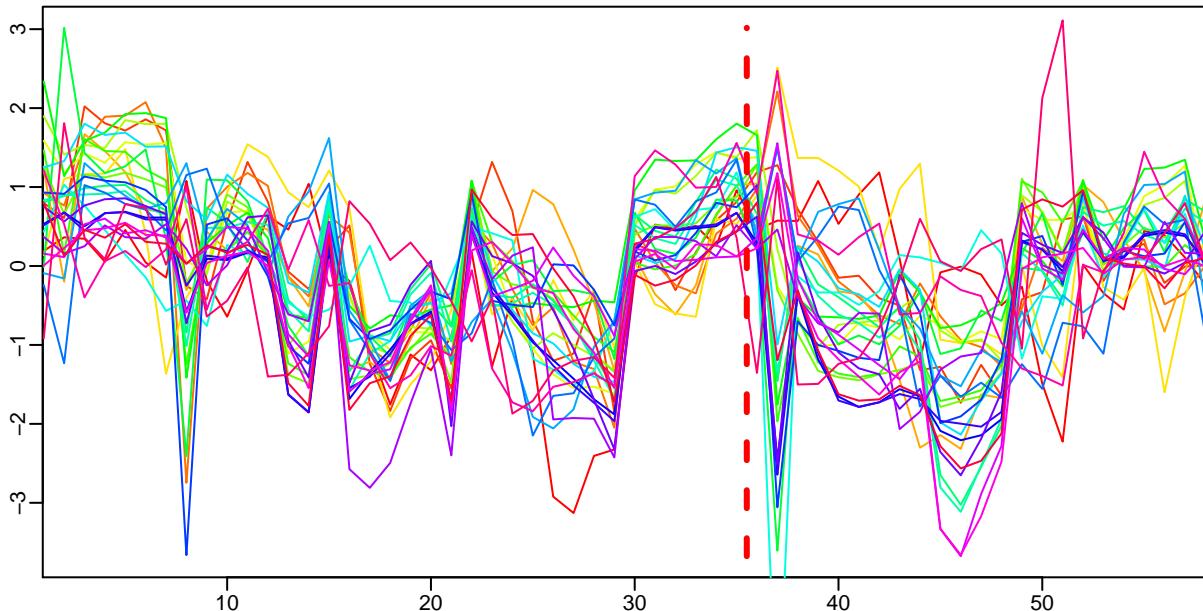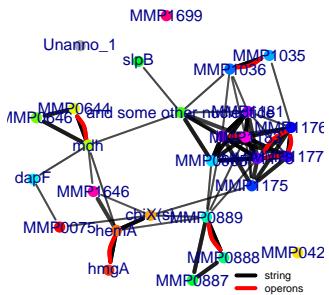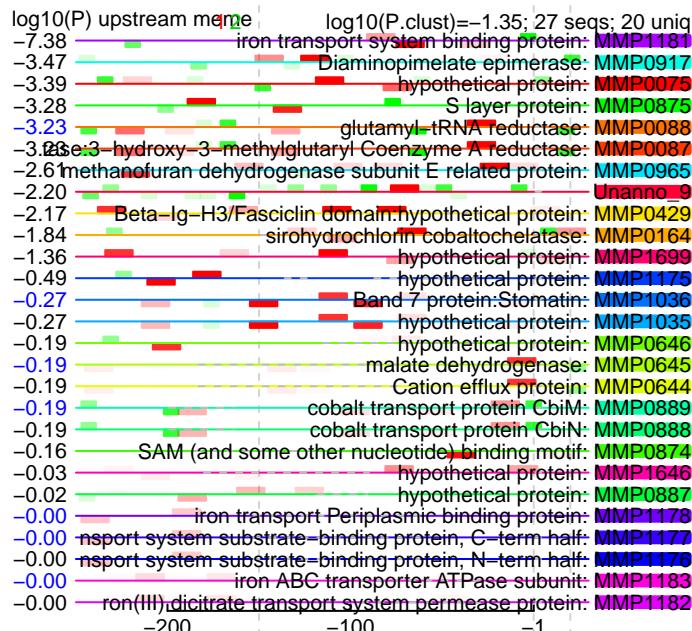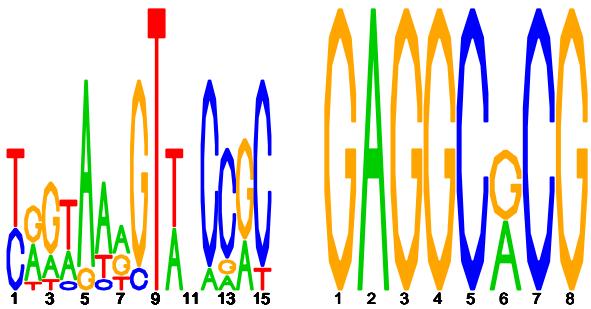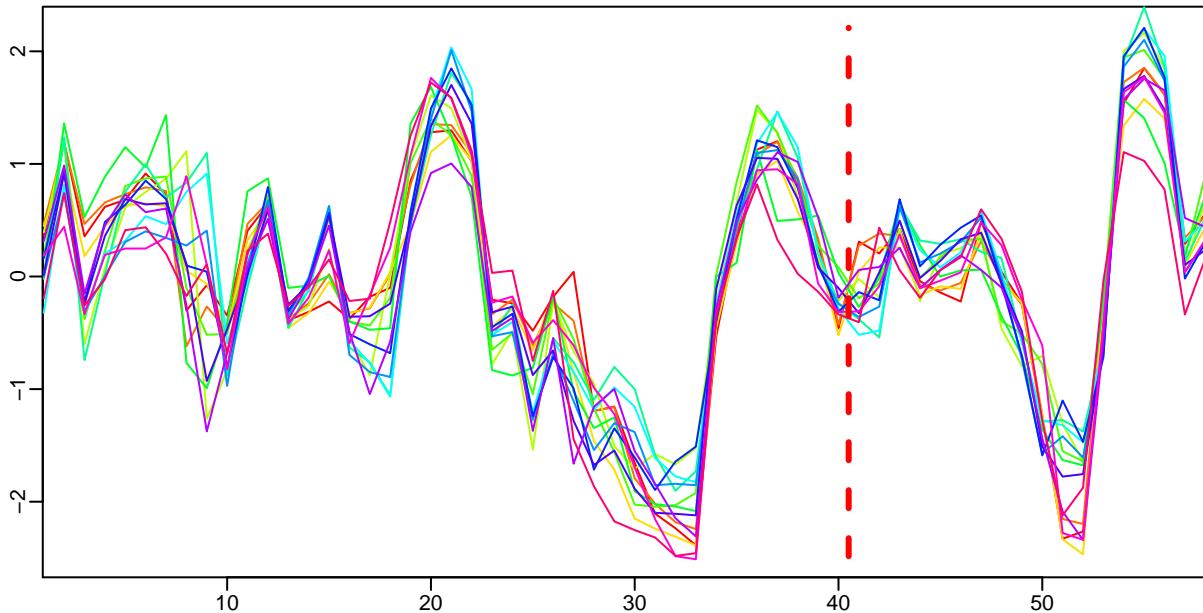upstream meme PSSM #1; e=2.6e+03   upstream meme PSSM #2; e=5.6e+03

log10(P) upstream meme   log10(P.clust)=−1.24; 26 seqs; 13 uniq

log10(P)	Annotation	Gene
−3.22	hypothetical protein	MMP0118
−2.10	putative HAD family hydrolase, a fragment	MMP1231
−2.10	DNA polymerase, beta−like region	MMP1230
−1.70	ing site motif A (P−loop):ABC transporter:AAA ATPase	MMP1630
−1.64	hypothetical protein	MMP0186
−1.42	hosphate transport system regulatory protein−related	MMP1199
−1.34	hypothetical protein	MMP1467
−1.34	hypothetical protein	MMP1466
−1.34	hypothetical protein	MMP1465
−1.34	hypothetical protein	MMP1464
−1.34	polyferredoxin	MMP1463
−1.31	UDP−glucose 4−epimerase related	MMP1090
−1.21		Unanno_59
−1.00	energy conserving hydrogenase A large subunit	MMP1462
−1.00	energy conserving hydrogenase A small subunit	MMP1461
−1.00	hypothetical protein	MMP1460
−1.00	hypothetical protein	MMP1459
−1.00	hypothetical protein	MMP1458
−1.00	conserving hydrogenase A integral membrane subunit	MMP1457
−1.00	hypothetical protein	MMP1456
−1.00	putative transmembrane subunit of a hydrogenase	MMP1455
−1.00		MMP1454
−0.86	chemotaxis protein CheR	MMP0930
−0.84	putative molybdenum cofactor biosynthesis protein C	MMP1066
−0.10	gamma−F420−2:alpha−L−glutamate ligase	MMP0170
−0.01	hypothetical protein	MMP0844

−200   −100   −1

string
operons

Cluster: 0134 mmp; resid: 0.06; r/c: 7/37

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp
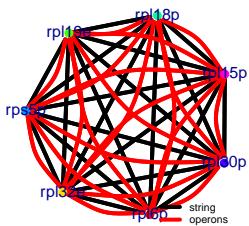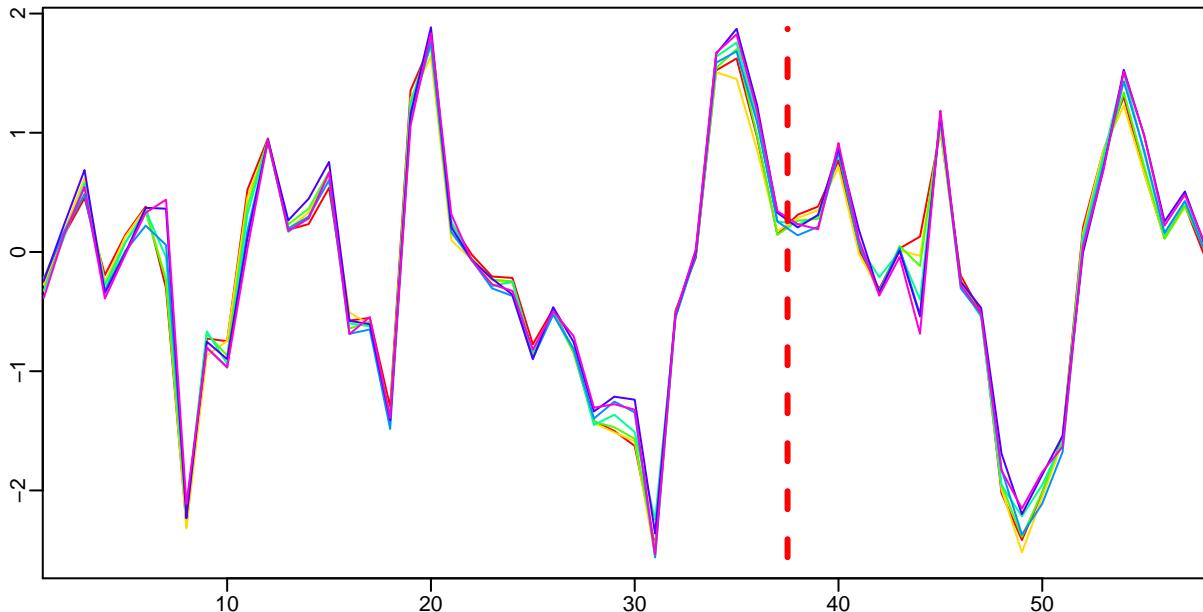
50S ribosomal protein L6P: MMP1415
50S ribosomal protein L32e: MMP1416
50S ribosomal protein L19e: MMP1417
50S ribosomal protein L18P: MMP1418
30S ribosomal protein S5P: MMP1419
50S ribosomal protein L30P: MMP1420
50S ribosomal protein L15P: MMP1421
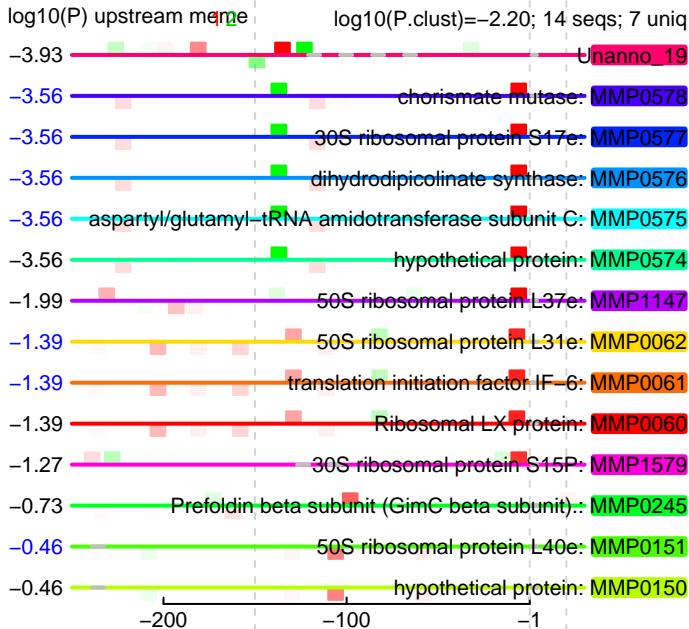
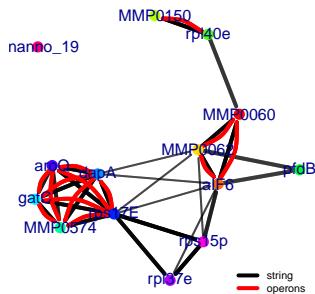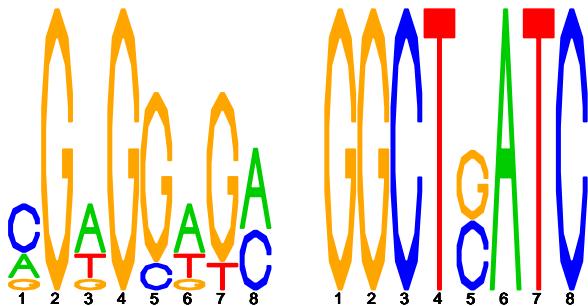−200   −100   −1

sequence position

Cluster: 0135 mmp; resid: 0.22; r/c: 16/40

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=1.6

upstream meme PSSM #2; e=650

log10(P) upstream meme

log10(P.clust)=−1.55; 16 seqs; 5 uniq

log10(P)	Annotation	Gene
−1.57	Unanno_1	Unanno_1
−1.57	elongation factor 1-alpha:	MMP1370
−1.57	hypothetical protein:	MMP1047
−1.57	V−type ATP synthase subunit D:	MMP1046
−1.57	V−type ATP synthase subunit B:	MMP1045
−1.57	V−type ATP synthase subunit A:	MMP1044
−1.57	V−type ATP synthase subunit F:	MMP1043
−1.57	V−type ATP synthase subunit C:	MMP1042
−1.57	A1A0 ATPase, subunit IE:	MMP1041
−1.57	V−type ATP synthase subunit K:	MMP1040
−1.57	V−type ATP synthase subunit I:	MMP1039
−1.57	A1A0 ATPase, subunit H:	MMP1038
−1.57	cell division protein FtsZ:	MMP1436
−1.57	preprotein translocase subunit SecE:	MMP1435
−1.43	preprotein translocase subunit SecF:	MMP1524
−1.43	preprotein translocase subunit SecD:	MMP1523

Cluster: 0136 mmp; resid: 0.41; r/c: 27/35

upstream meme PSSM #1; e=4.7e+03   upstream meme PSSM #2; e=9e+03

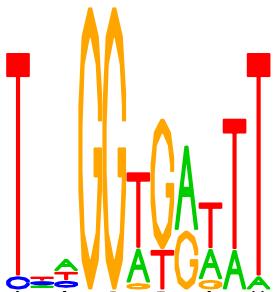| log10(P) upstream meme			log10(P.clust)=−1.35; 27 seqs; 20 uniq
−7.38			iron transport system binding protein: MMP1181
−3.47			Diaminopimelate epimerase: MMP0917
−3.39			hypothetical protein: MMP0075
−3.28			S layer protein: MMP0875
−3.23			glutamyl−tRNA reductase: MMP0088
−3.23			ase:3−hydroxy−3−methylglutaryl Coenzyme A reductase: MMP0087
−2.61			methanofuran dehydrogenase subunit E related protein: MMP0965
−2.20			Unanno_9
−2.17			Beta−Ig−H3/Fasciclin domain:hypothetical protein: MMP0429
−1.84			sirohydrochlorin cobaltochelatase: MMP0164
−1.36			hypothetical protein: MMP1699
−0.49			hypothetical protein: MMP1175
−0.27			Band 7 protein:Stomatin: MMP1036
−0.27			hypothetical protein: MMP1035
−0.19			hypothetical protein: MMP0646
−0.19			malate dehydrogenase: MMP0645
−0.19			Cation efflux protein: MMP0644
−0.19			cobalt transport protein CbiM: MMP0889
−0.19			cobalt transport protein CbiN: MMP0888
−0.16			SAM (and some other nucleotide) binding motif: MMP0874
−0.03			hypothetical protein: MMP1646
−0.02			hypothetical protein: MMP0887
−0.00			iron transport Periplasmic binding protein: MMP1178
−0.00			nsport system substrate−binding protein, C−term half: MMP1177
−0.00			nsport system substrate−binding protein, N−term half: MMP1176
−0.00			iron ABC transporter ATPase subunit: MMP1183
−0.00			ron(III)dicitrate transport system permease protein: MMP1182

string
operons

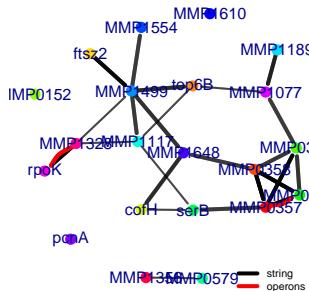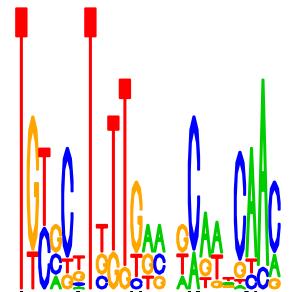**Cluster: 0137 mmp; resid: 0.25; r/c: 21/37**

11 Oct 11 16:14:07 iter=2000
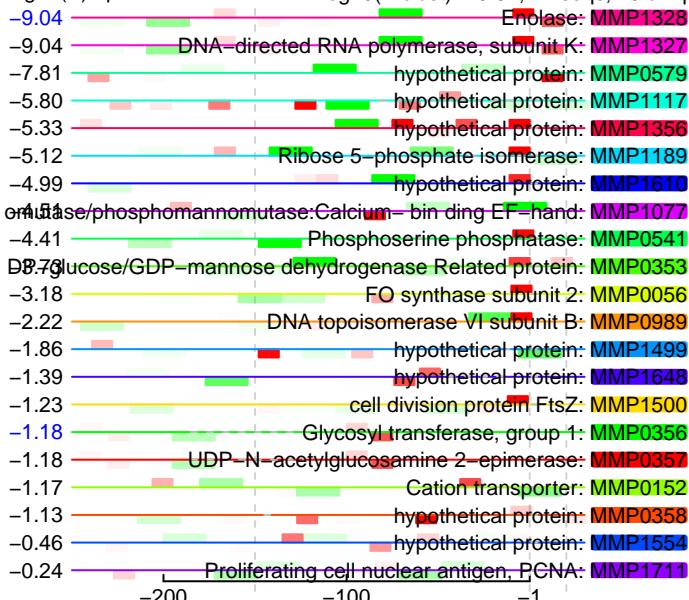cMonkey Version 4.8.8 mmp

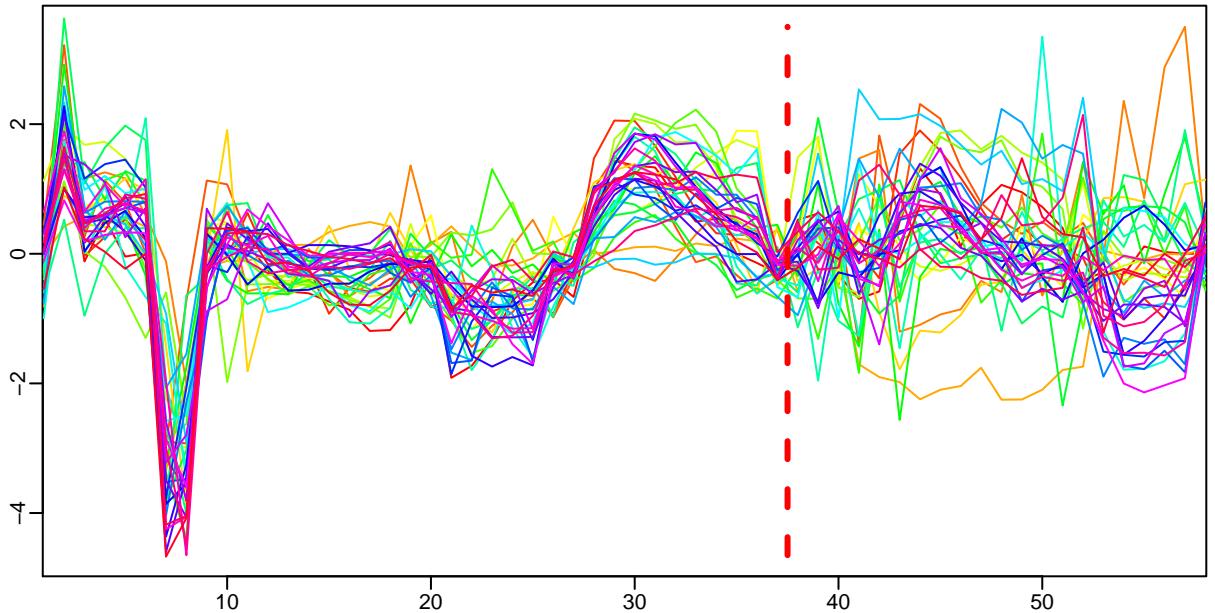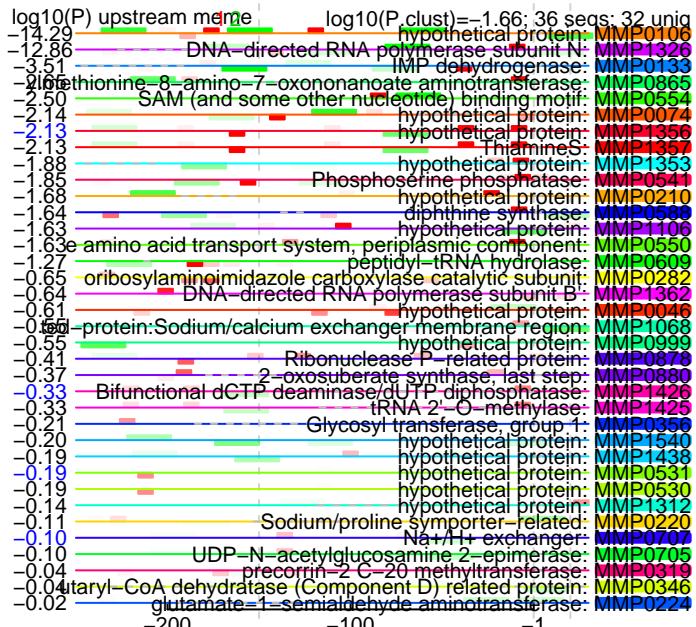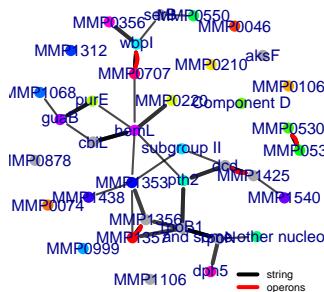upstream meme PSSM #1; e=2.3e+03   upstream meme PSSM #2; e=5.3e+03

log10(P) upstream meme   log10(P.clust)=−3.62; 21 seqs; 16 uniq

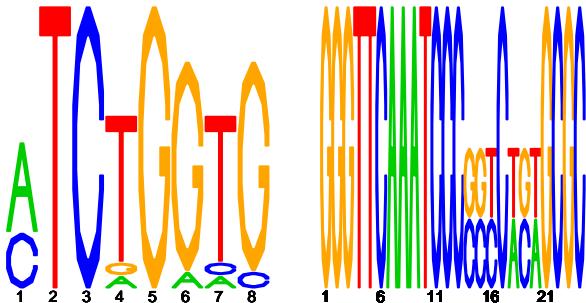| log10(P)	description	gene
−15.59	e pyridoxine biosynthetic glutamine amidotransferase:	MMP1656
−10.93	hypothetical protein:	MMP1106
−10.93	succinate−CoA ligase (ADP−forming), beta chain:	MMP1105
−7.71	translation−associated GTPase:	MMP1122
−4.29	hypothetical protein:	MMP1440
−3.95	LPPG:FO 2−phospho−(S)−lactate transferase:	MMP0404
−3.82	phosphoglycerate kinase:	MMP1532
−3.37	oxoglutarate ferredoxin oxidoreductase subunit beta:	MMP1316
−3.19	Amidophosphoribosyltransferase:	MMP1146
−1.56	Carbohydrate kinase, PfkB:	MMP0418
−1.56	e thylideneamino)imidazole−4−carboxamide isomerase:	MMP0417
−1.42	Transcriptional repressor of nif and glnA operons:	MMP0607
−1.42	similar to 23S ribosomal RNA methyltransferase:	MMP0606
−1.19	hypothetical protein:	MMP0881
−1.19	hypothetical protein:	MMP0146
−1.19	adenine phosphoribosyltransferase:	MMP0145
−0.73	imidazole glycerol phosphate synthase subunit HisF:	MMP1083
−0.73	putative LPS biosynthesis protein WbpG:	MMP1081
−0.66	thiamine biosynthesis protein ThiC:	MMP0187
−0.39	phenylalanyl−tRNA synthetase subunit alpha:	MMP1496
−0.22	glutamine synthetase:	MMP1206

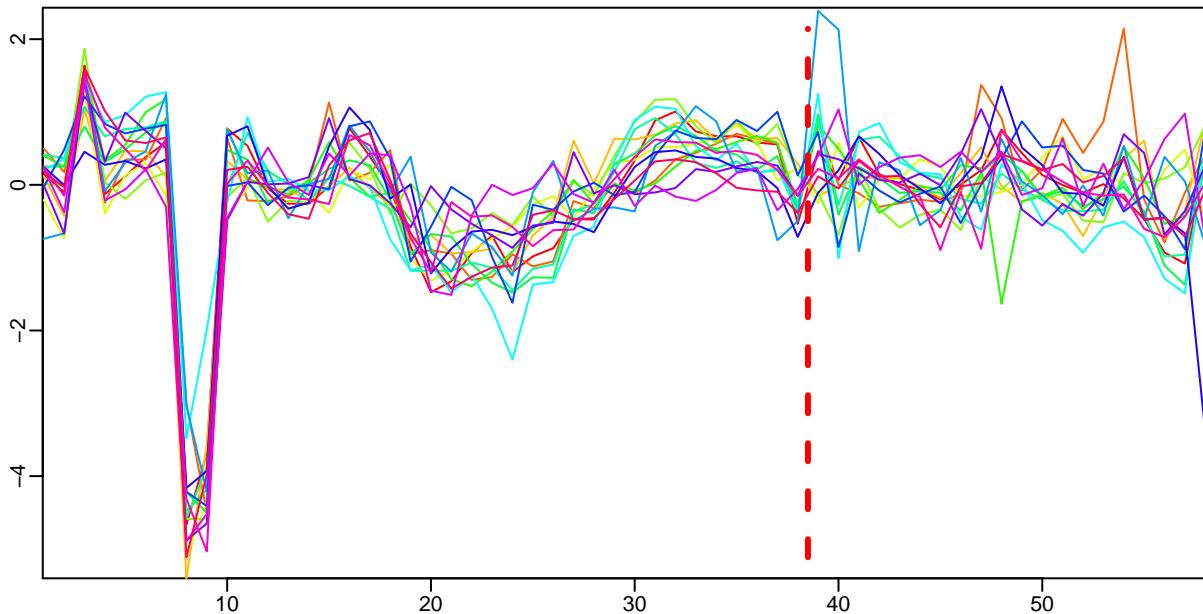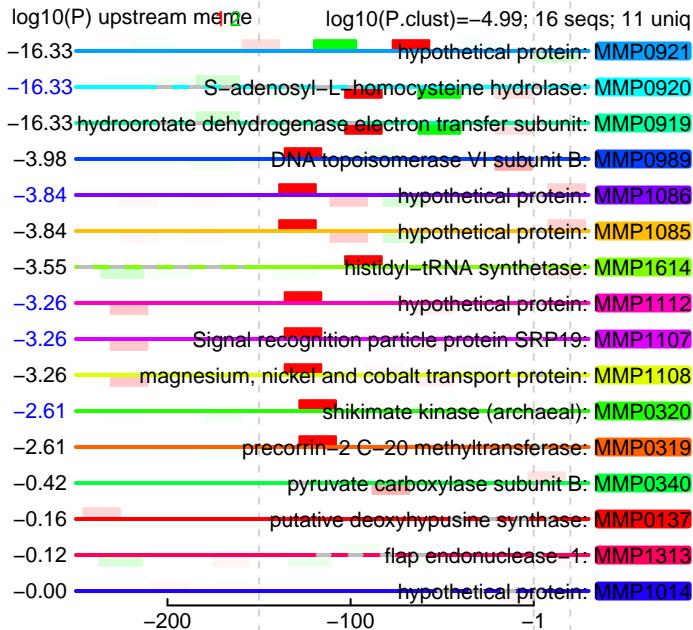**Cluster: 0138 mmp; resid: 0.22; r/c: 14/40**

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=120   upstream meme PSSM #2; e=4e+03

log10(P) upstream meme   log10(P.clust)=−2.20; 14 seqs; 7 uniq

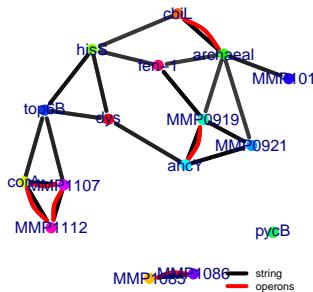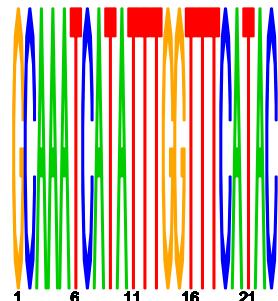| log10(P)	annotation
−3.93	Unanno_19
−3.56	chorismate mutase: MMP0578
−3.56	30S ribosomal protein S17e: MMP0577
−3.56	dihydrodipicolinate synthase: MMP0576
−3.56	aspartyl/glutamyl−tRNA amidotransferase subunit C: MMP0575
−3.56	hypothetical protein: MMP0574
−1.99	50S ribosomal protein L37e: MMP1147
−1.39	50S ribosomal protein L31e: MMP0062
−1.39	translation initiation factor IF−6: MMP0061
−1.39	Ribosomal LX protein: MMP0060
−1.27	30S ribosomal protein S15P: MMP1579
−0.73	Prefoldin beta subunit (GimC beta subunit).: MMP0245
−0.46	50S ribosomal protein L40e: MMP0151
−0.46	hypothetical protein: MMP0150

Cluster: 0139 mmp; resid: 0.33; r/c: 21/38

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=17

upstream meme PSSM #2; e=42

log10(P) upstream meme   log10(P.clust)=−3.57; 21 seqs; 19 uniq

log10(P)	Annotation
−9.04	Enolase: MMP1328
−9.04	DNA−directed RNA polymerase, subunit K: MMP1327
−7.81	hypothetical protein: MMP0579
−5.80	hypothetical protein: MMP1117
−5.33	hypothetical protein: MMP1356
−5.12	Ribose 5−phosphate isomerase: MMP1189
−4.99	hypothetical protein: MMP1610
	omutase/phosphomannomutase:Calcium−binding EF−hand: MMP1077
−4.41	Phosphoserine phosphatase: MMP0541
−3.79	UDP−glucose/GDP−mannose dehydrogenase Related protein: MMP0353
−3.18	FO synthase subunit 2: MMP0056
−2.22	DNA topoisomerase VI subunit B: MMP0989
−1.86	hypothetical protein: MMP1499
−1.39	hypothetical protein: MMP1648
−1.23	cell division protein FtsZ: MMP1500
−1.18	Glycosyl transferase, group 1: MMP0356
−1.18	UDP−N−acetylglucosamine 2−epimerase: MMP0357
−1.17	Cation transporter: MMP0152
−1.13	hypothetical protein: MMP0358
−0.46	hypothetical protein: MMP1554
−0.24	Proliferating cell nuclear antigen, PCNA: MMP1711

−200   −100   −1

Cluster: 0140 mmp; resid: 0.37; r/c: 36/37

11 Oct 11 16:14:07 iter=2000
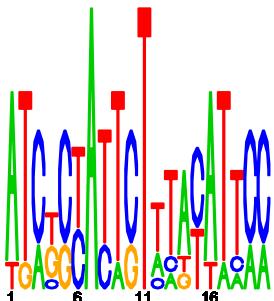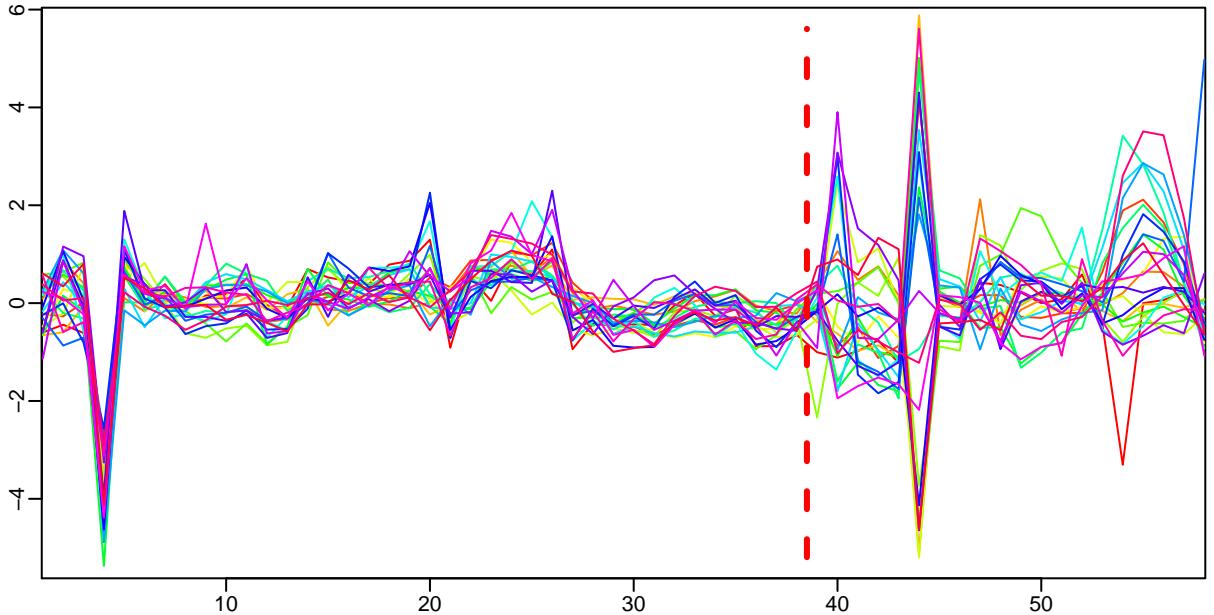cMonkey Version 4.8.8 mmp

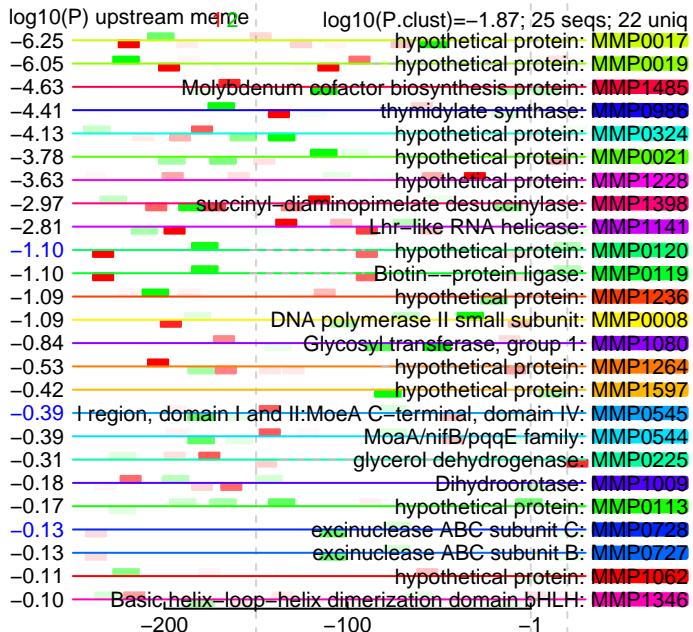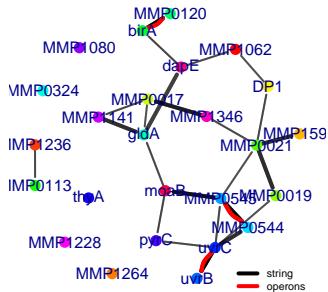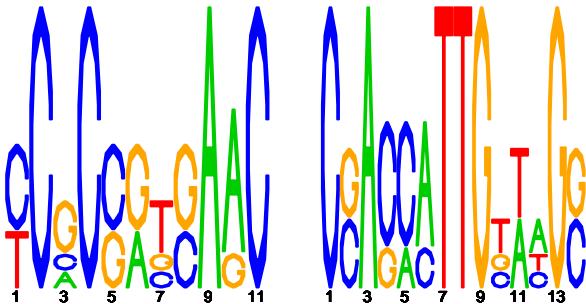upstream meme PSSM #1; e=0.011   upstream meme PSSM #2; e=110

log10(P) upstream meme   log10(P,clust)=−1.66; 36 seqs: 32 uniq

log10(P)	description	gene
−14.29	hypothetical protein:	MMP0106
−12.86	DNA−directed RNA polymerase subunit N:	MMP1326
−3.51	IMP dehydrogenase:	MMP0133
−2.66	methionine−8−amino−7−oxononanoate aminotransferase:	MMP0865
−2.50	SAM (and some other nucleotide) binding motif:	MMP0554
−2.14	hypothetical protein:	MMP0074
−2.13	hypothetical protein:	MMP1356
−2.13	ThiamineS:	MMP1357
−1.88	hypothetical protein:	MMP1353
−1.85	Phosphoserine phosphatase:	MMP0541
−1.68	hypothetical protein:	MMP0210
−1.64	diphthine synthase:	MMP0599
−1.63	hypothetical protein:	MMP1106
−1.63	e amino acid transport system, periplasmic component:	MMP0550
−1.27	peptidyl−tRNA hydrolase:	MMP0609
−0.65	oribosylaminoimidazole carboxylase catalytic subunit:	MMP0282
−0.64	DNA−directed RNA polymerase subunit B:	MMP1362
−0.61	hypothetical protein:	MMP0046
−0.60	protein:Sodium/calcium exchanger membrane region:	MMP1068
−0.55	hypothetical protein:	MMP0999
−0.41	Ribonuclease P−related protein:	MMP1540
−0.37	2−oxosuberate synthase, last step:	MMP0880
−0.33	Bifunctional dCTP deaminase/dUTP diphosphatase:	MMP1426
−0.33	tRNA 2'−O−methylase:	MMP1425
−0.21	Glycosyl transferase, group 1:	MMP0956
−0.20	hypothetical protein:	MMP1540
−0.19	hypothetical protein:	MMP1438
−0.19	hypothetical protein:	MMP0531
−0.19	hypothetical protein:	MMP0530
−0.14	hypothetical protein:	MMP1312
−0.11	Sodium/proline symporter−related:	MMP0220
−0.10	Na+/H+ exchanger:	MMP0707
−0.10	UDP−N−acetylglucosamine 2−epimerase:	MMP0705
−0.04	precorrin−2 C−20 methyltransferase:	MMP0319
−0.04	utaryl−CoA dehydratase (Component D) related protein:	MMP0346
−0.02	glutamate−1−semialdehyde aminotransferase:	MMP0224

Cluster: 0141 mmp; resid: 0.29; r/c: 16/38

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

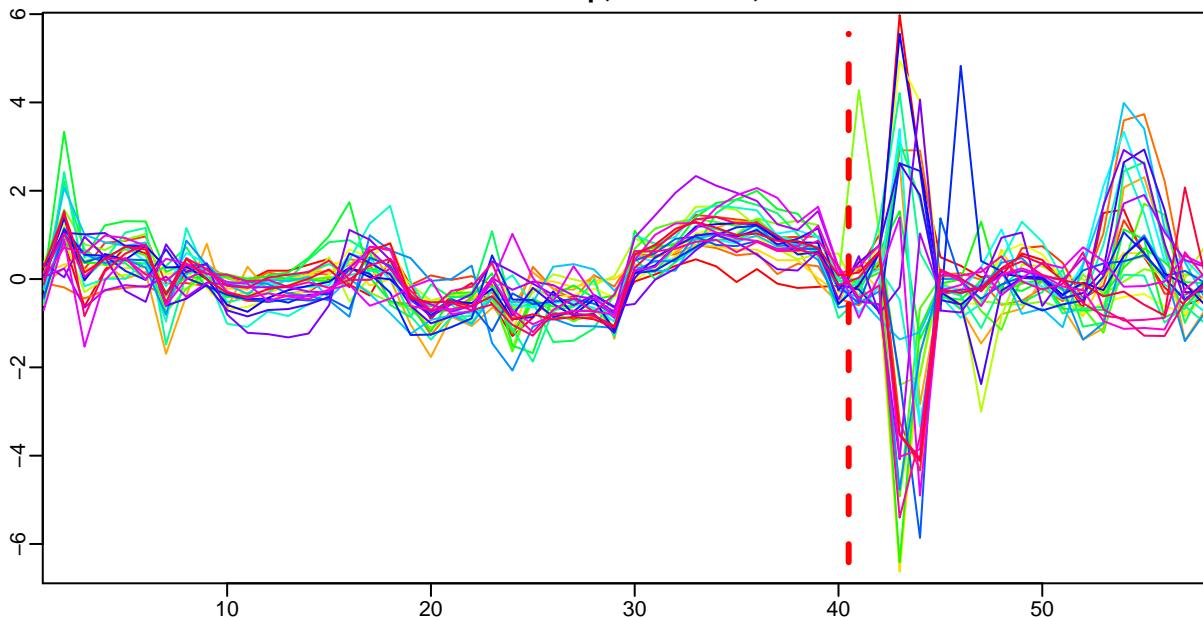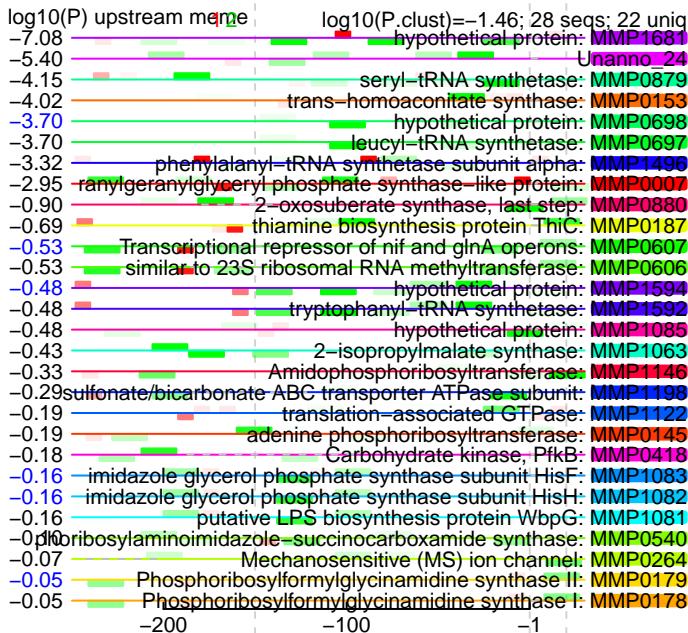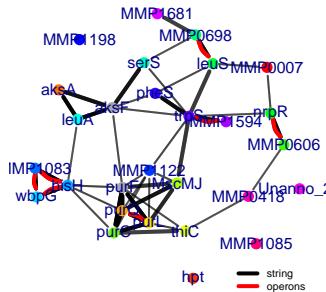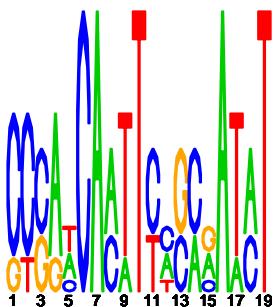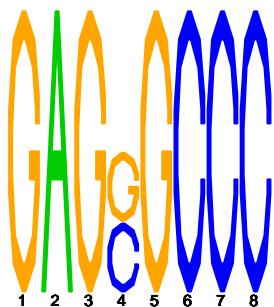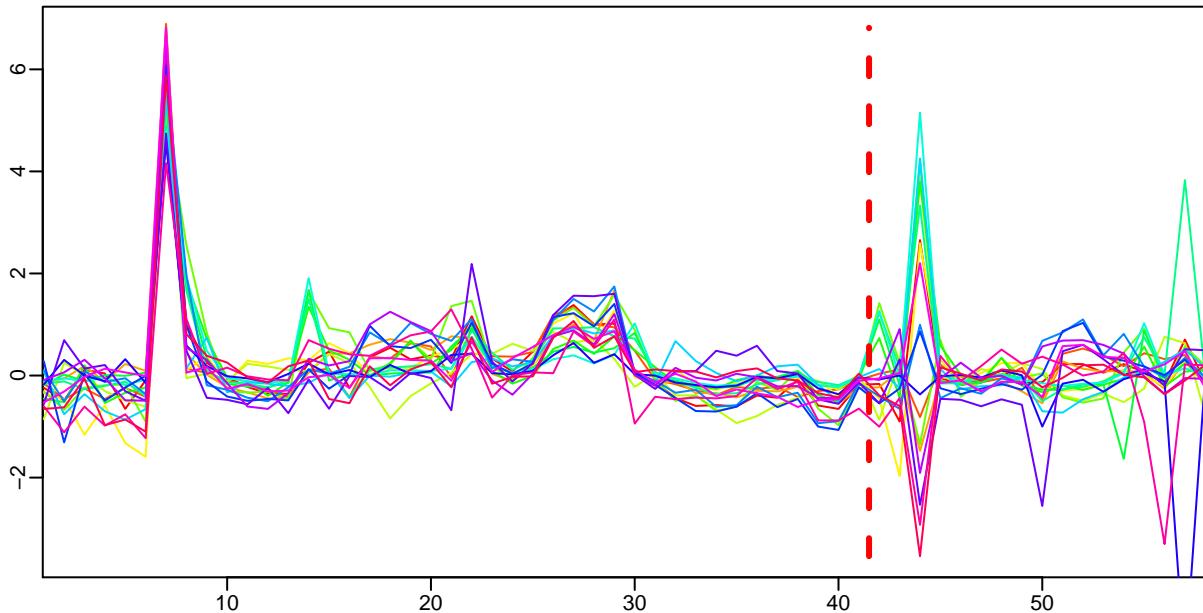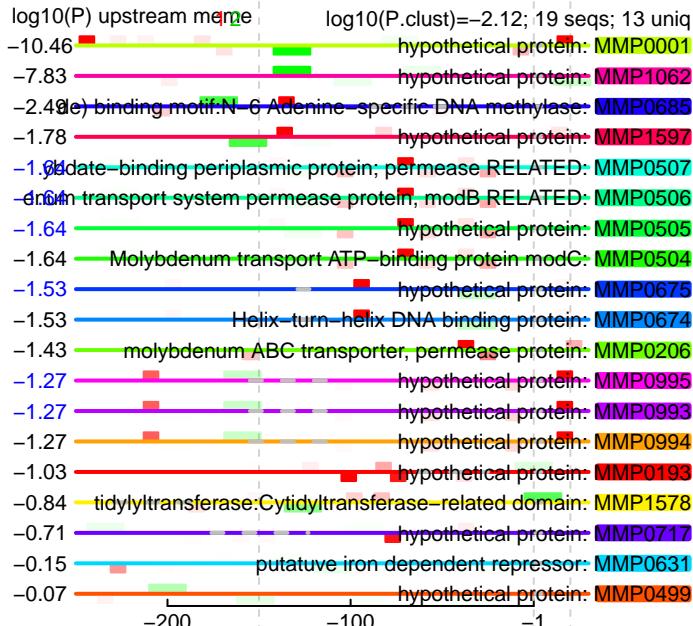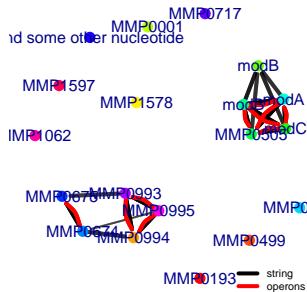upstream meme PSSM #1; e=71   upstream meme PSSM #2; e=6.2e+03

log10(P) upstream meme   log10(P.clust)=−4.99; 16 seqs; 11 uniq

log10(P)	Description	Gene
−16.33	hypothetical protein	MMP0921
−16.33	S−adenosyl−L−homocysteine hydrolase	MMP0920
−16.33	hydroorotate dehydrogenase electron transfer subunit	MMP0919
−3.98	DNA topoisomerase VI subunit B	MMP0989
−3.84	hypothetical protein	MMP1086
−3.84	hypothetical protein	MMP1085
−3.55	histidyl−tRNA synthetase	MMP1614
−3.26	hypothetical protein	MMP1112
−3.26	Signal recognition particle protein SRP19	MMP1107
−3.26	magnesium, nickel and cobalt transport protein	MMP1108
−2.61	shikimate kinase (archaeal)	MMP0320
−2.61	precorrin−2 C−20 methyltransferase	MMP0319
−0.42	pyruvate carboxylase subunit B	MMP0340
−0.16	putative deoxyhypusine synthase	MMP0137
−0.12	flap endonuclease−1	MMP1313
−0.00	hypothetical protein	MMP1014

Cluster: 0142 mmp; resid: 0.29; r/c: 25/38

upstream meme PSSM #1; e=960   upstream meme PSSM #2; e=7.3e+03

log10(P) upstream meme   log10(P.clust)=−1.87; 25 seqs; 22 uniq

log10(P)	annotation	gene
−6.25	hypothetical protein:	MMP0017
−6.05	hypothetical protein:	MMP0019
−4.63	Molybdenum cofactor biosynthesis protein:	MMP1485
−4.41	thymidylate synthase:	MMP0986
−4.13	hypothetical protein:	MMP0324
−3.78	hypothetical protein:	MMP0021
−3.63	hypothetical protein:	MMP1228
−2.97	succinyl–diaminopimelate desuccinylase:	MMP1398
−2.81	Lhr–like RNA helicase:	MMP1141
−1.10	hypothetical protein:	MMP0120
−1.10	Biotin−−protein ligase:	MMP0119
−1.09	hypothetical protein:	MMP1236
−1.09	DNA polymerase II small subunit:	MMP0008
−0.84	Glycosyl transferase, group 1:	MMP1080
−0.53	hypothetical protein:	MMP1264
−0.42	hypothetical protein:	MMP1597
−0.39	I region, domain I and II:MoeA C−terminal, domain IV:	MMP0545
−0.39	MoaA/nifB/pqqE family:	MMP0544
−0.31	glycerol dehydrogenase:	MMP0225
−0.18	Dihydroorotase:	MMP1009
−0.17	hypothetical protein:	MMP0113
−0.13	excinuclease ABC subunit C:	MMP0728
−0.13	excinuclease ABC subunit B:	MMP0727
−0.11	hypothetical protein:	MMP1062
−0.10	Basic helix−loop−helix dimerization domain bHLH:	MMP1346

Cluster: 0143 mmp; resid: 0.30; r/c: 28/40

upstream meme PSSM #1; e=2.4e+00   upstream meme PSSM #2; e=4.7e+03

log10(P) upstream meme   log10(P.clust)=−1.46; 28 seqs; 22 uniq

log10(P)	annotation
−7.08	hypothetical protein: MMP1681
−5.40	Unanno_24
−4.15	seryl−tRNA synthetase: MMP0879
−4.02	trans−homoaconitate synthase: MMP0153
−3.70	hypothetical protein: MMP0698
−3.70	leucyl−tRNA synthetase: MMP0697
−3.32	phenylalanyl−tRNA synthetase subunit alpha: MMP1496
−2.95	ranylgeranylglyceryl phosphate synthase−like protein: MMP0007
−0.90	2−oxosuberate synthase, last step: MMP0880
−0.69	thiamine biosynthesis protein ThiC: MMP0187
−0.53	Transcriptional repressor of nif and glnA operons: MMP0607
−0.53	similar to 23S ribosomal RNA methyltransferase: MMP0606
−0.48	hypothetical protein: MMP1594
−0.48	tryptophanyl−tRNA synthetase: MMP1592
−0.48	hypothetical protein: MMP1085
−0.43	2−isopropylmalate synthase: MMP1063
−0.33	Amidophosphoribosyltransferase: MMP1146
−0.29	sulfonate/bicarbonate ABC transporter ATPase subunit: MMP1198
−0.19	translation−associated GTPase: MMP1122
−0.19	adenine phosphoribosyltransferase: MMP0145
−0.18	Carbohydrate kinase, PfkB: MMP0418
−0.16	imidazole glycerol phosphate synthase subunit HisF: MMP1083
−0.16	imidazole glycerol phosphate synthase subunit HisH: MMP1082
−0.16	putative LPS biosynthesis protein WbpG: MMP1081
−0.10	phoribosylaminoimidazole−succinocarboxamide synthase: MMP0540
−0.07	Mechanosensitive (MS) ion channel: MMP0264
−0.05	Phosphoribosylformylglycinamide synthase II: MMP0179
−0.05	Phosphoribosylformylglycinamide synthase I: MMP0178

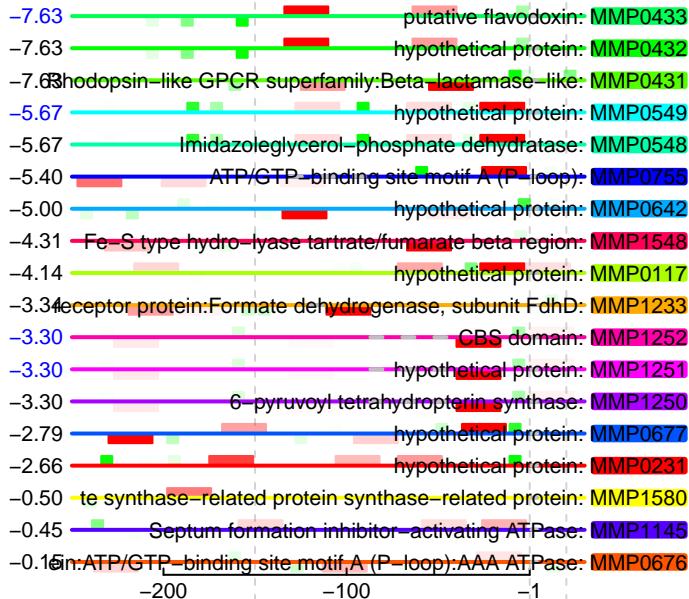Cluster: 0144 mmp; resid: 0.27; r/c: 19/41

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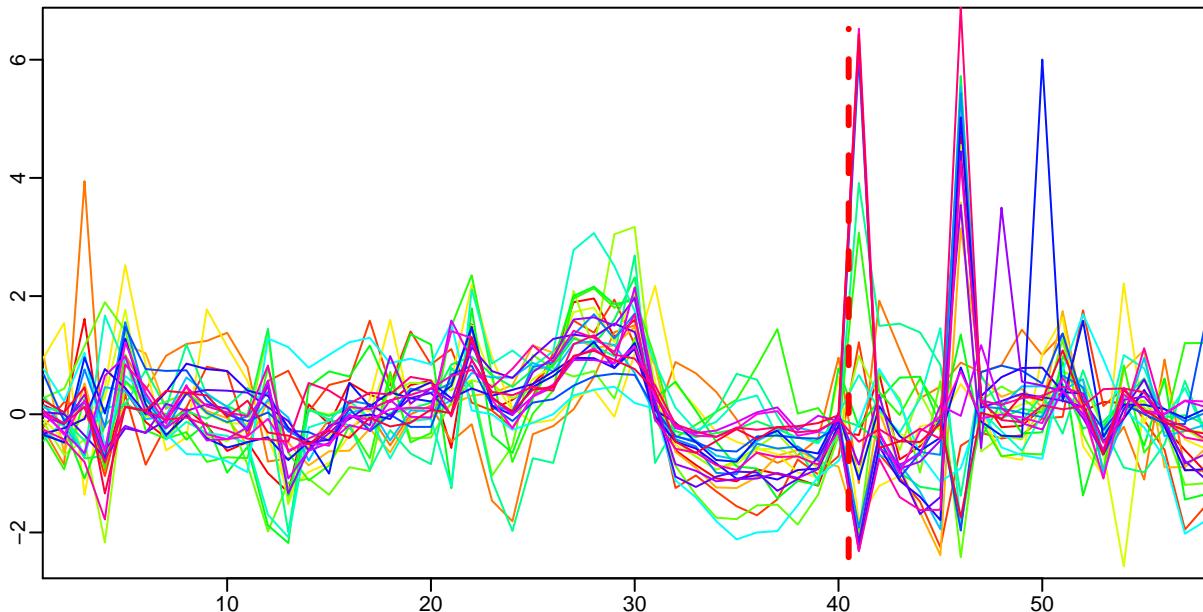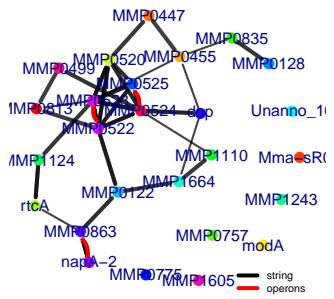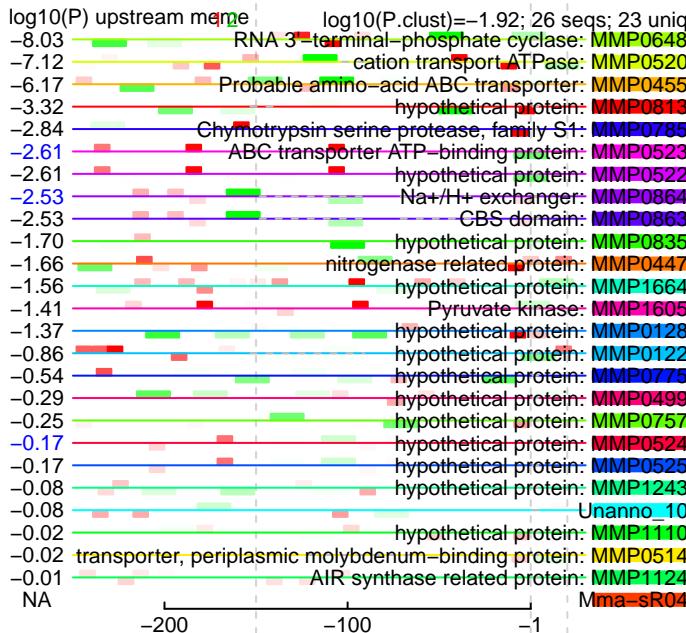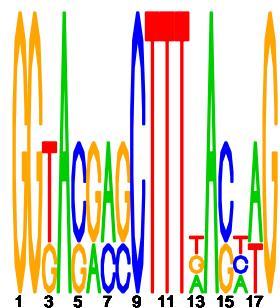upstream meme PSSM #1; e=6.3   upstream meme PSSM #2; e=1.9e+03

log10(P) upstream meme   log10(P.clust)=−2.12; 19 seqs; 13 uniq

log10(P)	description
−10.46	hypothetical protein: MMP0001
−7.83	hypothetical protein: MMP1062
−2.48	le) binding motif:N−6 Adenine−specific DNA methylase: MMP0685
−1.78	hypothetical protein: MMP1597
−1.9	ddate−binding periplasmic protein; permease RELATED: MMP0507
−1.6	dnum transport system permease protein, modB RELATED: MMP0506
−1.64	hypothetical protein: MMP0505
−1.64	Molybdenum transport ATP−binding protein modC: MMP0504
−1.53	hypothetical protein: MMP0675
−1.53	Helix−turn−helix DNA binding protein: MMP0674
−1.43	molybdenum ABC transporter, permease protein: MMP0206
−1.27	hypothetical protein: MMP0995
−1.27	hypothetical protein: MMP0993
−1.27	hypothetical protein: MMP0994
−1.03	hypothetical protein: MMP0193
−0.84	tidylyltransferase:Cytidylltransferase−related domain: MMP1578
−0.71	hypothetical protein: MMP0717
−0.15	putatuve iron dependent repressor: MMP0631
−0.07	hypothetical protein: MMP0499

Cluster: 0145 mmp; resid: 0.24; r/c: 18/39

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upstream meme PSSM #1; e=0.1   upstream meme PSSM #2; e=1e+03
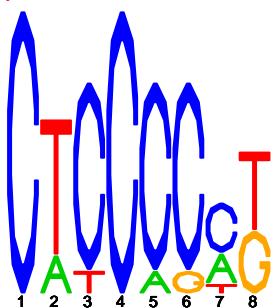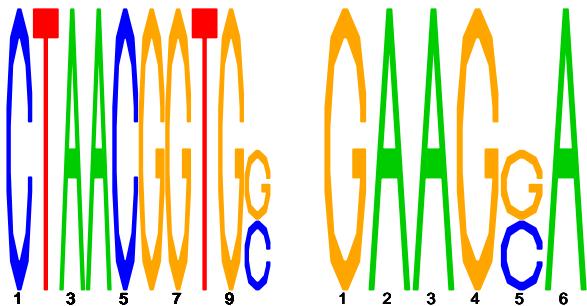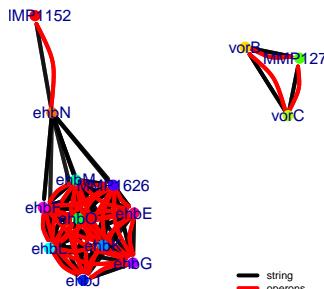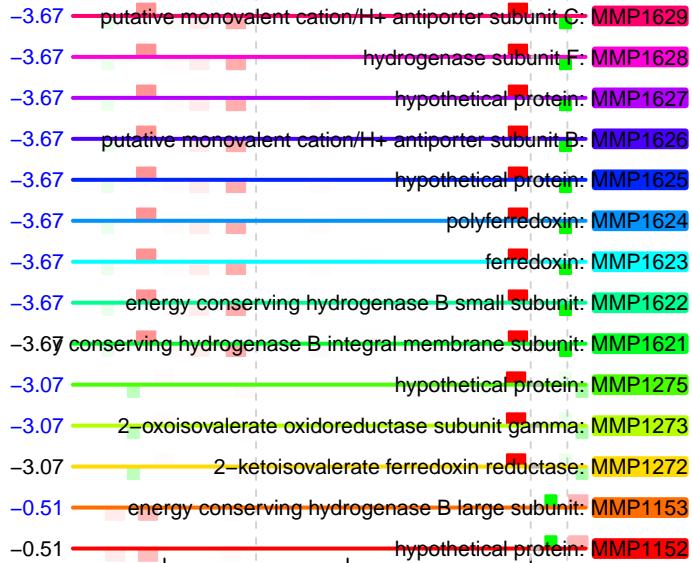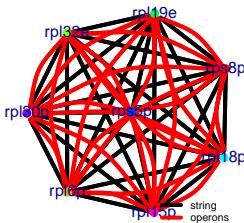
log10(P) upstream meme   log10(P.clust)=−4.05; 18 seqs; 14 uniq

log10(P)	Description	Gene
−7.63	putative flavodoxin	MMP0433
−7.63	hypothetical protein	MMP0432
−7.63	Rhodopsin−like GPCR superfamily:Beta−lactamase−like	MMP0431
−5.67	hypothetical protein	MMP0549
−5.67	Imidazoleglycerol−phosphate dehydratase	MMP0548
−5.40	ATP/GTP−binding site motif A (P−loop)	MMP0755
−5.00	hypothetical protein	MMP0642
−4.31	Fe−S type hydro−lyase tartrate/fumarate beta region	MMP1548
−4.14	hypothetical protein	MMP0117
−3.34	receptor protein:Formate dehydrogenase, subunit FdhD	MMP1233
−3.30	CBS domain	MMP1252
−3.30	hypothetical protein	MMP1251
−3.30	6−pyruvoyl tetrahydropterin synthase	MMP1250
−2.79	hypothetical protein	MMP0677
−2.66	hypothetical protein	MMP0231
−0.50	te synthase−related protein synthase−related protein	MMP1580
−0.45	Septum formation inhibitor−activating ATPase	MMP1145
−0.16	in:ATP/GTP−binding site motif A (P−loop):AAA ATPase	MMP0676

Cluster: 0146 mmp; resid: 0.42; r/c: 26/40

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upstream meme PSSM #1; e=1.3 **upstream meme PSSM #2; e=1.9e+04**

log10(P) upstream meme   log10(P.clust)=−1.92; 26 seqs; 23 uniq

log10(P)	Annotation
−8.03	RNA 3'−terminal−phosphate cyclase: MMP0648
−7.12	cation transport ATPase: MMP0520
−6.17	Probable amino−acid ABC transporter: MMP0455
−3.32	hypothetical protein: MMP0813
−2.84	Chymotrypsin serine protease, family S1: MMP0785
−2.61	ABC transporter ATP−binding protein: MMP0523
−2.61	hypothetical protein: MMP0522
−2.53	Na+/H+ exchanger: MMP0864
−2.53	CBS domain: MMP0863
−1.70	hypothetical protein: MMP0835
−1.66	nitrogenase related protein: MMP0447
−1.56	hypothetical protein: MMP1664
−1.41	Pyruvate kinase: MMP1605
−1.37	hypothetical protein: MMP0128
−0.86	hypothetical protein: MMP0122
−0.54	hypothetical protein: MMP0775
−0.29	hypothetical protein: MMP0499
−0.25	hypothetical protein: MMP0757
−0.17	hypothetical protein: MMP0524
−0.17	hypothetical protein: MMP0525
−0.08	hypothetical protein: MMP1243
−0.08	Unanno_10
−0.02	hypothetical protein: MMP1110
−0.02	transporter, periplasmic molybdenum−binding protein: MMP0514
−0.01	AIR synthase related protein: MMP1124
NA	Mma−sR04

Cluster: 0147 mmp; resid: 0.19; r/c: 14/39

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upstream meme PSSM #1; e=240   upstream meme PSSM #2; e=5.6e+03

log10(P) upstream meme   log10(P.clust)=−3.09; 14 seqs; 3 uniq

−3.67	putative monovalent cation/H+ antiporter subunit C: MMP1629
−3.67	hydrogenase subunit F: MMP1628
−3.67	hypothetical protein: MMP1627
−3.67	putative monovalent cation/H+ antiporter subunit B: MMP1626
−3.67	hypothetical protein: MMP1625
−3.67	polyferredoxin: MMP1624
−3.67	ferredoxin: MMP1623
−3.67	energy conserving hydrogenase B small subunit: MMP1622
−3.67	conserving hydrogenase B integral membrane subunit: MMP1621
−3.07	hypothetical protein: MMP1275
−3.07	2−oxoisovalerate oxidoreductase subunit gamma: MMP1273
−3.07	2−ketoisovalerate ferredoxin reductase: MMP1272
−0.51	energy conserving hydrogenase B large subunit: MMP1153
−0.51	hypothetical protein: MMP1152

Cluster: 0148 mmp; resid: 0.06; r/c: 8/37

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30S ribosomal protein S8P: MMP1414
50S ribosomal protein L6P: MMP1415
50S ribosomal protein L32e: MMP1416
50S ribosomal protein L19e: MMP1417
50S ribosomal protein L18P: MMP1418
30S ribosomal protein S5P: MMP1419
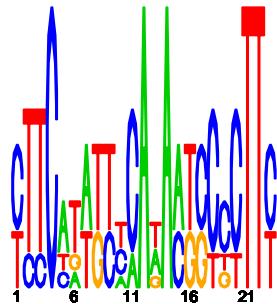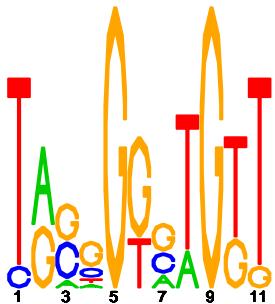50S ribosomal protein L30P: MMP1420
50S ribosomal protein L15P: MMP1421

string operons

−200   −100   −1

sequence position

Cluster: 0149 mmp; resid: 0.30; r/c: 26/39

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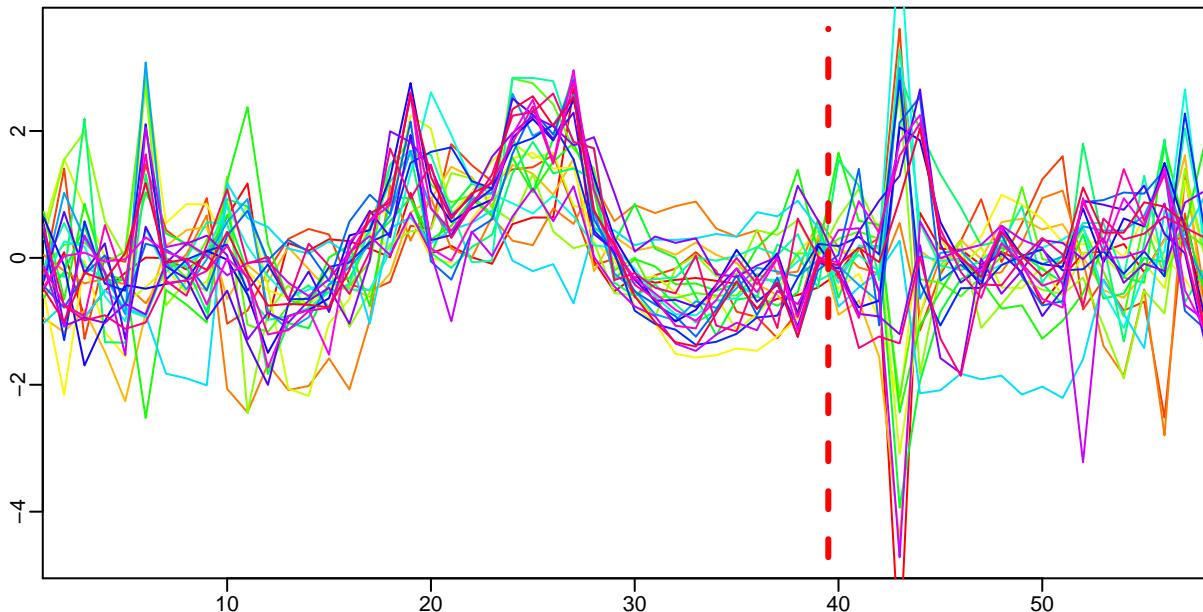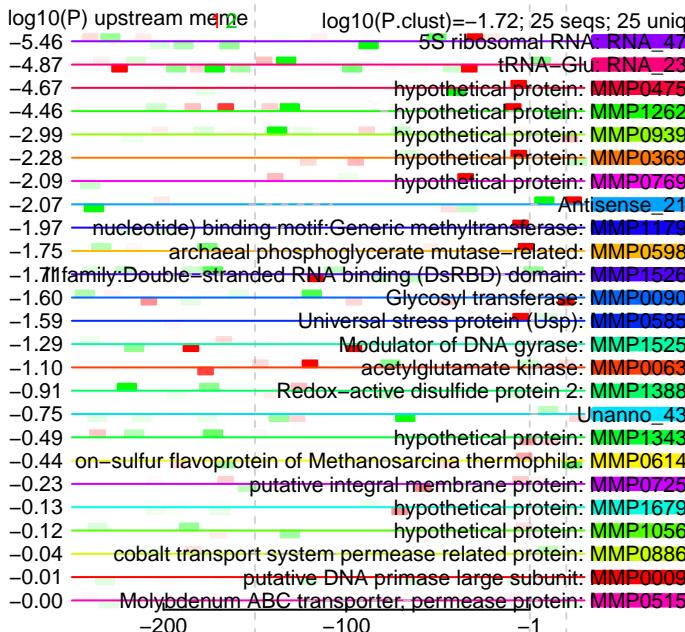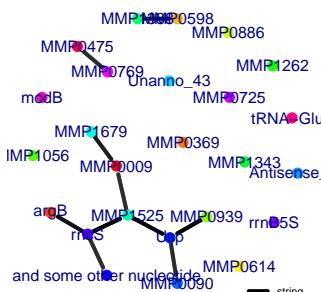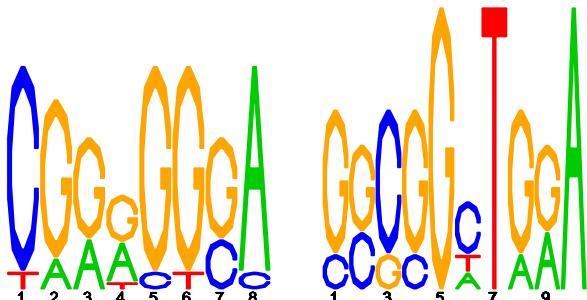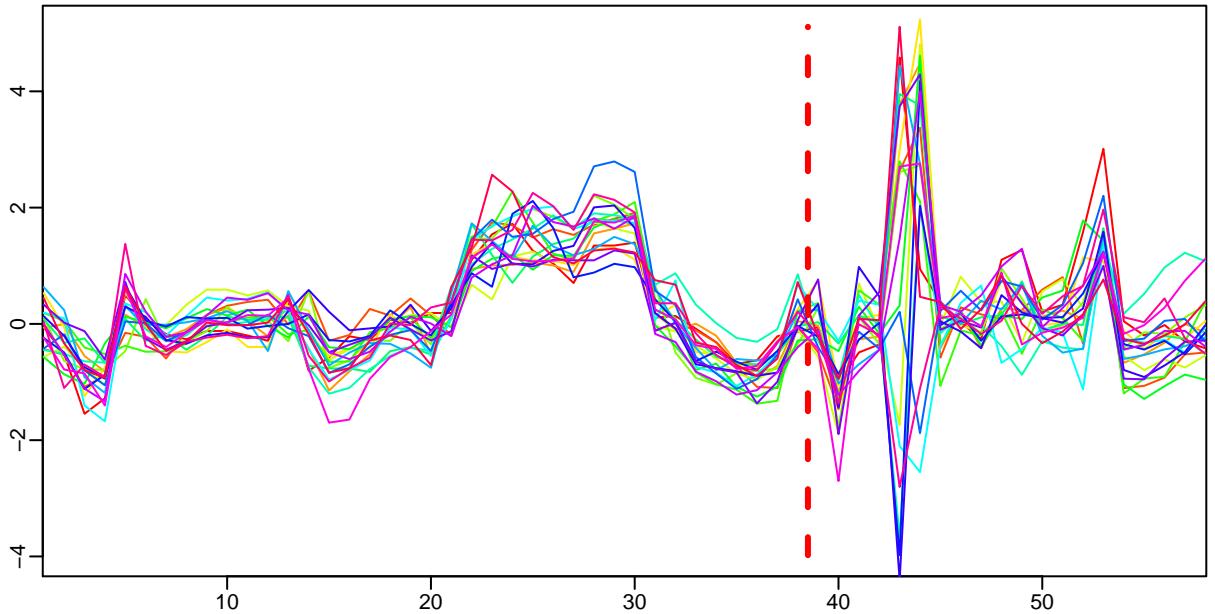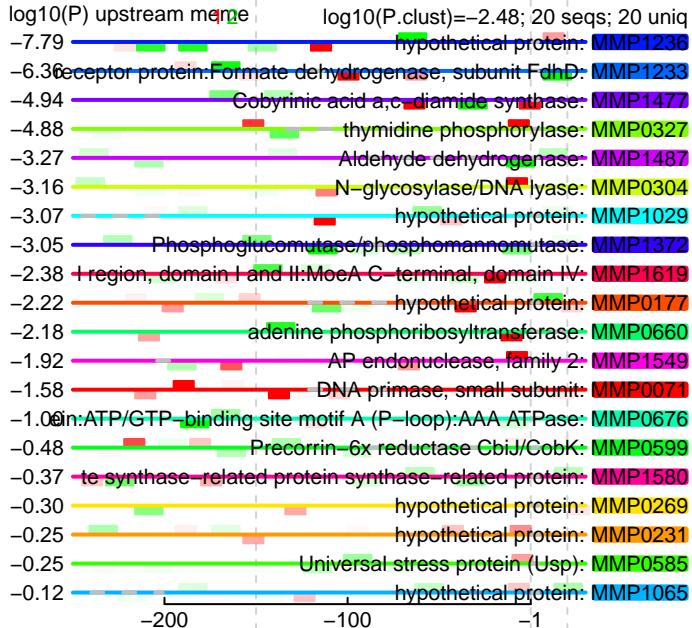upstream meme PSSM #1; e=0.6

upstream meme PSSM #2; e=150

log10(P) upstream meme

log10(P.clust)=−3.12; 26 seqs; 20 uniq

log10(P)	Description	Gene
−12.10	Enolase	MMP1328
−12.10	DNA−directed RNA polymerase, subunit K	MMP1327
−9.13	methyltransferase related protein	MMP1307
−5.99	translation initiation factor IF−2	MMP0284
−5.80	hypothetical protein	MMP0564
−4.74	hypothetical protein	MMP0034
−3.82	O−sialoglycoprotein endopeptidase/protein kinase	MMP0415
−3.22	precorrin−3B C17−methyltransferase	MMP0953
−3.04	predicted archaeal transcriptional regulator	MMP0907
−3.04	hypothetical protein	MMP0906
−3.04	hypothetical protein	MMP0905
−2.86	hypothetical protein	MMP0941
−2.27	Orotate phosphoribosyltransferase	MMP1492
−2.27	Chlorohydrolase	MMP1491
−1.85	pyruvate carboxylase subunit B	MMP0340
−1.43	putative deoxyhypusine synthase	MMP0137
−1.32	pyruvoyl−dependent arginine decarboxylase	MMP1582
−1.18	hypothetical protein	MMP1085
−0.98	histidyl−tRNA synthetase	MMP1614
−0.26	ThiamineS	MMP1357
−0.26	hypothetical protein	MMP1356
−0.14	precorrin−2 C−20 methyltransferase	MMP0319
−0.08	Beta−lactamase−like:KH domain	MMP0694
−0.04	hypothetical protein	MMP1112
−0.04	magnesium, nickel and cobalt transport protein	MMP1108
−0.02	DNA−directed RNA polymerase subunit beta"	MMP1361

Cluster: 0150 mmp; resid: 0.24; r/c: 17/41

upstream meme PSSM #1; e=510   upstream meme PSSM #2; e=2.1e+03

log10(P) upstream meme   log10(P.clust)=−3.48; 17 seqs; 15 uniq

log10(P)	Annotation	ID
−11.01	Glycosyl transferase, group 1:	MMP1294
−7.09	hypothetical protein:	MMP1237
−7.09	Molybdopterin biosynthesis MoaE:	MMP1235
−6.82		Antisense_10
−5.52	hypothetical protein:	MMP1608
−5.41	hypothetical protein:	MMP0086
−2.92	zein−L−isoaspartate(D−aspartate) O−methyltransferase:	MMP0102
−2.60	methyltransferase:	MMP0069
−2.31	hypothetical protein:	MMP1019
−2.26	hypothetical protein:	MMP1653
−1.98	hypothetical protein:	MMP0528
−1.90	hypothetical protein:	MMP1256
−1.20	lyase, 3−octaprenyl−4−hydroxybenzoate carboxy−lyase:	MMP1552
−0.38	hypothetical protein:	MMP1283
−0.38	hypothetical protein:	MMP1282
−0.13	hypothetical protein:	MMP0190
−0.09	hypothetical protein:	MMP1387

Cluster: 0151 mmp; resid: 0.49; r/c: 25/39

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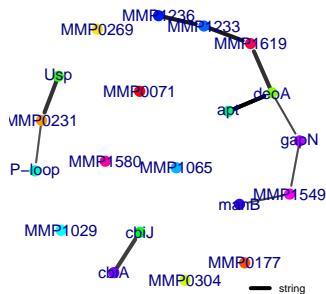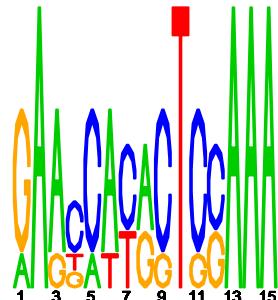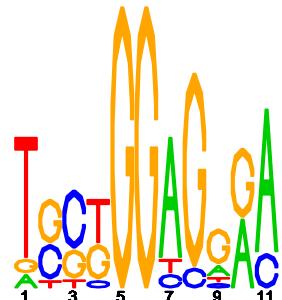upstream meme PSSM #1; e=0.017   upstream meme PSSM #2; e=970
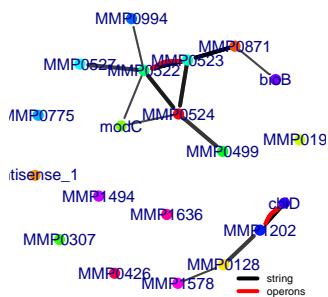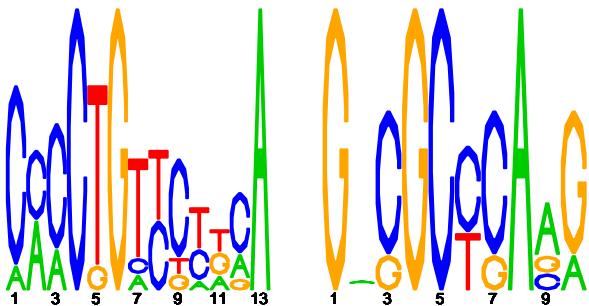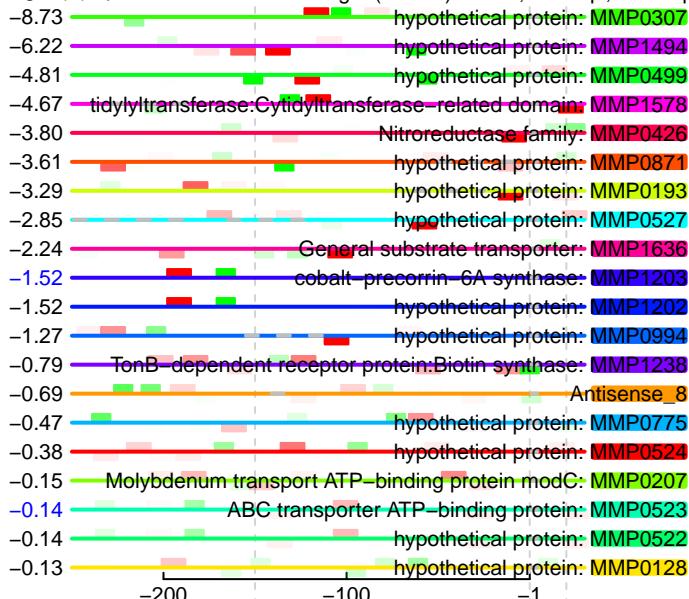
log10(P) upstream meme   log10(P.clust)=−1.72; 25 seqs; 25 uniq

−5.46	5S ribosomal RNA: RNA_47
−4.87	tRNA−Glu: RNA_23
−4.67	hypothetical protein: MMP0475
−4.46	hypothetical protein: MMP1262
−2.99	hypothetical protein: MMP0939
−2.28	hypothetical protein: MMP0369
−2.09	hypothetical protein: MMP0769
−2.07	Antisense_21
−1.97	nucleotide) binding motif:Generic methyltransferase: MMP1179
−1.75	archaeal phosphoglycerate mutase−related: MMP0598
−1.71	Ilfamily:Double−stranded RNA binding (DsRBD) domain: MMP1526
−1.60	Glycosyl transferase: MMP0090
−1.59	Universal stress protein (Usp): MMP0585
−1.29	Modulator of DNA gyrase: MMP1525
−1.10	acetylglutamate kinase: MMP0063
−0.91	Redox−active disulfide protein 2: MMP1388
−0.75	Unanno_43
−0.49	hypothetical protein: MMP1343
−0.44	on−sulfur flavoprotein of Methanosarcina thermophila: MMP0614
−0.23	putative integral membrane protein: MMP0725
−0.13	hypothetical protein: MMP1679
−0.12	hypothetical protein: MMP1056
−0.04	cobalt transport system permease related protein: MMP0886
−0.01	putative DNA primase large subunit: MMP0009
−0.00	Molybdenum ABC transporter, permease protein: MMP0515

−200   −100   −1

Cluster: 0152 mmp; resid: 0.25; r/c: 20/38

upstream meme PSSM #1; e=1.8   upstream meme PSSM #2; e=530

log10(P) upstream meme   log10(P.clust)=−2.48; 20 seqs; 20 uniq

log10(P)	Description	Gene
−7.79	hypothetical protein:	MMP1236
−6.36	receptor protein:Formate dehydrogenase, subunit FdhD:	MMP1233
−4.94	Cobyrinic acid a,c−diamide synthase:	MMP1477
−4.88	thymidine phosphorylase:	MMP0327
−3.27	Aldehyde dehydrogenase:	MMP1487
−3.16	N−glycosylase/DNA lyase:	MMP0304
−3.07	hypothetical protein:	MMP1029
−3.05	Phosphoglucomutase/phosphomannomutase:	MMP1372
−2.38	I region, domain I and II:MoeA C−terminal, domain IV:	MMP1619
−2.22	hypothetical protein:	MMP0177
−2.18	adenine phosphoribosyltransferase:	MMP0660
−1.92	AP endonuclease, family 2:	MMP1549
−1.58	DNA primase, small subunit:	MMP0071
−1.00	in:ATP/GTP−binding site motif A (P−loop):AAA ATPase:	MMP0676
−0.48	Precorrin−6x reductase CbiJ/CobK:	MMP0599
−0.37	te synthase−related protein synthase−related protein:	MMP1580
−0.30	hypothetical protein:	MMP0269
−0.25	hypothetical protein:	MMP0231
−0.25	Universal stress protein (Usp):	MMP0585
−0.12	hypothetical protein:	MMP1065

Cluster: 0153 mmp; resid: 0.21; r/c: 20/41

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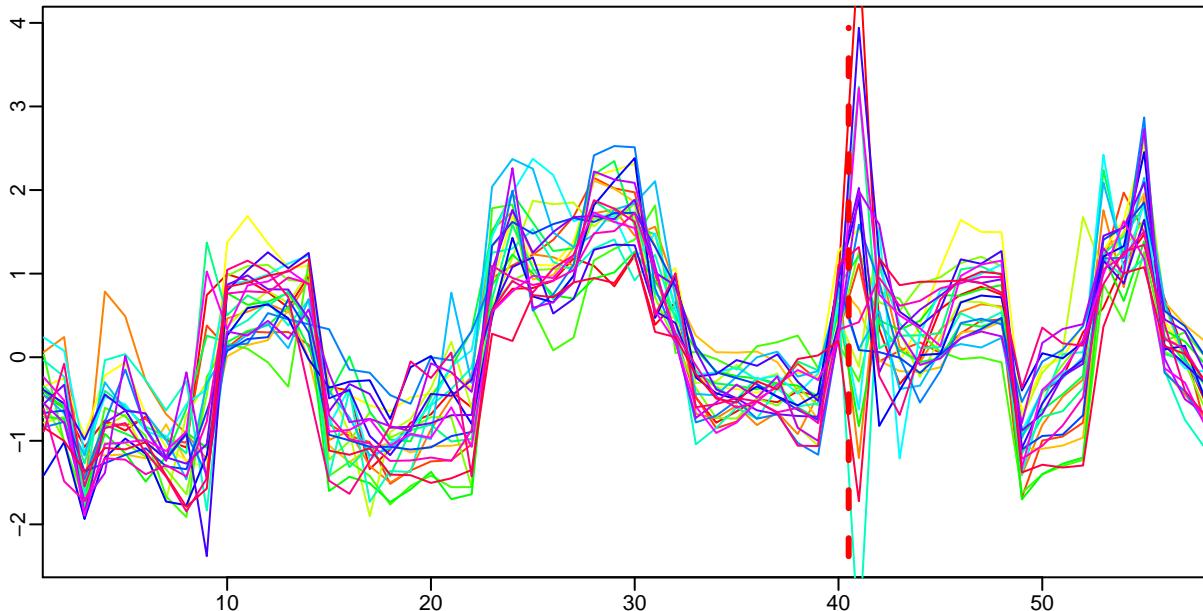upstream meme PSSM #1; e=0.48   upstream meme PSSM #2; e=190

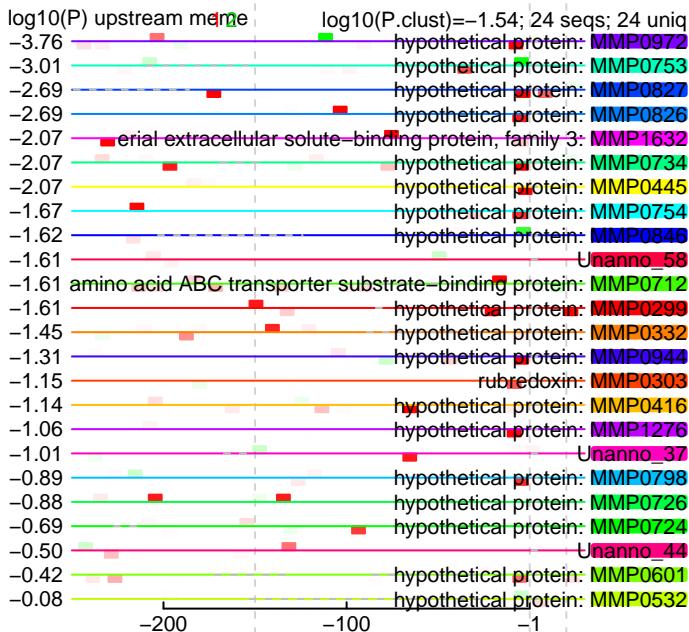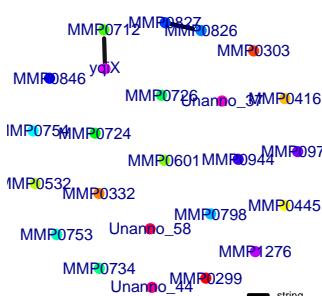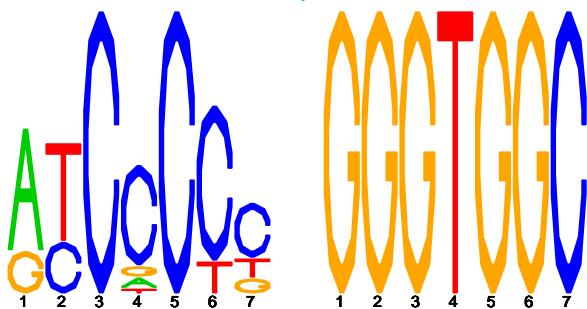log10(P) upstream meme   log10(P.clust)=−2.37; 20 seqs; 18 uniq

log10(P)	Description	ID
−8.73	hypothetical protein:	MMP0307
−6.22	hypothetical protein:	MMP1494
−4.81	hypothetical protein:	MMP0499
−4.67	tidylyltransferase:Cytidyltransferase−related domain:	MMP1578
−3.80	Nitroreductase family:	MMP0426
−3.61	hypothetical protein:	MMP0871
−3.29	hypothetical protein:	MMP0193
−2.85	hypothetical protein:	MMP0527
−2.24	General substrate transporter:	MMP1636
−1.52	cobalt−precorrin−6A synthase:	MMP1203
−1.52	hypothetical protein:	MMP1202
−1.27	hypothetical protein:	MMP0994
−0.79	TonB−dependent receptor protein:Biotin synthase:	MMP1238
−0.69		Antisense_8
−0.47	hypothetical protein:	MMP0775
−0.38	hypothetical protein:	MMP0524
−0.15	Molybdenum transport ATP−binding protein modC:	MMP0207
−0.14	ABC transporter ATP−binding protein:	MMP0523
−0.14	hypothetical protein:	MMP0522
−0.13	hypothetical protein:	MMP0128

string
operons

Cluster: 0154 mmp; resid: 0.30; r/c: 24/40
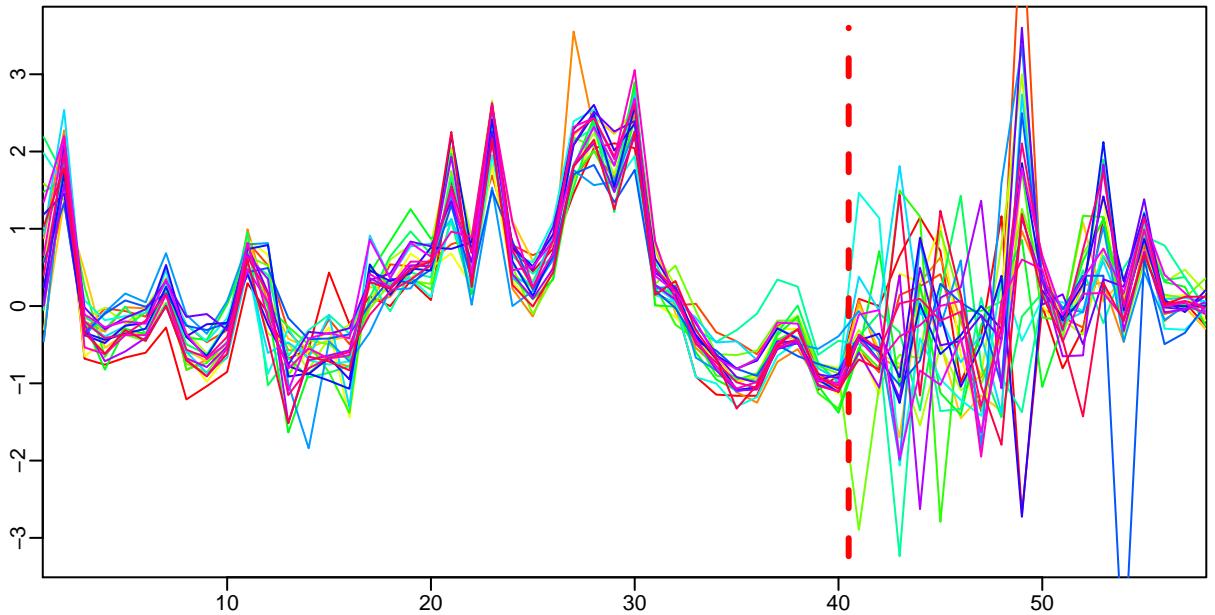

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cMonkey Version 4.8.8 mmp

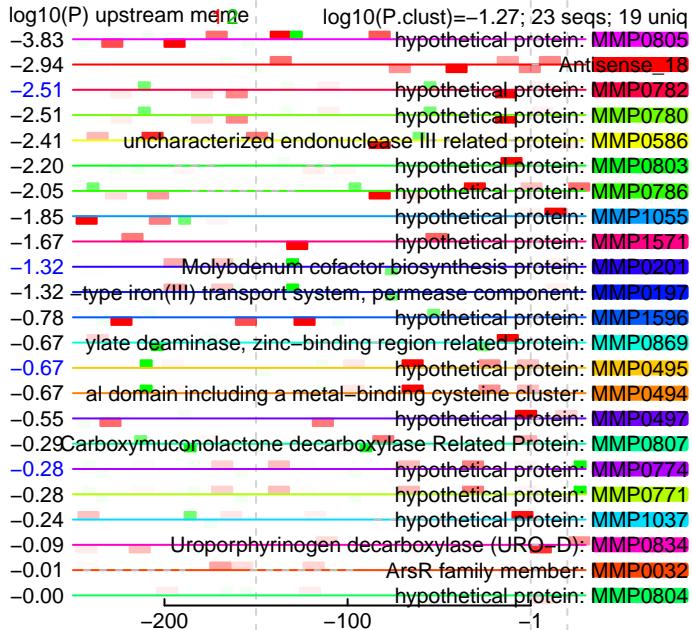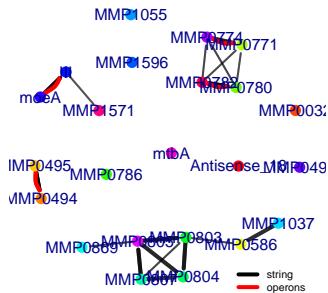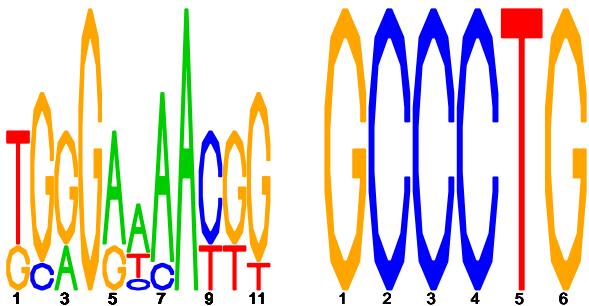upstream meme PSSM #1; e=7.2e-10   upstream meme PSSM #2; e=5.2e+03

log10(P) upstream meme   log10(P.clust)=−1.54; 24 seqs; 24 uniq

log10(P)	annotation	gene
−3.76	hypothetical protein:	MMP0972
−3.01	hypothetical protein:	MMP0753
−2.69	hypothetical protein:	MMP0827
−2.69	hypothetical protein:	MMP0826
−2.07	erial extracellular solute−binding protein, family 3:	MMP1632
−2.07	hypothetical protein:	MMP0734
−2.07	hypothetical protein:	MMP0445
−1.67	hypothetical protein:	MMP0754
−1.62	hypothetical protein:	MMP0846
−1.61		Unanno_58
−1.61	amino acid ABC transporter substrate−binding protein:	MMP0712
−1.61	hypothetical protein:	MMP0299
−1.45	hypothetical protein:	MMP0332
−1.31	hypothetical protein:	MMP0944
−1.15	rubredoxin:	MMP0303
−1.14	hypothetical protein:	MMP0416
−1.06	hypothetical protein:	MMP1276
−1.01		Unanno_37
−0.89	hypothetical protein:	MMP0798
−0.88	hypothetical protein:	MMP0726
−0.69	hypothetical protein:	MMP0724
−0.50		Unanno_44
−0.42	hypothetical protein:	MMP0601
−0.08	hypothetical protein:	MMP0532

Cluster: 0155 mmp; resid: 0.20; r/c: 23/40
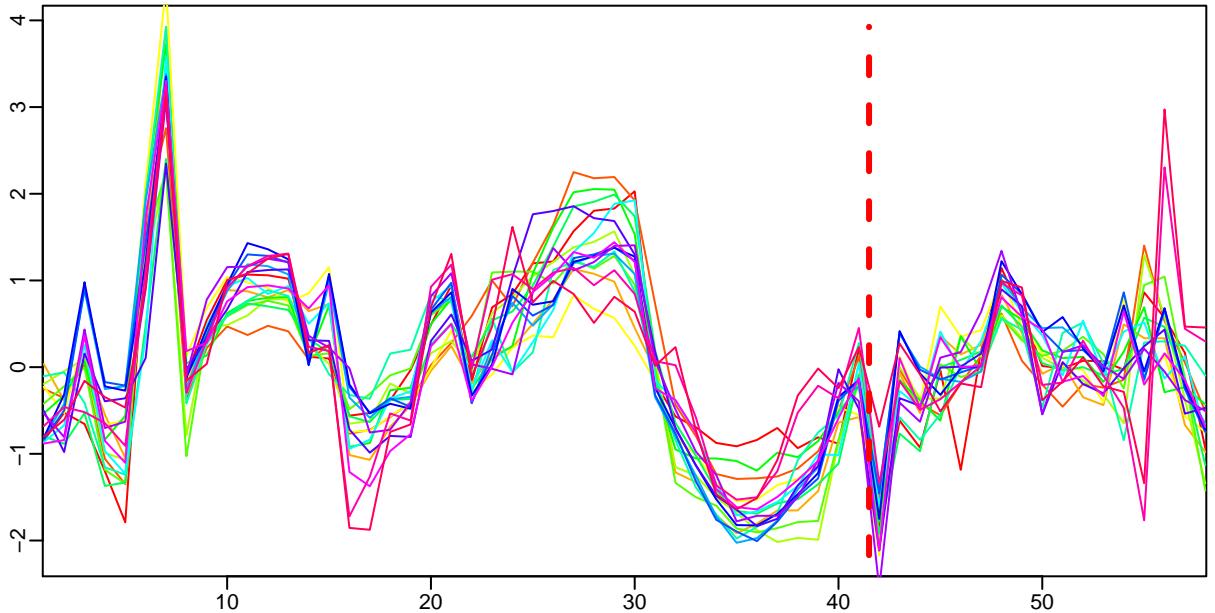
11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

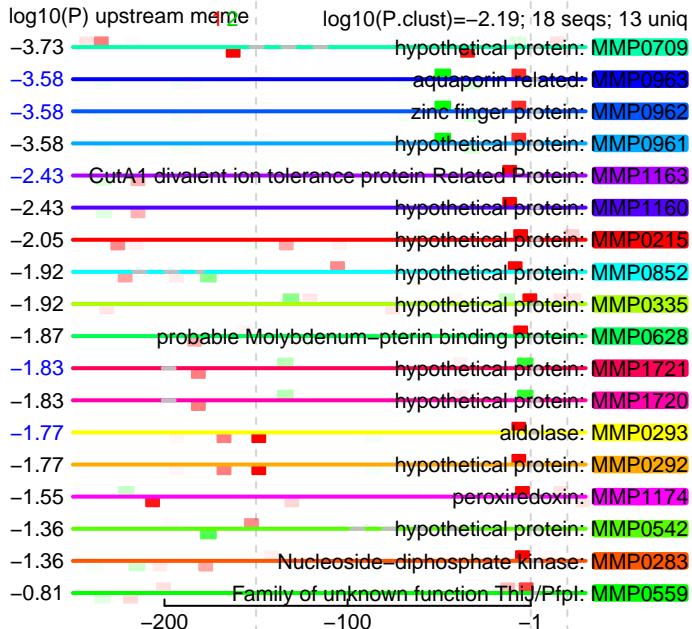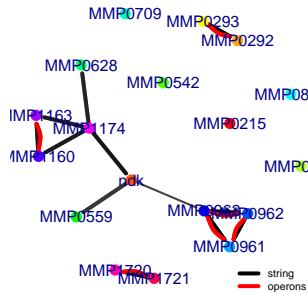upstream meme PSSM #1; e=920   upstream meme PSSM #2; e=1e+04

log10(P) upstream meme   log10(P.clust)=−1.27; 23 seqs; 19 uniq

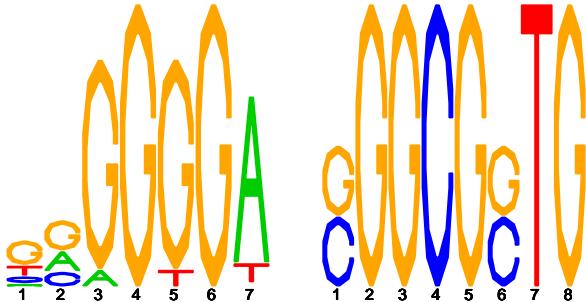| log10(P)	annotation
−3.83	hypothetical protein: MMP0805
−2.94	Antisense_18
−2.51	hypothetical protein: MMP0782
−2.51	hypothetical protein: MMP0780
−2.41	uncharacterized endonuclease III related protein: MMP0586
−2.20	hypothetical protein: MMP0803
−2.05	hypothetical protein: MMP0786
−1.85	hypothetical protein: MMP1055
−1.67	hypothetical protein: MMP1571
−1.32	Molybdenum cofactor biosynthesis protein: MMP0201
−1.32	type iron(III) transport system, permease component: MMP0197
−0.78	hypothetical protein: MMP1596
−0.67	ylate deaminase, zinc−binding region related protein: MMP0869
−0.67	hypothetical protein: MMP0495
−0.67	al domain including a metal−binding cysteine cluster: MMP0494
−0.55	hypothetical protein: MMP0497
−0.29	Carboxymuconolactone decarboxylase Related Protein: MMP0807
−0.28	hypothetical protein: MMP0774
−0.28	hypothetical protein: MMP0771
−0.24	hypothetical protein: MMP1037
−0.09	Uroporphyrinogen decarboxylase (URO−D): MMP0834
−0.01	ArsR family member: MMP0032
−0.00	hypothetical protein: MMP0804

Cluster: 0156 mmp; resid: 0.27; r/c: 18/41

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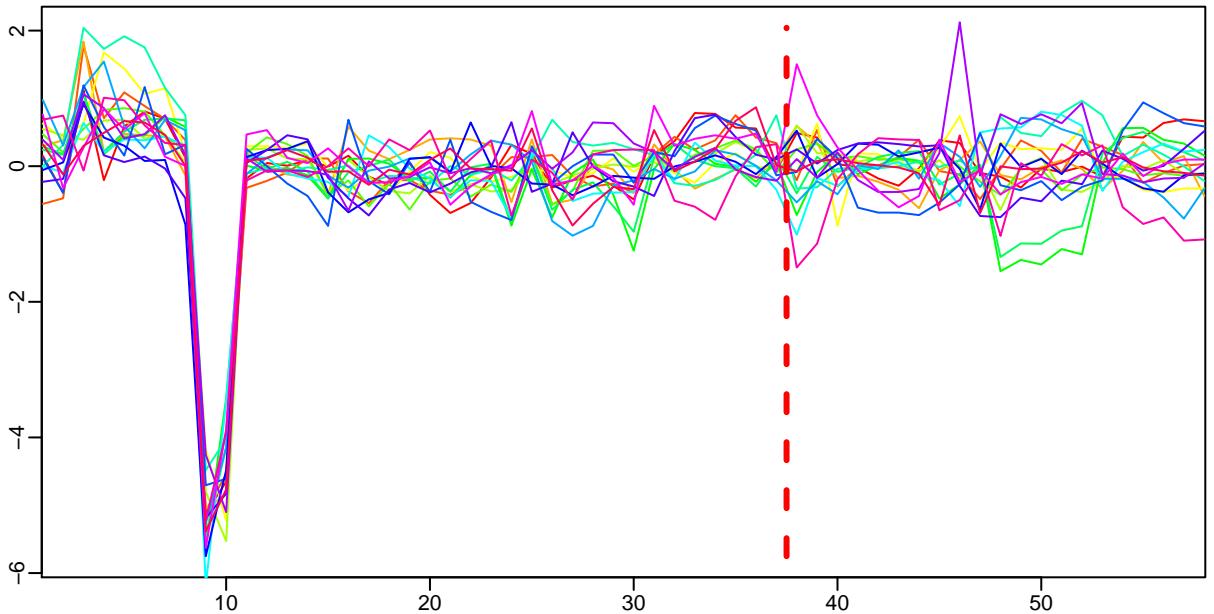
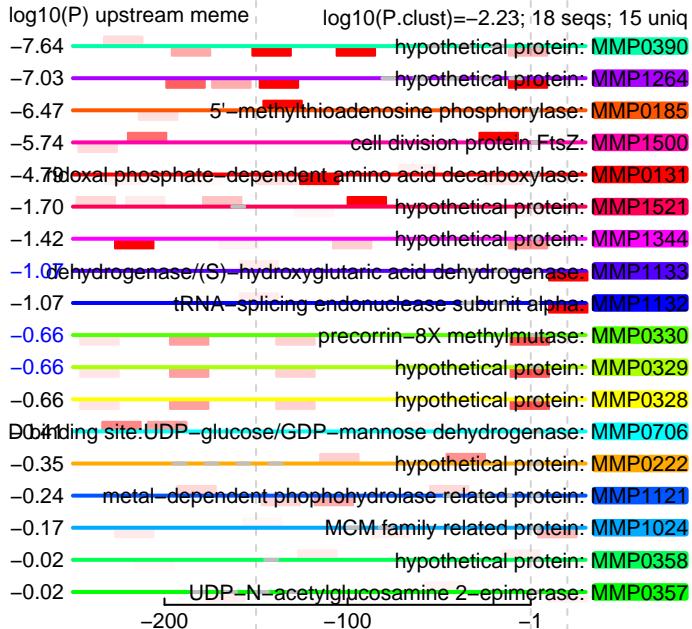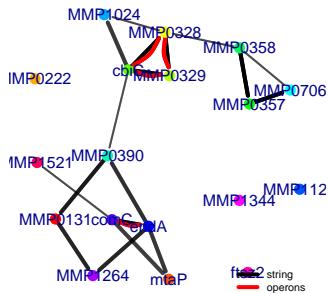upstream meme PSSM #1; e=4.5e−06 upstream meme PSSM #2; e=1.3e+03

log10(P) upstream meme   log10(P.clust)=−2.19; 18 seqs; 13 uniq

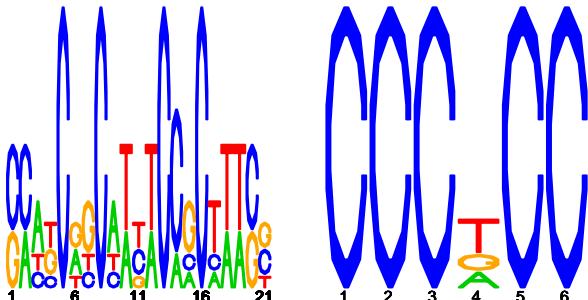| log10(P)	description	gene
−3.73	hypothetical protein	MMP0709
−3.58	aquaporin related	MMP0963
−3.58	zinc finger protein	MMP0962
−3.58	hypothetical protein	MMP0961
−2.43	CutA1 divalent ion tolerance protein Related Protein	MMP1163
−2.43	hypothetical protein	MMP1160
−2.05	hypothetical protein	MMP0215
−1.92	hypothetical protein	MMP0852
−1.92	hypothetical protein	MMP0335
−1.87	probable Molybdenum−pterin binding protein	MMP0628
−1.83	hypothetical protein	MMP1721
−1.83	hypothetical protein	MMP1720
−1.77	aldolase	MMP0293
−1.77	hypothetical protein	MMP0292
−1.55	peroxiredoxin	MMP1174
−1.36	hypothetical protein	MMP0542
−1.36	Nucleoside−diphosphate kinase	MMP0283
−0.81	Family of unknown function ThiJ/PfpI	MMP0559

Cluster: 0157 mmp; resid: 0.26; r/c: 18/37

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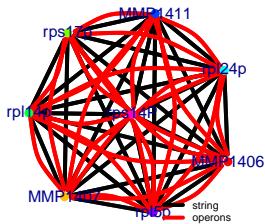upstream meme PSSM #1; e=210   upstream meme PSSM #2; e=2.4e+03

log10(P) upstream meme   log10(P.clust)=−2.23; 18 seqs; 15 uniq

log10(P)	Annotation	ID
−7.64	hypothetical protein:	MMP0390
−7.03	hypothetical protein:	MMP1264
−6.47	5′−methylthioadenosine phosphorylase:	MMP0185
−5.74	cell division protein FtsZ:	MMP1500
−4.79	pyridoxal phosphate−dependent amino acid decarboxylase:	MMP0131
−1.70	hypothetical protein:	MMP1521
−1.42	hypothetical protein:	MMP1344
−1.07	dehydrogenase/(S)−hydroxyglutaric acid dehydrogenase:	MMP1133
−1.07	tRNA−splicing endonuclease subunit alpha:	MMP1132
−0.66	precorrin−8X methylmutase:	MMP0330
−0.66	hypothetical protein:	MMP0329
−0.66	hypothetical protein:	MMP0328
−0.41	DNA binding site:UDP−glucose/GDP−mannose dehydrogenase:	MMP0706
−0.35	hypothetical protein:	MMP0222
−0.24	metal−dependent phophohydrolase related protein:	MMP1121
−0.17	MCM family related protein:	MMP1024
−0.02	hypothetical protein:	MMP0358
−0.02	UDP−N−acetylglucosamine 2−epimerase:	MMP0357

Cluster: 0158 mmp; resid: 0.08; r/c: 8/39

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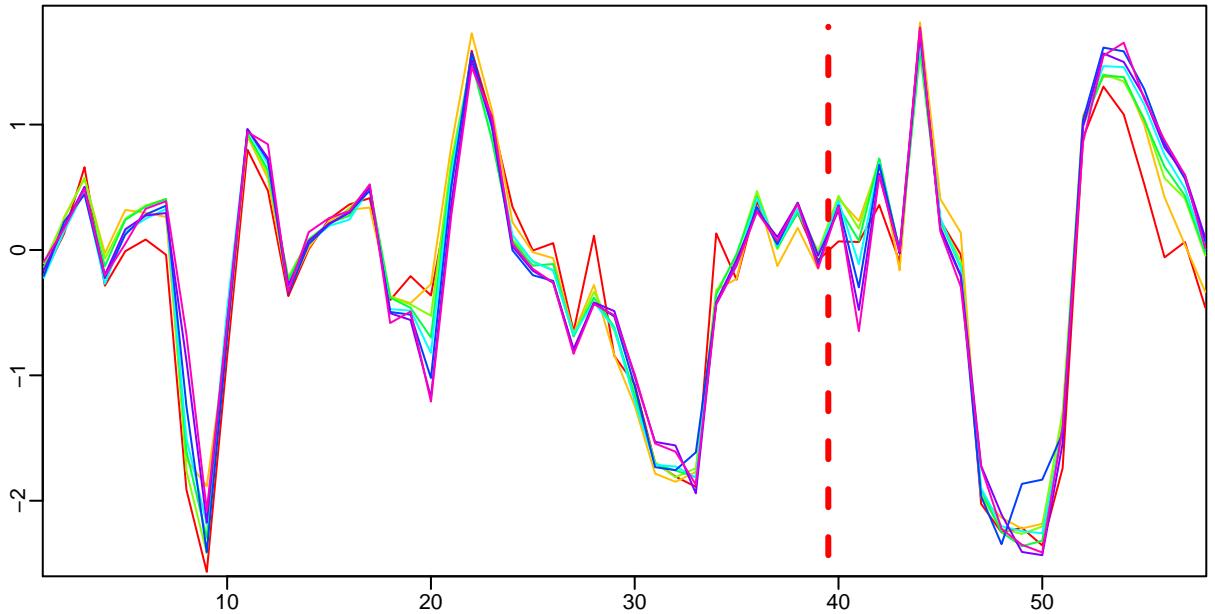
translation initiation factor Sui1: MMP1406
ribonuclease P protein component 1: MMP1407
30S ribosomal protein S17P: MMP1408
50S ribosomal protein L14P: MMP1409
50S ribosomal protein L24P: MMP1410
30S ribosomal protein S4e: MMP1411
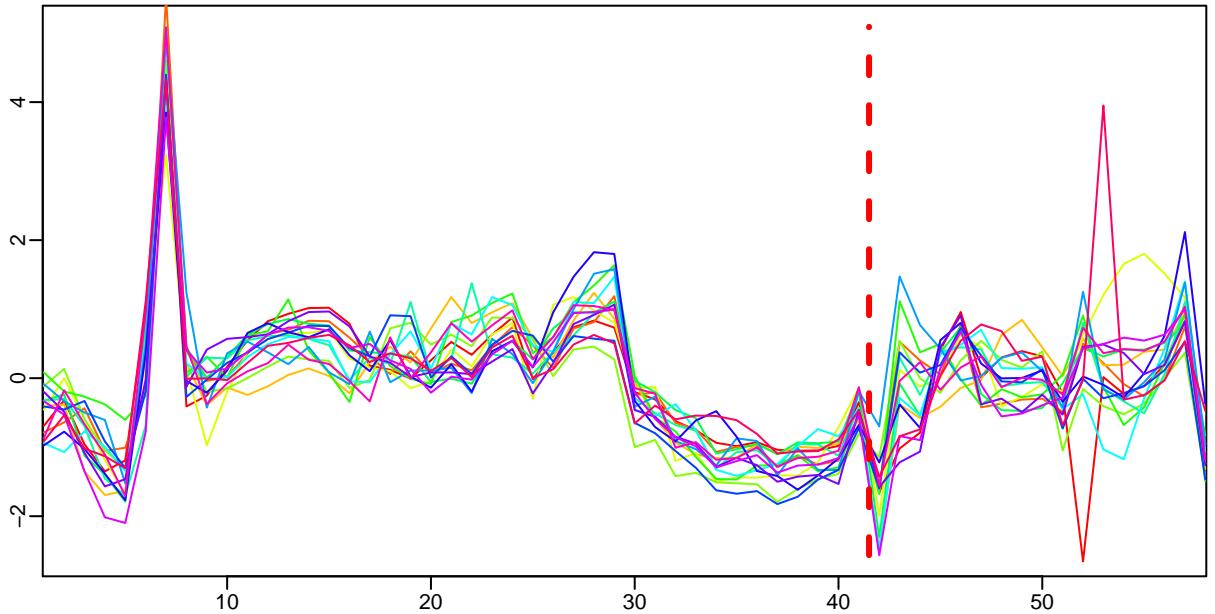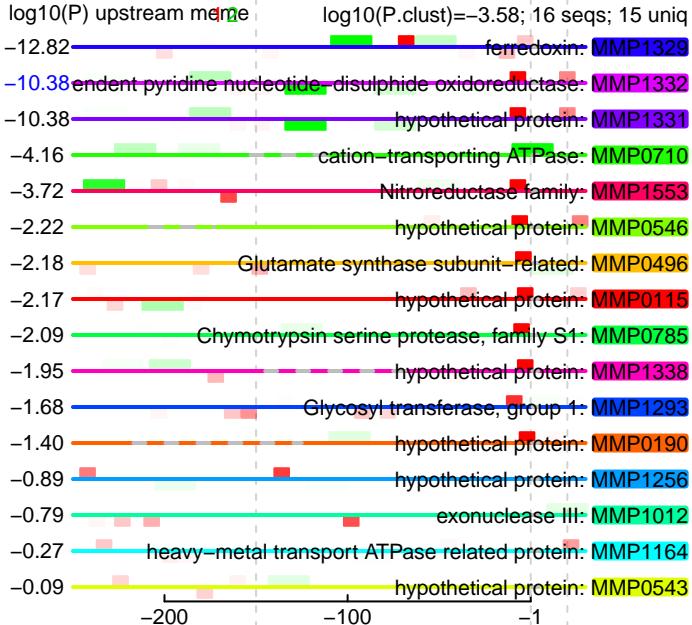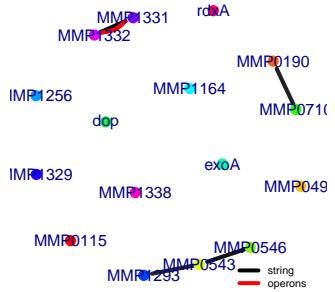50S ribosomal protein L5P: MMP1412
30S ribosomal protein S14P: MMP1413

MMP1411
rps17p
l24p
rpl14
MMP1406
MMP1407
rpl5p

string
operons

−200   −100   −1

sequence position

Cluster: 0159 mmp; resid: 0.23; r/c: 16/41

upstream meme PSSM #1; e=1.2e−09 upstream meme PSSM #2; e=2.4e+03

log10(P) upstream meme   log10(P.clust)=−3.58; 16 seqs; 15 uniq

log10(P)	annotation
−12.82	ferredoxin: MMP1329
−10.38	endent pyridine nucleotide–disulphide oxidoreductase: MMP1332
−10.38	hypothetical protein: MMP1331
−4.16	cation–transporting ATPase: MMP0710
−3.72	Nitroreductase family: MMP1553
−2.22	hypothetical protein: MMP0546
−2.18	Glutamate synthase subunit–related: MMP0496
−2.17	hypothetical protein: MMP0115
−2.09	Chymotrypsin serine protease, family S1: MMP0785
−1.95	hypothetical protein: MMP1338
−1.68	Glycosyl transferase, group 1: MMP1293
−1.40	hypothetical protein: MMP0190
−0.89	hypothetical protein: MMP1256
−0.79	exonuclease III: MMP1012
−0.27	heavy–metal transport ATPase related protein: MMP1164
−0.09	hypothetical protein: MMP0543

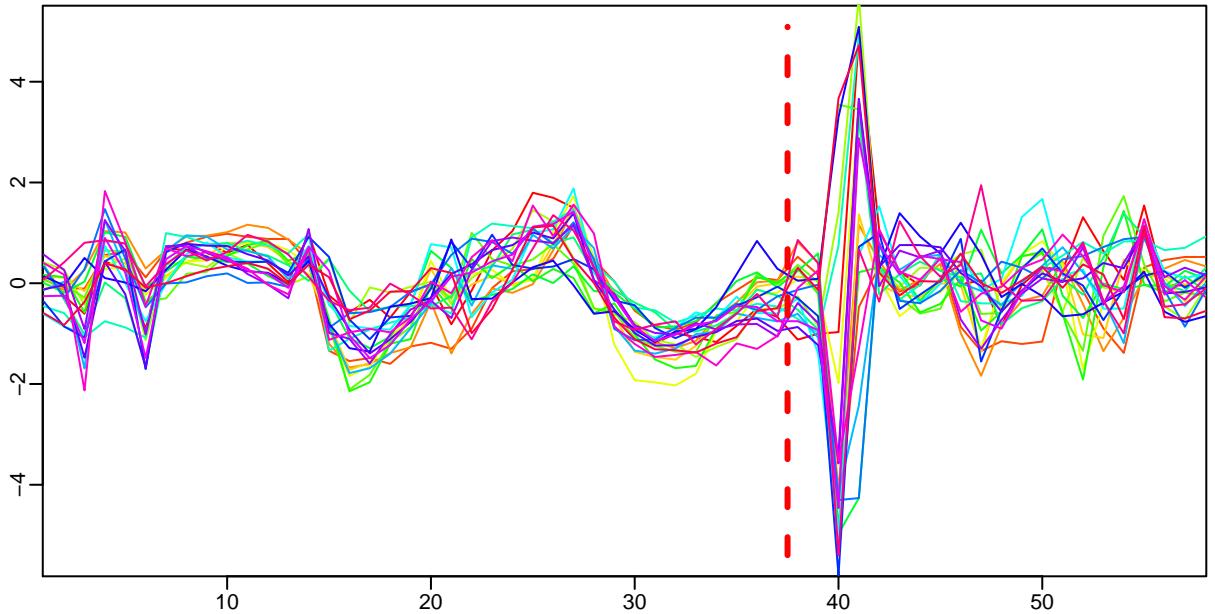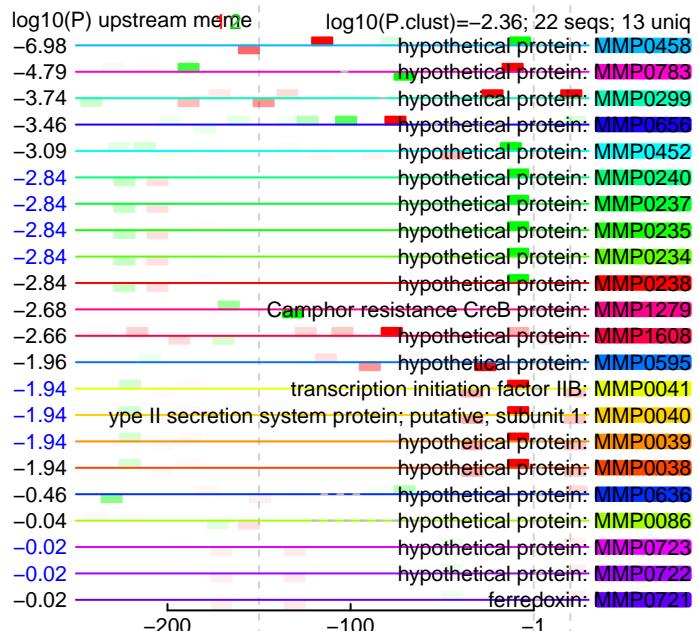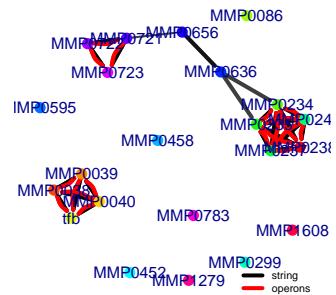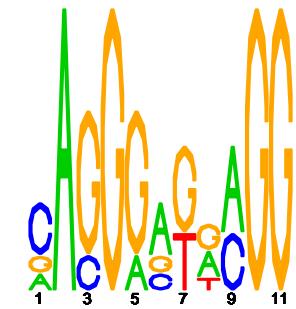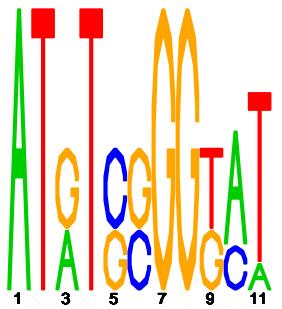**Cluster: 0160 mmp; resid: 0.33; r/c: 22/37**

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cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=0.87   upstream meme PSSM #2; e=320

log10(P) upstream meme   log10(P.clust)=−2.36; 22 seqs; 13 uniq

log10(P)	protein	gene
−6.98	hypothetical protein:	MMP0458
−4.79	hypothetical protein:	MMP0783
−3.74	hypothetical protein:	MMP0299
−3.46	hypothetical protein:	MMP0656
−3.09	hypothetical protein:	MMP0452
−2.84	hypothetical protein:	MMP0240
−2.84	hypothetical protein:	MMP0237
−2.84	hypothetical protein:	MMP0235
−2.84	hypothetical protein:	MMP0234
−2.84	hypothetical protein:	MMP0238
−2.68	Camphor resistance CrcB protein:	MMP1279
−2.66	hypothetical protein:	MMP1608
−1.96	hypothetical protein:	MMP0595
−1.94	transcription initiation factor IIB:	MMP0041
−1.94	ype II secretion system protein; putative; subunit 1:	MMP0040
−1.94	hypothetical protein:	MMP0039
−1.94	hypothetical protein:	MMP0038
−0.46	hypothetical protein:	MMP0636
−0.04	hypothetical protein:	MMP0086
−0.02	hypothetical protein:	MMP0723
−0.02	hypothetical protein:	MMP0722
−0.02	ferredoxin:	MMP0721

Cluster: 0161 mmp; resid: 0.19; r/c: 14/40

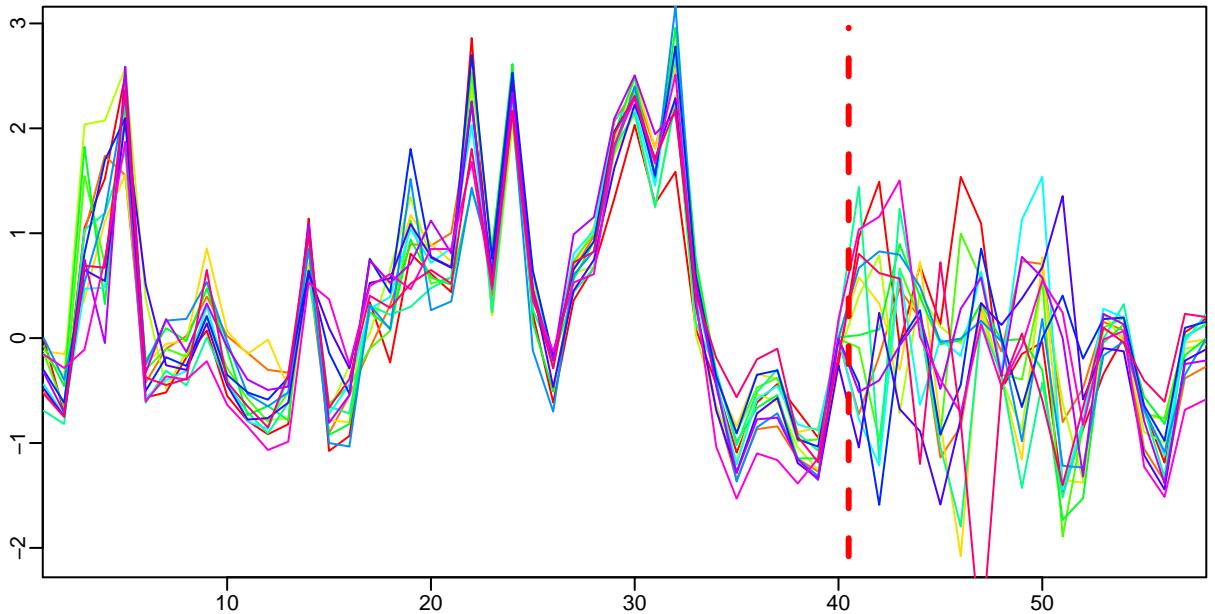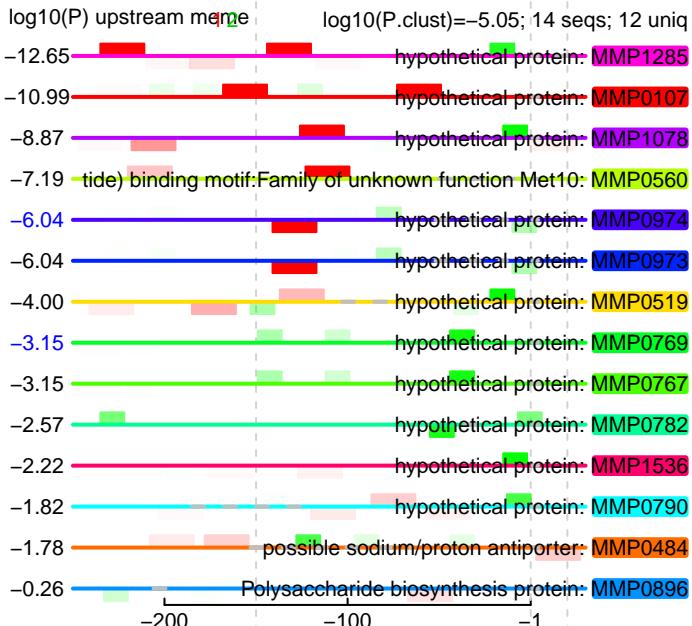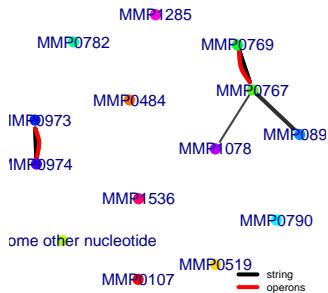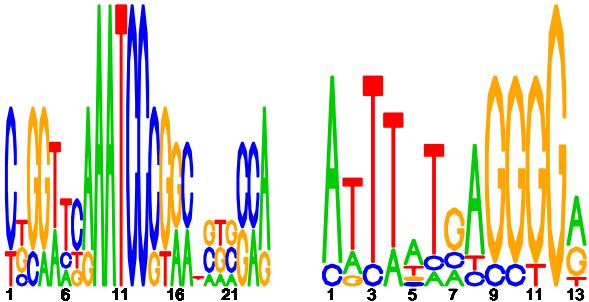11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=0.0012   upstream meme PSSM #2; e=3.3

log10(P) upstream meme   log10(P.clust)=−5.05; 14 seqs; 12 uniq

−12.65	hypothetical protein: MMP1285
−10.99	hypothetical protein: MMP0107
−8.87	hypothetical protein: MMP1078
−7.19	tide) binding motif:Family of unknown function Met10: MMP0560
−6.04	hypothetical protein: MMP0974
−6.04	hypothetical protein: MMP0973
−4.00	hypothetical protein: MMP0519
−3.15	hypothetical protein: MMP0769
−3.15	hypothetical protein: MMP0767
−2.57	hypothetical protein: MMP0782
−2.22	hypothetical protein: MMP1536
−1.82	hypothetical protein: MMP0790
−1.78	possible sodium/proton antiporter: MMP0484
−0.26	Polysaccharide biosynthesis protein: MMP0896

MMP1285
MMP0782   MMP0769
MMP0484   MMP0767
MMP0973   MMP1089
MMP0974   MMP1078
MMP1536
MMP0790
ome other nucleotide
MMP0519
MMP0107

string
operons

Cluster: 0162 mmp; resid: 0.29; r/c: 19/37
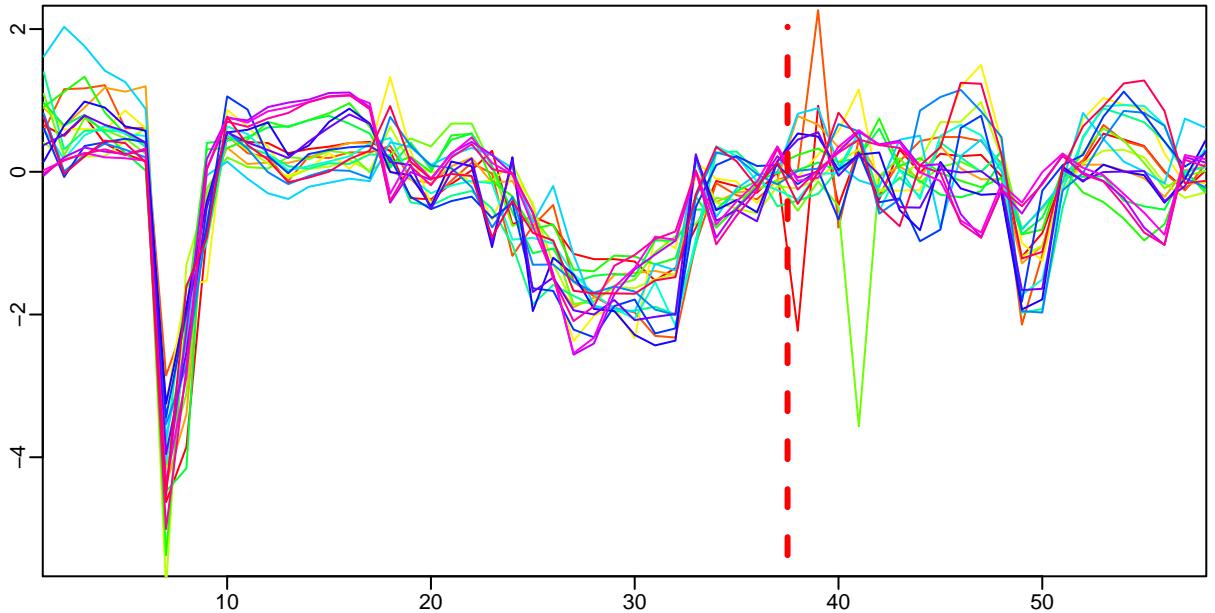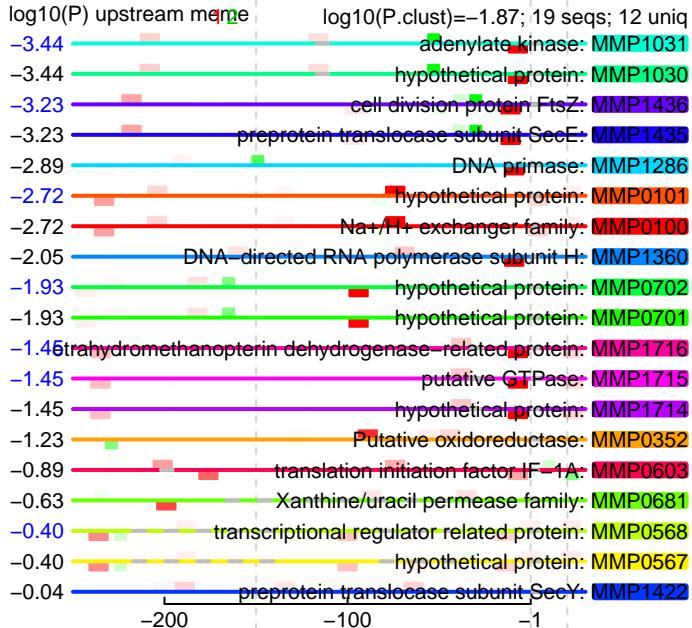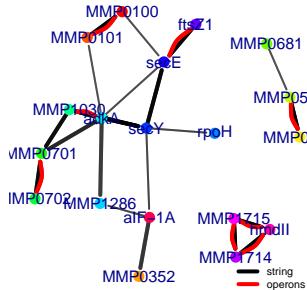
11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=420   upstream meme PSSM #2; e=1.2e+04

log10(P) upstream meme   log10(P.clust)=−1.87; 19 seqs; 12 uniq

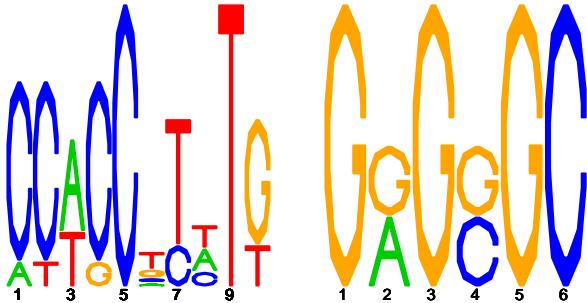| log10(P)	annotation	gene
−3.44	adenylate kinase:	MMP1031
−3.44	hypothetical protein:	MMP1030
−3.23	cell division protein FtsZ:	MMP1436
−3.23	preprotein translocase subunit SecE:	MMP1435
−2.89	DNA primase:	MMP1286
−2.72	hypothetical protein:	MMP0101
−2.72	Na+/H+ exchanger family:	MMP0100
−2.05	DNA-directed RNA polymerase subunit H:	MMP1360
−1.93	hypothetical protein:	MMP0702
−1.93	hypothetical protein:	MMP0701
−1.46	tetrahydromethanopterin dehydrogenase−related protein:	MMP1716
−1.45	putative GTPase:	MMP1715
−1.45	hypothetical protein:	MMP1714
−1.23	Putative oxidoreductase:	MMP0352
−0.89	translation initiation factor IF−1A:	MMP0603
−0.63	Xanthine/uracil permease family:	MMP0681
−0.40	transcriptional regulator related protein:	MMP0568
−0.40	hypothetical protein:	MMP0567
−0.04	preprotein translocase subunit SecY:	MMP1422

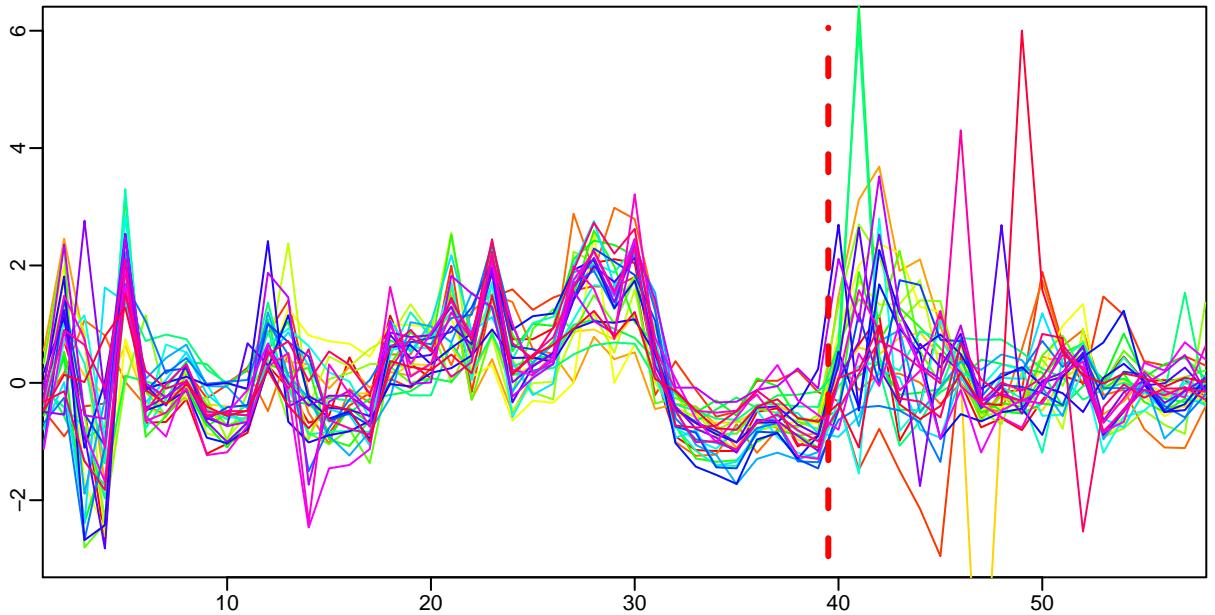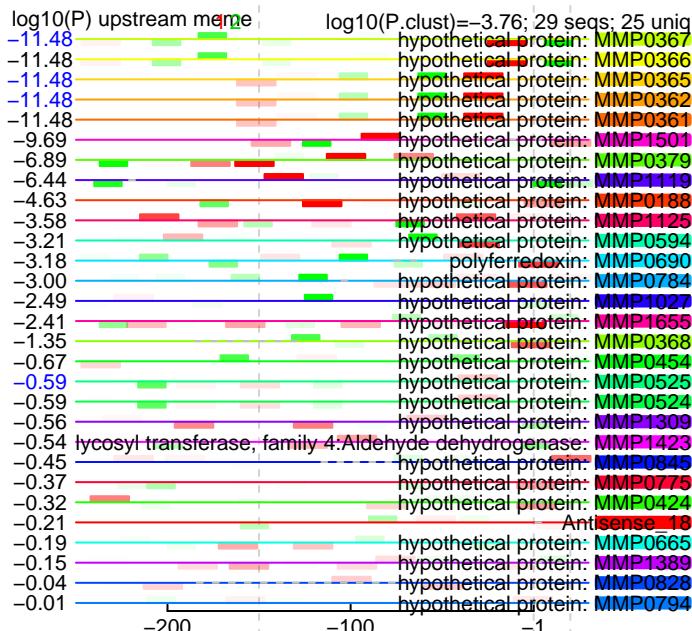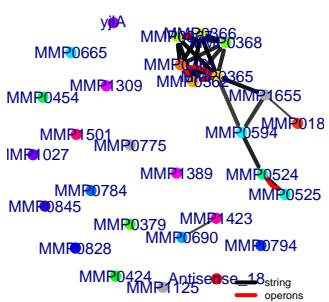**Cluster: 0163 mmp; resid: 0.42; r/c: 29/39**

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=19
upstream meme PSSM #2; e=380

log10(P) upstream meme
log10(P.clust)=−3.76; 29 seqs; 25 uniq

log10(P)	protein
−11.48	hypothetical protein: MMP0367
−11.48	hypothetical protein: MMP0366
−11.48	hypothetical protein: MMP0365
−11.48	hypothetical protein: MMP0362
−11.48	hypothetical protein: MMP0361
−9.69	hypothetical protein: MMP1501
−6.89	hypothetical protein: MMP0379
−6.44	hypothetical protein: MMP1119
−4.63	hypothetical protein: MMP0188
−3.58	hypothetical protein: MMP1125
−3.21	hypothetical protein: MMP0594
−3.18	polyferredoxin: MMP0690
−3.00	hypothetical protein: MMP0784
−2.49	hypothetical protein: MMP1027
−2.41	hypothetical protein: MMP1655
−1.35	hypothetical protein: MMP0368
−0.67	hypothetical protein: MMP0454
−0.59	hypothetical protein: MMP0525
−0.59	hypothetical protein: MMP0524
−0.56	hypothetical protein: MMP1309
−0.54	lycosyl transferase, family 4:Aldehyde dehydrogenase: MMP1423
−0.45	hypothetical protein: MMP0845
−0.37	hypothetical protein: MMP0775
−0.32	hypothetical protein: MMP0424
−0.21	Antisense_18
−0.19	hypothetical protein: MMP0665
−0.15	hypothetical protein: MMP1389
−0.04	hypothetical protein: MMP0828
−0.01	hypothetical protein: MMP0794

Cluster: 0164 mmp; resid: 0.16; r/c: 14/38

upstream meme PSSM #1; e=53   upstream meme PSSM #2; e=1.8e+03

log10(P) upstream meme   log10(P.clust)=−5.50; 14 seqs; 3 uniq

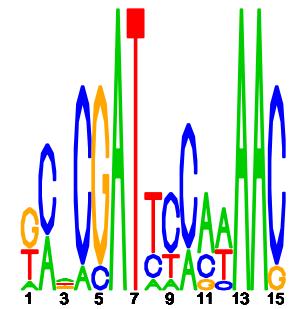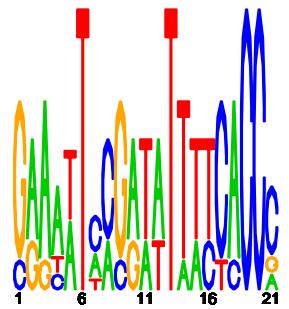|	
−5.97	flagella accessory protein I: MMP1675
−5.97	flagella accessory protein G: MMP1673
−5.97	flagella accessory protein F: MMP1672
−5.97	flagella accessory protein E: MMP1671
−5.97	flagella accessory protein D: MMP1670
−5.97	flagella accessory protein C: MMP1669
−5.97	flagellin: MMP1668
−5.97	flagellin: MMP1667
−5.97	flagellin: MMP1666
−4.65	Chemotaxis protein CheA: MMP0927
−4.65	chemotaxis protein CheB: MMP0926
−4.65	chemotaxis protein CheW: MMP0925
−4.65	hypothetical protein: MMP0924
−4.61	hypothetical protein: MMP1719

Cluster: 0165 mmp; resid: 0.23; r/c: 20/40

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cMonkey Version 4.8.8 mmp

upstream meme PSSM #1; e=3.7e−15   upstream meme PSSM #2; e=0.0016

log10(P) upstream meme   log10(P.clust)=−6.68; 20 seqs; 11 uniq

log10(P)	tRNA
−9.45	tRNA−Leu: RNA_26
−9.45	tRNA−Met: RNA_19
−9.42	tRNA−Phe: RNA_20
−8.01	tRNA−Leu: RNA_24
−8.01	tRNA−Glu: RNA_23
−8.01	tRNA−Met: RNA_22
−6.99	tRNA−Sec: RNA_50
−6.80	tRNA−Ala: RNA_9
−6.80	tRNA−Ala: RNA_8
−6.80	tRNA−Ala: RNA_7
−6.80	tRNA−Ala: RNA_6
−6.80	tRNA−Ala: RNA_5
−6.80	tRNA−Ala: RNA_3
−6.80	tRNA−Ala: RNA_2
−6.80	tRNA−Ala: RNA_1
−4.99	tRNA−Ser: RNA_13
−4.34	tRNA−Val: RNA_27
−3.99	tRNA−Ser: RNA_16
−3.65	tRNA−Trp: RNA_43
−2.88	tRNA−Ala: RNA_31

Cluster: 0166 mmp; resid: 0.30; r/c: 23/40

11 Oct 11 16:14:07 iter=2000
cMonkey Version 4.8.8 mmp

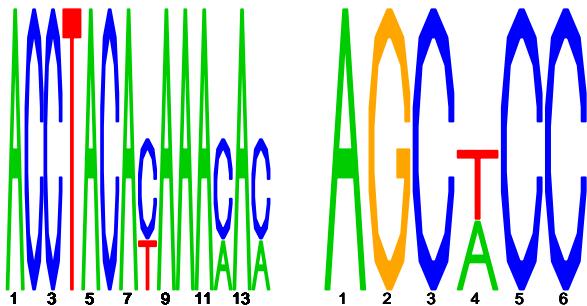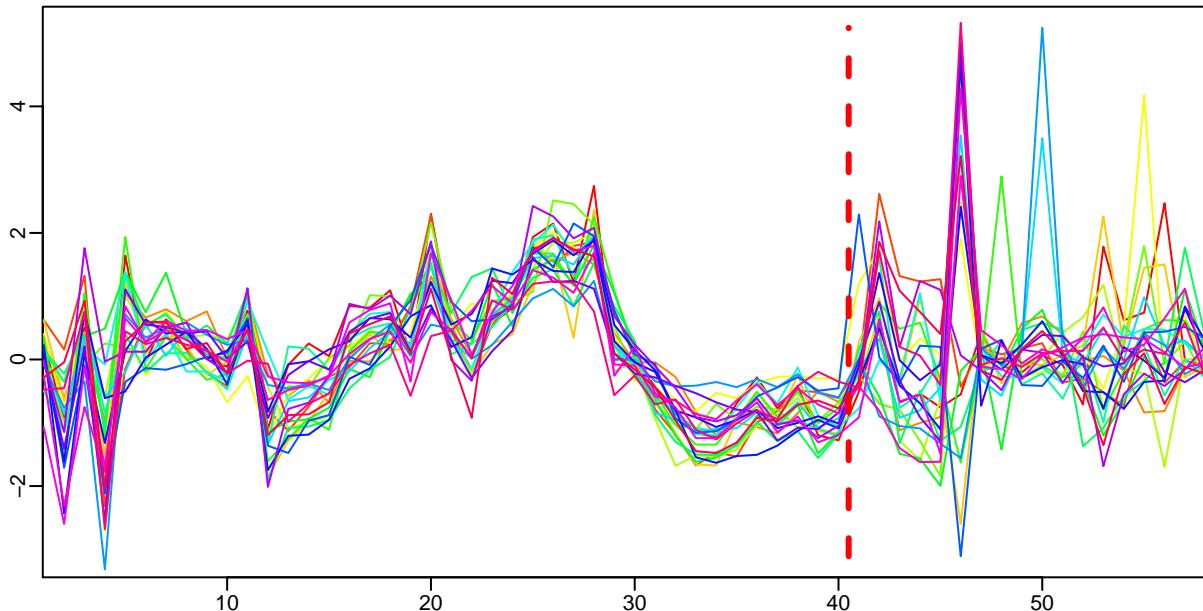upstream meme PSSM #1; e=1.7e−05   upstream meme PSSM #2; e=2

log10(P) upstream meme   log10(P.clust)=−3.68; 23 seqs; 19 uniq

−9.38	ADP−specific phosphofructokinase: MMP1296
−9.38	Glycosyl transferase, group 1: MMP1294
−9.38	glucan 1,4−alpha−glucosidase (glucoamylase): MMP1292
−9.38	Glycoside hydrolase, family 57: MMP1291
−9.09	Pyruvate kinase: MMP1605
−7.86	hypothetical protein: MMP1604
−6.05	RecJ related protein: MMP0547
−3.25	hypothetical protein: MMP0238
−2.54	hypothetical protein: MMP0813
−2.26	Na+/H+ exchanger: MMP0864
−2.03	hypothetical protein: MMP0842
−2.00	hypothetical protein: MMP0652
−1.85	hypothetical protein: MMP0756
−1.62	hypothetical protein: MMP0759
−1.62	HNH endonuclease:HNH nuclease: MMP0758
−1.44	hypothetical protein: MMP0538
−1.34	Transcriptional regulator, LysR Family Member: MMP0018
−1.12	hypothetical protein: MMP0558
−0.83	hypothetical protein: MMP1654
−0.83	hypothetical protein: MMP1653
−0.56	hypothetical protein: MMP0871
−0.46	criptional regulator protein, Helix−turn−helix motif: MMP0097
−0.37	hypothetical protein: MMP1268