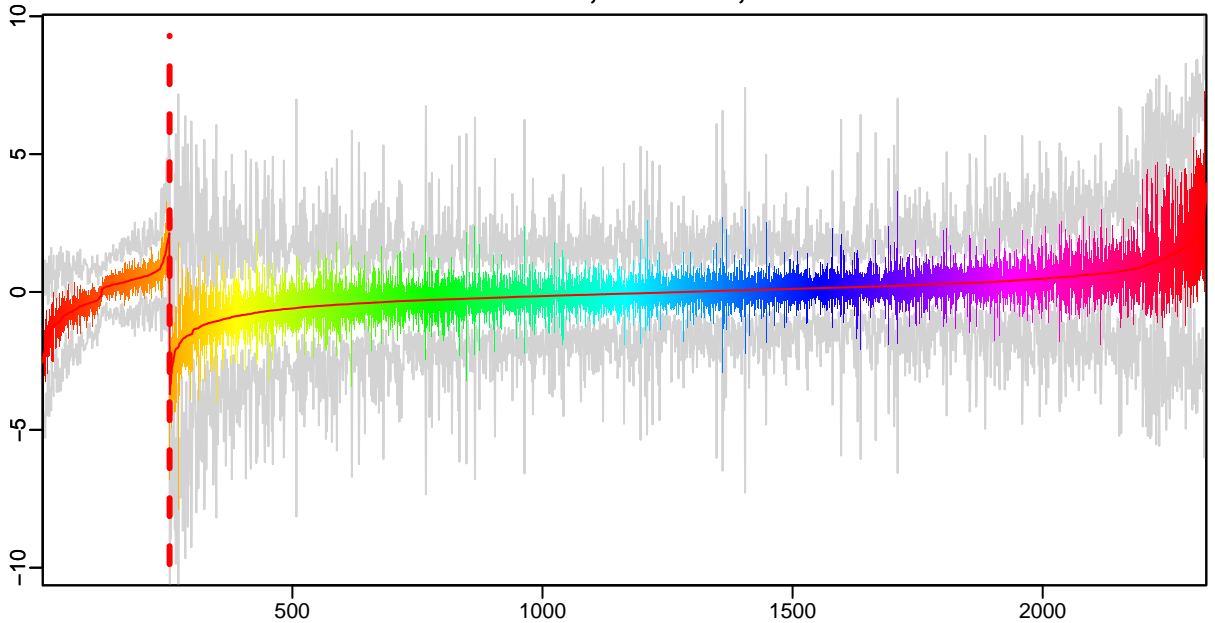
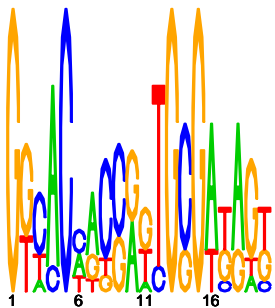


Cluster: 0063 mtu; resid: 0.56; r/c: 14/254

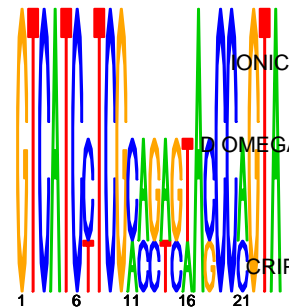
13 Oct 25 14:25:18 iter=2000
cMonkey Version 4.9.8 mtu



upstream meme PSSM #1; e=0.014



upstream meme PSSM #2; e=37



log10(P) upstream meme log10(P.clust)=-9.96; 14 seqs; 9 uniq

IONIC AMINO ACID TRANSPORT INTEGRAL MEMBRANE PROTEIN: RV3253C

-16.83 hypothetical protein: RV3254C

DI-Omega-HYDROXYLASE (ALKANE HYDROXYLASE-RUBREDOXIN): RV3252C

-16.83 PROBABLE RUBREDOXIN RUBA: RV3251C

-16.83 PROBABLE RUBREDOXIN RUBB: RV3250C

CRIPTONIN REGULATORY PROTEIN (PROBABLY TETR FAMILY): RV3249C

-11.12 POSSIBLE ESTERASE LIPOPROTEIN LPQC: RV3298C

CRIPTONIN REGULATORY PROTEIN (PROBABLY ASNC FAMILY): RV3291C

ALCOHOL DEHYDROGENASE P.6B (PIPERIDEINE-6-CARBOXYLATE DEHYDROGENASE): RV3293C

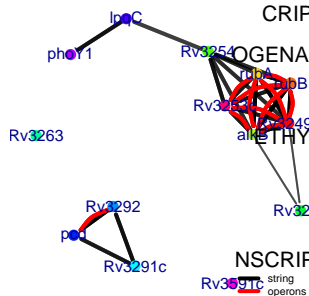
-5.56 hypothetical protein: RV3292C

METHYLASE (MODIFICATION METHYLASE) (METHYLTRANSFERASE): RV3263C

-3.21 POSSIBLE HYDROLASE: RV3591C

-2.55 hypothetical protein: RV3259C

TRANSCRIPTIONAL REGULATORY PROTEIN PHOU HOMOLOG 1 PHOY1: RV3301C



-200 -100 -1