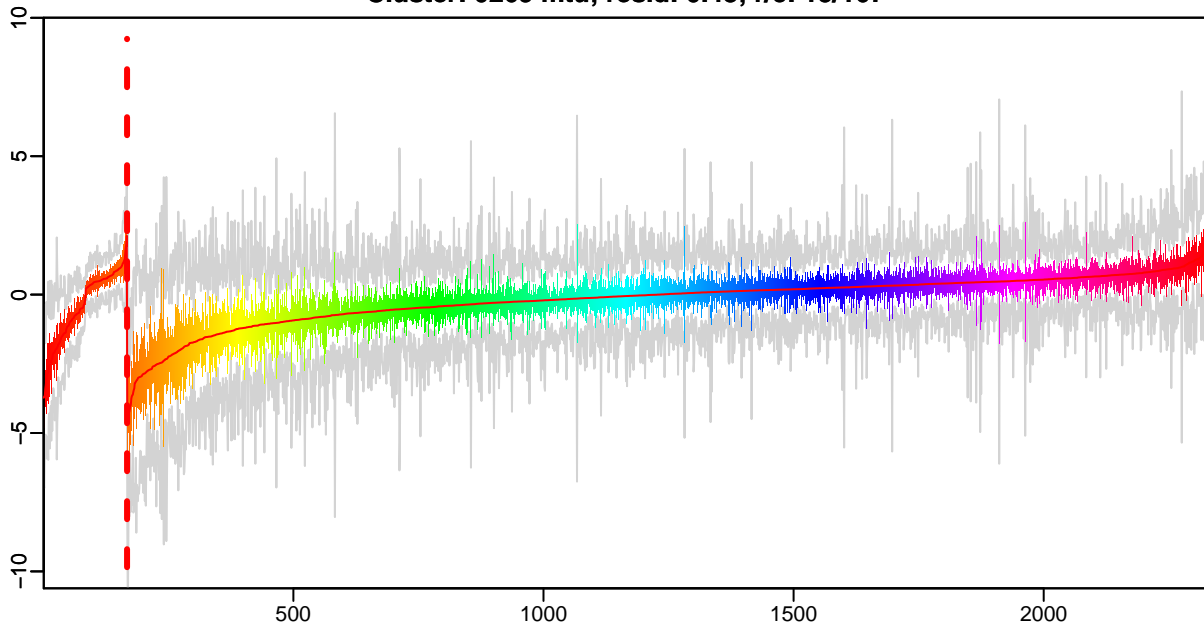
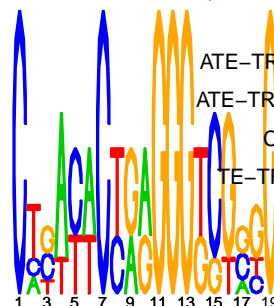
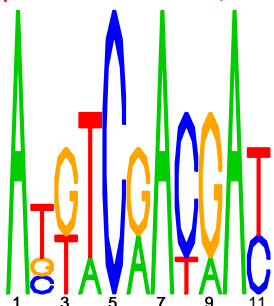


Cluster: 0269 mtu; resid: 0.48; r/c: 15/167

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



upstream meme PSSM #1; e=150 upstream meme PSSM #2; e=1.6e+03



log10(P) upstream meme log10(P.clust)=-6.84; 15 seqs; 5 uniq

ATE-TRANSPORT INTEGRAL MEMBRANE ABC TRANSPORTER PSTA2: RV0936

ATE-TRANSPORT INTEGRAL MEMBRANE ABC TRANSPORTER PSTC1: RV0935

C PHOSPHATE-BINDING LIPOPROTEIN PSTS1 (PBP-1) (PSTS1): RV0934

TE-TRANSPORT ATP-BINDING PROTEIN ABC TRANSPORTER PSTB: RV0933

-6.92 prolipoprotein diacylglycerol transferase: RV1614

-6.92 tryptophan synthase subunit alpha: RV1613

-6.92 tryptophan synthase subunit beta: RV1612

-6.56 fumarate reductase iron-sulfur subunit: RV0247C

Rv0249C E [MEMBRANE ANCHOR SUBUNIT] (SUCCINIC DEHYDROGENASE): RV0249C

OBABLE CONSERVED MCE ASSOCIATED TRANSMEMBRANE PROTEIN: RV0176

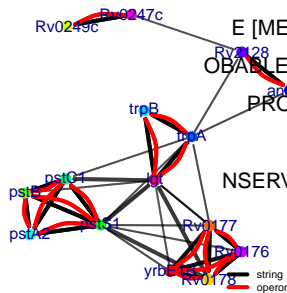
PROBABLE CONSERVED MCE ASSOCIATED MEMBRANE PROTEIN: RV0178

-6.25 PROBABLE CONSERVED MCE ASSOCIATED PROTEIN: RV0177

NSERVED HETEROLOGICAL INTEGRAL MEMBRANE PROTEIN YRBE1B: RV0168

-5.31 PROBABLE CONSERVED TRANSMEMBRANE PROTEIN: RV2128

-5.31 Probable L-asparagine permease ansP: RV2127



-200 -100 -1