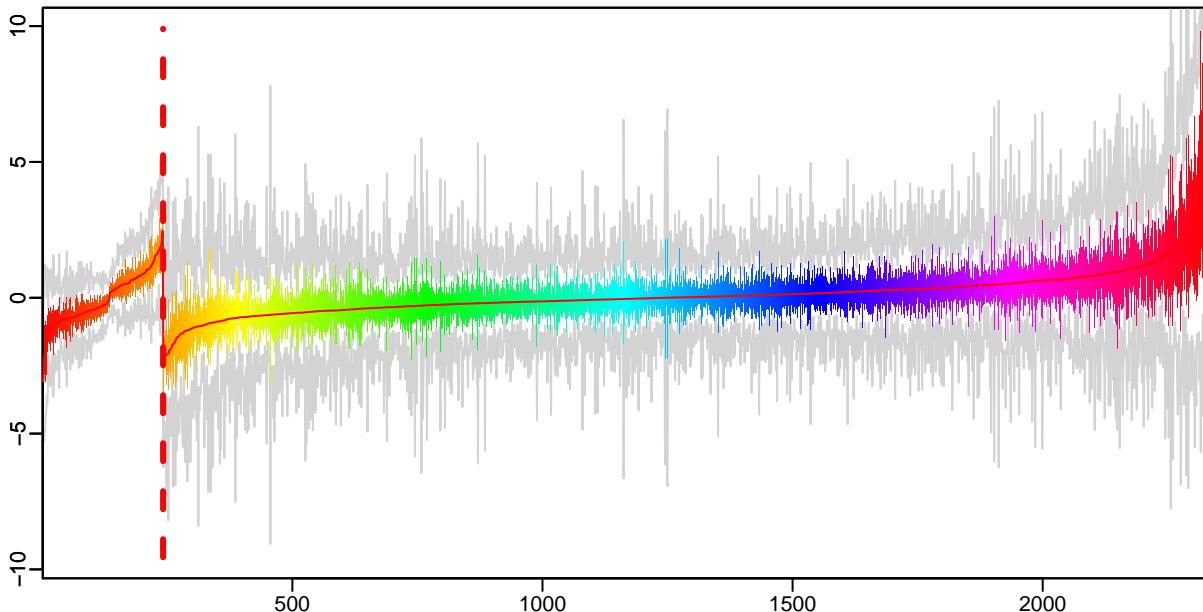
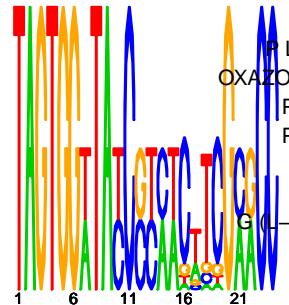
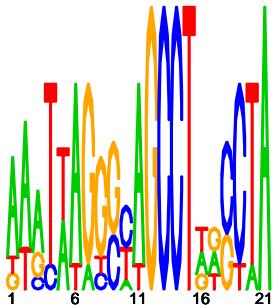


Cluster: 0502 mtu; resid: 0.52; r/c: 20/241

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

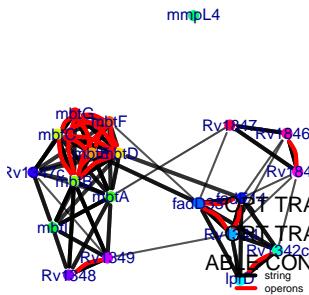


upstream meme PSSM #1; e=2e-16 upstream meme PSSM #2; e=1.2



log10(P) upstream meme log10(P.clust)=-10.91; 20 seqs; 10 uniq

- P LIGASE (SALICYL-AMP LIGASE) + SALICYL-S-AC P SYNTHETASE: RV2384
- OXAZOLINE SYNTHASE MBTB (PHENYLOXAZOLINE SYNTHETASE): RV2383C
- POLYKETIDE SYNTHETASE MBTC (POLYKETIDE SYNTHASE): RV2382C
- POLYKETIDE SYNTHETASE MBTD (POLYKETIDE SYNTHASE): RV2381C
- 17. PEPTIDE SYNTHETASE MBTE (PEPTIDE SYNTHASE): RV2380C
- 17. PEPTIDE SYNTHETASE MBTF (PEPTIDE SYNTHASE): RV2379C
- G (L-LYSINE)6-MONOOXYGENASE (LYSINE N6-HYDROXYLASE): RV2378C
- 13.48 PROBABLE CONSERVED LIPOPROTEIN LPRD: RV1343C
- 13.48 hypothetical protein: RV1342C
- 8.28 POSSIBLE ACYL-CoA DEHYDROGENASE FAD4: RV1346
- 8.28 acyl-CoA synthetase: RV1345
- 8.28 acyl carrier protein: RV1344
- 7.86 hypothetical protein: RV1847
- 7.86 POSSIBLE TRANSCRIPTIONAL REGULATORY PROTEIN: RV1846C
- 7.72 hypothetical protein: RV1845C
- 5.12 hypothetical protein: RV1347C
- 4.99 salicylate synthase MbtH: RV2386C
- TRANSMEMBRANE ATP-BINDING PROTEIN ABC TRANSPORTER: RV1349
- TRANSMEMBRANE ATP-BINDING PROTEIN ABC TRANSPORTER: RV1348
- ABC CONSERVED TRANSMEMBRANE TRANSPORT PROTEIN MMPL4: RV0450C



-200 -100 -1