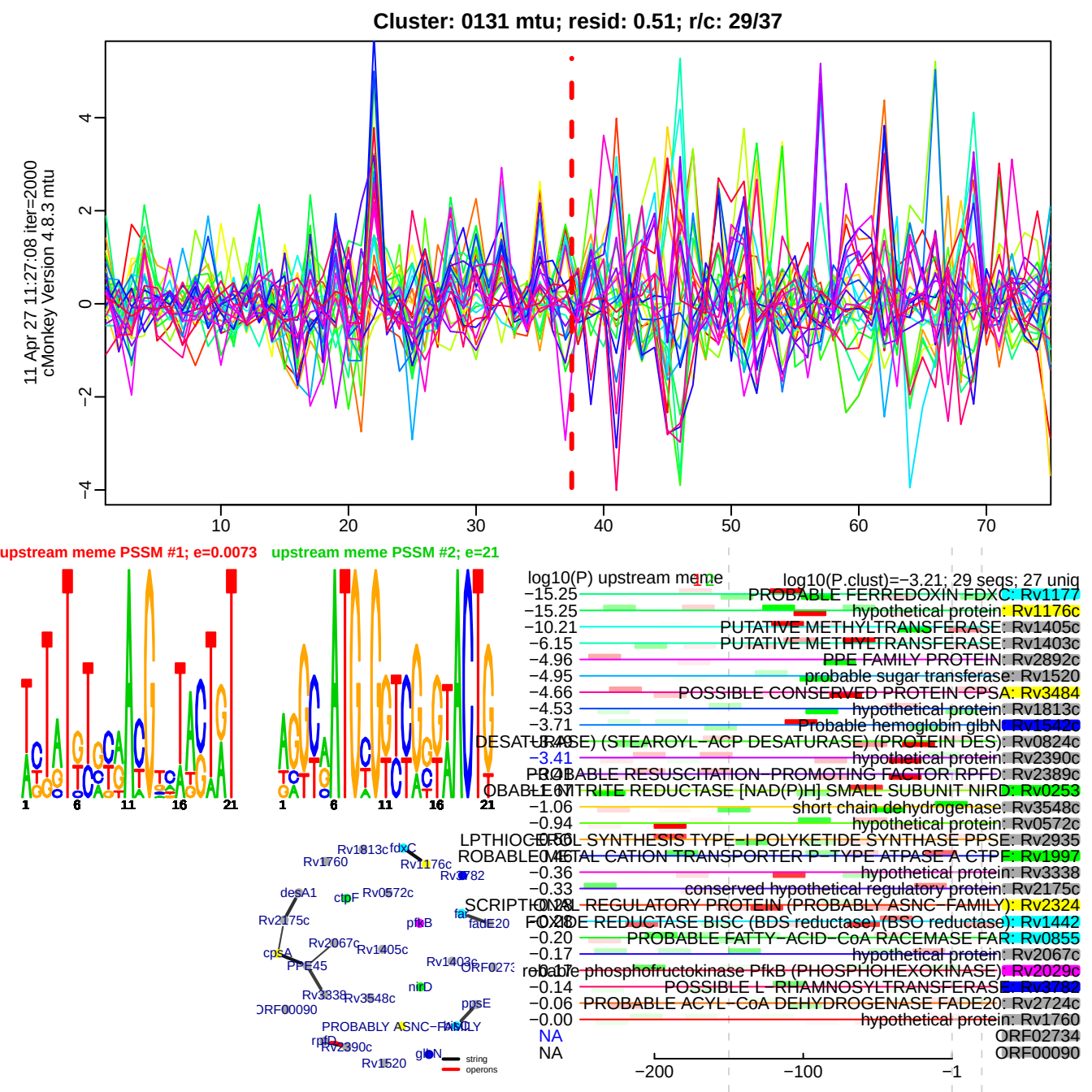
Cluster: 0131 mtu; resid: 0.51; r/c: 29/37
11 Apr 27 11:27:08 iter=2000
cMonkey Version 4.8.3 mtu
upstream meme PSSM #1; e=0.0073
upstream meme PSSM #2; e=21
log10(P) upstream meme
log10(P.clust)=−3.21; 29 seqs; 27 uniq
−15.25 PROBABLE FERREDOXIN FDXC: Rv1177
−15.25 hypothetical protein: Rv1176c
−10.21 PUTATIVE METHYLTRANSFERASE: Rv1405c
−6.15 PUTATIVE METHYLTRANSFERASE: Rv1403c
−4.96 PPE FAMILY PROTEIN: Rv2892c
−4.95 probable sugar transferase: Rv1520
−4.66 POSSIBLE CONSERVED PROTEIN CPSA: Rv3484
−4.53 hypothetical protein: Rv1813c
−3.71 Probable hemoglobin glbN: Rv1542c
−3.49 DESATURASE) (STEAROYL−ACP DESATURASE) (PROTEIN DES): Rv0824c
−3.41 hypothetical protein: Rv2390c
−3.21 PROBABLE RESUSCITATION−PROMOTING FACTOR RPFD: Rv2389c
−1.67 OBABLE NITRITE REDUCTASE [NAD(P)H] SMALL SUBUNIT NIRD: Rv0253
−1.06 short chain dehydrogenase: Rv3548c
−0.94 hypothetical protein: Rv0572c
−0.87 LPTHIOCIDYL SYNTHESIS TYPE−I POLYKETIDE SYNTHASE PPSE: Rv2935
−0.46 ROBABLE METAL CATION TRANSPORTER P−TYPE ATPASE A CTPF: Rv1997
−0.36 hypothetical protein: Rv3338
−0.33 conserved hypothetical regulatory protein: Rv2175c
−0.28 SCRIPTIONAL REGULATORY PROTEIN (PROBABLY ASNC−FAMILY): Rv2324
−0.28 FOXIDE REDUCTASE BISC (BDS reductase) (BSO reductase): Rv1442
−0.20 PROBABLE FATTY−ACID−CoA RACEMASE FAR: Rv0855
−0.17 hypothetical protein: Rv2067c
−0.17 robable phosphofructokinase PfkB (PHOSPHOHEXOKINASE): Rv2029c
−0.14 POSSIBLE L−RHAMNOSYLTRANSFERASE: Rv3782
−0.06 PROBABLE ACYL−CoA DEHYDROGENASE FADE20: Rv2724c
−0.00 hypothetical protein: Rv1760
NA ORF02734
NA ORF00090
−200
−100
−1
string
operons