deepBlockAlign v1.0

Block group alignment: *cluster-651-chr12-Trp-CCA with cluster-731-chr16-Arg-CCG* (Score: 0.845969)

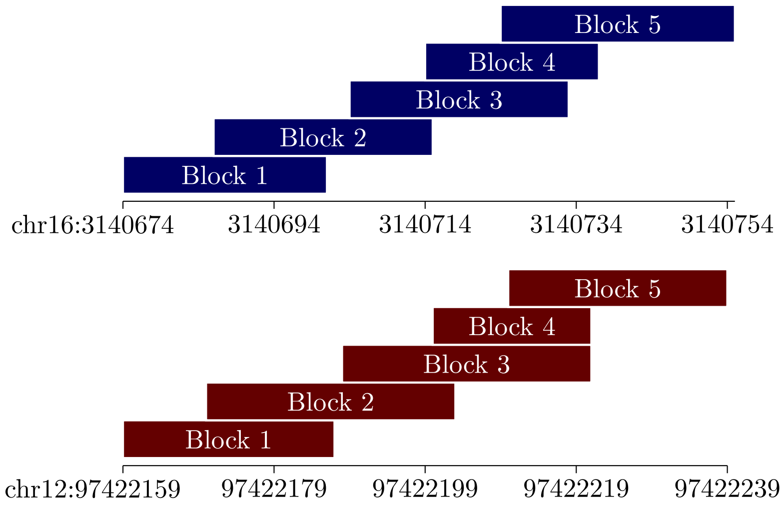
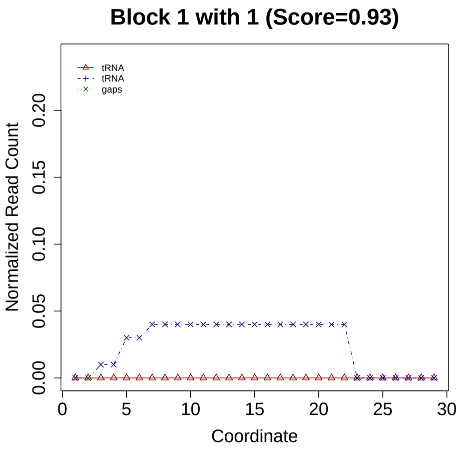


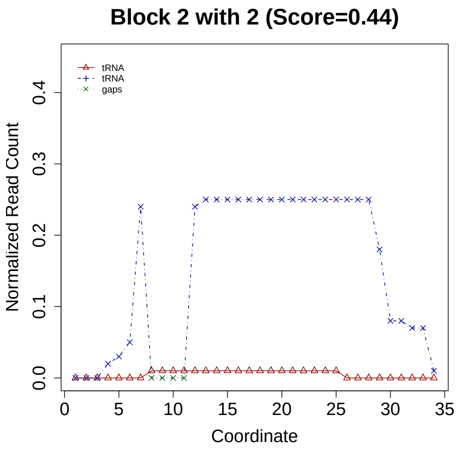
Table 1: Aligned Blocks

tRNA	tRNA
Block 1	Block 1
Block 2	Block 2
Block 3	Block 3
Block 4	Block 4
Block 5	Block 5

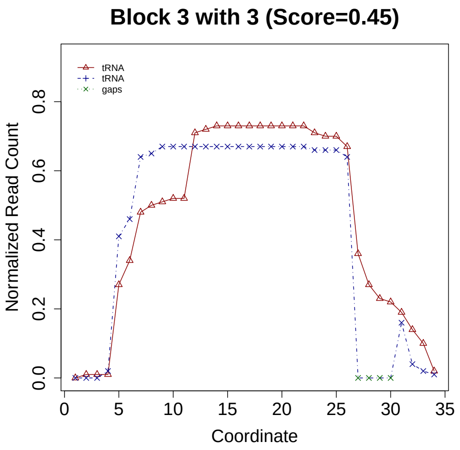
Block alignment:



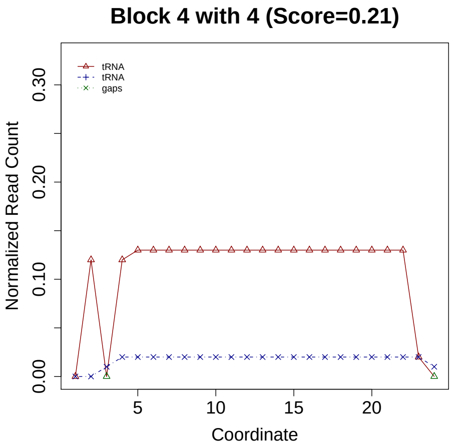
Block 1 with 1 (Score=0.93)



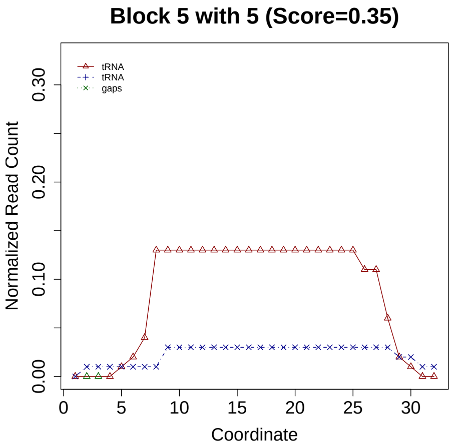
Block 2 with 2 (Score=0.44)



Block 3 with 3 (Score=0.45)



Block 4 with 4 (Score=0.21)



Block 5 with 5 (Score=0.35)