

deepBlockAlign v1.0

Alignment parameters:

[Input]

date and time Sun, 03 Feb 2013 02:25:39 +0100
first block group EscH1hesRep2-cluster.1646
first file /home/projects/users/sachin/frontier/putative_mirna//tmp500query.tmp
second block group bg_33
second file /home/projects/users/sachin/frontier/bgs/mirbase.all.map.bgs.flagged.sig

[Block group alignment]

distance weight 1
block weight 1
gap penalty -1

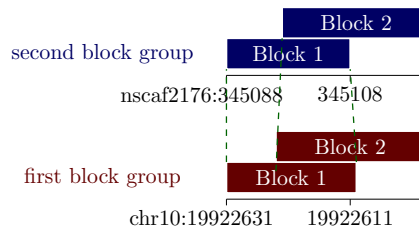
[Block alignment]

gap initialization penalty -2
gap extension penalty -1
threshold for expression difference 1
match score 1
mismatch score -1
profile shape difference penalty 1

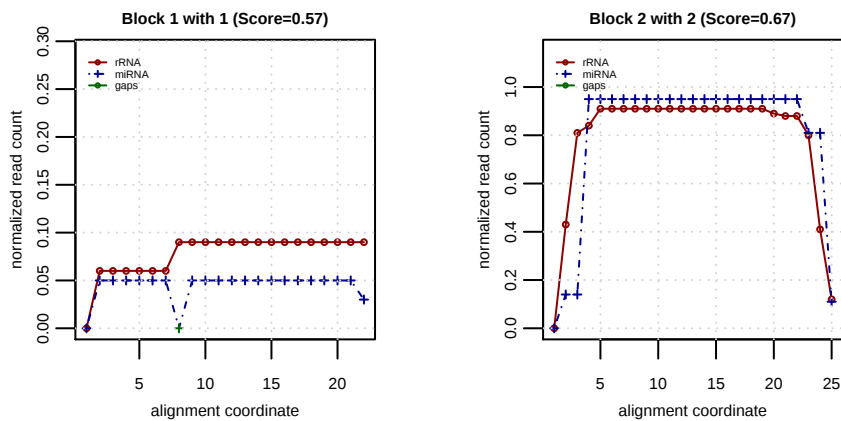
[Block group information]

Entropy (first block group) 1.88
Reads (first block group) 16.04
% Unique reads (first block group) 81
Entropy (second block group) 0.86
Reads (second block group) 37.00
% Unique reads (second block group) 100

Block group alignment: EscH1hesRep2-cluster-1646-5S-rRNA-related(-) with bg-33-bmo-mir-2851-2-MI0012990(+) [Score: 0.74]



Block alignment:



Citation: Langenberger, D*, Pundhir, S*, Ekstrøm, C.T., Stadler, P.F., Hoffmann, S., and Gorodkin, J.(2012). deepBlockAlign: A tool for aligning RNA-seq profiles of read block patterns. *Bioinformatics*, **28**(1),17-24. (*equal contribution)