

deepBlockAlign v1.0

Alignment parameters:

[Input]
date and time Sun, 03 Feb 2013 02:02:00 +0100
first block group BloodGm12878Rep1_cluster.3647
first file /home/projects/users/sachin/frontier/putative_mirna//tmp3500query.tmp
second block group bg_750
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

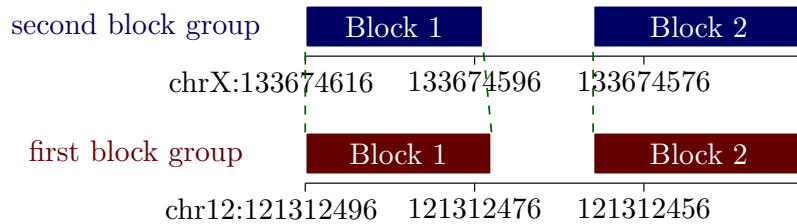
[Block alignment]

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

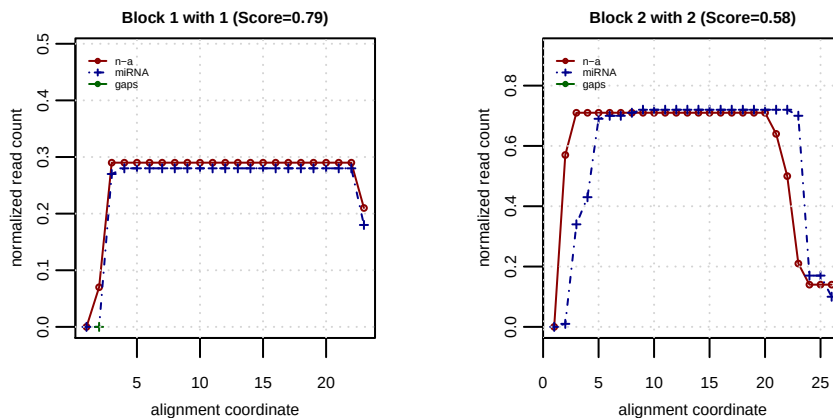
[Block group information]

Entropy (first block group) 1.61
Reads (first block group) 14.00
% Unique reads (first block group) 100
Entropy (second block group) 2.16
Reads (second block group) 321.00
% Unique reads (second block group) 100

Block group alignment: BloodGm12878Rep1-cluster-3647-n-a(-) with bg-750-hsa-mir-450a-2-MI0003187(-) [Score: 0.79]



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)