

deepBlockAlign v1.0

Alignment parameters:

[Input]
date and time Sun, 03 Feb 2013 02:07:40 +0100
first block group CervixHelas3Rep1_cluster_11363
first file /home/projects/users/sachin/frontier/putative_mirna//tmp4000query.tmp
second block group bg_67
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

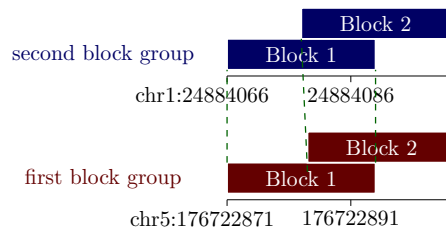
[Block alignment]

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

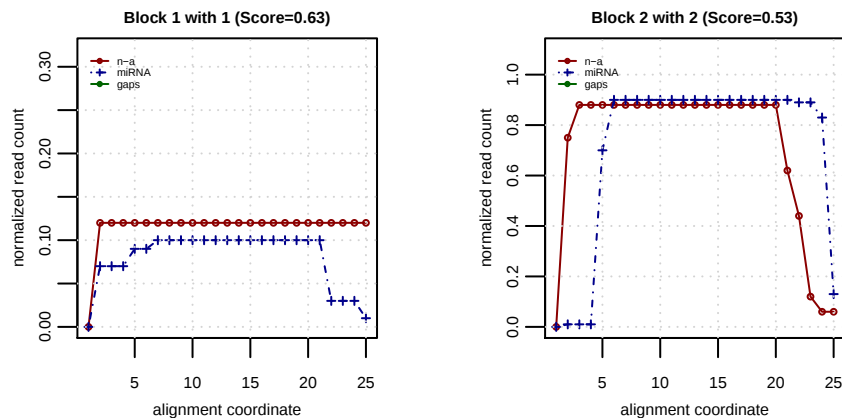
[Block group information]

Entropy (first block group) 1.06
Reads (first block group) 16.00
% Unique reads (first block group) 100
Entropy (second block group) 1.37
Reads (second block group) 89.00
% Unique reads (second block group) 100

Block group alignment: CervixHelas3Rep1-cluster-11363-n-a(+) with bg-67-ath-MIR163-MI0000196(+) [Score: 0.71]



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)