

deepBlockAlign v1.0

Alignment parameters:

[Input]
date and time Sun, 03 Feb 2013 02:11:53 +0100
first block group CervixHelas3Rep1_cluster_15886
first file /home/projects/users/sachin/frontier/putative_mirna//tmp4000query.tmp
second block group bg_127
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

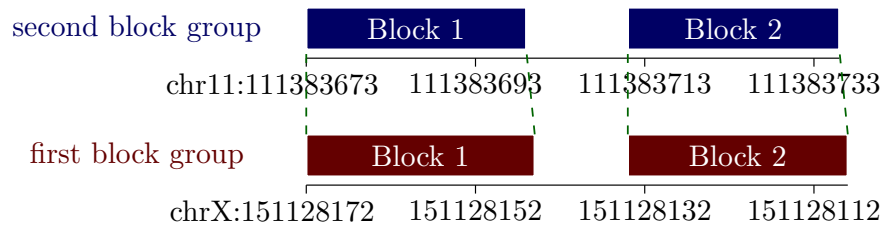
[Block alignment]

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

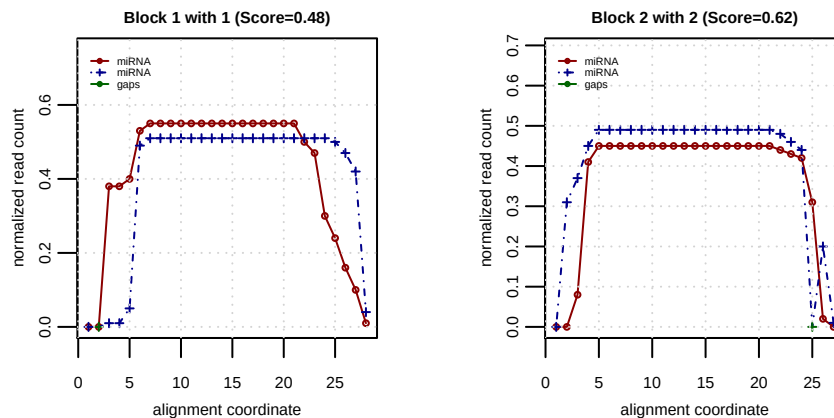
[Block group information]

Entropy (first block group) 2.20
Reads (first block group) 11183.06
% Unique reads (first block group) 97
Entropy (second block group) 2.09
Reads (second block group) 249.00
% Unique reads (second block group) 100

Block group alignment: CervixHelas3Rep1-cluster-15886-hsa-mir-452(-) with bg-127-hsa-mir-34b-MI0000742(+) [Score: 0.70]



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)