

deepBlockAlign v1.0

Alignment parameters:

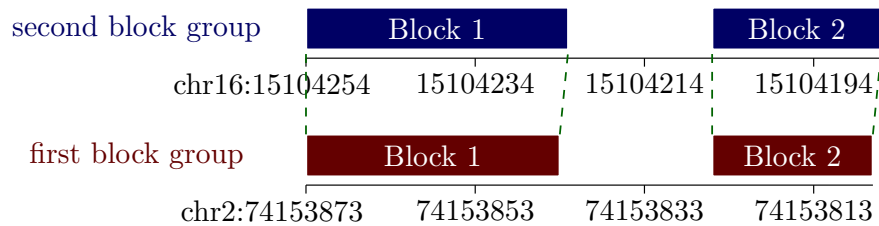
[Input]
date and time Sun, 03 Feb 2013 01:40:51 +0100
first block group CervixHelas3Rep2_cluster_7766
first file /home/projects/users/sachin/frontier/putative_mirna//tmp2500query.tmp
second block group bg_265
second file /home/projects/users/sachin/frontier/bgs/mirbase.all.map.bgs.flagged.sig

[Block group alignment]
distance weight 1
block weight 1
gap penalty -1

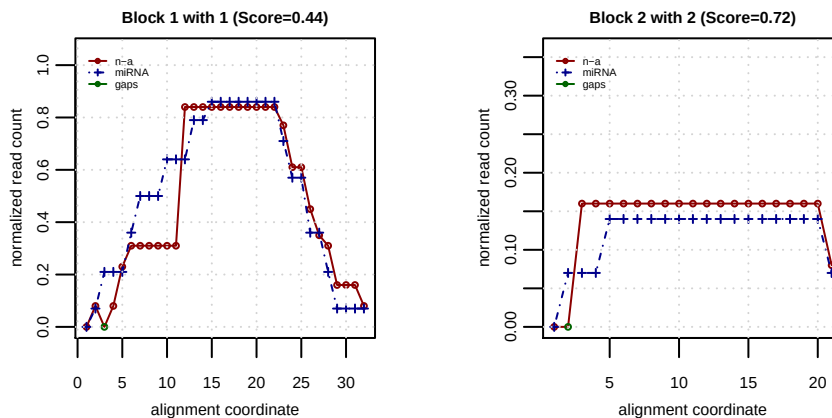
[Block alignment]
gap initialization penalty -2
gap extension penalty -1
threshold for expression difference 1
match score 1
mismatch score -1
profile shape difference penalty 1

[Block group information]
Entropy (first block group) 1.89
Reads (first block group) 12.83
% Unique reads (first block group) 94
Entropy (second block group) 3.09
Reads (second block group) 14.00
% Unique reads (second block group) 100

Block group alignment: CervixHelas3Rep2-cluster-7766-n-a(-) with bg-265-hsa-mir-1972-1-MI0009982(-) [Score: 0.72]



Block alignment:



Citation: Langenberger, D*, Pundhir, S*, Ekström, 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)