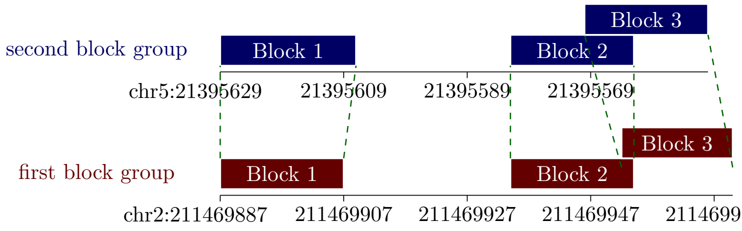
deepBlockAlign v1.0

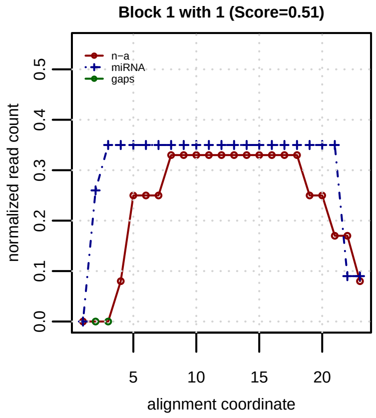
Alignment parameters:

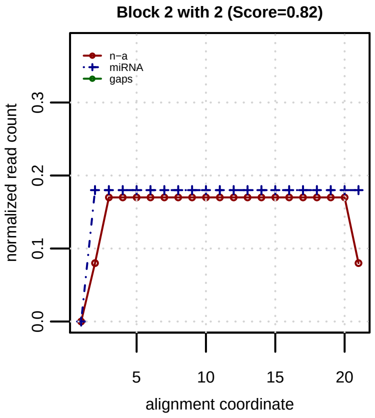
[Input]	
date and time	Sun, 03 Feb 2013 02:18:06 +0100
first block group	CervixHelas3Rep2_cluster_7499
first file	/home/projects/users/sachin/frontier/putative_mirna//tmp4500query.tmp
second block group	bg_257
second file	/home/projects/users/sachin/frontier/bgs/mirbase.all.map.bgs.flagged.sig
[Block 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)	2.86
Reads (first block group)	12.00
% Unique reads (first block group)	100
Entropy (second block group)	1.77
Reads (second block group)	34.00
% Unique reads (second block group)	100

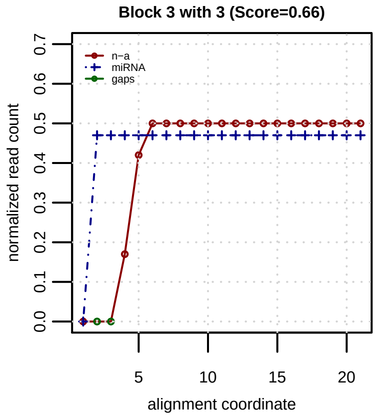
Block group alignment: *CervixHelas3Rep2-cluster-7499-n-a(+) with bg-257-ath-MIR870-MI0005448(-)* [Score: 0.75]



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)