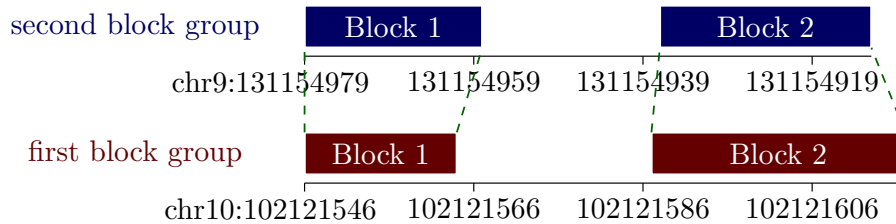


deepBlockAlign v1.0

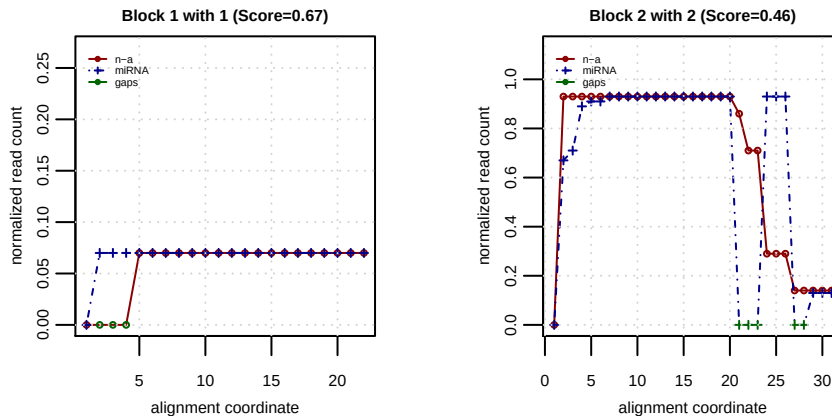
Alignment parameters:

[Input]	
date and time	Sun, 03 Feb 2013 01:55:22 +0100
first block group	CervixHelas3Rep1_cluster.1615
first file	/home/projects/users/sachin/frontier/putative_mirna//tmp3000query.tmp
second block group	bg_702
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)	0.37
Reads (first block group)	14.00
% Unique reads (first block group)	100
Entropy (second block group)	1.49
Reads (second block group)	55.00
% Unique reads (second block group)	100

Block group alignment: *CervixHelas3Rep1-cluster-1615-n-a(+)* with *bg-702-hsa-mir-219-2-MI0000740(-)* [Score: 0.70]



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)