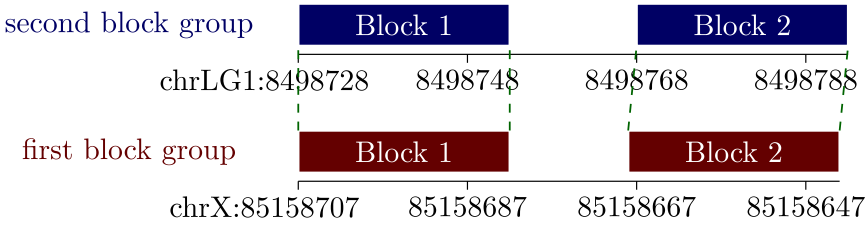
deepBlockAlign v1.0

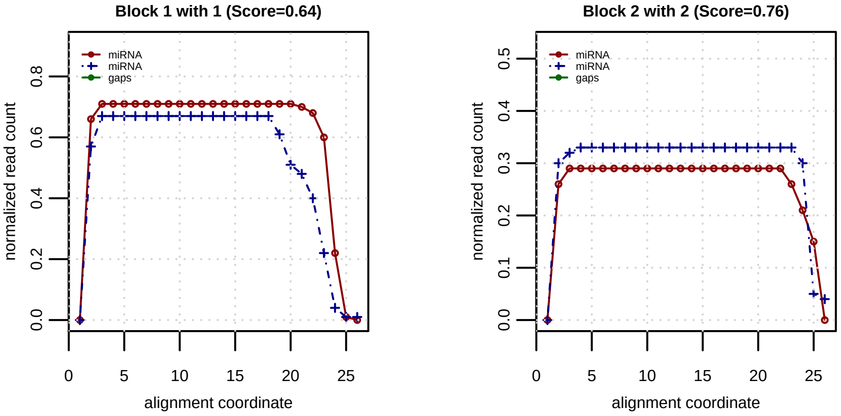
Alignment parameters:

[Input]	
date and time	Sun, 03 Feb 2013 01:38:54 +0100
first block group	BloodGm12878Rep1_cluster_16297
first file	/home/projects/users/sachin/frontier/putative_mirna//tmp2500query.tmp
second block group	bg_30
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)	1.25
Reads (first block group)	864.67
% Unique reads (first block group)	97
Entropy (second block group)	1.51
Reads (second block group)	2296.00
% Unique reads (second block group)	100

Block group alignment: *BloodGm12878Rep1-cluster-16297-hsa-mir-361(-) with bg-30-tca-mir-3811c-2-MI0016276(+)* [Score: 0.79]



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)