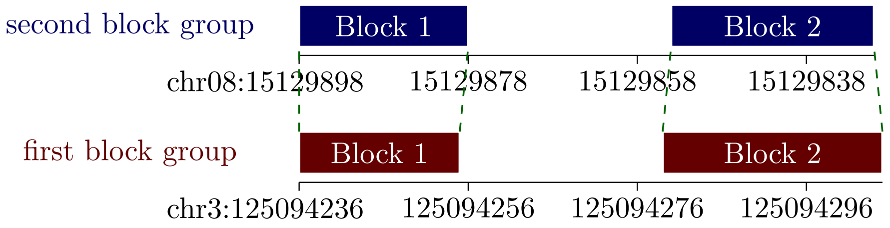
deepBlockAlign v1.0

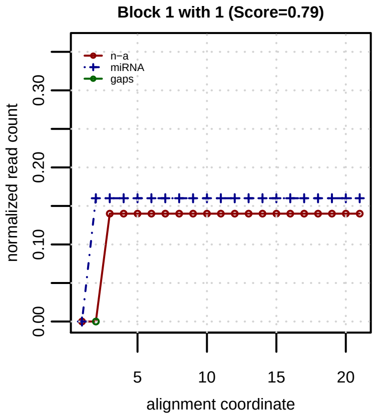
Alignment parameters:

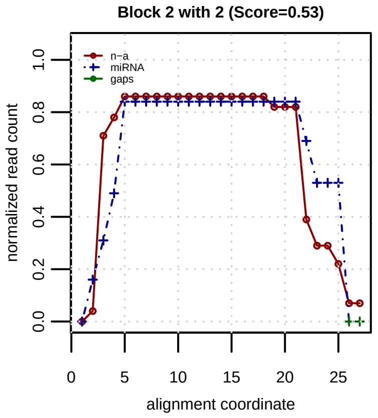
[Input]	
date and time	Sun, 03 Feb 2013 02:03:22 +0100
first block group	BloodGm12878Rep2_cluster_11786
first file	/home/projects/users/sachin/frontier/putative_mirna//tmp3500query.tmp
second block group	bg_351
second file	/home/projects/users/sachin/frontier/bgs/mirbase.all.map.bgs.flagged.sig
[Block 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)	1.51
Reads (first block group)	13.83
% Unique reads (first block group)	94
Entropy (second block group)	2.22
Reads (second block group)	134.00
% Unique reads (second block group)	100

Block group alignment: *BloodGm12878Rep2-cluster-11786-n-a(+) with bg-351-osa-MIR1861k-MI0008257(-)* [Score: 0.77]



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)