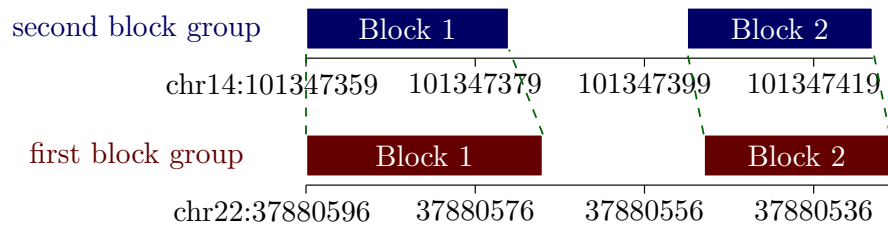


deepBlockAlign v1.0

Alignment parameters:

[Input]	
date and time	Sun, 03 Feb 2013 01:05:27 +0100
first block group	BloodGm12878Rep2_cluster.11333
first file	/home/projects/users/sachin/frontier/putative_mirna//tmp1500query.tmp
second block group	bg_190
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)	2.41
Reads (first block group)	13.00
% Unique reads (first block group)	100
Entropy (second block group)	1.81
Reads (second block group)	24.00
% Unique reads (second block group)	100

Block group alignment: BloodGm12878Rep2-cluster-11333-n-a(-) with bg-190-hsa-mir-431-MI0001721(+) [Score: 0.71]



Block alignment:

