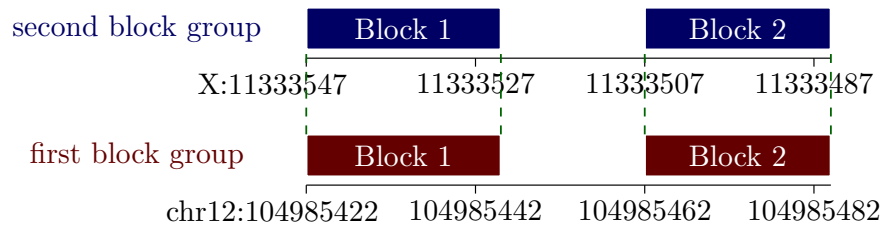


deepBlockAlign v1.0

Alignment parameters:

[Input]	
date and time	Sun, 03 Feb 2013 01:51:48 +0100
first block group	BloodGm12878Rep1_cluster.3203
first file	/home/projects/users/sachin/frontier/putative_mirna//tmp3000query.tmp
second block group	bg_93
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)	1.55
Reads (first block group)	20.62
% Unique reads (first block group)	97
Entropy (second block group)	1.43
Reads (second block group)	30.00
% Unique reads (second block group)	100

Block group alignment: BloodGm12878Rep1-cluster-3203-hsa-mir-3922(+) with bg-93-cel-mir-254-MI0000330(-) [Score: 0.78]



Block alignment:

