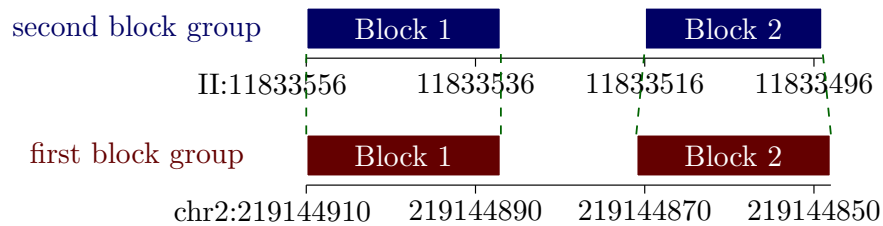


deepBlockAlign v1.0

Alignment parameters:

[Input]	
date and time	Sun, 03 Feb 2013 02:17:06 +0100
first block group	EpitheliumA549Rep1_cluster.6990
first file	/home/projects/users/sachin/frontier/putative_mirna//tmp4500query.tmp
second block group	bg_18
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)	0.99
Reads (first block group)	16.00
% Unique reads (first block group)	100
Entropy (second block group)	1.44
Reads (second block group)	17.00
% Unique reads (second block group)	100

Block group alignment: EpitheliumA549Rep1-cluster-6990-n-a(-) with bg-18-cel-mir-355-MI0000754(-) [Score: 0.85]



Block alignment:

