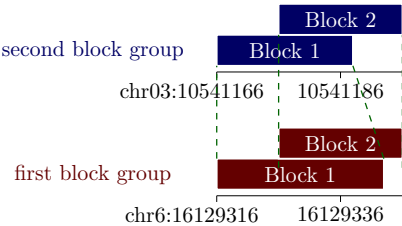


deepBlockAlign v1.0

Alignment parameters:

[Input]	
date and time	Sun, 03 Feb 2013 02:24:10 +0100
first block group	BloodGm12878Rep2_cluster.14813
first file	/home/projects/users/sachin/frontier/putative_mirna//tmp500query.tmp
second block group	bg_159
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)	1.66
Reads (first block group)	12.67
% Unique reads (first block group)	87
Entropy (second block group)	1.71
Reads (second block group)	164.00
% Unique reads (second block group)	100

Block group alignment: BloodGm12878Rep2-cluster-14813-n-a(+) with bg-159-osa-MIR164e-MI0001105(+) [Score: 0.71]



Block alignment:

