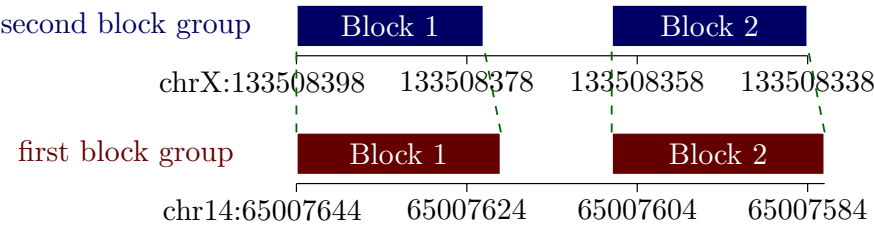


deepBlockAlign v1.3

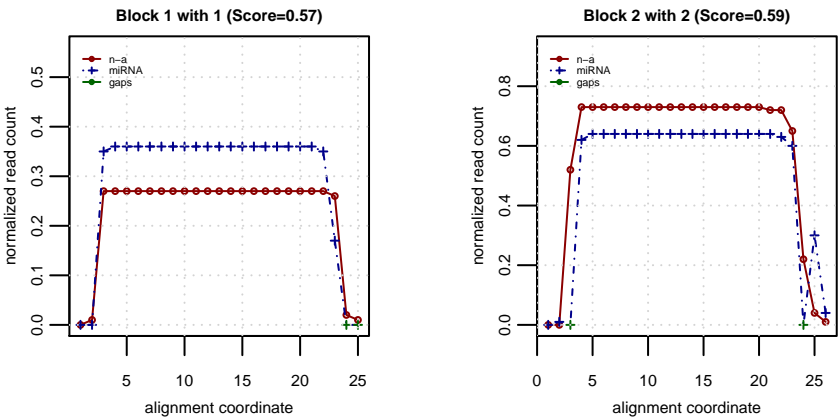
Alignment parameters:

[Input]	
date and time	Thu, 04 Dec 2014 16:27:41 +0100
first block group	cluster_176
first file	testsuite/human_eb.blockGroups
second block group	cluster_531
second file	testsuite/human_eb.blockGroups
[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)	1.57
Reads (first block group)	183.78
% Unique reads (first block group)	0
Entropy (second block group)	1.24
Reads (second block group)	121.67
% Unique reads (second block group)	0

Block group alignment: cluster-176-n-a(-) with cluster-531-hsa-mir-424(-) [Score: 0.72]



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)