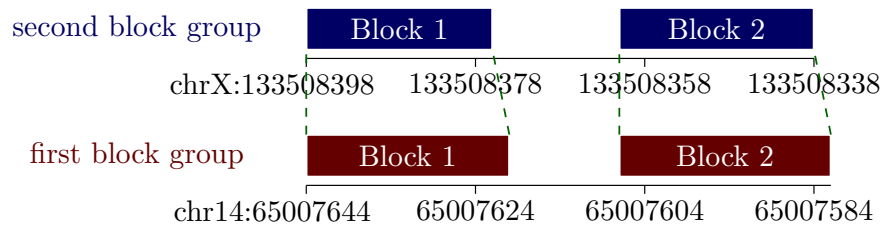


deepBlockAlign v1.0

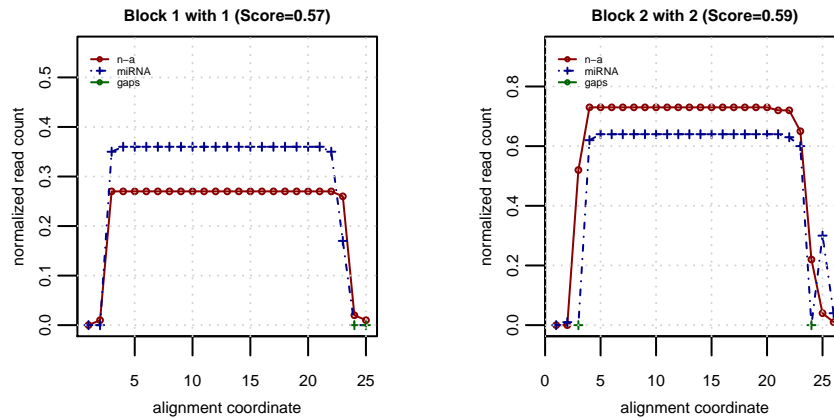
Alignment parameters:

[Input]	
date and time	Fri, 14 Dec 2012 16:18:57 +0100
first block group	cluster_176
first file	example/human_eb.blockGroups
second block group	cluster_531
second file	example/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 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)