

deepBlockAlign v1.0

Alignment parameters:

[Input]

date and time	Sun, 03 Feb 2013 00:47:52 +0100
first block group	CervixHelas3Rep2_cluster.8415
first file	/home/projects/users/sachin/frontier/putative_mirna//tmp0query.tmp
second block group	bg_98
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

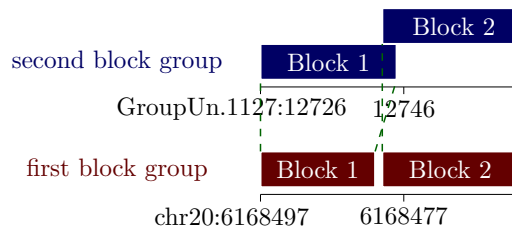
[Block alignment]

gap initialization penalty	-2
gap extension penalty	-1
threshold for expression difference	1
match score	1
mismatch score	-1
profile shape difference penalty	1

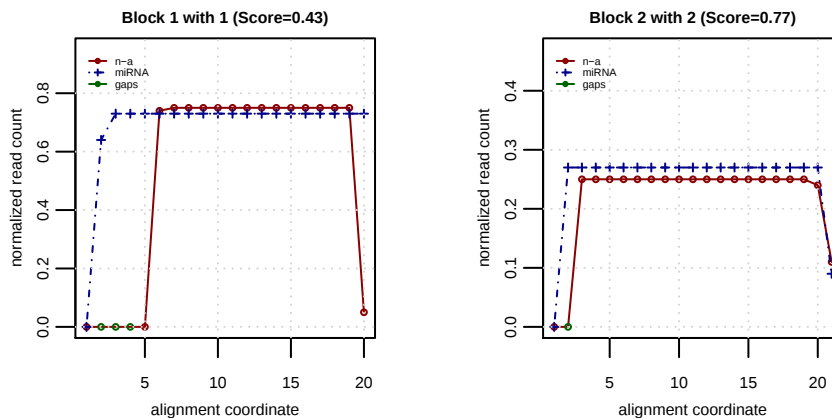
[Block group information]

Entropy (first block group)	0.93
Reads (first block group)	123.76
% Unique reads (first block group)	6
Entropy (second block group)	1.24
Reads (second block group)	11.00
% Unique reads (second block group)	100

Block group alignment: CervixHelas3Rep2-cluster-8415-n-a(-) with bg-98-ame-mir-3763-MI0016166(+) [Score: 0.73]



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)