

deepBlockAlign v1.0

Alignment parameters:

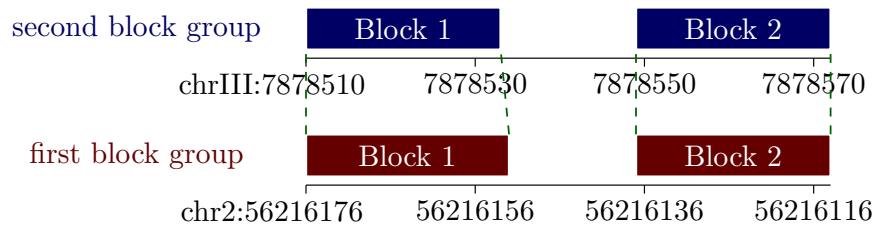
```
[Input]
date and time          Sun, 03 Feb 2013 01:31:56 +0100
first block group      CervixHelas3Rep1_cluster_7759
first file             /home/projects/users/sachin/frontier/putative_mirna//tmp2000query.tmp
second block group     bg_33
second file            /home/projects/users/sachin/frontier/bgs/mirbase.all.map.bgs.flagged.sig

[Block group alignment]
distance weight        1
block weight           1
gap penalty            -1

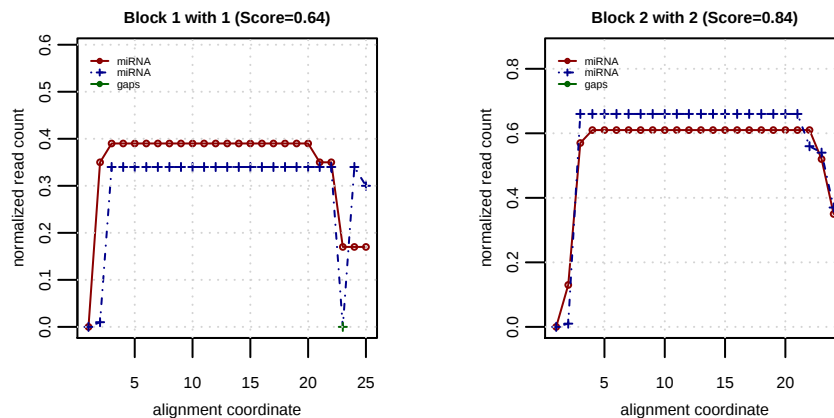
[Block alignment]
gap initialization penalty -2
gap extension penalty    -1
threshold for expression difference 1
match score              1
mismatch score           -1
profile shape difference penalty 1

[Block group information]
Entropy (first block group) 1.83
Reads (first block group) 23.00
% Unique reads (first block group) 100
Entropy (second block group) 1.08
Reads (second block group) 134.00
% Unique reads (second block group) 100
```

Block group alignment: *CervixHelas3Rep1-cluster-7759-hsa-mir-216a(-)* with *bg-33-cbr-mir-46-MI0000500(+)* [Score: 0.83]



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)