

# deepBlockAlign v1.0

## Alignment parameters:

[Input]  
date and time Sun, 03 Feb 2013 01:16:30 +0100  
first block group CervixHelas3Rep1\_cluster.8794  
first file /home/projects/users/sachin/frontier/putative\_mirna//tmp1500query.tmp  
second block group bg\_400  
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

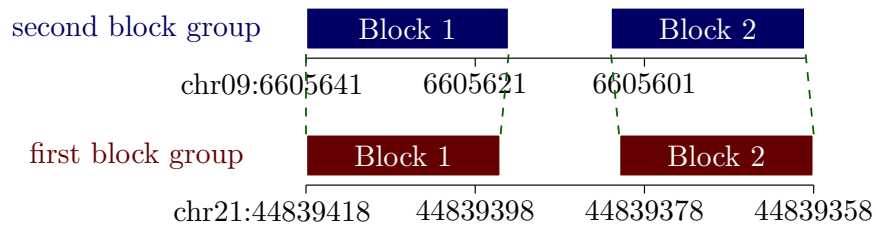
### [Block alignment]

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

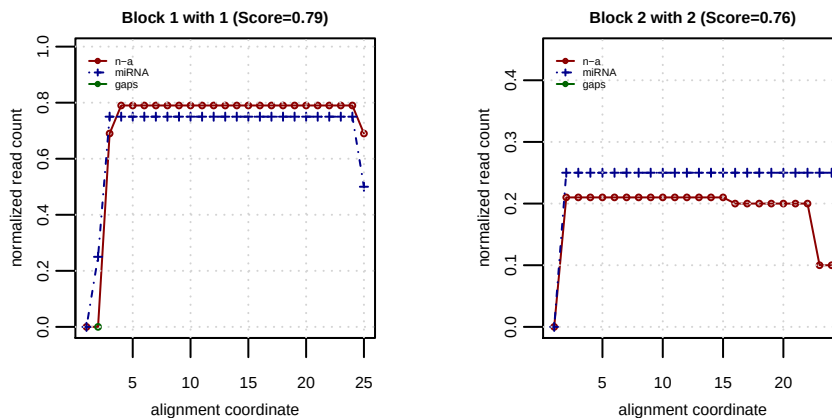
### [Block group information]

Entropy (first block group) 1.17  
Reads (first block group) 10.10  
% Unique reads (first block group) 99  
Entropy (second block group) 1.50  
Reads (second block group) 96.00  
% Unique reads (second block group) 100

**Block group alignment:** CervixHelas3Rep1-cluster-8794-n-a(-) with bg-400-osa-MIR395v-MI0005090(-) [Score: 0.84]



## 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)