

# deepBlockAlign v1.0

## Alignment parameters:

### [Input]

date and time Sun, 03 Feb 2013 01:27:30 +0100  
first block group BrainSknshraRep1\_cluster.4454  
first file /home/projects/users/sachin/frontier/putative\_mirna//tmp2000query.tmp  
second block group bg\_181  
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

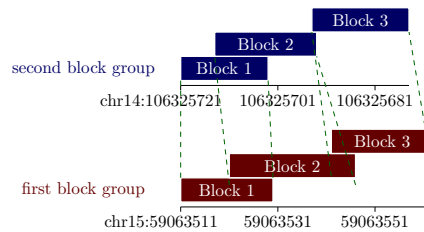
### [Block alignment]

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

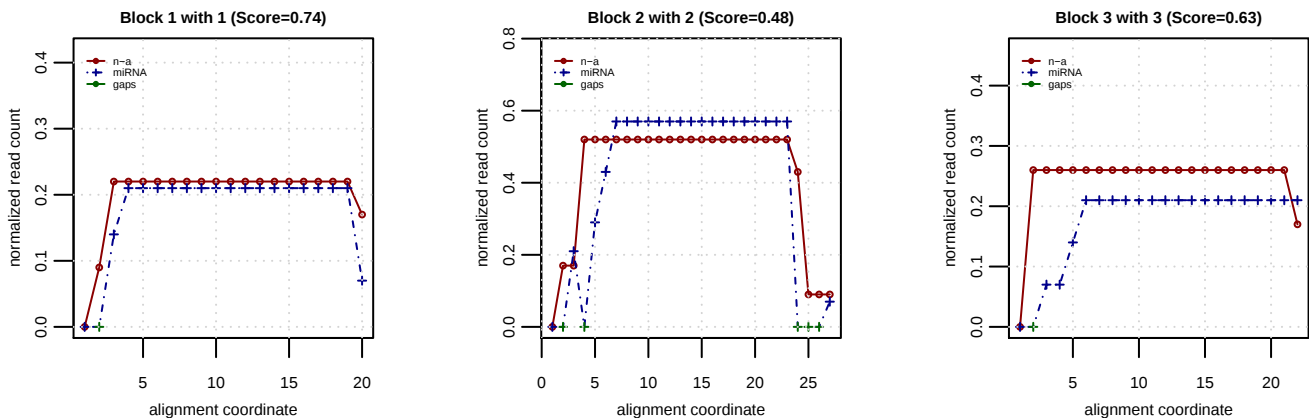
### [Block group information]

Entropy (first block group) 2.16  
Reads (first block group) 11.50  
% Unique reads (first block group) 96  
Entropy (second block group) 3.04  
Reads (second block group) 14.00  
% Unique reads (second block group) 100

**Block group alignment:** *BrainSknshraRep1-cluster-4454-n-a(+)* with *bg-181-hsa-mir-4537-MI0016908(-)* [Score: 0.71]



## 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)