

# deepBlockAlign v1.0

## Alignment parameters:

[Input]  
date and time Sun, 03 Feb 2013 01:58:45 +0100  
first block group BloodGm12878Rep2\_cluster.18223  
first file /home/projects/users/sachin/frontier/putative\_mirna//tmp3500query.tmp  
second block group bg\_368  
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

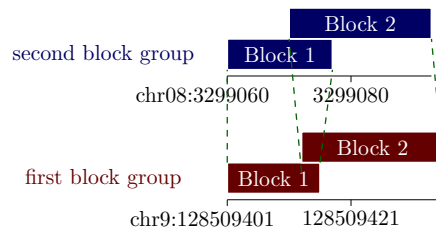
### [Block alignment]

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

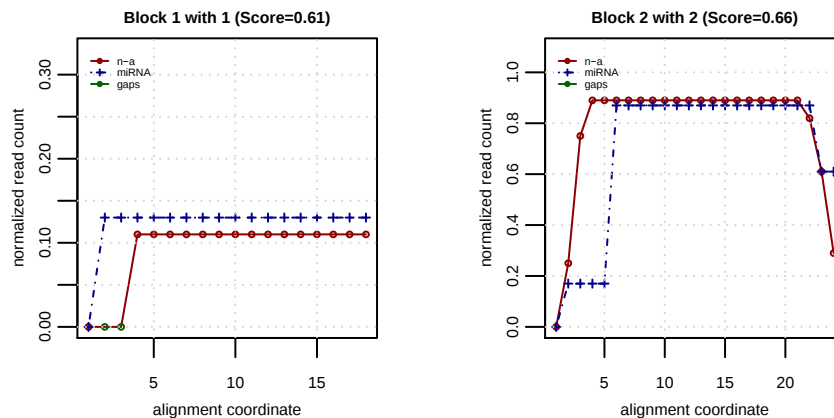
### [Block group information]

Entropy (first block group) 1.75  
Reads (first block group) 14.01  
% Unique reads (first block group) 86  
Entropy (second block group) 1.18  
Reads (second block group) 140.00  
% Unique reads (second block group) 100

**Block group alignment:** BloodGm12878Rep2-cluster-18223-n-a(+) with bg-368-osa-MIR395l-MI0001036(+) [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)