

# deepBlockAlign v1.0

## Alignment parameters:

### [Input]

date and time Sun, 03 Feb 2013 02:03:16 +0100  
first block group EscH1hesRep2-cluster.7244  
first file /home/projects/users/sachin/frontier/putative\_mirna//tmp3500query.tmp  
second block group bg\_518  
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

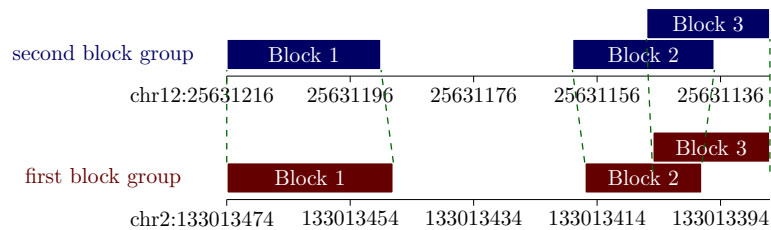
### [Block alignment]

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

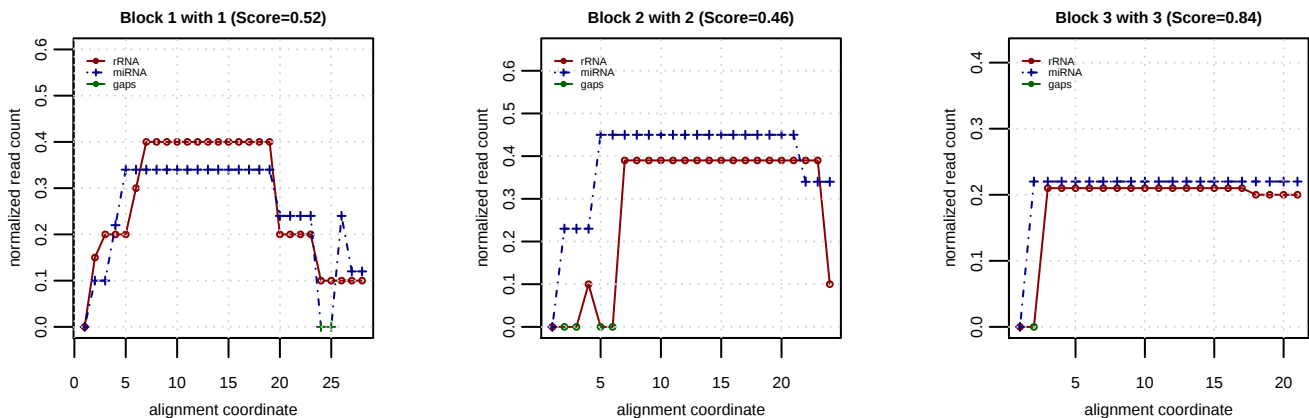
### [Block group information]

Entropy (first block group) 2.61  
Reads (first block group) 10.08  
% Unique reads (first block group) 60  
Entropy (second block group) 2.50  
Reads (second block group) 194.00  
% Unique reads (second block group) 100

**Block group alignment:** EscH1hesRep2-cluster-7244-18S-rRNA-related(-) with bg-518-osa-MIR2864-MI0013026(-) [Score: 0.70]



## 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)