

# deepBlockAlign v1.0

## Alignment parameters:

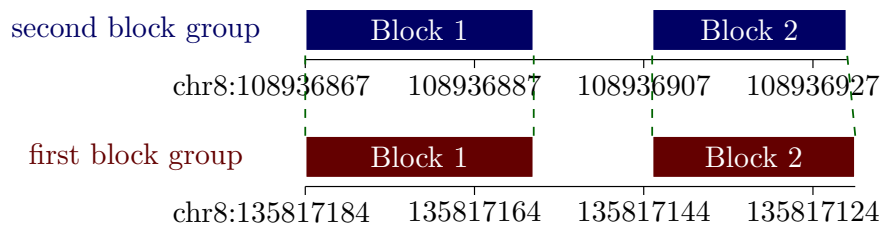
[Input]  
date and time Sun, 03 Feb 2013 02:04:33 +0100  
first block group BrainSknshraRep2\_cluster\_12075  
first file /home/projects/users/sachin/frontier/putative\_mirna//tmp3500query.tmp  
second block group bg\_588  
second file /home/projects/users/sachin/frontier/bgs/mirbase.all.map.bgs.flagged.sig

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

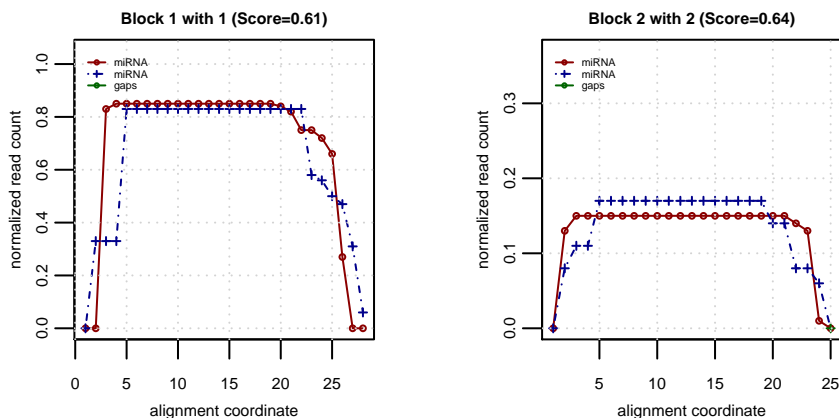
[Block alignment]  
gap initialization penalty -2  
gap extension penalty -1  
threshold for expression difference 1  
match score 1  
mismatch score -1  
profile shape difference penalty 1

[Block group information]  
Entropy (first block group) 0.83  
Reads (first block group) 7848.55  
% Unique reads (first block group) 99  
Entropy (second block group) 1.70  
Reads (second block group) 36.00  
% Unique reads (second block group) 100

**Block group alignment:** BrainSknshraRep2-cluster-12075-hsa-mir-30d(-) with bg-588-mmu-mir-3108-MI0014105(+) [Score: 0.75]



## Block alignment:



**Citation:** Langenberger, D\*, Pundhir, S\*, Ekström, 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)