

deepBlockAlign v1.0

Alignment parameters:

[Input]

date and time Sun, 03 Feb 2013 02:16:38 +0100
 first block group EpitheliumA549Rep2.cluster_5185
 first file /home/projects/users/sachin/frontier/putative_mirna//tmp4500query.tmp
 second block group bg_175
 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

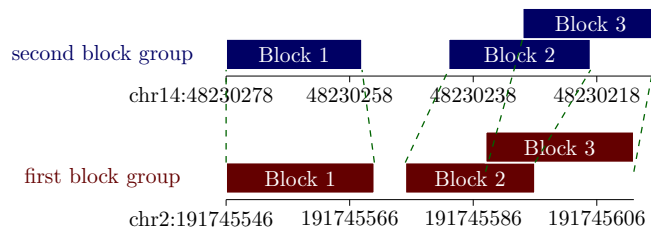
[Block alignment]

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

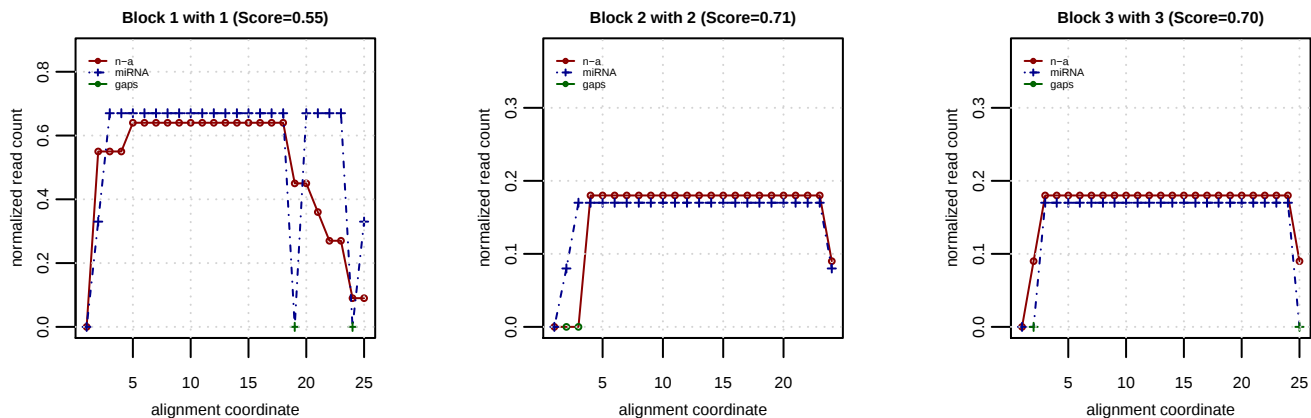
[Block group information]

Entropy (first block group) 1.87
 Reads (first block group) 11.00
 % Unique reads (first block group) 100
 Entropy (second block group) 2.08
 Reads (second block group) 12.00
 % Unique reads (second block group) 100

Block group alignment: EpitheliumA549Rep2-cluster-5185-n-a(+) with bg-175-hsa-mir-548y-MI0016595(-) [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)