

deepBlockAlign v1.0

Alignment parameters:

[Input]

date and time Sun, 03 Feb 2013 02:27:06 +0100
 first block group BloodGm12878Rep1_cluster.8745
 first file /home/projects/users/sachin/frontier/putative_mirna//tmp500query.tmp
 second block group bg_17
 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

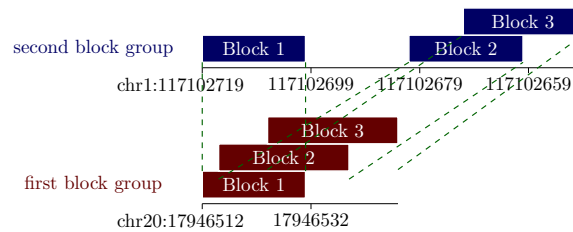
[Block alignment]

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

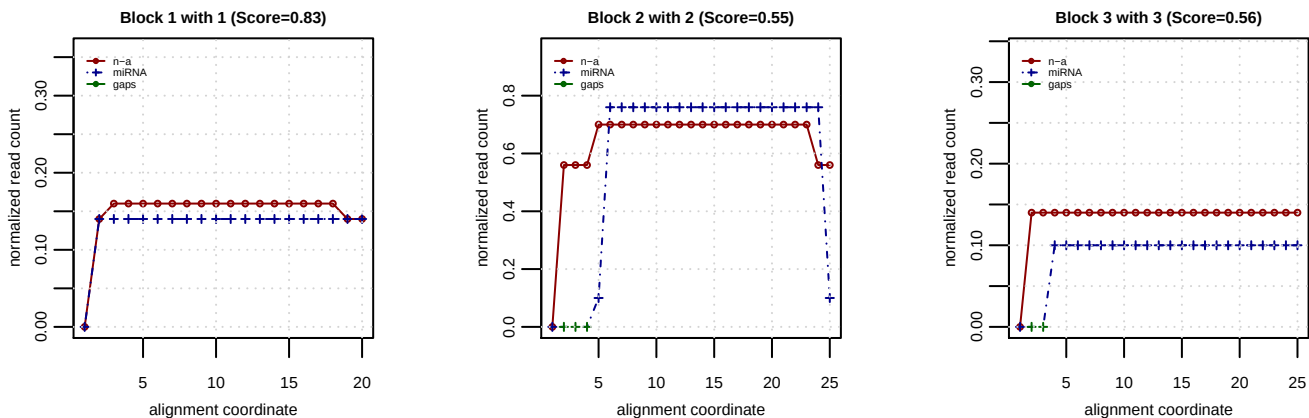
[Block group information]

Entropy (first block group) 1.79
 Reads (first block group) 7.17
 % Unique reads (first block group) 98
 Entropy (second block group) 1.44
 Reads (second block group) 21.00
 % Unique reads (second block group) 100

Block group alignment: BloodGm12878Rep1-cluster-8745-n-a(+) with bg-17-hsa-mir-548ac-MI0016762(-) [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)