

deepBlockAlign v1.0

Alignment parameters:

[Input]

date and time Sun, 03 Feb 2013 01:52:16 +0100
first block group LungAg04450Rep2_cluster.2755
first file /home/projects/users/sachin/frontier/putative_mirna//tmp3000query.tmp
second block group bg_392
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

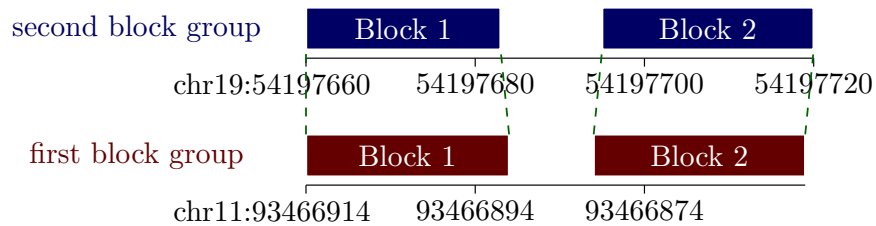
[Block alignment]

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

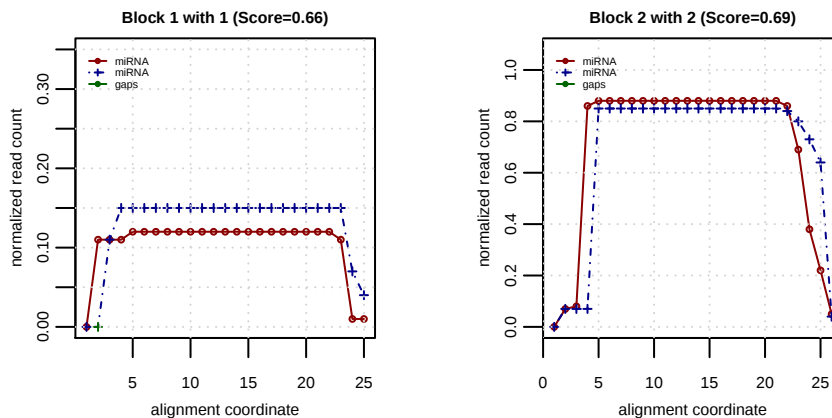
[Block group information]

Entropy (first block group) 1.19
Reads (first block group) 107.01
% Unique reads (first block group) 78
Entropy (second block group) 1.08
Reads (second block group) 55.00
% Unique reads (second block group) 100

Block group alignment: LungAg04450Rep2-cluster-2755-hsa-mir-1304(-) with bg-392-hsa-mir-526b-MI0003150(+) [Score: 0.77]



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)