

# deepBlockAlign v1.0

## Alignment parameters:

### [Input]

|                    |                                                                          |
|--------------------|--------------------------------------------------------------------------|
| date and time      | Sun, 03 Feb 2013 01:21:46 +0100                                          |
| first block group  | EscH1hescRep2-cluster_6053                                               |
| first file         | /home/projects/users/sachin/frontier/putative_mirna//tmp2000query.tmp    |
| second block group | bg_631                                                                   |
| 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 |

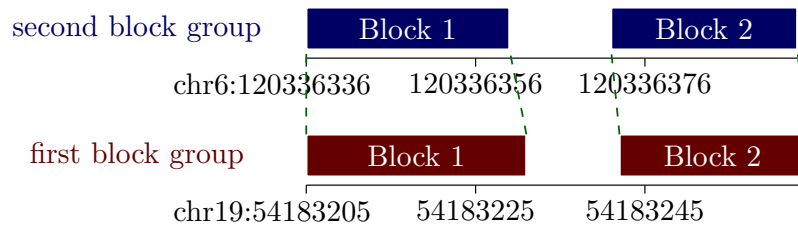
### [Block alignment]

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

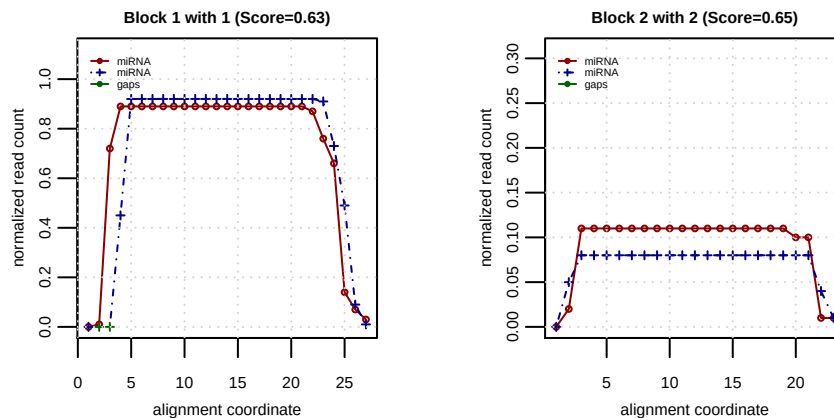
### [Block group information]

|                                     |        |
|-------------------------------------|--------|
| Entropy (first block group)         | 1.25   |
| Reads (first block group)           | 154.00 |
| % Unique reads (first block group)  | 97     |
| Entropy (second block group)        | 1.40   |
| Reads (second block group)          | 150.00 |
| % Unique reads (second block group) | 100    |

**Block group alignment:** *EscH1hescRep2-cluster-6053-hsa-mir-519e(+)* with *bg-631-hsa-mir-3144-MI0014169(+)* [Score: 0.75]



## 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)