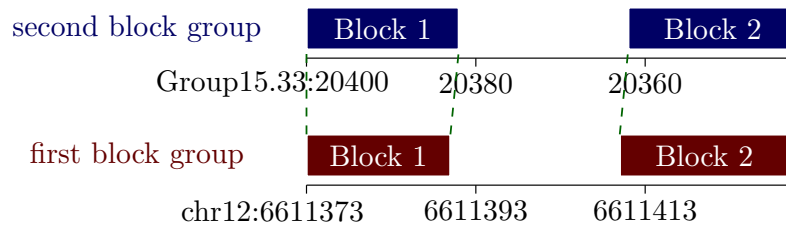


# deepBlockAlign v1.0

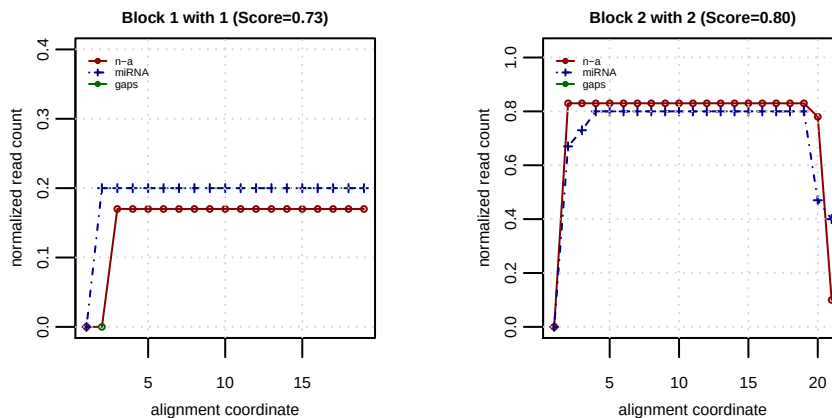
## Alignment parameters:

|                                     |                                                                          |
|-------------------------------------|--------------------------------------------------------------------------|
| <b>[Input]</b>                      |                                                                          |
| date and time                       | Sun, 03 Feb 2013 00:47:40 +0100                                          |
| first block group                   | CervixHelas3Rep2_cluster.2910                                            |
| first file                          | /home/projects/users/sachin/frontier/putative_mirna//tmp0query.tmp       |
| second block group                  | bg_33                                                                    |
| second file                         | /home/projects/users/sachin/frontier/bgs/mirbase.all.map.bgs.flagged.sig |
| <b>[Block group alignment]</b>      |                                                                          |
| distance weight                     | 1                                                                        |
| block weight                        | 1                                                                        |
| gap penalty                         | -1                                                                       |
| <b>[Block alignment]</b>            |                                                                          |
| gap initialization penalty          | -2                                                                       |
| gap extension penalty               | -1                                                                       |
| threshold for expression difference | 1                                                                        |
| match score                         | 1                                                                        |
| mismatch score                      | -1                                                                       |
| profile shape difference penalty    | 1                                                                        |
| <b>[Block group information]</b>    |                                                                          |
| Entropy (first block group)         | 0.66                                                                     |
| Reads (first block group)           | 10.25                                                                    |
| % Unique reads (first block group)  | 78                                                                       |
| Entropy (second block group)        | 1.38                                                                     |
| Reads (second block group)          | 15.00                                                                    |
| % Unique reads (second block group) | 100                                                                      |

**Block group alignment:** CervixHelas3Rep2-cluster-2910-n-a(+) with bg-33-ame-mir-9b-MI0001597(-) [Score: 0.83]



## 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)