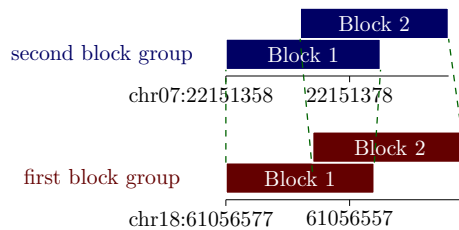


# deepBlockAlign v1.0

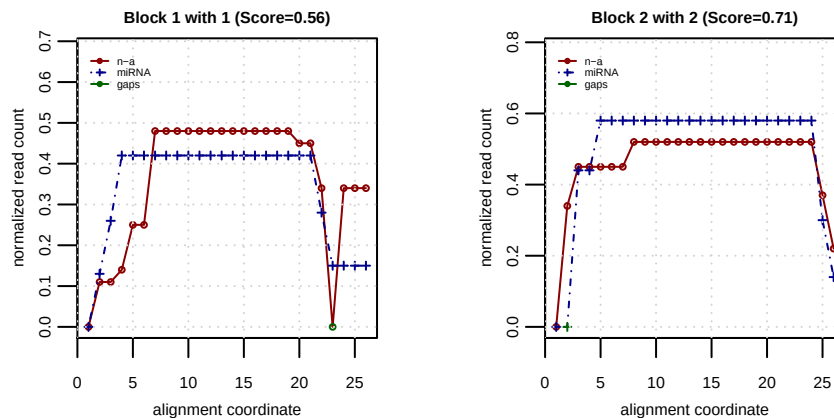
## Alignment parameters:

|                                     |                                                                          |
|-------------------------------------|--------------------------------------------------------------------------|
| [Input]                             |                                                                          |
| date and time                       | Sun, 03 Feb 2013 01:22:31 +0100                                          |
| first block group                   | CervixHelas3Rep2_cluster.6475                                            |
| first file                          | /home/projects/users/sachin/frontier/putative_mirna//tmp2000query.tmp    |
| second block group                  | bg_337                                                                   |
| 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)         | 2.50                                                                     |
| Reads (first block group)           | 8.92                                                                     |
| % Unique reads (first block group)  | 90                                                                       |
| Entropy (second block group)        | 2.11                                                                     |
| Reads (second block group)          | 159.00                                                                   |
| % Unique reads (second block group) | 100                                                                      |

**Block group alignment:** CervixHelas3Rep2-cluster-6475-n-a(-) with bg-337-osa-MIR812i-MI0008298(+) [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)