# deepBlockAlign v1.3

## Alignment parameters:

**[Input]**

| | |
|---|---|
| date and time | Wed, 15 Oct 2014 23:15:09 +0200 |
| first block group | cluster_176 |
| first file | human_eb.blockGroups |
| second block group | cluster_531 |
| second file | human_eb.blockGroups |

**[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) | 1.57 |
| Reads (first block group) | 183.78 |
| % Unique reads (first block group) | 0 |
| Entropy (second block group) | 1.24 |
| Reads (second block group) | 121.67 |
| % Unique reads (second block group) | 0 |

**Block group alignment:** *cluster-176-n-a(-)* with *cluster-531-hsa-mir-424(-)* [Score: 0.72]
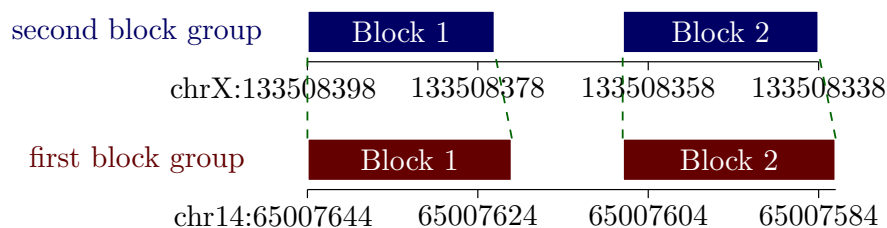


## Block alignment:
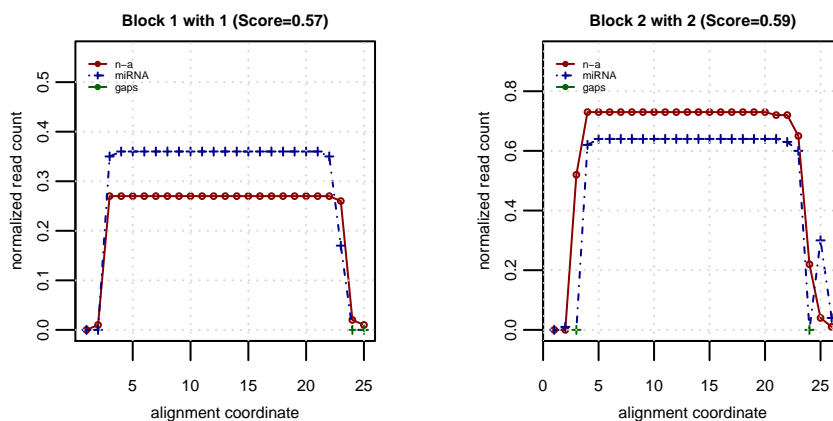


**Citation:** Langenberger, D*., Pundhir, S*., Ekstrøm, C.T., Stadler, P.F., Hoffmann, S., and Gorodkin, J.(2012). deepBlockAlign: A tool for aligning RNA-seq profiles of read block patterns. *Bioinformatics*, **28(1)**,17-24. (*equal contribution)