

deepBlockAlign v1.0

Block group alignment: cluster-403-chr6-Arg-ACG with cluster-520-hsa-mir-361 (Score: 0.835477)

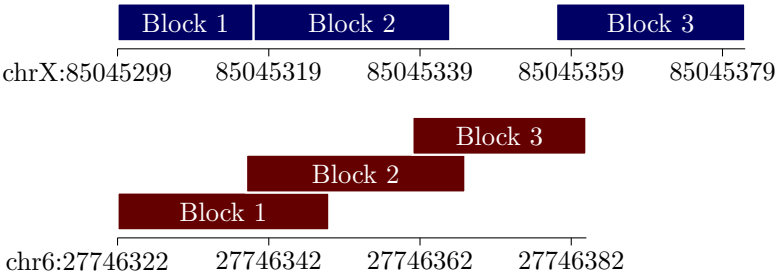


Table 1: Aligned Blocks

tRNA	miRNA
Block 1	Block 1
Block 2	Block 2
Block 3	Block 3

Block alignment:

