##In columns **“mip\_target\_start\_position”** and **“mip\_target\_stop\_position”** the range has to overlap the next one by at least one nucleotide.##

##The bigger the overlap, the better; however, the quality is more important##

for **“feature\_start\_position”**, **“feature\_stop\_position”** of record n = **“feature\_start\_position”**, **“feature\_stop\_position”** of record n+1 ##exon definition##

1. for records “n” **“probe\_strand”**=”-“ AND records n+1, n+2 **“probe\_strand”**=”+”

OR

for records “n” **“probe\_strand”**=”+“ AND records n+1, n+2 **“probe\_strand”**=”-”

* 1. if **“mip\_target\_start\_position”** of record n => **“mip\_target\_stop\_position”** of record n+1 AND **“mip\_target\_start\_position”** of record n => **“mip\_target\_stop\_position”** of record n+2 goto b
  2. if **“mip\_target\_start\_position”** of record n+1 < **“mip\_target\_start\_position”** of record n+2, AND **“rank\_score”** of record n+1 => **“rank\_score”** of record n+2, delete record n+2
  3. check if exon is covered; if not, undo last operation and delete record n+1 instead

## In columns L and M the range has to overlap the next one by at least one nucleotide.##

1. check overlap: **“mip\_target\_start\_position”** of record n =< **“mip\_target\_stop\_position”** of record n+1
2. If there are any redundant probes (target is covered sufficiently), remove them. The ones with lower quality (**“rank\_score”**) should be preferentially removed.
3. check if exon is covered
4. If there are any parts missing, create a tab separated text output file with the lines:

1st row track name=MIP\_candidates description="MIP\_candidates" visibility=1 color=0,255,0

Then columns without column names:

A: chromosome (format: chrN, where N=number); B region start, C region end

1. When final design done:

Create unique MIP name per gene, based on sorted target position:

–BLIND-ANIMAL-CAND\_GENEA\_MIP1

–BLIND-ANIMAL-CAND \_GENEA\_MIP2 etc. etc.

•MIP count per gene (with count per score)