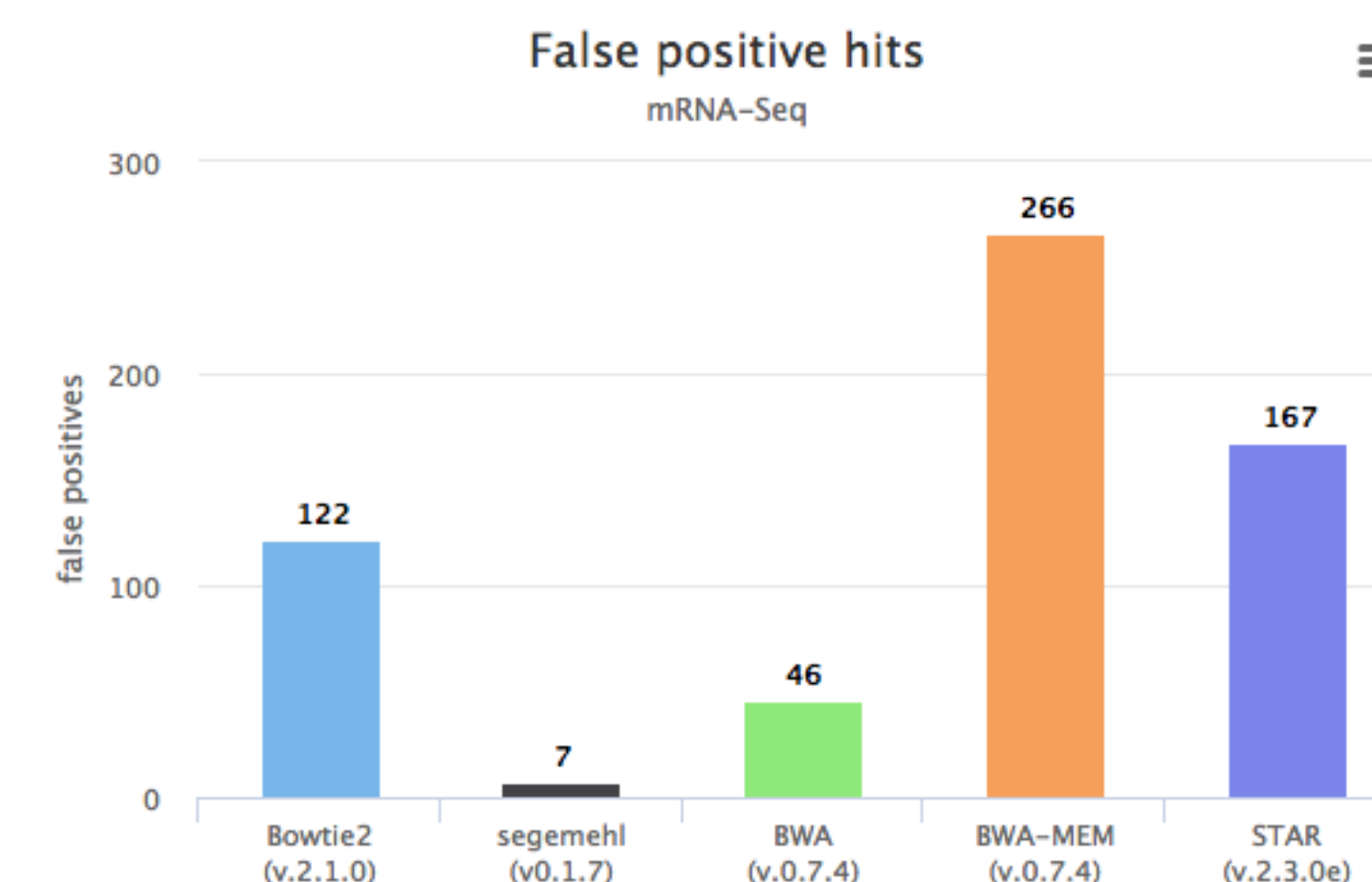
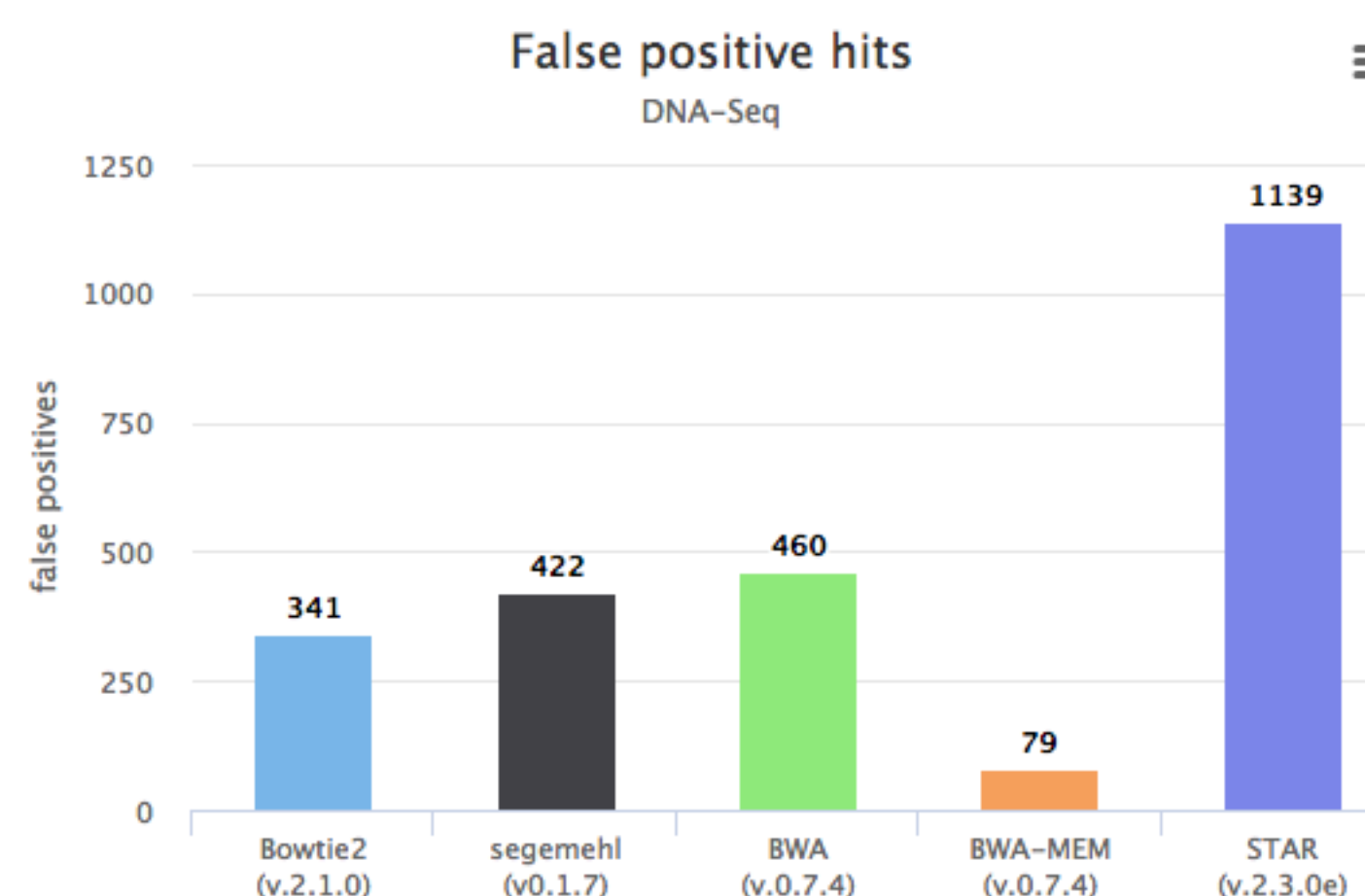
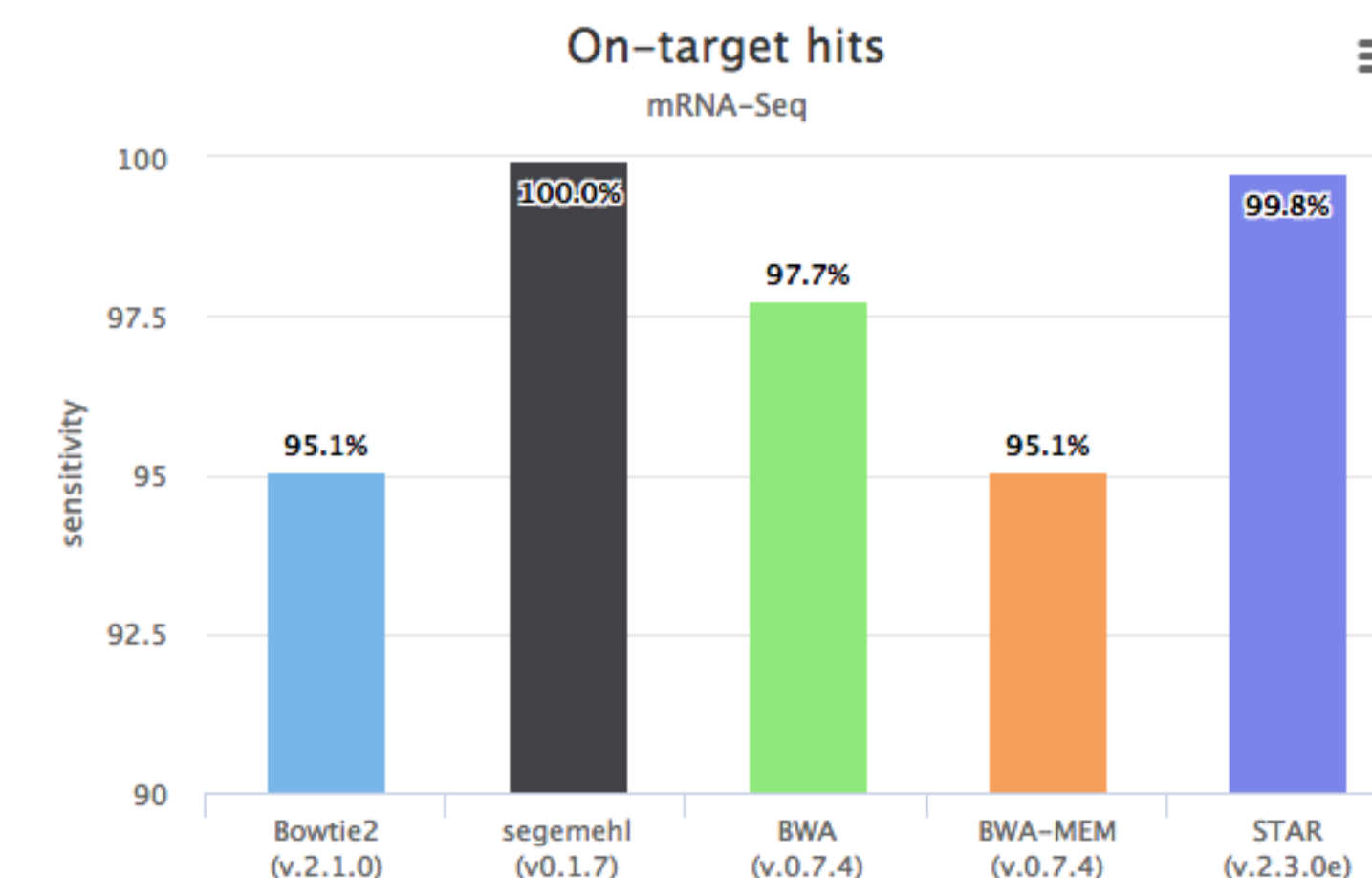
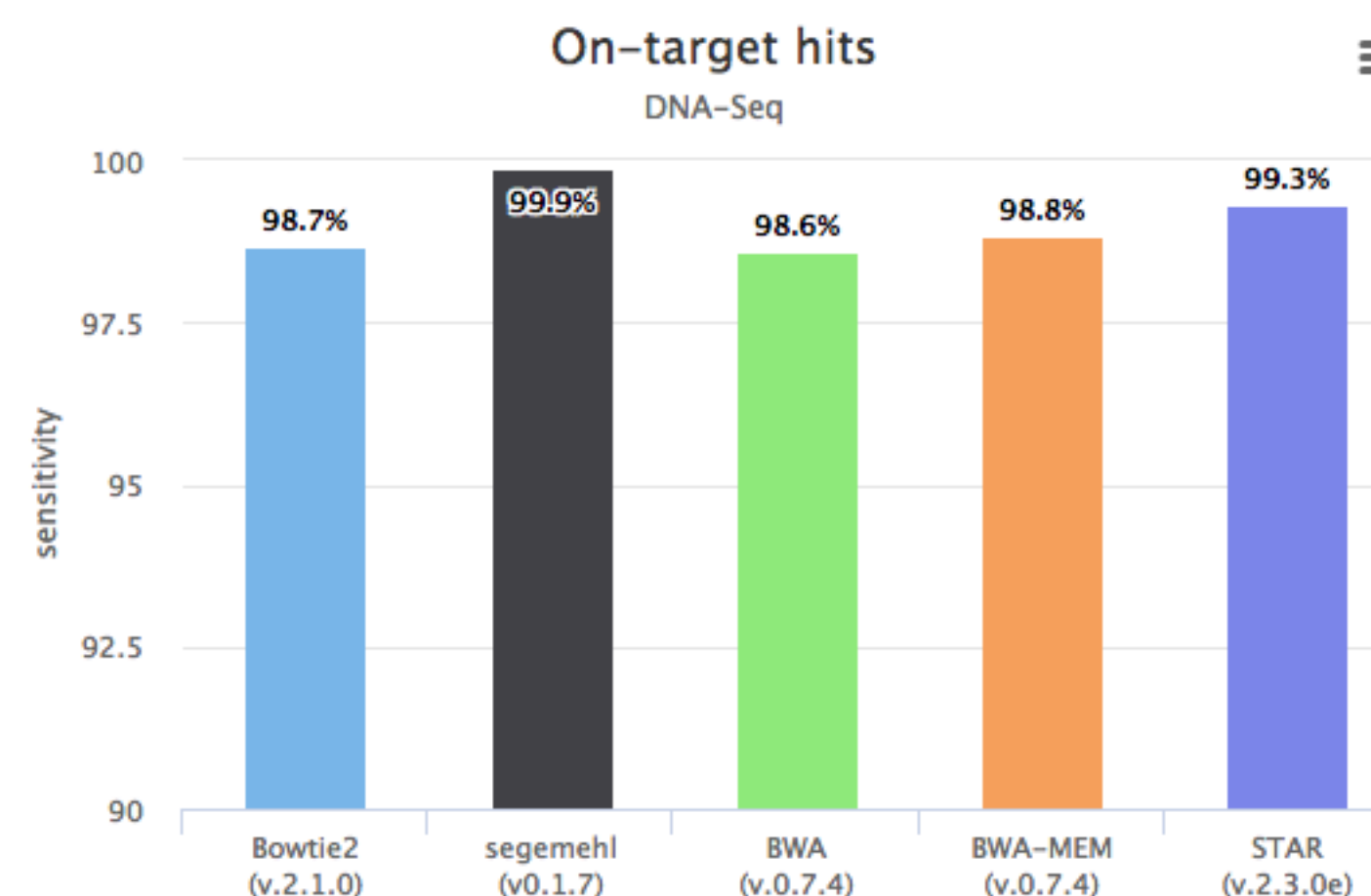
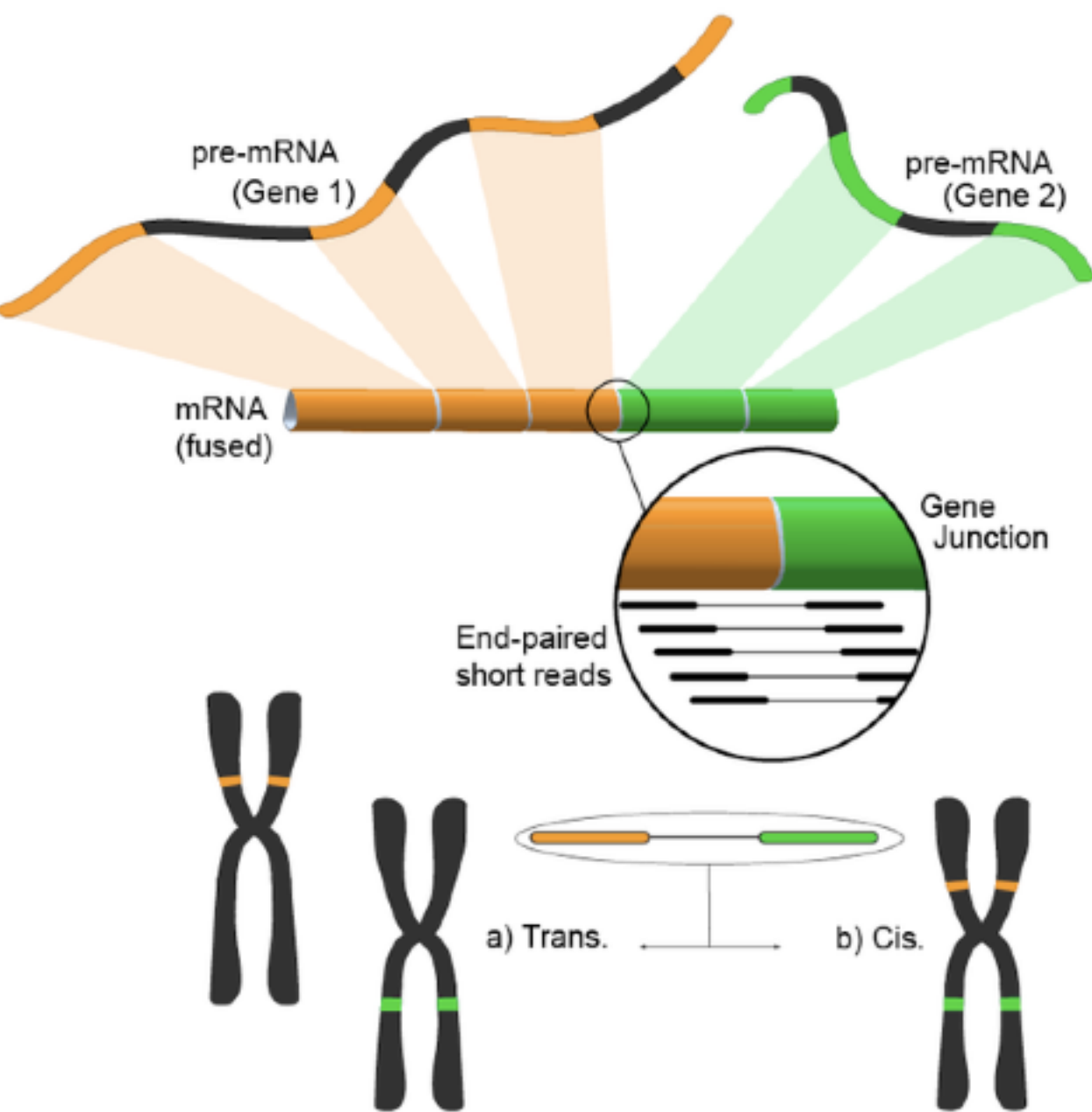


- Identificação de variantes:
 - Poucos falso positivos
 - Alinhamento global (identifica indel)
- Quantificação:
 - Alta sensibilidade
 - Alinhamento local (splice aware)



Contar o que?

- A medida base é o número de reads.
- Contam-se o número de reads mapeadas a uma feature.
- Reads curtos
- Single read (quantificação) - paired-end (splice)



##gff-version 3						
ctg123	.	mRNA	1300	9000	.	ID=mrna0001;Name=sonichedgehog
ctg123	.	exon	1300	1500	.	ID=exon00001;Parent=mrna0001
ctg123	.	exon	1050	1500	.	ID=exon00002;Parent=mrna0001
ctg123	.	exon	3000	3902	.	ID=exon00003;Parent=mrna0001
ctg123	.	exon	5000	5500	.	ID=exon00004;Parent=mrna0001
ctg123	.	exon	7000	9000	.	ID=exon00005;Parent=mrna0001

