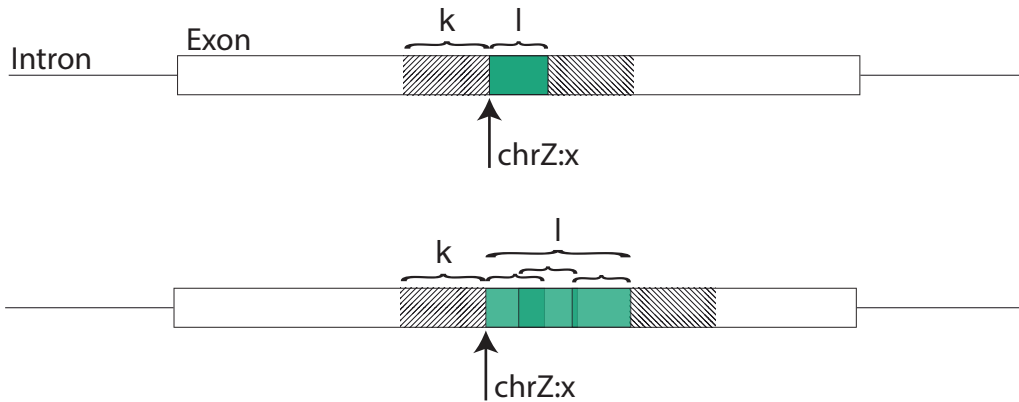


Case 1: The variant region is in middle of coding region, see:

- DNMT3A_R882_exon_23.fa
- MYC_T58A_P59R_exon2.fa
- FLT3-TKD_exon_20.fa

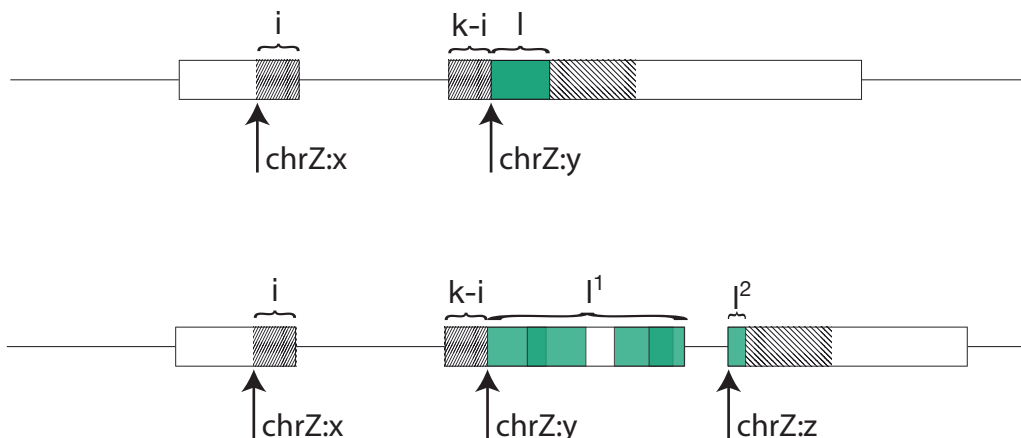
Target sequence fasta file



```
>chrZ:(x - k)-(x + l + k)
[ACGT]{k+l+k}
```

Case 2: The variant region is close or overlap an extremite of coding region, see:

- IDH1_R132.fa
- NPM1_4ins_exons_10-11utr.fa
- FLT3-ITD_exons13-15.fa

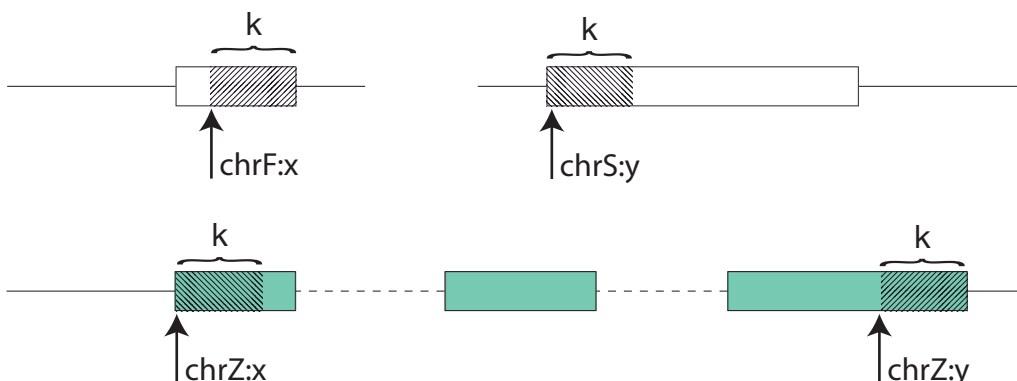


```
>chrZ:x-(x+i)
[ACGT]{i}
>chrZ:(y - (k-i))-(y + l + k)
[ACGT]{k-i+l+k}
```

```
>chrZ:x-(x+i)
[ACGT]{i}
>chrZ:(y - (k-i))-(y + l1)
[ACGT]{k-i+l1}
>chrZ:z-(z+l2)
[ACTG]{l2}
```

Case 3: Fusion or large tandem duplication, see:

- NSD1_exon6-NUP98_exon13.fa
- NUP98_exon11-NSD1_exon7.fa
- KMT2A-PTD_8-2.fa



```
>chrF:x-(x + k)
[ACGT]{k}
>chrS:y-(y + k)
[ACGT]{k}
```

```
>chrZ:y-(y + k)
[ACGT]{k}
>chrZ:x-(x + k)
[ACGT]{k}
```