```
pp1    45_5_chr        1866817 1905496 1868451 1868465 1904385 1904399 AATTATCATTATTT  AAATAATGATAATT  Longest Repeat flanking phage and within 2000 bp
pp2    45_5_plasmid    4016    20200   2352    2365    17134   17147   TTAAAATATGATT   AATCATATTTTAA   Longest Repeat flanking phage and within 2000 bp
prophage_coordinates.tsv (END)
```

as shown in the figure，this is an output file by using PhisPy(4.2.19).the start position and end position of attL are 1868451 and 1868465,then the sequence is "AATTATCATTATTT".However,I used seqkit tools(seqkit subseq -r 1868451:1868465 genome.fa) to extract sequence from start position and end position,the sequence is "AATTATCATTATTTA" .Obviously,the result I extracted have an extra base("A") at the end,comparing to the sequence of output.That is to say,the description of postion and sequence is not matched.By the way,the positon of prophage also doesn't match with sequence in "phage.fasta" generating by PhiSpy.Which result should I choose?By position or sequence?