ALIGNMENTS IN BOWTIE 2
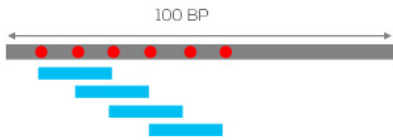
@HWI-ST974:58:C059FACXX:2:1201:10589:110434 1:N:0:TGACCA
TGCACACTGAACGTGCCGFGCCCAAAATCTGTCAAATGAATTTAGG
ACGTG

MULTISEED ALIGNMENT (UNGAPPED)   SEED LENGTH: 16 NT, EVERY 10 NT
100 BP   # MISMATCHES: 0

```
@PG ID:bowtie2  PN:bowtie2   VN:2.2.1     CL:"/
read1   16   chr10   6    255 100M      *   0   0
read2   16   chr7    4    255 99M1S     *   0   0
read3   0    chr7    4    31  100M      *   0   0
read4   256  chr10   4    31  100M      *   0   0
read5   0    chr5    38   37  2S90M8S   *   0   0
read6   256  chr6    40   37  3D97M     *   0   0
read7   0    chr1    40   38  100M      *   0   0
```

Bowtie2 is a fast alignment algorithm based on the FM-index approach on seeds substrings to align them to the genome.

For more info please see:

Langmead B, Salzberg SL. Fast gapped-read alignment with Bowtie 2. Nat Methods. 2012;9(4):357-359. doi:10.1038/nmeth.1923.

This job takes reads in fq, fa files, aligns these onto the reference genome and gives mapping result in SAM format. Each row of the SAM file contains input read name, reference read name, position on the reference read and number of mapped/skipped/inserted/deleted positions