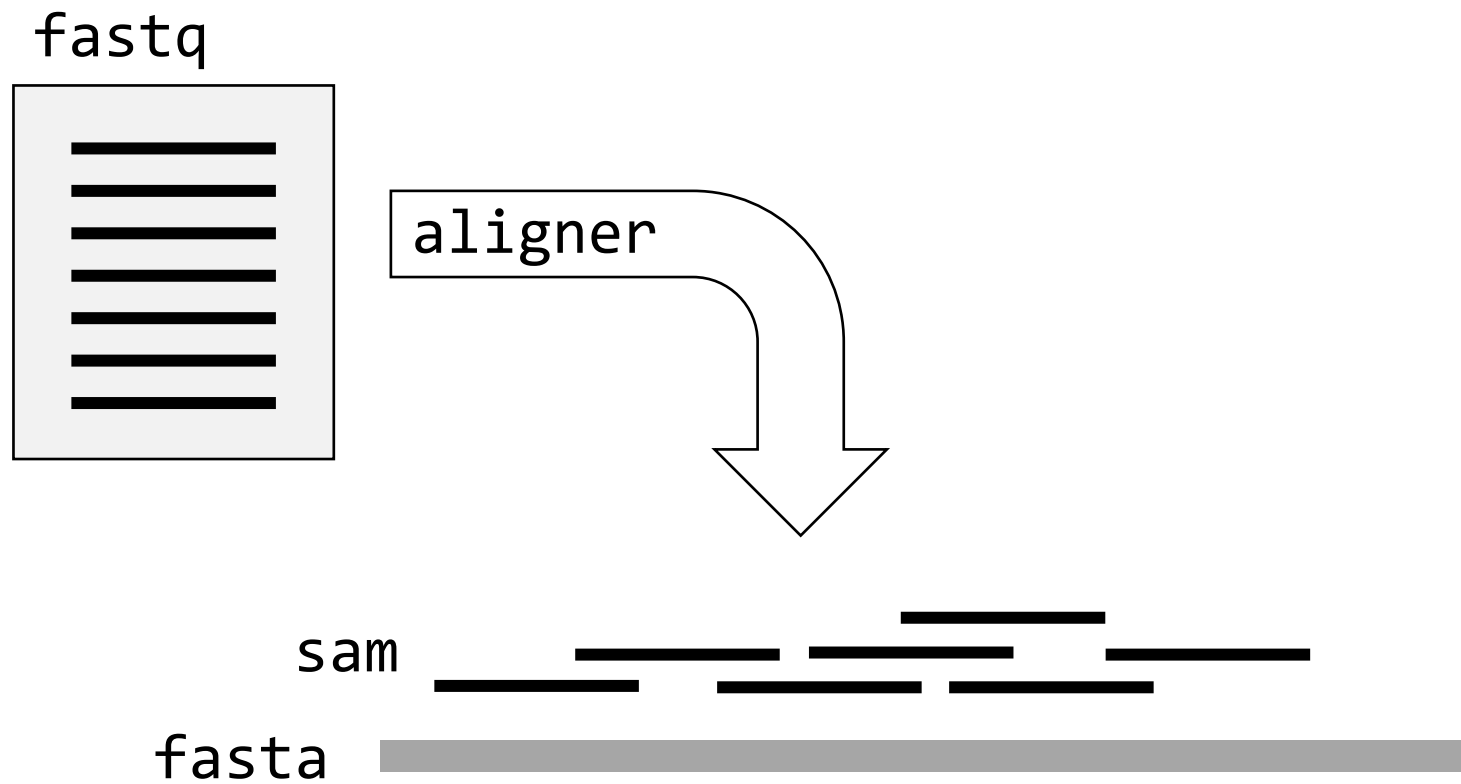
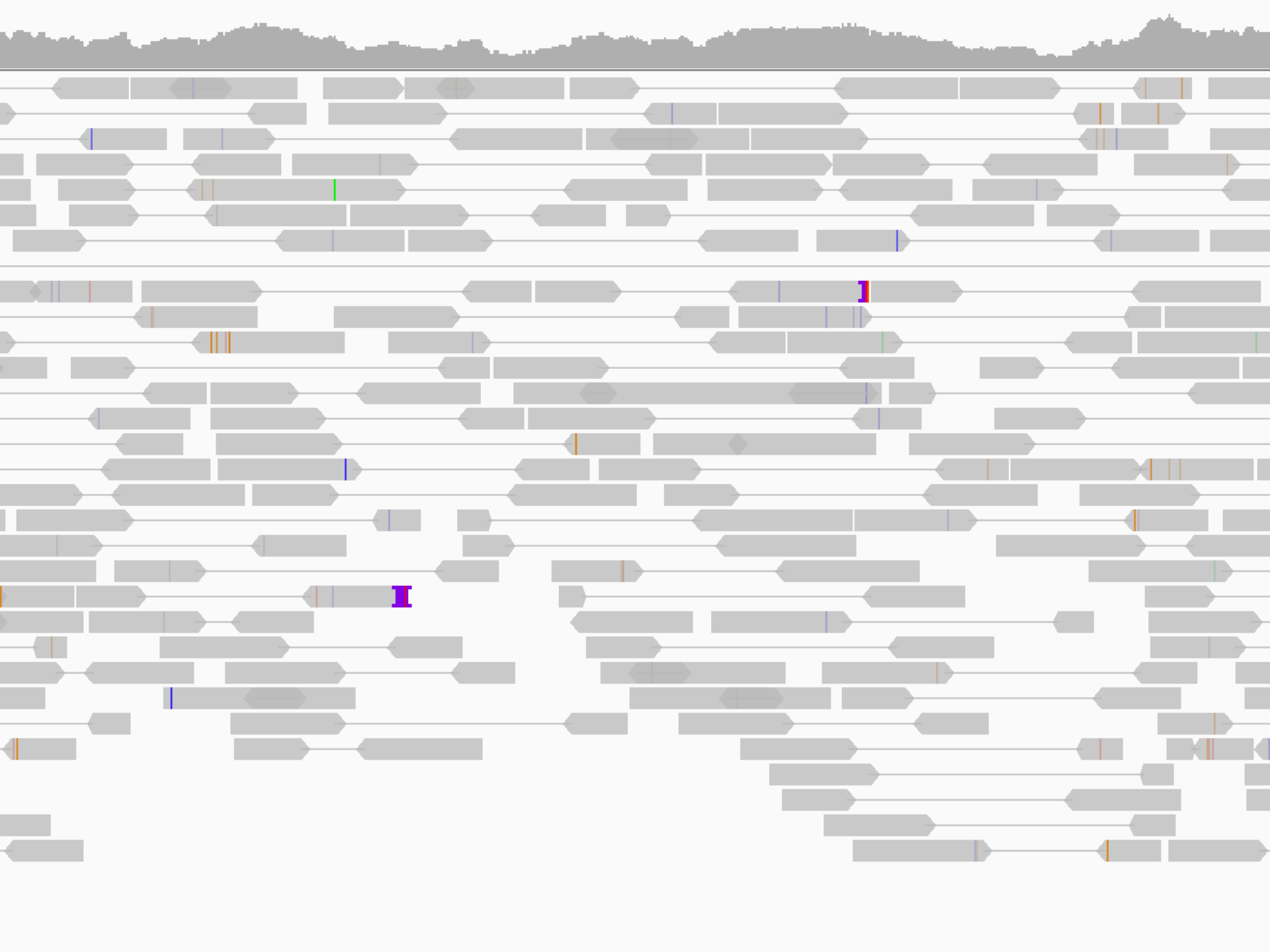


NGS - quality control, alignment, visualisation

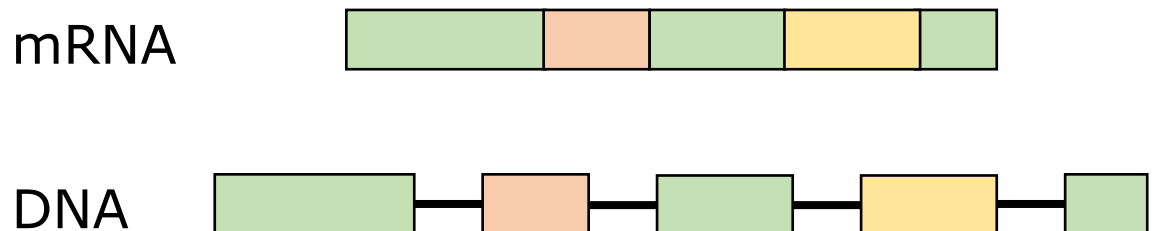
Read alignment



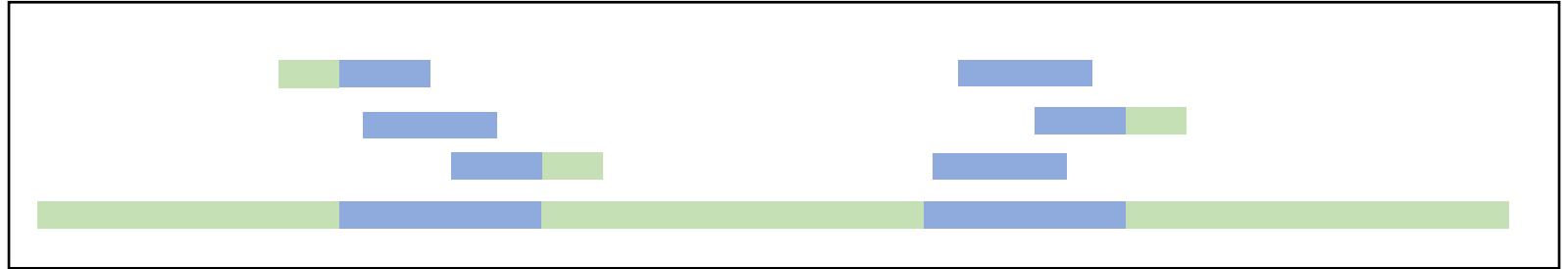


Software

- Basic alignment:
 - bowtie2
 - bwa-mem
- Splice-aware (RNA-seq):
 - hisat2
 - STAR
- Long reads + short reads + splice-aware:
 - minimap2



Mapping quality



$MAPQ$

$= -10\log_{10} \Pr\{\text{mapping position is wrong}\}$

$$-10\log_{10} (0.01) = 20$$

$$-10\log_{10} (0.5) = 3$$