# Translatome workbench
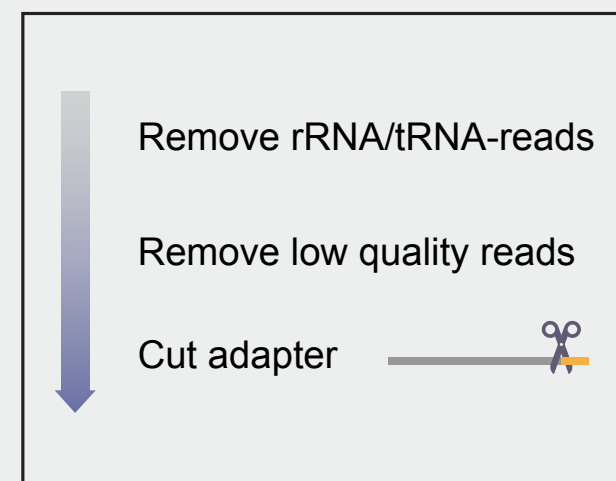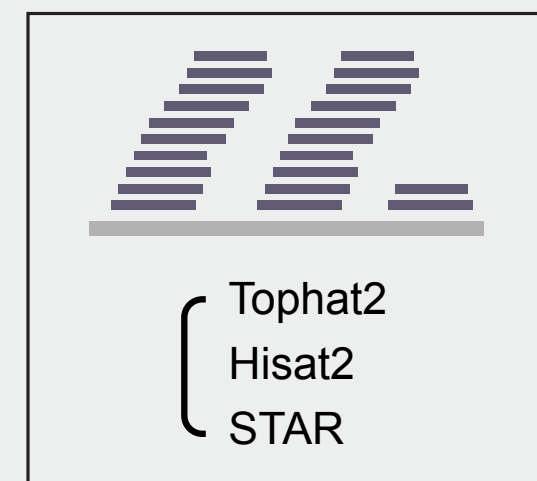
**Fastq** → **QC** → **Mapping** → **Post-alignment QC** → **Normalization**
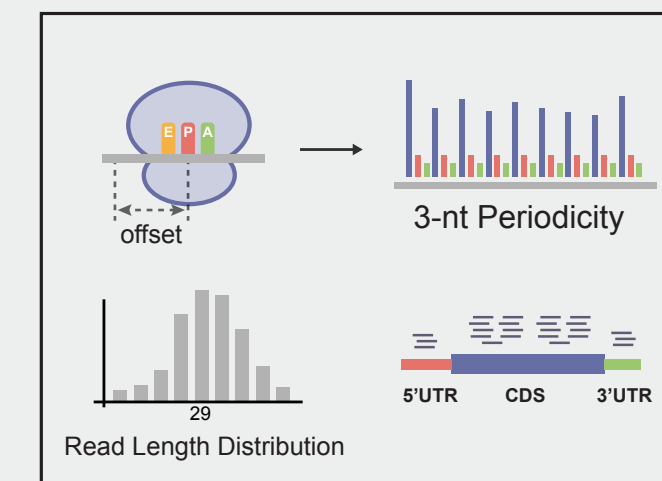
QC:
- Remove rRNA/tRNA-reads
- Remove low quality reads
- Cut adapter

Mapping:
- Tophat2
- Hisat2
- STAR

Post-alignment QC:
- offset → 3-nt Periodicity
- Read Length Distribution (29)
- 5'UTR | CDS | 3'UTR

Normalization:

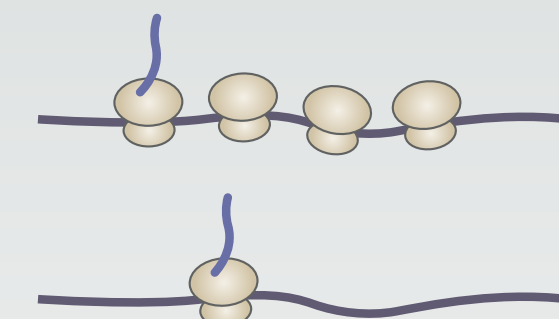|    | S1 | S2 | $\cdots$ | Sn |
|----|----|----|----------|----|
| G1 | *  | *  | $\cdots$ | *  |
| G2 | *  | *  | $\cdots$ | *  |
| $\vdots$ | $\vdots$ | $\vdots$ | | $\vdots$ |
| Gn | *  | *  | $\cdots$ | *  |
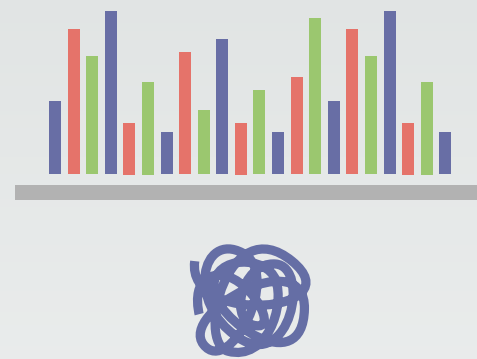
**Non-ribosomal enclosed regions**
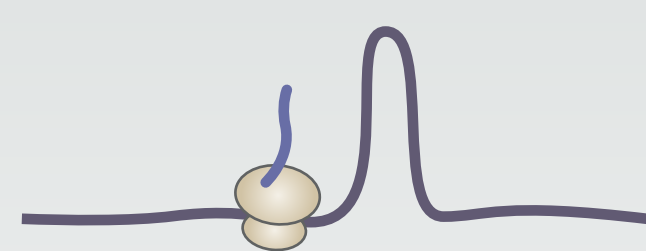
**Ribosome pausing**

**Isoform level**

**Translational efficiency**

**Activate translation**