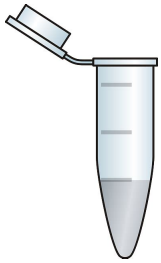
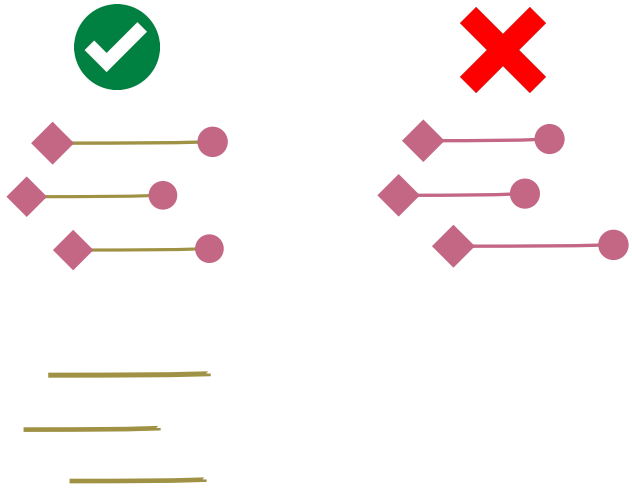


CUT&RUN experiment

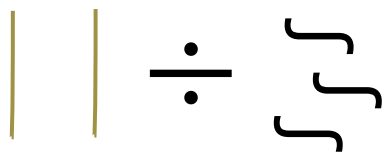
Quality check with FastQC

Trim sequence adapters

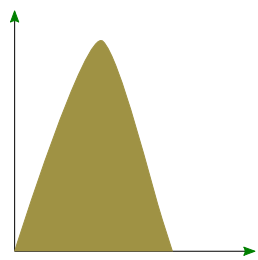
Align trimmed reads to reference genome



Filter reads to keep 20 bp ≤ fragments ≤ 120 bp



Calibrate size filtered reads with spike-in *E. coli* reads



Call CUT&RUN peaks using MACS2