

# Paired-end vs Single-end Sequencing

## Single-end (SE)



**Method:** Sequence from one end only

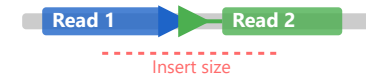
**Read Length:** 50-150 bp

**Cost:** Lower (\$)

**Time:** Faster

**Use Case:** Gene expression, small RNA-seq

## Paired-end (PE)



**Method:** Sequence from both ends

**Read Length:**  $2 \times (75-300)$  bp

**Cost:** Higher (\$\$)

**Time:** Longer

**Use Case:** Variant calling, de novo assembly, structural variants

## Paired-end Advantages

- ✓ Better alignment accuracy - confirms read location
- ✓ Detect structural variants and rearrangements
- ✓ Improved de novo assembly quality

- ✓ Span repetitive regions more effectively