

Paired-end vs Single-end Sequencing

Single-end (SE)



Method: Sequence from one end only

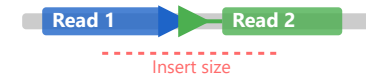
Read Length: 50-150 bp

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