Efficiency

Refers to how effectively a sequencing platform converts input resources (time, cost, sample material) into usable genetic data.

High efficiency means:

Lower cost per base

Faster turnaround time

Minimal sample waste

Fewer errors requiring re-sequencing

Depth (Sequencing Depth)

Also called read depth.

Indicates how many times a particular nucleotide or region of DNA is read during sequencing.

Example: A depth of 30× means each base was read 30 times.

Higher depth improves confidence in detecting variants, especially rare ones.

Coverage

Refers to the proportion of the genome or target region that is successfully sequenced.

Types:

Breadth of coverage: Percentage of the genome covered at least once.

Uniformity of coverage: How evenly the reads are distributed across the genome.

High coverage ensures that important regions aren’t missed.

Accuracy

Measures how correctly the sequencer identifies the actual DNA bases.

Influenced by:

Sequencing technology

Base calling algorithms

Error correction methods

High accuracy is crucial for clinical diagnostics and variant detection.