



Nex-StoCT workgroup definitions of CLIA performance characteristics for NGS

Performance Characteristics	Workgroup established definition for NGS applications
Accuracy	The degree of agreement between the nucleic acid sequences derived from the assay and a reference sequence.
Precision	The degree to which repeated sequence analyses give the same result-repeatability (within-run precision) and reproducibility (between-run precision).
Analytical Sensitivity	The likelihood that the assay will detect the targeted sequence variations, if present.
Analytical Specificity	The probability that the assay will not detect a sequence variation when none are present (the false positive rate is a useful measure for sequencing assays).
Reportable Range	The region of the genome in which sequence of an acceptable quality can be derived by the laboratory test.
Reference Range	Reportable sequence variations the assay can detect that are expected to occur in an affected person (likely pathogenic and pathogenic variants reported and cataloged in ClinVar and elsewhere).

Reference: Gargis AS, K. L. (2012). Assuring the quality of next-generation sequencing in clinical laboratory practice. *Nature biotechnology*, 0(11):10.1038/nbt.2403. doi:10.1038/nbt.2403.