



DRAGEN™ secondary analysis

Efficient secondary analysis of NGS data with award-winning accuracy

DRAGEN secondary analysis allows labs of all sizes and disciplines to maximize their genomic insights with award-winning accuracy,^{1,2} a broad menu of applications, and efficient workflows. Get comprehensive coverage with hardware-accelerated genomic analysis algorithms, continuous innovations using machine learning, Multigenome (graph) references, and more.

Maximize the value of the genome



Accurate

Enable a 99.84% accuracy score using Multigenome (Graph) and machine learning with the Precision FDA Truth Challenge V2 benchmark data¹



Comprehensive

Analyze whole genomes, exomes, methylomes, and transcriptomes with a single platform that would take 30 open-source tools to partially replicate³



Efficient

Process an entire human genome at 30× coverage in approximately 25 minutes² and reduce FASTQ file sizes up to 5× with DRAGEN ORA compression

Access DRAGEN software on your platform of choice



DRAGEN on-premises

Analyze and store data locally with an on-premises server in a fraction of the time compared with a traditional CPU-based system



DRAGEN onboard

Analyze data directly on the NovaSeq™ X Series, or NextSeq™ 1000, or NextSeq 2000 Systems without additional computing infrastructure or bioinformatics resources



DRAGEN on cloud

Stream data from sequencing systems to BaseSpace™ Sequence Hub or Illumina Connected Analytics for rapid analysis at scale with no hardware investment



Awards

Won the Precision FDA Truth Challenge V2 for "Difficult-to-Map" and "All Benchmark" regions, Won "Best Precision" and "Best Overall" on Panel X and "Best Applicability" in the Precision FDA NCTR Indel Calling from OncoPanel.^{1,2}

Product highlights

Application	On-premises		Onboard		On-cloud	
	DRAGEN server	NovaSeq X Series	NextSeq 1000 NextSeq 2000 Systems	BaseSpace Sequence Hub	ILLUMINA Connected Analytics	
BCL conversion	✓	✓	✓	✓	✓	✓ (custom only)
DRAGEN ORA compression	✓	✓	✓			
DRAGEN FASTQ + MultiQC	✓	✓	✓	✓	✓	✓
Whole genome	Germline + somatic	Germline only Somatic <i>coming soon</i>	Germline only	Germline + somatic	Germline + somatic	Germline + somatic
Enrichment (including exome)	Germline + somatic	Germline + somatic	Germline + somatic	Germline + somatic	Germline + somatic	Germline + somatic
DNA amplicon	✓		✓	✓	✓	✓
RNA	✓	✓	✓	✓	✓	✓
Single-cell RNA	✓		✓	✓	✓	✓
Differential expression		✓	✓	✓	✓	
NanoString GeoMx NGS			✓	✓	✓	
RNA amplicon	✓			✓	✓	<i>Coming soon</i>
Methylation	✓	<i>Coming soon</i>		✓	✓	✓
Metagenomics	✓			✓	✓	
RNA pathogen detection				✓	✓	
COVID	COVIDSeq. COVID Lineage		COVIDSeq. (cloud only)	COVIDSeq. COVID Lineage		
TruSight™ Oncology 500	ctDNA available, solid <i>coming soon</i>			✓ enabled in 3.10	✓	
ScATAC-Seq	✓			✓	✓	✓
Imputation	✓			✓	✓	✓
PGx Star Allele Caller	✓	<i>Coming soon</i>		✓	✓	✓
Illumina Complete Long Reads				✓	✓	
DRAGEN secondary analysis for RPIP and UPIP	✓			✓	✓	✓



Learn how [customers are using DRAGEN](#) secondary analysis.



Read about DRAGEN secondary analysis in population genomics initiatives on our [resource page](#).



Explore recent [DRAGEN publications](#).

Learn more

1. Food and Drug Administration. Truth Challenge V2: Calling Variants from Short and Long Reads in Difficult-to-Map Regions. precision.fda.gov/challenges/10. Accessed July 14, 2023.
2. Food and Drug Administration. NCTR Indel Calling from Oncopanel Sequencing Data Challenge Phase 1. precision.fda.gov/challenges/21. Accessed July 14, 2023.
3. Internal data on file. Illumina, Inc., 2023.



1.800.809.4566 toll-free (US) | +1.858.202.4566 tel

techsupport@illumina.com | www.illumina.com

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