Call variants. Find meaning. Take action.

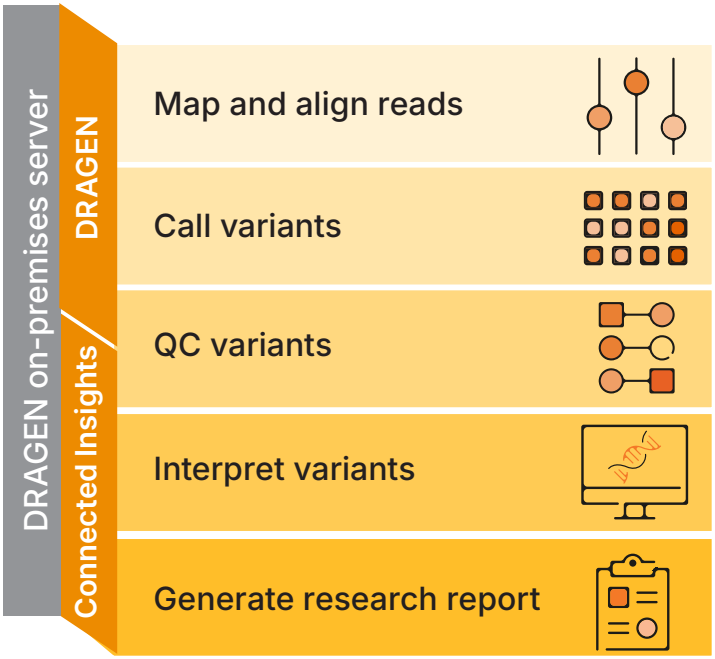
From a single server: DRAGEN™ secondary analysis and Connected Insights variant interpretation and reporting for oncology clinical research.

illumina®

Your DRAGEN server now does more for oncology

Streamline your oncology clinical research, leveraging variant calling through interpretation and report generation on a single DRAGEN server. Connected Insights and DRAGEN on-premises enable access to:

- Award-winning accuracy of DRAGEN variant calling and Connected Insights in one server
- Seamless data ingestion enabling quality control and sample to insight workflows
- Hardware and software tested together by a trusted provider
- Adherence to institutional and regional guidelines, enterprise-level security, and privacy



Unlock meaning for a wide range of oncology applications and assays within a single server

Applications

- Solid tumor testing (tissue)
- Liquid biopsy
- Hematological cancer
- Methylation*
- Expression*
- MRD[1] and monitoring*

Assays**

Targeted panels | CGP[2] | WTS[3], WES[4], WGS[5]

Variants & biomarker signatures

SNV[6] MNV[7] CNV[8] SV[9] Fusions Indels[10] LOH[11]
TMB[12] MSI[13] GIS[14] Tumor Ploidy Tumor Purity

*Application currently supported by DRAGEN secondary analysis. Support within Connected Insights coming soon.
**Including Illumina, Illumina-partnered, or third-party kits

For Research Use Only. Not for use in diagnostic procedures.

The combined power of DRAGEN and Illumina Connected Insights

Accurate results

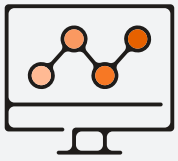
- Achieve high accuracy variant calling with DRAGEN secondary analysis, proven with 99.89% accuracy score in all benchmark regions in the Precision FDA Truth Challenge V2[14-15]
- Benefit from the latest machine learning (ML) and pangenome technology within DRAGEN secondary analysis

Comprehensive solution

- Uncover more insights across a broad range of oncology-specific variant classes and biomarker signatures
- Harness the power of 55+ integrated knowledge sources, with variant classifications, drug labels, and clinical trials all in a single view
- Leverage a comprehensive suite of cutting-edge predictors to call, annotate, and predict oncogenicity classification of variants*

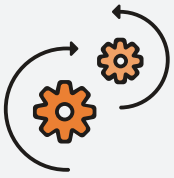
Efficient analysis

- Achieve rapid turnaround times and process NGS data faster compared to open source methods leveraging exceptionally high speeds of DRAGEN[16-17]
- Save time by seamlessly transferring data between secondary and tertiary analysis
- Automatically launch Connected Insights for a no-touch workflow



Powerful visualizations

- Perform variant QC with gene- and exon-level coverage plots and IGV
- Visualize complex variants in whole genome views, including Circos, B-allele ratio, fusion plots, and more



Optimized workflow

- Expand and re-use past variant interpretations maintained in your private knowledge base
- Speed up interpretation with automated, guidelines-based variant oncogenicity prediction, supported with AI algorithms*
- Get started fast with an automatically generated partial draft report, ready for lab review and edits

Customizable reporting

- Customize report template based on customer brand and content requirements (logo, layout, design)
- Incorporate region-specific tiering guidelines for user-defined interpretation and research reporting
- Generate reports in 18+ different languages

*Including PrimateAI-3D and SpliceAI

Discover the power of DRAGEN secondary analysis

Learn more about Connected Insights

References

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4. Whole Exome Sequencing
5. Whole Genome Sequencing
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7. Multi-Nucleotide Variant
8. Copy Number Variant
9. Structural Variant
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