

Connections bring meaning to cancer testing

Identify insights faster while
scaling NGS operations
for somatic oncology
applications





Move precision medicine forward

Streamlined

Accelerate time to report by harnessing the power of automation, user-defined workflow configuration, and > 45 knowledge sources

Integrated

Remove unnecessary touchpoints and manual data movement by connecting data analysis with upstream sequencing to simplify and secure the comprehensive workflow

Powered for growth

Scale the volume and throughput of your NGS workflows without increasing headcount to keep pace with evolving science, technology, and demand

Connected Insights harnesses > 45 knowledge sources to bring insights to diverse applications

Comprehensive knowledge in one place

Apply the power of API integrations to connect LIMS, storage, pipelines, and third-party knowledge bases; integrate variant classifications, relevant drug labels, and pertinent clinical trials within a single view

Evidence-based clinical content

Leverage comprehensive solid and hematological cancer content, somatic gene variant annotations, and related content powered by The Jackson Laboratory Clinical Knowledgebase (JAX-CKB™), a trusted knowledge base of over 100,000 users worldwide

Flexible regionality

Incorporate relevant lab- and region-specific practices within user-defined workflow; support customized variant interpretation and reporting based on regional-tiering guidelines

Regular updates

Access up-to-date, relevant variant annotations, insights, guidelines, and more, with Connected Insights-Research and integral regular, automated content updates (as frequently as monthly for some knowledge sources)

Unlock meaning for a wide range of applications within a single, customizable platform



Solid tumor testing (tissue)

Assess comprehensive gene panels covering multiple variant types, including TMB, MSI, and GIS to assess HRD



Liquid biopsy

Detect and analyze cancer variants with high analytical sensitivity and specificity using low levels of ctDNA found in the bloodstream



Hematological cancer

Streamline insight generation for myeloid leukemia, lymphoma, and other hematologic malignancies



Hereditary disease*

Uncover insights by interpreting genome-wide disease biomarker signatures (STR, paralog) with increasing relevance to precision medicine

*Capabilities expected in future roadmap.

Powerful features to streamline integration and adoption of a single-vendor workflow

Enterprise-level security and privacy standards

Protect the privacy of your genomic data with industry-leading global and local security standards

User-defined SOPs and advanced filters

Implement SOPs on the platform by creating sets of predefined custom filters or using the advanced filtering system

Streamlined workflow and collaboration

Facilitate teamwork; save time and remove manual data movement steps with autoingestion of variant data and autolaunch of Connected Insights

Broad portfolio of tests and variant types

Evolve your analysis to comprehensive panels, exomes, or genomes; analyze across a range of DNA and RNA variant and biomarker types, including TMB, MSI, and GIS to assess HRD

Lab-specific curation

Maintain a private knowledge base of your organization's curated data, including information about past variant interpretations and reporting

Automated custom reporting

Customize, edit, and automatically populate reports with minimal manual interaction; generate reports in 18+ different languages as needed

Available in select countries.

Integrate and streamline your workflows from library prep, sequencing, and data analysis

White paper



[GenomeWeb KOL white paper](#)

Learn the thoughts of key opinion leaders on the current challenges and promise of NGS interpretation and reporting in clinical oncology

Data sheet



[Connected Insights data sheet](#)

Read how Connected Insights streamlines, integrates, and powers laboratories for scale and growth

Video



[Connected Insights animated video](#)

Understand how Connected Insights can connect various knowledge sources to streamline operations for powerful insights

Learn more at [illumina.com/connected-insights](https://www.illumina.com/connected-insights)

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Abbreviations

API application programming interface

CNV copy number variant

ctDNA circulating tumor DNA

GIS genomic instability score

HRD homologous recombination deficiency

Indels insertion/deletion

KOL key opinion leader

LIMS laboratory information management system

MSI microsatellite instability

NGS next-generation sequencing

SNV single nucleotide variant

SOP standard operating procedure

SV structural variant

TMB tumor mutational burden

WES whole-exome sequencing

WGS whole-genome sequencing