Connections bring meaning to cancer testing

Identify insights faster while scaling NGS operations for somatic oncology applications today, genetic disease testing tomorrow

Available in select countries.
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 touch points and manual data movement by connecting to sequencing systems to simplify and secure assay workflows

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

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

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 (TM)), a trusted knowledgebase of over 100,000 clinicians worldwide

Regular updates
Access the most up-to-date, relevant content, with Connected Insights updates made on a monthly basis

Available in select countries.
Unlock meaning for a wide range of applications within a single, customizable platform

**Solid tumor testing (tissue)**
Assess comprehensive gene panels across multiple variant types, including TMB, MSI, and more

**Liquid biopsy**
Detect and analyze cancer with high sensitivity and specificity using low levels of ctDNA 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.

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**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

**Broad portfolio of tests and variant types**
Evolve with confidence, broadening 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

**User-defined SOPs and advanced filters**
Implement SOPs on the platform by creating sets of predefined custom filters or using the advanced filtering system

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

**Streamlined workflow and collaboration**
Facilitate teamwork; autoingestion of variant data and autolaunch of Connected Insights save time and remove manual data movement steps

**Automated custom reporting**
Customize, edit, and automatically populate reports; minimal manual interaction

Available in select countries.
Integrate and streamline your workflows from library prep, sequencing, and data analysis

**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

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

**Connected Insights animated video**
Watch to understand how Connected Insights can connect various knowledge sources to streamline operations for powerful insights

Learn more at illumina.com/connected-insights

Abbreviations

- API: application programming interface
- CNV: copy number variant
- ctDNA: circulating tumor DNA
- GIS: genomic instability score
- HRD: homologous recombination deficiency
- Indels: insertion/deletion
- 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

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