



Biomedical Genomics Workbench

Biomedical Genomics Workbench enables you to find the signal in the noise in your cancer and hereditary disease NGS data with ease

Unravel the complexity of NGS analysis and discover novel insights with greater than 95% sensitivity and high specificity for unsurpassed accuracy. Biomedical Genomics Workbench provides a comprehensive suite of intuitive analysis workflows, tools, and visualization modules that guide you through a customizable analysis of your genome, exome, targeted amplicon, transcriptome, and epigenetic NGS sequencing data for accelerated discovery, verification, and validation of novel cancer and hereditary disease biomarkers.

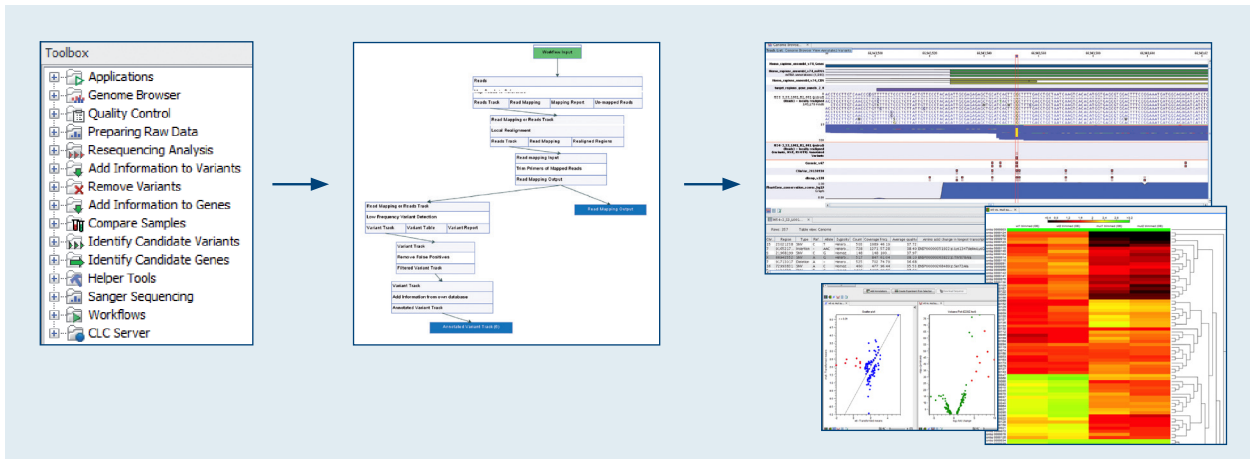


Figure 1. Biomedical Genomics Workbench offers a comprehensive toolbox, gives you the flexibility to build analysis workflows, and allows you to quickly visualize and verify your results.

Discover the signals that lead to answers

- Complete end-to-end, and customizable analysis workflows for the comprehensive discovery, verification, and validation of novel biomarkers.
- Specialized functionalities such as primer and primer-dimer removal for highly accurate targeted amplicon sequencing results.
- High sensitivity for detection of germline as well as low frequency variants from DNA-Seq and RNA-Seq data.
- Accelerate the verification and testing of known actionable variants without variant calling.
- Copy number detection for exome and targeted amplicon sequencing for unsurpassed accuracy.
- Integrated visualization, validation, reporting, and filtering tools, enable simple and fully customizable analysis workflows.
 - Visualization of results and mapped sequencing reads in a Genome Browser format
 - Variant visualization on protein 3D structure for pathogenicity detection
 - Filtering and annotation with dbSNP, ClinVar, COSMIC and others

Biomedical Genomics Workbench is part of QIAGEN's sample-to-insight workflow!

- Realize one-step analysis on QIAGEN GeneRead DNASeq Amplicon panel data!
- Streamline your data analysis and interpretation simply by adding Ingenuity® Variant Analysis™ with HGMD®, and Ingenuity® Pathway Analysis for an integrated solution.
- Direct access to Genome Trax™ within the software.
- Combine with TRANSFAC® for the identification and annotation of transcription factor binding sites.

To learn more, visit qiagenbioinformatics.com