

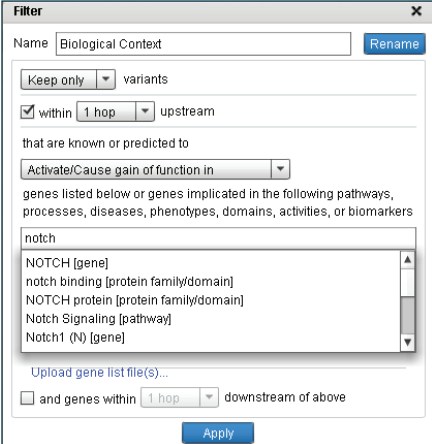
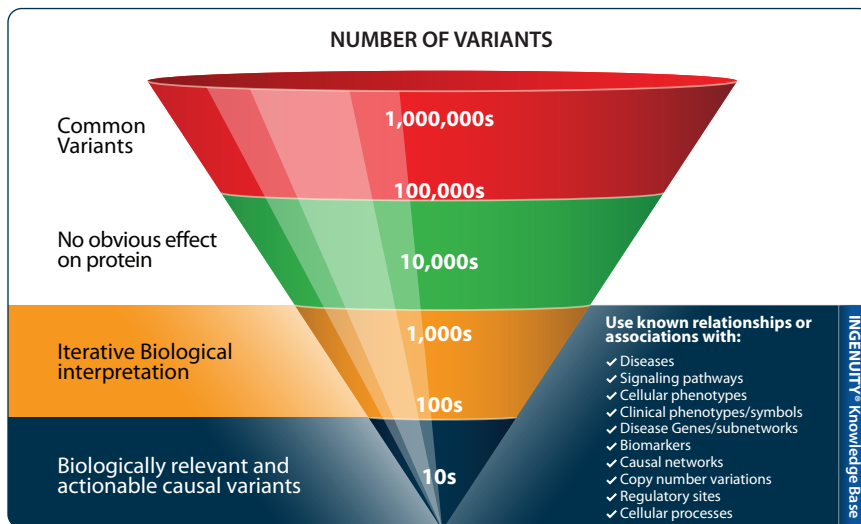
Variant Analysis™

Identify causal variants from human resequencing data in just minutes.

Ingenuity® Variant Analysis™ combines analytical tools and integrated content to help you rapidly identify a short list of compelling variants using selection criteria based both upon published biological evidence and your own knowledge of disease biology.

FOR: Researchers who need to identify causal variants from human resequencing data.

HOW: Drill down on biologically relevant variants based on information in the Ingenuity® Knowledge Base, including primary literature on human mutations in patients with particular diseases or abnormal phenotypes.



Interactive filters let you rapidly zero in on the most biologically interesting and relevant variants

Interactive Filtering to Prioritize Variants

- Quickly select for uncommon variants anywhere in the genome that likely cause loss or gain of function
- Identify variants that impact symptoms, pathways, processes, and genes implicated in drug response or disease progression
- Interactively adjust variant selection criteria in real-time
- Apply genetic selection criteria appropriate for your study design, from one to hundreds of samples

Integrated Evidence for Fast, Accurate Results

- Nearly 4 million manually-curated findings from the literature, including effects of mutations on human disease and phenotypes
- Mutation content from databases including COSMIC and OMIM
- Known and inferred effects on protein function resulting from variants in coding and regulatory regions, copy number variation, and fusions
- Cancer disease models that enable rapid causally-consistent identification of driver variants

Learn more in the Products section of www.ingenuity.com

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