

An Exploration of Clinical Workflows in VarSeq

Steve Hystad - Field Application Scientist

Darby Kammeraad – Field Application Scientist





Top 10 Analytics Solution Providers



Hype Cycle for Life sciences

Golden Helix – Who We Are

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Golden Helix is a global bioinformatics company founded in 1998.





Variant Calling Filtering and Annotation Clinical Reports CNV Analysis Pipeline: Run Workflows



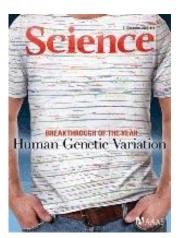
Variant Warehouse Centralized Annotations Hosted Reports Sharing and Integration GWAS Genomic Prediction Large-N-Population Studies RNA-Seq Large-N CNV-Analysis

SNP &

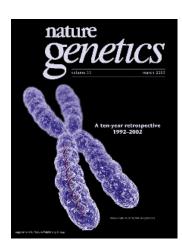


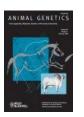
Cited in over 1100 peer-reviewed publications



























Over 350 customers globally



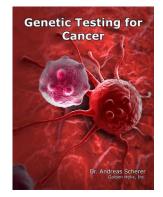




When you choose a Golden Helix solution, you get more than just software

- REPUTATION
- TRUST
- EXPERIENCE





- INDUSTRY FOCUS
- THOUGHT LEADERSHIP
- COMMUNITY

- TRAINING
- SUPPORT
- RESPONSIVENESS



- TRANSPARENCY
- INNOVATION and SPEED
- CUSTOMIZATIONS





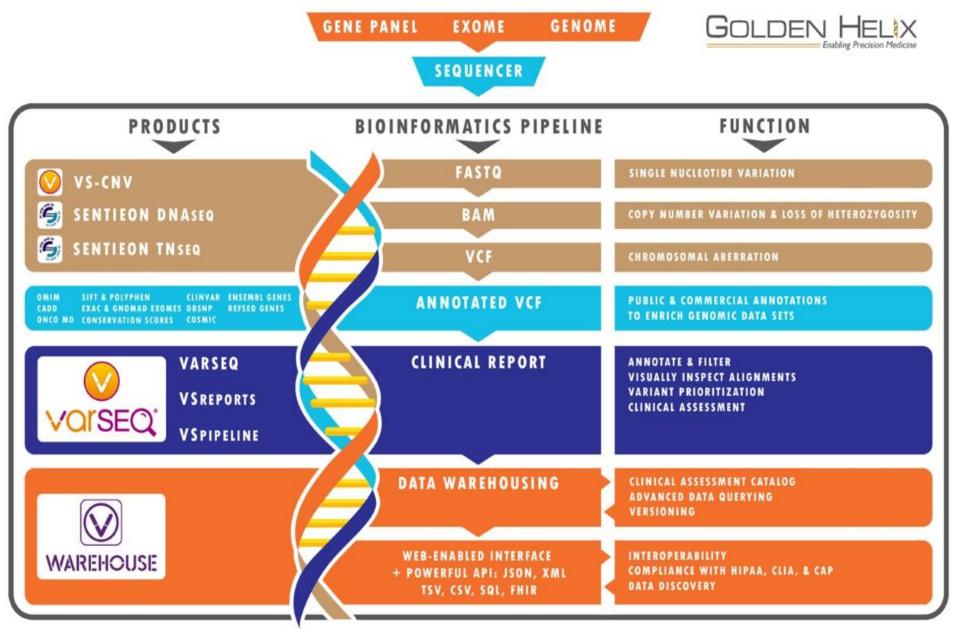


- Variant annotation, filtering, and interpretation
- Powerful GUI with rich visualizations
- Repeatable workflows & command-line interfaces



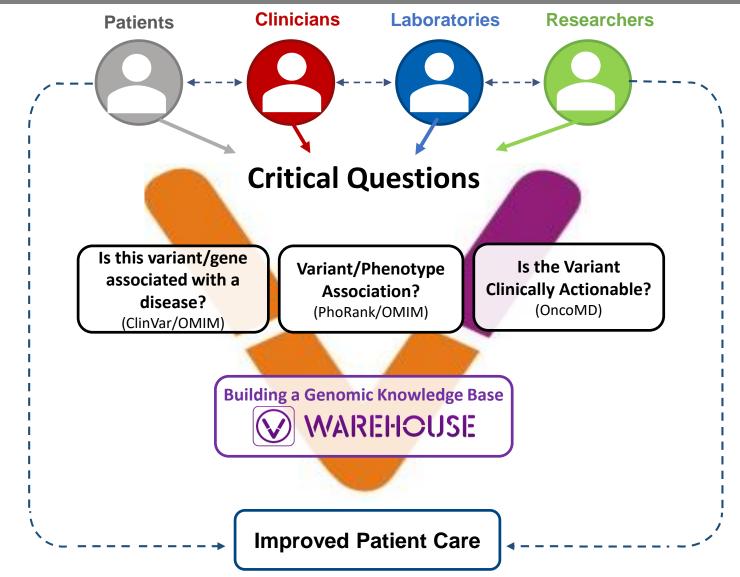
VarSeq Complete Stack





VarSeq Clinical Workflow







TruSight Cancer Gene Panels



TruSight Cancer Sequencing Kit from Illumina

- 6 samples; 1 with Lung Cancer Phenotype
- Key mutations in Tumor Suppressor Genes or Known Oncogenes?

Drugs Target Protein Products of Oncogenes

- Epidermal Growth Factor (EGFR)
- Anaplastic lymphoma kinase (ALK).
 - Crizotinib & Ceritinib inhibitors of oncogenesis.

Does this sample possess key variants in Oncogenes?

- If so, is it pathogenic?
- Drug targeting information, ongoing clinical trials?
 - Create a clinical report.



VarSeq Demonstration





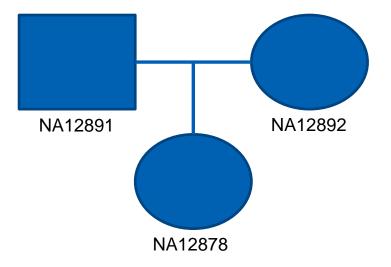


Trio Exome Analysis



From International HapMap Project

- BAM file from 1000 Genomes Phase 3 Illumina Exome Alignment
- Used Sentieon tools for variant calling.
- Mutations in the CTFR gene (cystic fibrosis) and BRCA1 gene (breast cancer)





VarSeq Demonstration





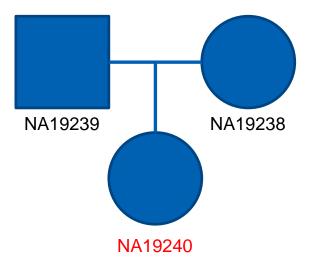


Single Exome Analysis



NA19240 from International HapMap Project – Yoruba in Ibadan, Nigeria

- BAM file from 1000 Genomes Phase 3 Illumina Exome Alignment
- Used Sentieon tools for variant calling.
- Has a mutation in the SMAD4 gene which is associated with Myrhe Syndrome.





VarSeq Demonstration









Questions or more info:

- Email info@goldenhelix.com
- Request an evaluation of the software at <u>www.goldenhelix.com</u>



