GOLDEN HELIX

Enabling Precision Medicine

Processing Hereditary Cancer Panels in VarSeq

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CIOReview

20 most promising Biotech Technology Providers

pharma TECH OUTLOOK

Top 10 Analytics Solution Providers

Gartner

Hype Cycle for Life sciences

Q & A

Please enter your questions into your GoToWebinar Panel

Golden Helix – Who We Are

Golden Helix is a global bioinformatics company founded in 1998.

GlaxoSmithKline

varSEQ®

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

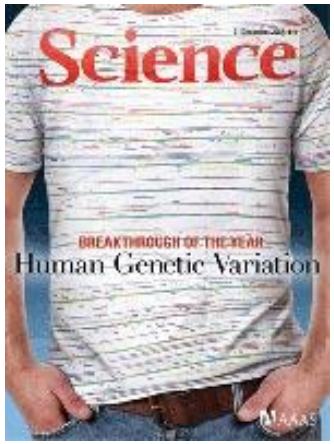
VARIANT WAREHOUSE

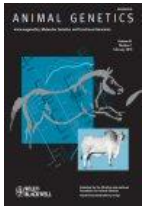
Variant Warehouse
Centralized Annotations
Hosted Reports
Sharing and Integration

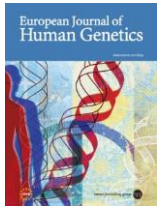
SNP & VARIATION SUITE

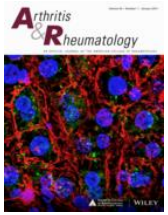
GWAS
Genomic Prediction
Large-N-Population Studies
RNA-Seq
Large-N CNV-Analysis

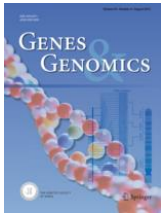
Cited in over 1200 peer-reviewed publications











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Over 350 customers globally

SickKids
THE HOSPITAL FOR SICK CHILDREN

Cincinnati Children's
Hospital Medical Center

The Children's Hospital of Philadelphia

Stanford University

UBC

Ucla

Yale

The Feinstein Institute for Medical Research
North Shore-Long Island Jewish Health System

North Shore LIJ

PREVENTION GENETICS
DISEASE PREVENTION THROUGH GENETIC TESTING

MAYO CLINIC

LINEAGEN

MOFFITT CANCER CENTER

Dartmouth-Hitchcock
NORRIS COTTON CANCER CENTER

BAYER

Lilly

abbvie

TEVA

GOLDEN HELIX
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NATIONAL CANCER INSTITUTE

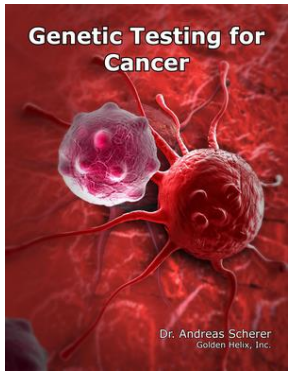
USDA
USDA Agricultural Research Service

FDA

Golden Helix – Who We Are

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

- REPUTATION
- TRUST
- EXPERIENCE



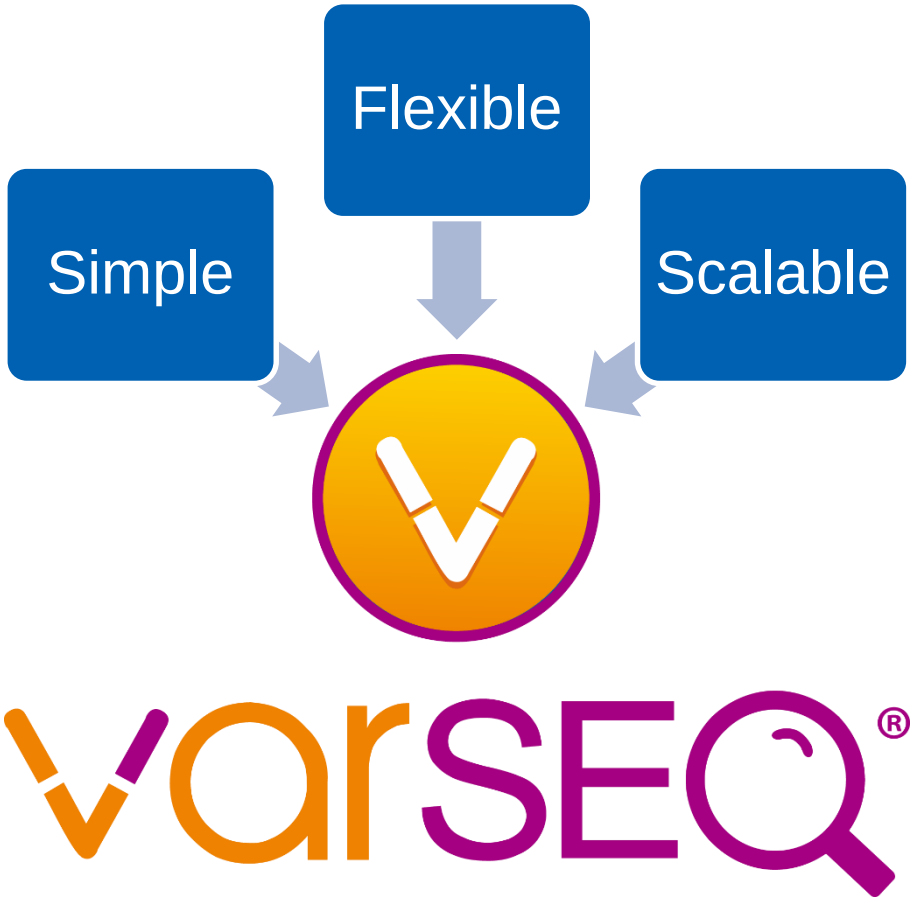
- INDUSTRY FOCUS
- THOUGHT LEADERSHIP
- COMMUNITY

- TRAINING
- SUPPORT
- RESPONSIVENESS

- INNOVATION and SPEED

PRODUCTS	BIOINFORMATICS PIPELINE	FUNCTION
DNAseq (Sentieon) TNseq (Sentieon) VS-CNV	FASTQ BAM VCF	▸ Single nucleotide variation ▸ Copy number variation & loss of heterozygosity ▸ Chromosomal aberration
Annotations	Annotated VCF	▸ Public & commercial annotations to enrich genomic data sets
VarSeq VSReports VSPipeline	Clinical Report	▸ Annotate & filter ▸ Visually inspect alignments ▸ Variant prioritization ▸ Clinical assessment
VSClinical	Automated ACMG Guidelines	▸ Clinical variant interpretation in concordance with ACMG Guidelines
VSWarehouse	Data Warehousing Web-Enabled Interface + Powerful API: JSON, XML, TSV, CSV, SQL, FHIR	▸ Clinical assessment catalog ▸ Advanced data querying ▸ Versioning ▸ Interoperability ▸ Compliance with HIPPA, CLIA & CAP data discovery

VarSeq Suite



- **Variant annotation, filtering, and interpretation**
- **Powerful GUI with rich visualizations**
- **Repeatable workflows + pipeline**

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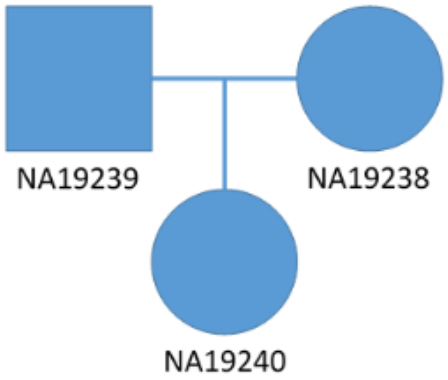
Goals for the Webcast

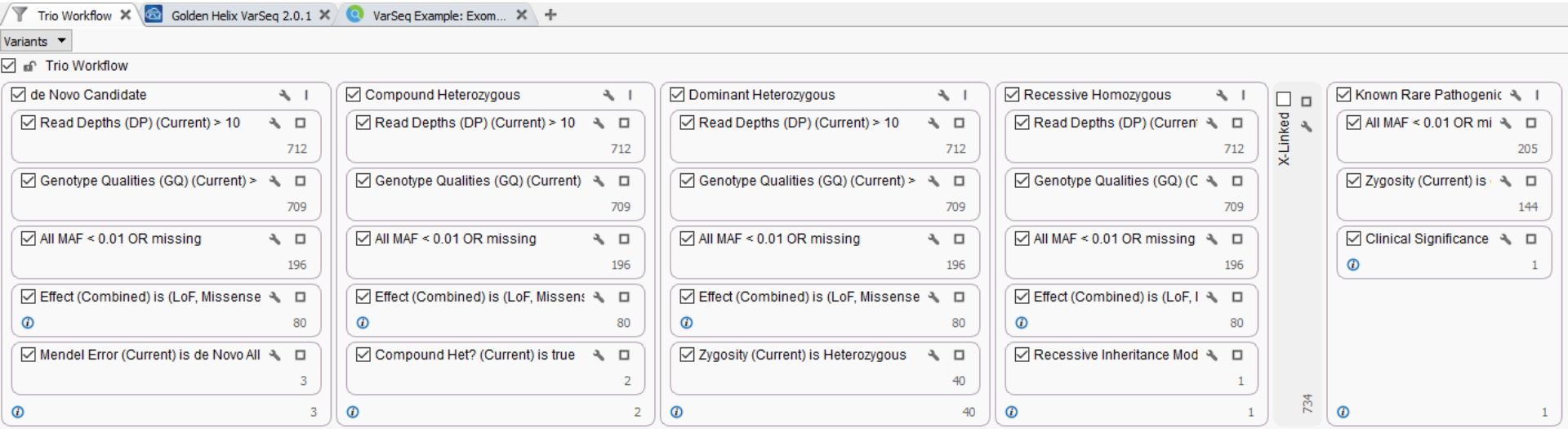
- **Building a project template**
  - **Focus on cancer panel**
  - **Target specific phenotypes/genes**
  - **Useful annotations**
- **Investigate interesting Variants**
  - **VSClinical/ACMG Guidelines – variant deep dive**
  - **Include variant in clinical report**
- **Save project as template**
  - **Demonstrate speed/efficiency of using template**
  - **Discuss other options for workflow efficiency**

Example Trio Project

- **Background – Public Data**
  - Yoruban Trio
    - Mother NA12938
    - Father - 39
    - Proband (female) - 40



- **Trio Analysis including**
  - De Novo Candidate
  - Dominant Heterozygous
  - Compound Heterozygous
  - Recessive Homozygous
  - X-Linked
  - Known Rare Pathogenic



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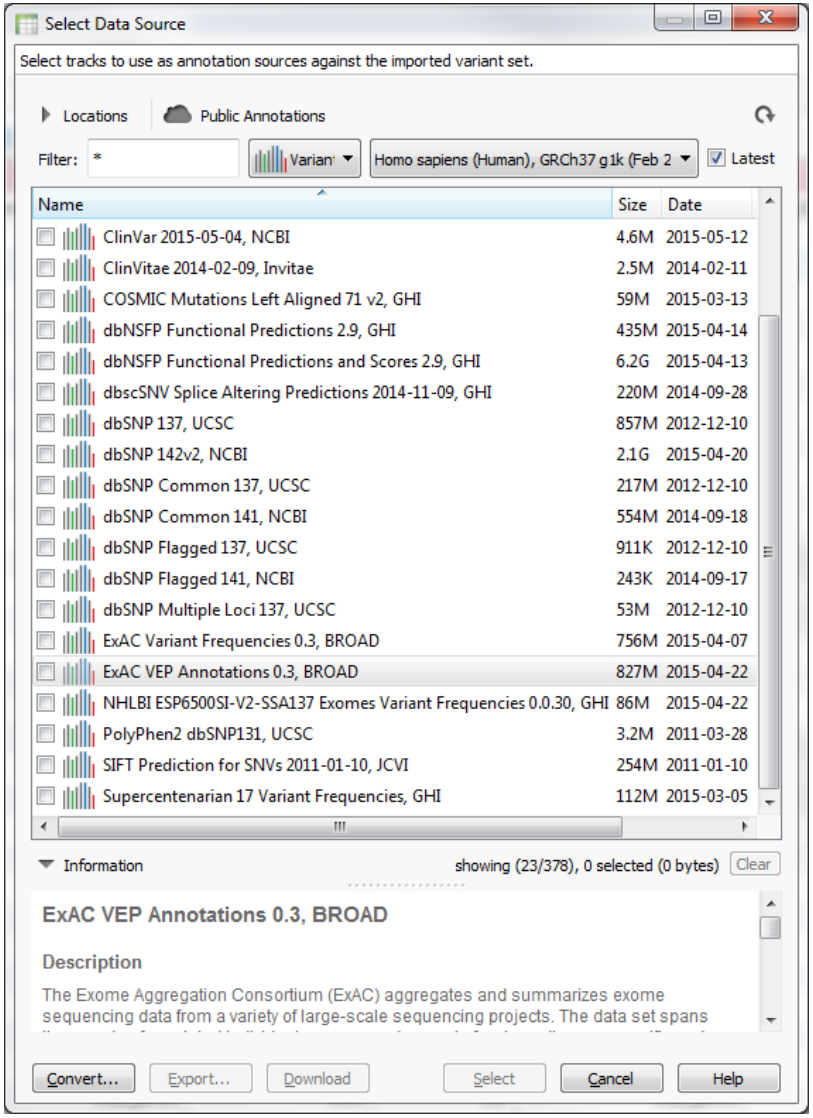
VarSeq Overview

- **Included Default Workflows**
  - **Trio Analysis including**
    - De Novo Candidate
    - Dominant Heterozygous
    - Compound Heterozygous
    - Recessive Homozygous
    - X-Linked
    - Known Rare Pathogenic
  - **Hereditary Gene Panel**
  - **Somatic Mutation Workflows**
    - Cancer Gene Panels
    - Tumor/Normal Pair Analysis
- **Example Projects**
  - Example TruSight Cardio Gene Panel
  - Example YRI Exome Trio Analysis
  - Example Tumor-Normal Pair Analysis

Data Curation of Annotation Sources

- **VarSeq is backed by an extensive list of curated public data sources**
  - 1kG Phase3 Variant Frequencies
  - ClinVar, NCBI
  - COSMIC
  - dbNSFP Functional Predictions
  - dbSNP
  - ExAC
  - RefSeq Genes, NCBI
  - ClinGen Dosage Sensitivity Mapping
- **Your workflows lock down specific versions**
- **Cloud Annotations:**
  - **OMIM** Genes, Phenotypes and Variants
  - **CADD**, tool for scoring deleteriousness of SNVs and Indels in the human genome.



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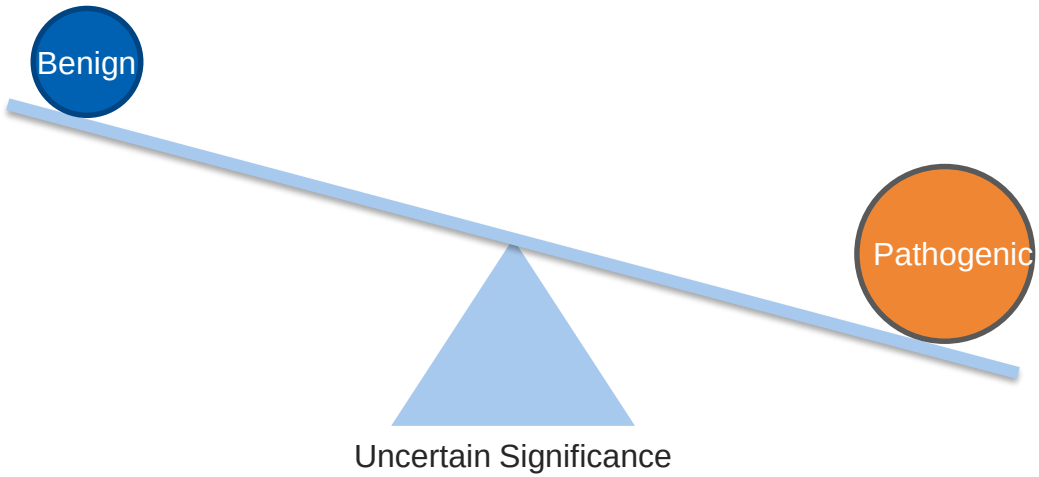
VS Clinical - Variant Interpretation

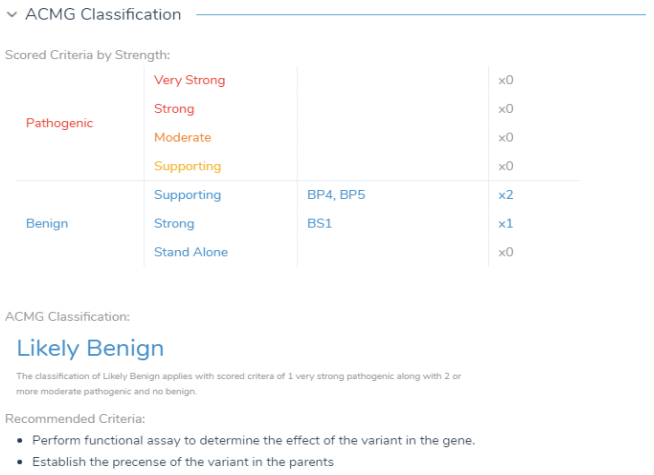
- **Evaluation of Evidence:**
  - Clinical presentation
  - Gene function
  - Bioinformatic evidence
  - Population frequencies
- **ACMG Guidelines:**
  - 33 criteria for evaluating evidence
  - 5 classifications from the scored criteria
  - Caveats and discussion about how to evaluate criteria in different context



VSClinical

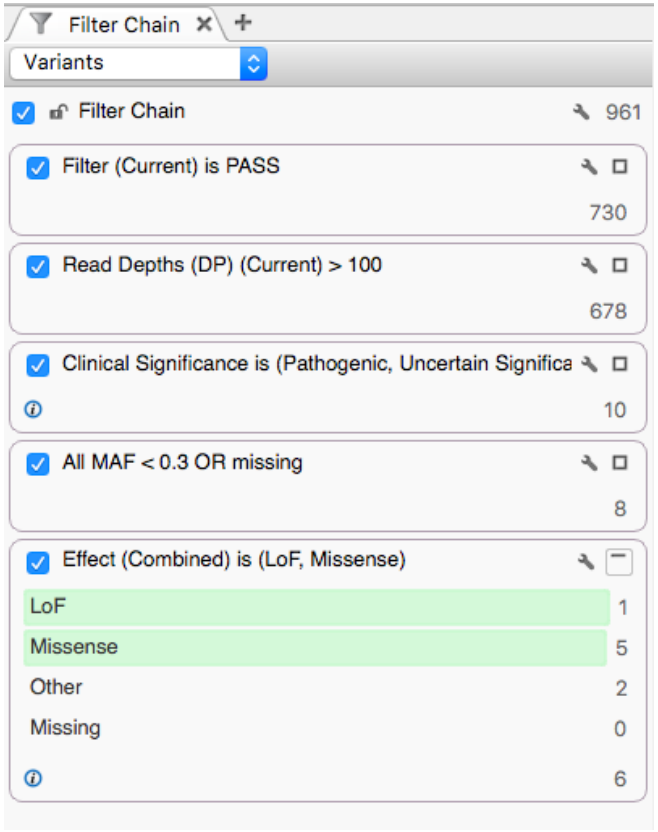
- **High level**
- **Consistent results**
  - Time irrelevant
  - No fatigue impact
- **Up to speed quickly**
- **Ramping up workforce**
- **We working on developments and you benefit**

VSClinical®



Analysis Workflow with VSClinical

1. **Follow your existing VarSeq annotation and filtering workflow**
2. **Add new ACMG Auto Classifier algorithm:**
   - Looks up if variant annotated in previous sample
   - Scores 18 criteria based on available evidence from 7 sources
3. **Select variants to evaluate using the ACMG Guidelines**
4. **Score and Finalize each variant, selecting which to report**
5. **Finalize the sample, review and report**



VSReports

- **Prepared "Templates"**
  - ACMG Standard Germline Report
  - Configurable Global Settings
    - Logo
    - Lab Information
    - Test Description / Disclaimers
- **Customizable Sample Inputs**
  - Patient Information
  - Test Results
- **Selected Variants Added**
  - Per-variant information
- **Customizable**
  - Default values are scriptable
  - Rendering is entirely programmatic

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Patient Information

Name	Gender	Date of Birth	Id
NA19240	Male	July 10, 2018	1234

Mother Information

Name	Date of Birth	Id
NA19238	July 10, 2018	1235

Father Information

Name	Date of Birth	Id
NA19239	July 10, 2018	1236

Reference Information

Physician	Identification Number	Institution
Case Id		

Sample Information

Sample Site	Sample Type	Collection Method	Collection Date	Receipt Date	Report Date
			July 10, 2018	July 10, 2018	July 10, 2018

Results - Positive

Mutations with an established link detected.

Primary Findings

Gene	Exon	Variant	Zygosity	Pathogenicity
SMAD4	12	NM_005359.5:c.1498A>G (NP_005350.1:p.Ile500Val)	Heterozygous	Pathogenic

Affected Genes

SMAD4 (1)

Interpretation Summary

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VSPipeline - High throughput

- **Command-line interface that automates pipelines and workflows**
- **Build template in VarSeq then automate with VSpipeline**

UP-TO-DATE ANNOTATIONS

POWER AND FLEXIBILITY FOR HIGH THROUGHPUT ENVIRONMENTS

REPEATABLE CLINICAL WORKFLOWS

BUILT FOR CLINICAL SETTINGS

VarSeq Demonstration

Q & A

Please enter your questions into your GoToWebinar Panel

20th Anniversary License Specials

20-month license for the price of a 12-month license

- (~~2~~ 1 left) SVS License *1 user - $2,995*
- (~~3~~ 1 left) VarSeq License *1 user - $4,795*
- (1) VarSeq License (w/ VSReports & VS-CNV) *1 user - $12K*
- (~~3~~ 1 left) VSClinical License (w/ VarSeq, VSReports, CADD & OMIM) *1 user - $12K*
- (2) VSClinical & VS-CNV License (Small Lab Starter) *2 user - $24K*
- (2) VarSeq, VS-Reports, VS-CNV, Tier 1 Sentieon (1 users) *$17.5K*
- (~~3~~ 2 left) Sentieon Tier 2 License - *$10K*
- (2) Small Warehouse License (VS-CNV, VSClinical, Sentieon Tier 1, VSReports, VSPipeline) *2 user - $48K*
- ~~(1) Warehouse License (VS-CNV, VSClinical, Sentieon Tier 1, VSReports, VSPipeline) *Up to 10 users - $120K*~~
- ~~(1) SVS Server License with Imputation *2 user - $7,995*~~

These offers will expire on September 15, 2018

Q & A

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