



Authoring Clinical Reports in VarSeq

September 23, 2015

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VP Product & Engineering



1 Clinical NGS Testing Workflows

2 One Click Clinical Reporting

3 VarSeq: Clinical NGS Testing Platform

4 VSPipeline & VarSeq Viewer

Golden Helix – Who We Are



Golden Helix is a global bioinformatics company founded in 1998.



We are cited in over 900 peer-reviewed publications



Our Customers



Over 200 organizations world wide, and thousands of users, trust our software.



Stanford University



MAYO CLINIC



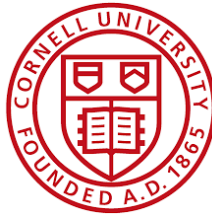
Cincinnati Children's
Hospital Medical Center



CEDARS-SINAI



BabyGenes



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



THE STATE UNIVERSITY OF NEW JERSEY
RUTGERS



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SCHOOL of MEDICINE



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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

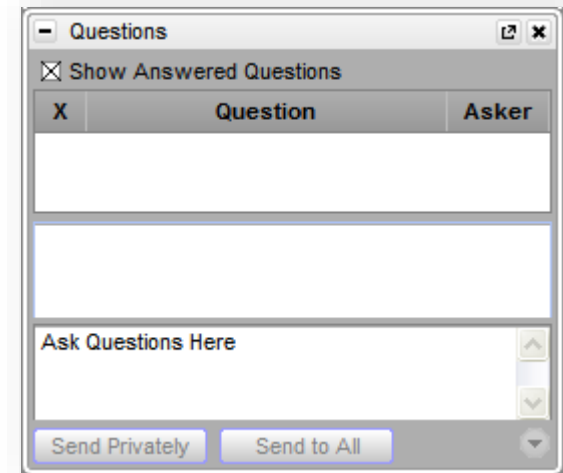


- TRANSPARENCY
- INNOVATION and SPEED
- CUSTOMIZATIONS



Questions during the presentation

Use the Questions pane in your GoToWebinar window





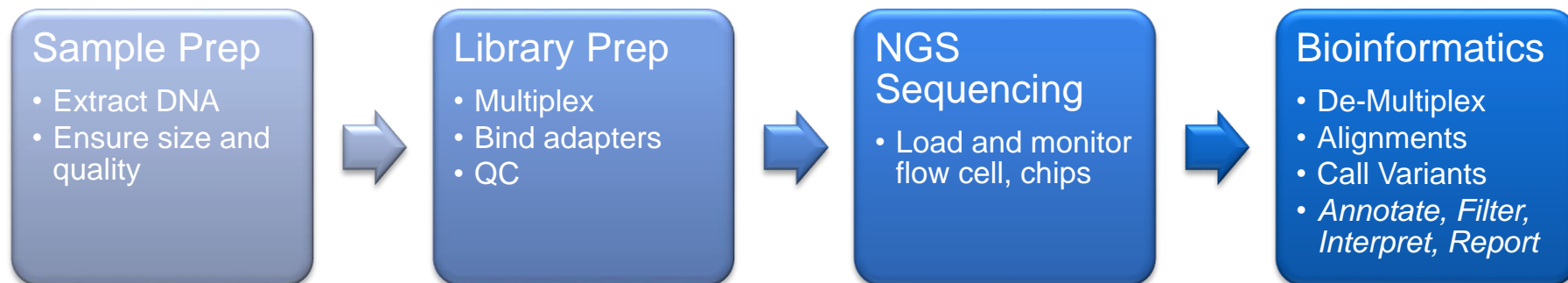
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Clinical Gene Panel Tests



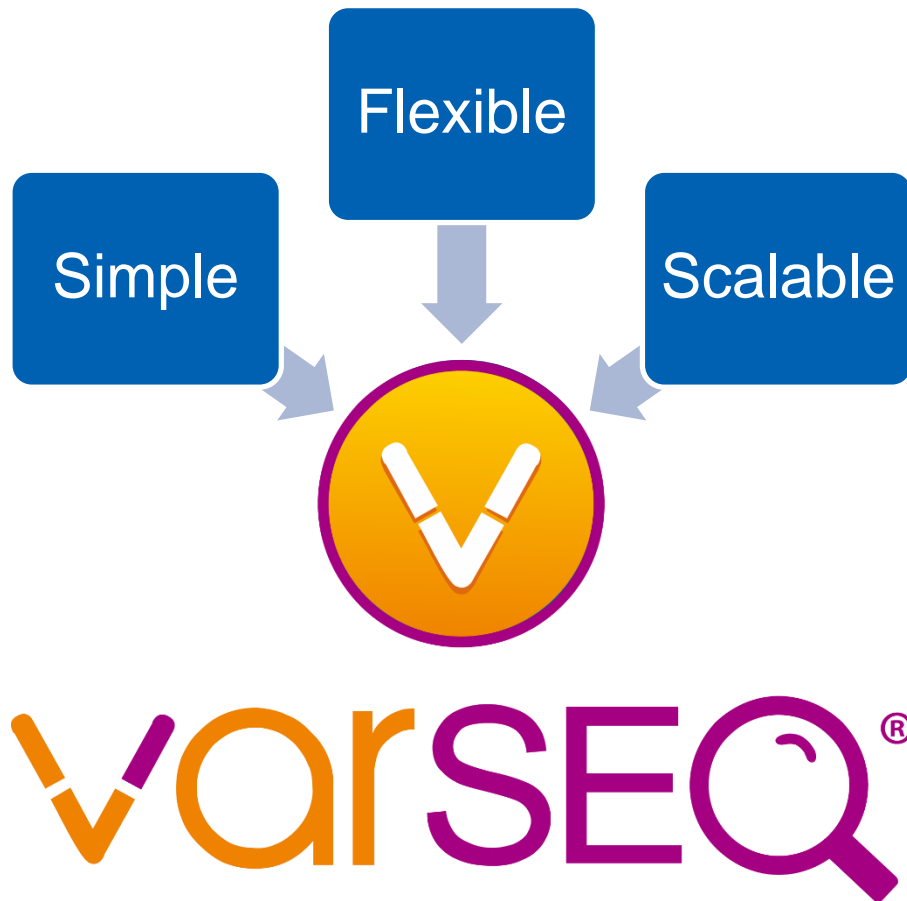
Annotate, Filter, Interpret, Report

- QC variants and target regions
- Annotations current & accurate
- Visualize NGS alignment, context
- Capture variant assessments, results
- Export captured and computed data

Economics

- Human hands-on-time most variable
- Lab tech and MD time highly valued
- Some analytics can be automated
- Interpretation platform optimizes for:
 - Efficient interpretation
 - Integrated with lab workflow

What is VarSeq?



- Variant annotation, filtering and interpretation
- Repeatable workflows
- Rich visualizations with GenomeBrowse built-in
- Powerful GUI and command-line interfaces



VarSeq

- Gene panel testing
- Whole exome and whole genome analysis
- Cancer diagnostics
- Repeatable workflows
- Coverage statistics
- Multiple sample support
- Variant assessment database

VSPipeline

- Command line runner
- Integrate with your current bioinformatics pipeline
- Create repeatable clinical workflows for CLIA and CAP certified analysis
- Supports high throughput scenarios

VSReports

- Tertiary analysis to report in **one click**
- Focused and actionable data
- Modeled on ACMG guidelines
- Hereditary and cancer templates
- OMIM included



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varSEQTM

[Demonstration]



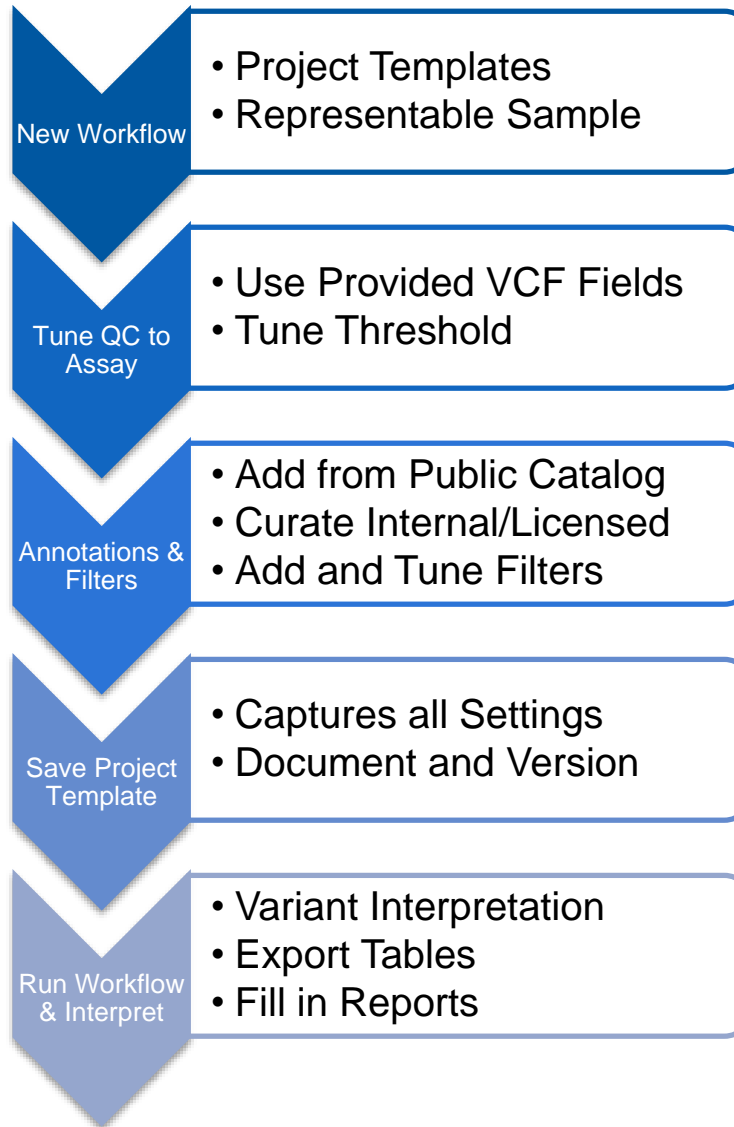
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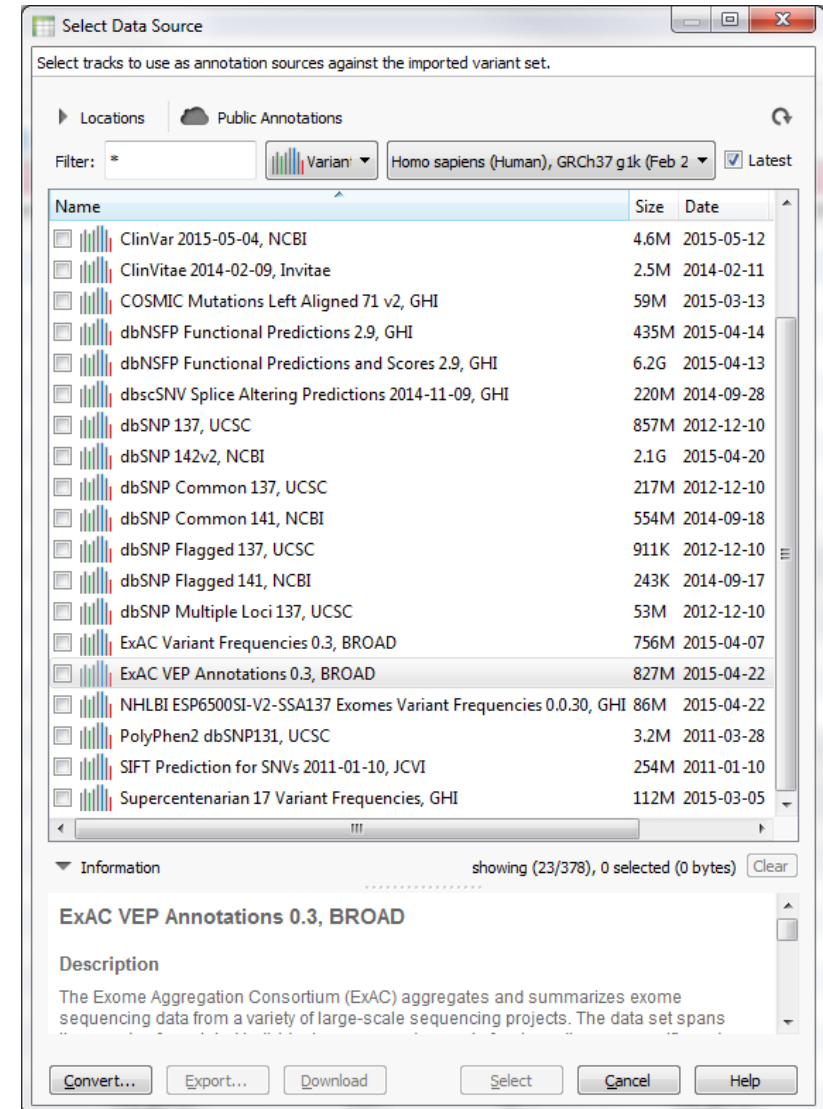
Setting up a Clinical Test with VarSeq



Data Curation of Annotation Sources



- **OMIM – Variant, Gene and Phenotype**
 - Bundled with Clinical Reports
 - Updated monthly
 - Rich integration of hyperlinks, references
- **VarSeq is backed by an extensive list of curated data sources**
 - 1kG Phase3 Variant Frequencies
 - ClinVar, NCBI
 - ClinVitae, Invitae
 - COSMIC
 - dbNSFP Functional Predictions
 - dbSNP
 - ExAC
 - RefSeq Genes, NCBI
 - Supercentenarian 17 Variant Frequencies
- **Your workflows lock down specific versions**



Workflows: What is it Capturing and How?



■ Save as Template

- Import Settings
- Annotations and Algorithms
- Filters (can be locked)
- View choices (Reports, Browser etc)

■ Create New Projects

- Shipped “starter” templates
- Your custom template


■ Automated and Logged

- Log contains what, when, whom
- Prompts to download missing sources

ACMG Template			
Log			
All			
Time	User	Event	Detail
2015-09-22 12:41 pm	rudy@goldenhelix.com	Report Saved	Report Details <ul style="list-style-type: none">• Template: Cardio Gene Panel Report• Sample: NA12877_Rep1
2015-09-22 12:34 pm	rudy@goldenhelix.com	Task Finished	<p>Variants in dbscSNV Splice Altering Predictions 2014-11-09, GHI completed successfully in about 2 minutes.</p> Annotation Source Details <ul style="list-style-type: none">• Name: dbscSNV Splice Altering Predictions 2014-11-09, GHI• File: dbscSNVSpliceAlteringPredictions2014-11-09-GHI_2014-11-09_GRCh_37_Homo_sapiens.tsf• Location: C:\Users\grudy\AppData\Local\Golden Helix\Common Data\Annotations• Features: 15,030,435• Curated: 2014-09-28• Series: dbscSNV• Version: 2014-11-09• UUID: {0bed8de2-06d9-4fba-b5a1-3e2cc5d5662e}



- **Customize a “Report Template”**
 - ACMG Standard Germline Report
 - Configurable Global Settings
 - Logo
 - Lab Information
 - Test Description / Disclaimers
- **Customizable Sample Inputs**
 - Patient Information
 - Test Results
- **Select Variants to Include**
 - Per-variant classification
 - Interpretation prefilled from project data
- **Customizable**



Molecular Golden Genetics Inc.
 214 Enterprise Blvd
 Bozeman, 12345-6789
 Phone: 123-456-7890
 Fax: 123-456-7891

Reference Information

Physician	Dr. Jane Smith
Institution	Any Town General
Case Id	ABC123345

Patient Information

Name	L1207497
Gender	Male
Date of Birth	8/25/15
Id	1234

Sample Information

Sample Site	Blood	Avg. Read Depth	1500x
Sample Type	Blood	Collection Date	8/25/15
Collection Method	Peripheral Draw	Receipt Date	8/25/15
Panel Coverage	98%		

Results

Positive An established cause of the Phenotype was found.

Genetic Variants
No variants specified

Interpretation Summary
Recommendations

Individual Variant Interpretations
No variants specified

Background
 The Pan Cardiomyopathy Panel sequences 46 genes associated with various forms of cardiomyopathy (HCM, DCM, ARVC and LVNC). Cardiomyopathy is typically inherited in an autosomal dominant pattern, though some genes are X-linked. For information regarding the clinical presentation or genetics of a specific type of cardiomyopathy, please visit our website.

Method



varSEQ™

[Demonstration]



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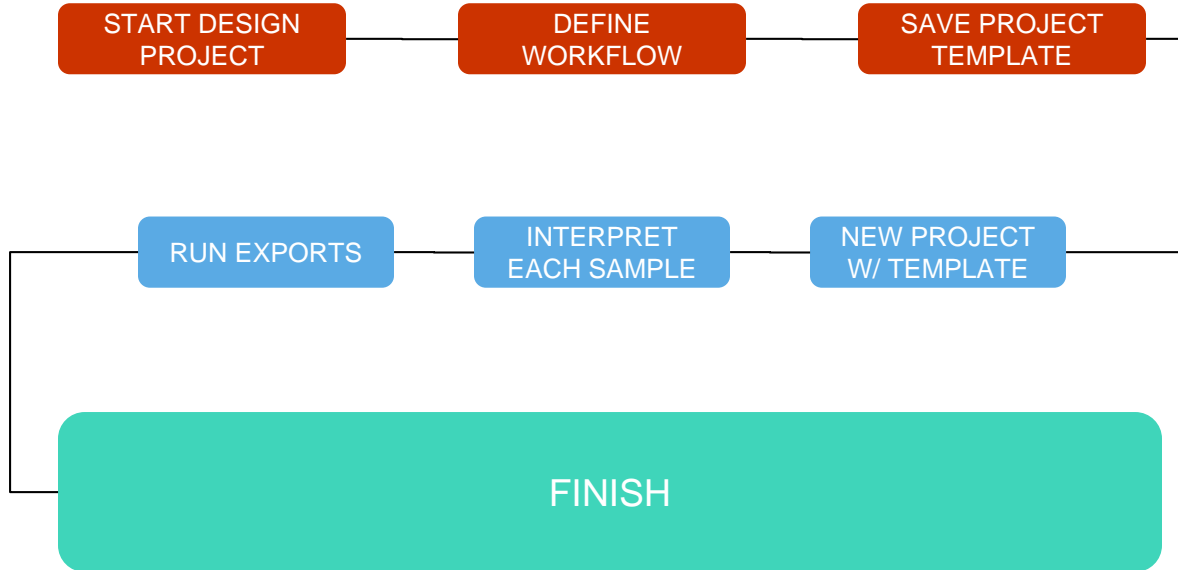
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Batch Analysis Workflow



Define a Workflow that is Repeated for “Batches” of Samples



- Steps in **RED** are done once when designing a new workflow to be tuned to the upstream pipeline and test thresholds
- Steps in **BLUE** are done for each sample or set of samples that should repeat the workflow
- Steps in **BLUE** can be automated with **VSPipeline**

VSPipeline: High Throughput, Automated



■ Produce Automated “Deliverables”

- Filtered and annotated variant lists
- Exported to Excel, VCF, Text
- VarSeq Projects (openable by VarSeq, VarSeq Viewer)

■ Deploy a Project Template

- Support validation (like CAP/CLIA)
- All steps logged

■ Integrated

- Run as part of pipeline that produces BAM/VCF files.

■ Works with VSReports!

```
grudy@LinServerDev:~/scratch$ vspipeline -c batch file=panel_workflow.vsbatch
Loading...
Importing variants...
[0%] Starting...
[0%] Preparing source reader
[0%] Writing new file
[0%] Writing new file
[0%] Writing new file
[0%] Writing new file
[0%] Writing new file
[0%] Writing new file
[0%] Writing new file
[0%] Writing new file
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[0%] Writing new file
[0%] Writing new file
[0%] Writing new file
[0%] Writing new file
[0%] Writing new file
[0%] Writing new file
[15%] Writing new file - About 10 Seconds remaining
[16%] Writing new file - About 10 Seconds remaining
[22%] Writing new file - About 10 Seconds remaining
[27%] Writing new file - About 10 Seconds remaining
[29%] Writing new file - About 10 Seconds remaining
[34%] Writing new file - About 10 Seconds remaining
[35%] Writing new file - About 10 Seconds remaining
[40%] Writing new file - Less than 10 Seconds remaining
[43%] Writing new file - Less than 10 Seconds remaining
[45%] Writing new file - Less than 10 Seconds remaining
```

Available Now: VarSeq Viewer



FREE Reader of VarSeq Projects

VIEW FILTERED

View tables
Investigate results



VISUALIZE

GenomeBrowse
BAM and VCF
Save Screenshots



EXPORT

Excel Rich Reports
Text and VCF



SHARE

Relocatable Projects
Efficient Storage
Anybody can Open



VarSeq projects are a perfect preservation of an analysis, and can be opened at any time with the FREE VarSeq Viewer.

VarSeq Viewer is VarSeq without an active subscription license. It can be downloaded by anyone at anytime.



Questions or more info:

- Email info@goldenhelix.com
- Request an evaluation of the software at www.goldenhelix.com





Questions?

Use the Questions pane in
your GoToWebinar window

