Introducing VarSeq:
Variant Discovery & Gene Panels Made Easy

Gabe Rudy with intro from Andreas Scherer
October 1, 2014
We are building the MRI for the genome!

The analysis of genomic data and the prediction of outcomes reshapes the way we diagnose disorders, predict outcomes and select the best possible care options for a patient.
Thousands of Users in Research and Translational Labs

Hundreds of Customers Across the Globe

Over 850 Citations
### Genetics Adoption Curve

<table>
<thead>
<tr>
<th>Early Stage</th>
<th>Moderate Adoption</th>
<th>High Adoption</th>
</tr>
</thead>
<tbody>
<tr>
<td>Market focus is on science and research, lack of infrastructure, clinical evidence and physician education.</td>
<td>Clinical genetic standard for selected targets and therapeutic areas. Bioinformatics increasingly crucial for diagnosis and treatment selection.</td>
<td>Greater availability of data around testing with genetic services becoming standard of care for a majority of patients.</td>
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</tbody>
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<thead>
<tr>
<th>Regulatory Landscape</th>
<th>Reimbursement</th>
<th>Bioinformatics</th>
</tr>
</thead>
<tbody>
<tr>
<td>Testing Technology</td>
<td>Physician Adoption</td>
<td>Consumer Demand</td>
</tr>
</tbody>
</table>
Introducing VarSeq:
Variant Discovery & Gene Panels Made Easy

Gabe Rudy
VP of Product Development
October 1, 2014
Agenda

1. Roots of VarSeq
2. Demo
3. What’s Next at Golden Helix
4. Questions
Questions During the Presentation

Use the Questions pane in your GoToWebinar window
Built on Strength

- Experience empowering users to solve hard problems
- Tight feedback loop with users and stakeholders
- Support users with licensing models aligned with customer interests
- Evolve and share core technologies across products
Showing not Telling

Flexible

Simple

Scalable
Simple

- Get started easily
- Utilize pre-built best practice workflows
- Analyze samples in batches
- Focus workspaces to accelerate sample turn-around
[Demonstration]
Showing not Telling

Flexible

Simple

Scalable
Flexible

- Drilldown with context
- Annotate from extensive library of public databases
- Filter on any field of a data source
- Visualize sample and public data with GenomeBrowse
- Arrange quadrants to support multiple vantage points
- Document insights with supporting evidence
Showing not Telling

Flexible

Simple

Scalable
Scalable

- Analyze millions of variants
- Investigate multiple hypotheses in tandem
- Validate robustness of filtering thresholds
- Export results to VCF, text, and multi-tab Excel files
[Demonstration]
Acknowledgements

- Stakeholders
  - Jason Byars
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  - Sam Strom
  - Jeff Moore
  - Jeff Rosenfeld
  - Scott Ness
October

Announcement
End of 2014

Commercially Available

Golden Helix gives back

GWAS

Dr. Andreas Scherer
Golden Helix, Inc.
Q1 of 2015

More features and capabilities

Release of 8.3:
More Genomic Prediction,
More Methods to Study Complex Diseases

Molecular Med
TRI-CON 2015

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Golden Helix
Accelerating the Quest for Significance™
Do You Have Any Questions?

Use the Questions pane in your GoToWebinar window