

Application Note

Flexible Lab and Data Management for the Applied Biosystems SOLiD™ Next Generation Sequencing System

The Applied Biosystems SOLiD™ system is revolutionizing genetic analysis. Its massively parallel sequencing of clonally-amplified DNA fragments provides accurate, high-throughput results for growing applications in transcriptomics, epigenomics, and whole genome and targeted resequencing, all in one platform.

The SOLiD™ technology can swamp existing lab systems. With the explosion of data and flexible experimental workflows, changes in the lab operations and informatics are not small. GenoLogics has the capability to address these challenges with Geneus through flexible configuration. Geneus centrally manages data, activities and results across the workflow and provides the right level of tracking and information access. With Geneus, results come easier for collaborators, managers, technicians and bioinformaticians.

The screenshot displays the Geneus software interface, which is used for managing sample preparation and sequencing workflows. It features several panels:

- Submit Samples:** A table listing samples with columns for Name, ID, Status, and Project. Samples include Brain-1001, Brain-1002, Brain-1003, Brain-1004, Brain-1005, and Brain-1006, all with a 'Received' status and 'Brain (Tapihan SHP)' project.
- Manage Sample Preparation:** A detailed view of a sample's preparation process, including fields for Tissue Type, Sample Group, Parent 1, Date Collected, Model Organism, Biological Source ID, and Dose.
- Workflow Hierarchy:** A tree view showing the sequence of steps: ERF-GroupA, QC Isolated DNA, DNA Gel Image, DNA QC File, ERF-GroupA Validated, Prepare Library, Library Gel Image, ERF-GroupA Prepared, Amplify ePCR, SOLiD Bead Conc., ERF-GroupA Library, SOLiD WFA, WFA Run Definition, WFA Report, ERF-GroupA Slide, SOLiD Sequencing, Analysis Link, and Analyze SNPs DiBayes.
- Bottom Navigation:** Buttons for 'View Sample Annotations', 'Automate Pipelines', and 'Results'.

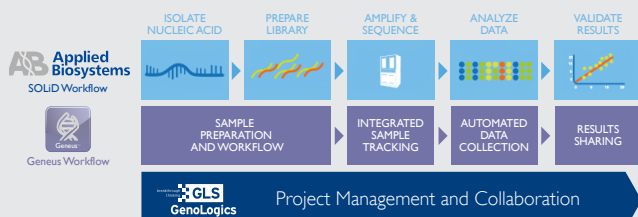
Why Integrate SOLiD™ Lab and Data Management?

- Streamline communications with centrally accessible information
- Increase quality with sample traceability
- Optimize lab operations with centralized workflows and tasks

Why use Geneus™ with SOLiD™ Workflows?

- Flexible configuration to support rapidly changes systems
- End-to-End tracking from submissions, to lab work and analysis results
- Integrate with in-house or commercial QC and data analysis tools
- Broad omics technology support including NGS, Microarray and real-time PCR

End-to-end next generation sequencing sample and data genealogy

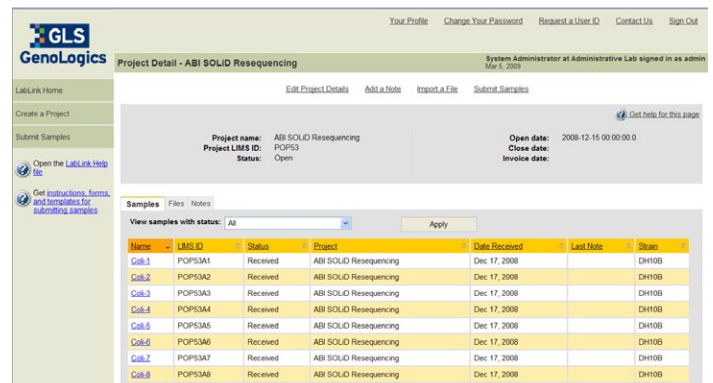


Genueus end-to-end data management for ABI SOLiD™ sequencing

To illustrate the application of Geneus lab and data management, a six step SOLiD™ next generation sequencing workflow process is outlined.

1. Electronic Sample Submission

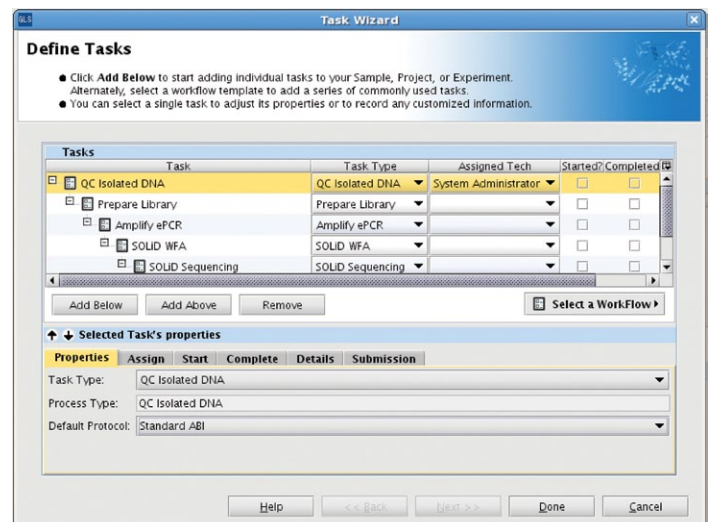
The collaborator submits sample annotations electronically through the Geneus web interface. All clinical, project, and sample information for next generation sequencing sample submission is entered into a customized form. Once the samples are submitted by the collaborator the sample information can be viewed in the Geneus lab client.



Submit and request samples with a secure online interface

2. Workflow Management

The lab manager opens the Geneus client and sees that new samples have been submitted, and that resequencing is needed. The samples are assigned to a resequencing workflow and steps are assigned to specific lab researchers, who will process the samples. The samples are automatically moved to the next step in the workflow as each step is performed. Geneus automatically provides work status visibility by tracking where the samples are throughout the workflow.



3. Sample and Library Preparation

The sample and library preparation is broken down into several steps. The first step of the resequencing workflow is sample and library preparation. As the lab researcher prepares to do this step, the required sample information (i.e. sample concentration, volume, etc.) is available in Geneus. The lab researcher performs sample preparation (DNA fragmentation) and then prepares the library according to the ABI resequencing protocol that is attached to the process and printed from Geneus. The final step of library preparation is amplification. After amplification the library passes quality control and is placed on the slide for sequencing. As the sample and library preparation is performed, the lab researcher can enter reagent lot numbers, notes and other information required from this step into user-configured fields in Geneus. Once the preparation is complete the samples in Geneus are moved to the next step of the workflow.

4. Sample and Library QC

The lab researcher determines DNA quality and quantity by measuring the absorbance (260/280nm ratio) on a UV spectrophotometer and runs a PAGE gel. The UV results are uploaded and stored into Geneus and the gel image is attached. The lab researcher views the 260/280 ratios in Geneus and flags the samples pass/fail.

ABI Library QC and Quantitation Wizard

Specify QC Flag, Volume and Concentration

- Select samples you would like to adjust on the Inputs or Outputs tabs. To select all the samples, click Ctrl-A.
- Specify whether you would like to automatically calculate the values.
- Enter the desired values and click Apply.

Automatically calculate volume or concentration: ☒ None ☐ Volume ☐ Concentration

New volume: 5 μ L Apply to Selection Apply to All

New concentration: 5 μ g / mL Apply to Selection Apply to All

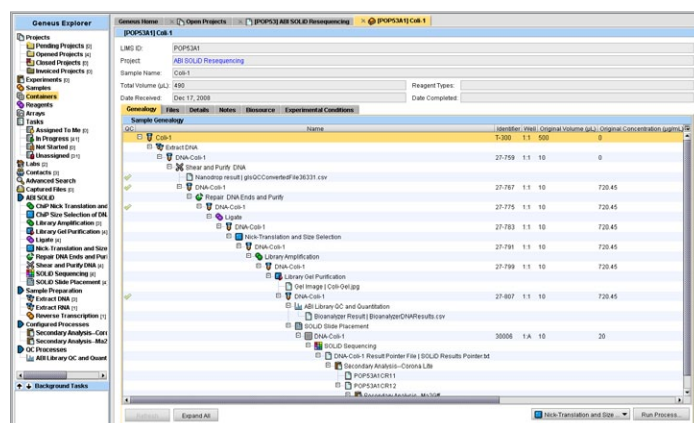
New QC Flag: Apply to Selection Apply to All

Input QC	Name	LIMS ID	Container Placement	Original Volume (μ L)	Original Conc. (μ g/mL)	New Volume (μ L)	New Conc. (μ g/mL)
<input checked="" type="checkbox"/>	Coli-1	POP53A1PA1	T-300 [1:1]	500	0	490	0
<input checked="" type="checkbox"/>	Coli-2	POP53A2PA1	T-301 [1:1]	500	0	490	0
<input checked="" type="checkbox"/>	Coli-3	POP53A3PA1	T-302 [1:1]	500	0	490	0
<input checked="" type="checkbox"/>	Coli-4	POP53A4PA1	T-303 [1:1]	500	0	490	0
<input checked="" type="checkbox"/>	Coli-5	POP53A5PA1	T-304 [1:1]	500	0	490	0
<input checked="" type="checkbox"/>	Coli-6	POP53A6PA1	T-305 [1:1]	500	0	490	0
<input checked="" type="checkbox"/>	Coli-7	POP53A7PA1	T-306 [1:1]	500	0	490	0
<input checked="" type="checkbox"/>	Coli-8	POP53A8PA1	T-307 [1:1]	500	0	490	0

Help << Back Next >> Done Cancel

5. Data Pipeline and Analysis

The Geneus automated informatics module connects command-line driven algorithms to form a data pipeline. The flexible design allows data pipelines to be easily modified to accommodate new algorithms or for new pipelines



to be defined for different applications or instruments. Bioinformaticians are now enabled to spend more of their time on analysis and developing new algorithms.

In this workflow example, once the sequencing run is complete, a Geneus script automatically writes a file, called a pointer file, indicating the location of the results. The data pipeline can easily be modified to plug-in a different alignment algorithm or to include subsequent analysis steps.

Within Geneus, the lab manager, researcher and bioinformatician can all see when the final step is complete and the history of what has happened, including the data produced at each step. After the data pipeline is completed, a file at each step indicates where the data is located, what data analysis steps were performed and the parameters used for analysis, thereby providing a historical record of the workflow.

From a single view of the sample genealogy, the researcher, lab manager and bioinformatician can easily view the project, sample or clinical information. This enables all members of the team to have easy access to sample and clinical information while maintaining the association between this information and the next generation sequencing results. Furthermore, sample QC data can easily be retrieved if questions regarding data quality arise during analysis.

6. Delivering Results and Publishing Reports

Finally, analyzed results can be packaged and provided to the researcher. Geneus can generate customized billing, operational and scientific results reports, which can be published to the Geneus web interface and easily accessed by collaborators or customers.

Conclusion

Research teams incorporate workflow management because well structured and accessible information accelerates their work. This means finding details, right down to sample records, becomes simple. Geneus ensures sample traceability and improves lab operation efficiency by being flexible: allowing the level of structure and detail be to configured to the appropriate level for the laboratory. With that right level of well structured and accessible end-to-end information, Geneus enables the multitude of people, projects, and platforms used in next generation sequencing labs today.

About GenoLogics

Breakthrough Informatics Solutions for Translational Research

GenoLogics is the leading provider of informatics solutions for translational research, covering both the clinical and research domains. Our vision is to catalyze life sciences research with a collaborative data management software platform, advancing the early detection, prevention and treatment of disease.

GenoLogics works with a wide range of prominent customers at academic institutions, research institutes and pharmaceutical and biotechnology facilities across North America and Europe. Customer solutions range from implementing a data management system for a genomics or proteomics lab to deploying an enterprise system across multiple facilities and sciences to enable translational research or systems biology initiatives. To provide our customers with integrated end-to-end solutions, GenoLogics also partners with best-in-class instrument and software vendors.

GenoLogics works closely with its customers in a collaborative approach to ensure solutions are deployed that increase productivity, streamline lab operations and accelerate scientific results.

For more information on GenoLogics or to request a demonstration, please contact us:



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