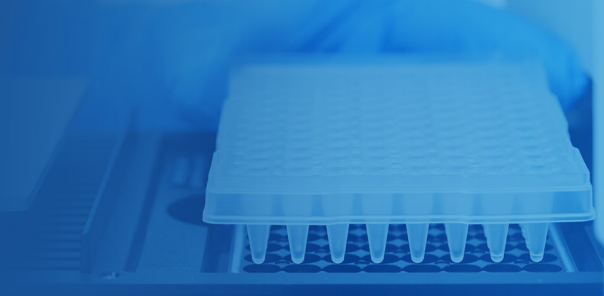


Enhanced sample tracking boosts genotyping throughput



CUSTOMER STORY

Partially filled plates reduce qPCR throughput

A large biopharmaceutical company uses genetically engineered mice to model disease states. Its team of scientists performs quantitative polymerase chain reaction (qPCR) to verify the genomic modification in each mouse pup.

The team receives tail snips in 96-well plates, usually 40 per plate. DNA is purified from these samples, mixed with reagents, and analyzed on a qPCR instrument (Figure 1). Two factors complicate sample preparation: (1) several intermediate plates are generated in the process and (2) each genetic modification requires a unique set of probes for detection.

To simplify sample tracking throughout the workflow, the scientists process and analyze samples in batches that match the original source plate (i.e., the same number and arrangement of samples). The barcode on the source plate is reused in all downstream microplates, including the final qPCR assay plate.

Because most wells in the source plate are empty, scientists generate partially filled plates during sample preparation. Assay throughput is 40 percent of capacity. Combining samples from different source plates would require well-by-well tracking, which is too slow and error prone to do manually.

Automated records for well-by-well tracking

The Tetra Scientific Data Cloud allows per-well tracking by automatically assembling raw scientific data and instrument log files from multiple sources and engineering them into harmonized records for every well (Figure 2). Fully automated pipelines create a genealogy that details the complete history of each sample from source plate to genotyping results. The final records are sent to a laboratory information management system (LIMS).

Higher throughput and richer data

The new workflow enabled scientists to easily combine samples from different source plates to create full qPCR plates. Assay throughput has now increased by roughly 33 percent and is projected to increase by 150 percent in the near future once all pending process changes are implemented. The team expects to analyze over 500,000 samples per year.

The Tetra-enabled solution also generates higher-quality, future-proof data. The Tetra Scientific Data Cloud enriches the qPCR results with metadata, adding scientific context and facilitating sample traceability.

AI readiness

The Tetra Scientific Data Cloud converts raw scientific data—including instrument logs and qPCR results—into large-scale, liquid, purpose-engineered, and compliant data. These data sets are optimized for AI, empowering biopharmaceutical companies to gain AI-driven insights from its genotyping data.

Challenge:

A top 20 biopharma company operates its qPCR-based genotyping workflow at 40% capacity due to limitations in sample tracking.

Solution:

The Tetra Scientific Data Cloud enables per-well sample tracking by replatforming and engineering scientific data.

Result:

33% increase in genotyping throughput so far; expected to increase by 150% total soon.

Learn more

To learn additional ways the Tetra Scientific Data Cloud can help leading biopharmas achieve AI insights, visit tetrascience.com.

tetrascience.com

Figure 1. Initial workflow

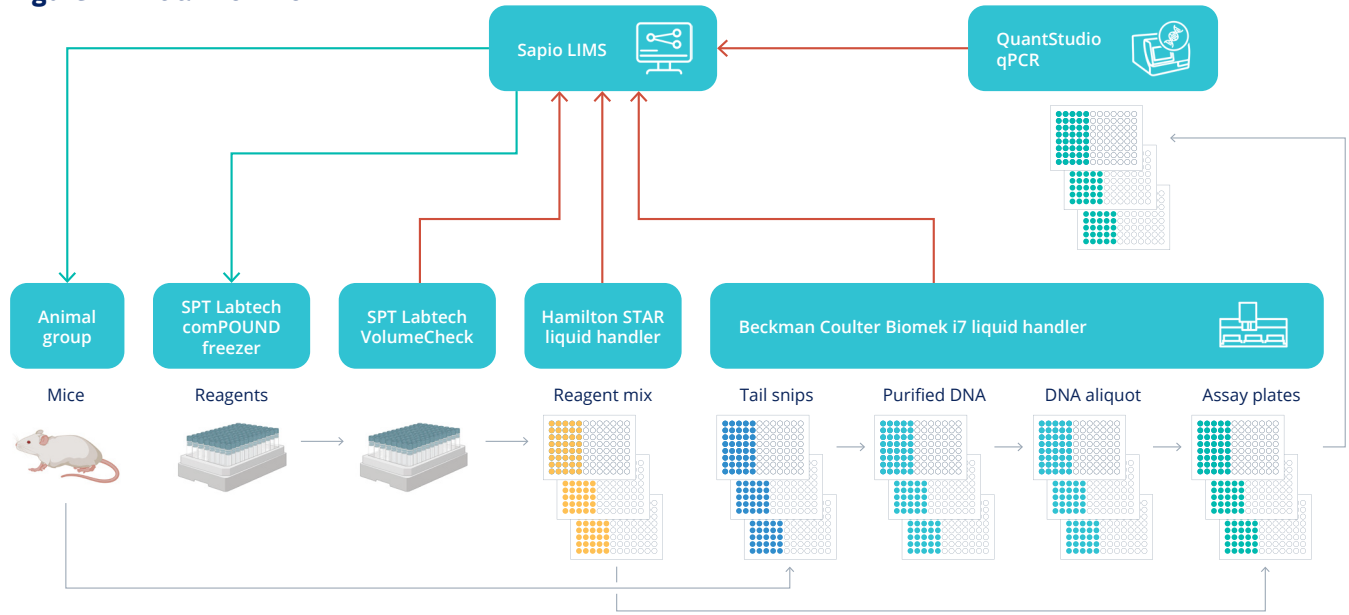
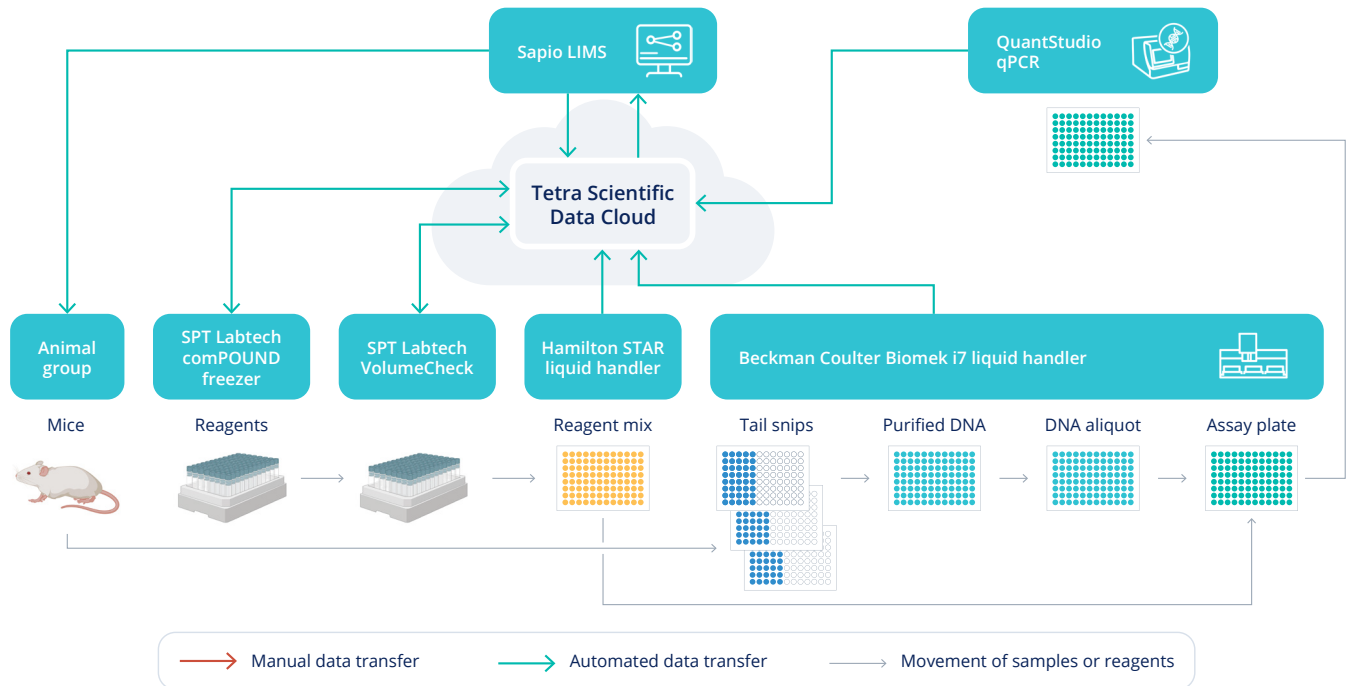


Figure 2. Tetra workflow



The Tetra Scientific Data Cloud integrates with the following systems.

- **Sapio LIMS:** tracks all microplates, tubes, and associated metadata used in lab workflows—including sample volume, location, and parent-child relationships of samples
- **SPT Labtech comPOUND automated freezer:** stores the tubes of qPCR reagents, including gene-specific probes
- **SPT Labtech VolumeCheck:** detects liquid volumes in tubes
- **Hamilton Microlab STAR liquid handler:** prepares the master mix of reagents
- **Beckman Coulter Biomek i7 liquid handler:** performs DNA extraction and prepares the final plates for qPCR
- **Thermo Fisher QuantStudio Real-Time PCR system:** analyzes the samples