From start to sequence: enabling high-impact research

How integrated services empower teams to achieve scientific breakthroughs

---

Executive Summary

In research, ambition is often limited not by ideas, but by resources. Whether you're part of a small, agile team or a large, well-established institution, budgets, personnel, and access to specialized equipment can all shape what's possible. High-risk, high-reward projects – such as endangered species genomics, ancient DNA recovery, or novel pathogen detection – require precision, speed, and reliability from the first pipette to the final dataset.

This case study explores how bundling services like myBaits® target capture and myReads® NGS services creates a seamless, efficient workflow that allows research teams of any size to tackle ambitious projects without sacrificing quality or scope.

Introduction

Background

Research teams often face a paradox: they have the ideas, expertise, and drive to tackle high-impact projects, but balancing time, resources, and bandwidth can be a challenge. In fields like environmental DNA analysis, agrigenomics, and ancient DNA research, precision and speed are critical, yet the complexity of managing multiple service providers can slow progress, strain budgets, and jeopardize results.

Bundling services like myBaits target capture and myReads NGS services offers a streamlined approach that aligns processes from start to finish, ensuring efficiency without compromising quality.

Problem Statement

Research teams working under tight budgets and timelines face:

- Limited personnel for labor-intensive library prep and sequencing workflows
- Coordinating overhead when managing multiple vendors, resulting in delays and inconsistencies
- Risk of sample loss or degradation during repeated shipping and handling/during extraction
- Resource restraints

Solution Overview

By bundling library preparation, hybridization capture, and sequencing through a single provider, labs can:

- Reduce turnaround times by eliminating inter-vendor delays
- Ensure consistent QC standards across the entire workflow
- Lower costs through bundled pricing and decreased risk of processing errors

---

Case study

Objective

A comparative genomics analyst is looking to complete targeted sequencing on 500 DNA samples – comprising both standard and degraded DNA – to construct a phylogenetic analysis of several angiosperm species.

Methodology

- Utilized Daicel Arbor Biosciences' myBaits target capture and myReads extraction services
- Sent raw samples directly to Daicel Arbor Biosciences's lab for integrated library prep, capture, and sequencing
- Maintained single-point communication with the project manager from Daicel Arbor Biosciences to align timelines and QC milestones

Results

- Reduced turnaround time by 8 weeks compared to previous multi-vendor approach

- Streamlined QC milestones and sample processing, avoiding errors in sample preparation and preserving precious DNA samples
- Delivered high-quality, consistent sequencing data in time for grant submission

Customer Testimonial

> *"When I used Arbor Biosciences, communication was excellent through Arbor's staff. I worked closely with staff to ensure my sample preparation–which uses fresh and degraded samples–was adequate to maximize sequencing results. The datasets have led to [discovering] new species and expanded my research program."*

Justin Bernstein, PhD, Postdoctoral research fellow at the National Science Foundation and The University of Kansas, author of Phylogenomics of Fresh and Formalin Specimens Resolves the Systematics of Old World Mud Snakes (Serpentes: Homalopsidae) and Expands Biogeographic Inference.

Comparative Analysis

Workflow step	**Multi-vendor approach**	**Bundled approach**	**Benefit**
Vendor coordination	3-4 handoffs	1 point of contact	Less admin time, fewer communication bottlenecks
QC standards	Variable	Consistent	Lower risk of QC-related delays and sample loss
Sample shipping	Multiple shipping	Single shipping	Reduced handling risk, preserves sample integrity
Cost efficiency	Full price at each step	Bundled pricing*	Keeps projects within budget, fewer repeat costs
Turnaround time	12-14 weeks	4-6 weeks	Faster delivery of usable data, accelerating next research phase

*Bundled pricing may vary based on the scope and objective of a project. For standard projects, bundling myBaits and myReads can save an average of $25 per sample for a total of $12,500 in savings for a 500 sample project when compared to custom per-sample pricing options.

Conclusion

For teams with big ambitions, bundling services is more than a convenience, it’s a measurable advantage. Maintaining a single touchpoint for NGS services offers strategic advantages from removing bottlenecks to protecting valuable samples and accelerating the path to actionable data.

By partnering with a Daicel Arbor Biosciences for library prep, capture, and sequencing, it becomes possible to gain more than efficiency, but an ally that is invested in success from start to finish. Projects that may have been perceived as out of reach may come into scope, with the added benefits of faster data delivery and fewer risks.