

Building the Largest Feline Imputation Panel for Population-Scale Genomics

Fulcrum Genomics is partnered with Darwin's Ark to develop a high-resolution imputation reference panel for domestic cats, enabling accurate low-pass whole genome sequencing at scale.

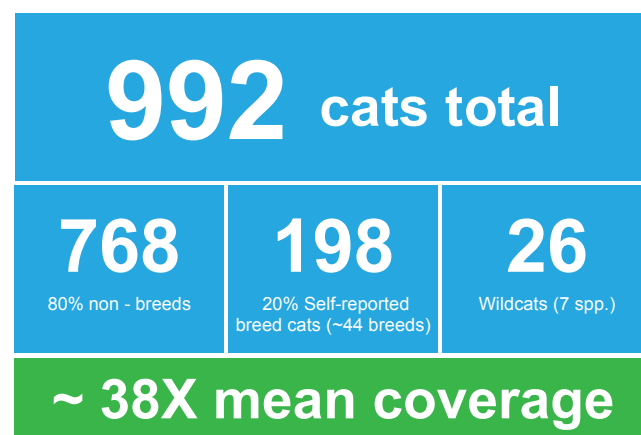
Darwin's Ark is a citizen science initiative that engages cat owners directly in research, building a large, community-powered dataset linking genetics to traits and behavior. As the project grows, they need a way to generate reliable genomic data from thousands of samples without relying on deep sequencing for every cat.

The Challenge

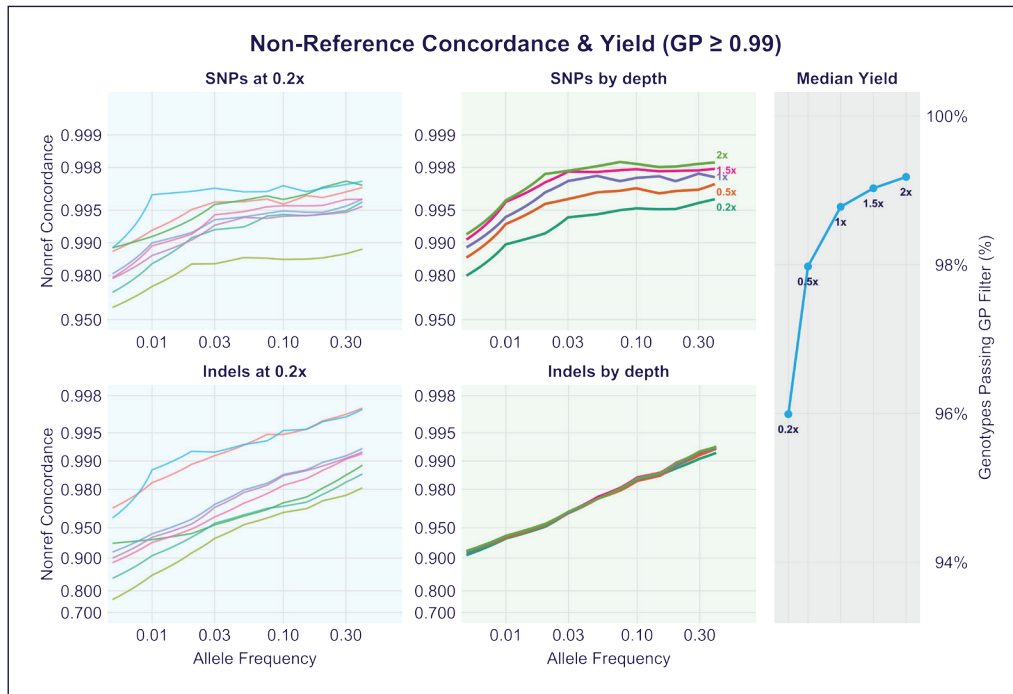
Darwin's Ark is building one of the largest community-powered datasets linking feline genetics to traits and behavior, with over 20,000 cats enrolled and 2,500 DNA sequencing participants. But the genomics infrastructure for cats lags far behind human and agricultural species. Existing imputation panels are small and unrepresentative, public sequencing data varies widely in quality, and variant resources are limited. To make low-pass sequencing viable at the scale Darwin's Ark needed, they required a larger, higher-quality reference panel and a reproducible framework for integrating diverse genomic data.

The Results

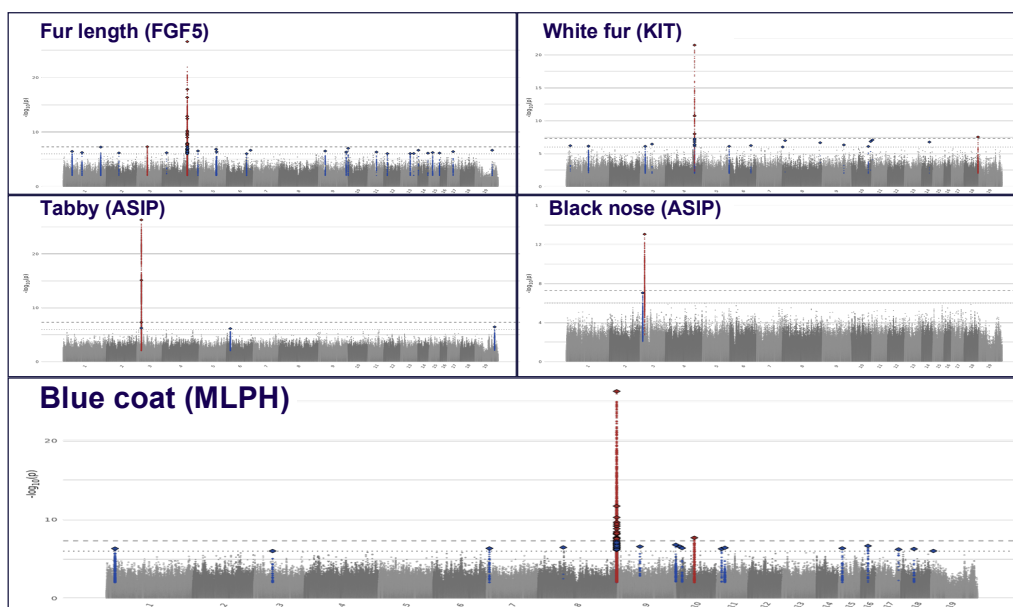
► **Developed the largest feline imputation reference panel to date**



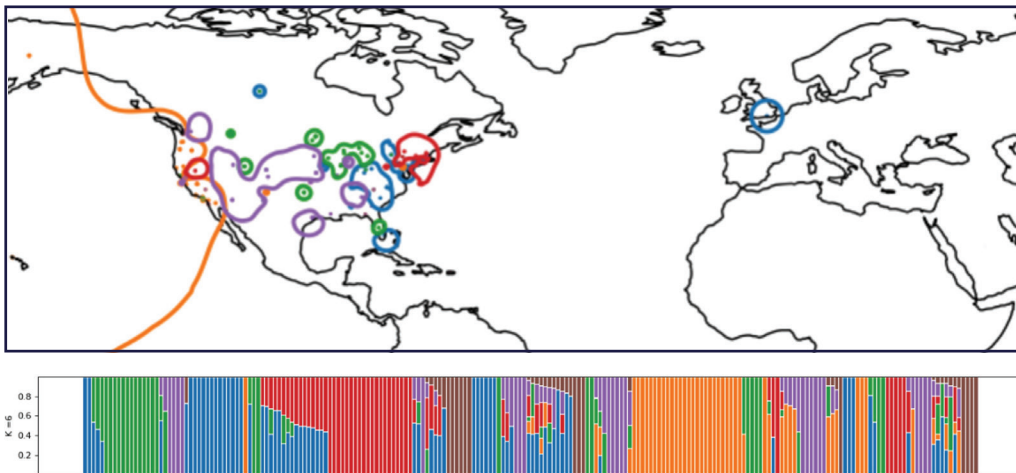
► Achieved up to 99.5% accuracy from as low as 0.2X coverage



► Reproduced known genotype–phenotype associations



► **Population structure revealed geographic rather than breed-based clustering**



"Fulcrum has been a game changer for us. When we took on a major new project in cat genetics, we knew we'd face technical hurdles — and we did, including some we never anticipated. Our partnership with Fulcrum allowed us to address every one of them without derailing our timeline. We now have pipelines that outperform anything else available and produce data of such high quality that we've expanded our vision for the entire project."

**Elinor Karlsson, Co-Founder & Chief Scientist,
 Darwin's Ark**

Fulcrum's Approach



Specialized Bioinformatics Team

Fulcrum staffed the project with experienced bioinformatics scientists, combining expertise in large-scale variant calling, imputation, and population genetics to support both methodological rigor and practical execution.



Aggregation and Standardization of Genomic Data

More than 1,100 cat genomes were collected from public repositories and sequencing efforts, then processed through a consistent pipeline to ensure comparability across samples.



Rigorous Quality Control

Samples were filtered based on coverage thresholds, duplication, relatedness, and missingness, resulting in a high-confidence dataset suitable for joint analysis.



Joint Variant Calling and Phasing

Variants were called using established best practices and phased to generate high-quality haplotypes across the cohort.



Imputation Workflow Development

A GLIMPSE2-based imputation pipeline was implemented in a containerized, reproducible framework, enabling efficient processing and future scalability.

Next Steps

Want to build imputation panels, scale low-pass sequencing, or develop genomic resources for non-model species?

Or did you see something that made you think “we need that level of analysis”? Let’s talk about how Fulcrum can help.