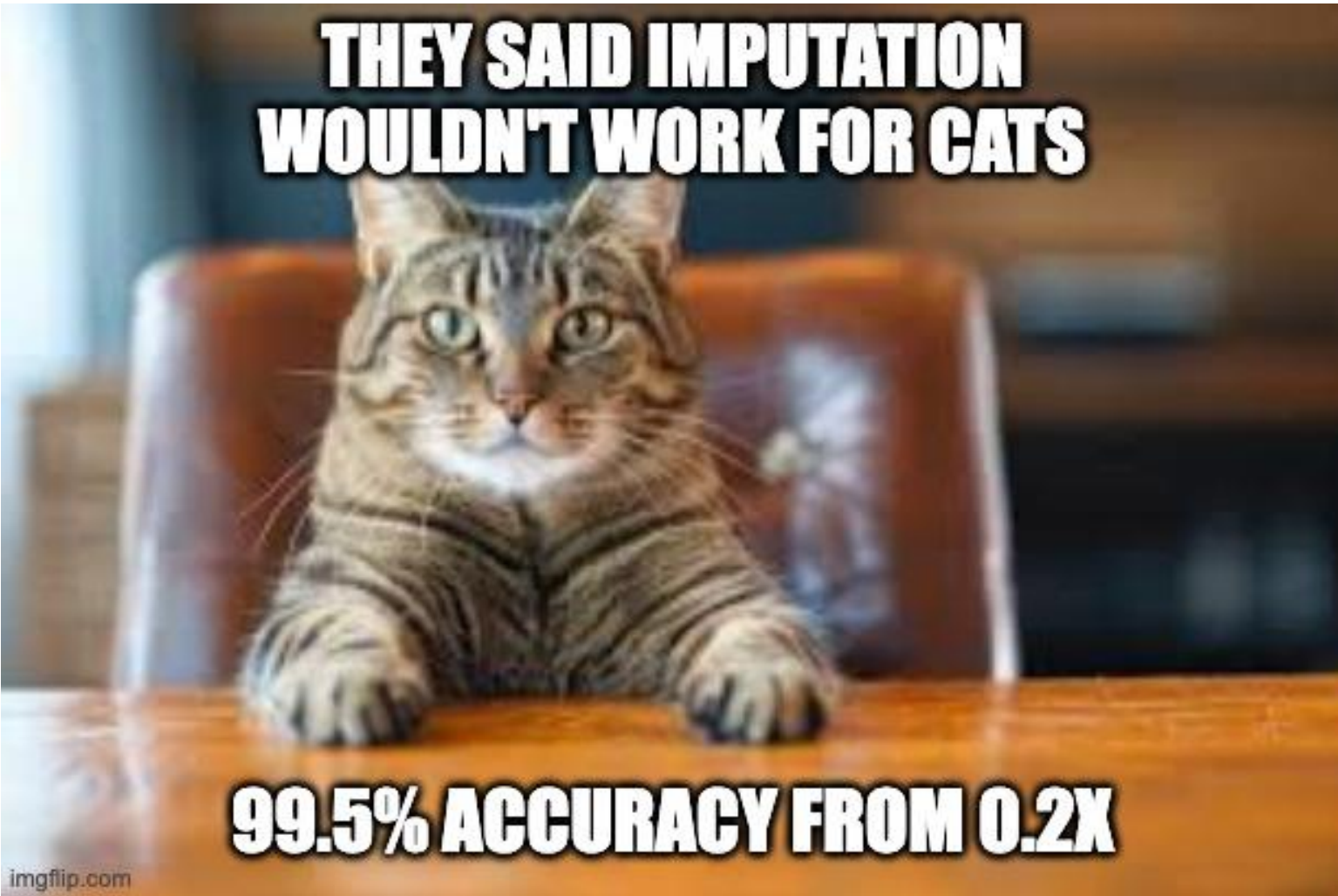


Cat-alyzing Feline Genomics

A Comprehensive Imputation Reference Panel for Domestic Cats

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Poster #128

Introduction

Genomic imputation has transformed human and agricultural genomics, enabling cost-effective large-scale studies from low-coverage data.

However, most non-model species still lack the reference panels needed.

Domestic cats (Felis catus):

- Share >250 hereditary diseases with humans
- Live in human-relevant environments
- Over 20,000 enrolled in Darwin's Ark

We developed the first high-resolution imputation reference panel for feline genomics.

Panel Construction

992 cats total **966** domestic (44 breeds)

26 wildcats (7 spp.) **~38X** mean coverage

Reference: F.catus_Fca126_mat1.0

Pipeline: BWA-MEM2 → GATK → SHAPEIT5

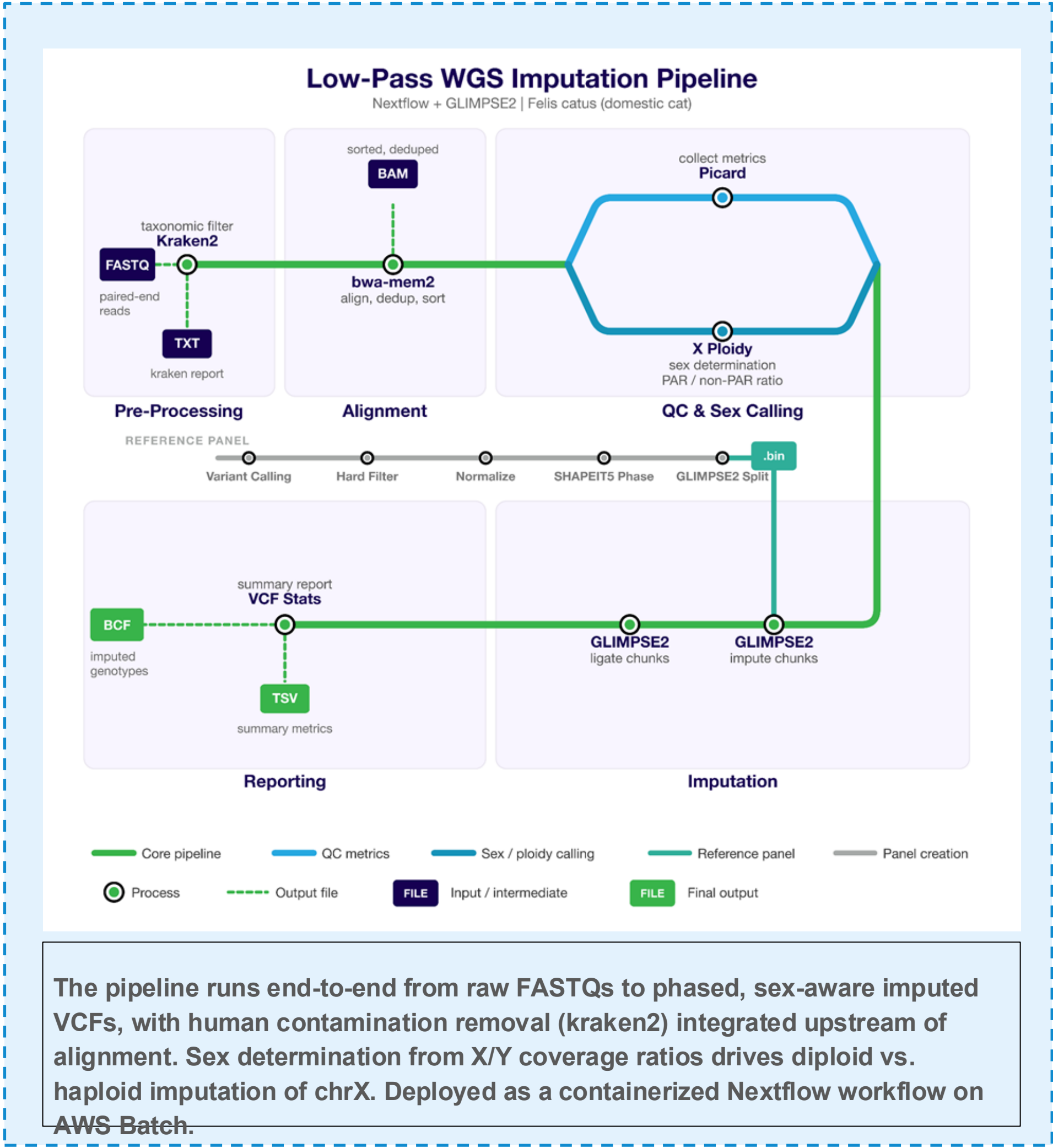
QC: coverage, relatedness, missingness

Result: 99M variants, 2,000 haplotypes

The largest feline genomic resource to date, spanning 44 domestic breeds and 7 wild Felidae species

Imputation Pipeline

Containerized GLIMPSE2-based workflow optimized for efficiency and reproducibility.



Case Study

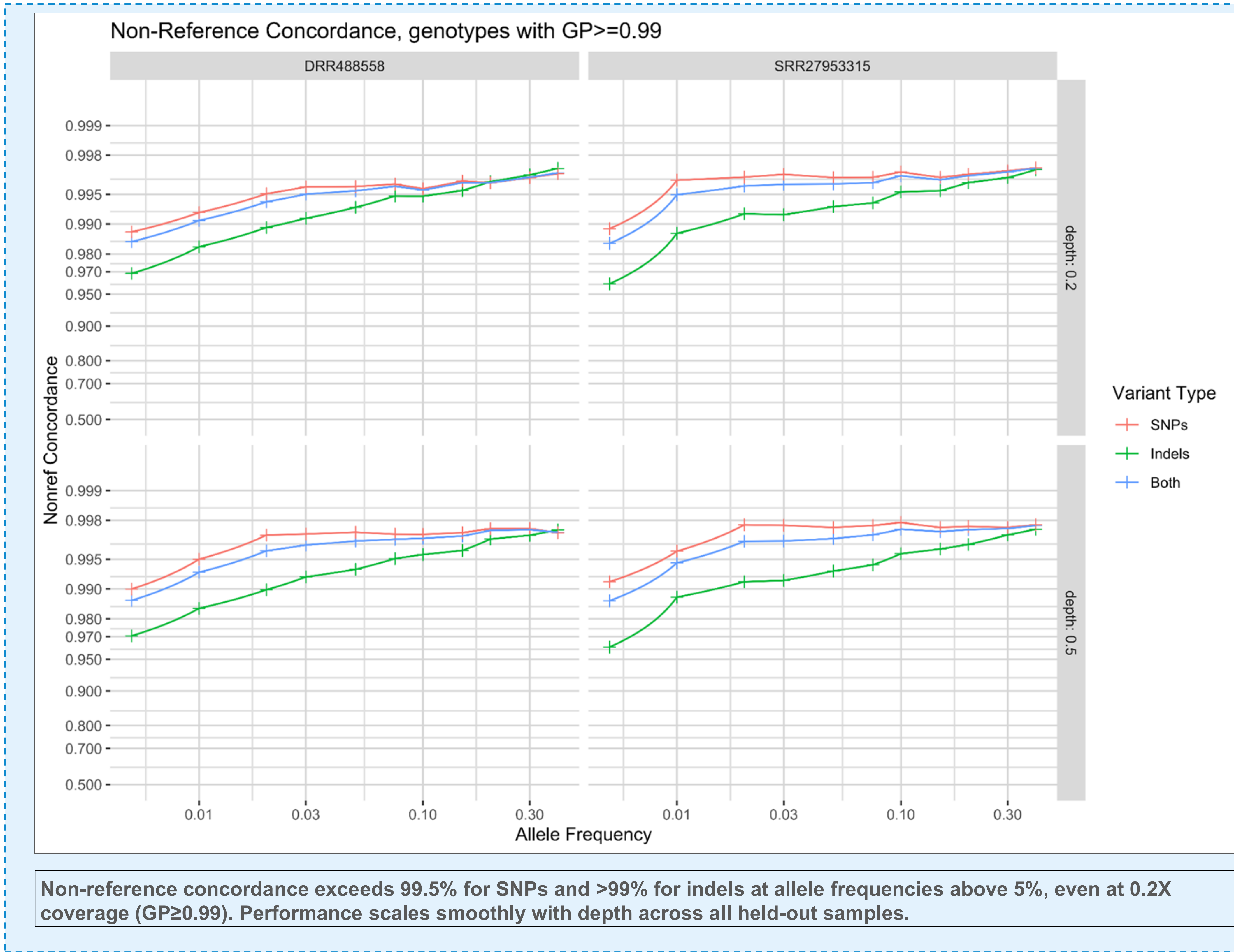
A template for any species

1. Built from public sequence archives
2. Containerized, reproducible pipeline
3. Dog panel (Dog10K) in progress
4. 20,000+ cats in Darwin's Ark



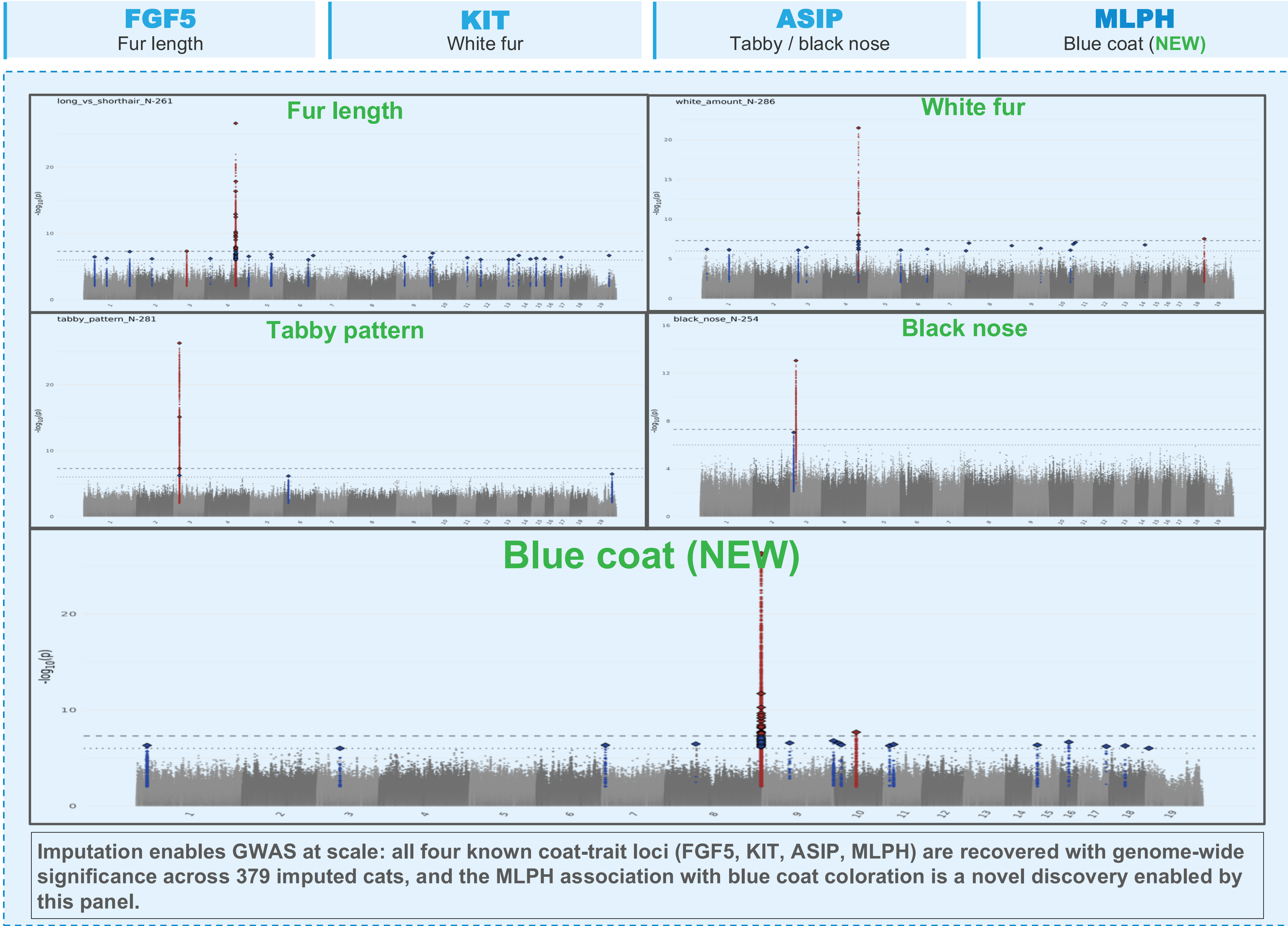
Imputation Accuracy

99.5% accuracy from 0.2X coverage



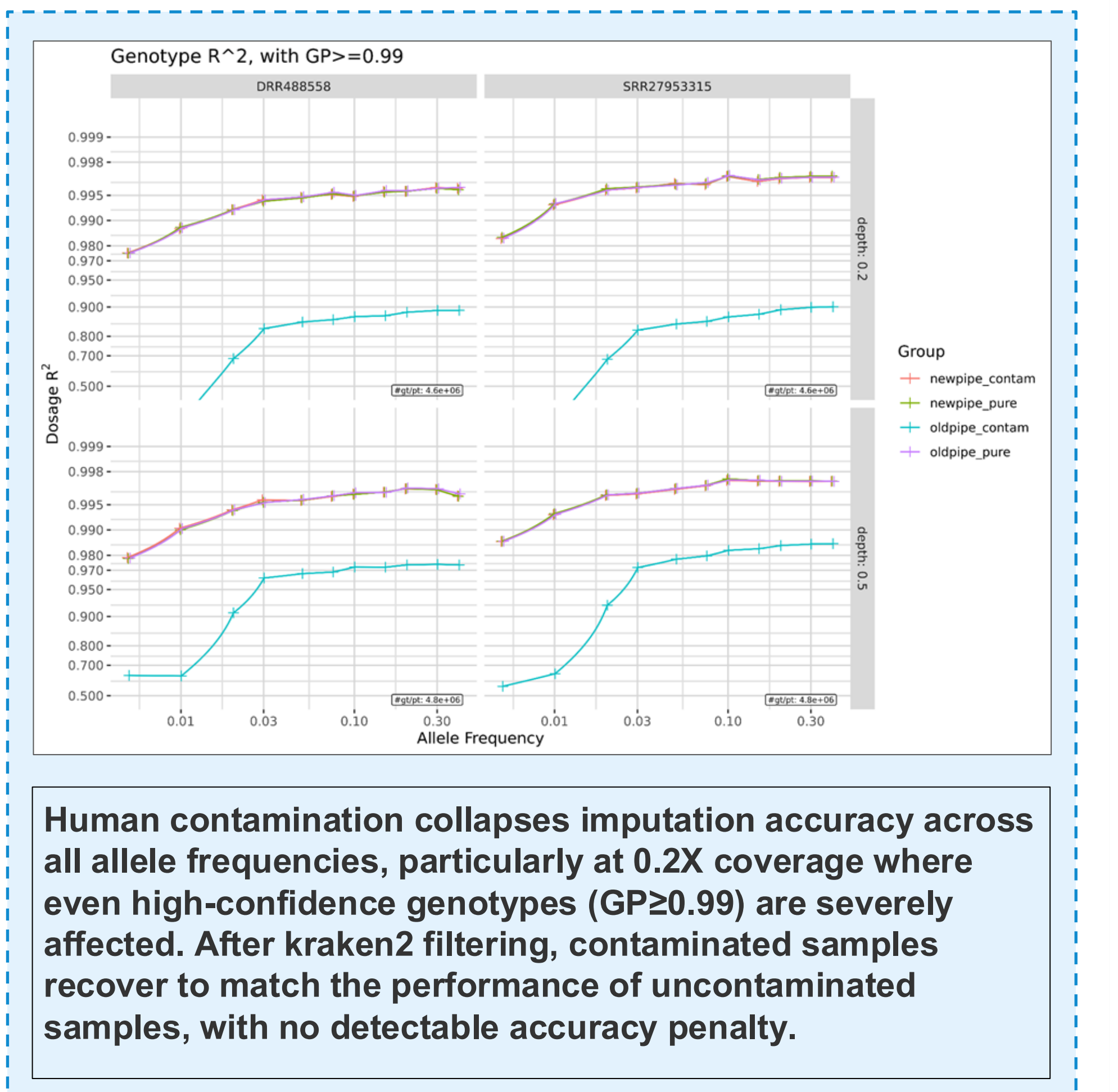
GWAS Validation

4 loci mapped, 1 novel — in 379 cats



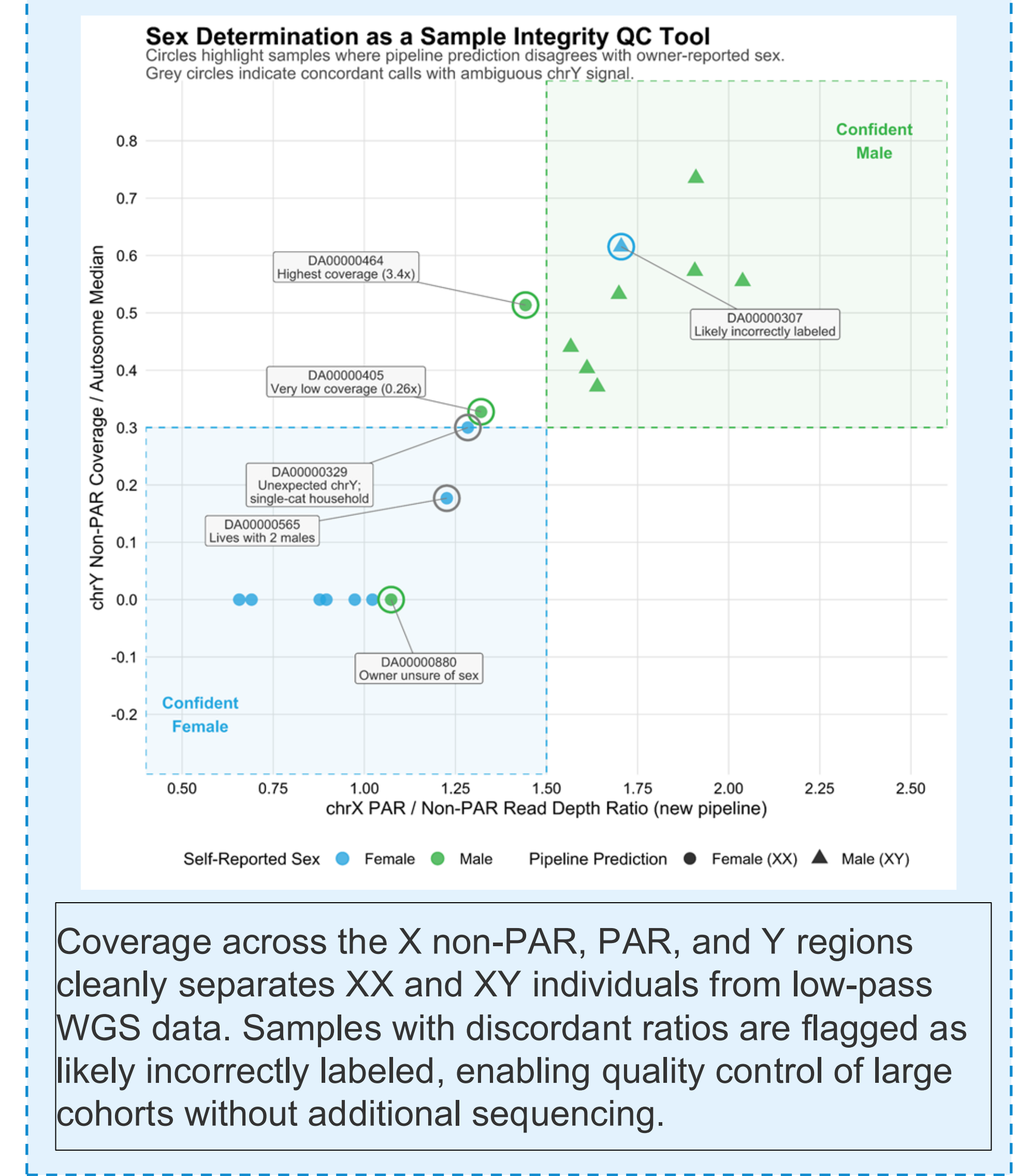
Human Contamination Removal

Saliva/fur samples often contain human DNA. Even modest contamination severely degrades imputation at low coverage.



chrY & Sex Determination

Maine Coon chrY integrated with 3 PAR regions masked to prevent X read loss, enabling sex determination and sample QC from low-pass WGS.



Population Structure & Conclusions

