
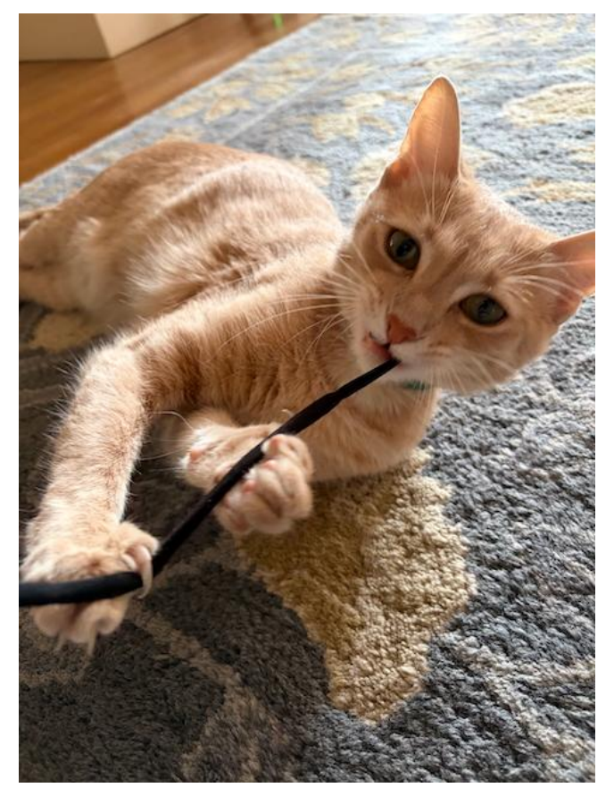
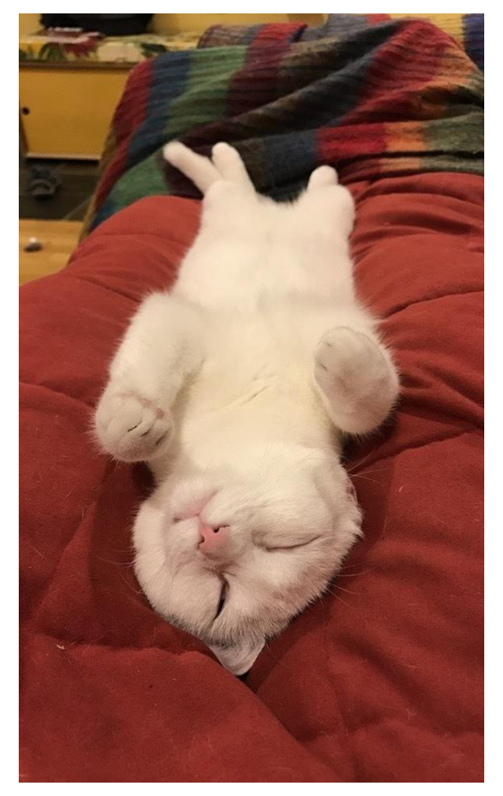

Enabling Community-Driven Genetics of the Domestic Cat at Large Scale

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SCAN HERE to sign up your cat

Darwin's Ark

A community science nonprofit catalyzing groundbreaking research by engaging pets and their people in scientific discovery

Our goal: to create a scientific resource to accelerate large-scale domestic cat research

Join now! You and your cat can participate in cat science!

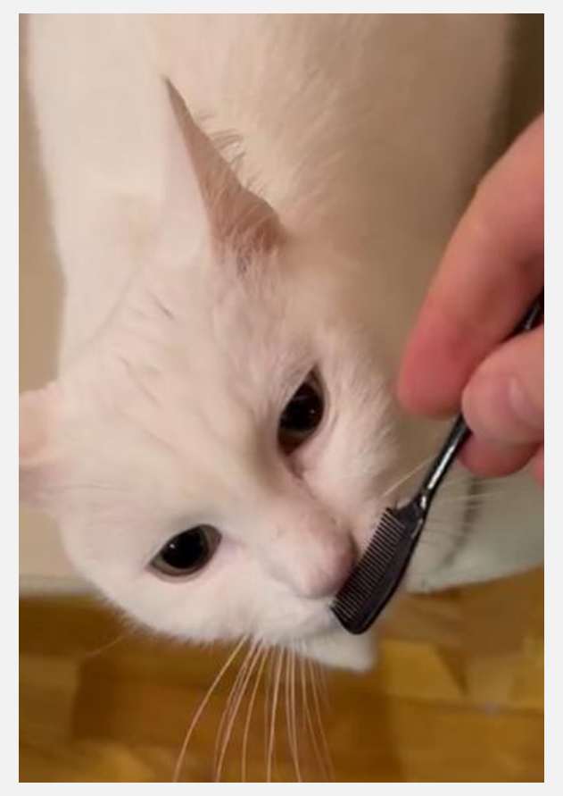
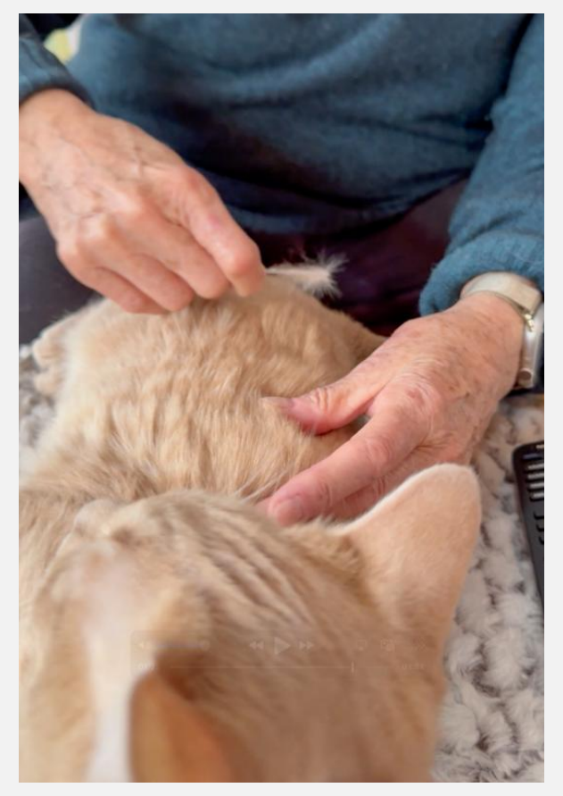
- Sign up on Darwin's Cats website
- Give a detailed description of your cat – this is key phenotypic data!
- Make a modest donation to support sample sequencing costs (~$150)
- Contribute a fur sample for low pass sequencing
- Be part of cat population genetic analysis
- Receive interesting genetic results

Fur-seq: Why sequence fur?

- Non-invasive, nontechnical sample collection
- Sample collection easy to do by any person
- Samples extremely stable at room temperature
- Good source of DNA of suitable quality and quantity
- No animal welfare concerns- cats often (but not always since they are cats…) seem to enjoy being combed

Fur sample collection

- Each cat receives a barcoded tube and a collection comb


- When kits arrive, cats are simply combed a few times to collect fur, then the comb goes into the tube and then into the preaddressed mailer

Fur-seq sample processing

Making fur into DNA sequencing libraries

1. Samples are digested with proteinase K
2. Bead-based DNA purification and cleanup
3. Tagmented libraries made with SeqWell MosiaX v2 kit
4. Bead-based library cleanup
5. Quantitation and QC
6. Fur-seq is scalable: Many steps automated on Hamilton
7. One lane of NovaSeq yields ~1x genome coverage of 192 samples, plenty for imputation of genotypes

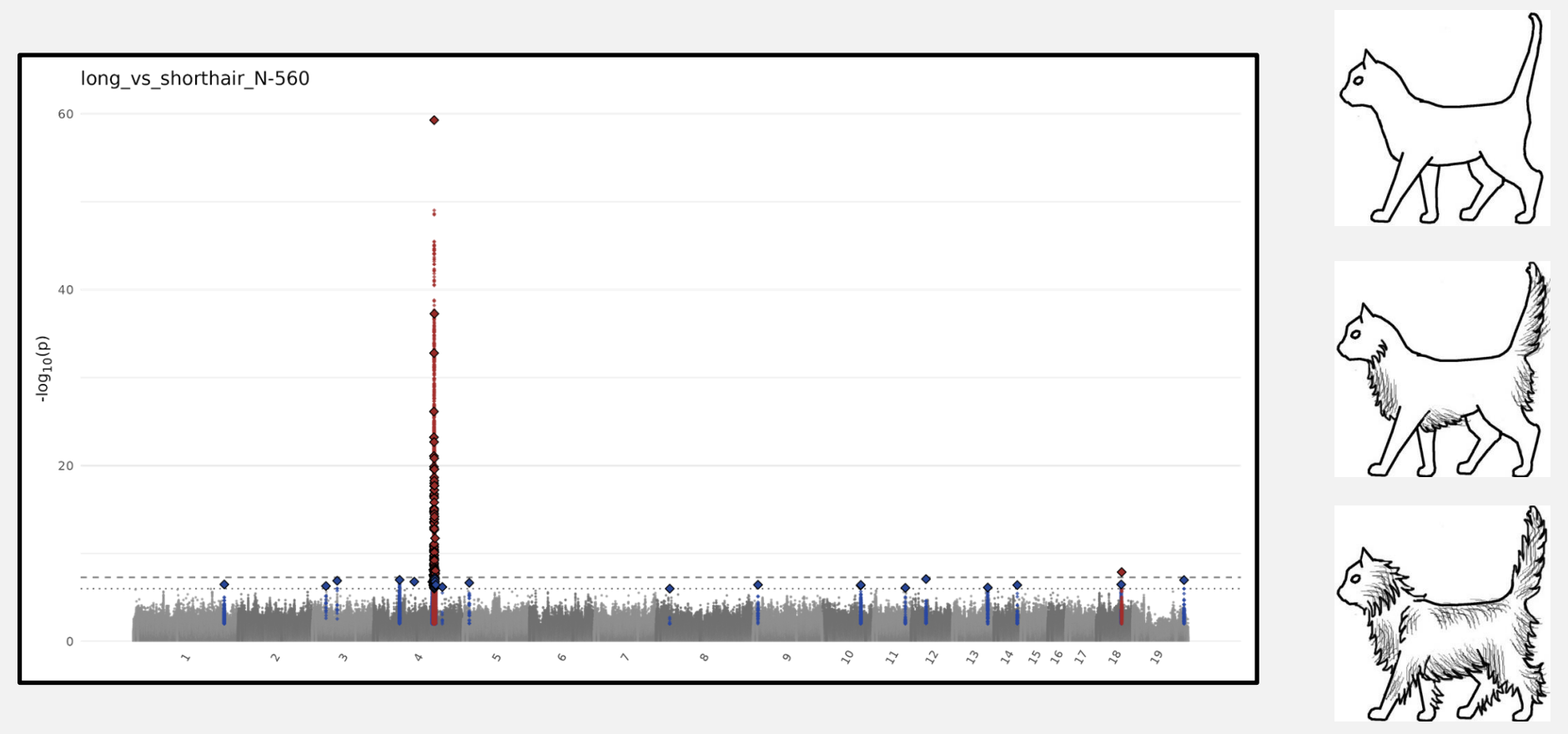
Data Quality

- Fur-seq reliably yields DNA concordant with blood-based sequencing
- Fur-seq contamination rates are much lower than saliva samples: 94% of Fur-derived sequences align to cat, vs 65% of saliva-derived
- Fur-derived DNA quality and quantity are sufficient to reliably support generation of high quality tagmented libraries for low pass (1-2X) sequencing

Results: Initial GWAS hits for aesthetic phenotypes

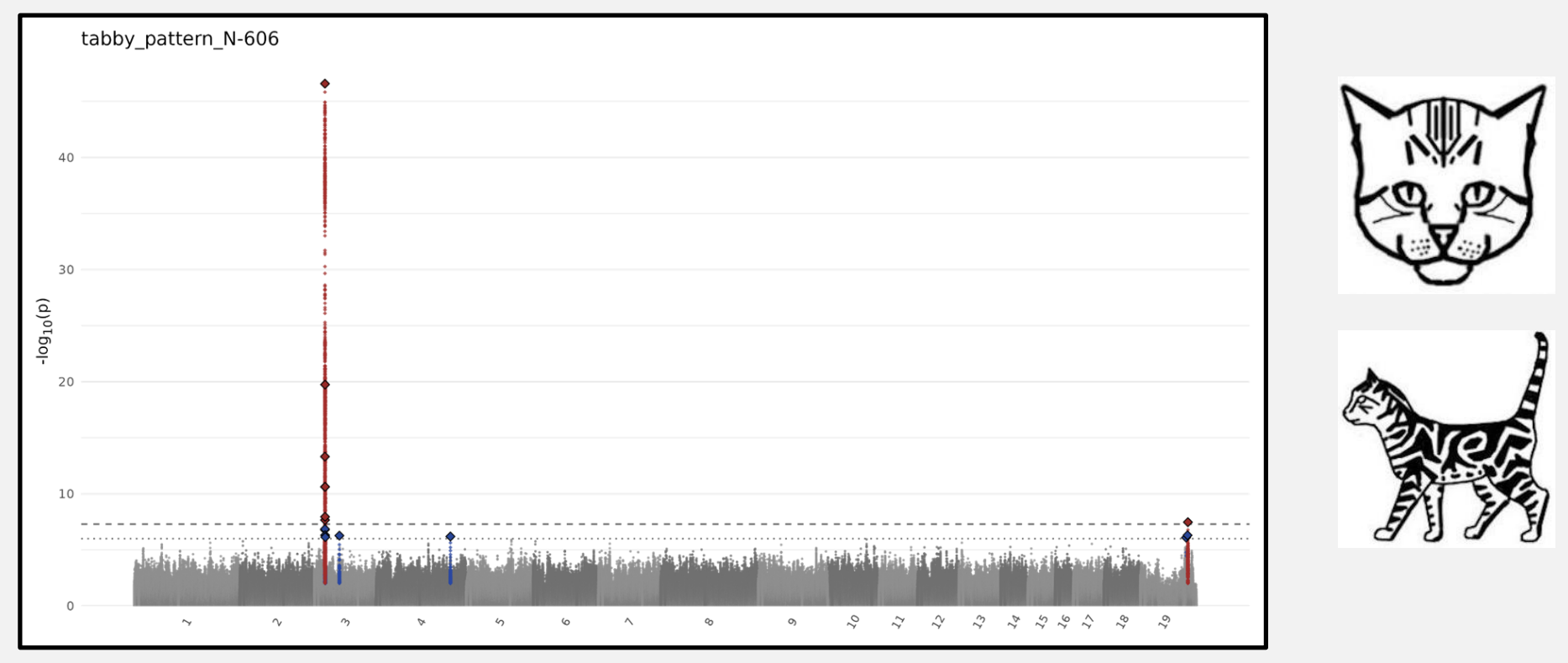
Fur Length

Strong signal at **FGF5**, inhibitor of hair growth



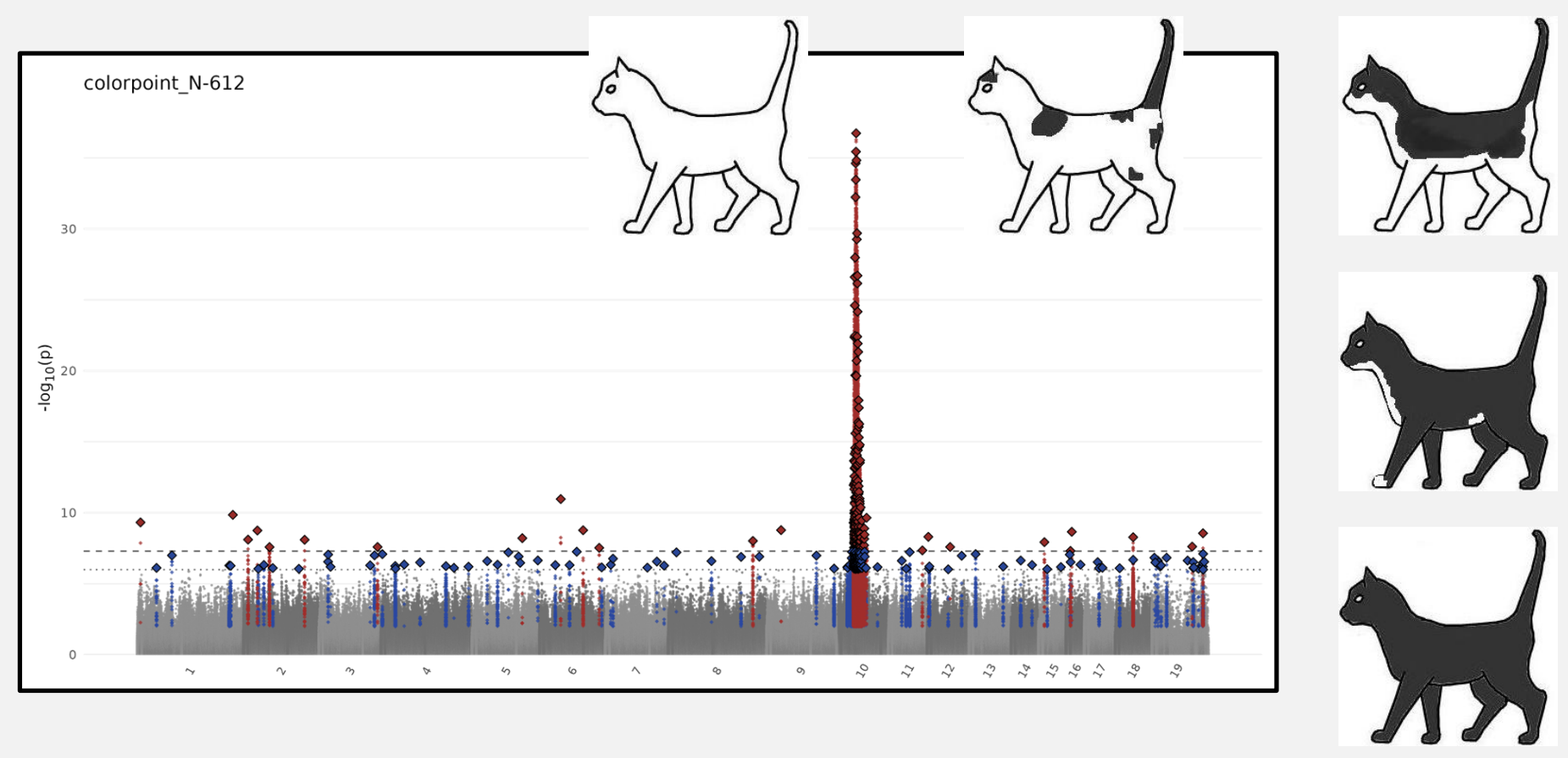
Tabby Pattern

Strong signal at **ASIP**, regulates pigment distribution



White Spotting

TYR Tyrosinase gene, essential for melanin production; controls temperature-sensitive pigment restriction (colorpoint) & albinism



Genotyping and Imputation

- Computational pipeline developed and run by Fulcrum Genomics
- Imputation panel of 992 deep sequenced cats; yielding 99 million variants across ~2000 haplotypes
- Since target coverage is ~1x, validation was done using held-out samples downsampled to 0.2–2X coverage. After quality filtering, imputation accuracy for common variants is 99.5%
- X chromosome accuracy is comparable to autosomes

Wider applications of Fur-seq

Effective on all 13 tested mammals

- Samples obtained in collaboration with Zoo New England
- Wide range of hair/fur types

➽ Demonstrates an opportunity to sample mammals previously inaccessible to DNA sequencing at low cost: rare, protected, sensitive or even extinct

Spotted Hyena

Potui Donkey

Two Toed Sloth

Red Panda

Giant Anteater

Western Lowland Gorilla

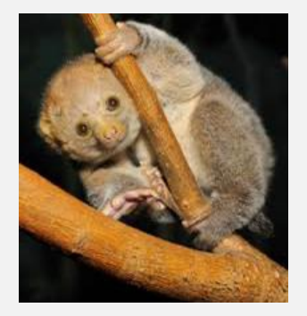
Ring Tailed Lemur

Black Welsh Sheep

Dexter Cattle

Miniature Horse

Potto



Bactrian Camel

Our funders include:

- Our participants
- Hills Pet Nutrition

Partners

- Broad Technology Space
- Zoo New England
- UMass Chan Medical School
- Fulcrum Genomics
- SeqWell

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