



# Population Structure & Genetic Improvement in Livestock

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# Overview

## Research focus

- Population structure
- Trait association

## Research projects

- Thermo-tolerance in tropical cattle
- African Goat Improvement Project

## Research goal

- Genetic improvement of livestock





# **THERMO-TOLERANCE IN TROPICAL CATTLE**



# Thermo-tolerance in Tropical Cattle



- **Importance** of thermo-tolerance in cattle
  - Milk Production
  - Reproduction
- **SLICK** hair-coat: short, fine, sleek hair-coat found in tropically adapted cattle
- **Objective:** improve diagnostic markers & identify causative mutation



**Senepol**  
St. Croix



**Carora**  
Venezuela



**Romosinuano**  
Venezuela

# Research Roll



- Identify breed relationship of SLICK- tropical cattle
- Investigate ancestral origins of SLICK- hair coat
- Conduct the Genome-wide association analysis of SLICK phenotype

# Research Approach

- Use a variety of analyses to assess trait association across the genome
  - Runs Of Homozygosity
  - Signatures of selection (iHS)
  - Genome-wide Association Study
  - Haplotype blocks



# Ancestry of Senepol cattle

- Composite Breed of the St. Croix Virgin Island



Senepol

Red Poll



N'Dama



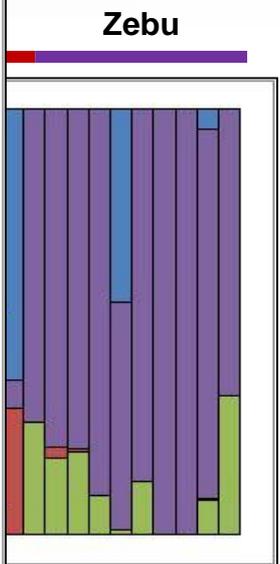
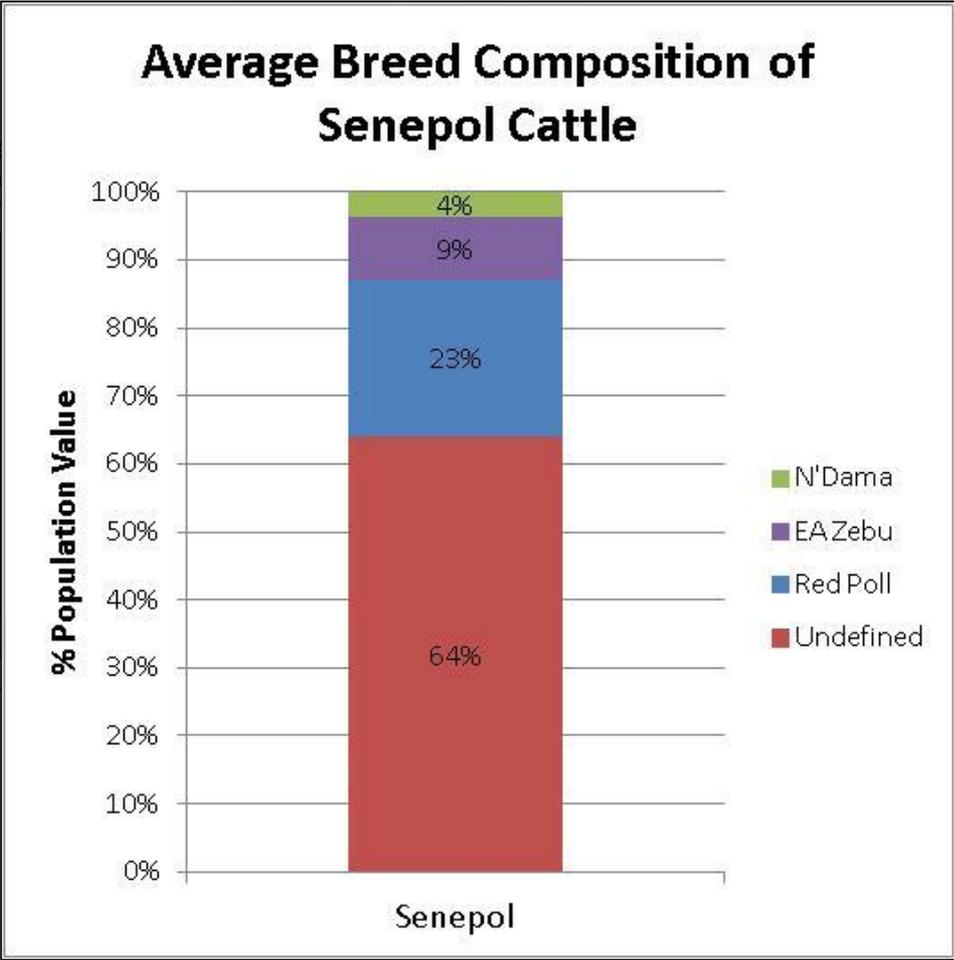
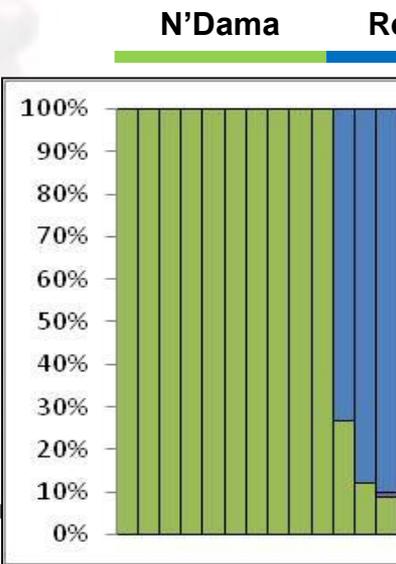
East African Zebu





# Genomic verification of Senepol ancestry

K=4



# GWAS of SLICK hair-coat



- ✓ Use ancestral breeds as controls to balance SLICK cases

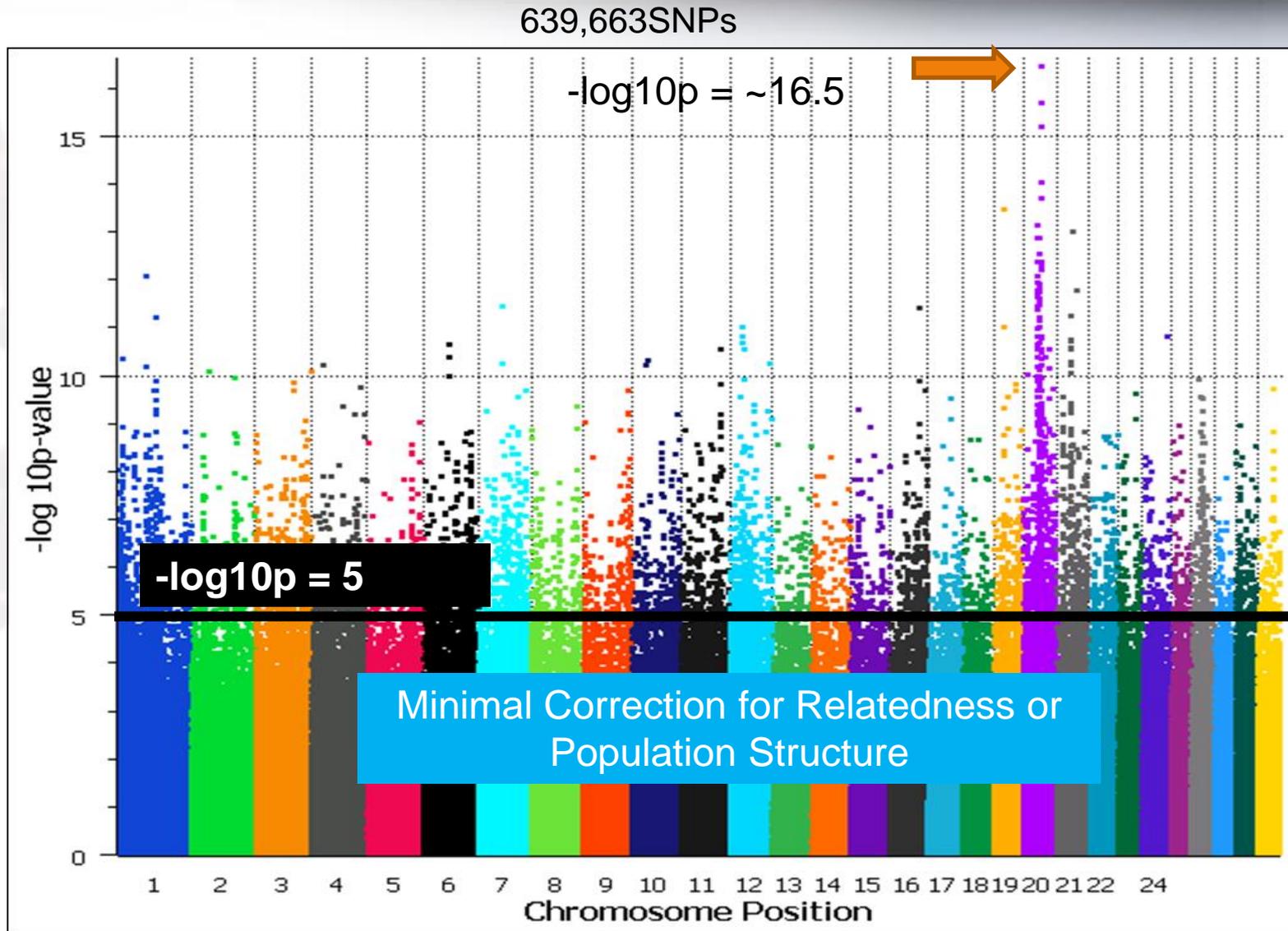
## Cases= 72

- Senepol- 36
- Senepol x Angus-3
- Senepol/Angus x Angus-1
- Romosinuano- 2
- Romosinuano/Angus x Angus-1
- Romosinuano x Angus-11
- Holstein x Senepol- 7
- Carora- 10

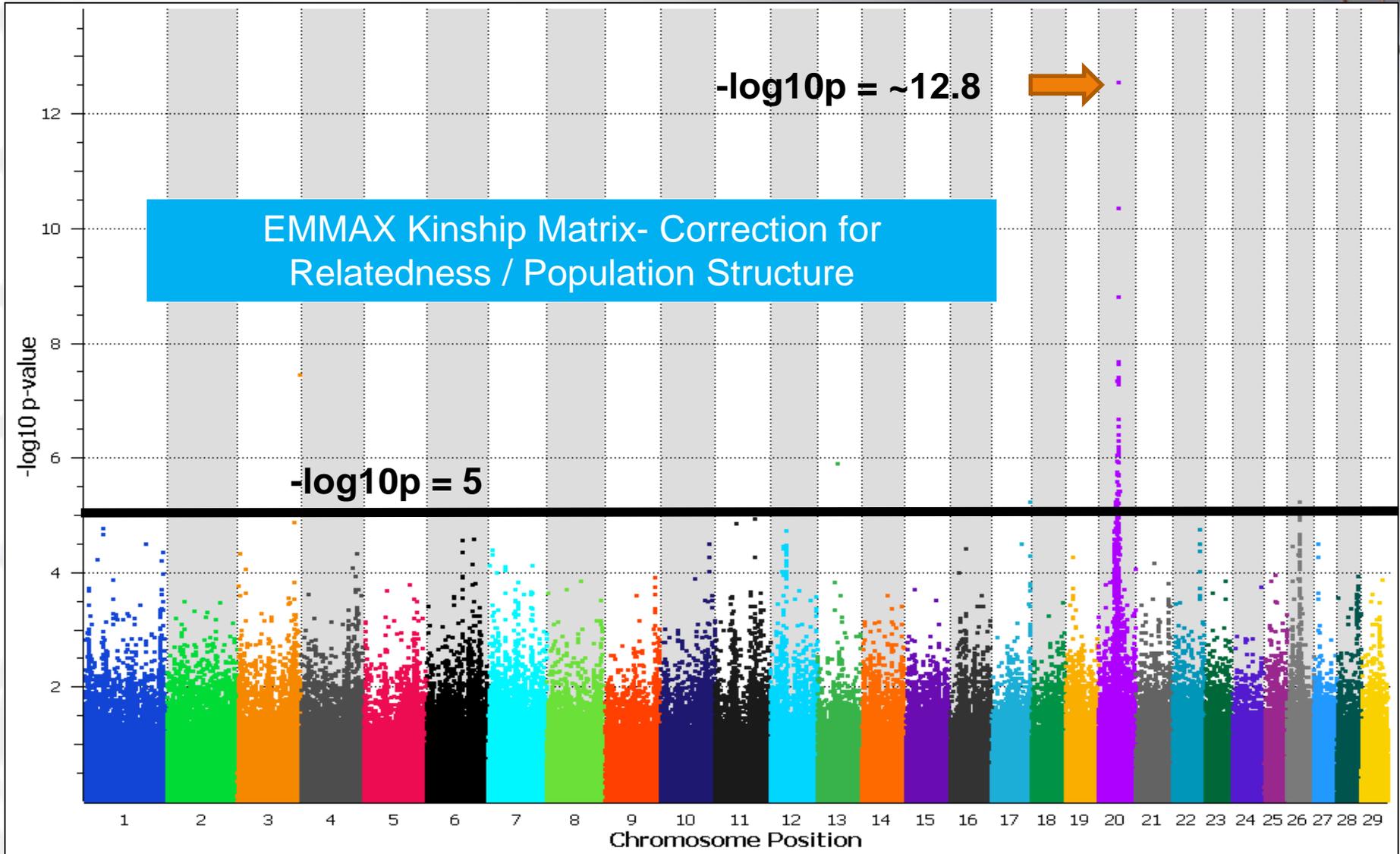
## Controls= 61

- Senepol-2
- Red Pole-10
- N'Dama-10
- Zebu- 10
- Senepol x Angus-1
- Senepol/Angus x Angus-1
- Angus-10
- Holstein- 7
- Brown Swiss- 10

# GWAS of SLICK hair-coat



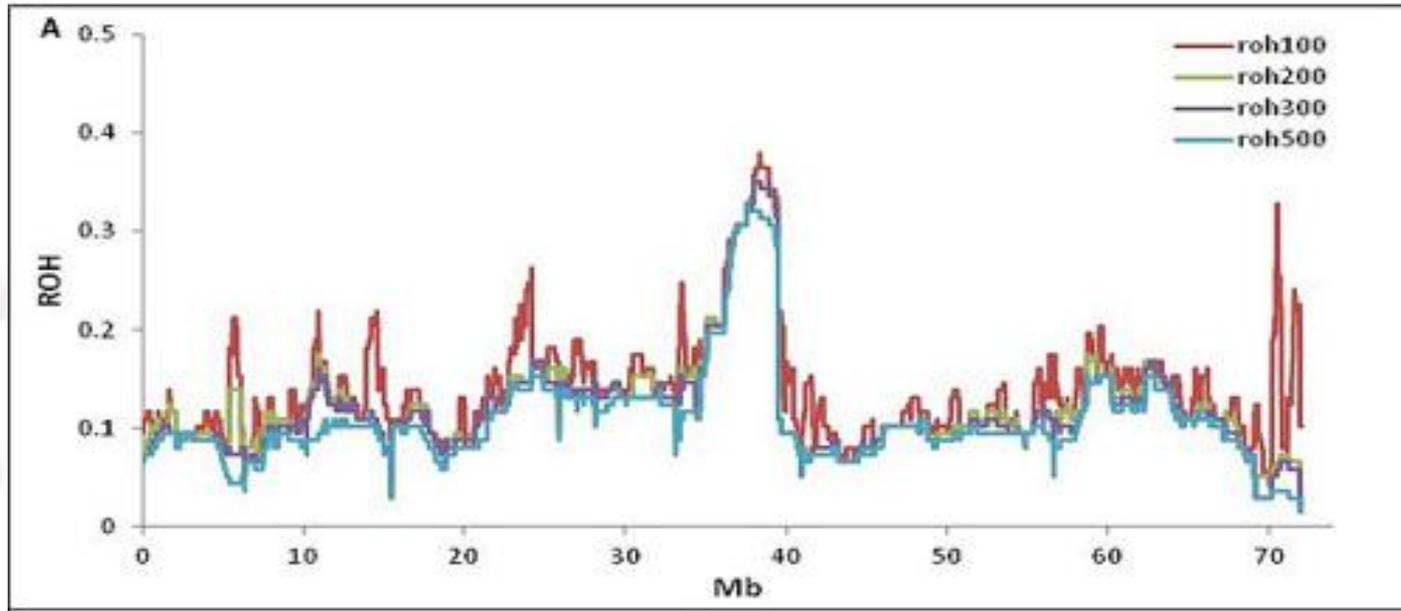
# Improved GWAS of SLICK hair-coat



# Runs of Homozygosity



Dr. Eui-Soo Kim, Iowa State University



SNP Threshold	Approximate distance
100 consecutive SNPs	0.3 Mb
200	0.6
300	1.0
500	1.6

# Haplotype Blocks



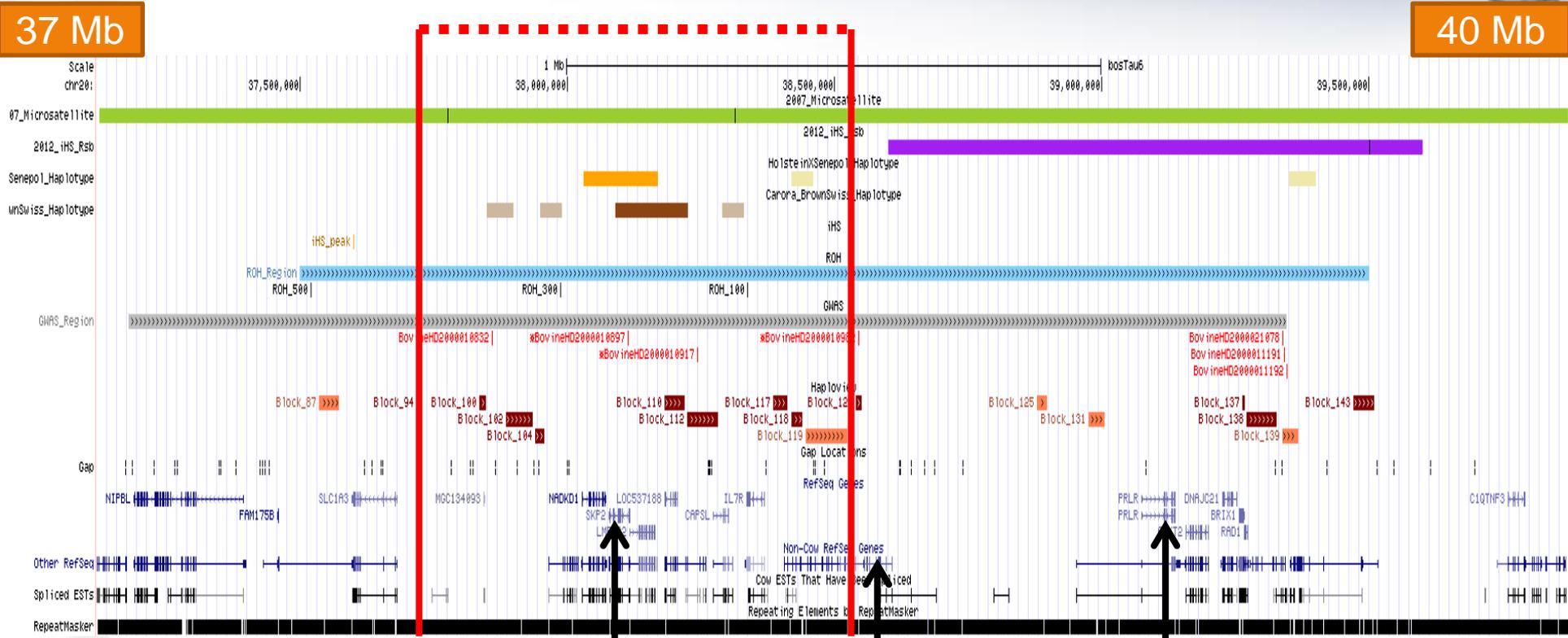
- ✓ 24 significantly associated haplotype patterns
- ✓ 3 haplotype patterns identified only in SLICK

Block ID	Start bp	End bp	Block Distance (bp)	Haplotype	Frequency SLICK	Frequency Non-SLICK	P Value
94	37718791	37721846	3,055	GGG	0.833	0.314	3.58E-12
104	37940179	37957238	17,059	GGGGA	0.292	0	4.96E-10
112	38224054	38281493	57,439	GGGGAGG	0.278	0	1.44E-09
143	39469953	39508807	38,854	GGGAGGGCAGCGGGAGGAGA	0.264	0	4.06E-09

# Multiple Genetic Analyses



## BTA 20



Keratinocyte proliferation and skin homeostasis

**SKP2**

**SPEF2**

**PRLR**

Hair cycling and localized to skin tissue

Spermatogenesis defects.  
Late feathering in male chickens.

# Outcomes

- Breed relationship and ancestry of SLICK-haired tropical cattle
- Narrowed SLICK locus to 0.5 Mb on BTA 20
- Identified new diagnostic markers
  - 3 haplotypes found only in SLICK haired individuals
- Huson *et al.* ***Frontiers in Genetics***, March 2014



# Future Directions



- Potentially 2 mutations effecting same gene
  - Related to breeds
- Sequencing region to determine causative mutation
- Genotyping additional SLICK breeds



**Senepol**  
St. Croix



**Romosinuano**  
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**Carora**  
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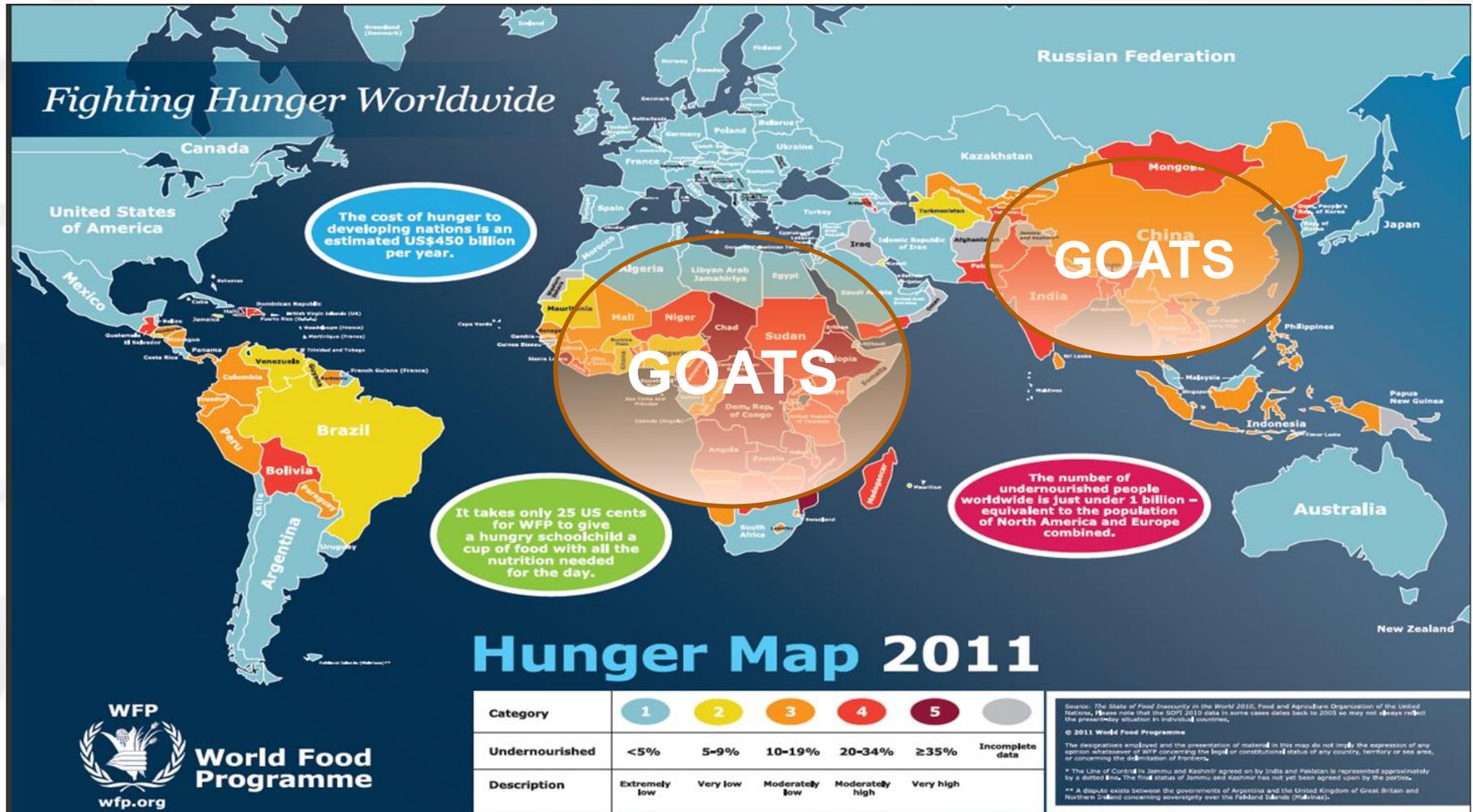
USAID: Feed the Future Initiative

# AFRICAN GOAT IMPROVEMENT NETWORK (AGIN)



# Global Food Security

- 90% of global population located in “Hunger Zones”
- Target: African small-holder farmers



# Why Goats?

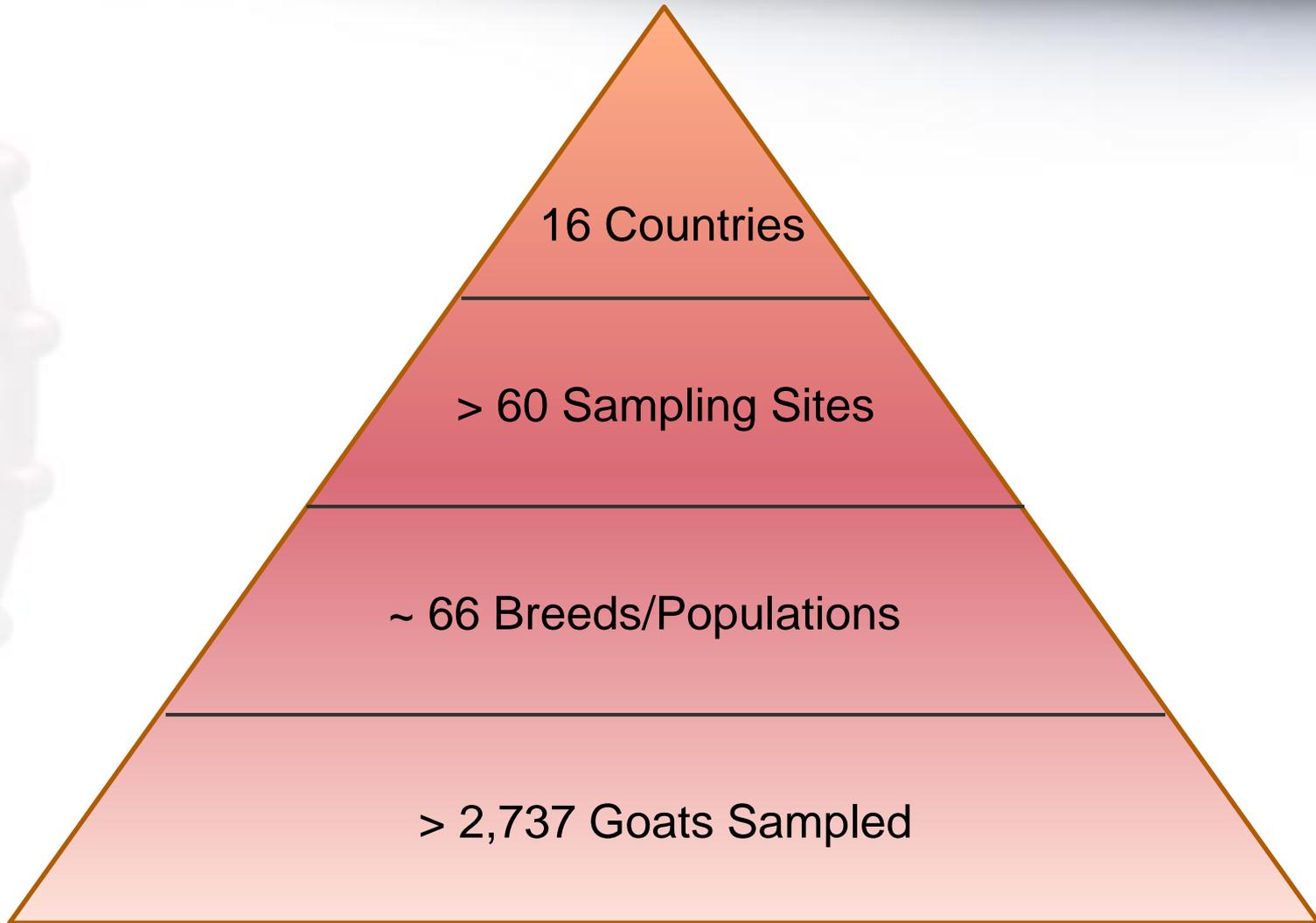
- Most common livestock species in Africa
  - Small-holder farmers (women)
- Diverse & hardy species
  - Thrive in harsh climates with sparse forage
- Large potential growth with selection
- Economically efficient



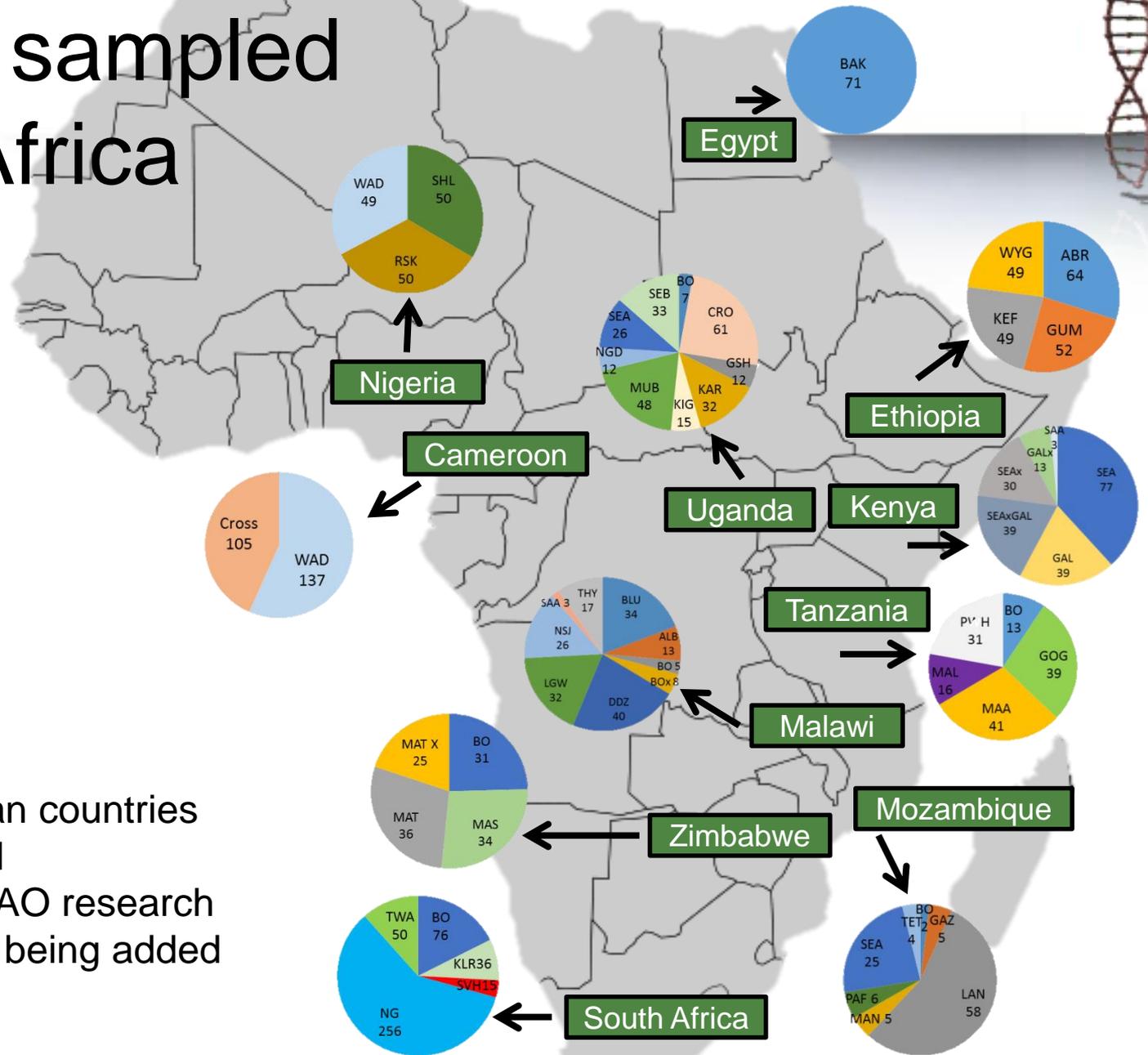


# SAMPLING STATUS

# Total Sampling Dataset



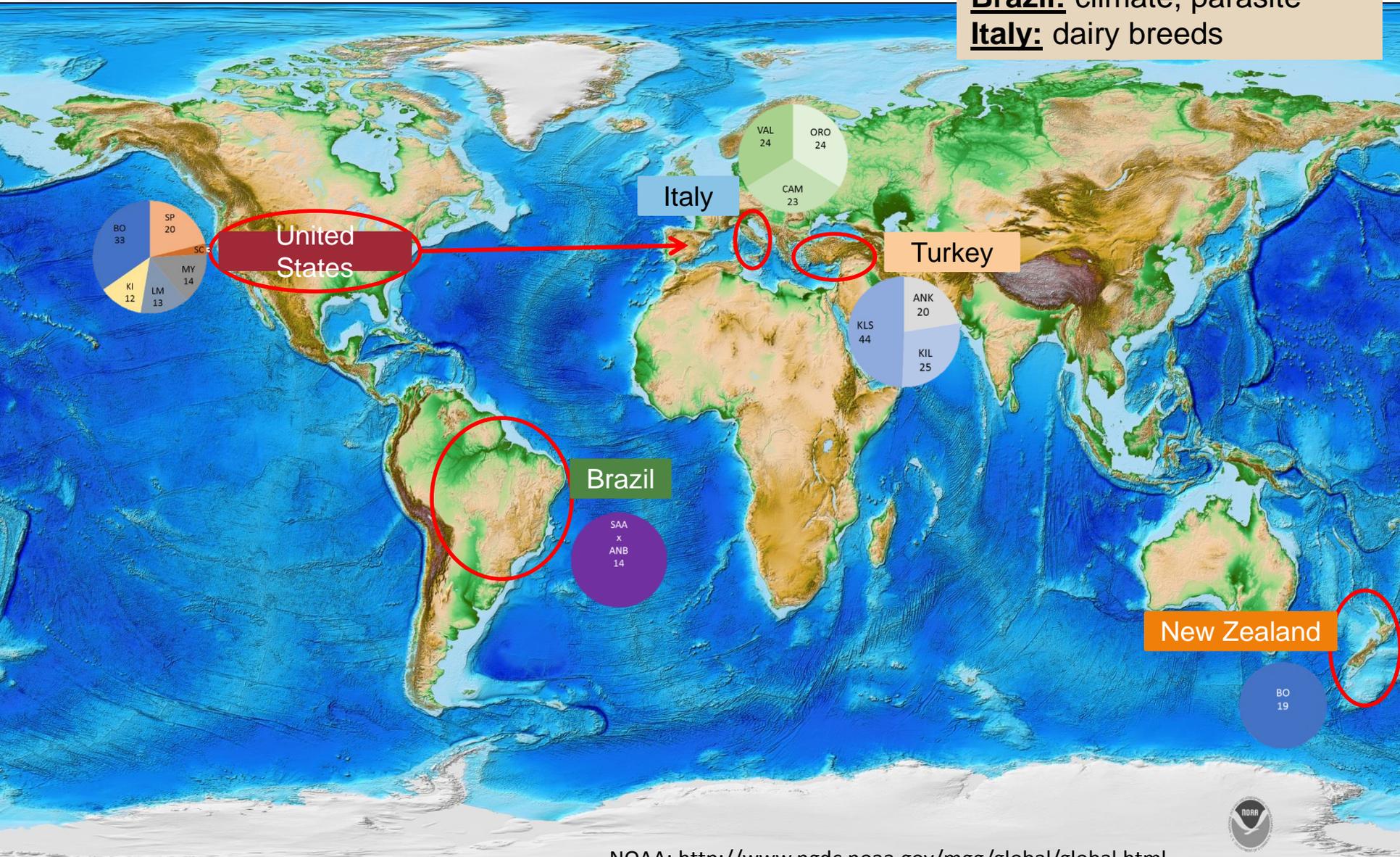
# Breeds sampled within Africa



- 11 African countries sampled
- 4 new FAO research projects being added

# Global Comparison

**US:** Spanish derived  
**New Zealand:** Boer  
**Turkey:** domestication  
**Brazil:** climate, parasite  
**Italy:** dairy breeds





# PHENOTYPING

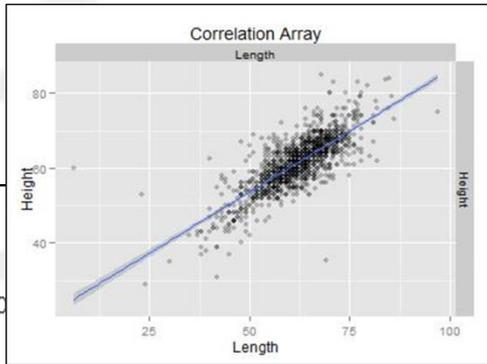
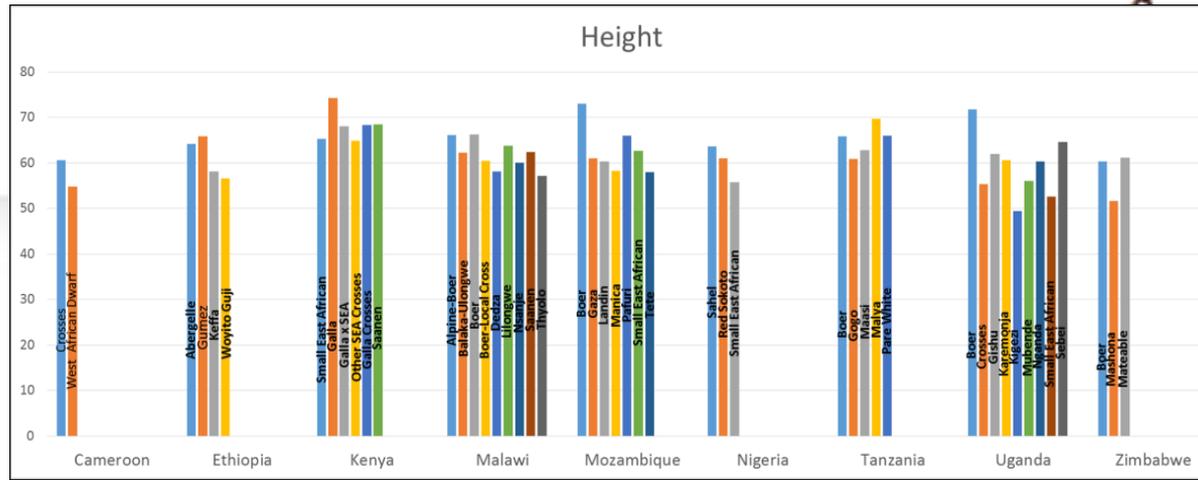
# Standardized Sampling Protocol



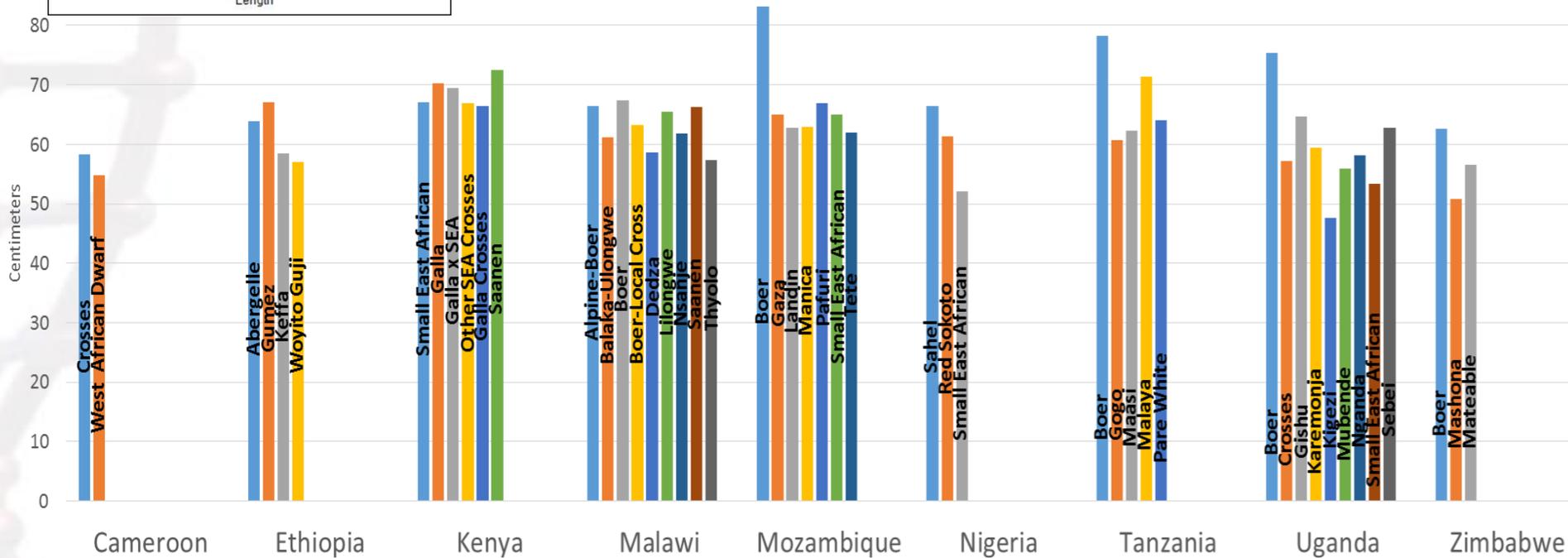
- Geographical information system (GIS) data
  - Latitude, longitude, elevation
- Physical body measurements
  - Chest girth, height, length, shoulder width, pin-bone width, weight
- Photo characterization
- Biological sample (DNA)



# Variation in body size



## Length

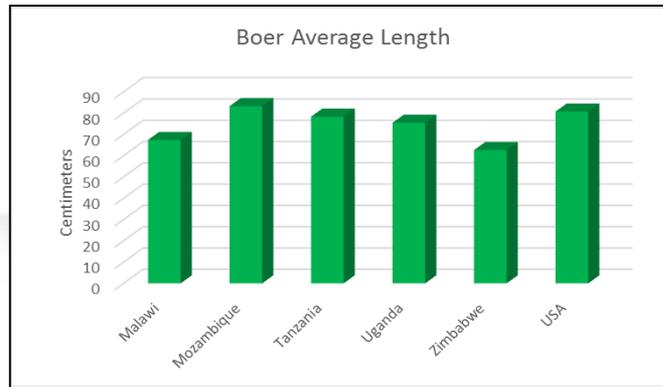


Is there a significance to size variation of breeds across different countries?



# Boer

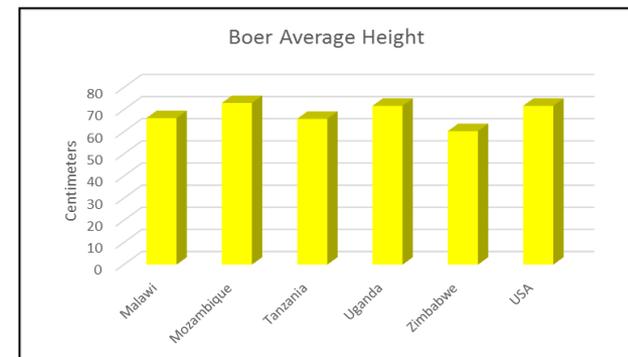
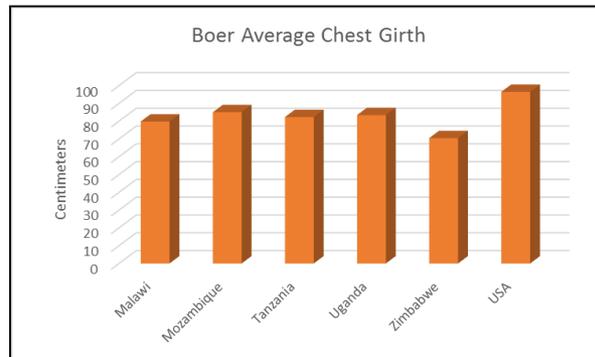
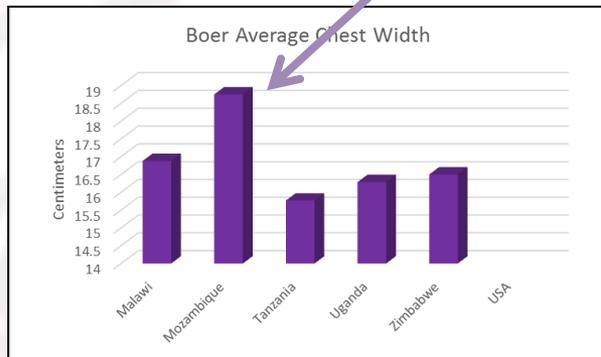
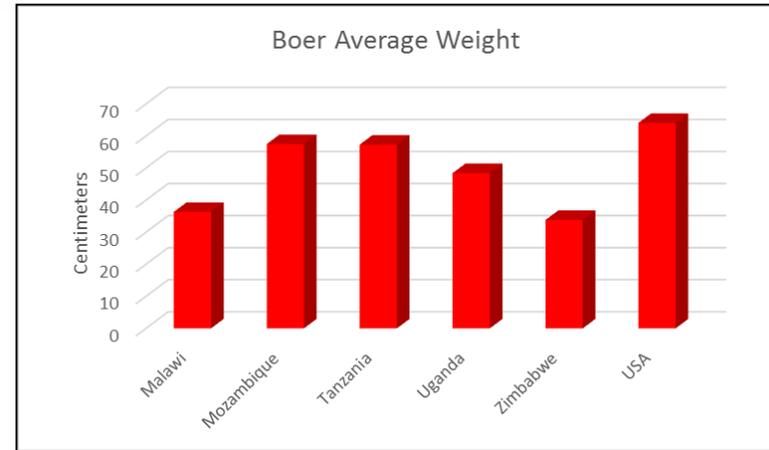
Country	# Goats
Malawi	18
Mozambique	2
Tanzania	13
Uganda	6
Zimbabwe	31
USA	15



## Points of Note:

**USA**- Are individuals significantly heavier?  
**Mozambique**- only 2 individuals  
**South Africa**???

*Develop plan to pursue Boer investigation...*



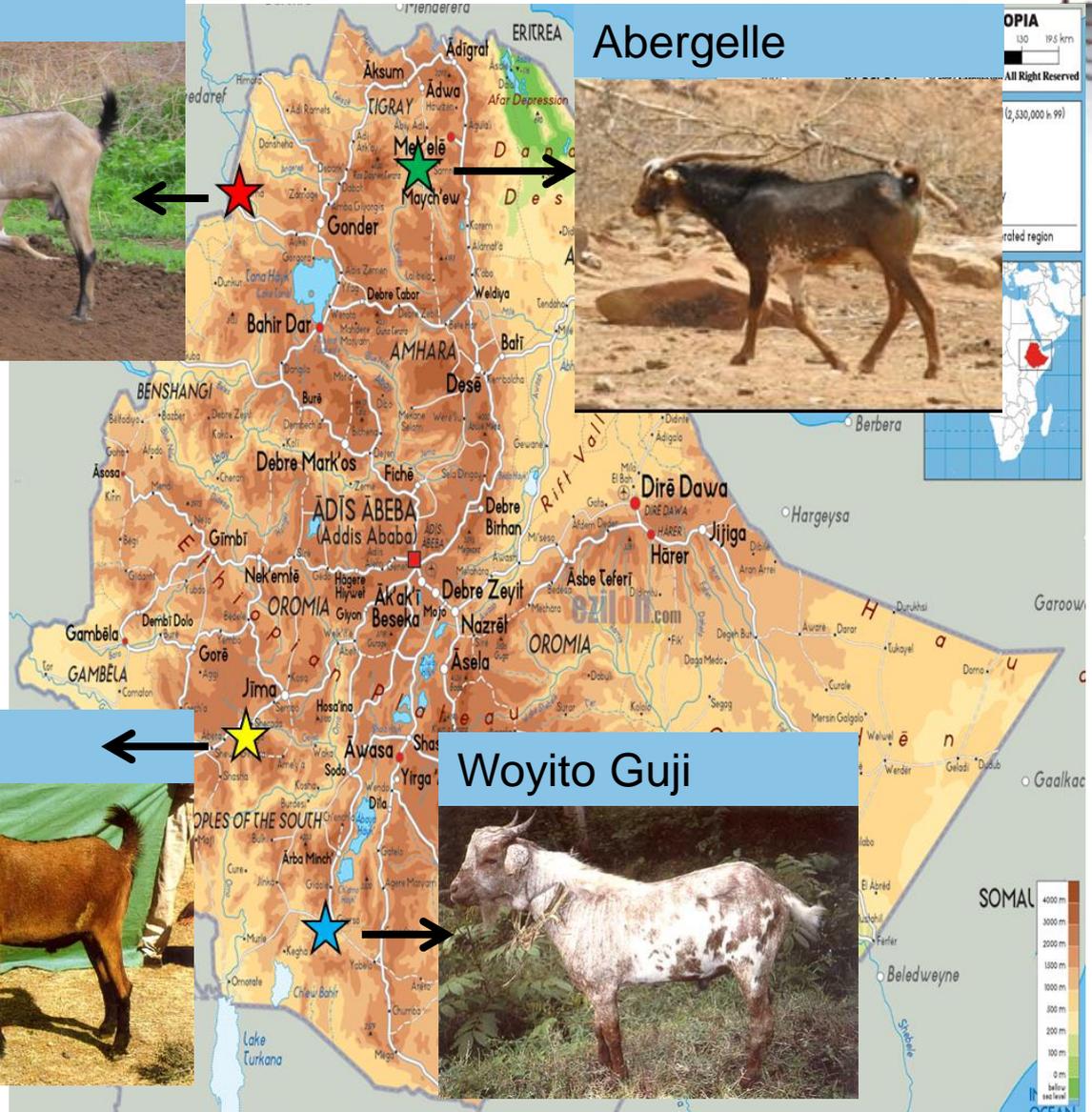
# Ethiopia



Gumez



Abergelle



Breed	# Goats
Abergelle	64
Gumez	53
Keffa	50
Woyito Guji	50

Keffa



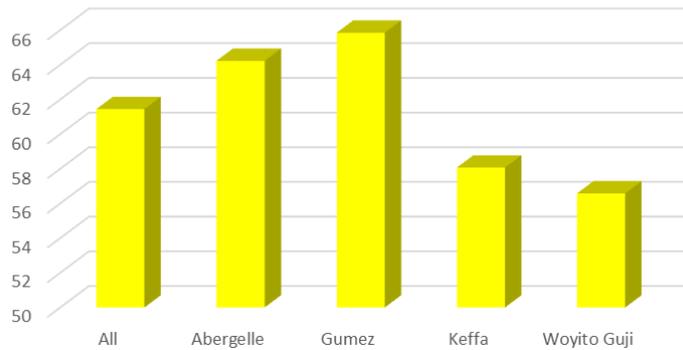
Woyito Guji



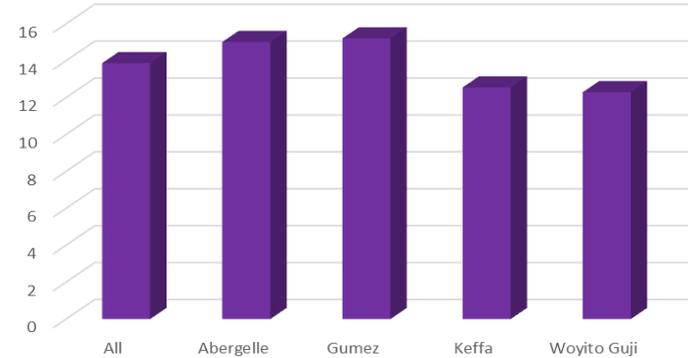
# Ethiopian Goats



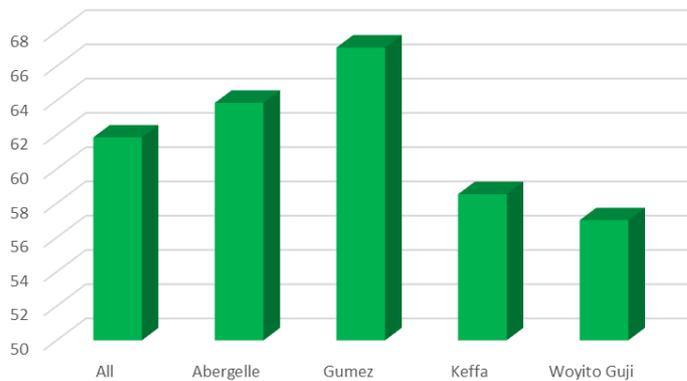
Ethiopia - Average Height



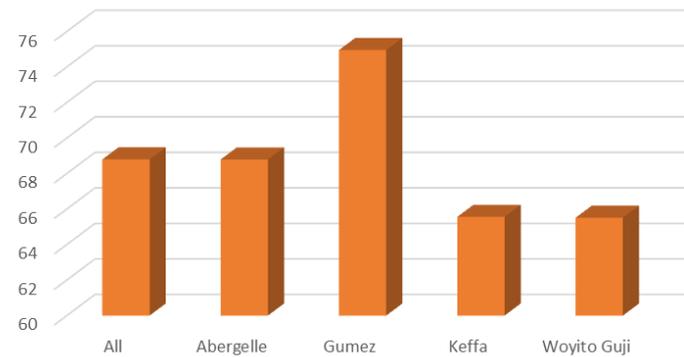
Ethiopia - Average Chest Width



Ethiopia - Average Length



Ethiopia - Average Chest Girth



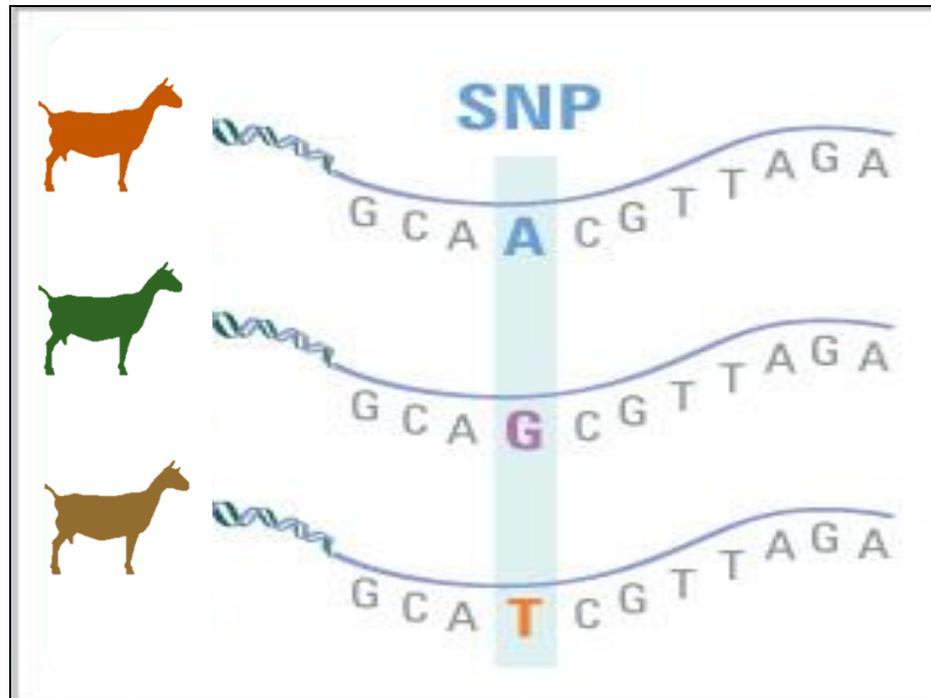


# GENOTYPING STATUS

# Quality Control Filtering



11 Countries, ~41 breeds/populations  
952 individuals  
53,347 SNPs



# Quality Control Filtering



**11 Countries, ~41 breeds/populations**

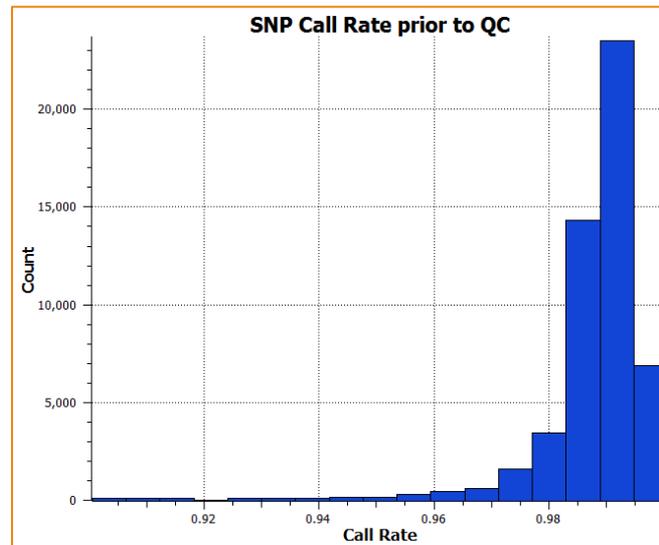
952 individuals

53,347 SNPs

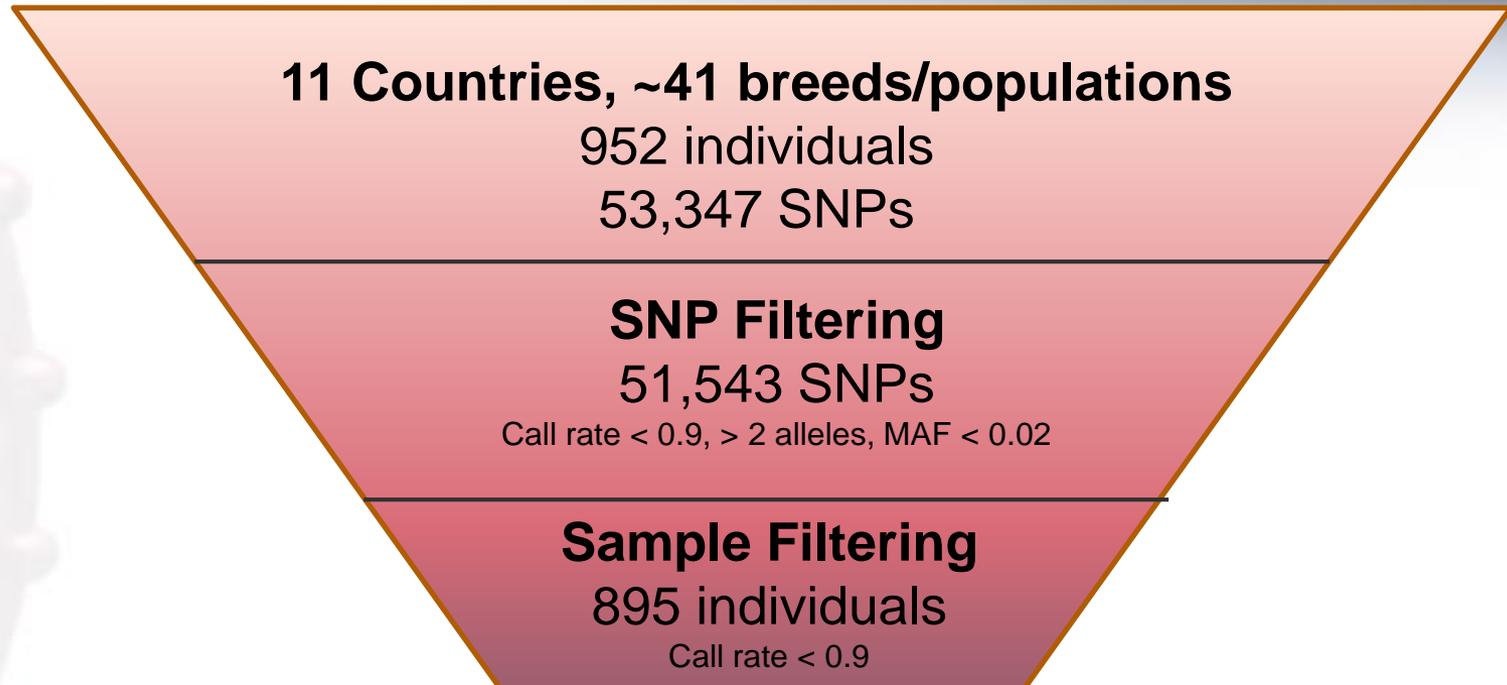
**SNP Filtering**

51,543 SNPs

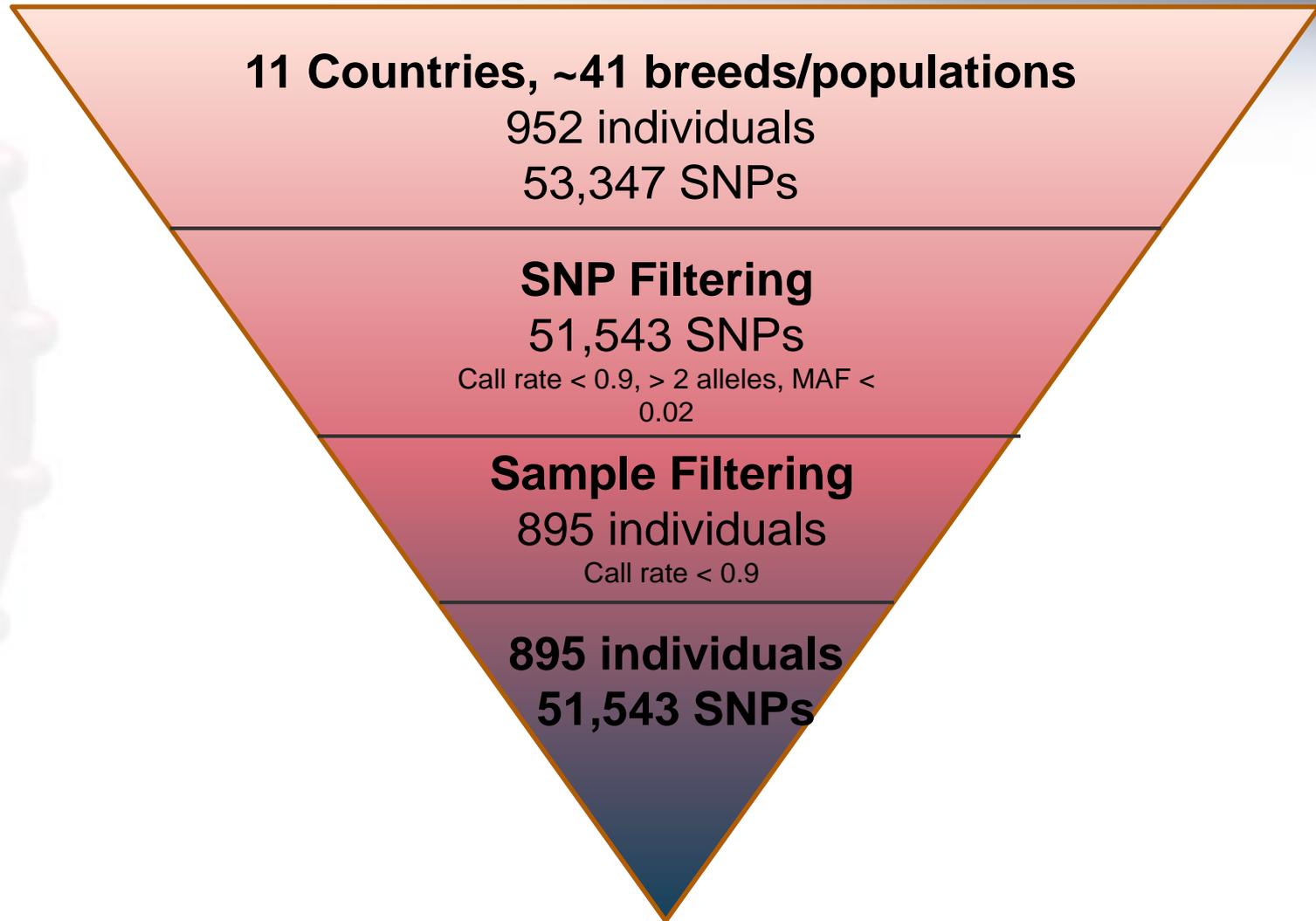
Call rate < 0.9, > 2 alleles, MAF < 0.02



# Quality Control Filtering



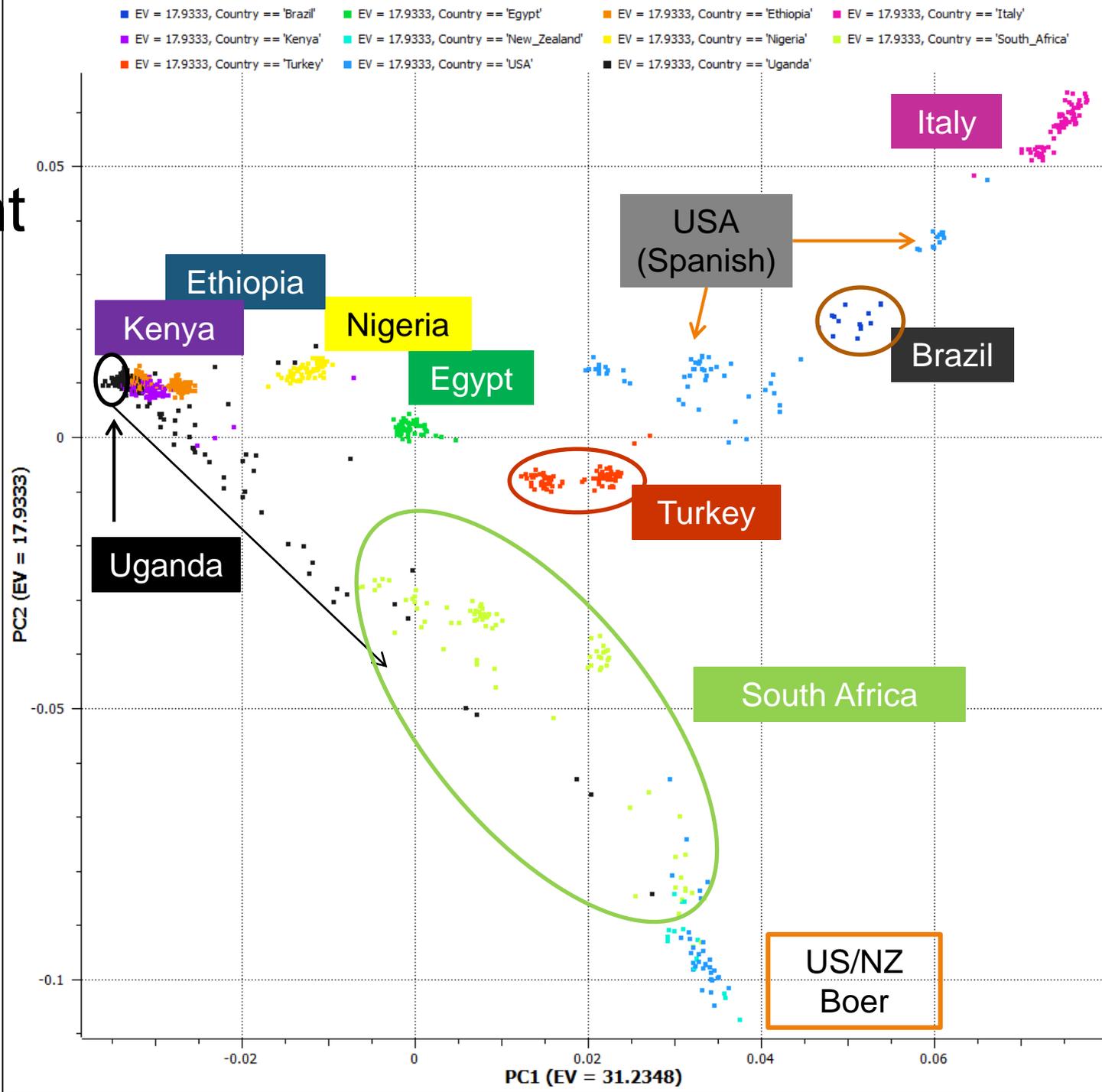
# Quality Control Filtering





# PROJECT ANALYSES

# Principle Component Analysis: PC1 vs PC2



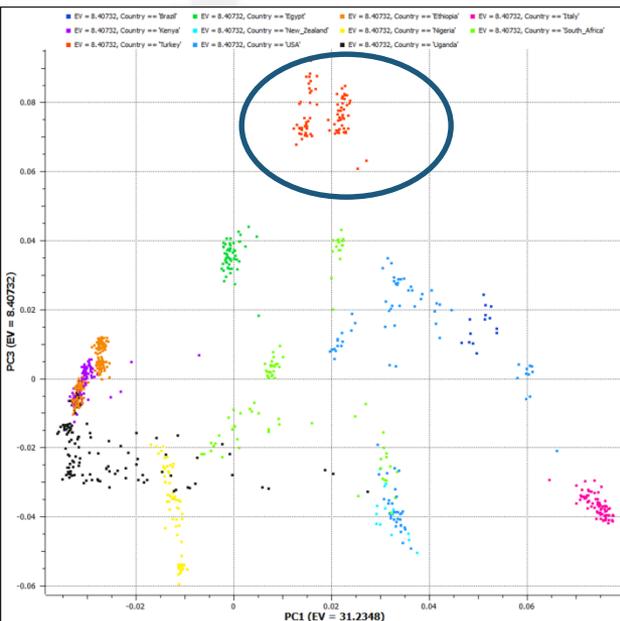
# Population dynamics from the PCA



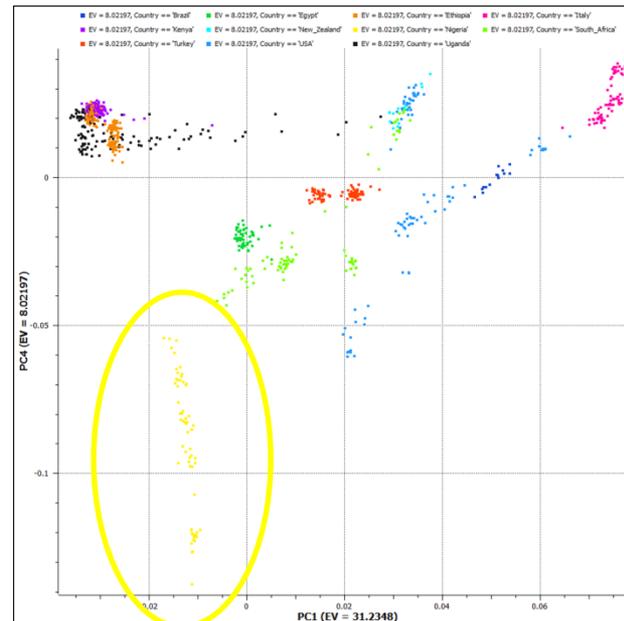
PC	Eigenvalue	Factor
1	31.23479	European – African
2	17.93332	Boer breed- South Africa
3	8.407324	Turkish breeds
4	8.021972	Nigerian breeds
5	5.329341	South African breeds

**Eigenvalue:** provides a measure of variation within the dataset for that component

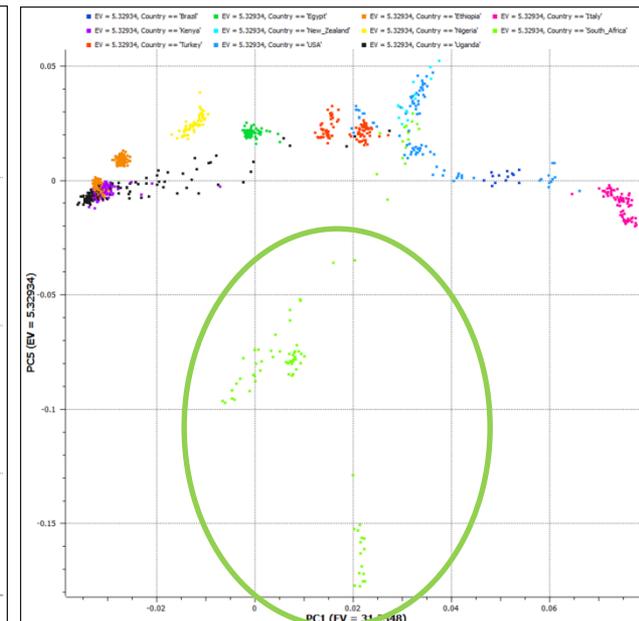
PC 3



PC 4



PC 5



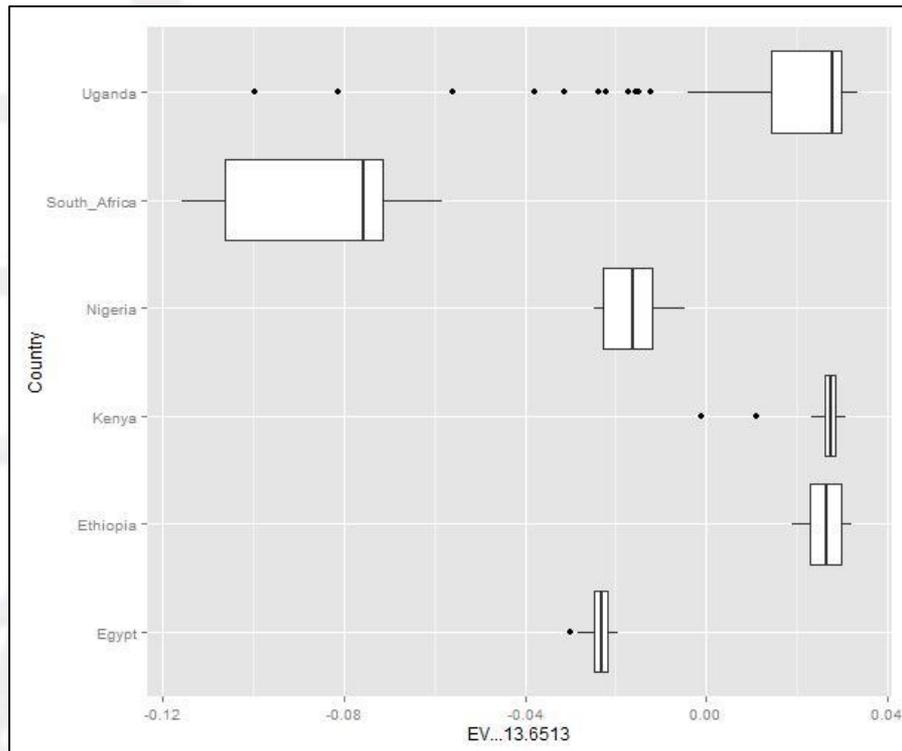
# PCA of African Countries Only



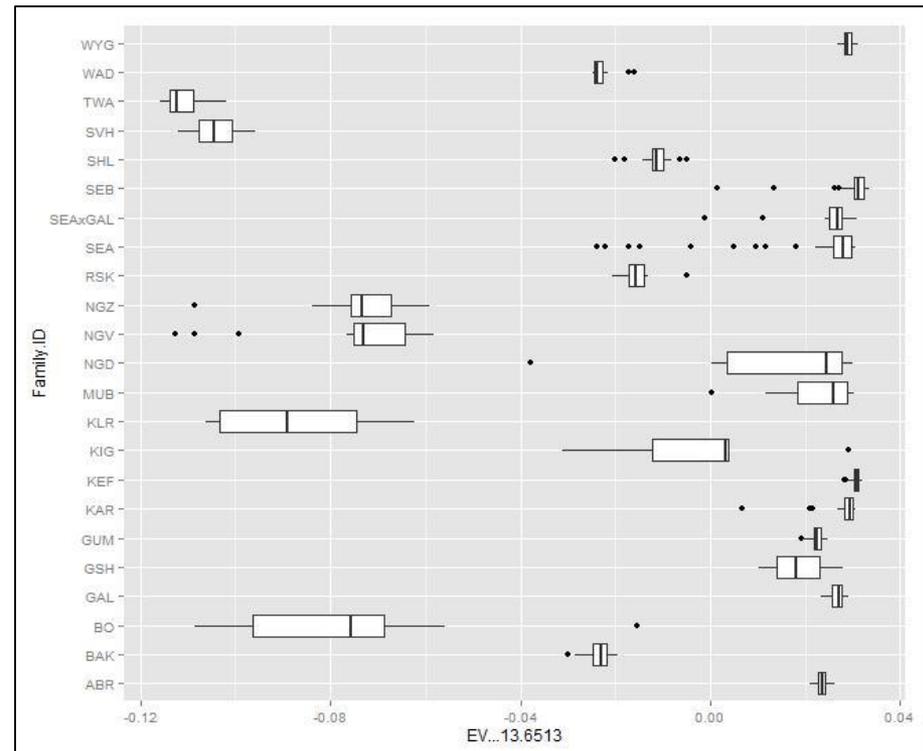
## Principle Component 1

EV = 13.65

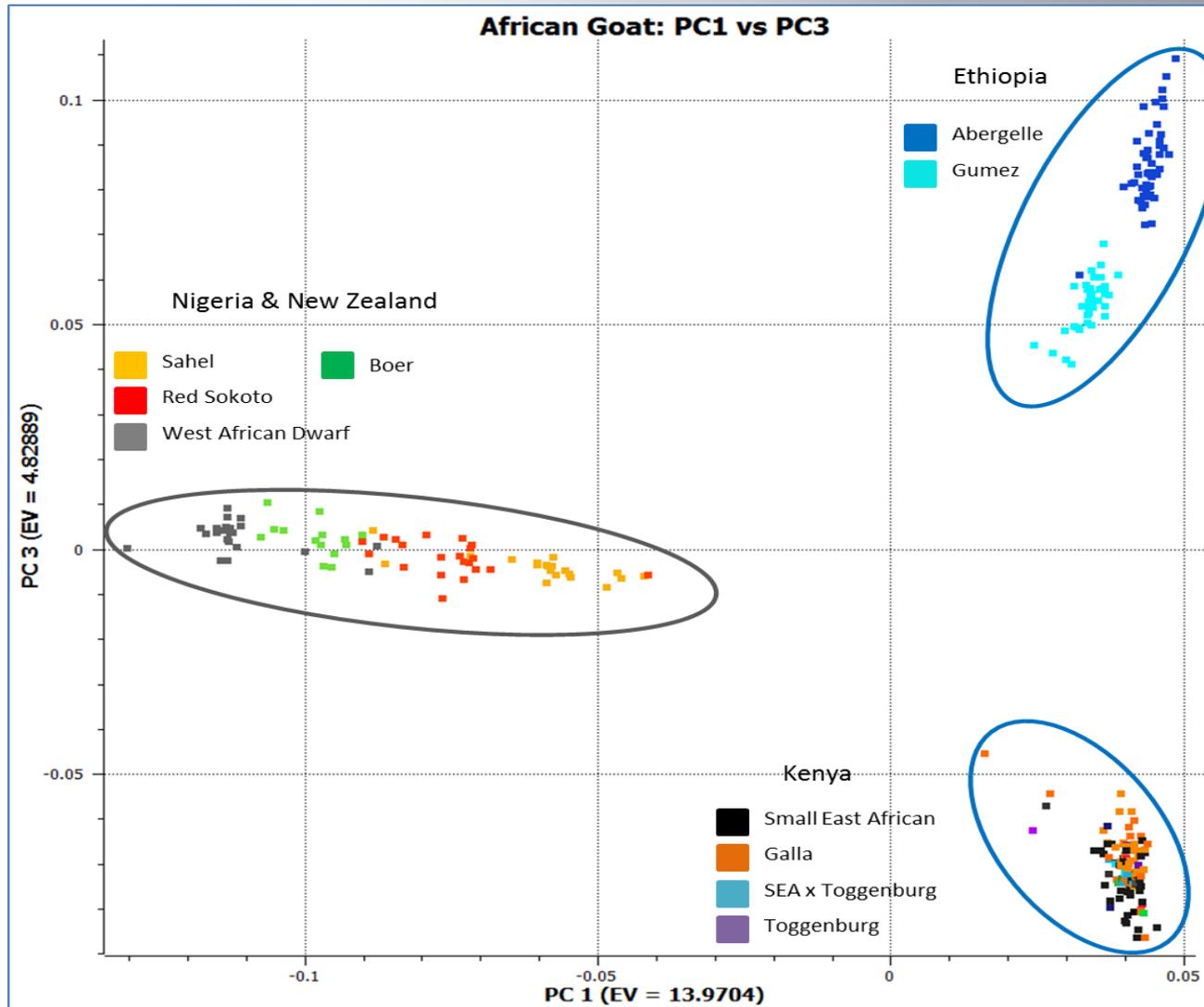
By Country



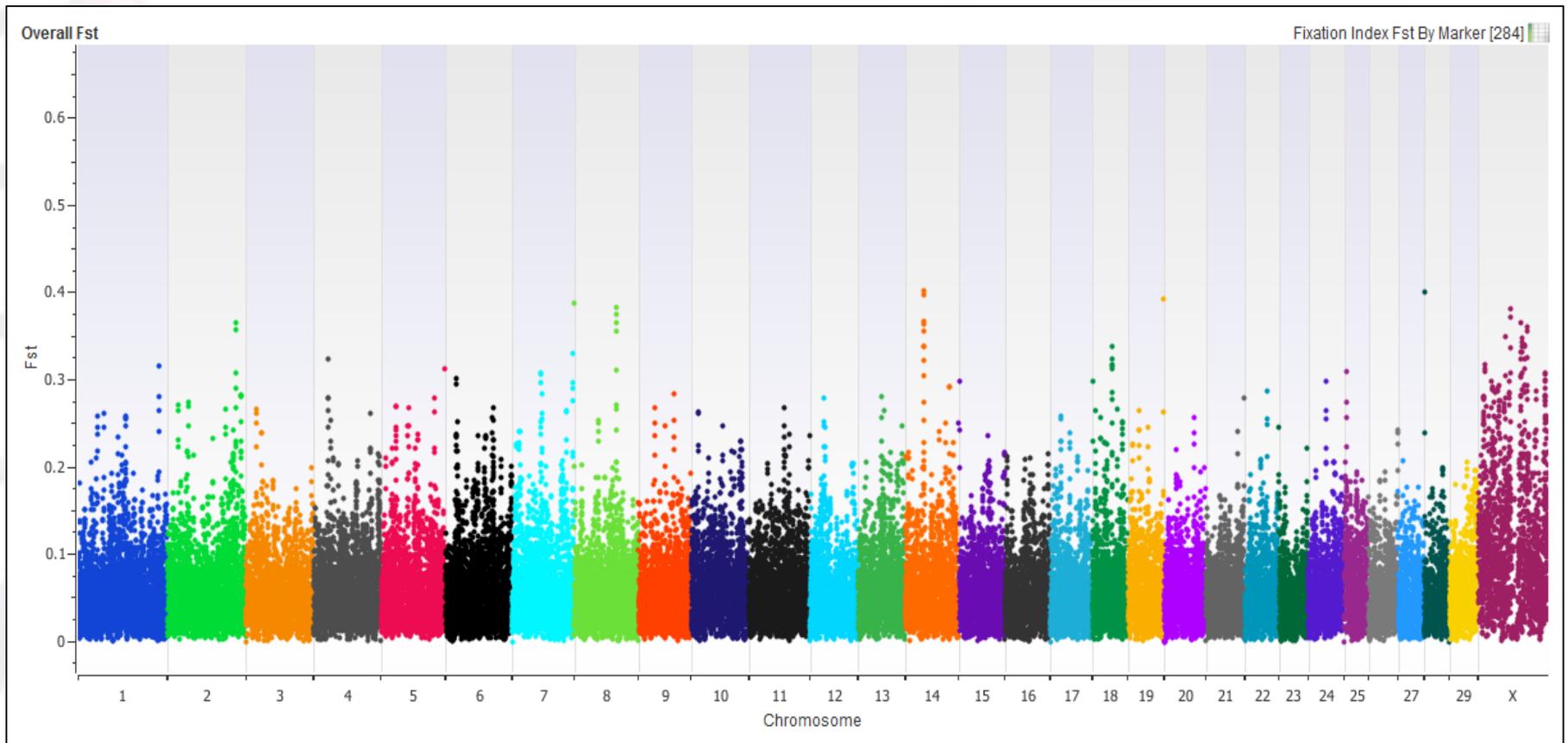
By Breed



# 3 African Countries & NZ Boer



# Signature of Selection- $F_{ST}$



# Outcomes



- Both body size and genetic investigation show variation among goat breeds
  - Level of significance?
- Genomic analysis of population structure through PCA shows both country and breed divergence
  - Further investigation into development of breeds and migration may provide insight into divergence patterns
- Genomic analysis demonstrates potential regions of the genome under selective pressure distinguishing African and European ancestry

# Research Strategy

- Genome-wide investigation
  - Thousands of markers across the genome
- Population Structure
  - Relatedness of individuals, breeds, ancestry
    - Inbreeding measures
    - Uniqueness of genetic signatures
    - Selection for conservation / improvement
- Genome-wide Association Studies
  - Identify regions of the genome in association with a trait (performance/production, morphology, health, adaptation)
    - Identify genetic regulation of trait
    - Identify diagnostic markers



# Acknowledgements



- ❖ Huson Lab, Cornell University
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  - ❖ Dr. Curt Van Tassell, USDA
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  - ❖ Dr. Antonio Landaeta-Hernandez, Univ. Venezuela
  - ❖ Dr. Tad Sonstegard, USDA



- ❖ African Goat Improvement Network
  - ❖ USAID
  - ❖ USDA
  - ❖ International Livestock Research Institute
  - ❖ Association for Strengthening Agricultural Research in Eastern & Central Africa
  - ❖ BOKU- University of Vienna
  - ❖ Agricultural Research Council
  - ❖ AgResearch- New Zealand
  - ❖ FAO



# Questions?

