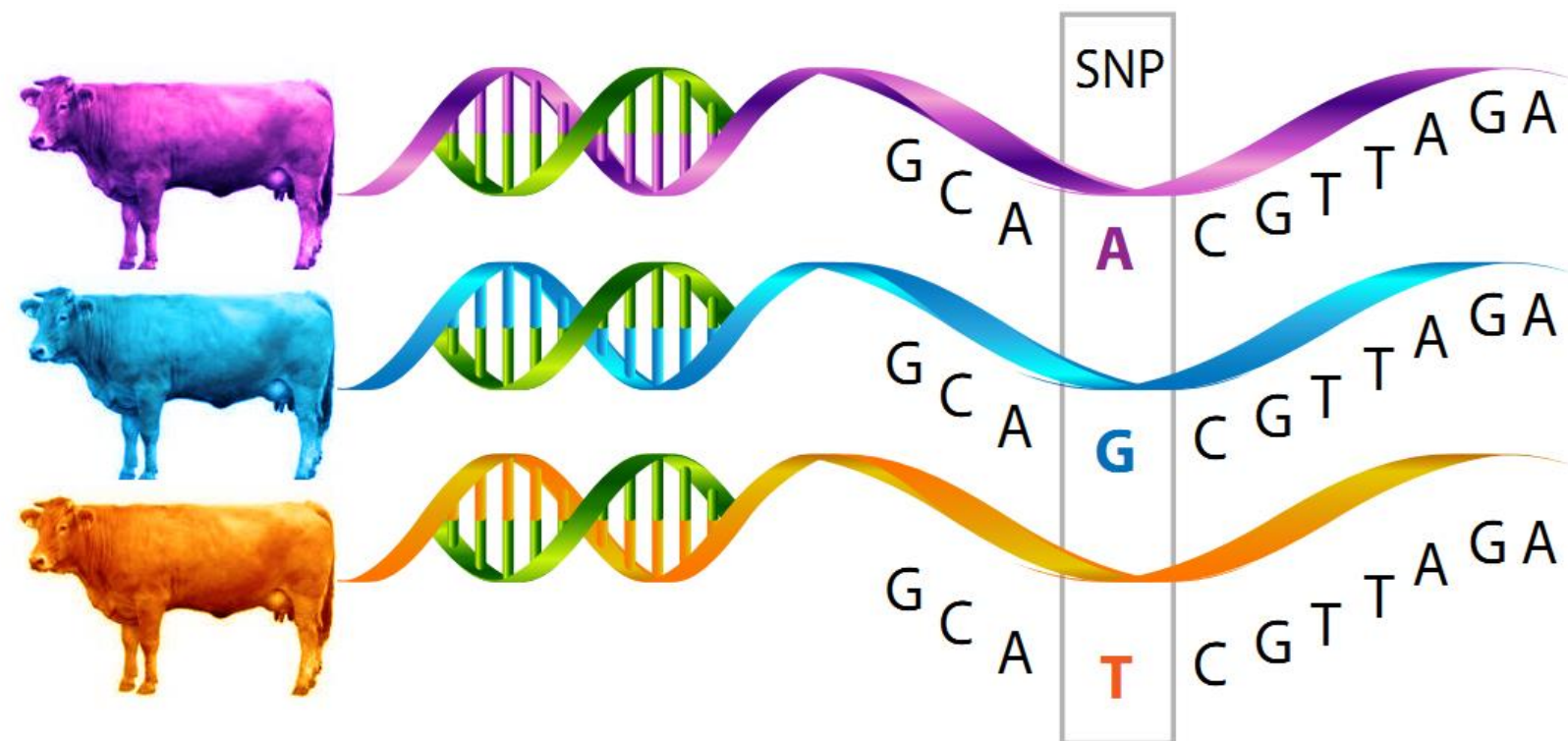


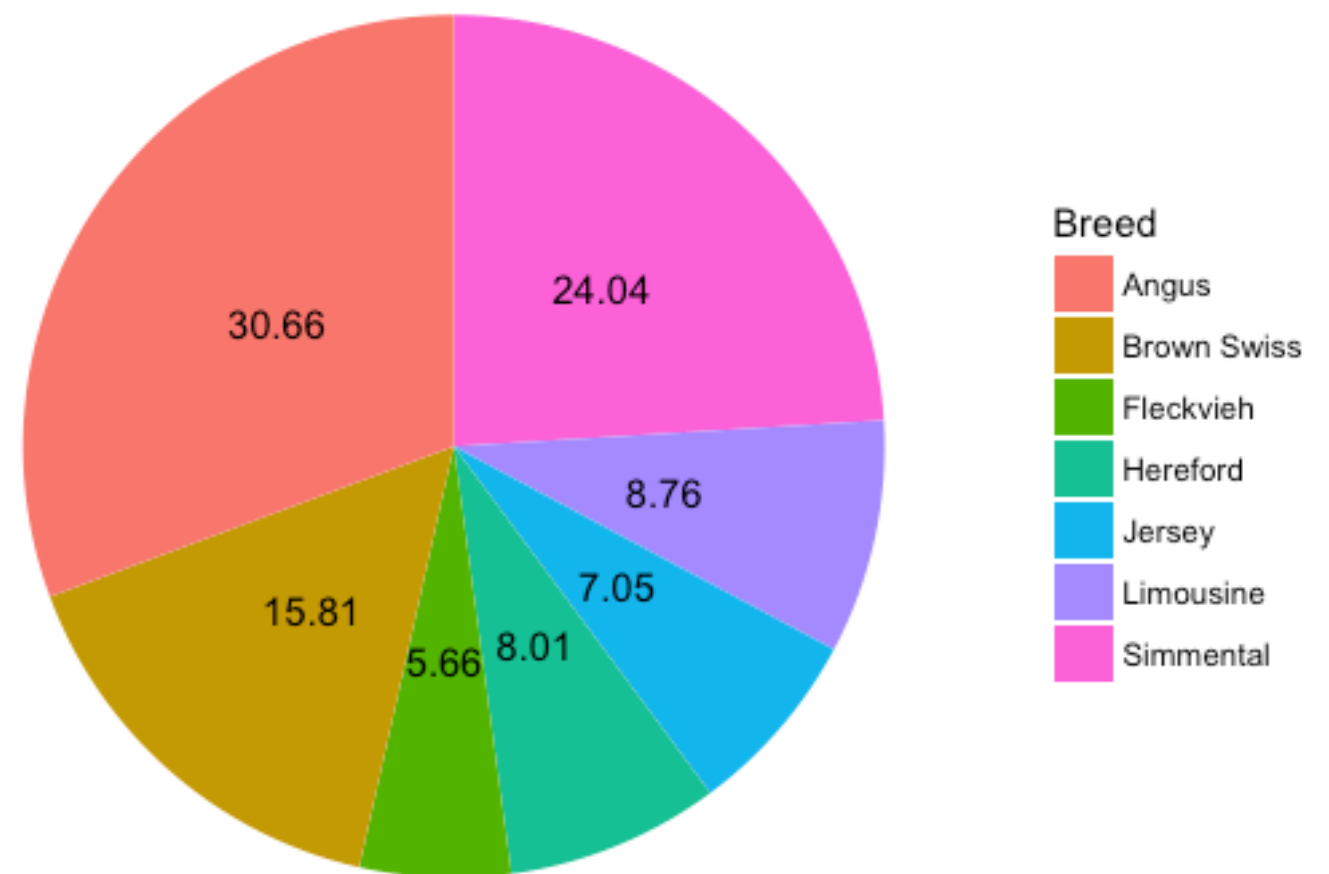
Objectives

- Identification of breed-specific SNPs
- Creating breed-specific reference genomes
- Annotation of breed-specific SNPs



Material

- Whole genome DNA-seq – 936 individuals
- Reference genome UMD 3.1

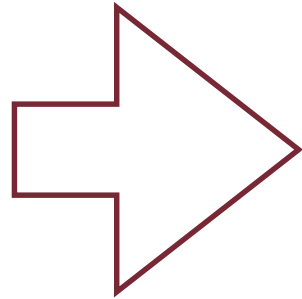


Methods

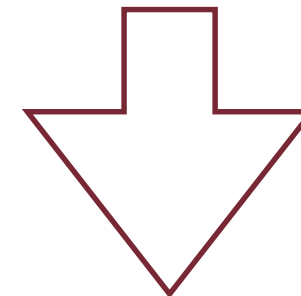
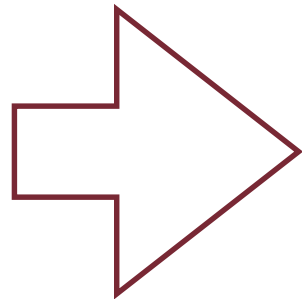
ALIGNMENT

BWA-MEM

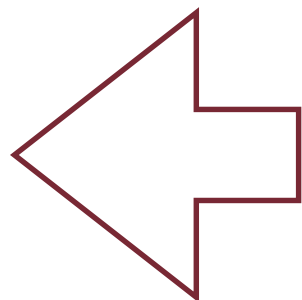
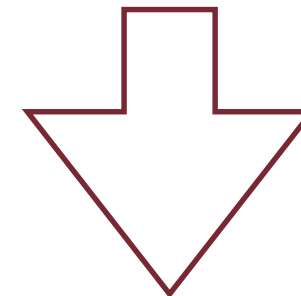
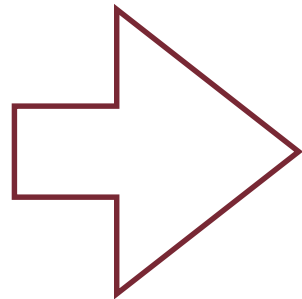
Methods



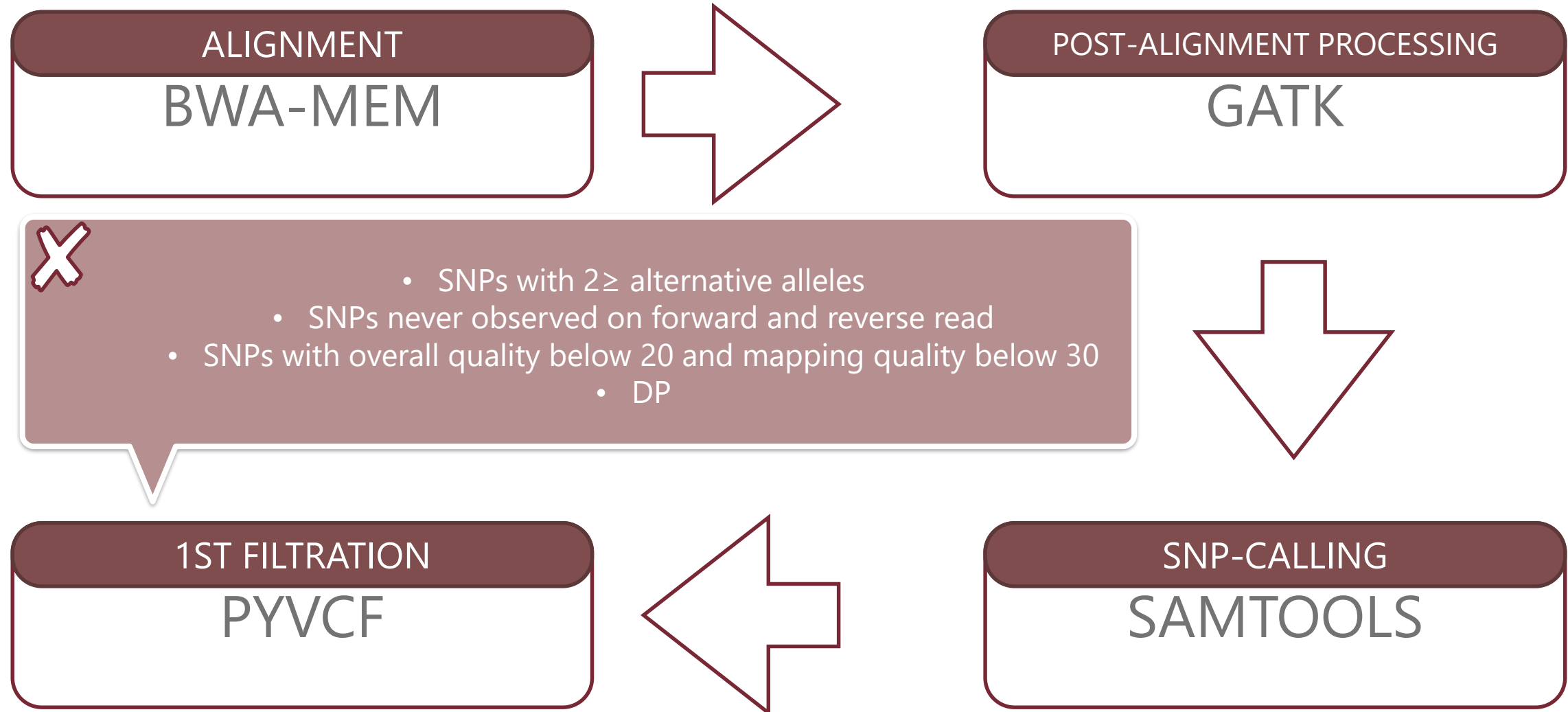
Methods



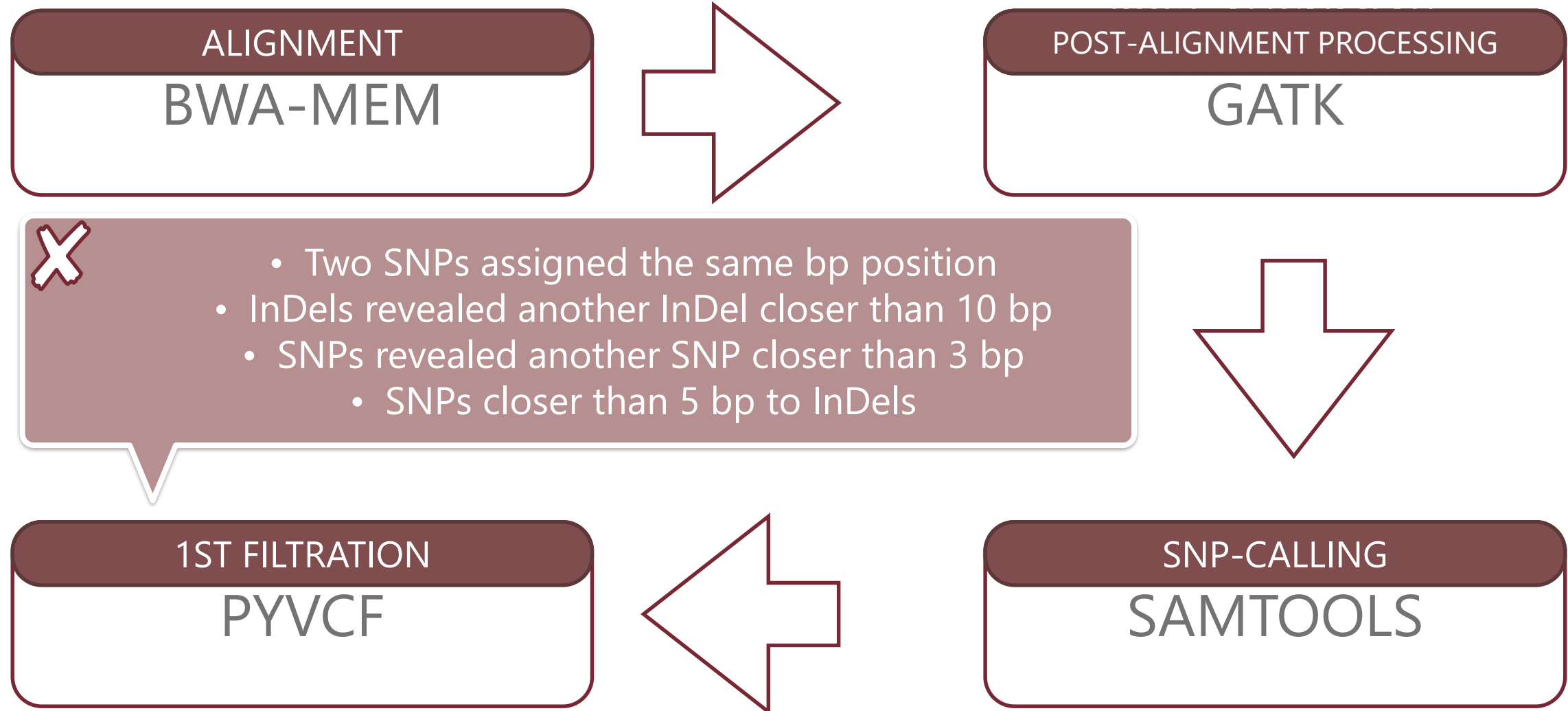
Methods



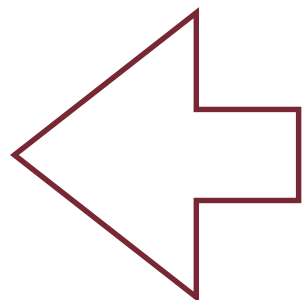
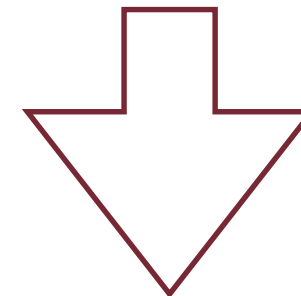
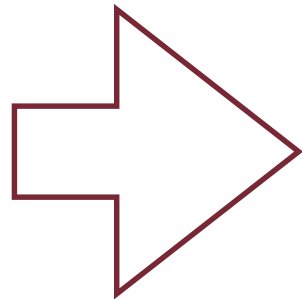
Methods



Methods



Methods



Methods

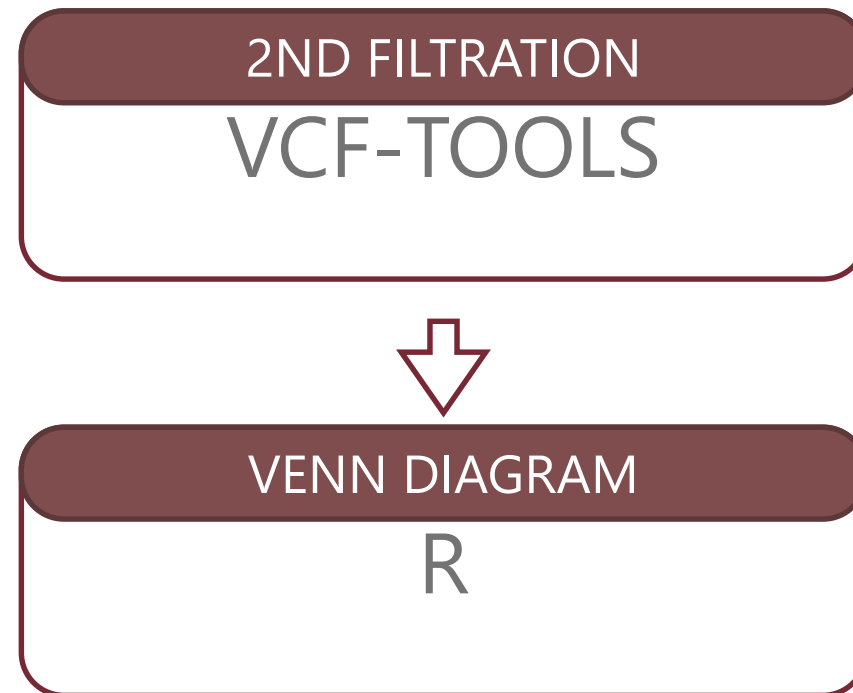


- AF \neq 1
- Missing genotypes >7%

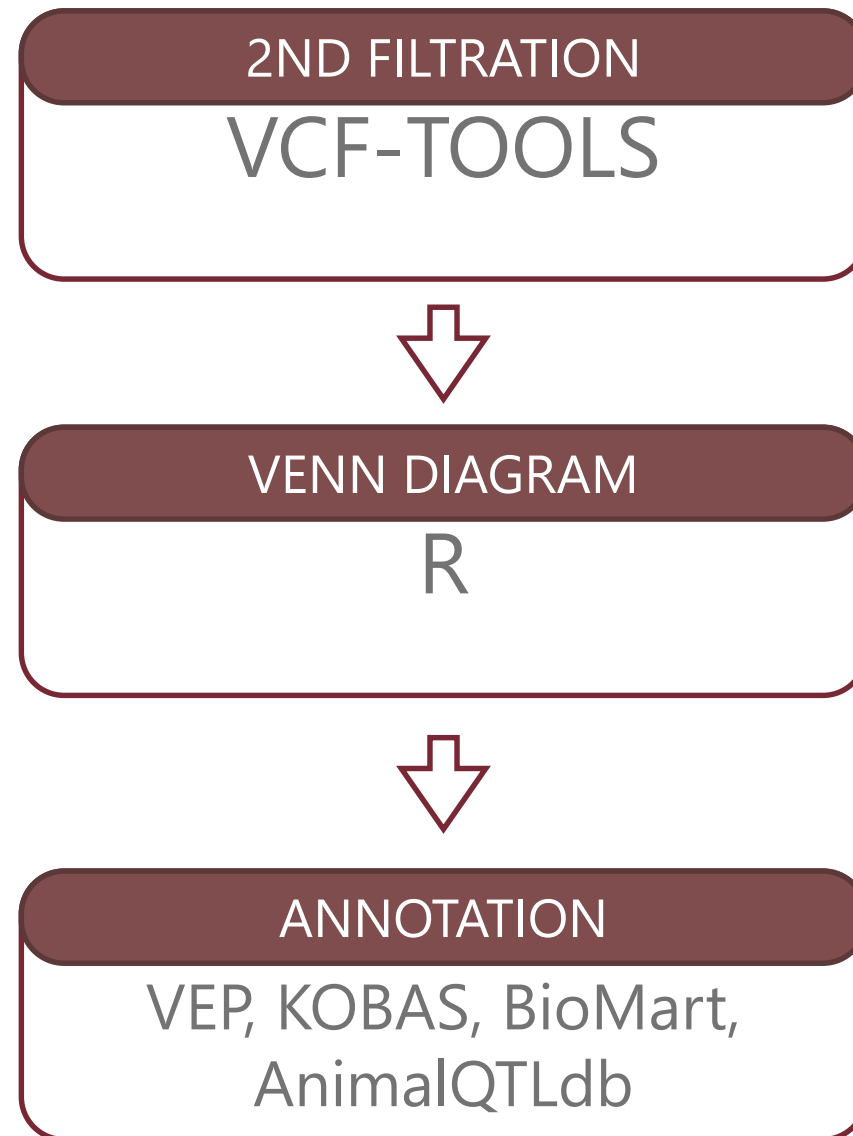
2ND FILTRATION

VCF-TOOLS

Methods



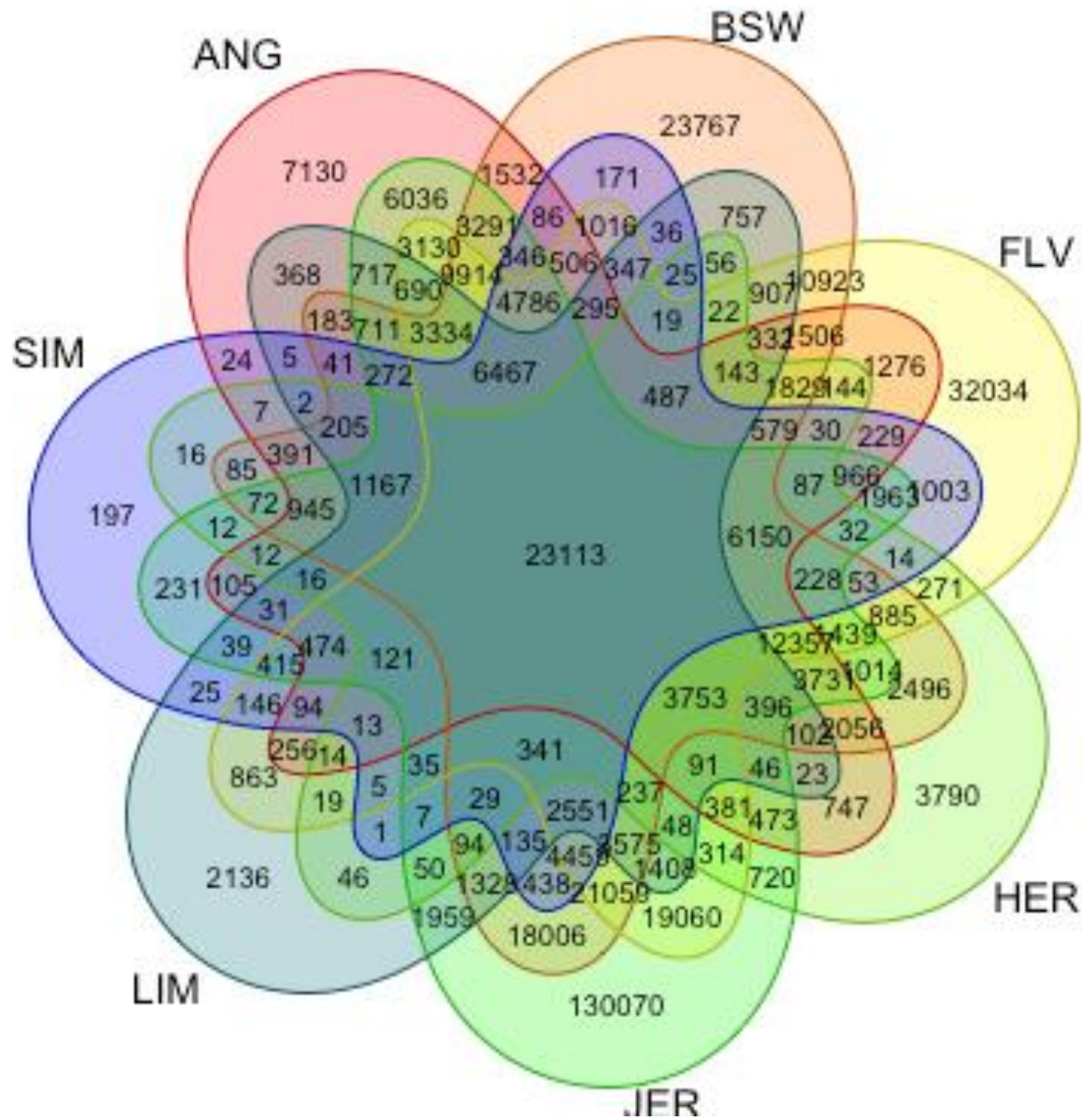
Methods



Results

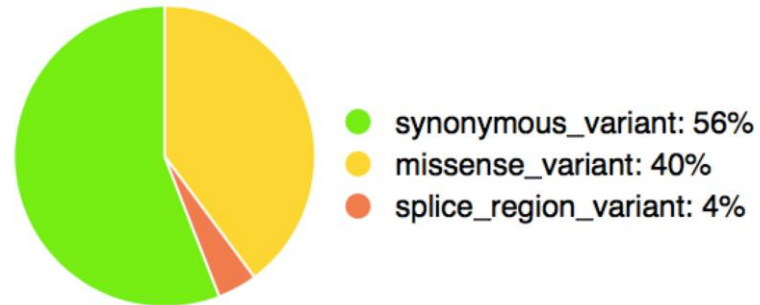
Breed	Total number of SNPs	Number of breed-specific SNPs	% of breed-specific SNPs
Angus	61 823 312	117 744	0.186
Brown Swiss	61 814 873	187 576	0.303
Fleckvieh	61 780 912	189 238	0.306
Hereford	61 813 028	73 772	0.119
Jersey	61 797 641	305 477	0.494
Limousin	61 820 287	61 623	0.100
Simmental	61 824 209	60 582	0.098

Results

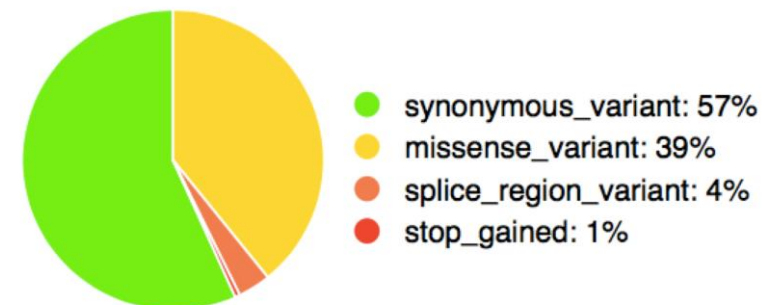


Results

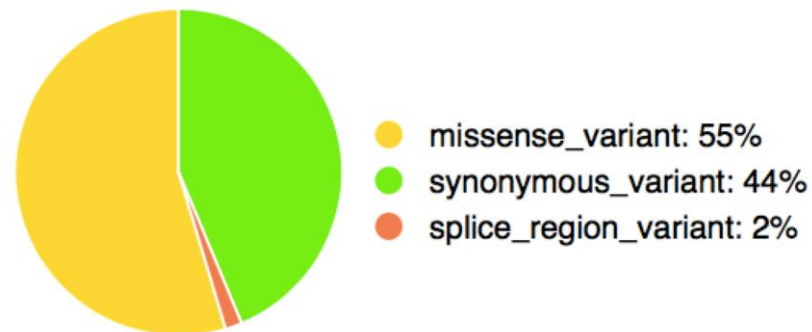
ANGUS



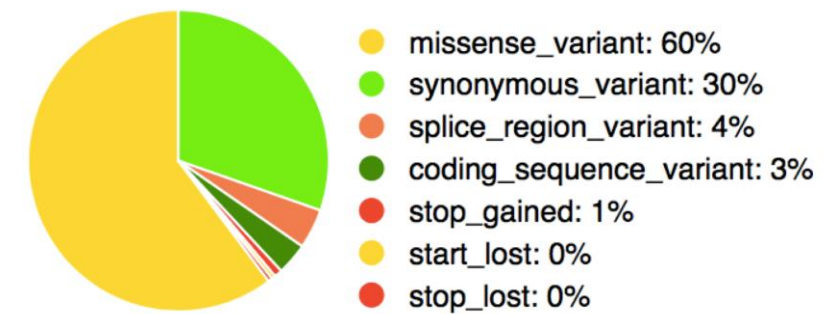
BROWN SWISS



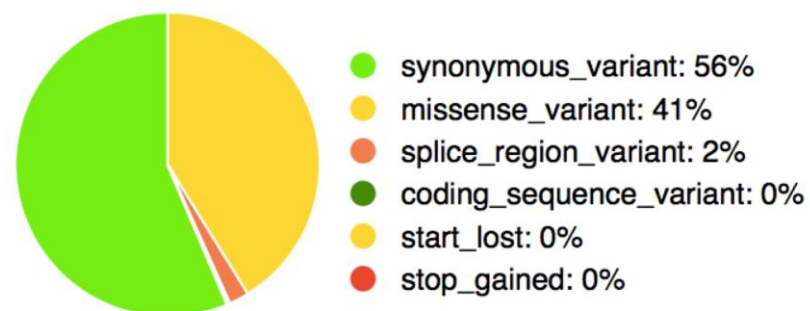
FLECKVIEH



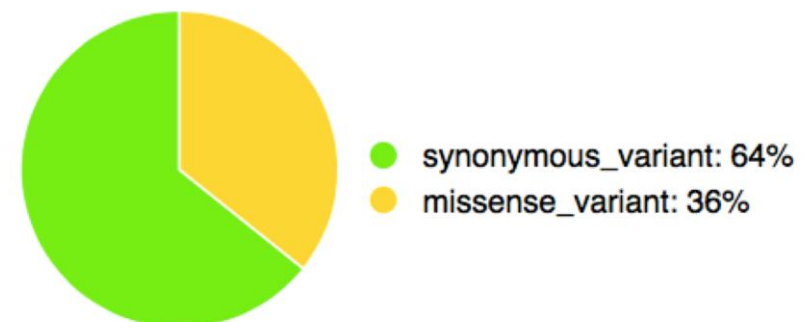
HEREFORD



LIMOUSINE



SIMMENTAL



Results



ANGUS

- *SLC39A4* (BTA14) –
Acrodermatitis enteropathica

JERSEY

- *GON4L* (BTA3) – dwarfism
- *APOB* (BTA11) – cholesterol deficiency
- *TG* (BTA14) – familial goitre
 - *COL7A1* (BTA22) -
Epidermolysis bullosa

BROWN SWISS

- *SLC4A2* (BTA4) –
Osteopetrosis
- *LAMA3* (BTA24) –
Epidermolysis bullosa

LIMOUSINE

- *PFAS* (BTA19) – abortion

Results

Animal QTLdb

ANGUS

- iron content in mussels

BROWN SWISS

- milk characteristics: milk solids, overall proteins, alpha-casein, alpha-lactalbumin, kappa-casein, beta-casein percentages, milk lactose content and yield
 - somatic cell score
- growth traits: body weight, longissimus muscle area and gastrointestinal nematode burden

Conclusions

- Differences observed between breeds express the dynamics of changes in the *Bos taurus* genome
- Breed specific reference genomes increase the accuracy of GWAS and SNP genotypes imputation

Acknowledgement



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POLAND



The Leading National
Research Centre

Wroclaw Centre of Biotechnology 2014-2018



1000 bull genomes project

1000 bull genomes project consortium



Thank you for your attention!



Czech B, Frąszczak M, Mielczarek M, Szyda J (2018)
Identification and annotation of breed-specific single nucleotide
polymorphisms in *Bos taurus* genomes. PLoS ONE 13(6): e0198419.
<https://doi.org/10.1371/journal.pone.0198419>