Economic Development,
Jobs, Transport
and Resources

Red Breed genomics
The science update

Irene van den Berg

AGRICULTURE VICTORIA

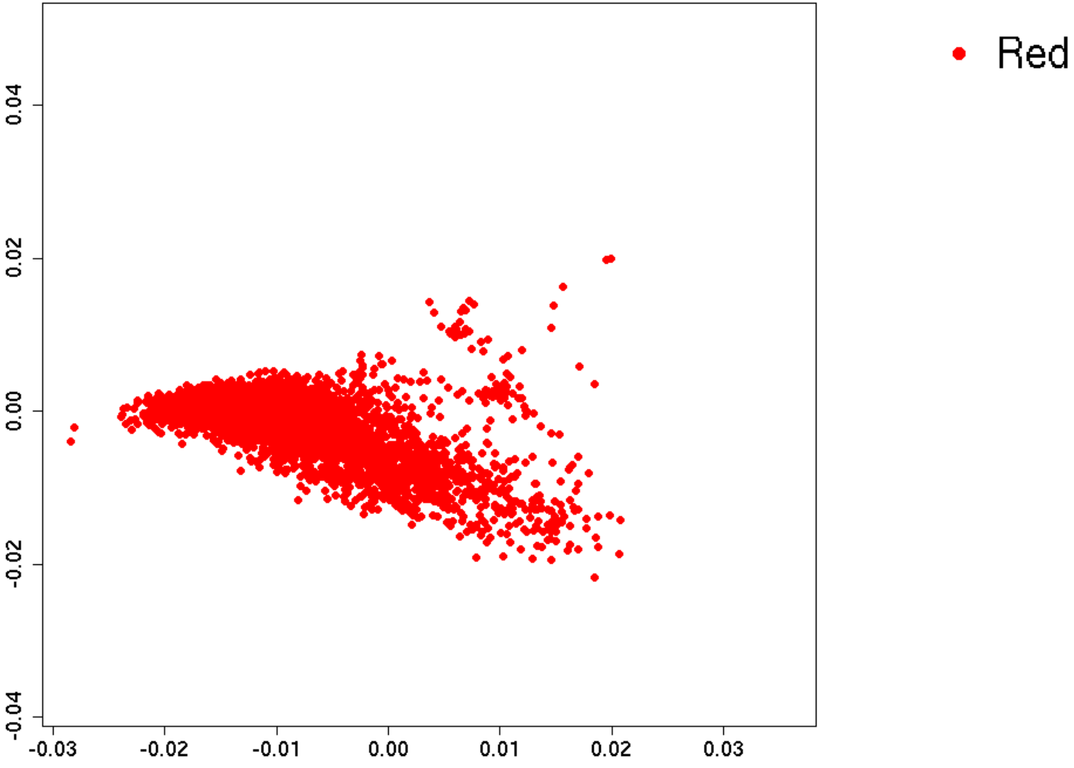
Australian Red cattle

Combining different Red dairy breeds:

- Scandinavian Red
- Ayrshire
- Dairy shorthorn
- Illawarra
- Red and white Holstein

AustralianReds
THE AUSTRALIAN RED DAIRY BREED

Australian Red cattle – relationships to other cattle breeds



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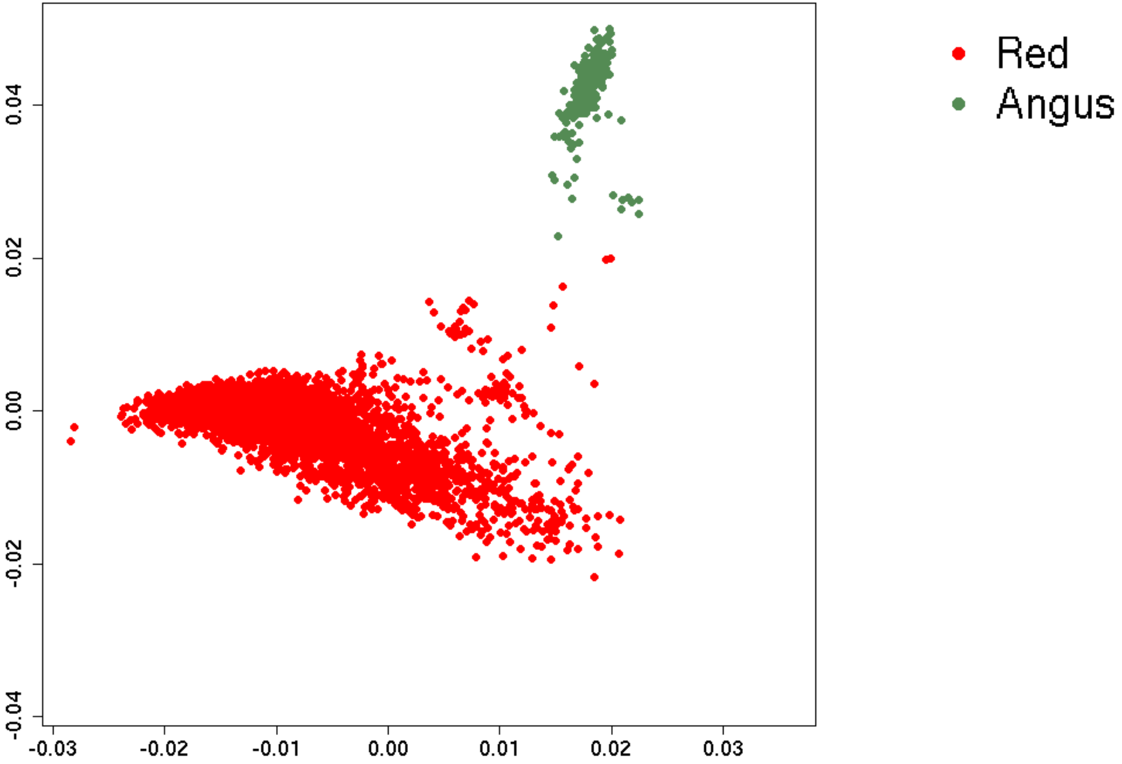

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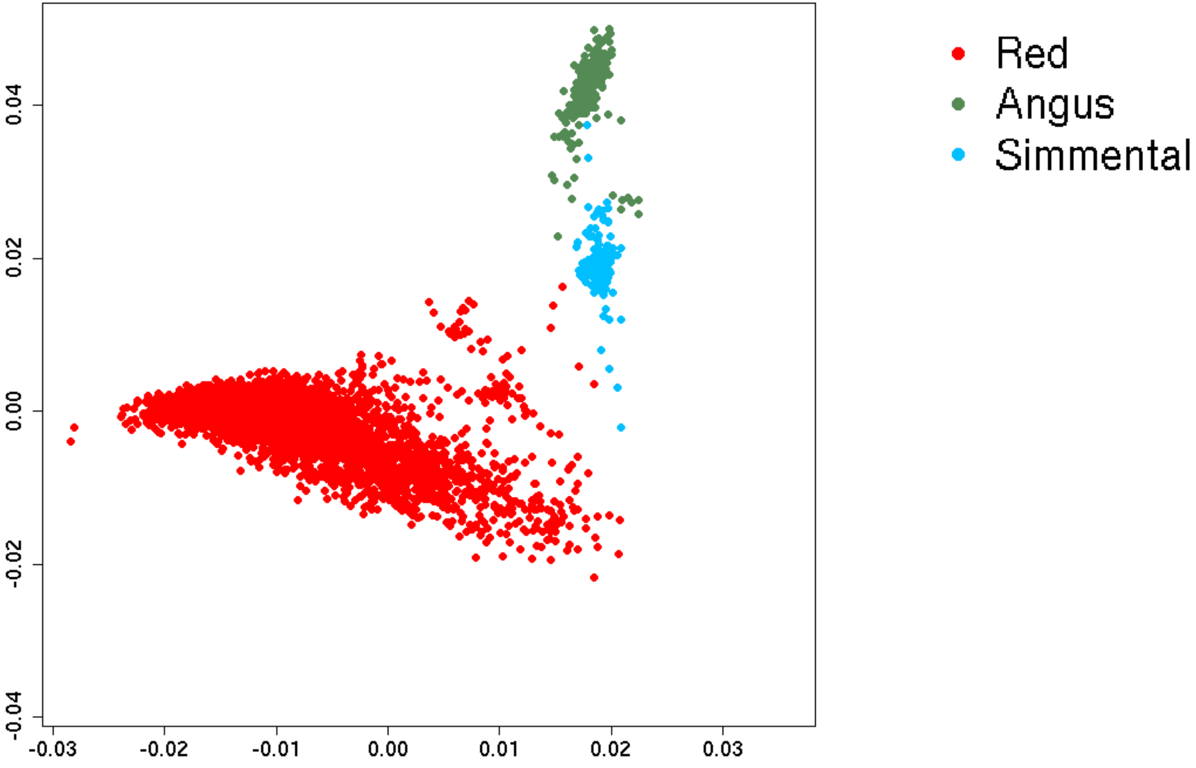

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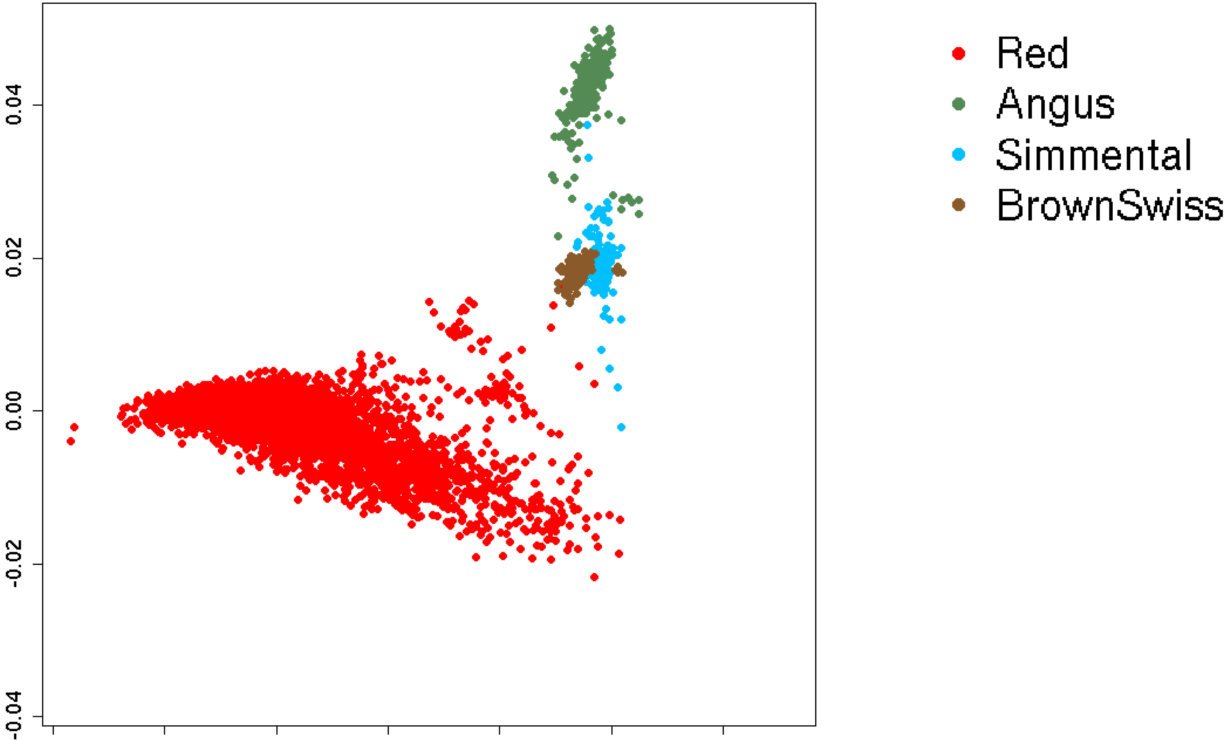

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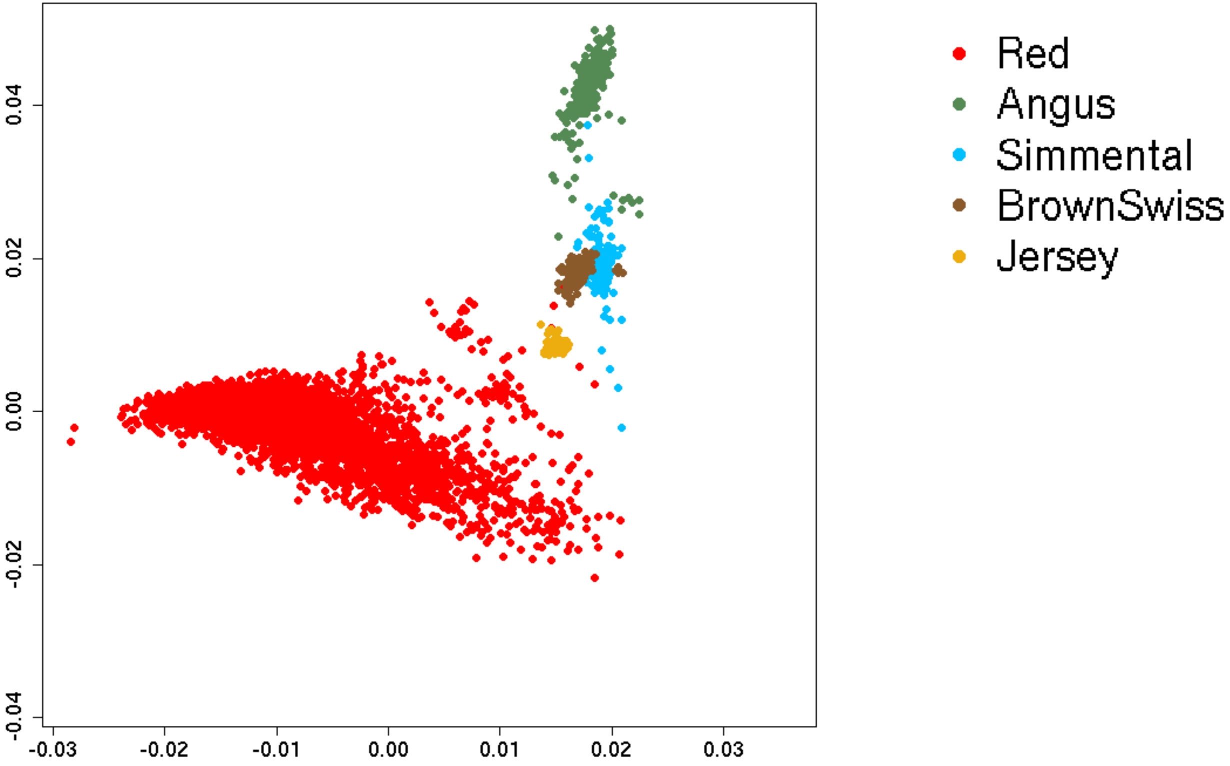

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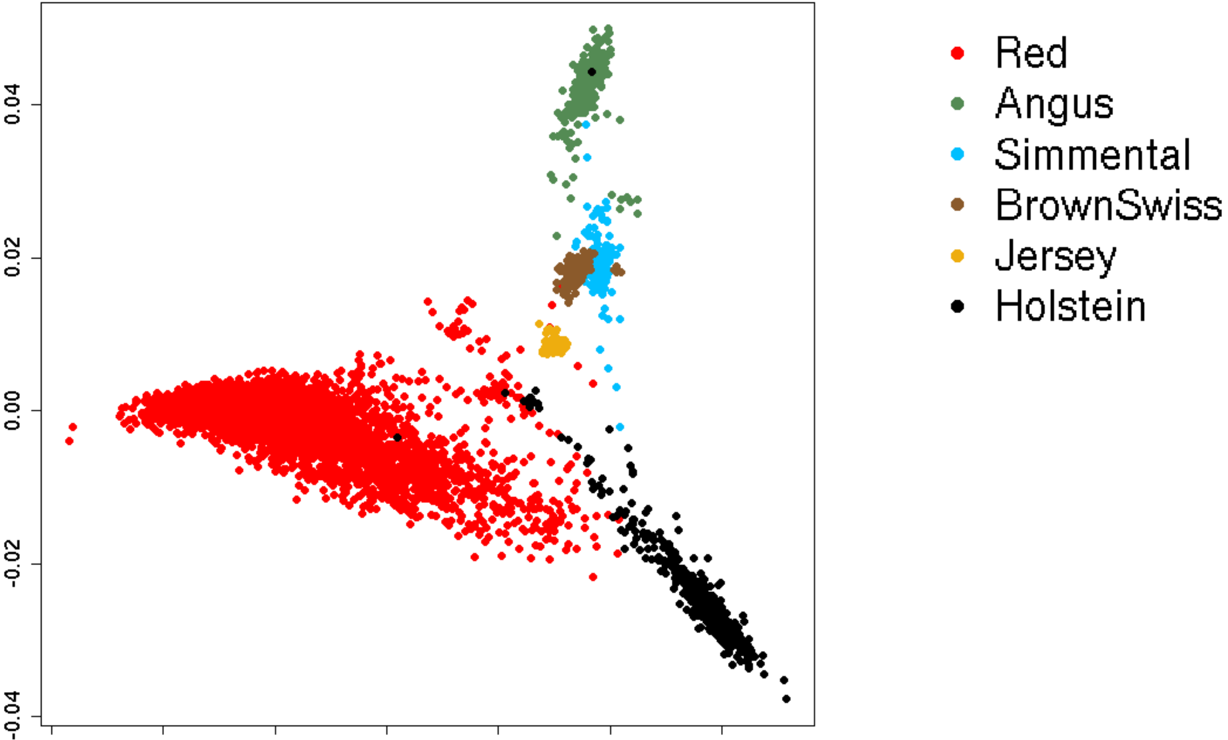
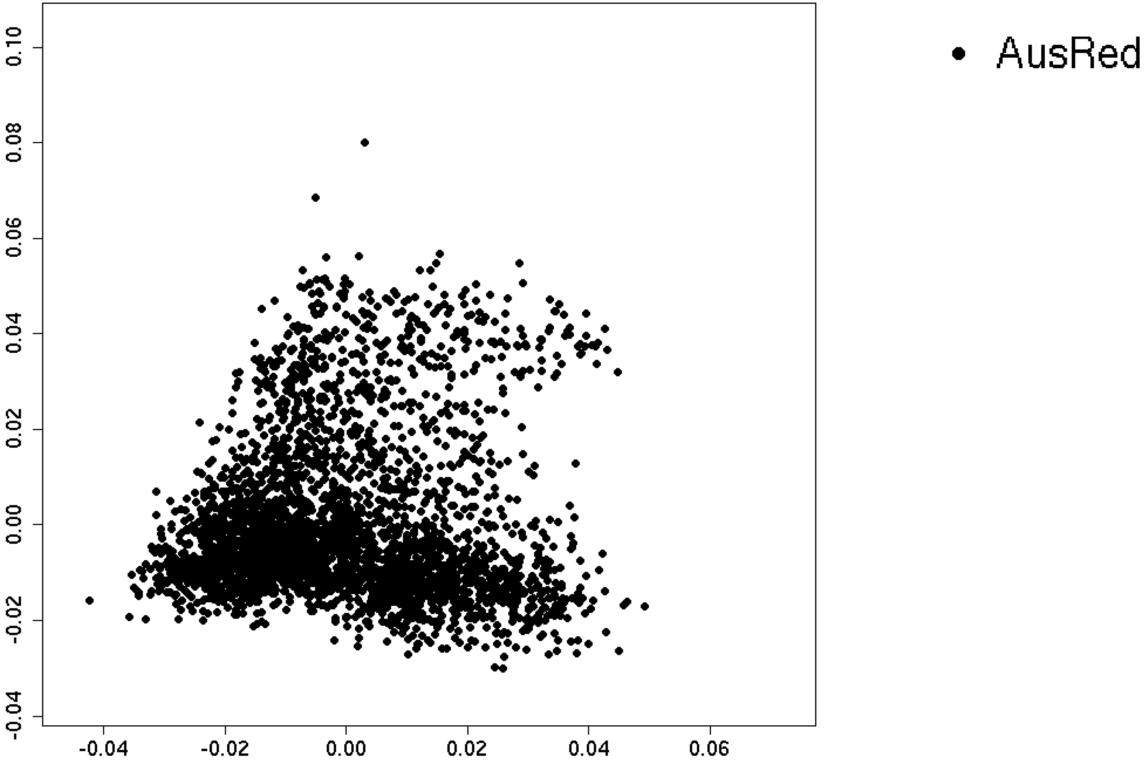


Australian Red cattle – diversity within Red cattle breeds



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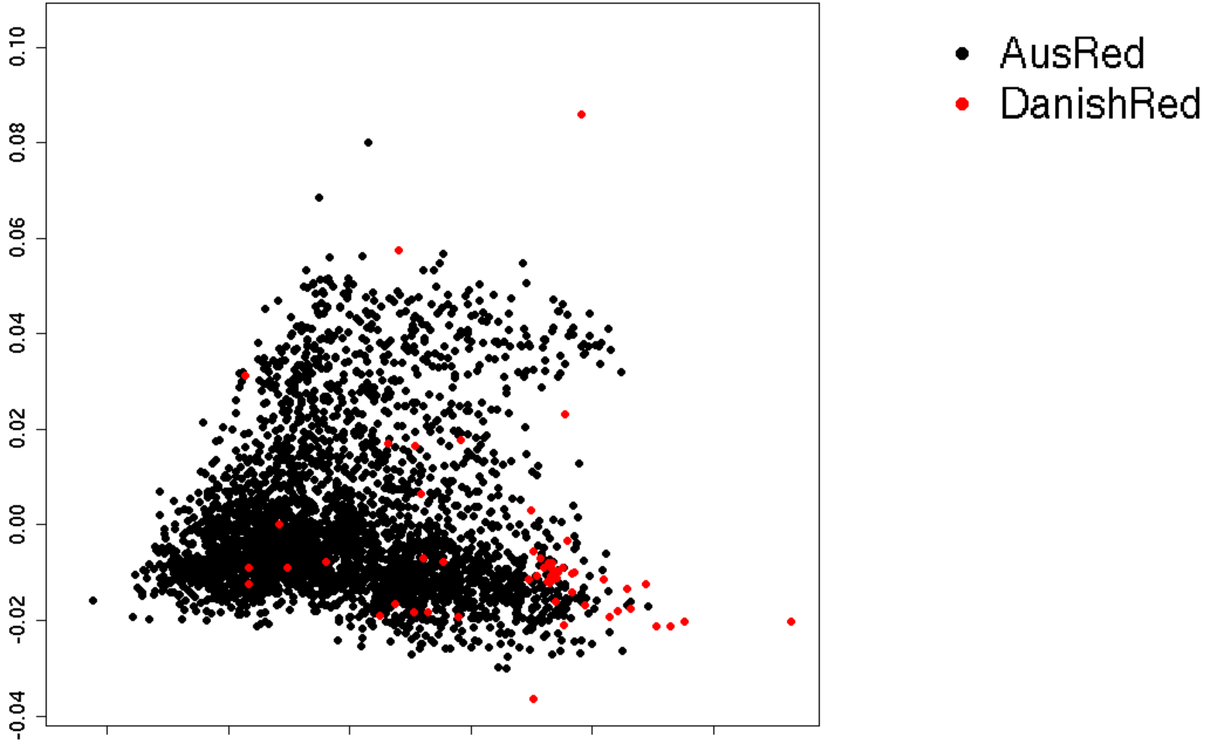

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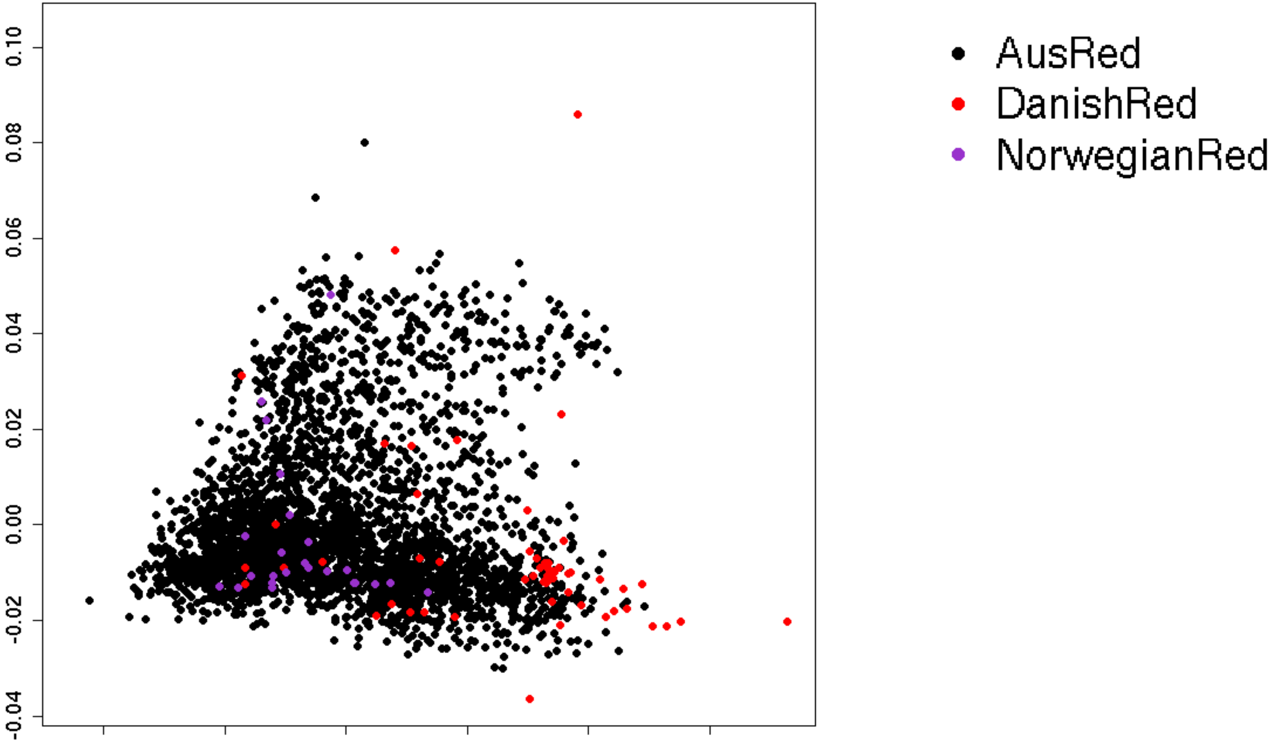

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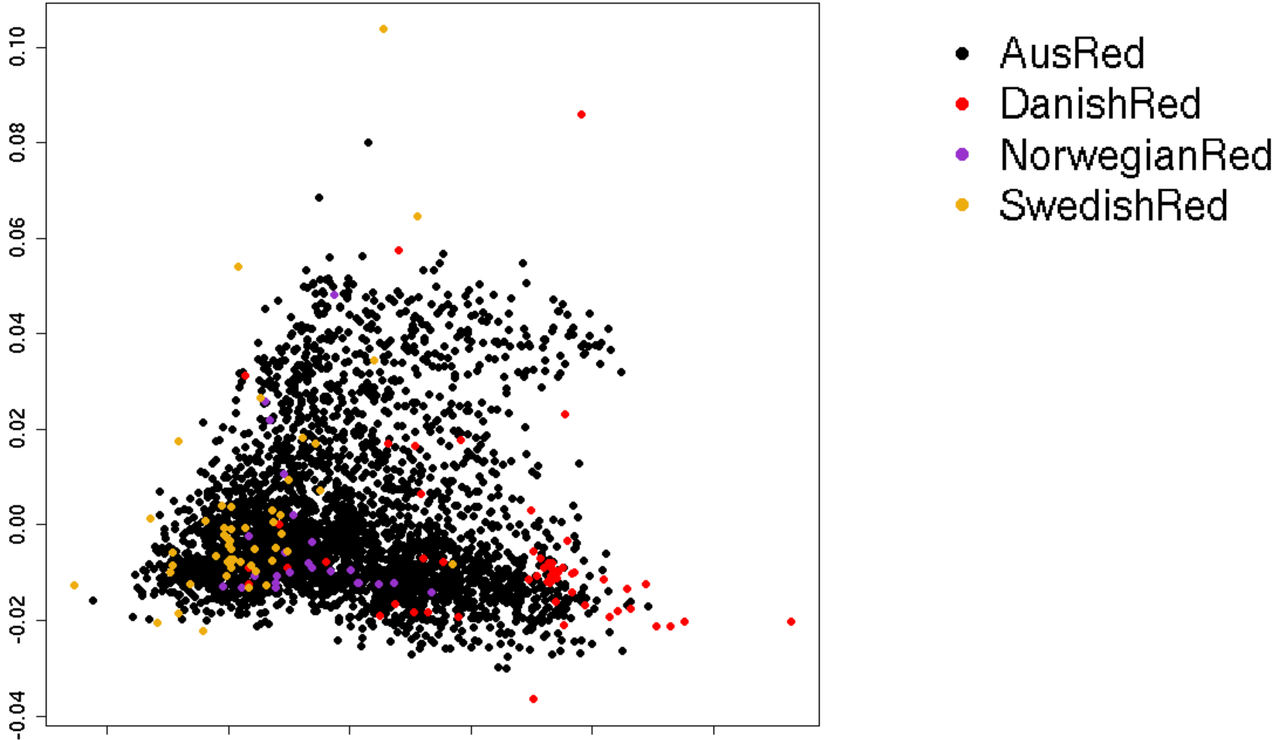

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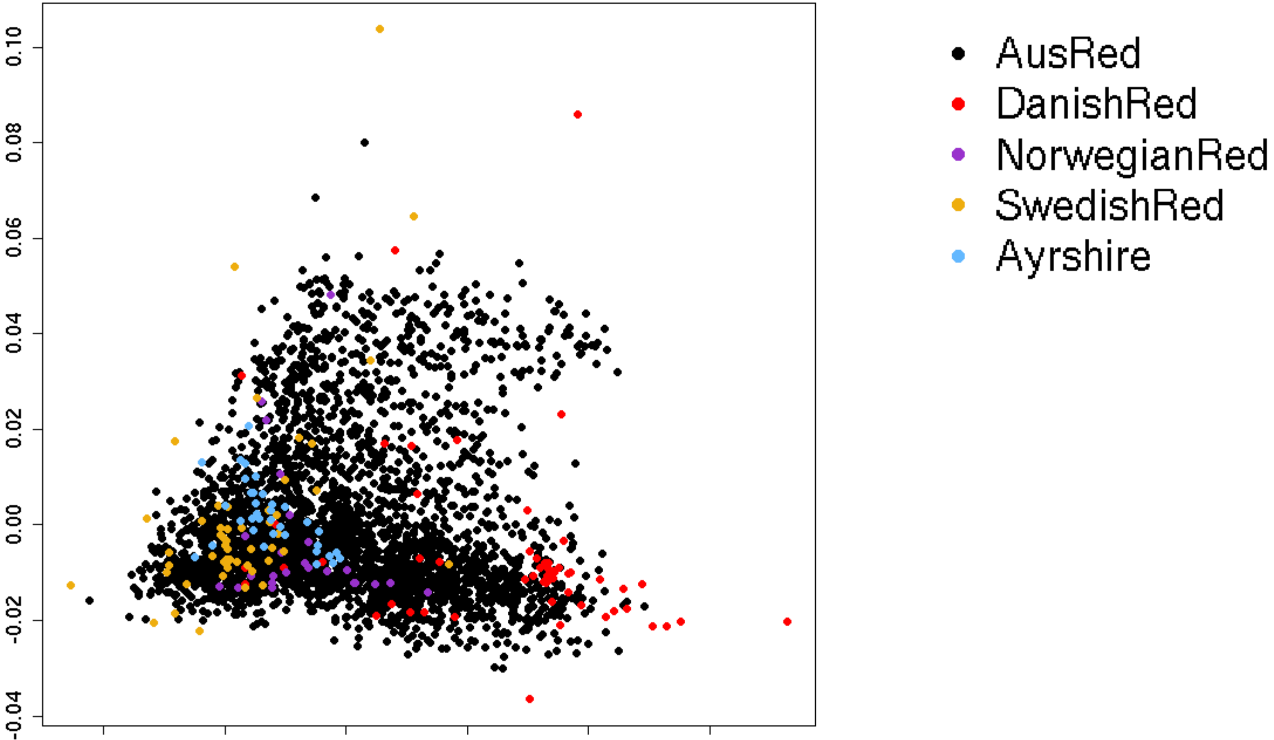

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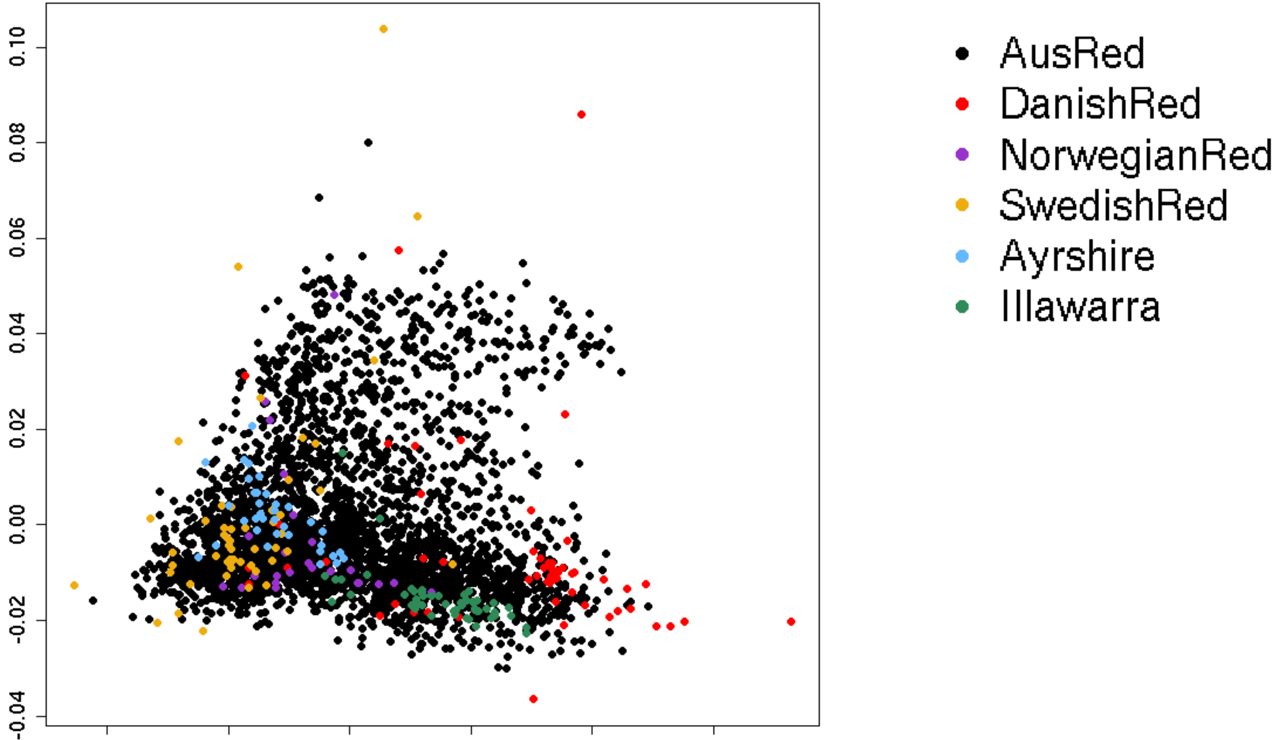

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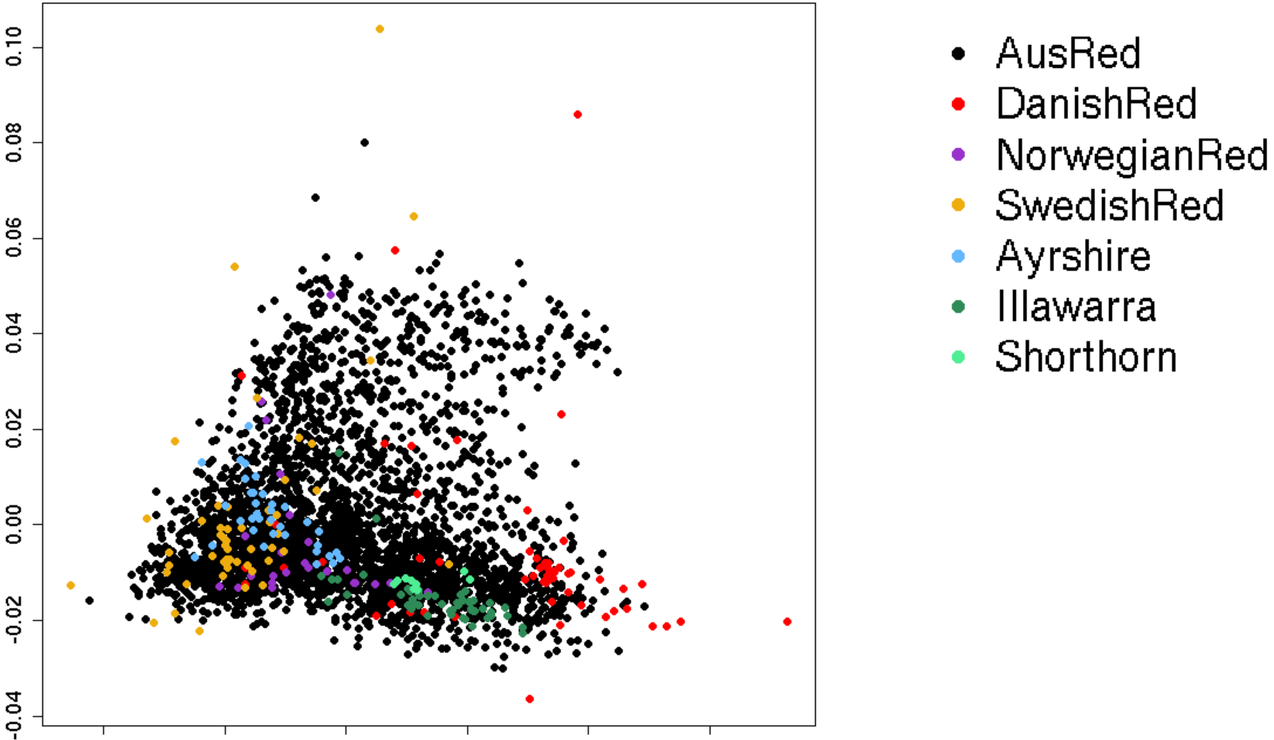
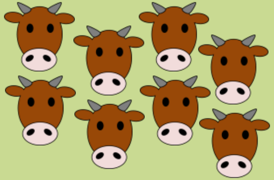


Genomic prediction

Reference population



Known genotypes and phenotypes

Genomic prediction

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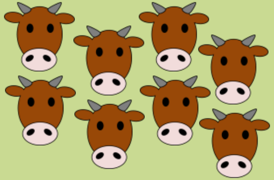

Known genotypes and phenotypes

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Prediction equation

Genomic breeding value = $w_1x_1 + w_1x_1 + w_1x_1$ ……

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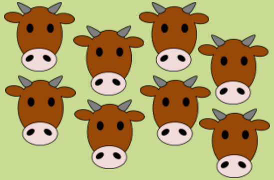

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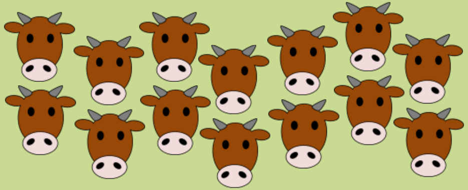

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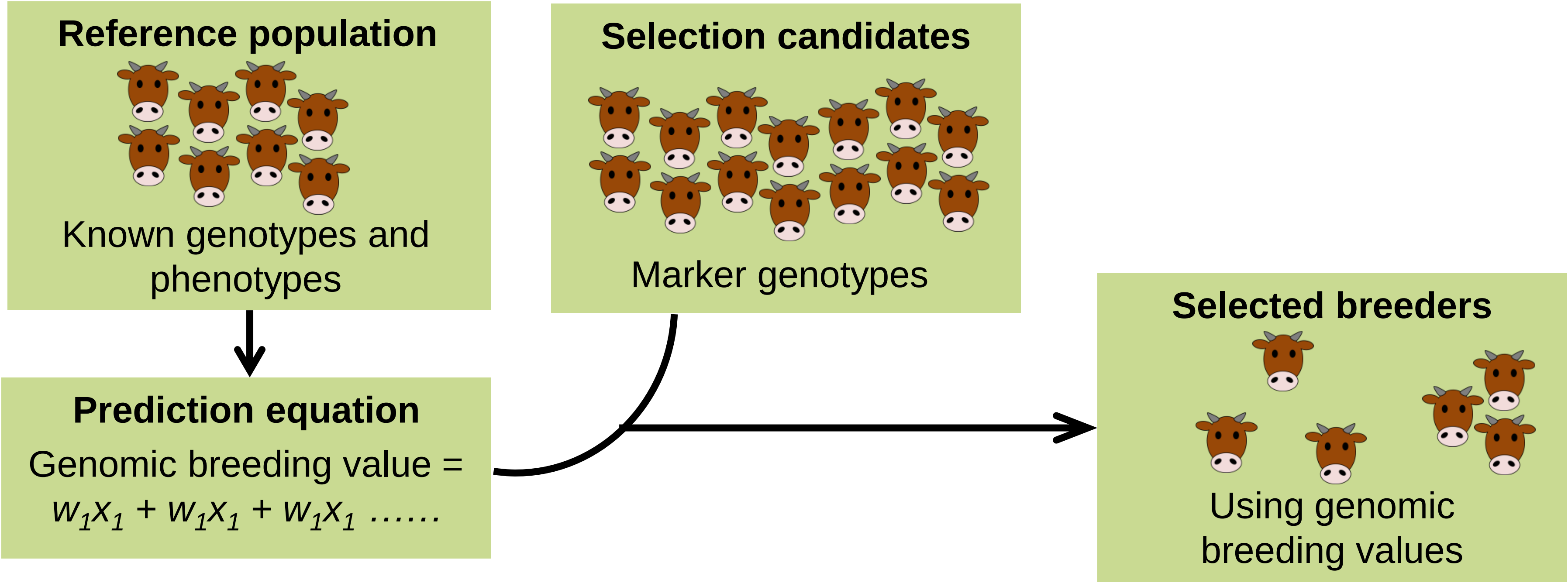

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Selected breeders

Using genomic breeding values

Genomic prediction: effect of reference population on accuracy

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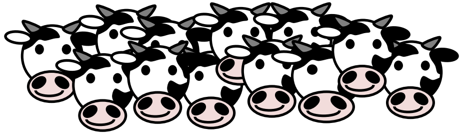

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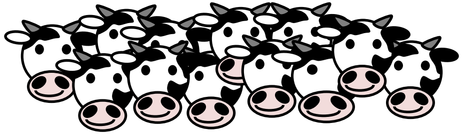

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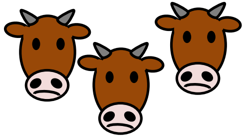

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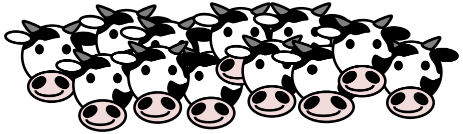

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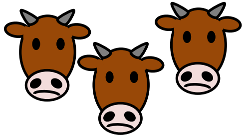

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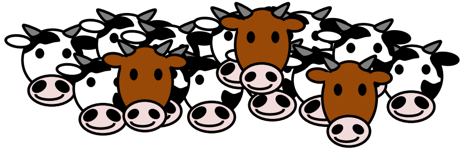

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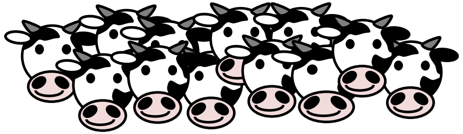

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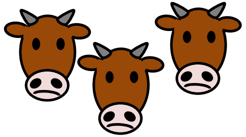

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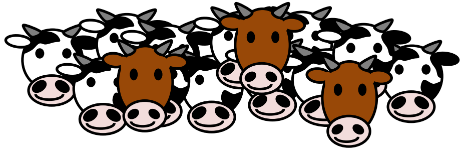
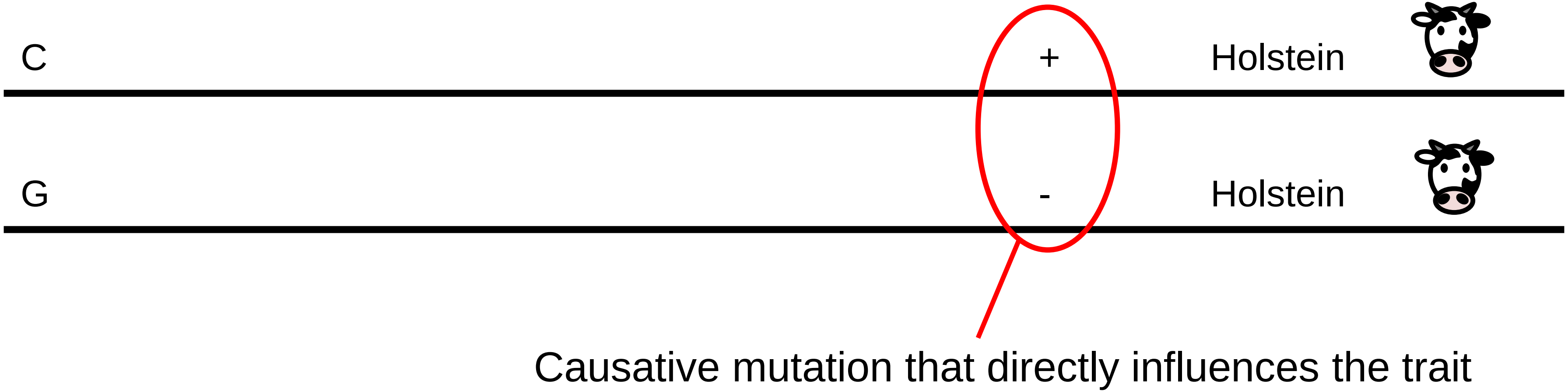


- It's also important which animals are in the reference population: accuracy is higher when relationships are stronger

Genomic prediction: within breed vs multi breed prediction

C	+	Holstein	🐮
G	-	Holstein	🐮

Genomic prediction: within breed vs multi breed prediction

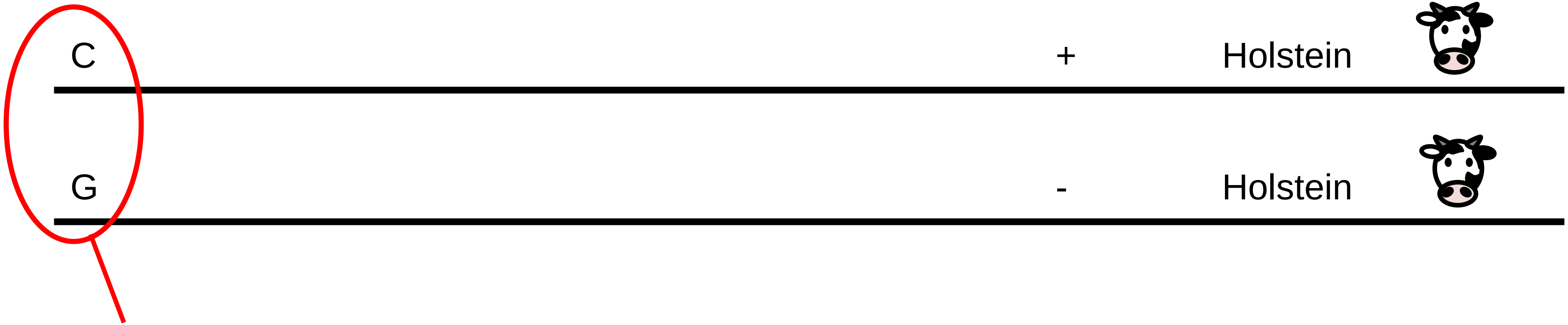


C + Holstein

G - Holstein

Causative mutation that directly influences the trait

Genomic prediction: within breed vs multi breed prediction



Prediction marker: linked to the causative mutation, has no effect on the trait itself, but can be used to predict the effect of the causative mutation

Genomic prediction: within breed vs multi breed prediction

C	+	Holstein
G	-	Holstein
C	-	Australian Red
G	+	Australian Red

Genomic prediction: within breed vs multi breed prediction

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Genomic prediction: within breed vs multi breed prediction

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Markers can be linked differently to causative mutations in different breeds
→ not useful to predict across breed

C	-	Australian Red
G	+	Australian Red

Genomic prediction: within breed vs multi breed prediction

C	C	+	Holstein
G	G	-	Holstein
C	G	-	Australian Red
G	C	+	Australian Red

Genomic prediction: within breed vs multi breed prediction

C	C	+	Holstein
G	G	-	Holstein
C	G	-	Australian Red
G	C	+	Australian Red

→ Prediction markers should be closer to the causative mutations for across breed prediction than within breed

Which reference population is better?

Same breed, multi country

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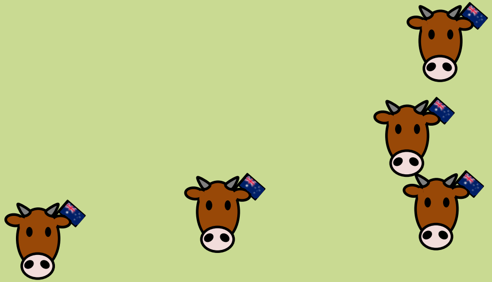

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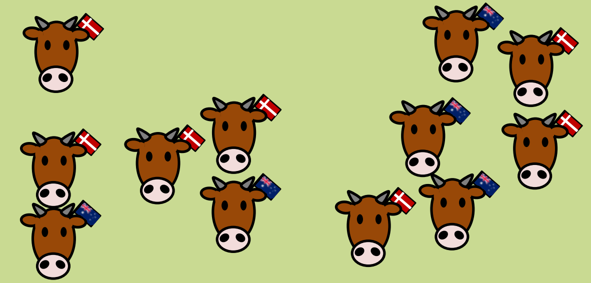

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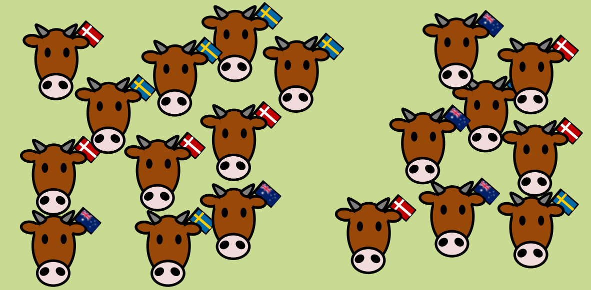

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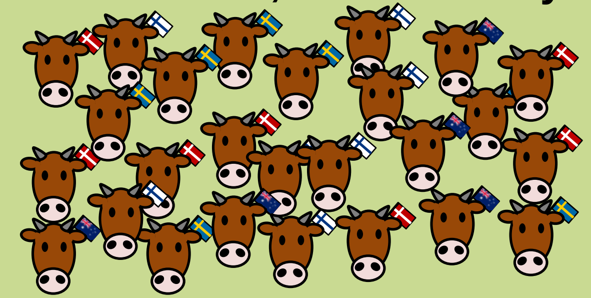

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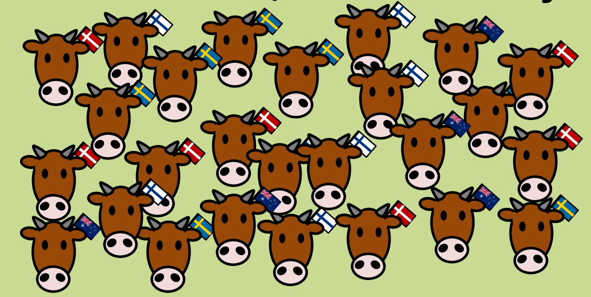

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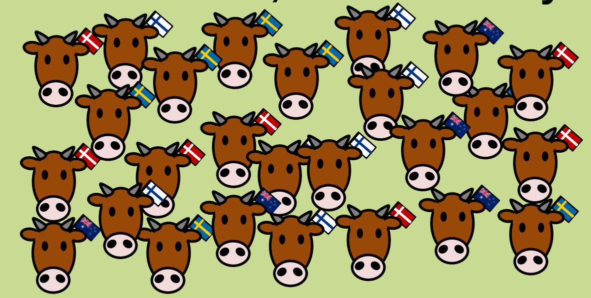

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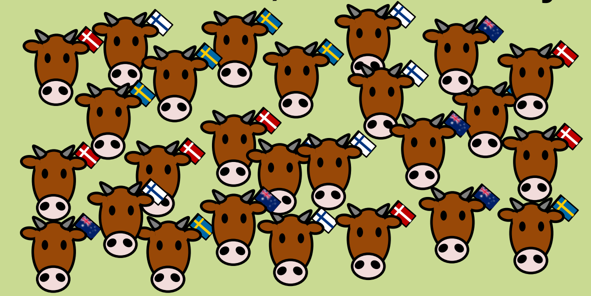

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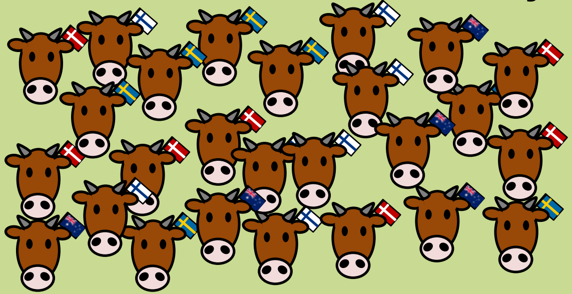

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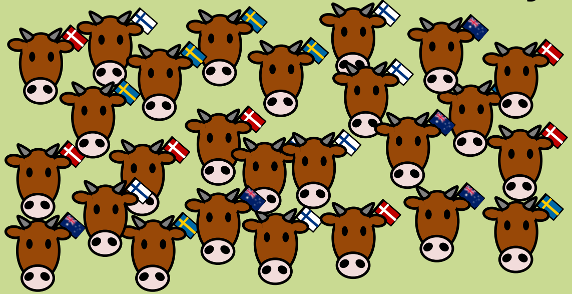

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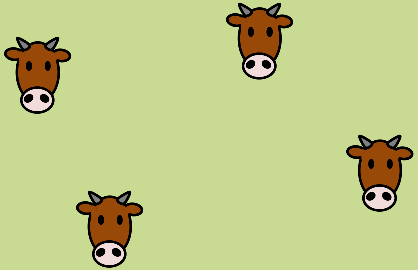

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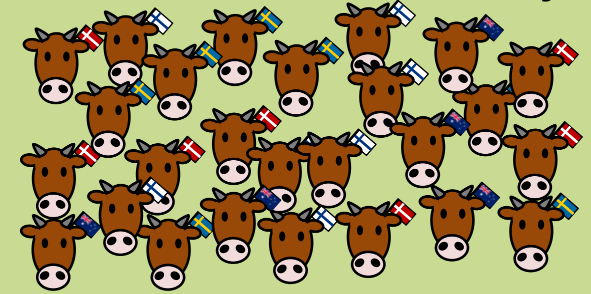

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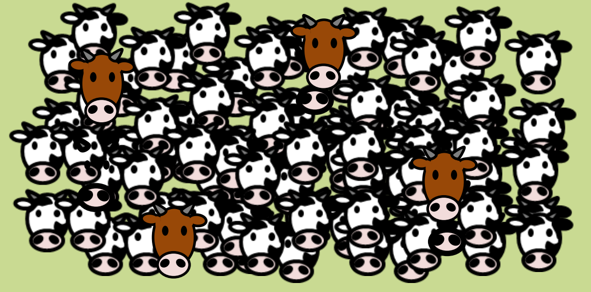

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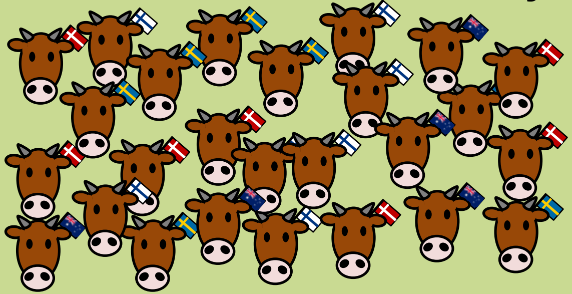

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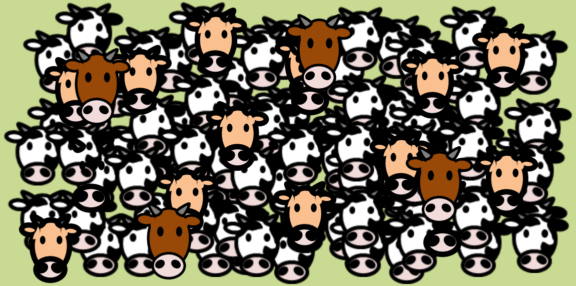

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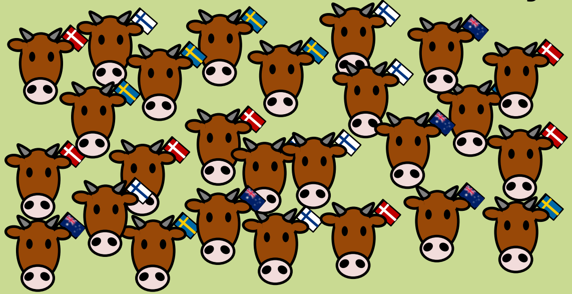

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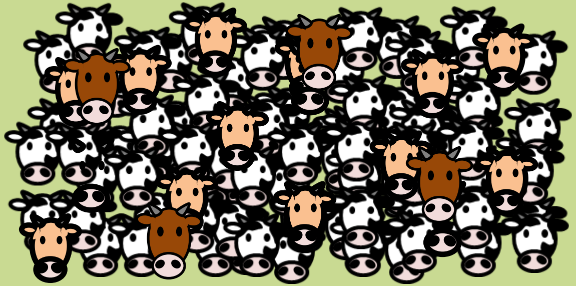

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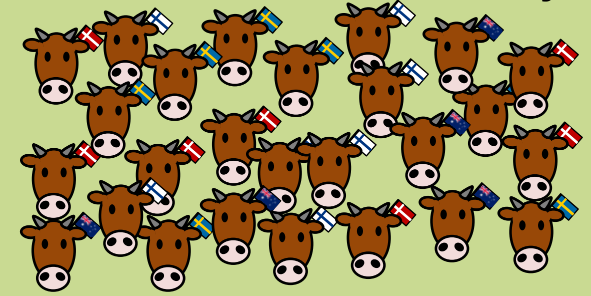

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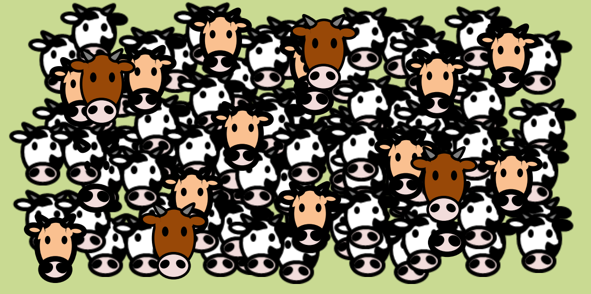

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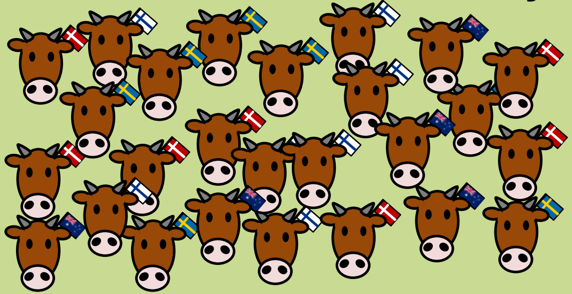

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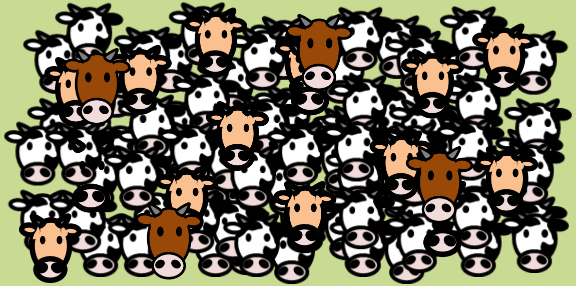

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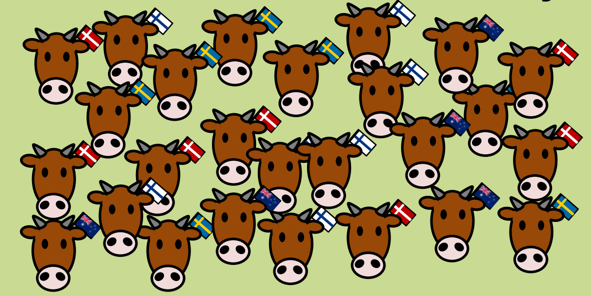

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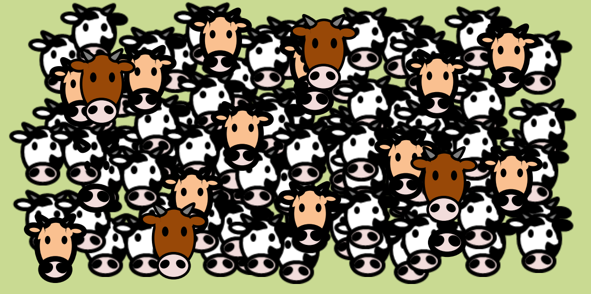

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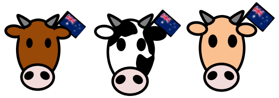

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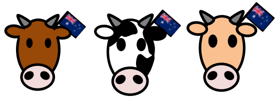

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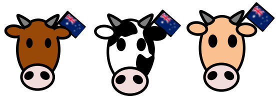

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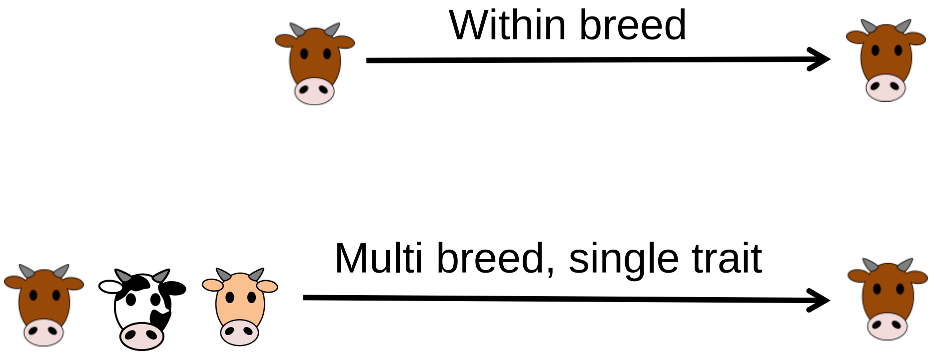

Within breed

Multi breed, single trait

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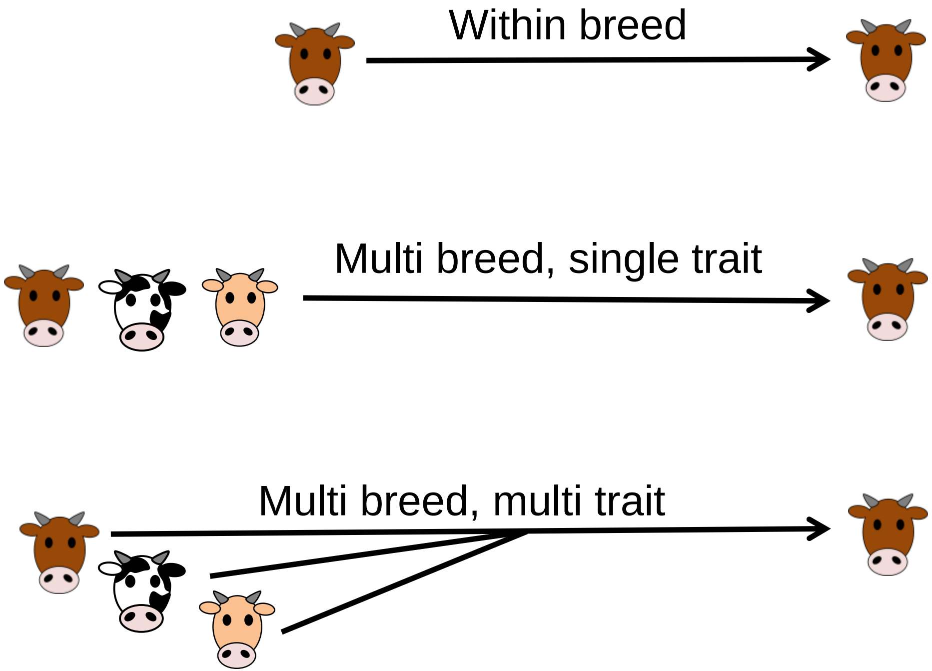

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Data – Traits

Milk yield, fat yield, protein yield, somatic cell count, fertility and survival

Data – Reference and validation populations

Reference population

within breed

3,041 Australian Red cows

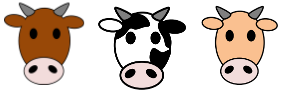
Data – Reference and validation populations

Reference population

within breed

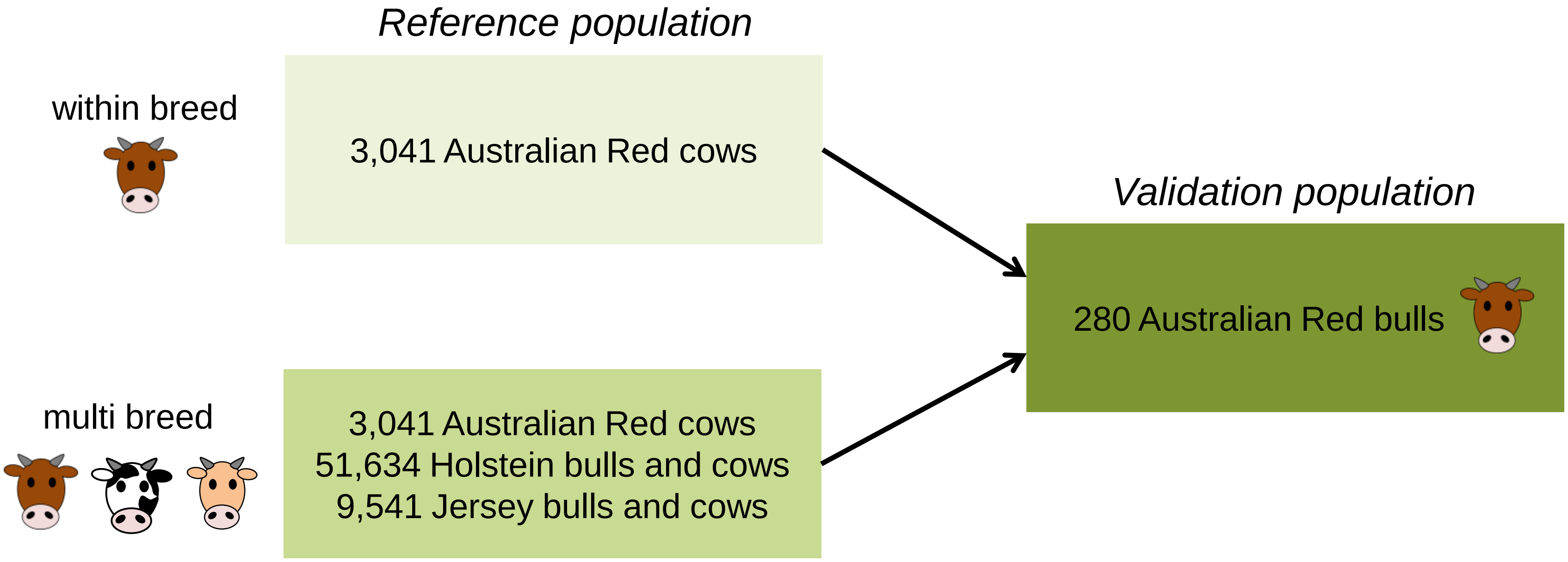
3,041 Australian Red cows

multi breed



3,041 Australian Red cows
51,634 Holstein bulls and cows
9,541 Jersey bulls and cows

Data – Reference and validation populations



Reference population

within breed

3,041 Australian Red cows

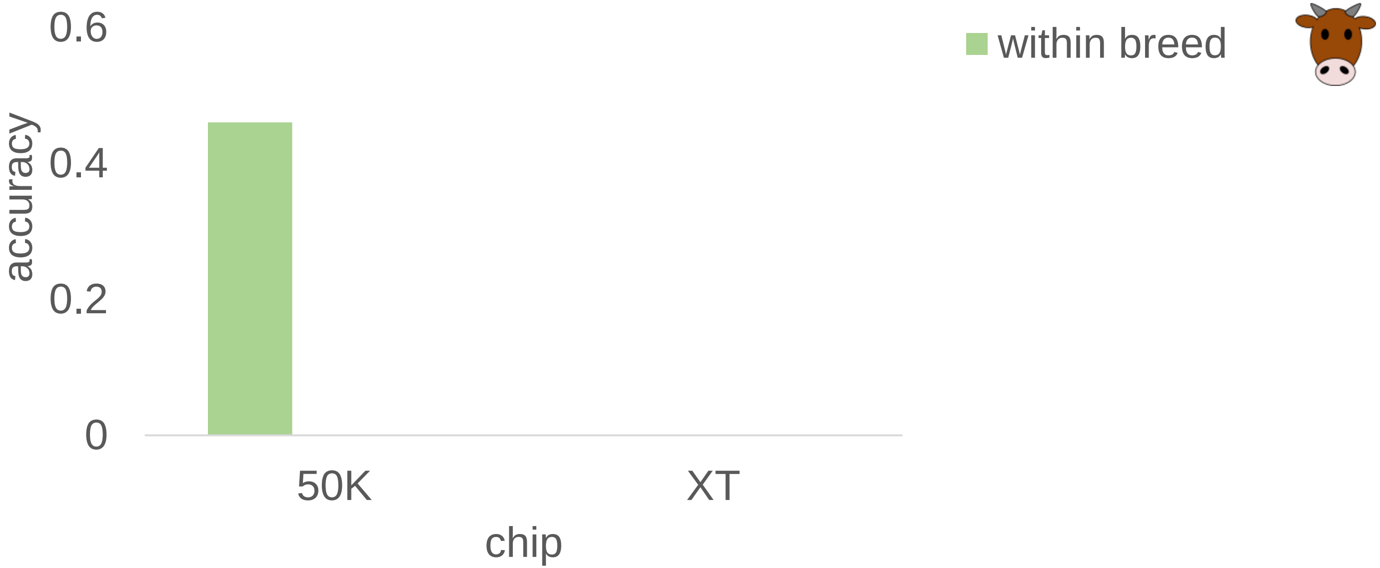
multi breed

3,041 Australian Red cows
51,634 Holstein bulls and cows
9,541 Jersey bulls and cows

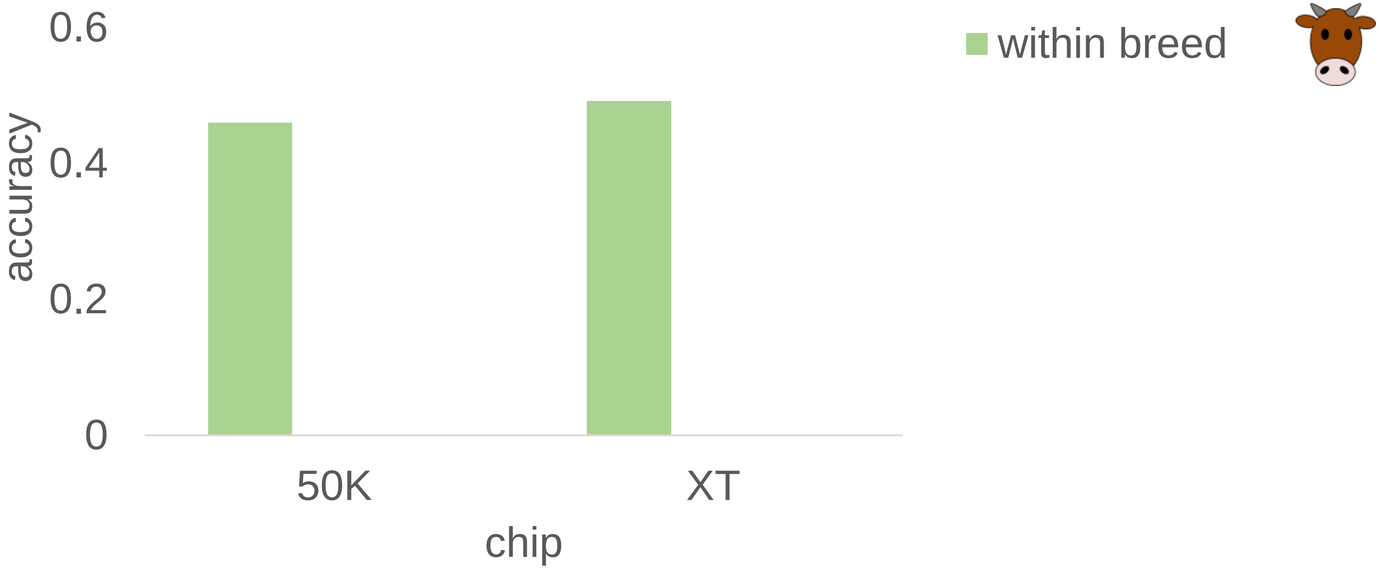
Validation population

280 Australian Red bulls

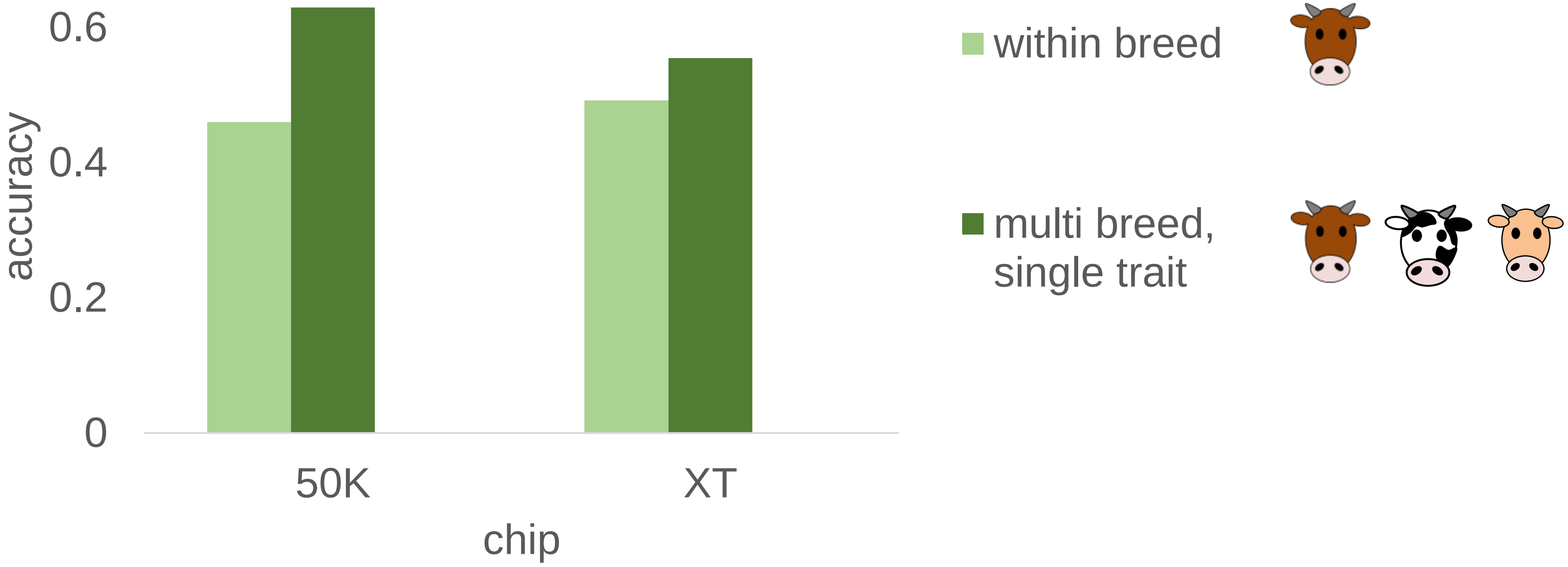
Results – Fat yield



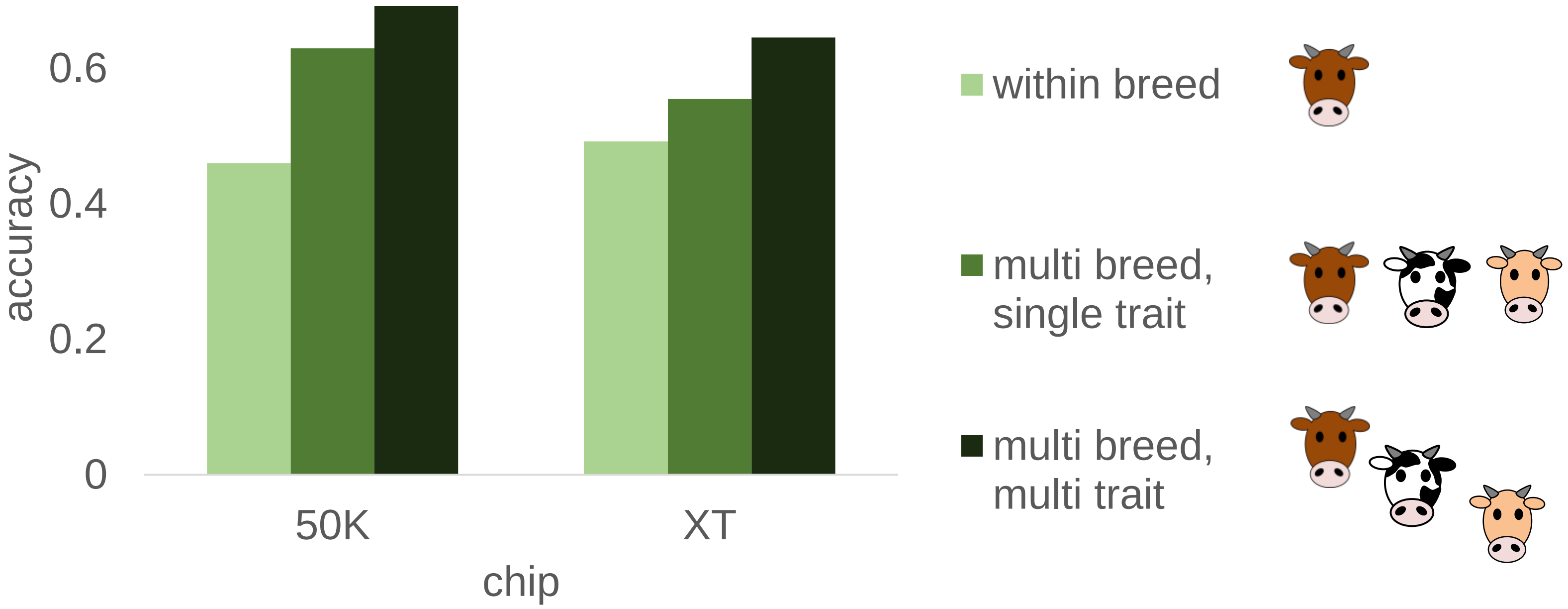
Results – Fat yield



Results – Fat yield

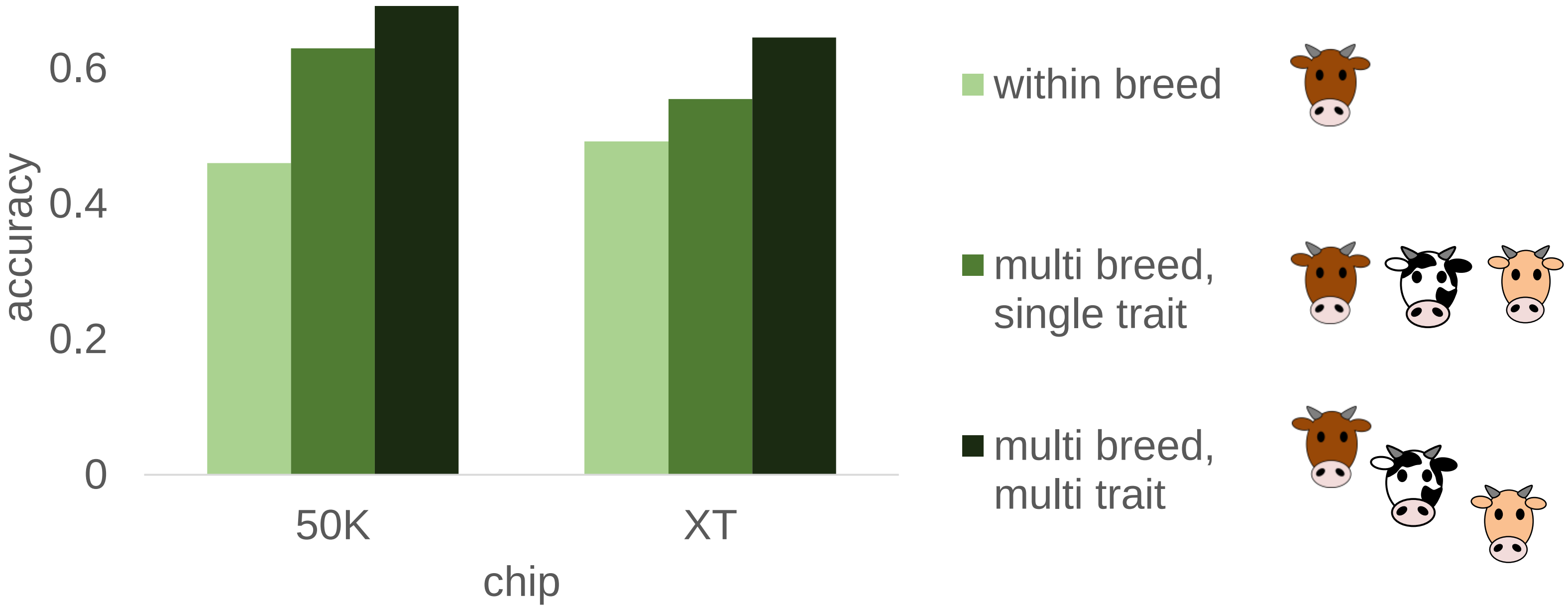


Results – Fat yield

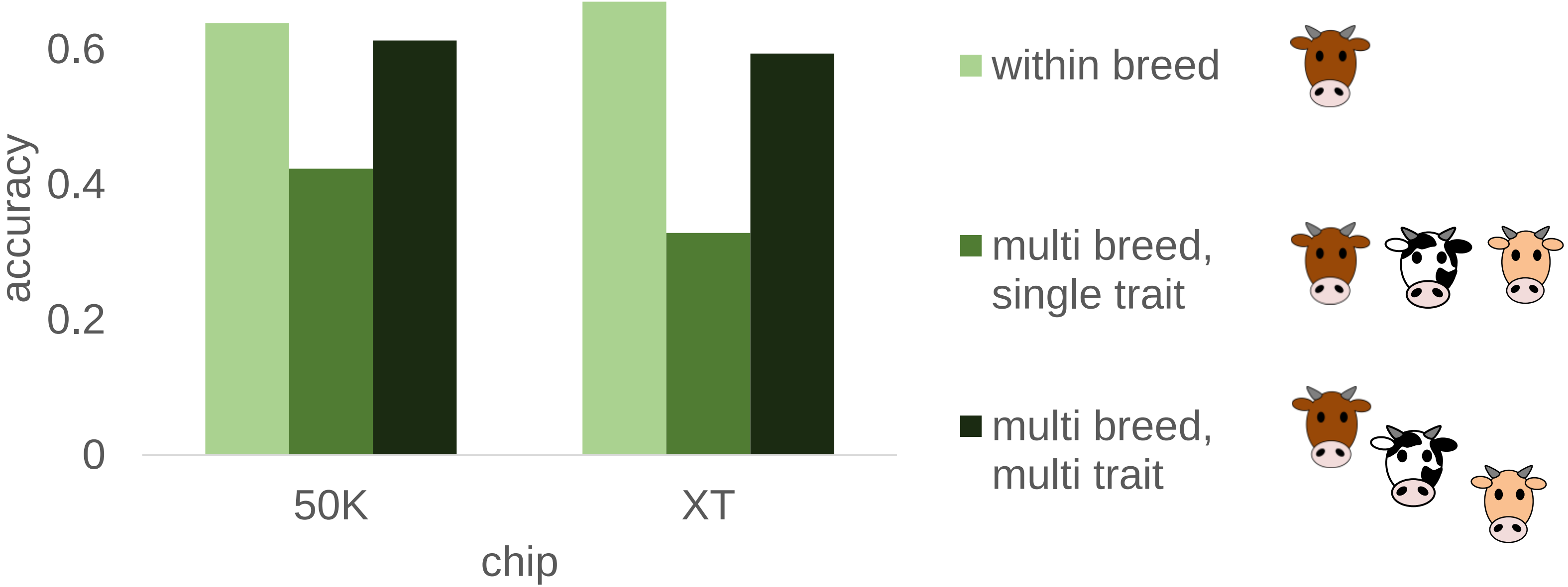


Results – Fat yield

→ *Increase in accuracy by using multi breed reference population & XT variants*

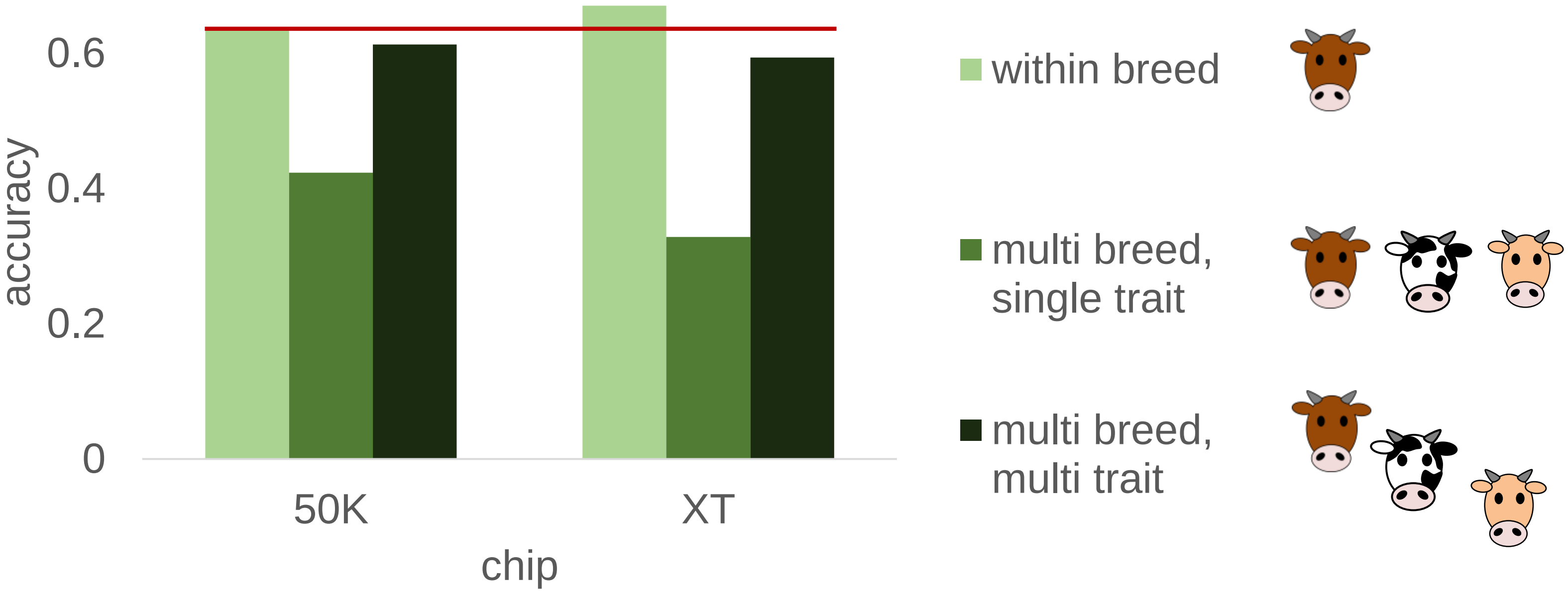


Results – Protein yield

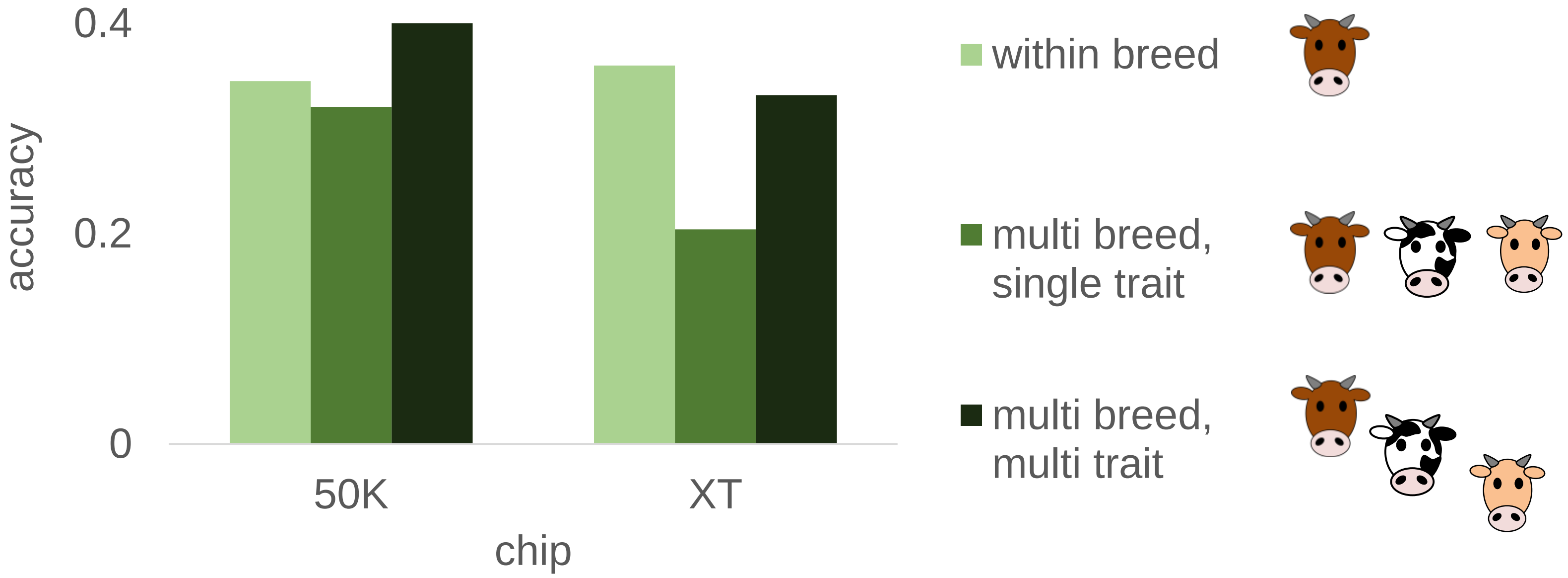


Results – Protein yield

→ *Higher accuracy for within breed prediction than multi breed prediction*

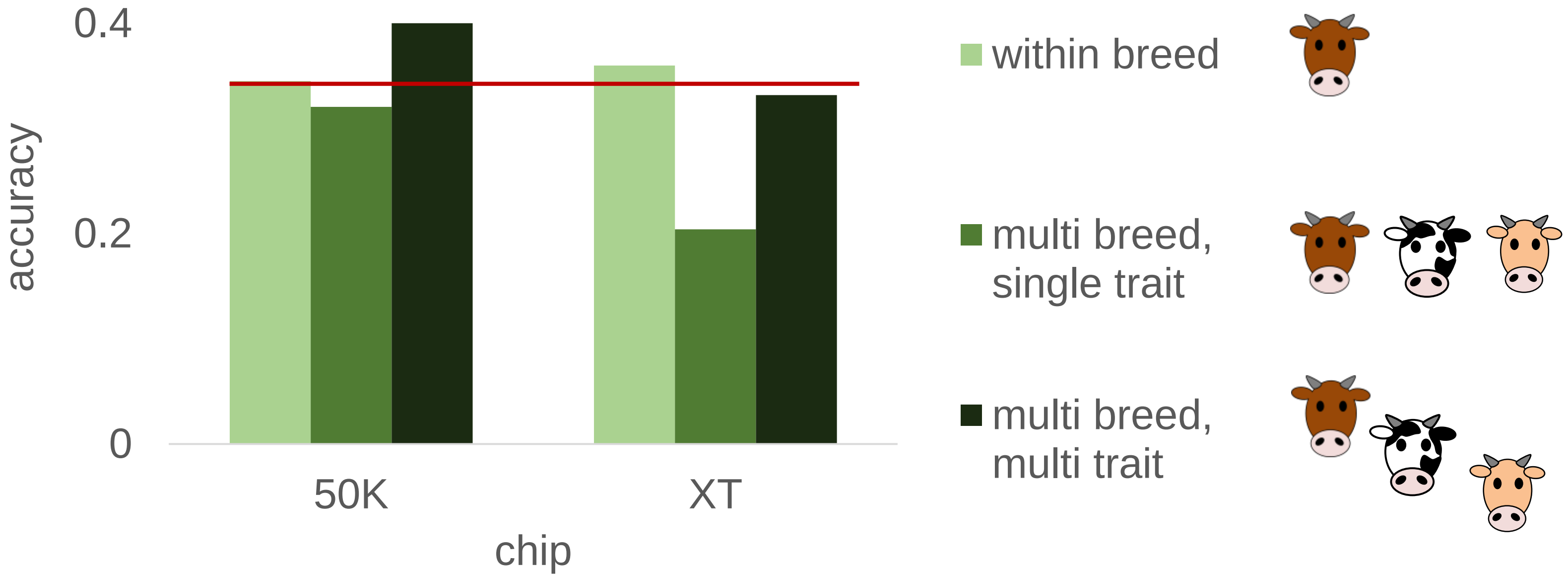


Results – Milk yield

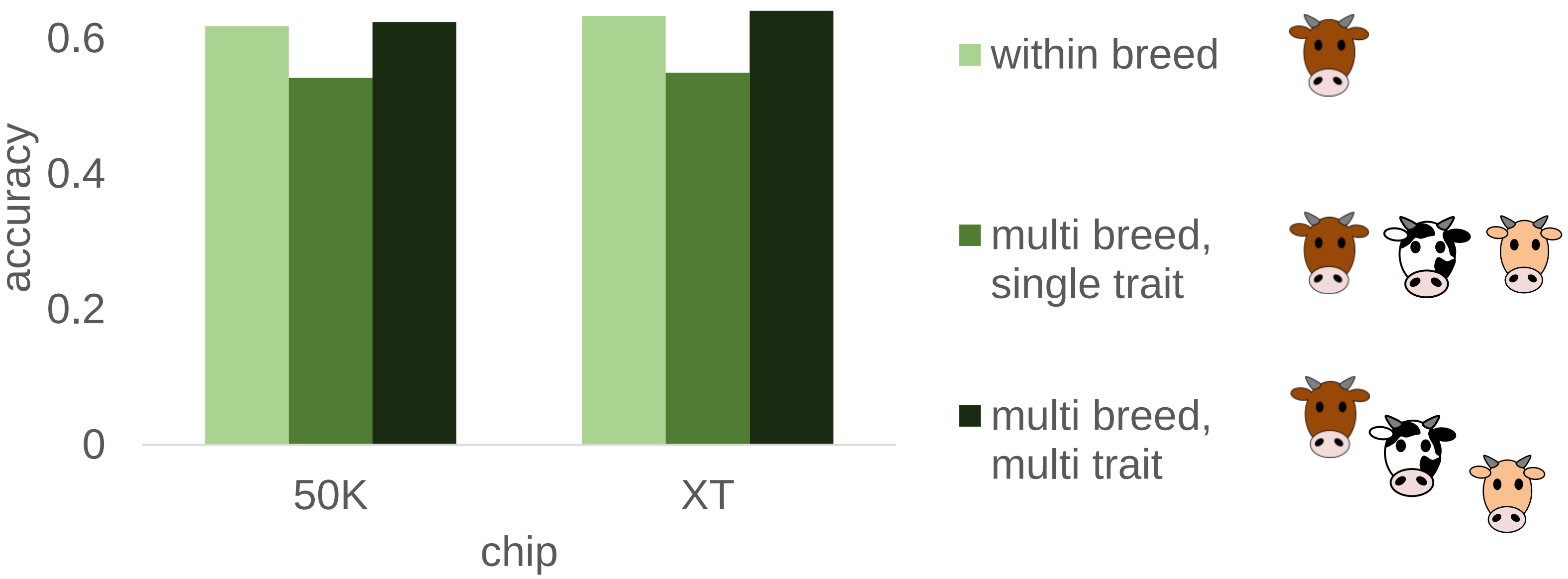


Results – Milk yield

→ *Inconsistent results*

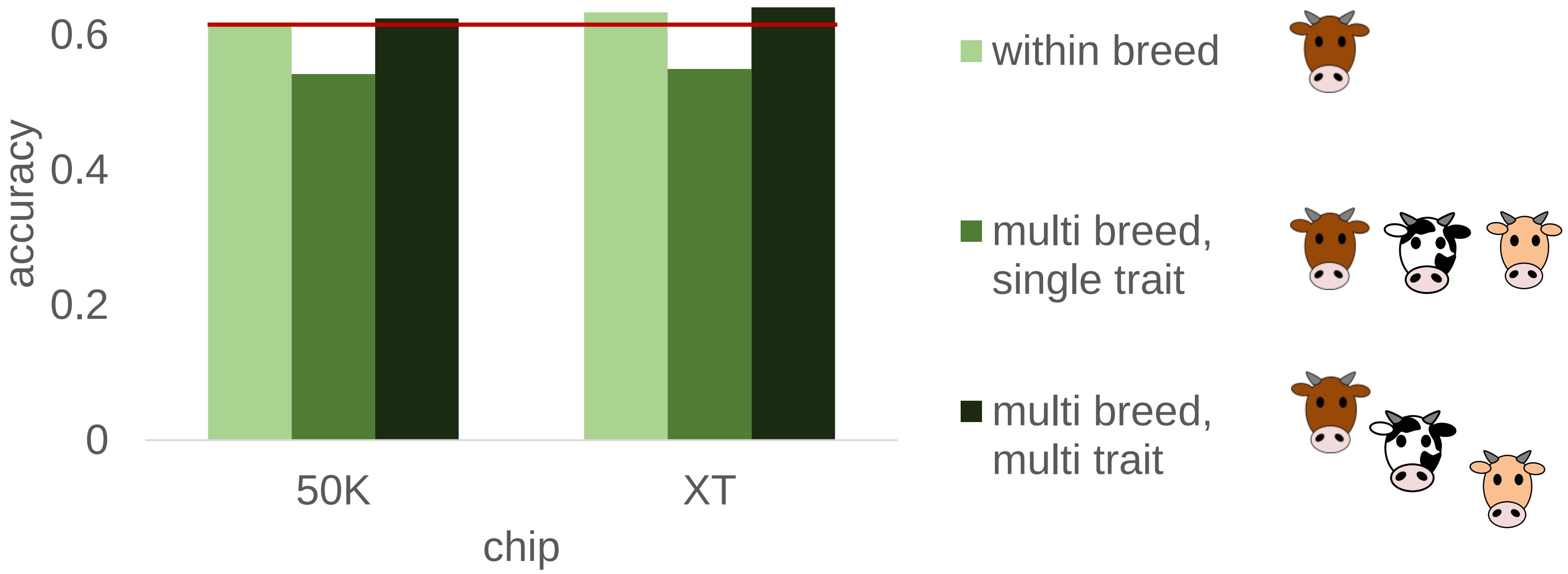


Results – Somatic cell count

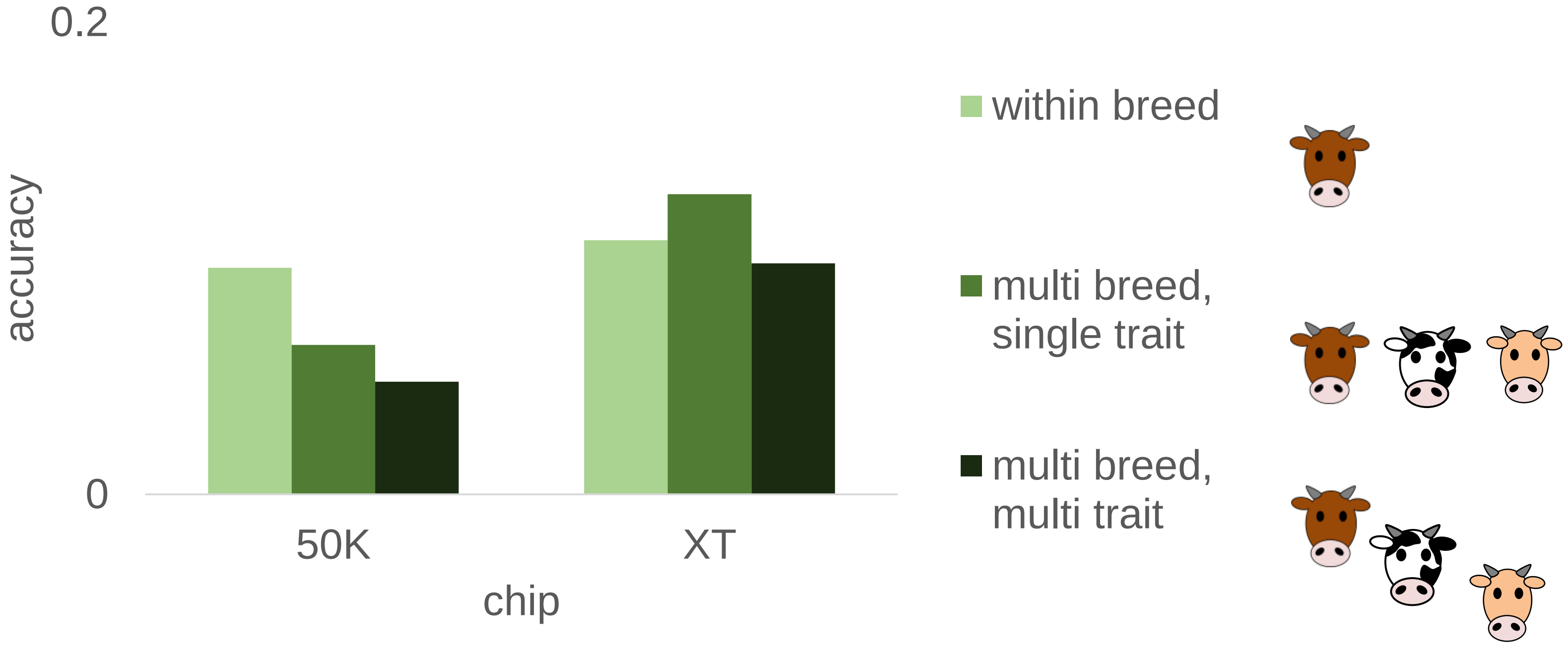


Results – Somatic cell count

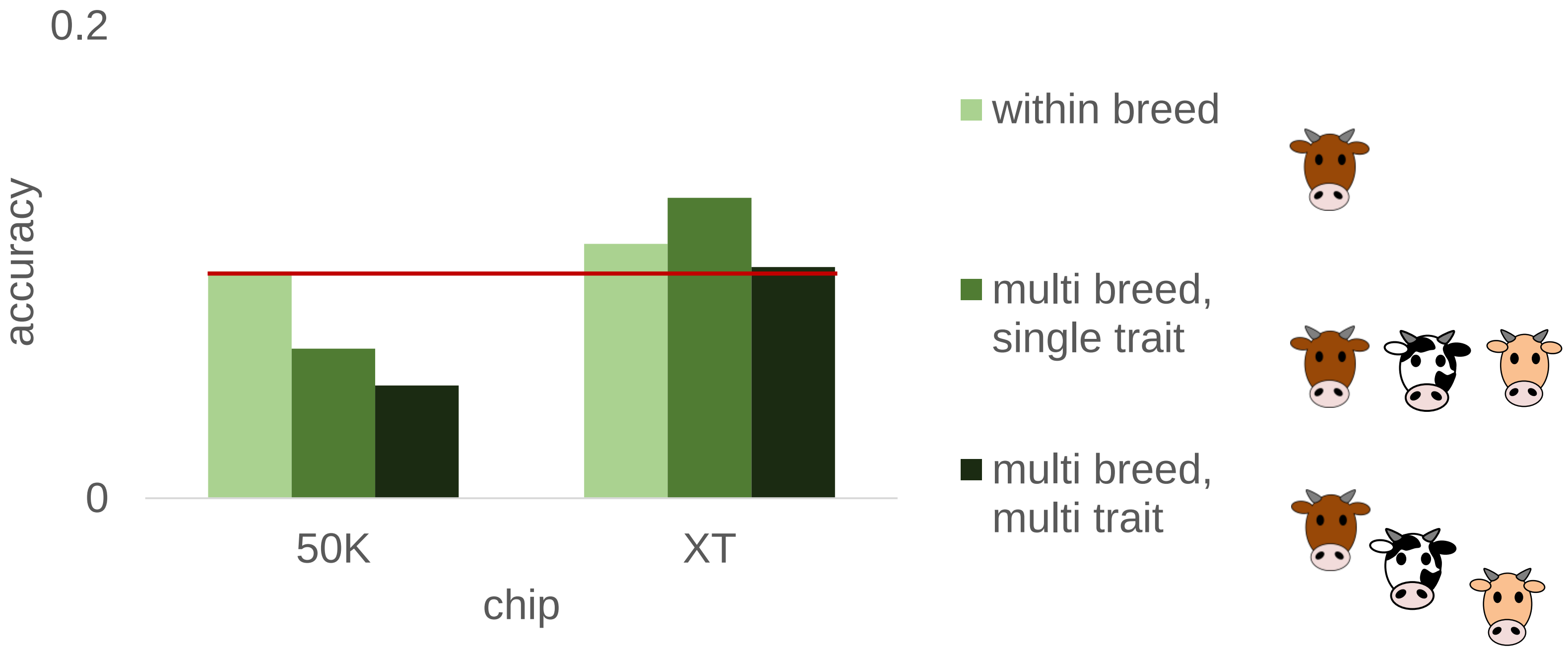
→ Small increase in accuracy for multi breed multi trait model and XT chip



Results – Fertility

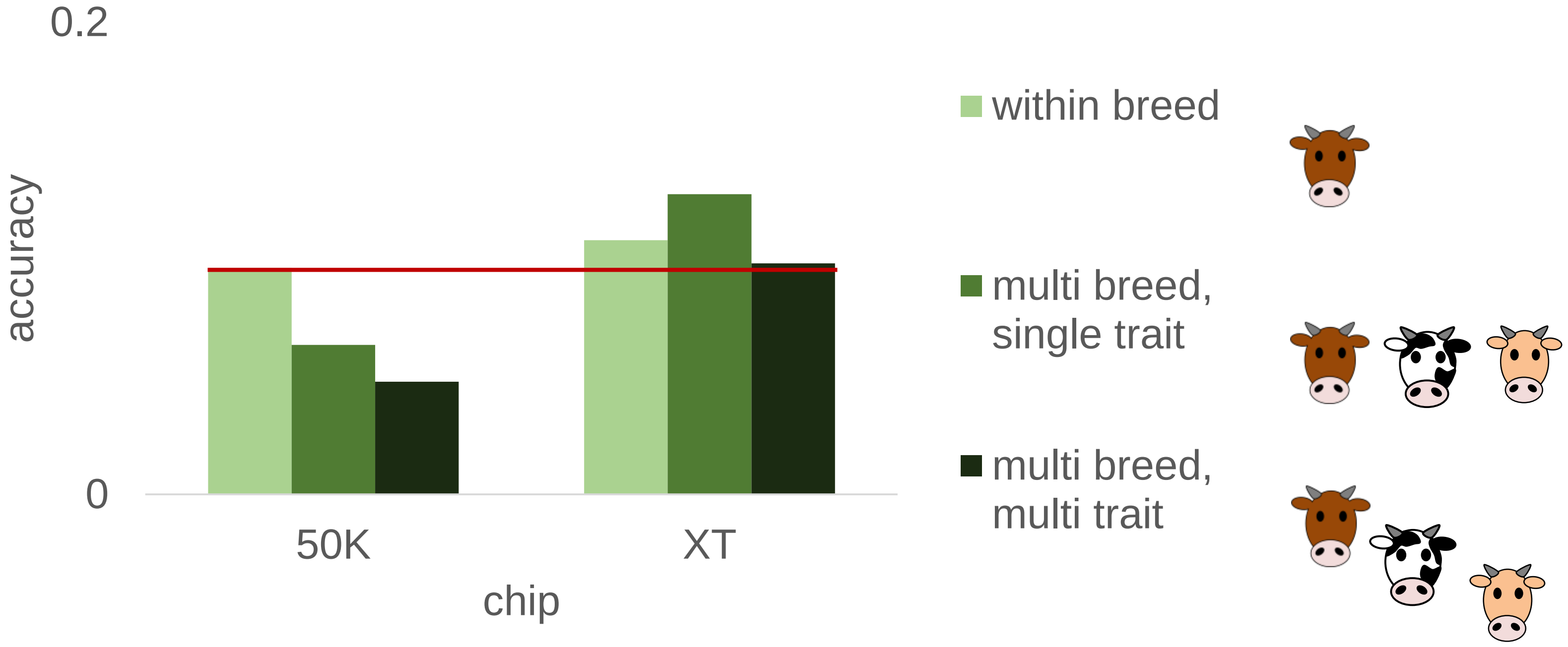


Results – Fertility



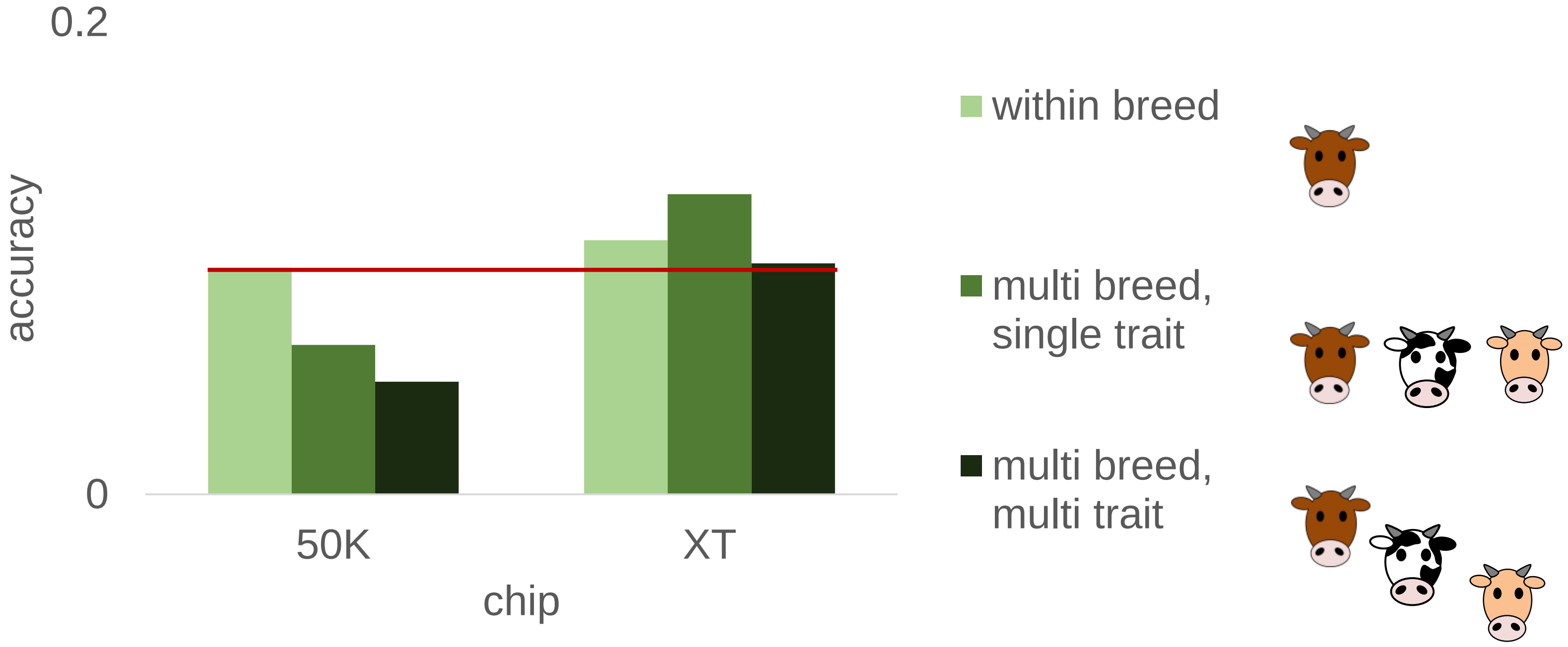
Results – Fertility

→ *Best model depends on the variants that are used*



Results – Fertility

→ *Best model depends on the variants that are used*



Survival: accuracies very low with all models

Conclusions

- Best strategy depends on trait and set of variants

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- Prediction especially difficult for traits with a lower heritability

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- Best strategy depends on trait and set of variants
- Prediction especially difficult for traits with a lower heritability
- Need a reference population with more Reds to have a higher accuracy

Future plans

- Some variants more important to others → put more weight on these variants

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- Multi breed reference population with only the Holstein individuals that are genetically closest to Australian Red cattle

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- Some variants more important to others → put more weight on these variants
- Multi breed reference population with only the Holstein individuals that are genetically closest to Australian Red cattle
- Compare results with breeding values provided by Viking Genetics

Acknowledgements

Agriculture Victoria
Jennie Pryce
Iona MacLeod
Coralie Reich
Amanda Chamberlain
Ruidong Xiang
Mike Goddard
BASC team

DataGene

Dairy Bio

GARDINER FOUNDATION

Dairy Australia

DataGene
Solutions for Herd Development

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