

Genomic prediction for Australian Red Dairy cattle

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Australian Red cattle

Combining different Red dairy breeds:

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



Genomic prediction: effect of reference population on accuracy

- Larger reference population → higher accuracy

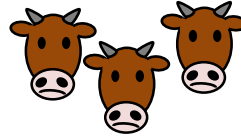
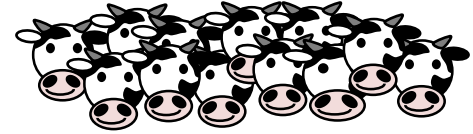
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- Holstein: very large reference populations → high accuracy



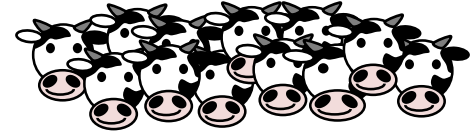
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- Breeds with smaller populations, for example Australian Red → size of the reference population limits prediction accuracy

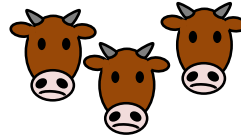


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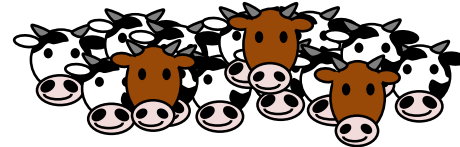
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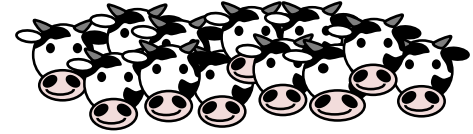


- Multi breed prediction: increase size of the reference population

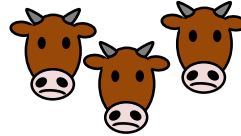


Genomic prediction: effect of reference population on accuracy

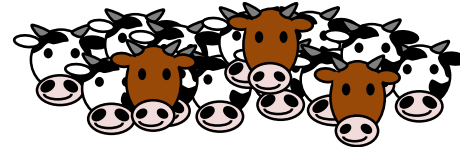
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- Multi breed prediction: increase size of the reference population



- But accuracy is higher when relationships are stronger → low relationships between breeds limit the accuracy of multi breed prediction

Objective: compare the reliability obtained with within breed and several multi breed reference populations for genomic prediction in Australian Red dairy cattle



Data

- Genotypes: 50K SNP chip
- Traits: milk yield, fat yield, protein yield, somatic cell count, fertility & survival

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Statistical analyses

- GBLUP (using MTG2):
 - ST = single trait, same trait in different breeds fitted as a single trait, account for breed differences with fixed effects
 - MT = multi trait, same trait in different breeds fitted as multiple correlated traits

Data – Reference and validation populations

Reference population

within breed



3,041 Australian Red cows

Data – Reference and validation populations

Reference population

within breed



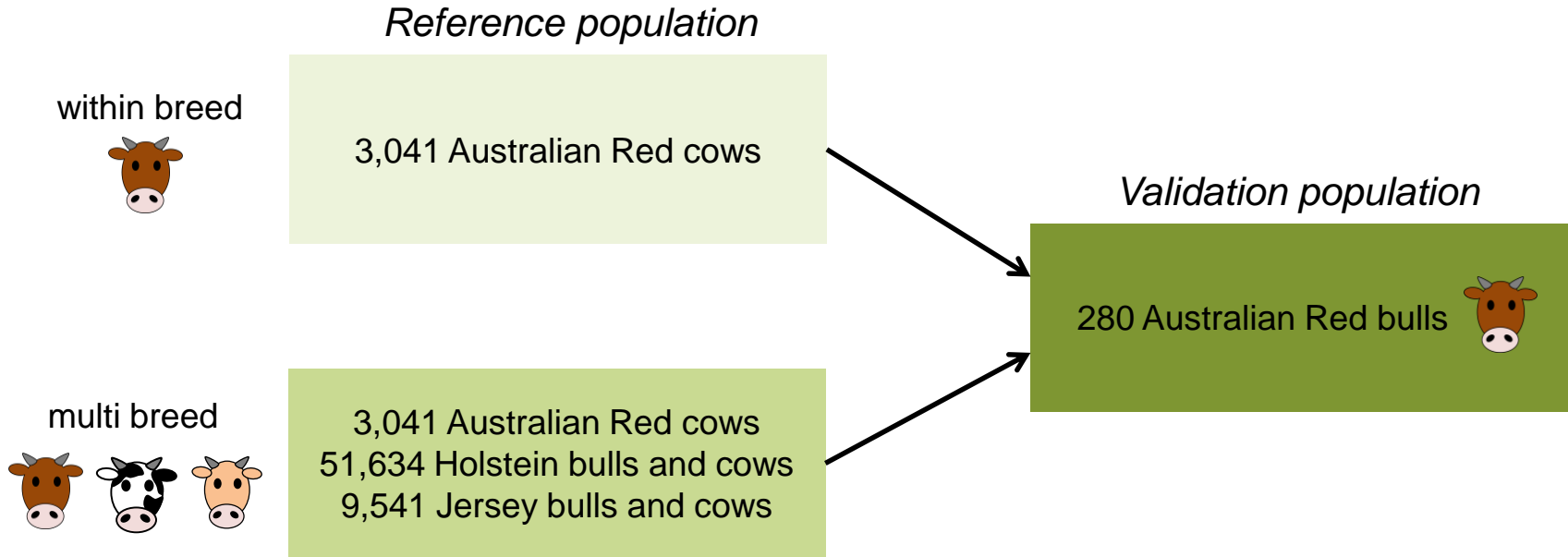
3,041 Australian Red cows

multi breed

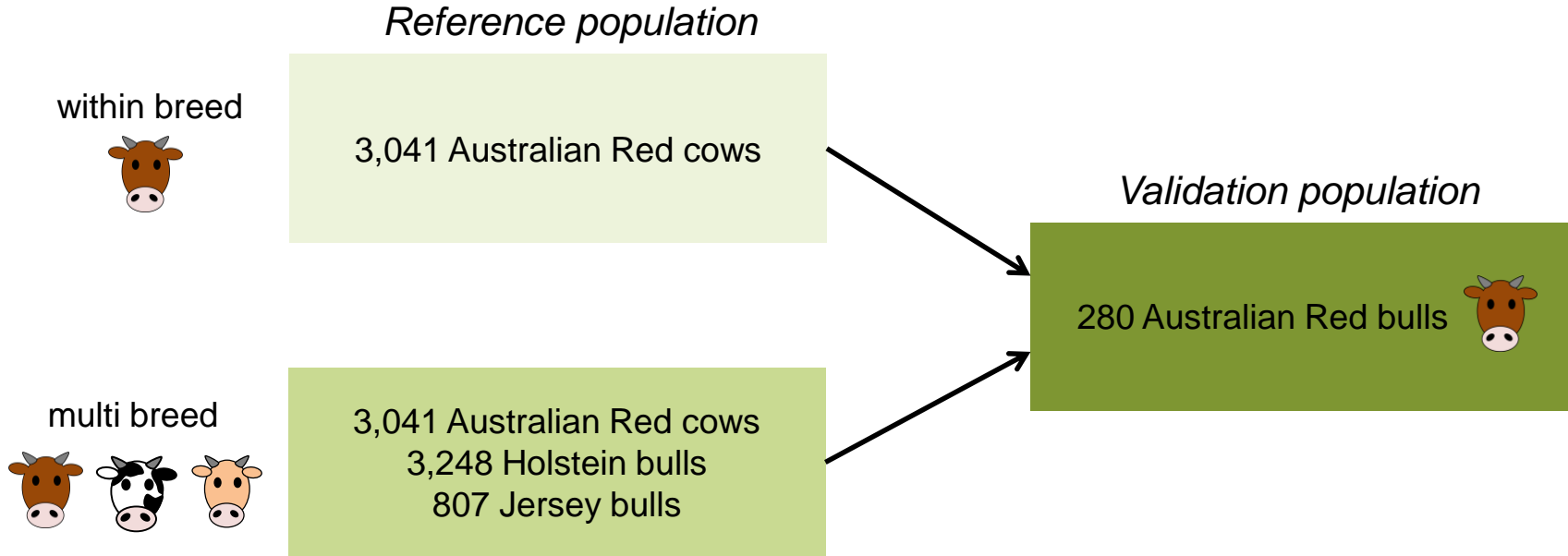


3,041 Australian Red cows
51,634 Holstein bulls and cows
9,541 Jersey bulls and cows

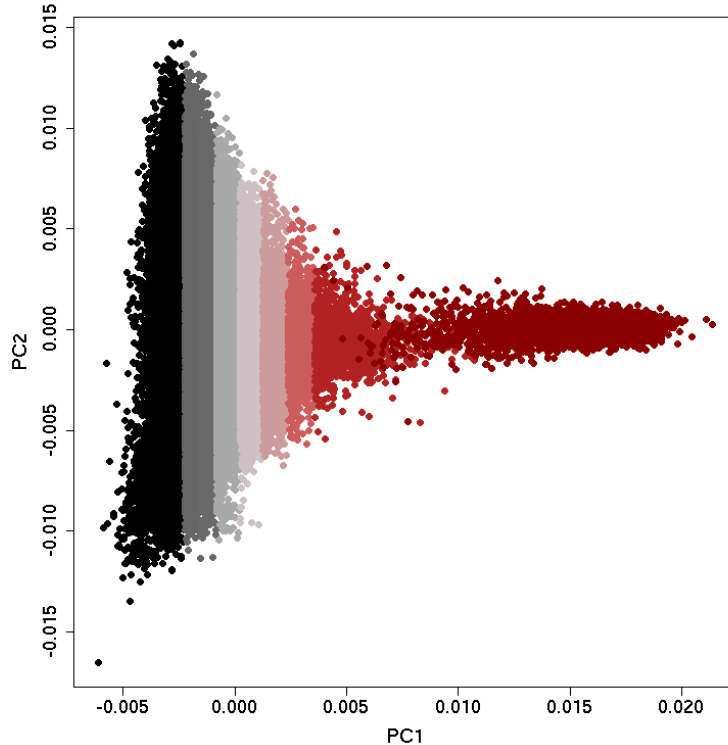
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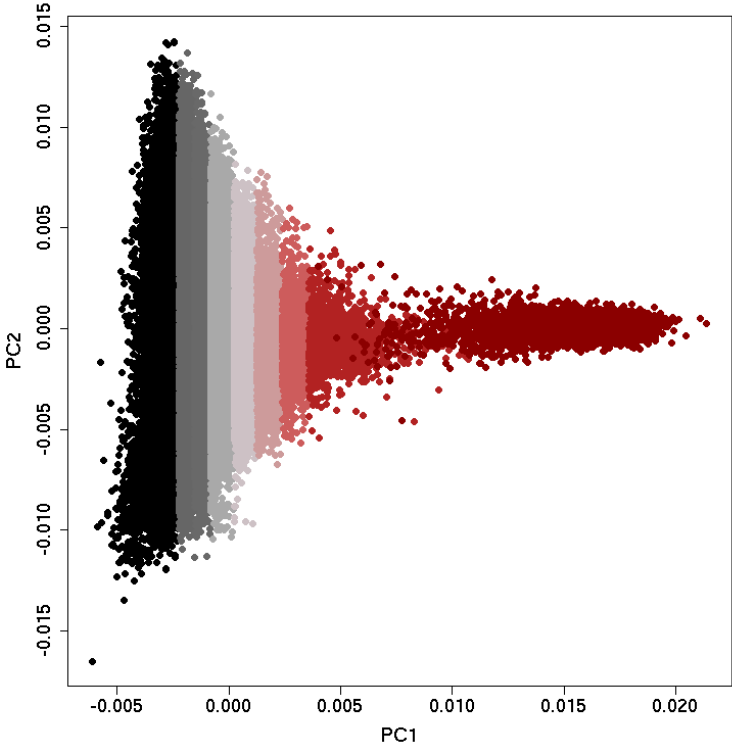


Data – More multi breed reference populations

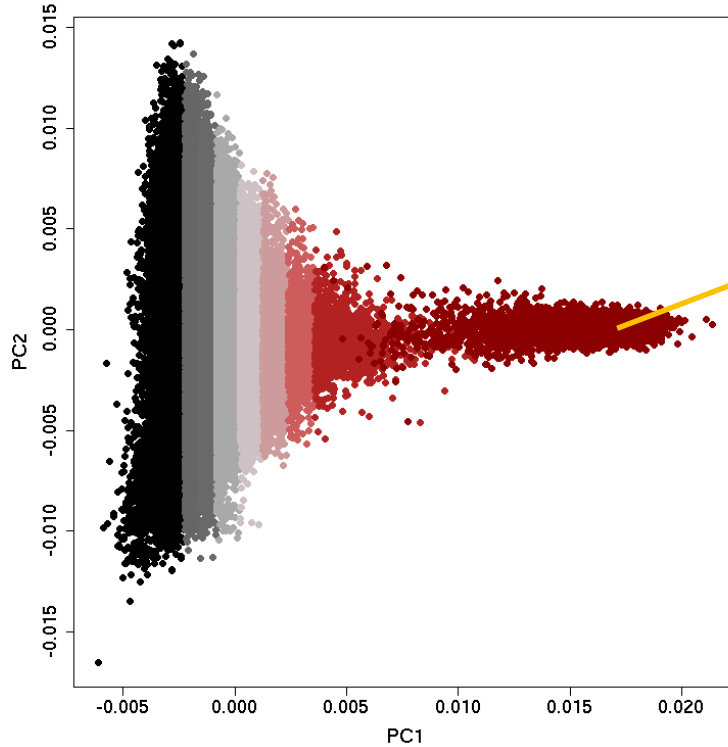


Is it better to use all Holstein / Jersey individuals or only the ones closest to the Australian Reds?

Data – More multi breed reference populations

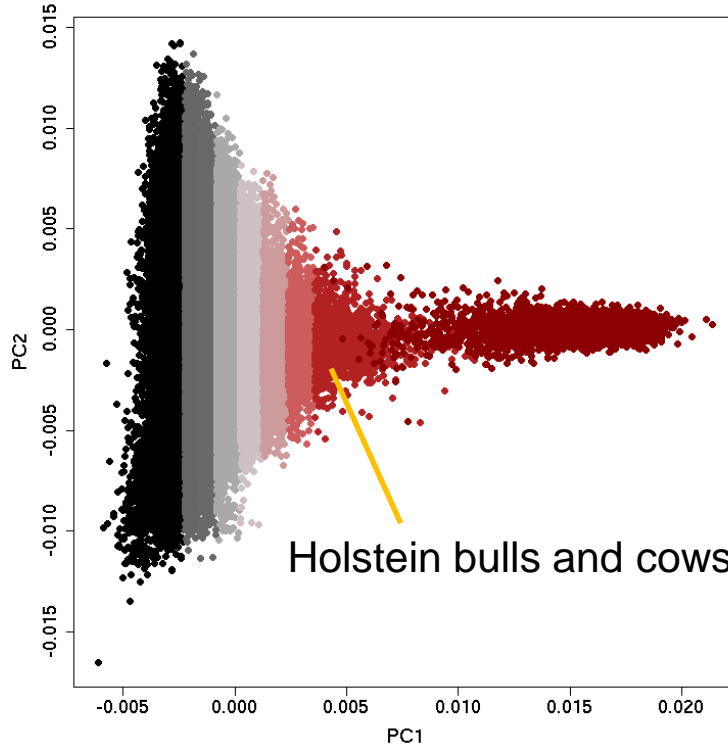


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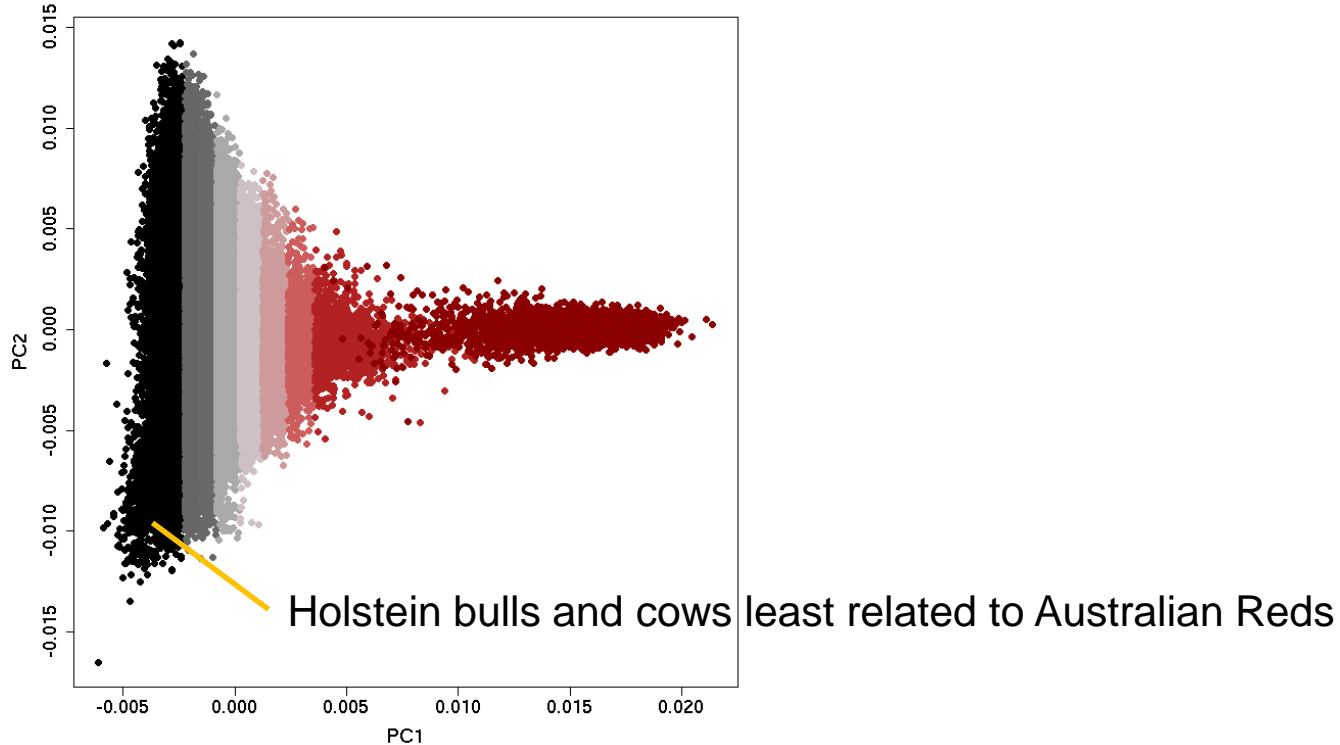
Australian Red cows

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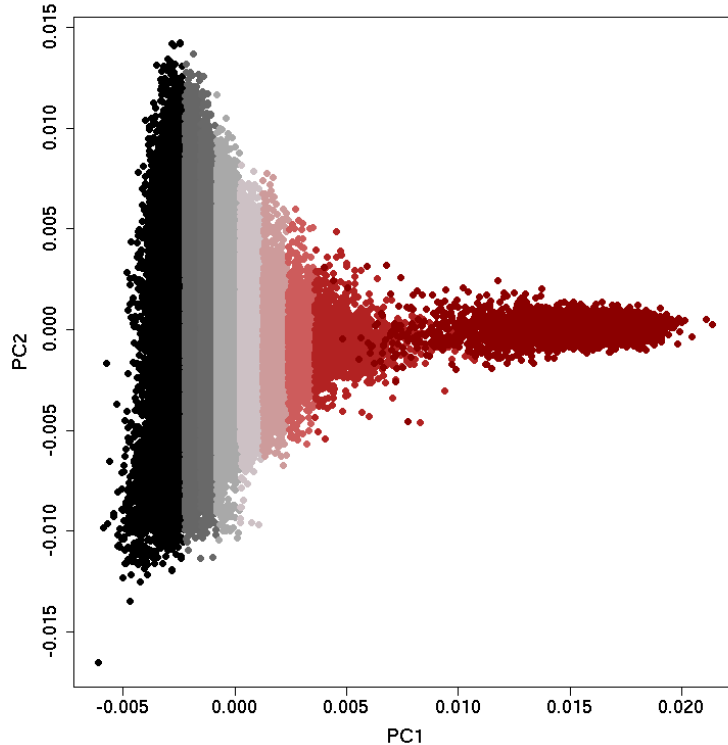


Holstein bulls and cows closest related to Australian Reds

Data – More multi breed reference populations

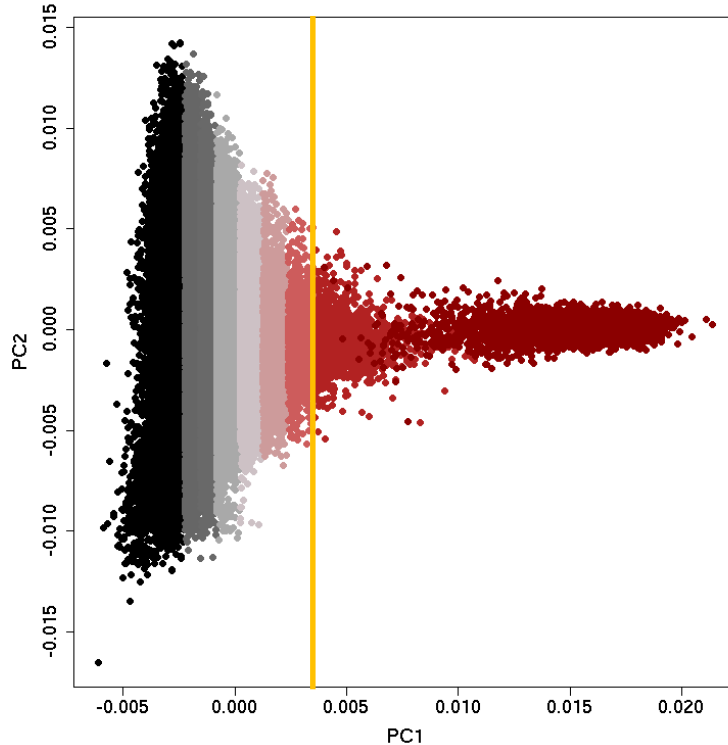


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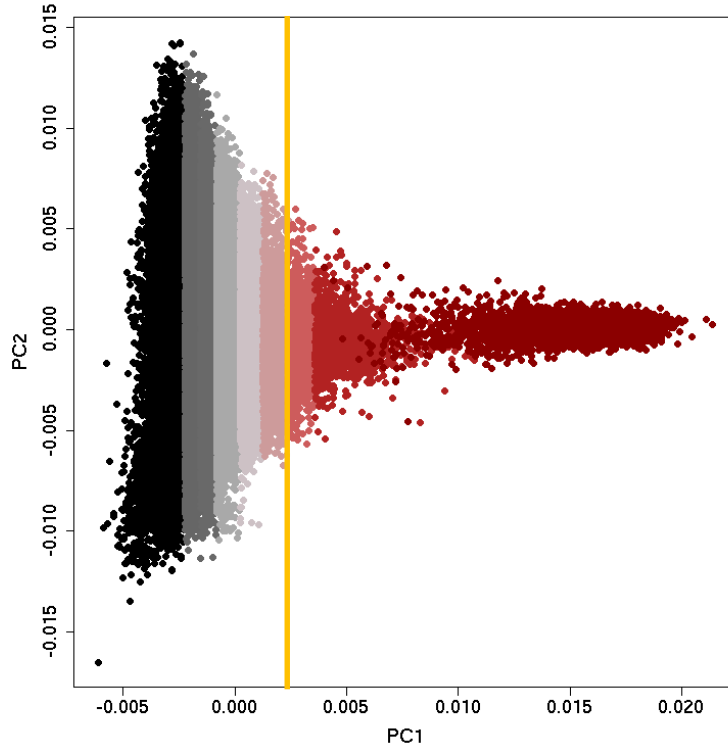
→ PCA used to construct 7 reference populations with increasing size but decreasing average relatedness to Australian Reds

Data – More multi breed reference populations



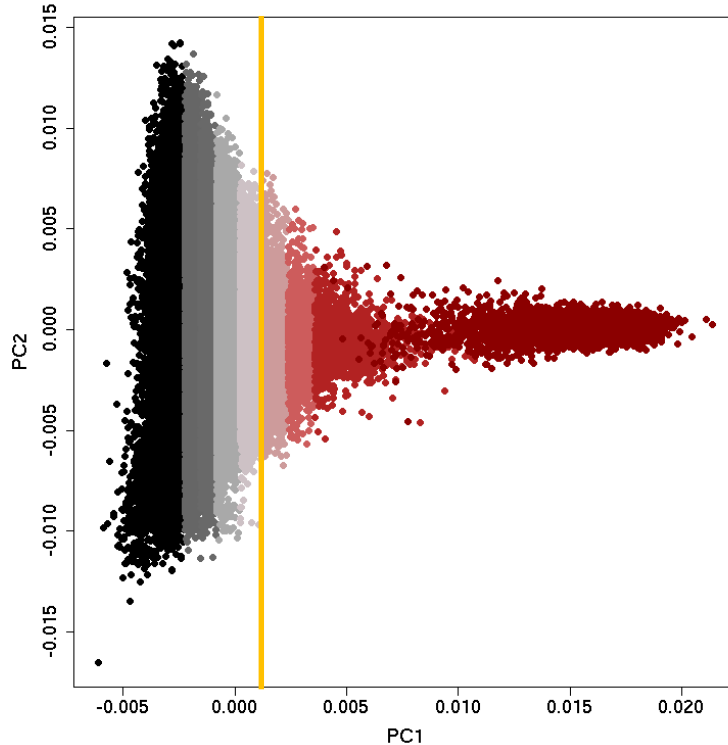
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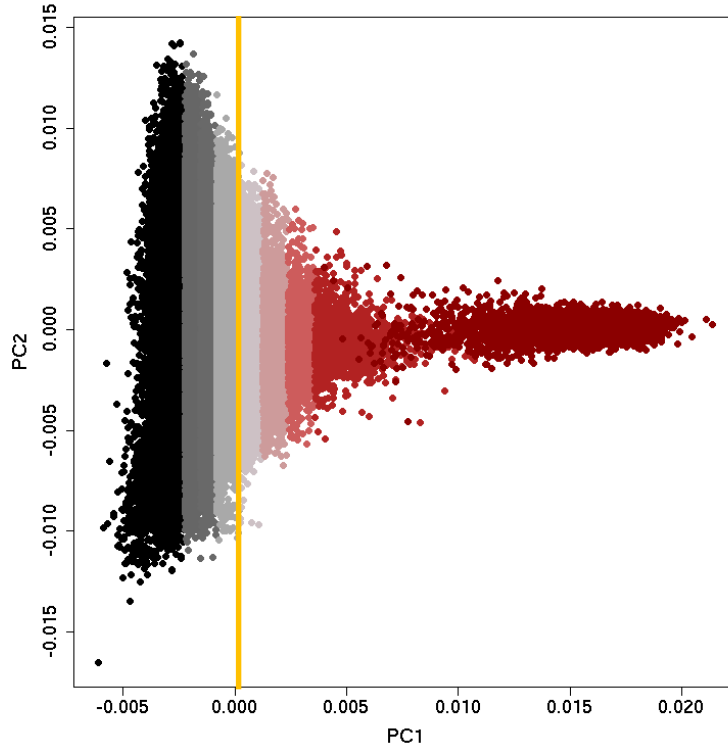
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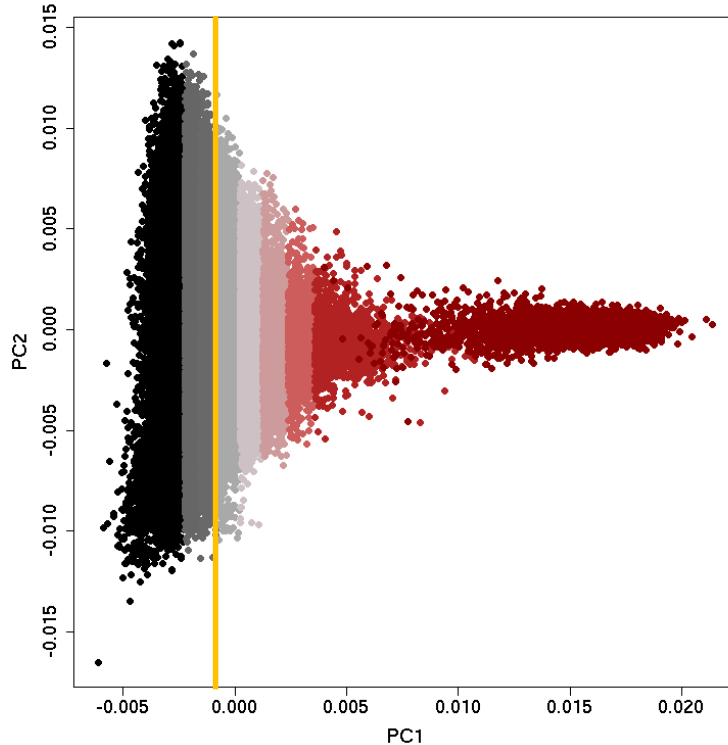
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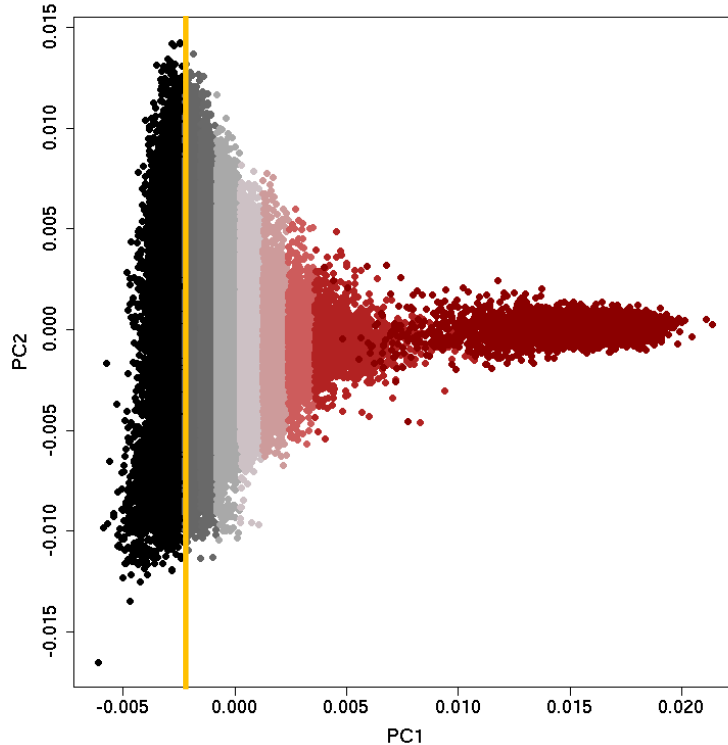
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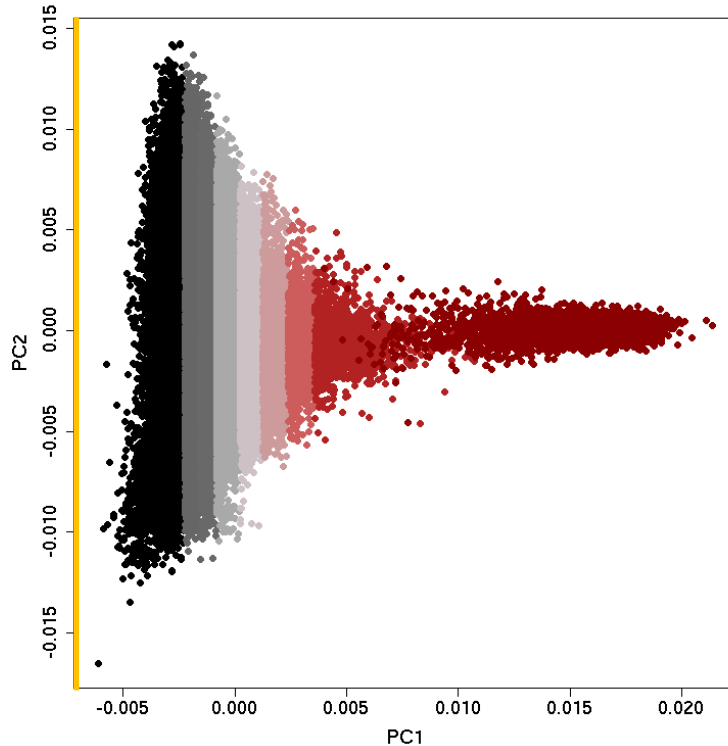
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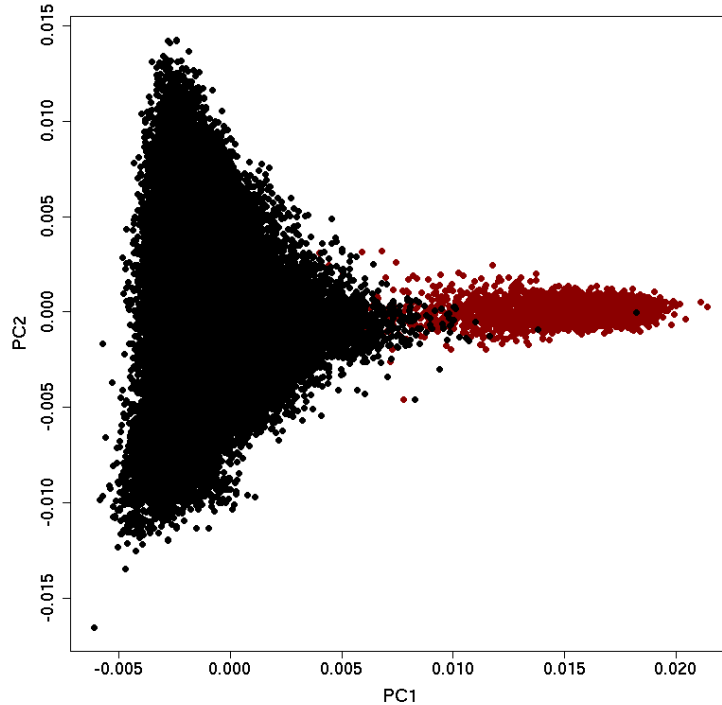
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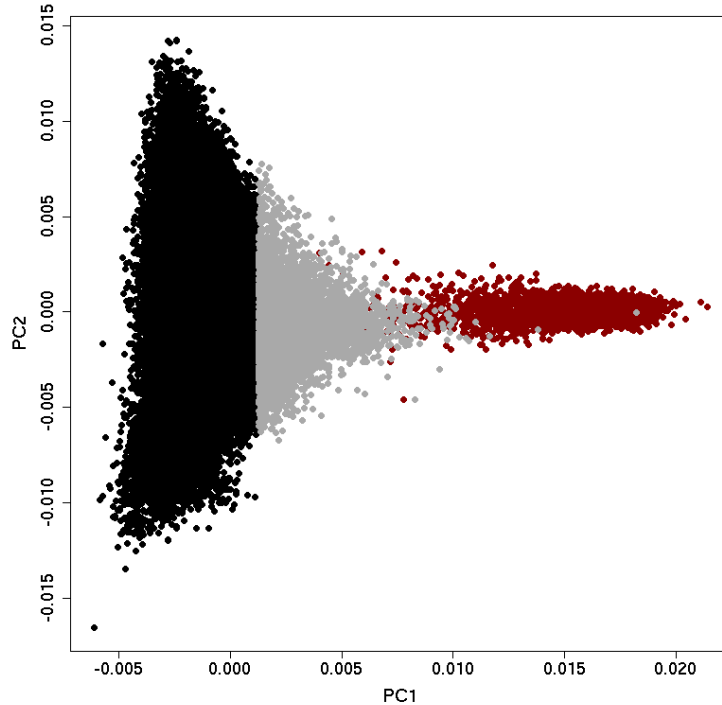
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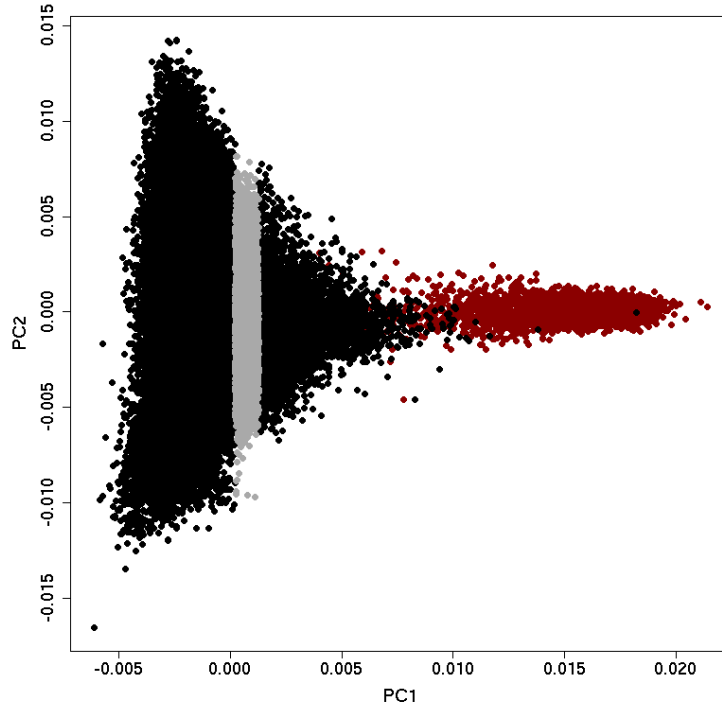
Constant number of Holsteins (10,000 bulls & cows) with varying relatedness to Australian Reds

Data – More multi breed reference populations



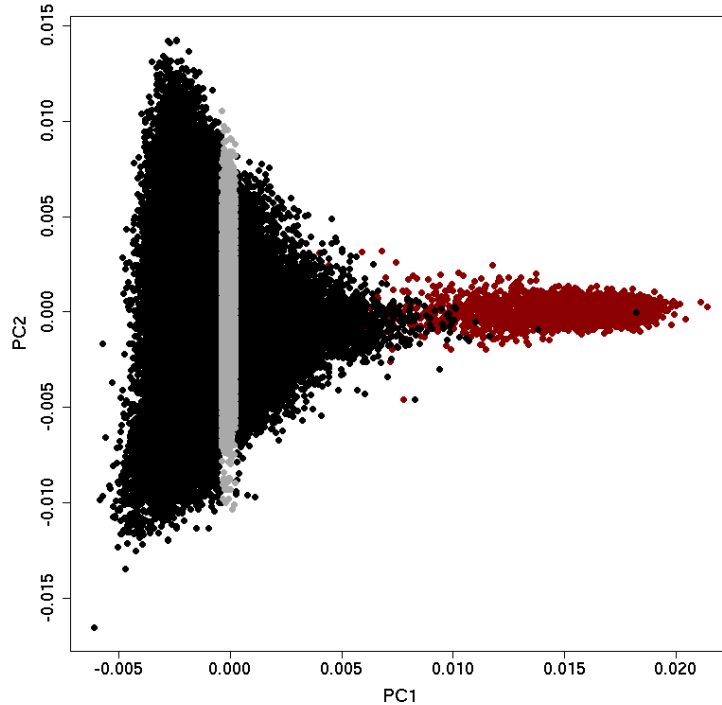
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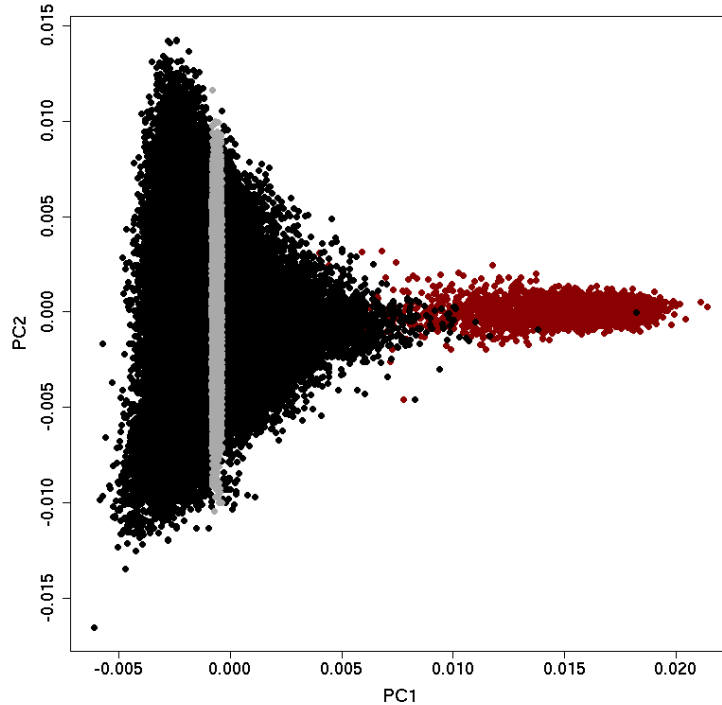
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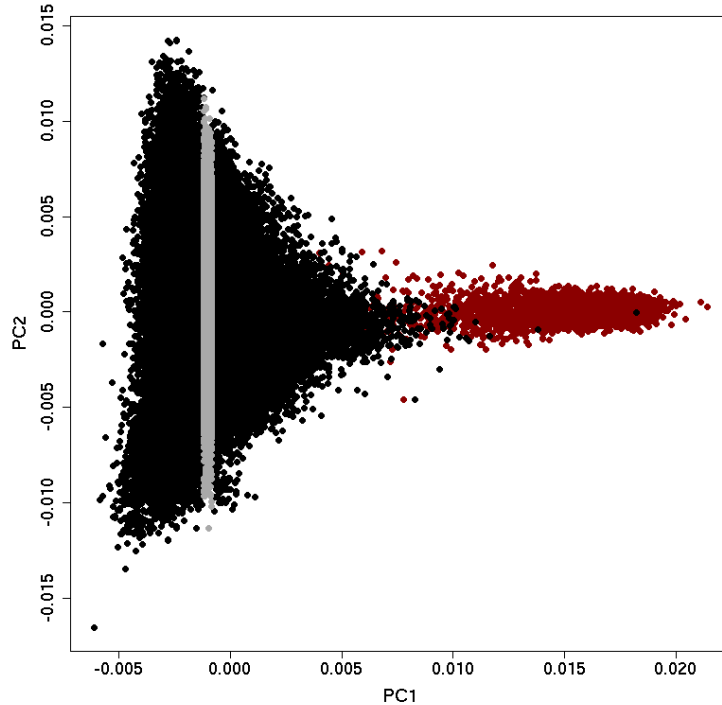
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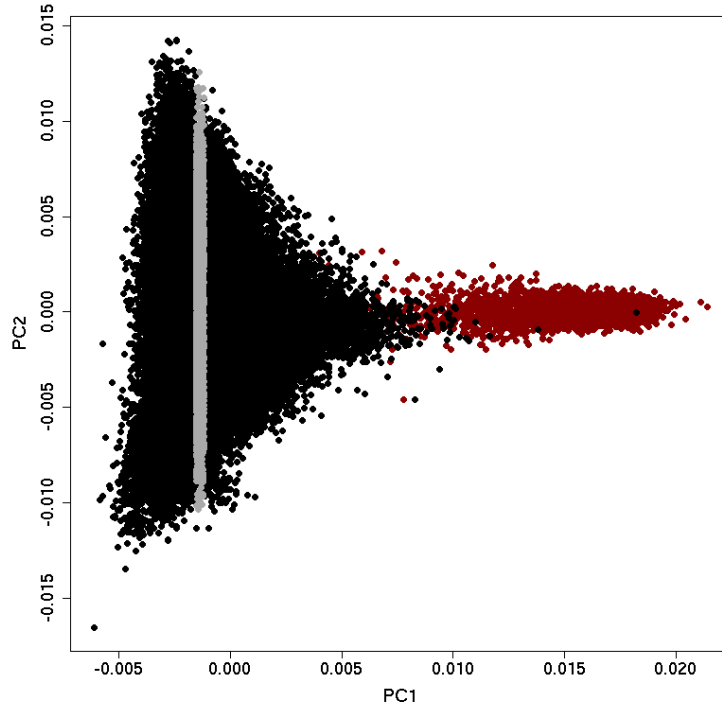
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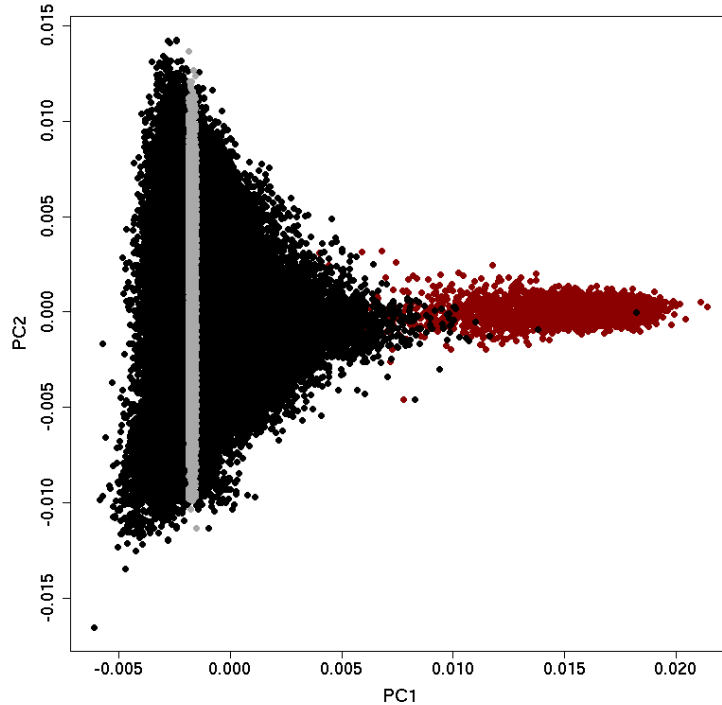
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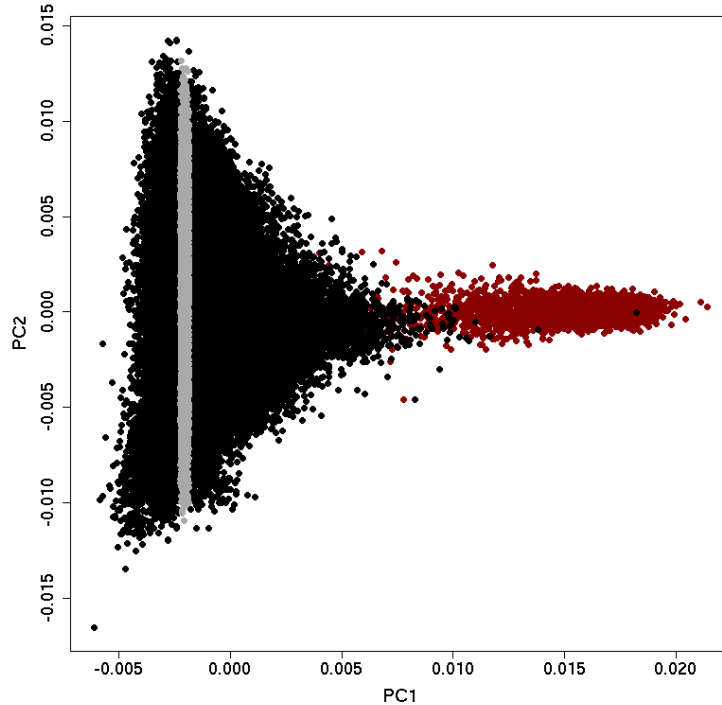
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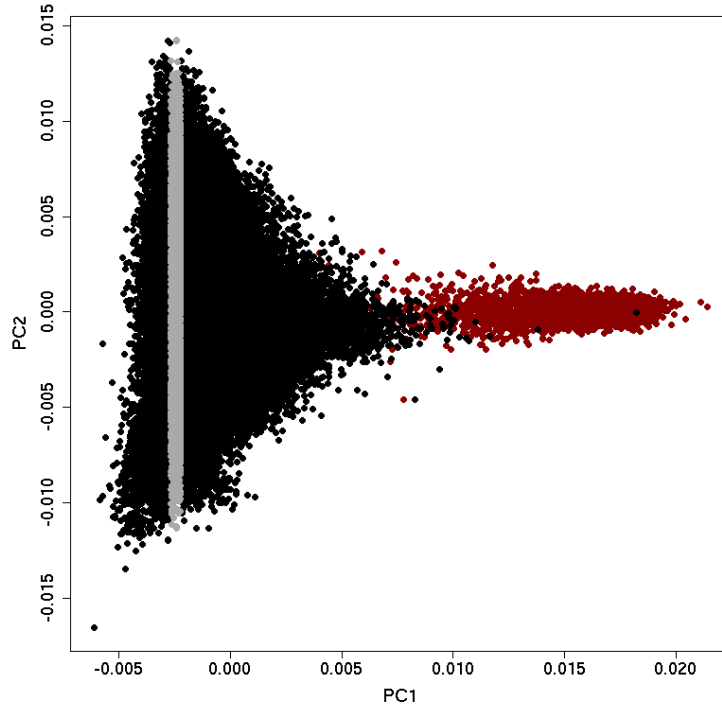
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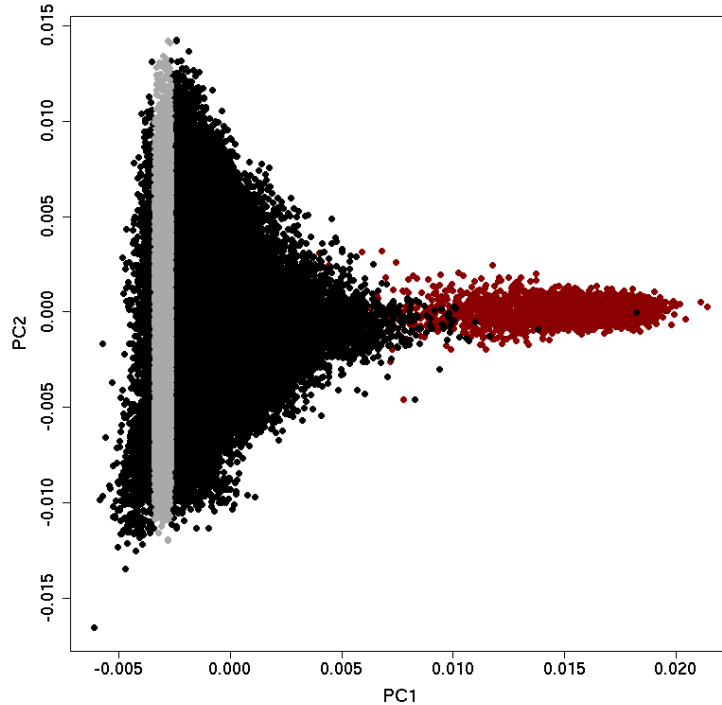
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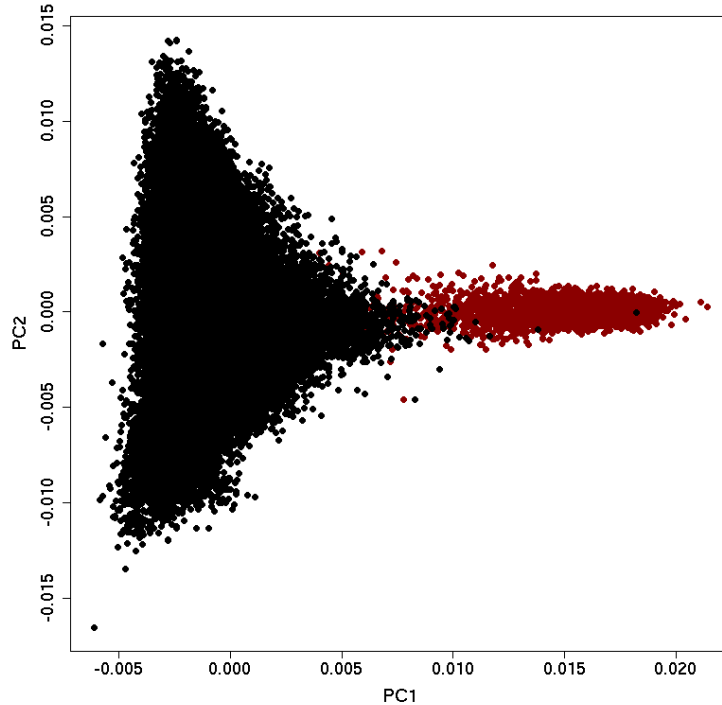
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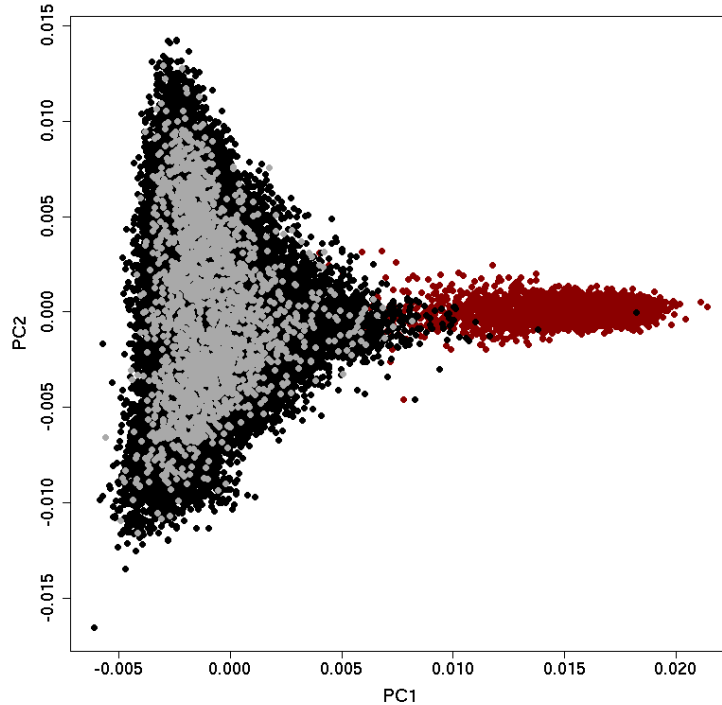
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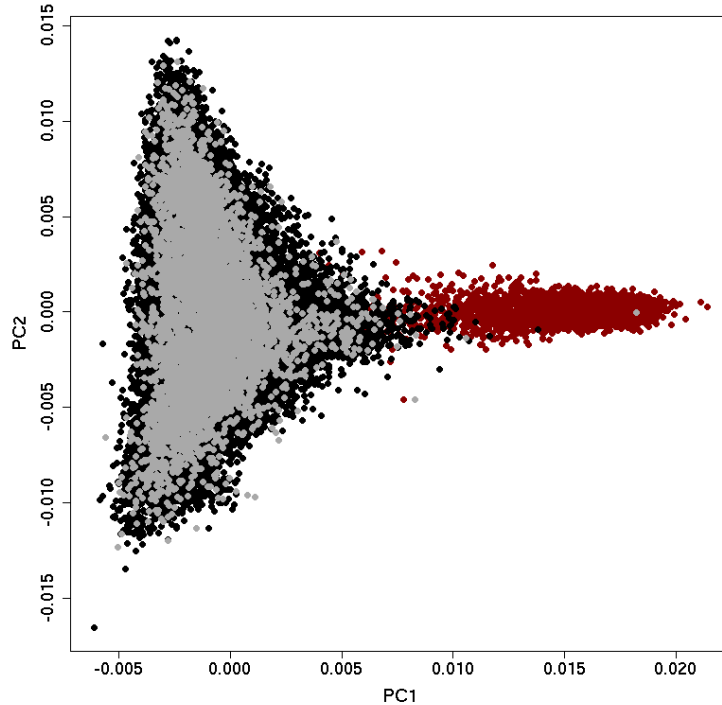
Similar relatedness but varying the number of Holsteins: randomly sampling 2,000 / 5,000 or 10,000 Holsteins (10 repeats)

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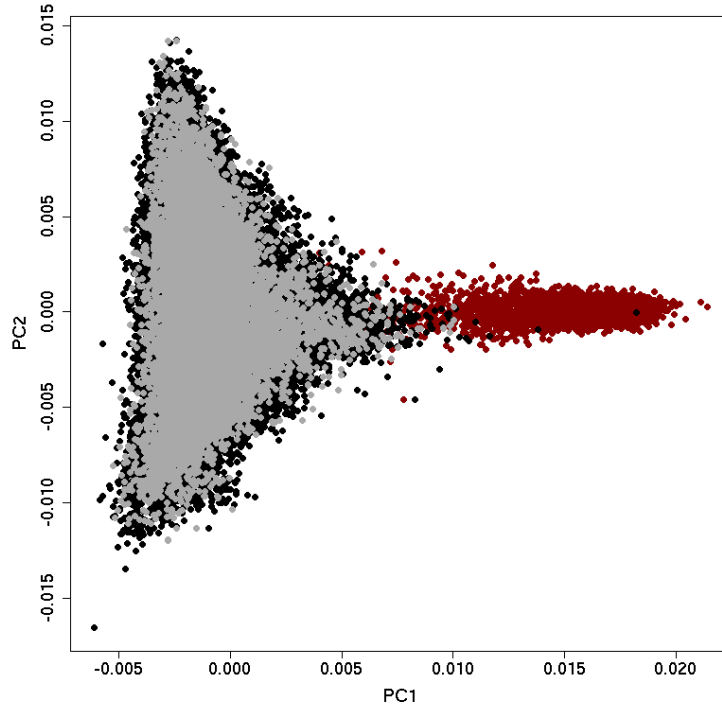
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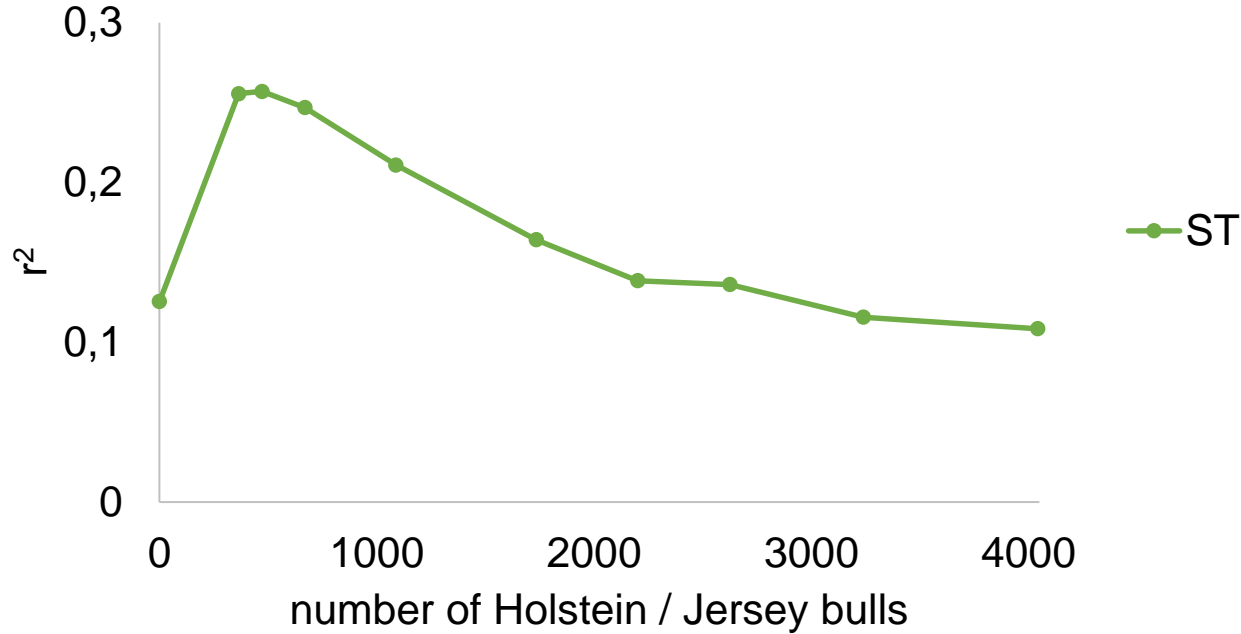
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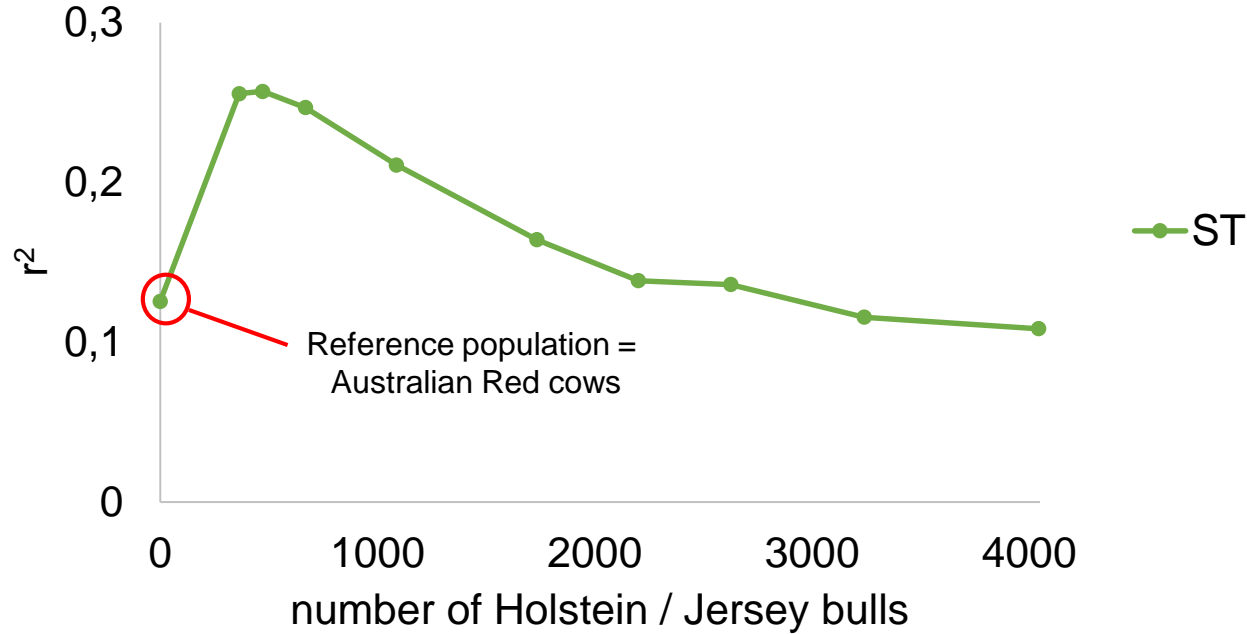


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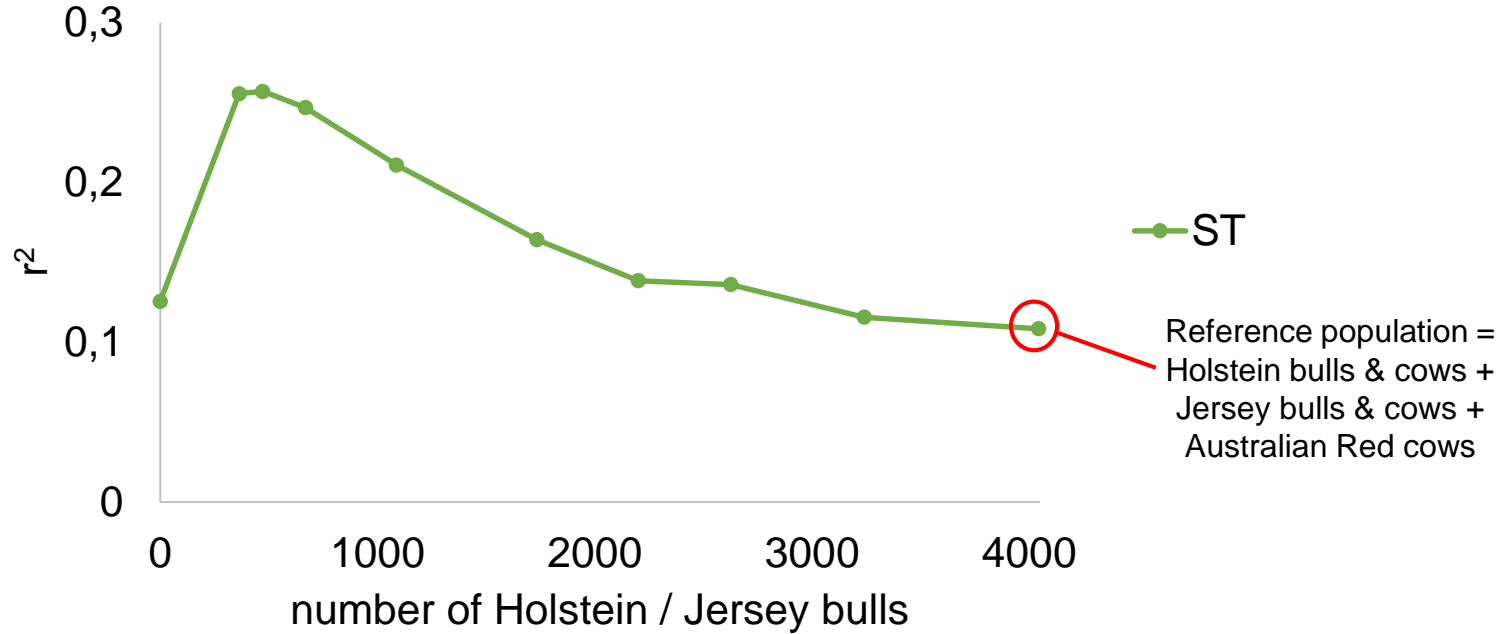
Results: size and relatedness of reference population – Milk yield



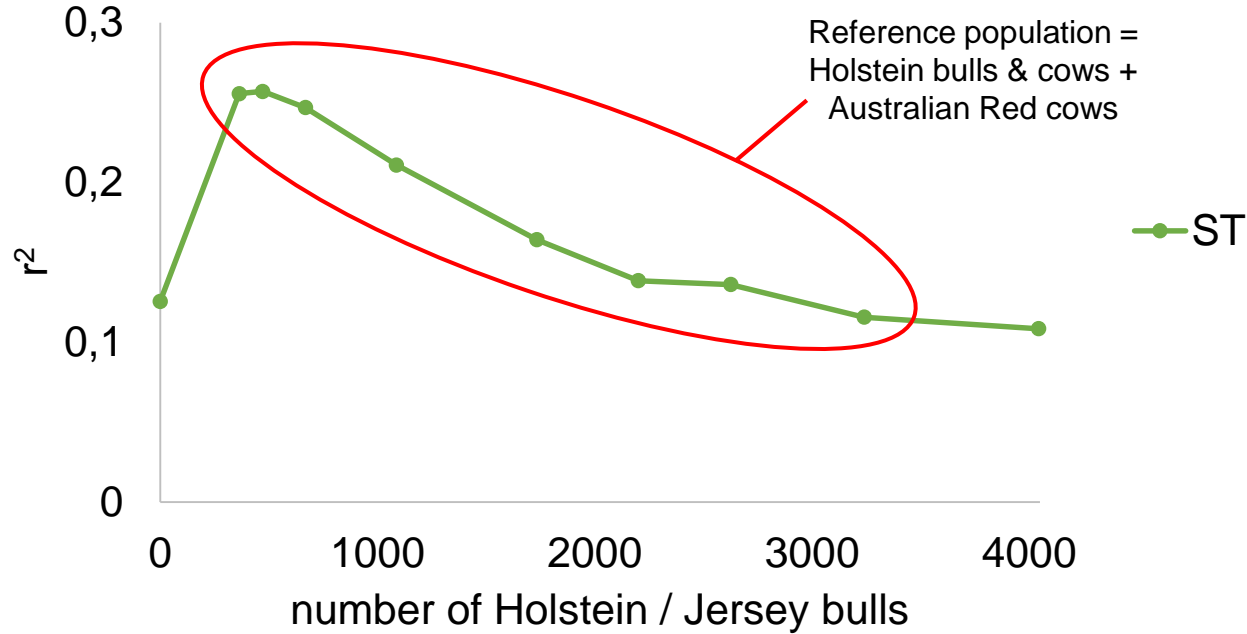
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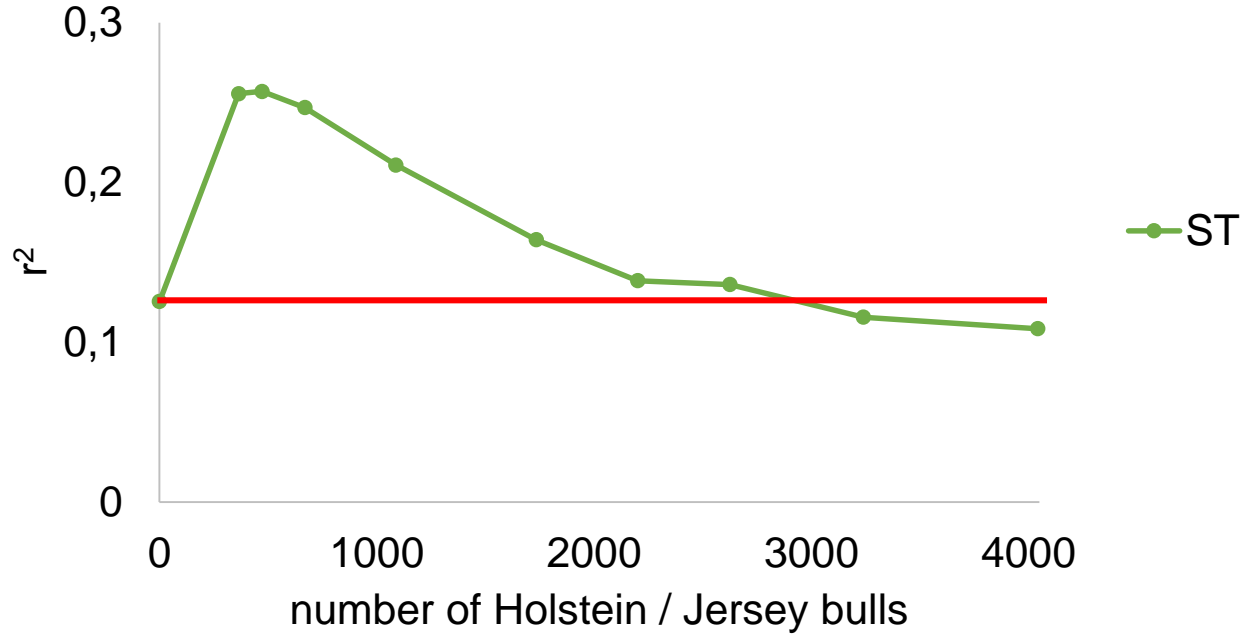
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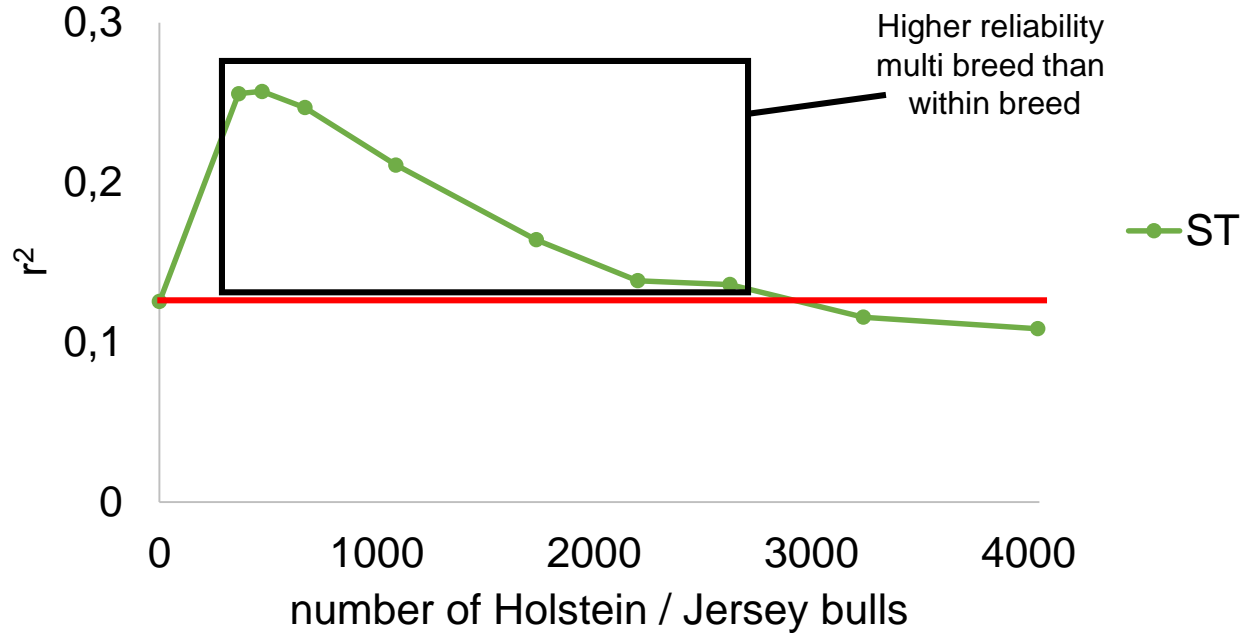
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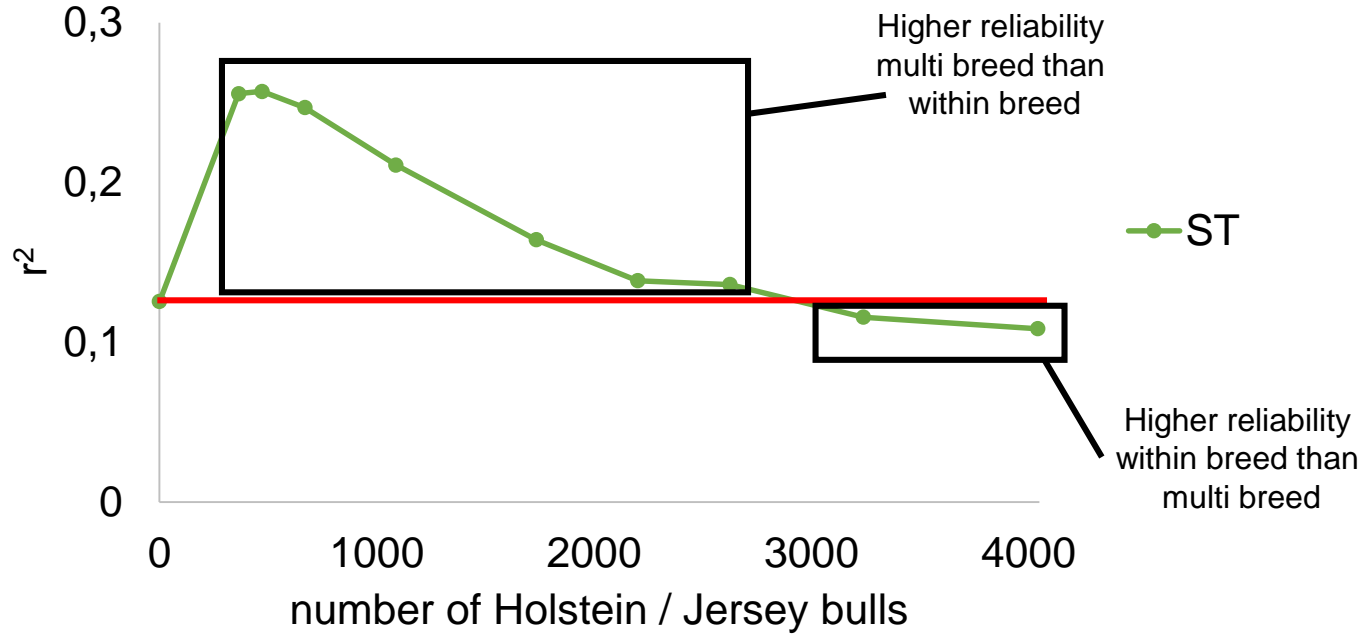
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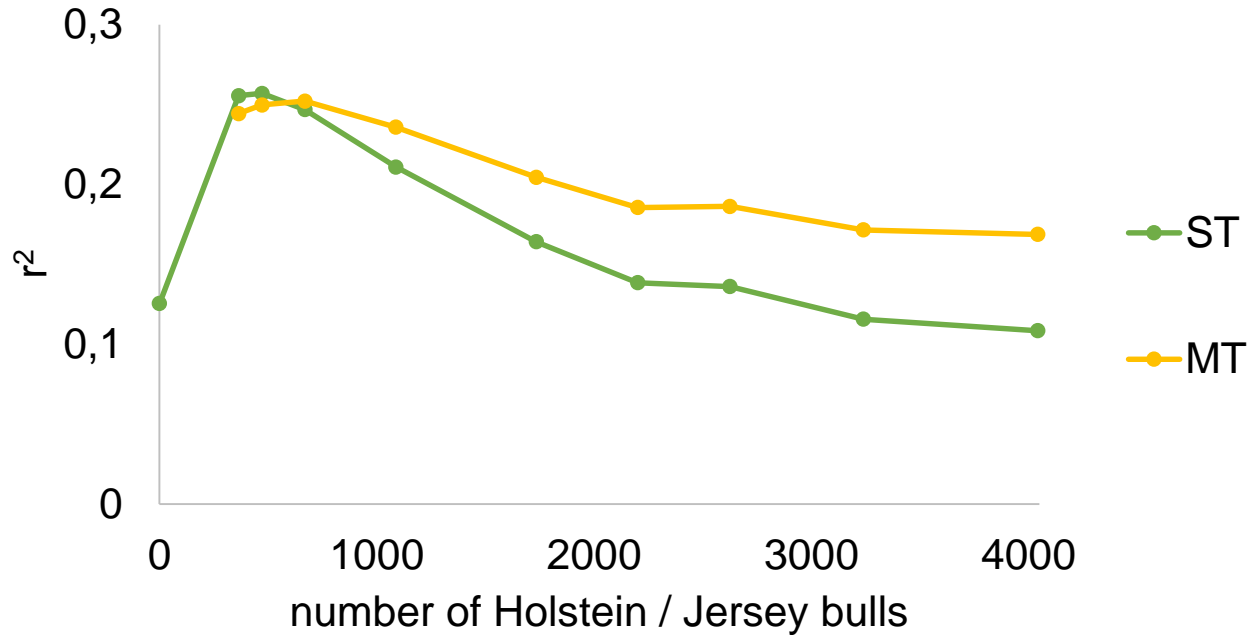
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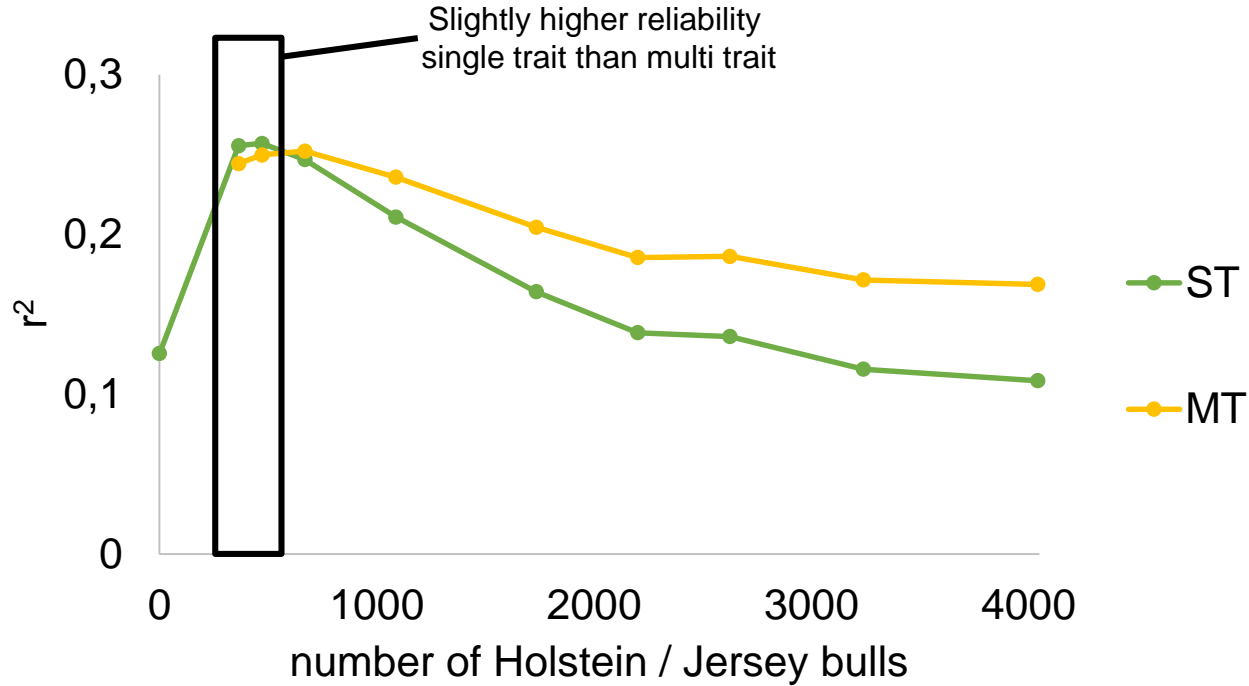
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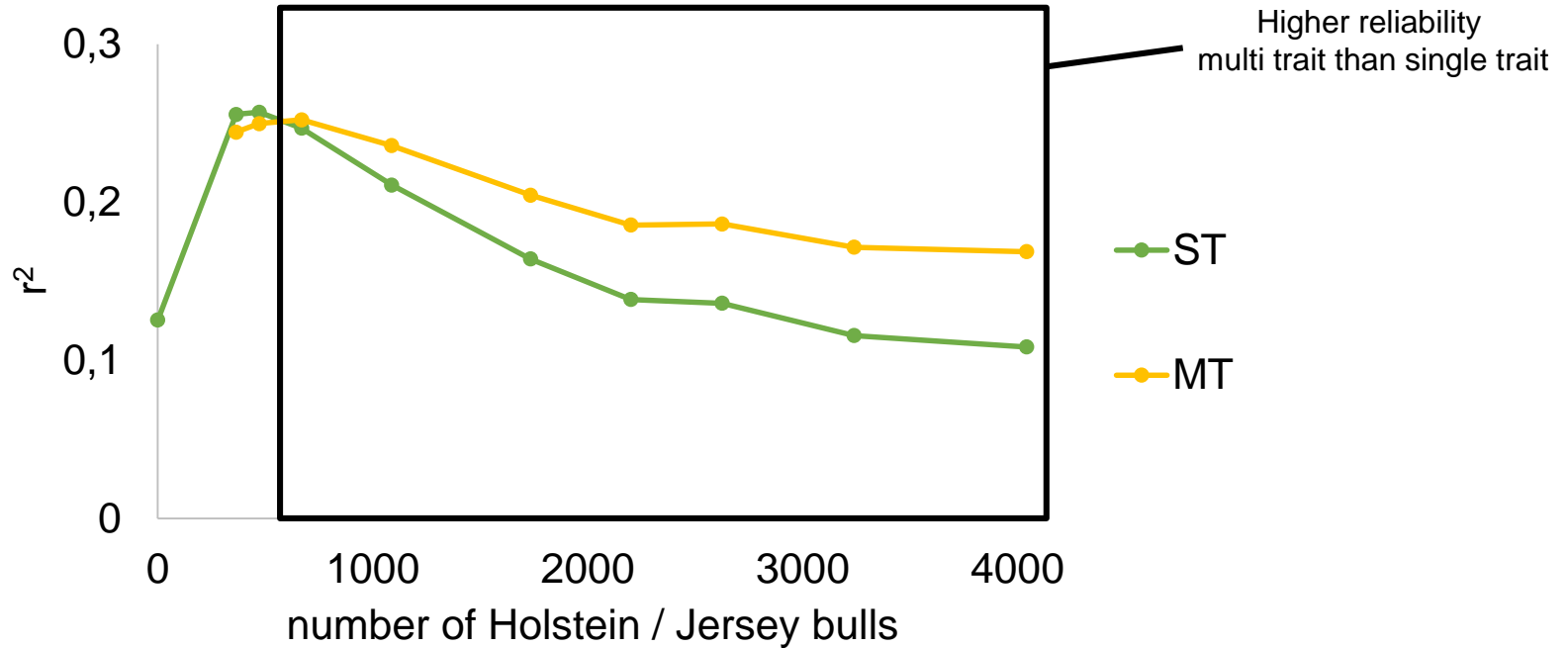
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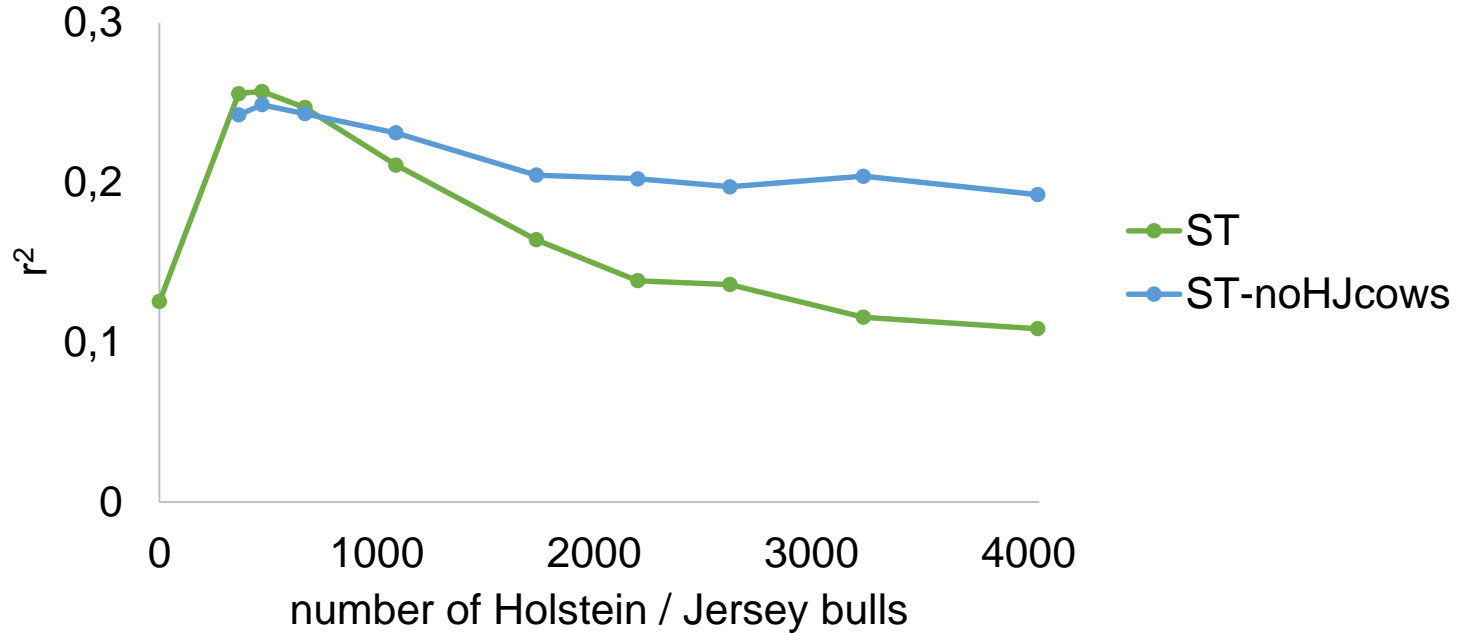
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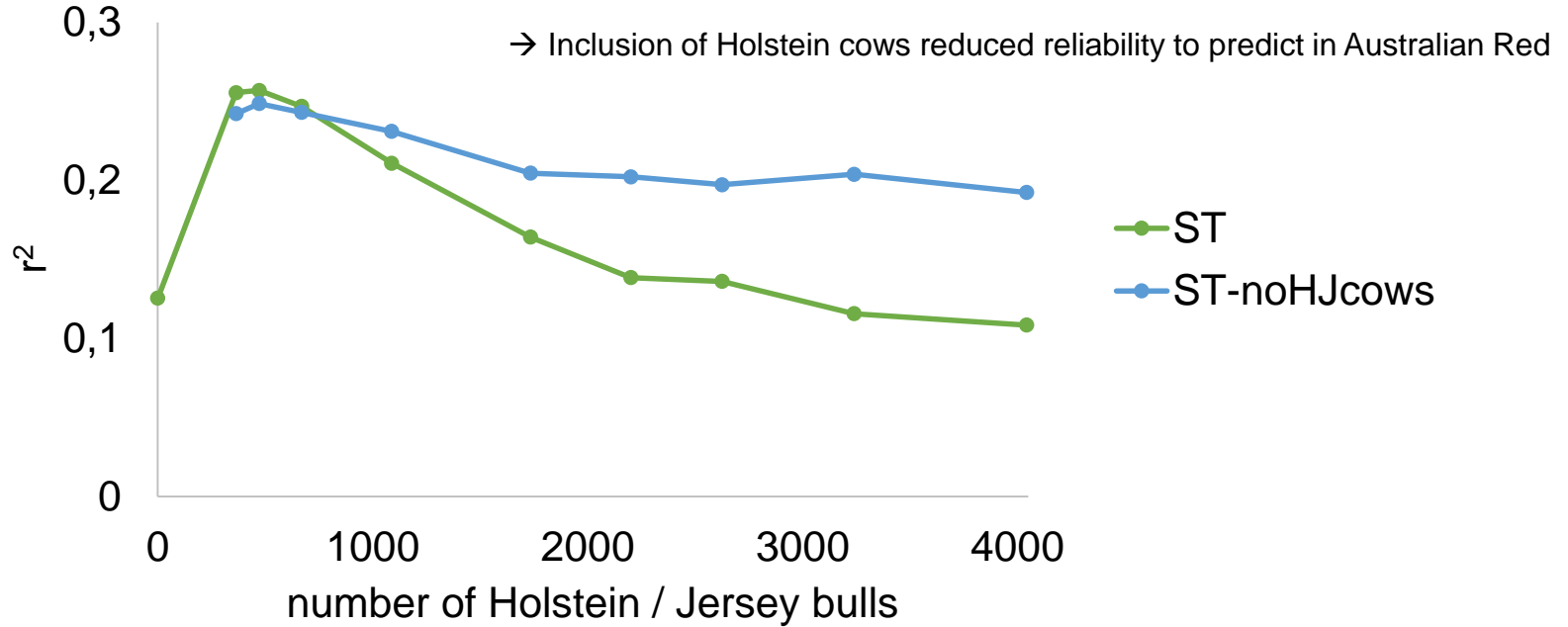
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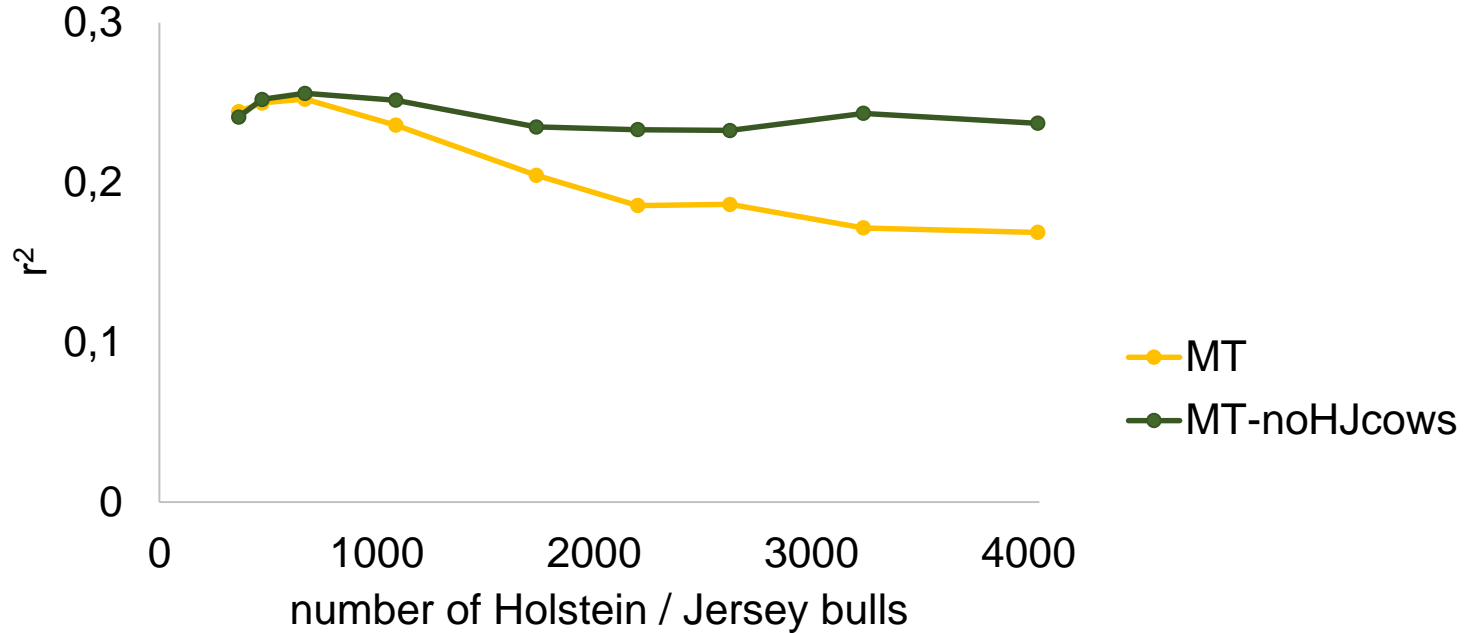
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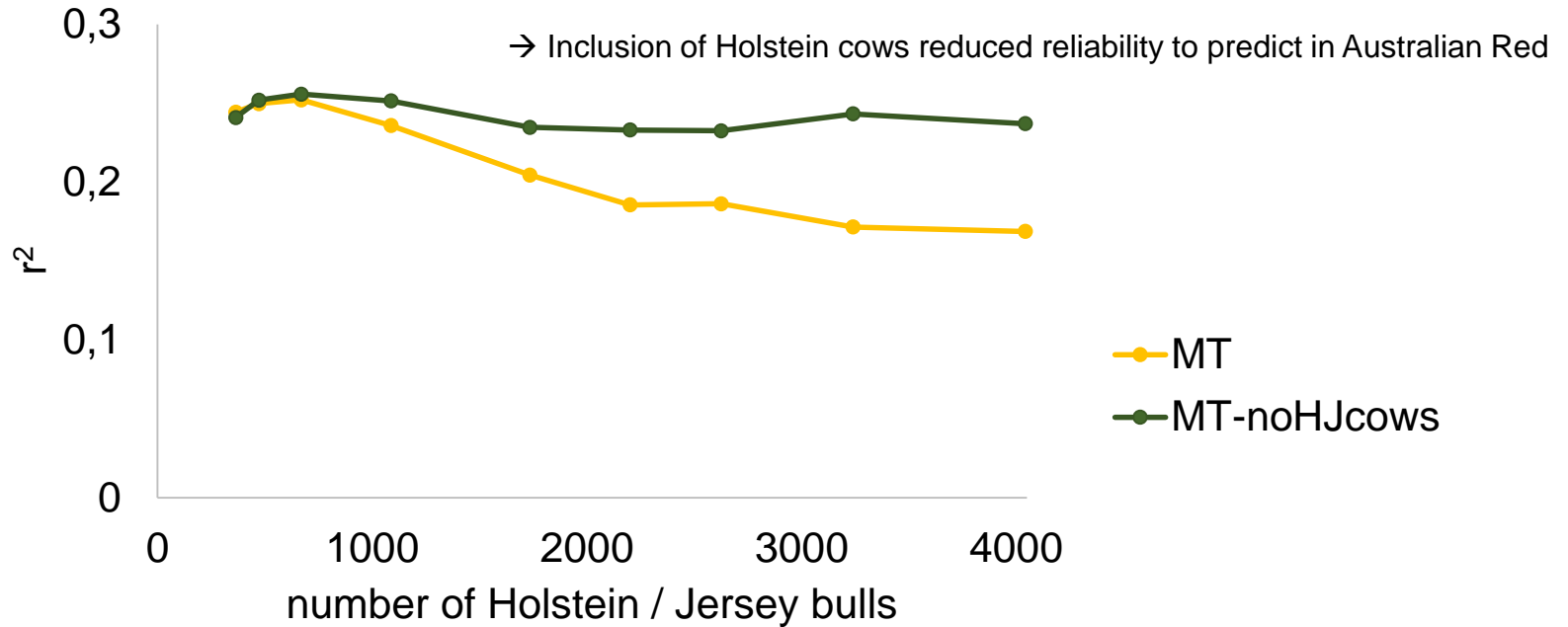
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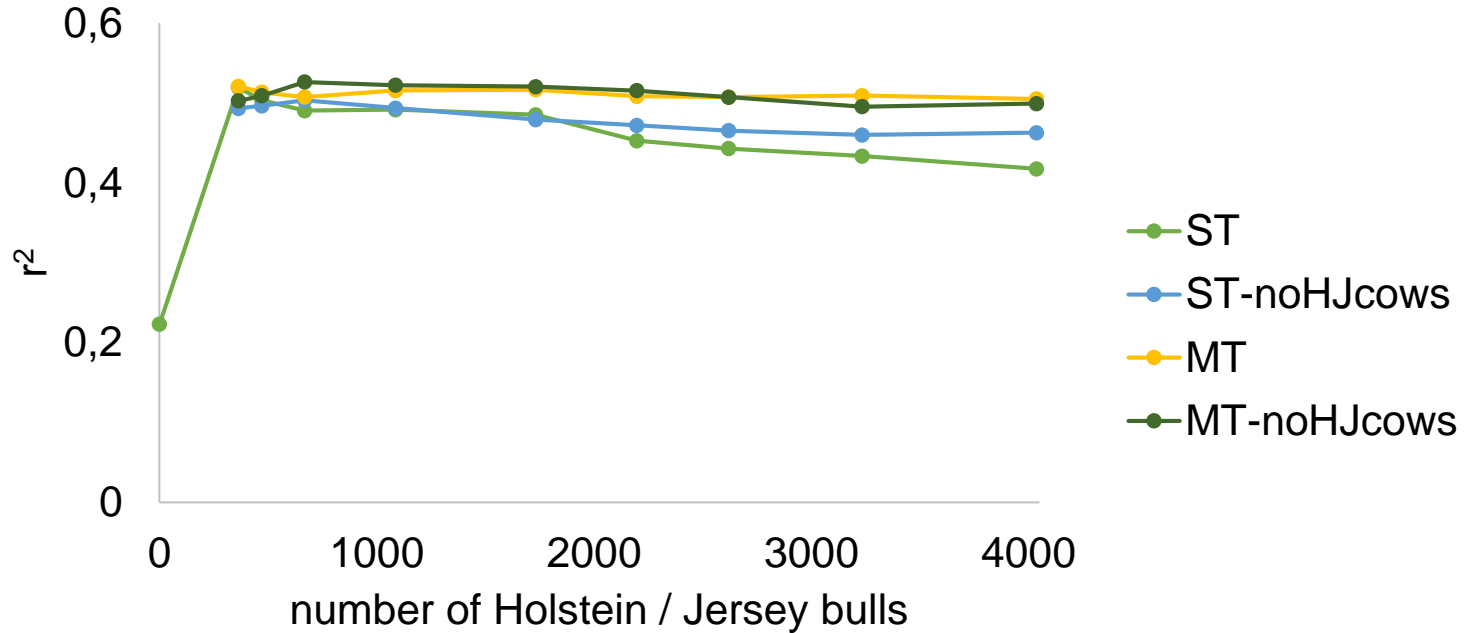
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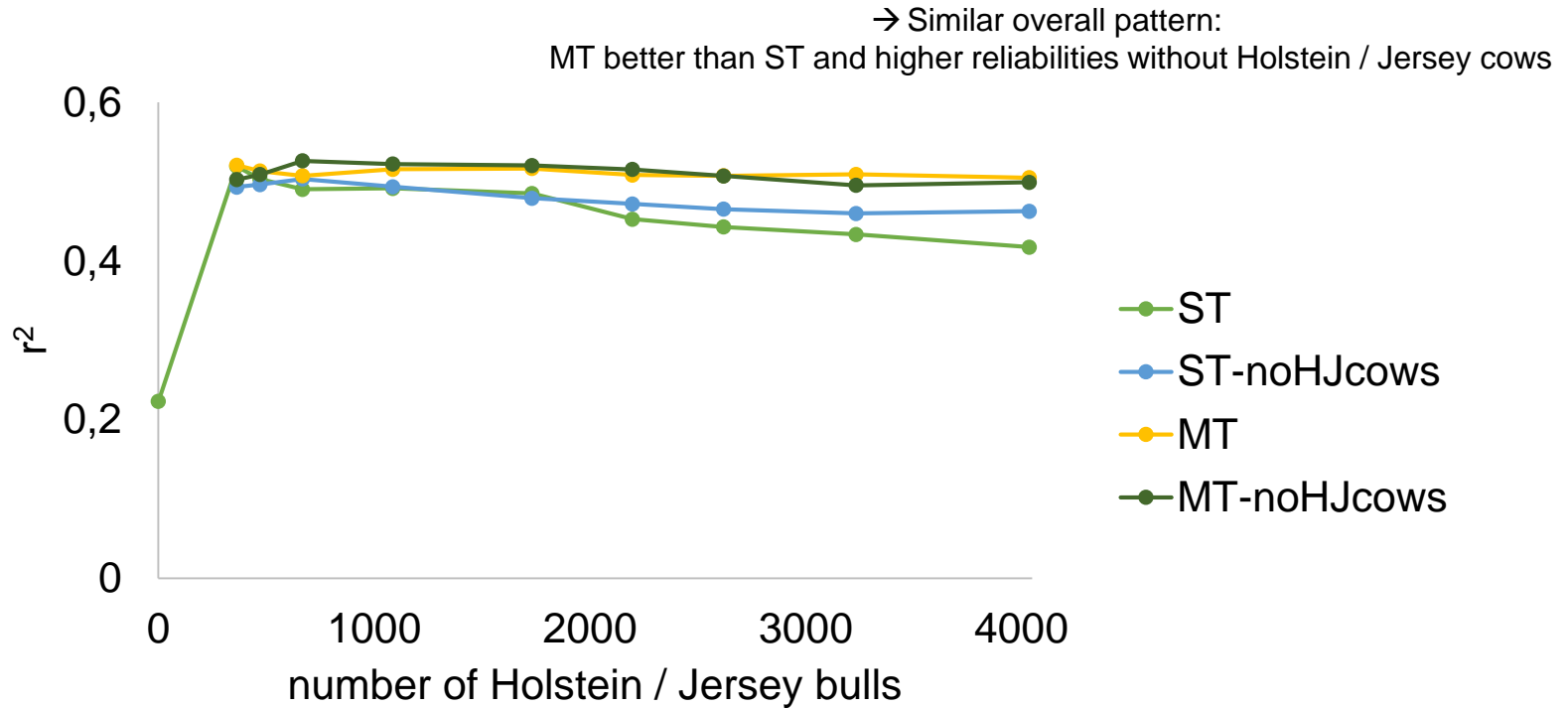
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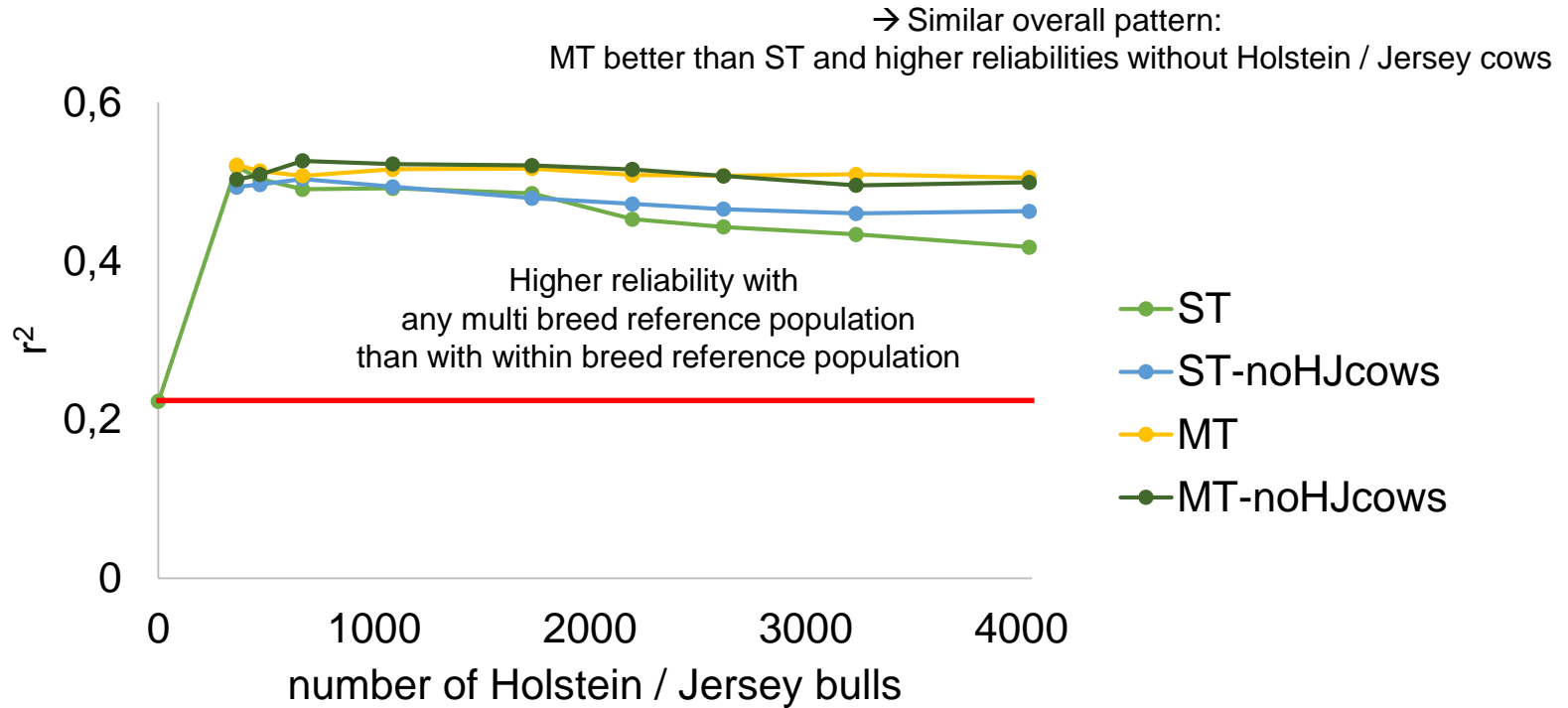
Results: size and relatedness of reference population – Fat yield



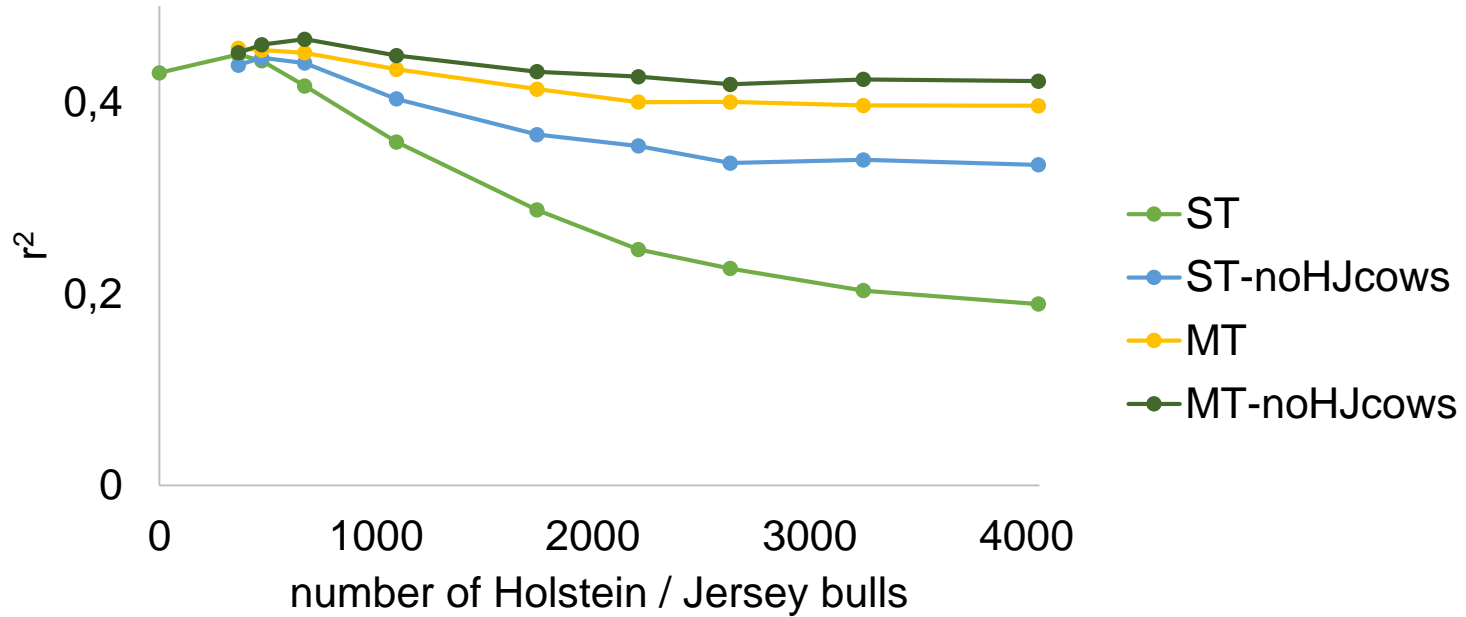
Results: size and relatedness of reference population – Fat yield



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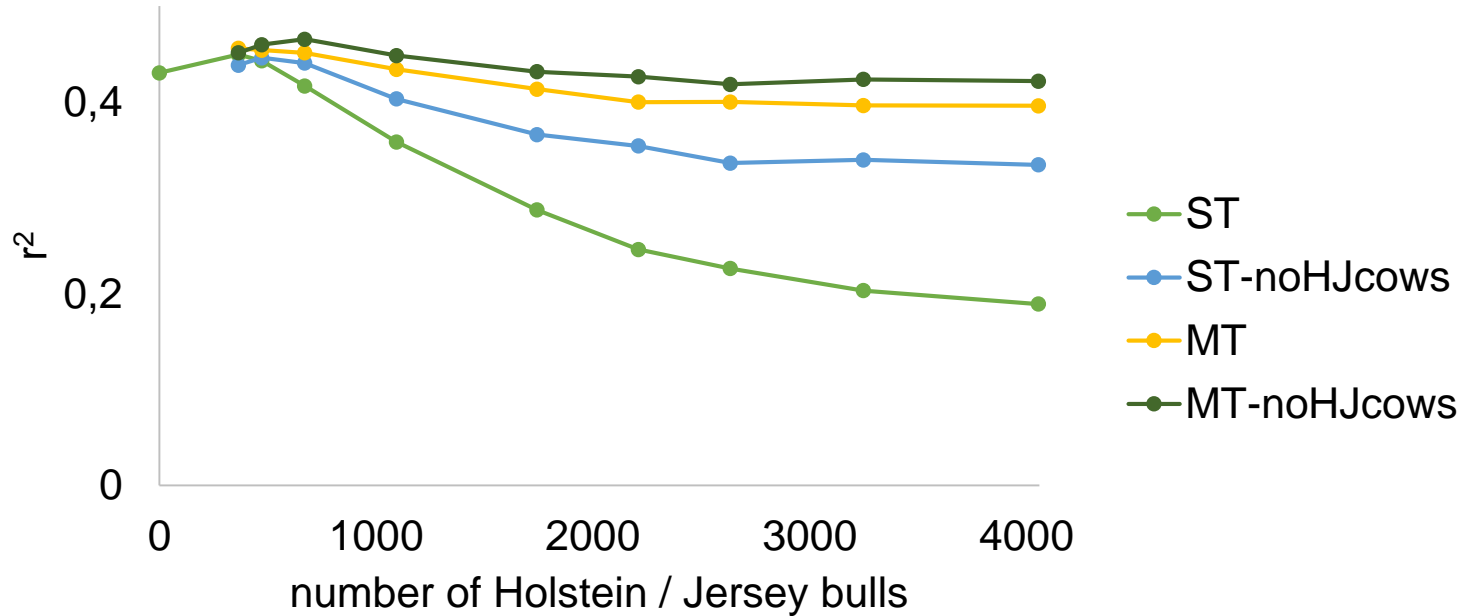
Results: size and relatedness of reference population – Fat yield



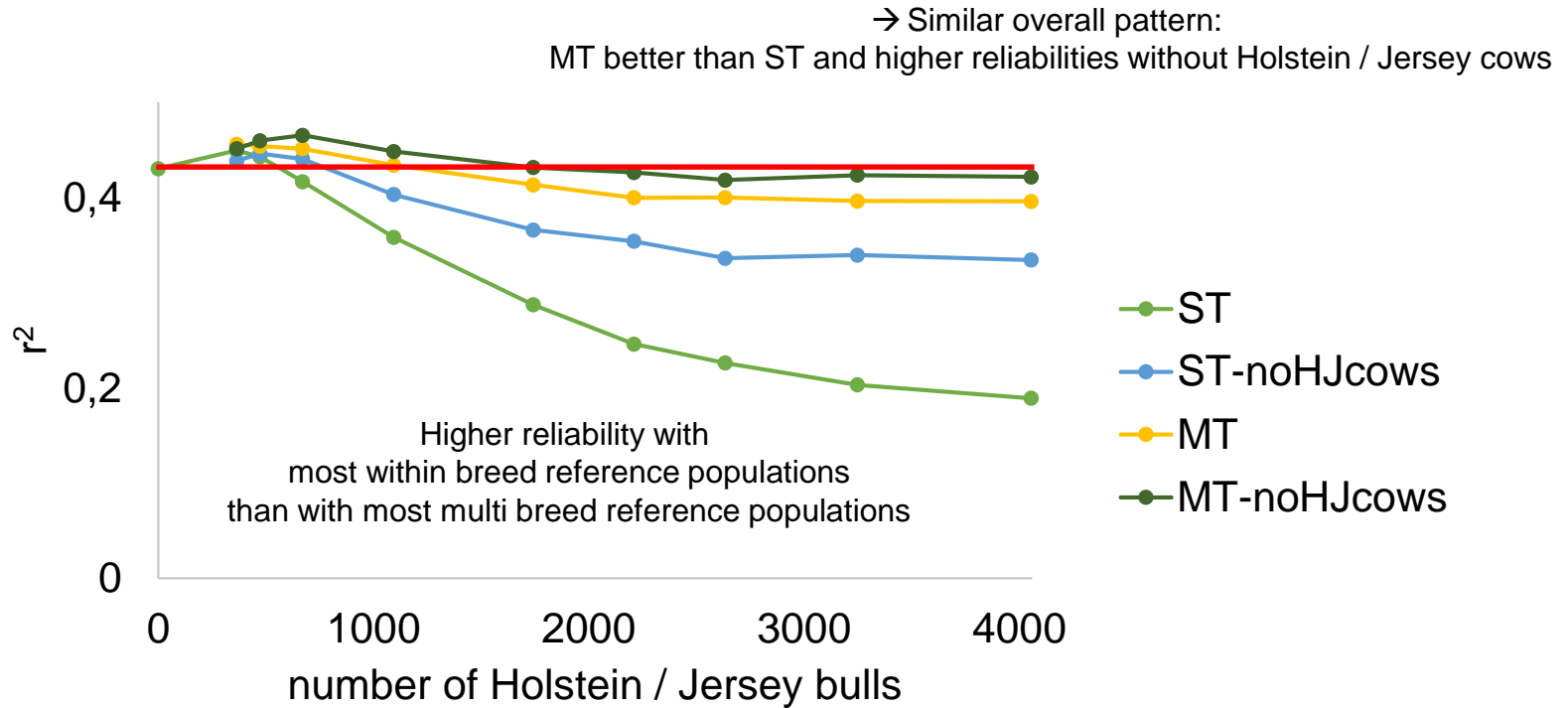
Results: size and relatedness of reference population – Protein yield

→ Similar overall pattern:

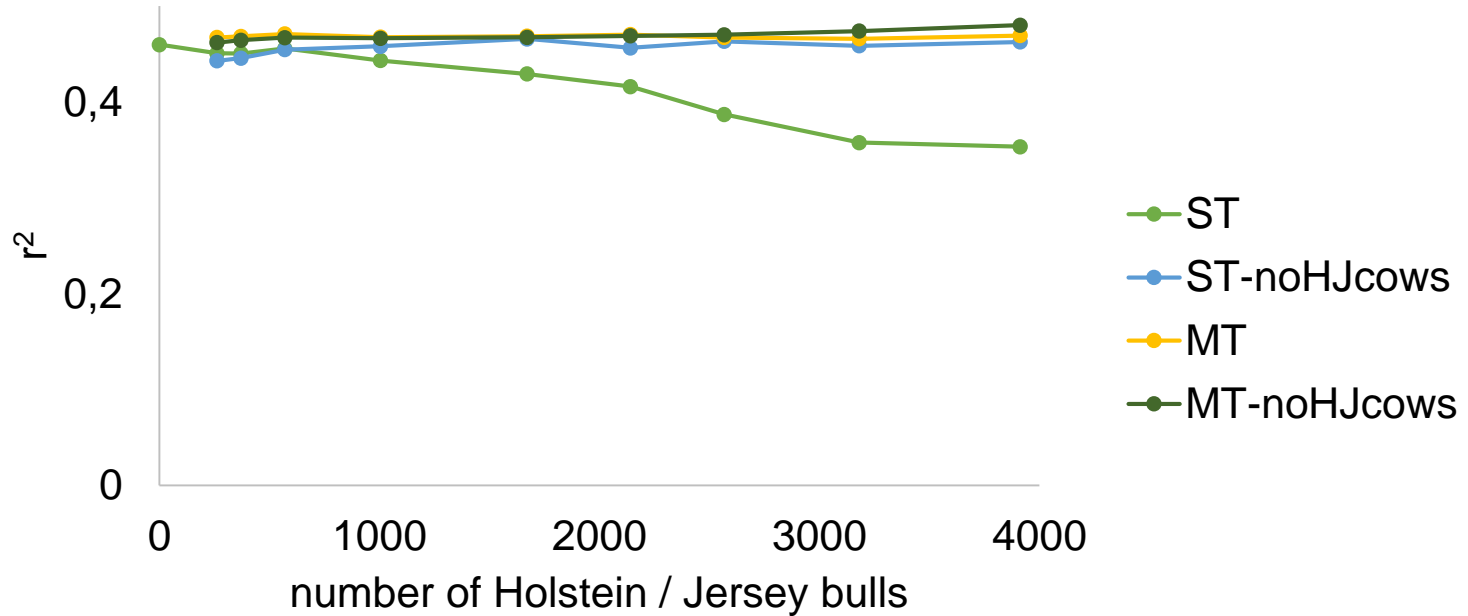
MT better than ST and higher reliabilities without Holstein / Jersey cows



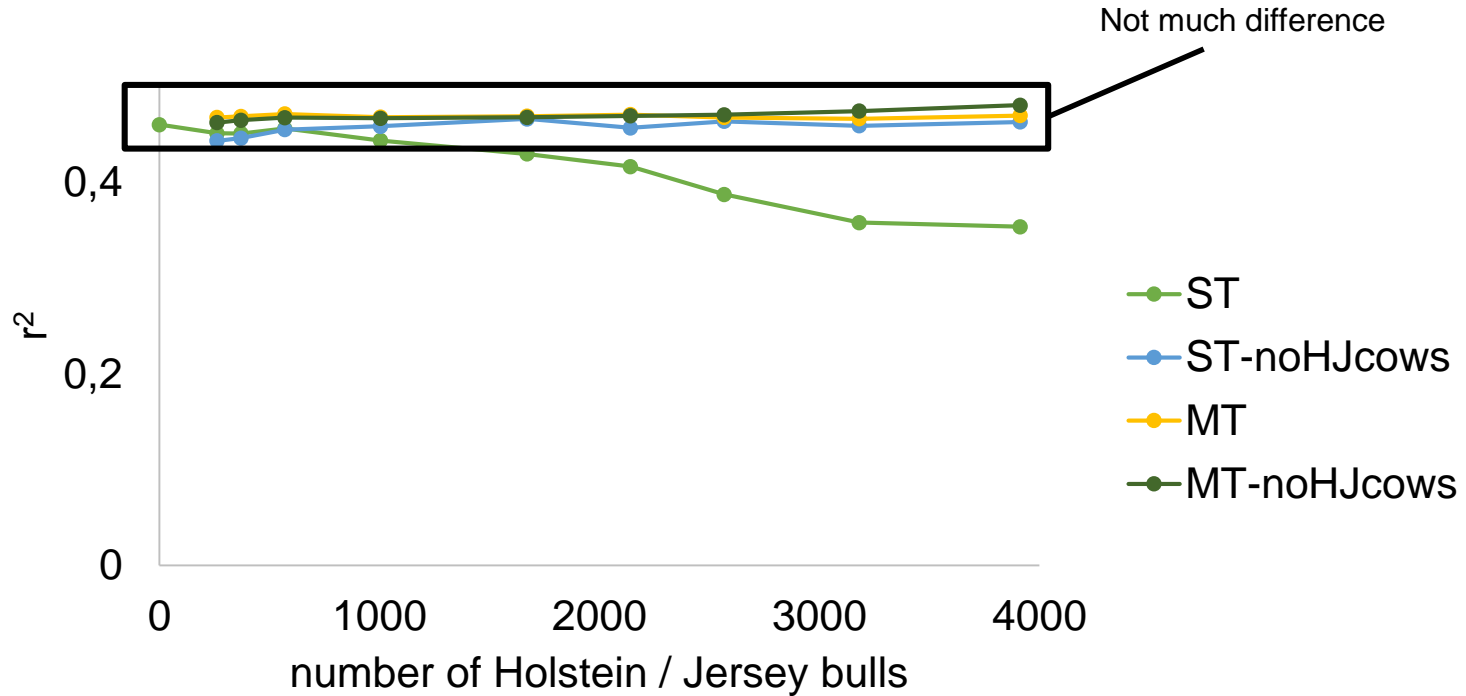
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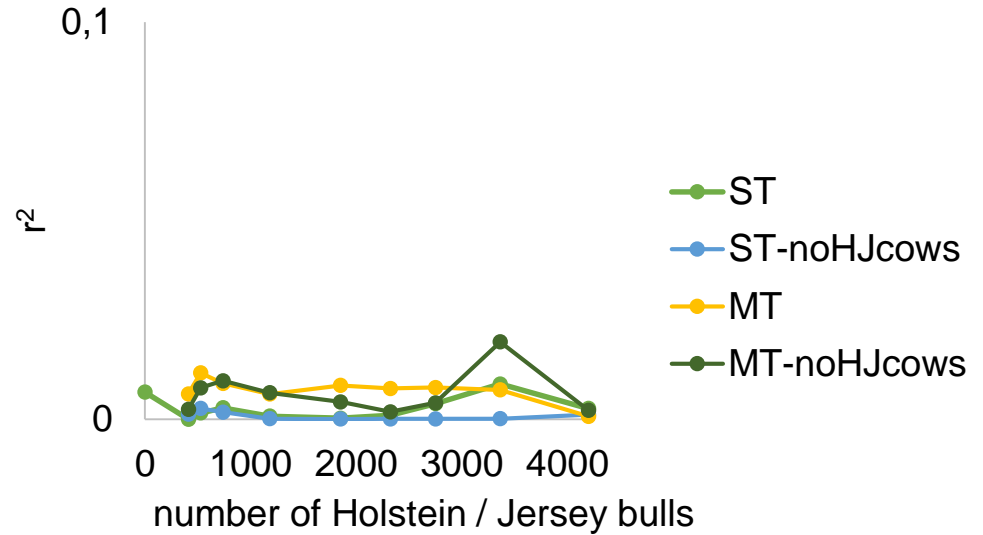
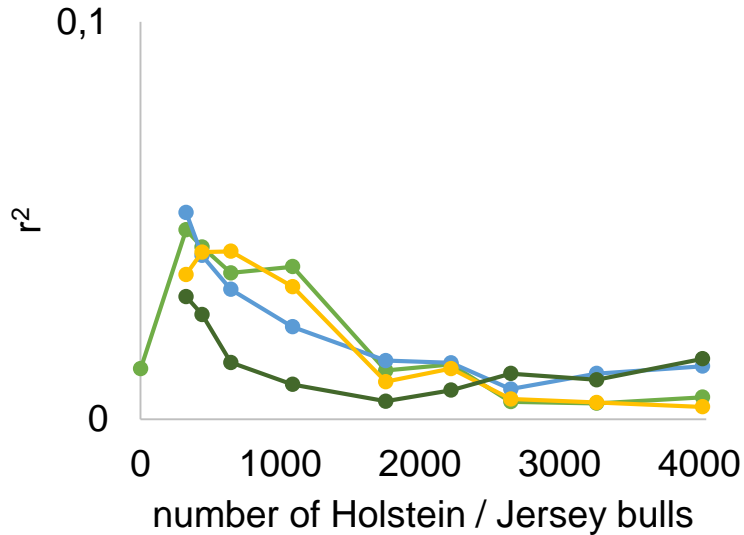
Results: size and relatedness of reference population – Somatic cell count



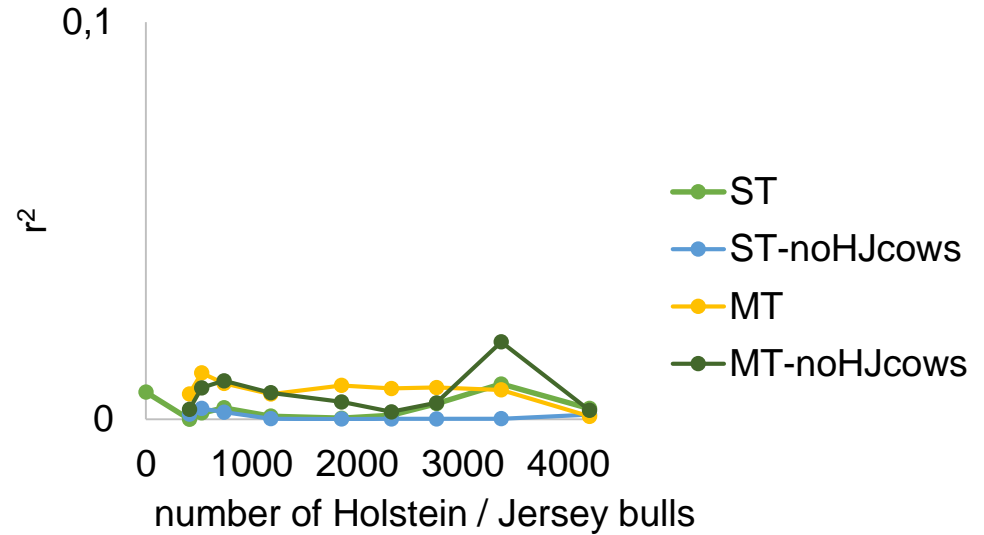
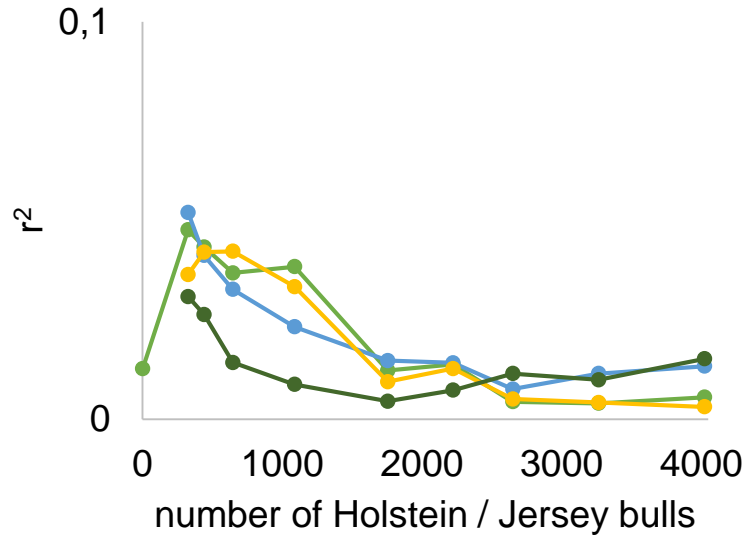
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Results: size and relatedness of reference population – Fertility & Survival

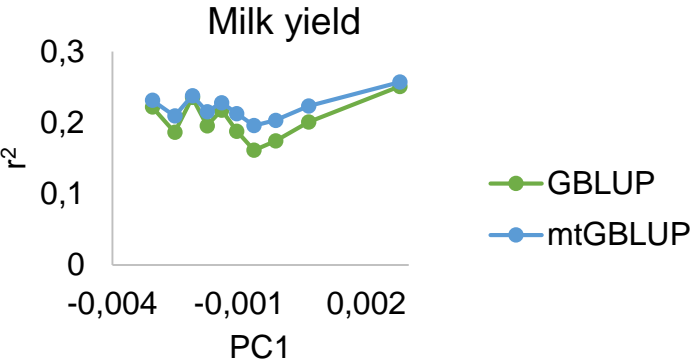


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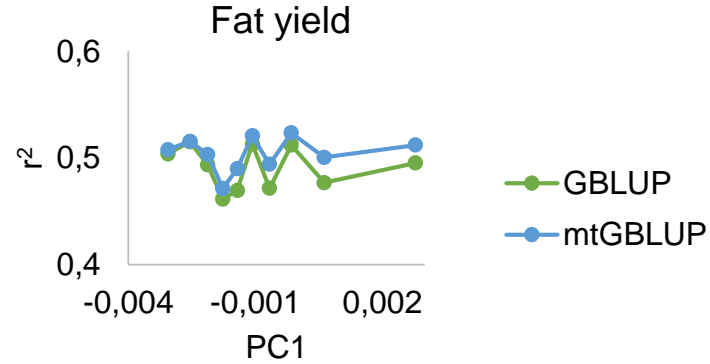
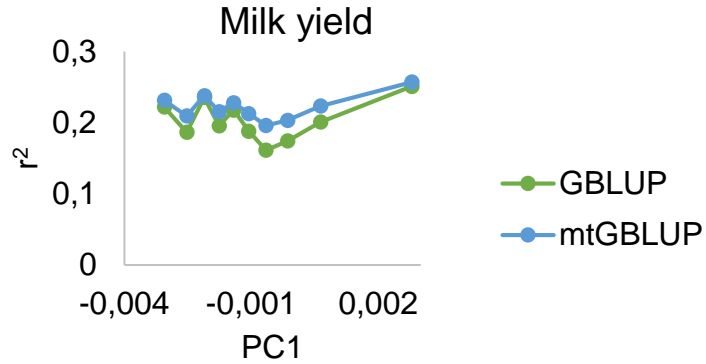


→ Low reliability regardless of model and reference population, probably due to low heritabilities

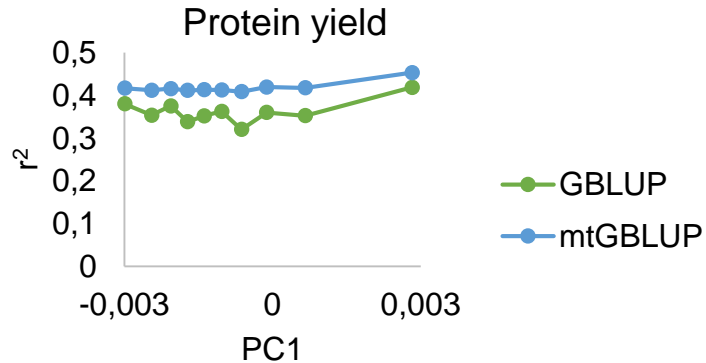
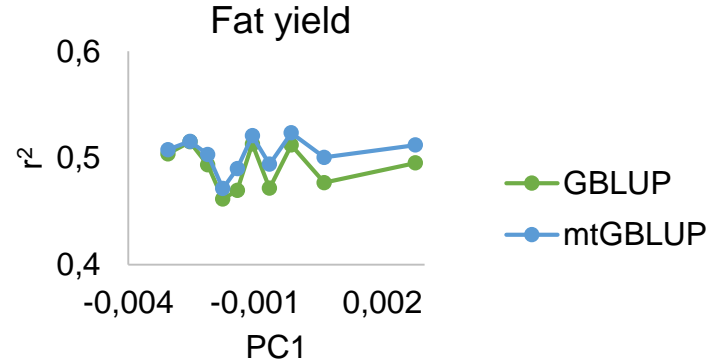
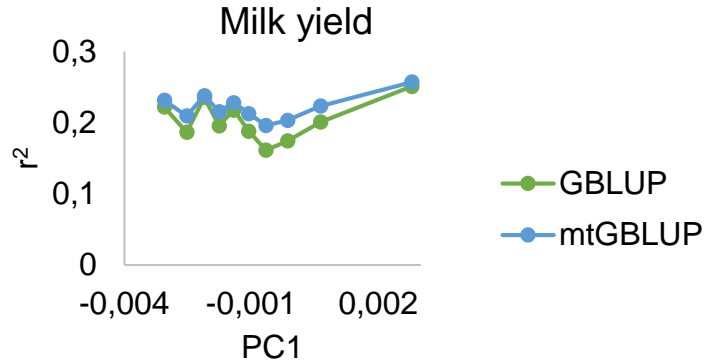
Results: relatedness of reference population



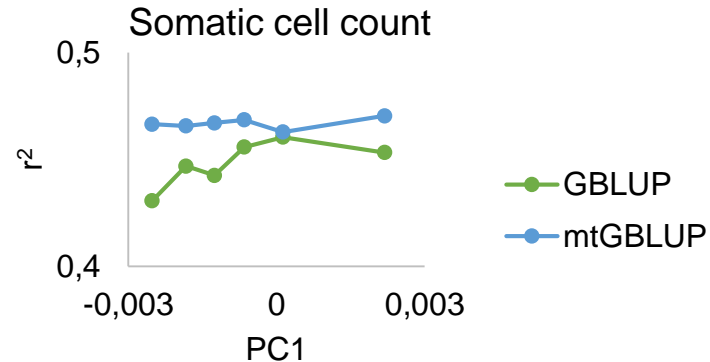
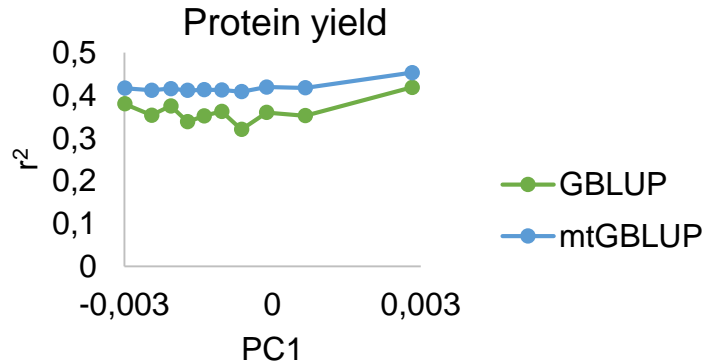
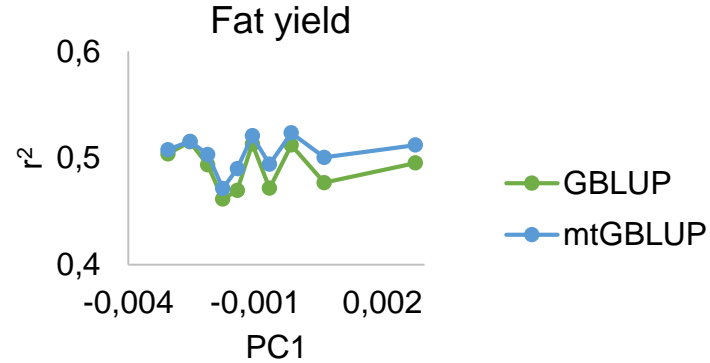
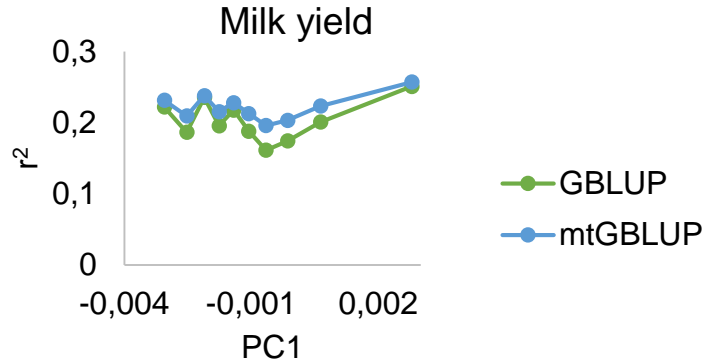
Results: relatedness of reference population



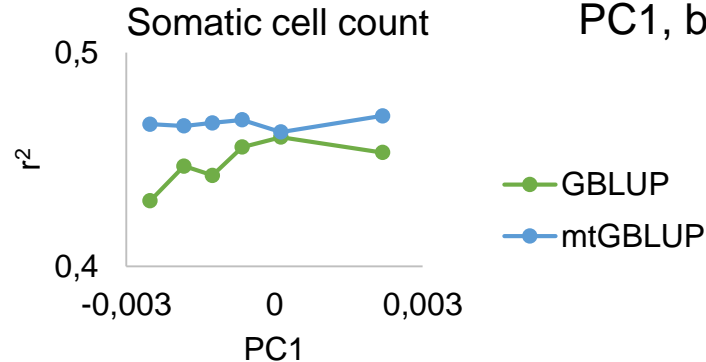
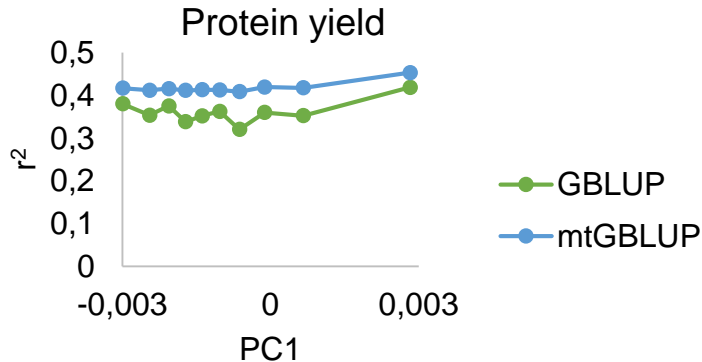
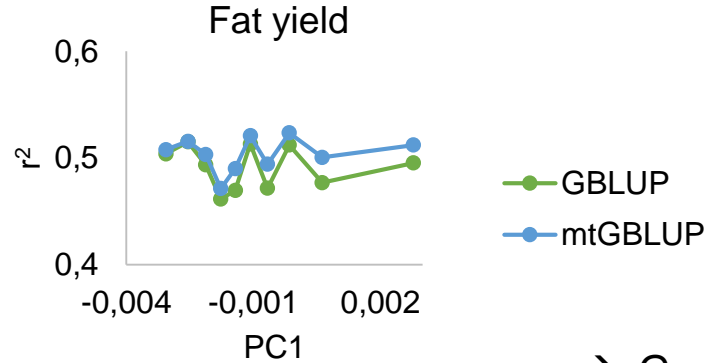
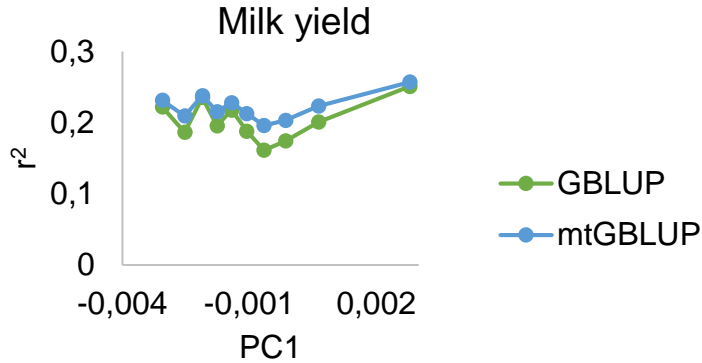
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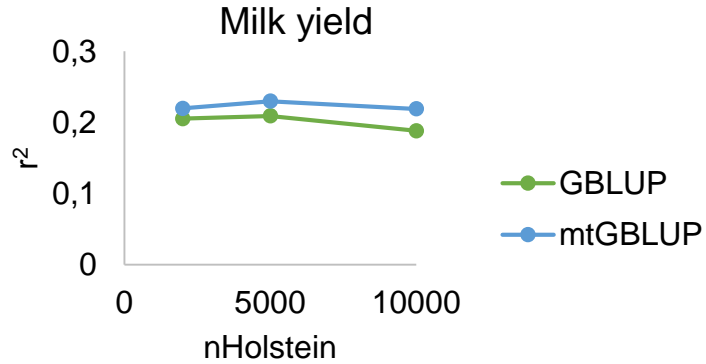


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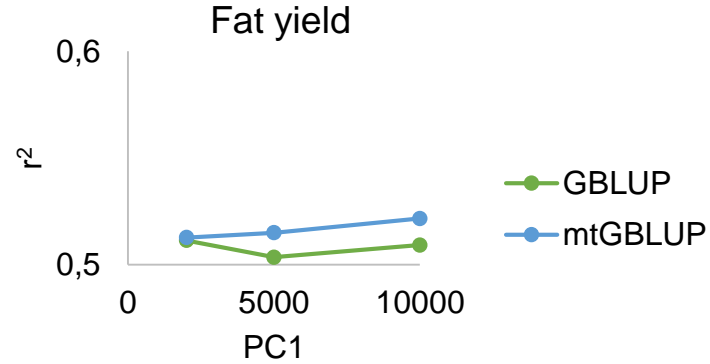
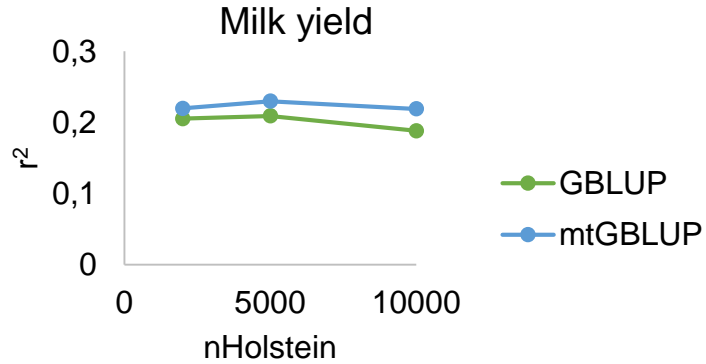


→ Generally largest reliability with largest PC1, but not consistent

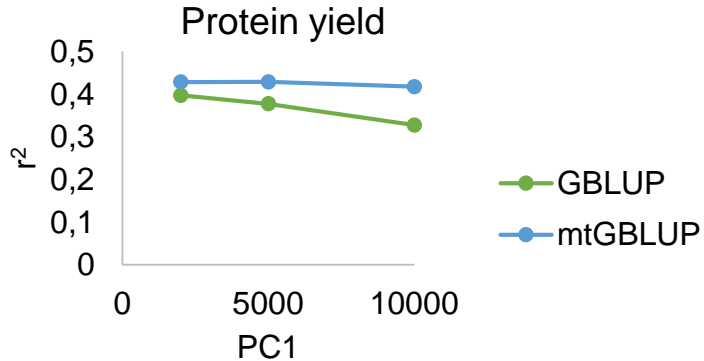
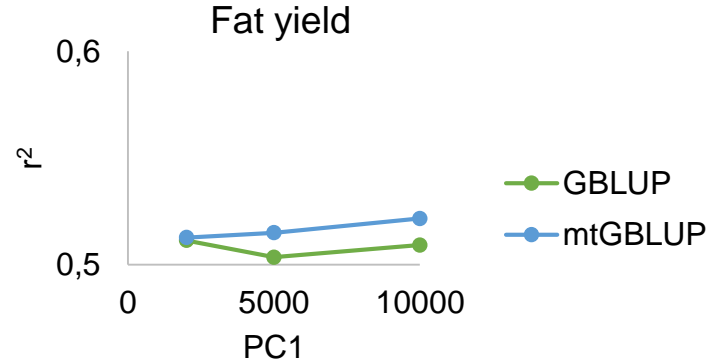
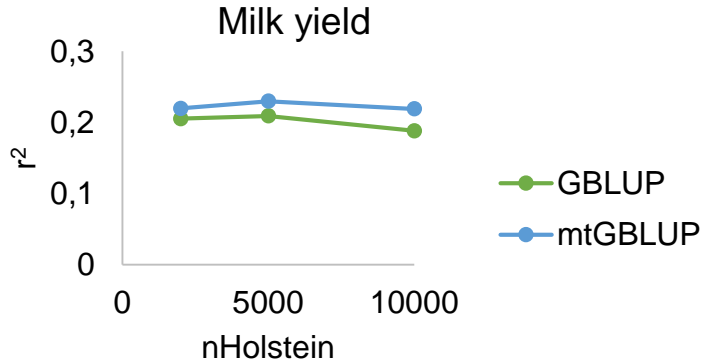
Results: number of Holsteins in the reference population



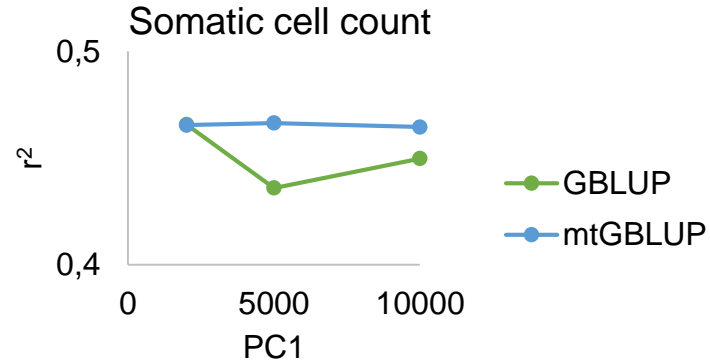
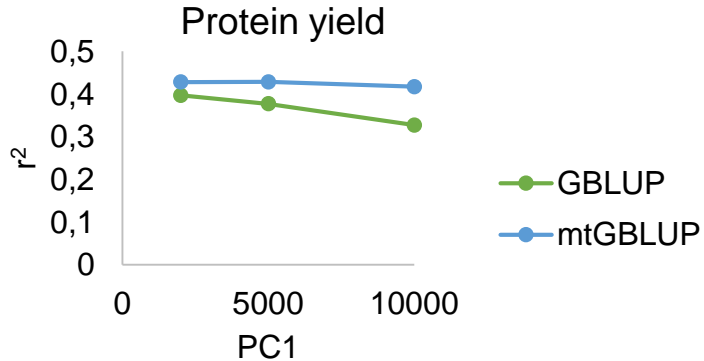
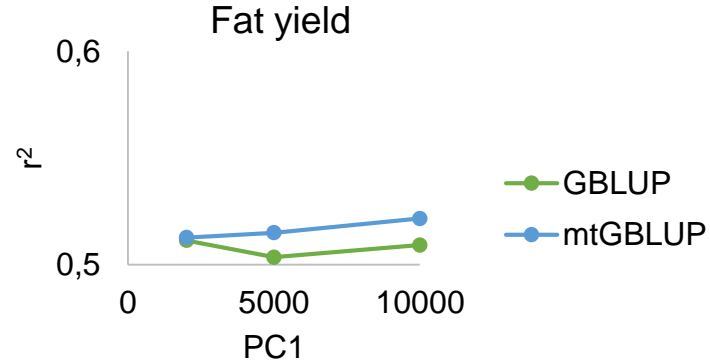
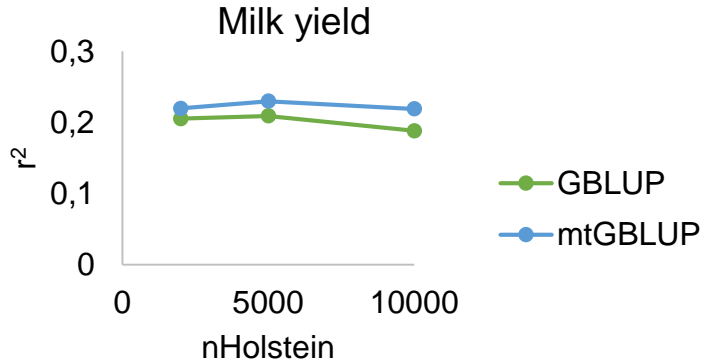
Results: number of Holsteins in the reference population



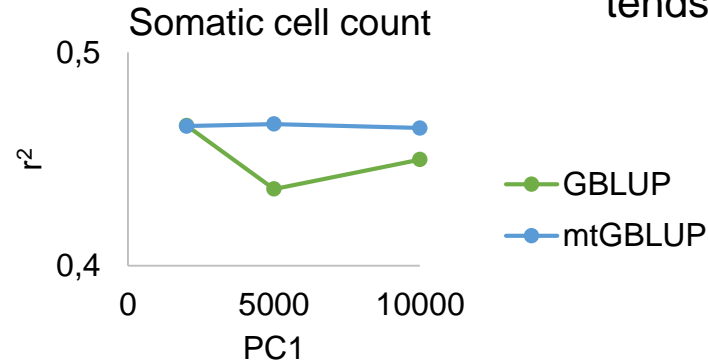
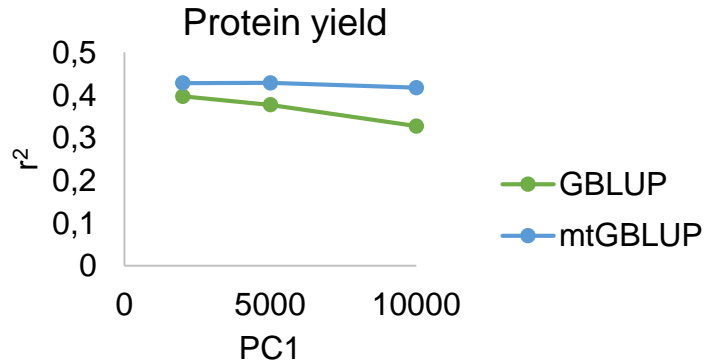
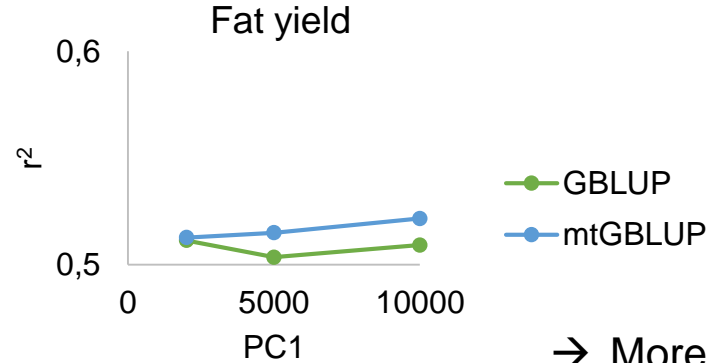
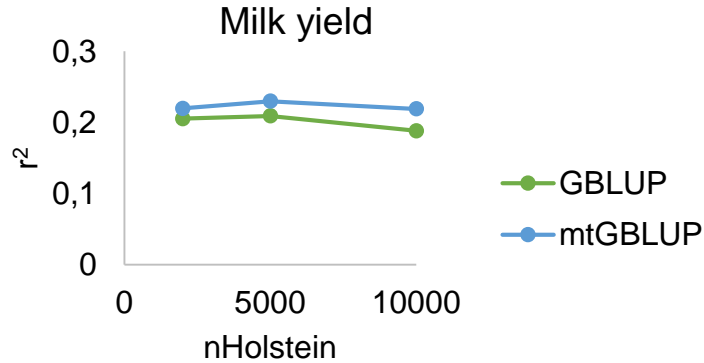
Results: number of Holsteins in the reference population



Results: number of Holsteins in the reference population



Results: number of Holsteins in the reference population



→ More Holsteins in the reference population tends to decrease the reliability

Conclusions

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Conclusions

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- Higher reliabilities using few Holstein bulls that are relatively closely related to Australian Red than more, less related individuals
- Better results with multi trait than single trait model
- Reliabilities only sufficiently high for few traits → need more data
- International collaboration may result in higher reliabilities?



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