

*Continuing the transformation*



# Genomic Selection in Sheep Breeding Programs



**une**  
University of  
New England

# Outline

- What is different in sheep?
- Potential benefits to sheep breeding programs?
- Accuracy of prediction: expected and realized
- Reference population requirements
- Strategies for implementation
- Future developments

# What is different in sheep?



- Existing data of high value as a RefPop
- Small Ne
- Only 1 breed (maybe 2)
- High genomic pred. acc.
- High Benefit/Cost ratio
- Large operators



- Existing data of limited value as a RefPop
- Higher Ne
- Many breeds
- Lower genomic pred. acc.
- Lower Benefit/Cost ratio
- Small operators/low cost

# Challenges of implementing GS in sheep

- Economically viable? Cost vs benefit
  - How much genetic variation in profit?
  - How much increase in genetic gain?

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  - How much increase in genetic gain?
- Accuracy of genomic predictions?
  - Large genetic diversity, both within and across breeds

# Challenges of implementing GS in sheep

- Economically viable? Cost vs benefit
  - How much genetic variation in profit?
  - How much increase in genetic gain?
- Accuracy of genomic predictions?
  - Large genetic diversity, both within and across breeds
- Breeding program structure
  - Many small operators
  - Genetic improvement tends to be 'low cost'

# The multibreed nature of Australian sheep

Three “breed groups” each with separate genetic evaluations  
(1.5m+ animals)



Fine wool

Medium wool

Strong wool

Border  
Leicester

Coopworth

Composites

Poll Dorset

White  
Suffolk

Texel, ...

# Genomic breeding values

Hard to measure, late in life traits

HTML

- Lean meat yield, meat quality
- Number of lambs weaned
- Adult wool traits
- Parasite Resistance
- Milk production





# Infrastructure for GS in ozz sheep

## ■ Reference population

– Information Nucleus Flock	18,000	50k (500)
– Sheep Genomics Flock	4,000	50k (500)
– Validation sires	1,000	50k (500)
– Industry sires	5,000	12k (500)
– Resource Flocks	3x2,000	12k (500)

4 breeds

- ~2000 HD genotypes (mainly sires)
- Currently sequencing 500 key sires

# Genotyping last 3 years

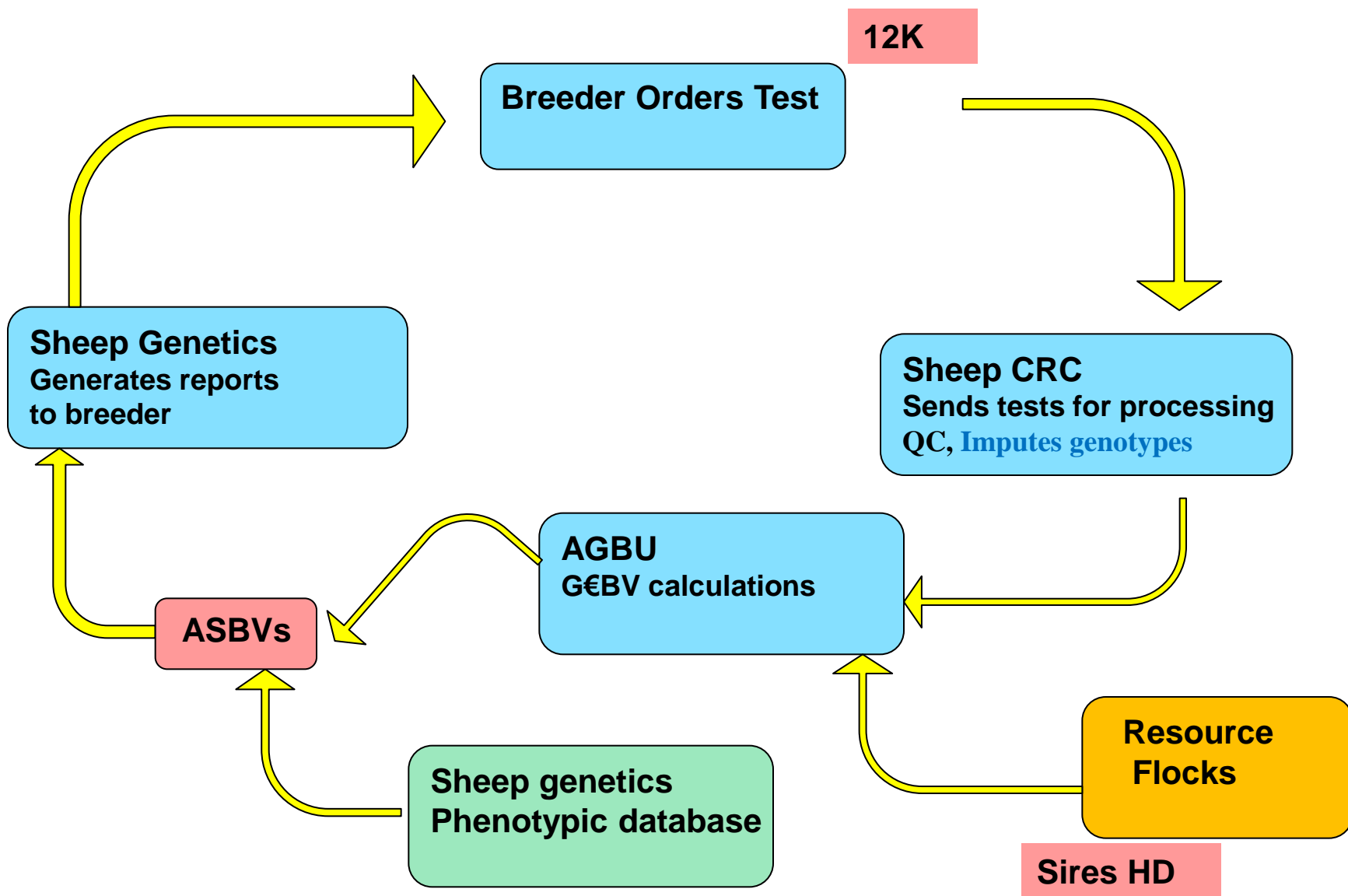
Test Type	Total Tests
<b>50k Total</b>	<b>5,976</b>
EOI Large Scale Trial	1,296
Resource Flock	248
INF	2,811
PPIII - 50k	1,478
Industry Sires	143
<b>12k Total</b>	<b>9,818</b>
Resource Flock	6,927
12k Commercial	2,891
<b>Parentage Total</b>	<b>48,048</b>
Resource Flock	8,449
INF	7,866
Parentage Commercial	30,252
<b>INF 700k</b>	<b>2,067</b>
<b>Full sequence</b>	<b>10</b>

# Genomic prediction accuracies in sheep now

Trait group	Merino	Maternal	Terminal
Wool	0.30 to 0.50		
Body weight, muscle & fat scans	0.25 to 0.50	0.25 to 0.50	0.15 to 0.40
Worm egg count	0.30	< 0.10	0.30
Carcass	0.20	0.15	0.20
Reproduction	0.11 to 0.31	0.05 to 0.15	

Prediction across breeds has not been effective at 50K

# Pipeline for delivering genomic breeding values 2013



# Potential benefits of genomic selection for sheep

## Wool Objective



1 <sup>st</sup> selection	GS	Relative response/year	
2	No	100%	
1	No	110%	100%
2	Yes	108%	
1	Yes	125%	114%

Accuracy -3%

Male generation interval -39%

**Some of benefit is achieved w/o GS**

# Potential benefits of genomic selection for sheep

## Meat Objective



1 <sup>st</sup> selection	GS	Relative response/year
1	No	100%
1	Yes	108%

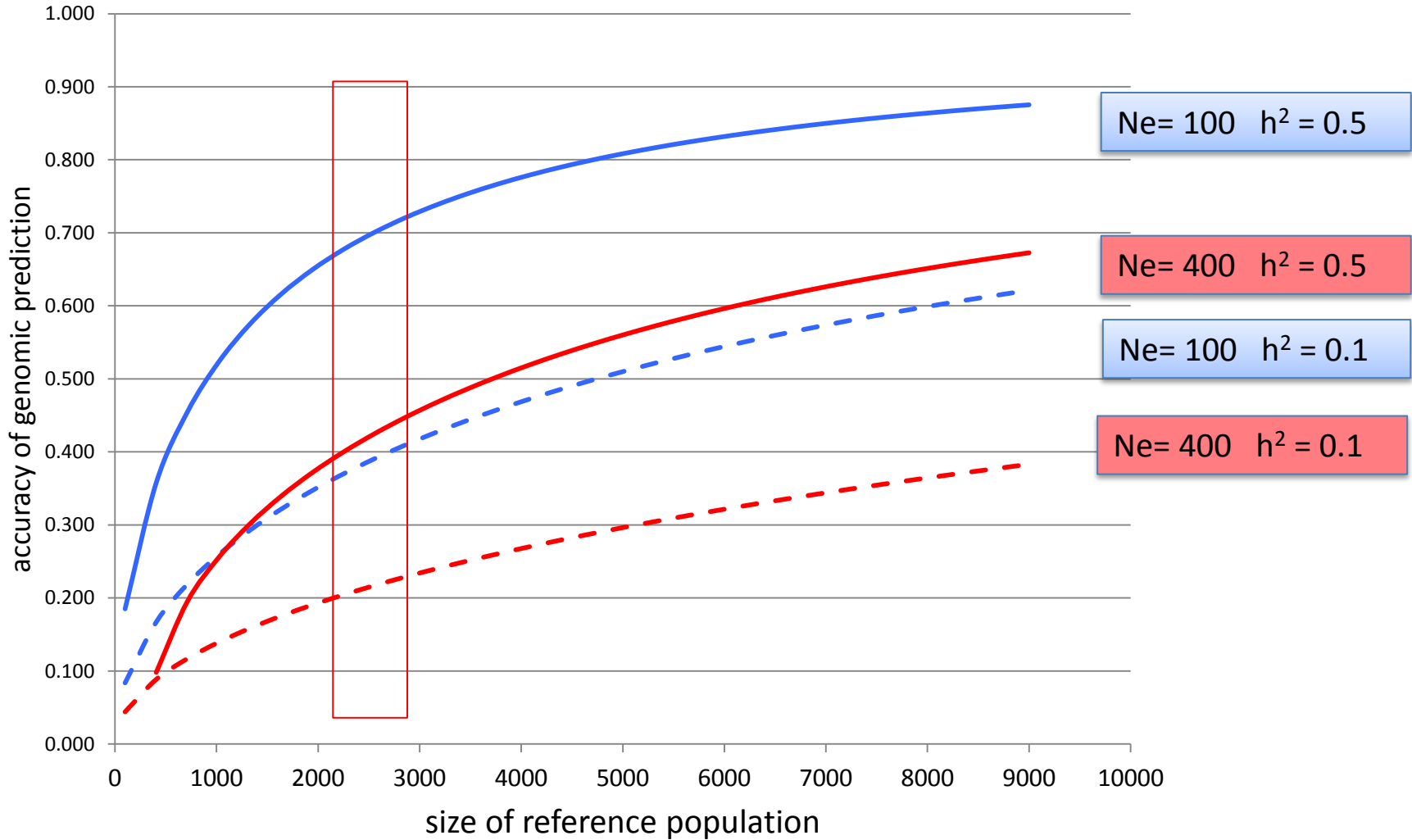
Accuracy +5%

Male generation interval -1%

# Summary Potential Benefits

- 5 -15% more benefits for meat/wool objectives
- Not all benefits captured by current indexes
- Also a shift in benefit between traits

# Genomic prediction accuracy *Using Goddard et al, 2011*





# What effective population size?

*Kijas et al 2012*

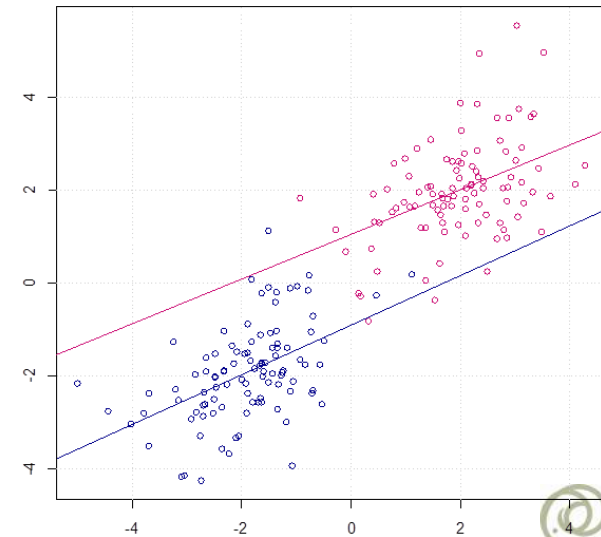
- Sampling?



Populations not homogeneous.

Within and between breed/line accuracies

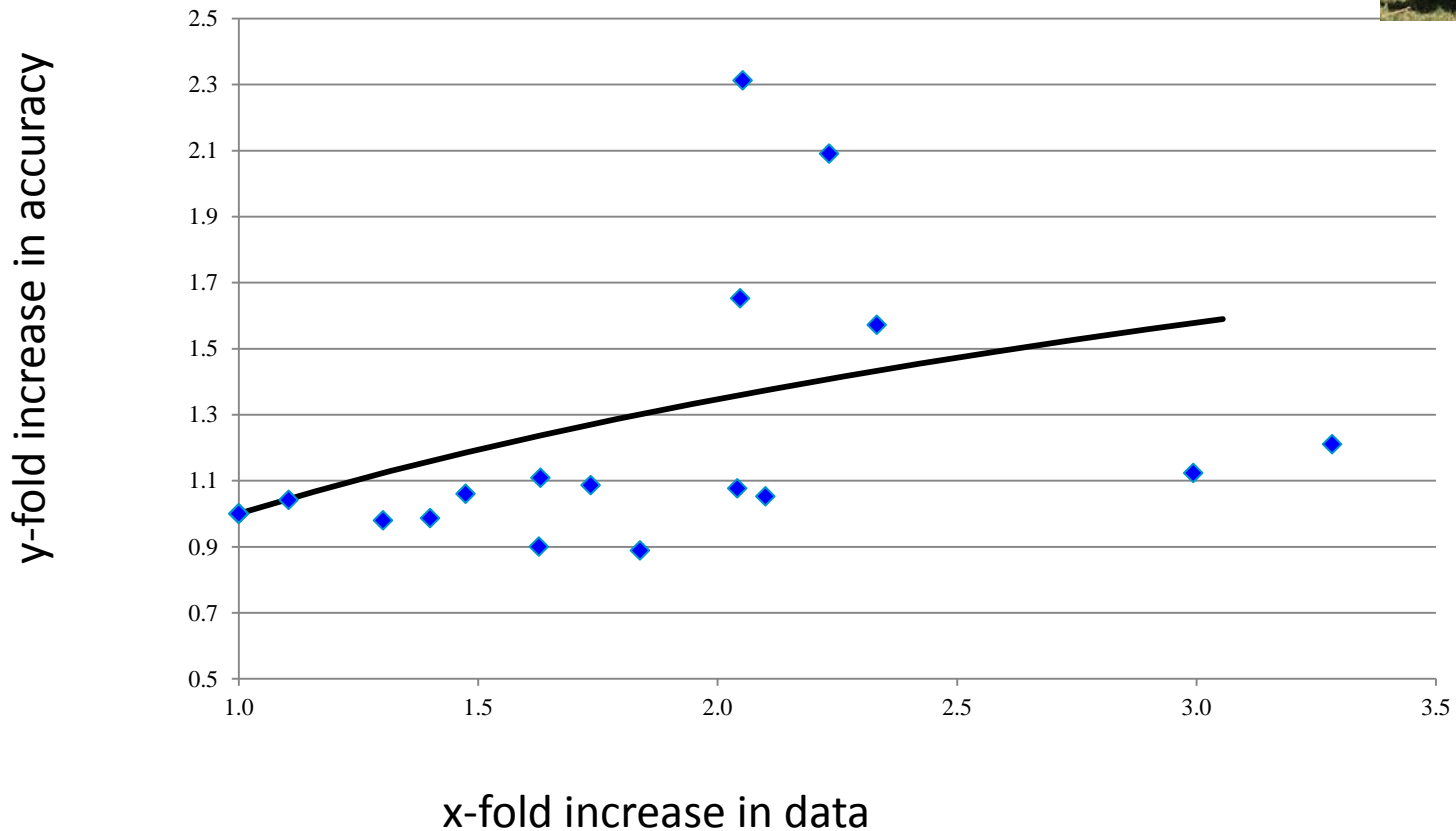
Some accuracy due to population structure



# Validating 'Genomic Prediction Accuracy'

More data is always good

But does it increase accuracy as expected?

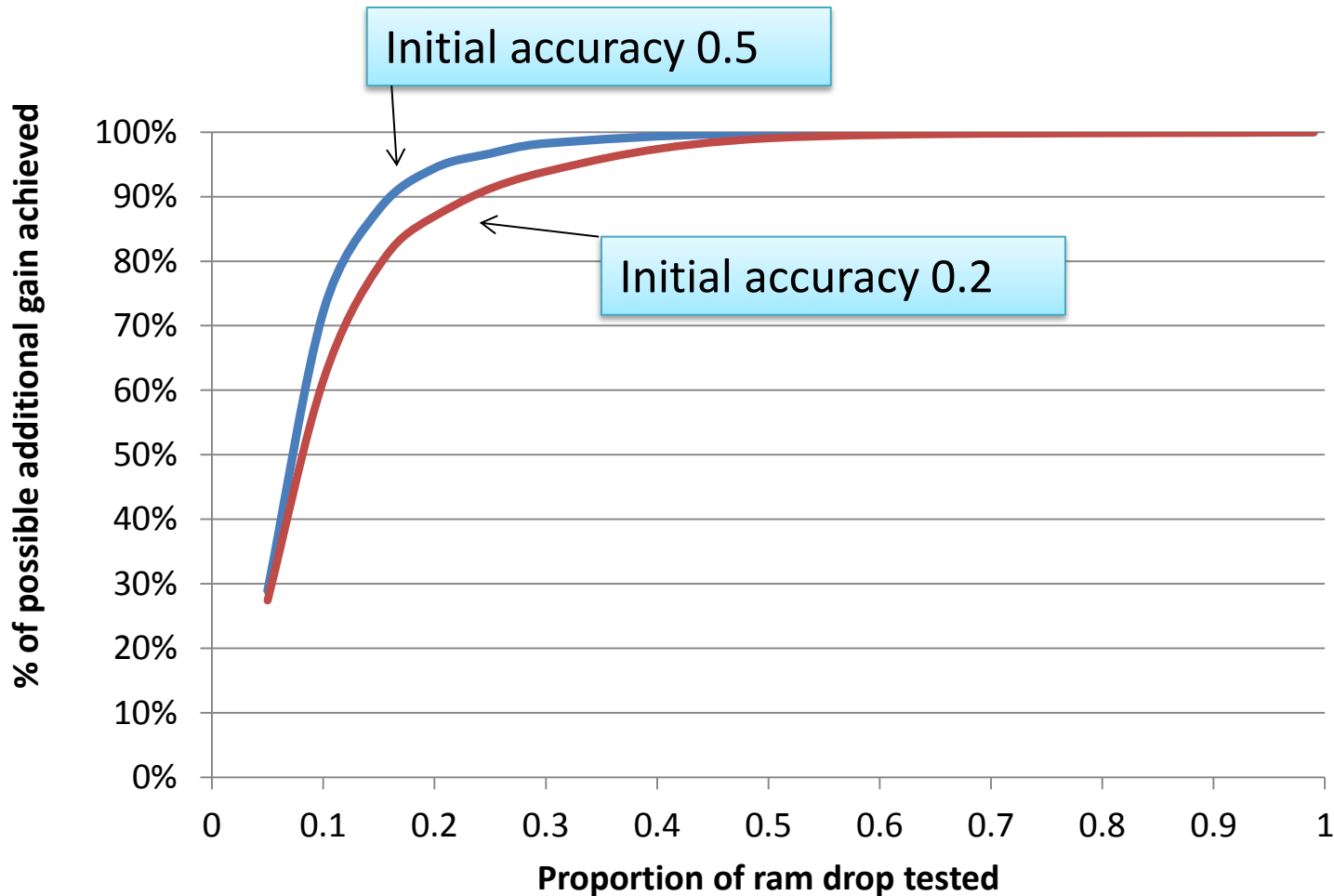


# Strategies for implementation

- Reduce genotyping cost
  - Genotype males only ~ 3% loss
  - Genotype only the top ~20% ~10-15% loss
- Increase potential benefits
  - Earlier selection of candidates
  - Increase accuracy
- Benefit of reproductive technologies

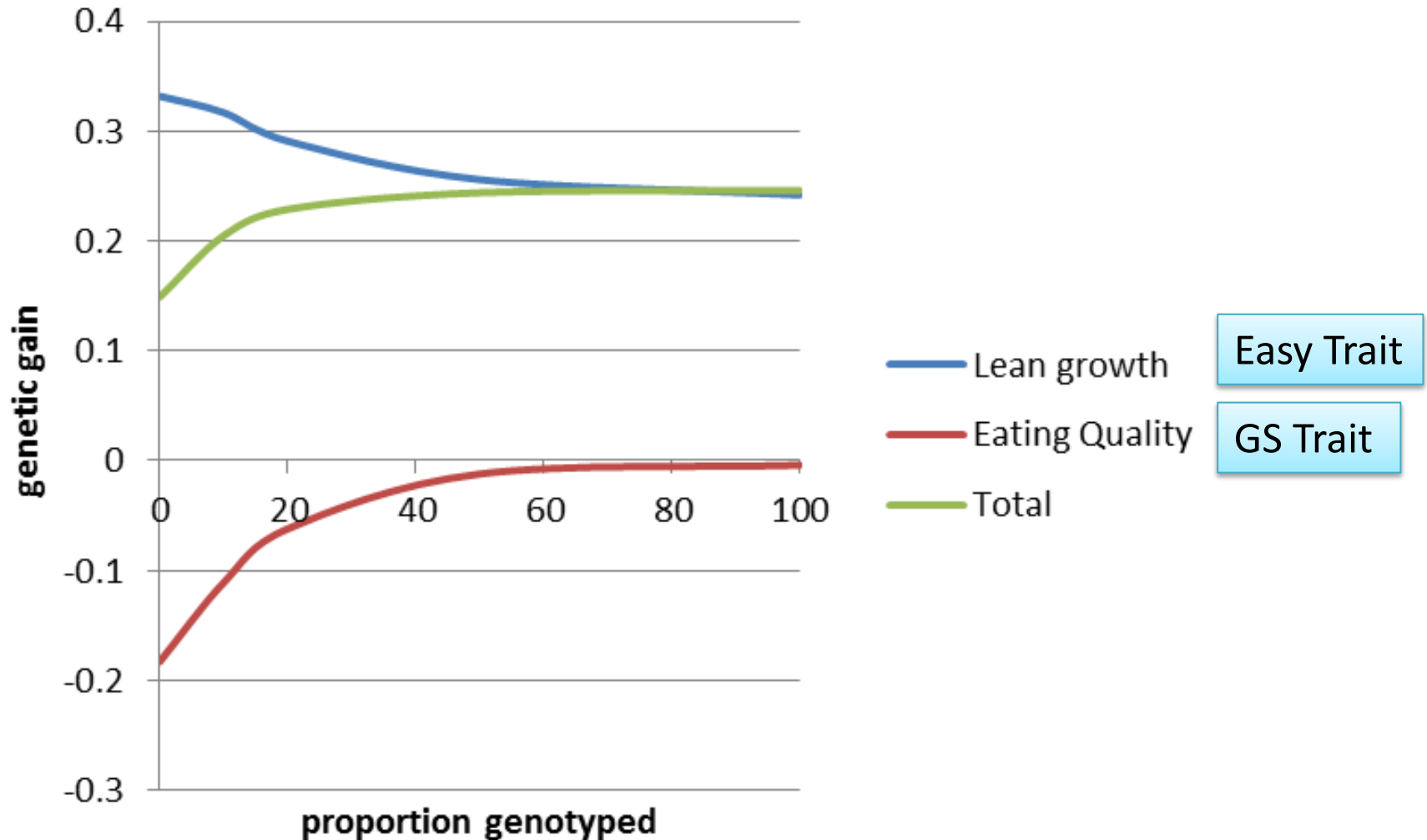
# 2-stage selection:

## Testing 20% of drop gives most of benefit



## 2-stage selection

More traits and unfavourable correlations?



## Multi breed reference

- Genomic prediction from larger reference population is desirable
- Theoretical predictions usually consider homogenous populations
- In sheep and beef cattle industry we have multiple breeds, strains and crossbred animals in reference populations

# Previous results fro multi-breed genomic predictions

## Simulation

- Some to little extra accuracy from across breed information  
(e.g. Ibanez -Escriche *et al* 2009 ; Toosi *et al* 2010 ; De Roos *et al* 2009 )

## Real Data

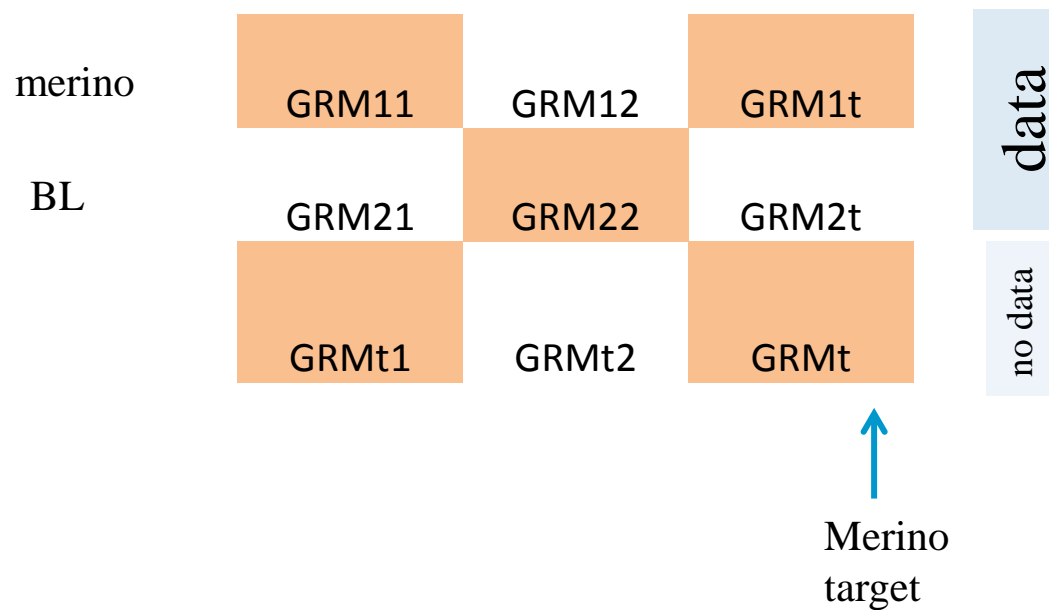
- Accuracy of GEBV lower for lower represented breeds
- Genomic prediction does not extend across breeds  
(based on 50k, Daetwyler *et al*)

# Questions

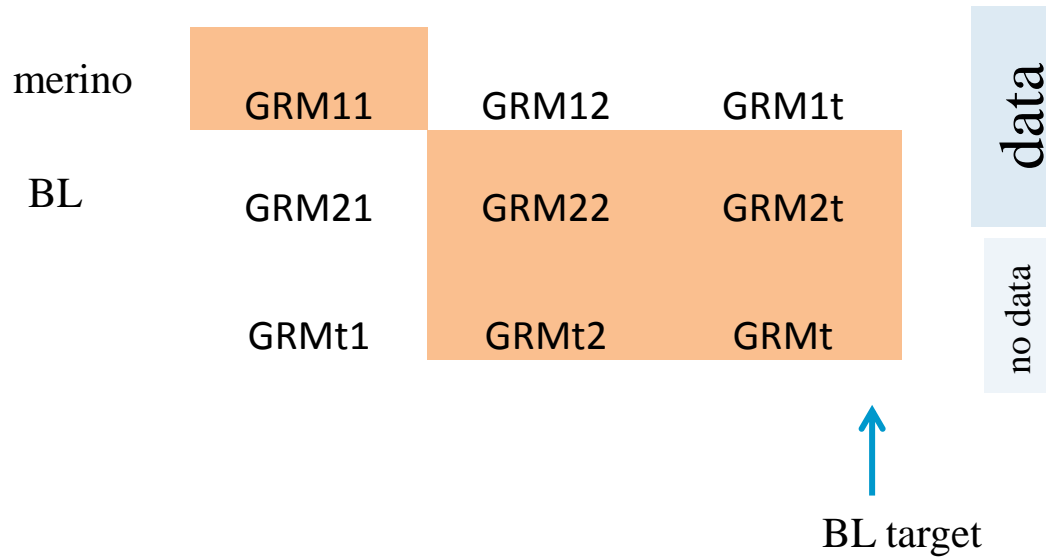
- Benefit of combining multiple breeds – real data ?
- Is it better to have breed specific reference populations?
- Value of crossbreds?



# Thinking GBLUP



# Thinking GBLUP



GRM

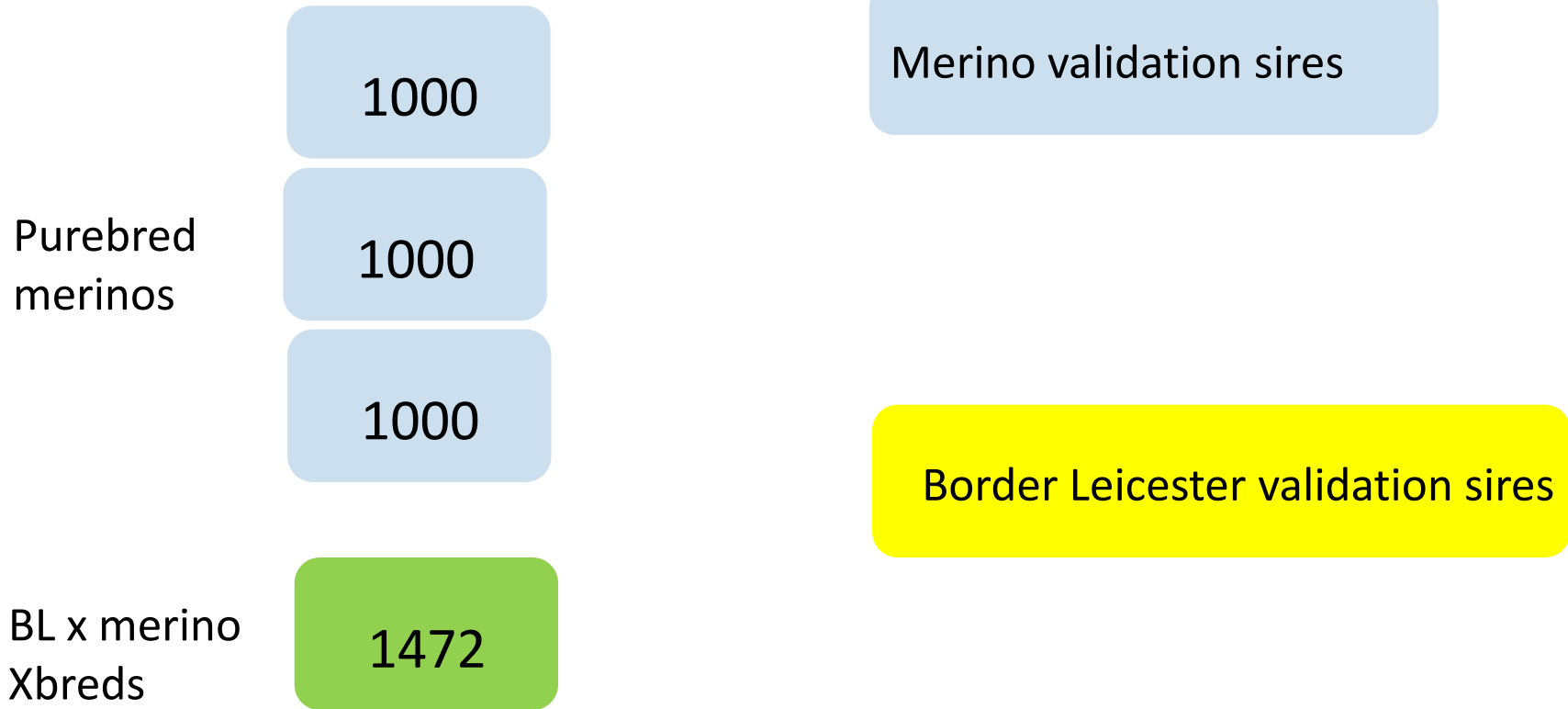
G1 = overall allele frequency

G2 = breed haplotypes frequency

# Design of study:

## Reference Populations

## Validation



# Results: Accuracy of genomic prediction for Birth Weight

Reference population		GEBV accuracy <sup>1</sup>	
Type	Size	G1	
(1) = Merino	1000	Merino	
		0.38 <sup>bc</sup>	
(2) = Merino	2000	0.42 <sup>cd</sup>	
(3) = Merino	3000	0.47 <sup>d</sup>	

# Accuracy of genomic prediction for Birth Weight

Reference population		GEBV accuracy <sup>1</sup>	
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(1) = Merino	1000		Merino
(2) = Merino	2000		0.38 <sup>bc</sup>
(3) = Merino	3000		0.42 <sup>cd</sup>
			0.47 <sup>d</sup>
BLxMerino	1472		0.29 <sup>a</sup>
BLxMerino + (1)	2472		0.36 <sup>b</sup>
BLxMerino + (2)	3472		0.39 <sup>bc</sup>
BLxMerino + (3)	4472		0.42 <sup>cd</sup>

# Accuracy of genomic prediction for Birth Weight

Reference population		GEBV accuracy <sup>1</sup>		
Type	Size	G1		
		BL	Merino	
(1) = Merino	1000	-0.03 <sup>b</sup>	0.38 <sup>bc</sup>	
(2) = Merino	2000	-0.10 <sup>ab</sup>	0.42 <sup>cd</sup>	
(3) = Merino	3000	-0.16 <sup>a</sup>	0.47 <sup>d</sup>	
BLxMerino	1472	0.24 <sup>c</sup>	0.29 <sup>a</sup>	
BLxMerino + (1)	2472	0.23 <sup>c</sup>	0.36 <sup>b</sup>	
BLxMerino + (2)	3472	0.17 <sup>c</sup>	0.39 <sup>bc</sup>	
BLxMerino + (3)	4472	0.18 <sup>c</sup>	0.42 <sup>cd</sup>	

## Accuracy of genomic prediction for Birth Weight

Reference population		GEBV accuracy <sup>1</sup>			
		G1		G2	
Type	Size	BL	Merino	BL	Merino
(1) = Merino	1000	-0.03 <sup>b</sup>	0.38 <sup>bc</sup>	-0.03 <sup>b</sup>	0.38 <sup>bc</sup>
(2) = Merino	2000	-0.10 <sup>ab</sup>	0.42 <sup>cd</sup>	-0.10 <sup>ab</sup>	0.42 <sup>cd</sup>
(3) = Merino	3000	-0.16 <sup>a</sup>	0.47 <sup>d</sup>	-0.14 <sup>a</sup>	0.47 <sup>d</sup>
BLxMerino	1472	0.24 <sup>c</sup>	0.29 <sup>a</sup>	0.24 <sup>c</sup>	0.29 <sup>a</sup>
BLxMerino + (1)	2472	0.23 <sup>c</sup>	0.36 <sup>b</sup>	0.24 <sup>c</sup>	0.39 <sup>bc</sup>
BLxMerino + (2)	3472	0.17 <sup>c</sup>	0.39 <sup>bc</sup>	0.17 <sup>c</sup>	0.39 <sup>bc</sup>
BLxMerino + (3)	4472	0.18 <sup>c</sup>	0.42 <sup>cd</sup>	0.18 <sup>c</sup>	0.42 <sup>cd</sup>

# Accuracy of genomic prediction for Weaning Weight

Reference population		GEBV accuracy <sup>1</sup>	
Type	Size	BL	Merino
(1) = Merino	1000	-0.07 <sup>b</sup>	0.42 <sup>b</sup>
(2) = Merino	2000	-0.13 <sup>b</sup>	0.49 <sup>c</sup>
(3) = Merino	3000	-0.26 <sup>a</sup>	0.51 <sup>c</sup>
BLxMerino	1547	0.32 <sup>d</sup>	0.31 <sup>a</sup>
BLxMerino + (1)	2547	0.22 <sup>c</sup>	0.43 <sup>b</sup>
BLxMerino + (2)	3547	0.16 <sup>c</sup>	0.46 <sup>b</sup>
BLxMerino + (3)	4547	0.17 <sup>c</sup>	0.47 <sup>bc</sup>



# Accuracy of genomic prediction for Post Weaning Weight

Reference population		GEBV accuracy	
		G1	
Type	Size	BL	Merino
(1) = Merino	1000	-0.02 <sup>a</sup>	0.53 <sup>b</sup>
(2) = Merino	2000	-0.04 <sup>a</sup>	0.57 <sup>bc</sup>
(3) = Merino	3000	-0.08 <sup>a</sup>	0.59 <sup>c</sup>
BLxMerino	1514	0.49 <sup>c</sup>	0.45 <sup>a</sup>
BLxMerino + (1)	2514	0.42 <sup>bc</sup>	0.56 <sup>bc</sup>
BLxMerino + (2)	3514	0.37 <sup>b</sup>	0.54 <sup>bc</sup>
BLxMerino + (3)	4514	0.36 <sup>b</sup>	0.56 <sup>bc</sup>

# Accuracy of genomic prediction for PW-EMD

Reference Population		GEBV Accuracy	
		G1	
Type	Size	BL	Merino
(1) = Purebred Merino	1000	0.00 <sup>a</sup>	0.23 <sup>a</sup>
(2) = Purebred Merino	2000	0.00 <sup>a</sup>	0.33 <sup>b</sup>
(3) = Purebred Merino	3000	-0.01 <sup>a</sup>	0.34 <sup>b</sup>
BL*Merino	1602	0.18 <sup>b</sup>	0.22 <sup>a</sup>
BL*Merino + (1)	2602	0.14 <sup>b</sup>	0.25 <sup>a</sup>
BL*Merino + (2)	3602	0.13 <sup>b</sup>	0.30 <sup>a</sup>
BL*Merino + (3)	4602	0.13 <sup>b</sup>	0.35 <sup>b</sup>
		<b>PD</b>	<b>Merino</b>
PD*Merino	1890	0.46 <sup>b</sup>	0.18 <sup>a</sup>
PD*Merino + (1)	2890	0.41 <sup>ab</sup>	0.26 <sup>b</sup>
PD*Merino + (2)	3890	0.40 <sup>a</sup>	0.33 <sup>c</sup>
PD*Merino + (3)	4890	0.40 <sup>a</sup>	0.35 <sup>c</sup>
		<b>WS</b>	<b>Merino</b>
WS*Merino	1257	0.13 <sup>a</sup>	0.13 <sup>a</sup>
WS*Merino + (1)	2257	0.11 <sup>a</sup>	0.19 <sup>a</sup>
WS*Merino + (2)	3257	0.11 <sup>a</sup>	0.25 <sup>b</sup>
WS*Merino + (3)	4257	0.09 <sup>a</sup>	0.27 <sup>b</sup>

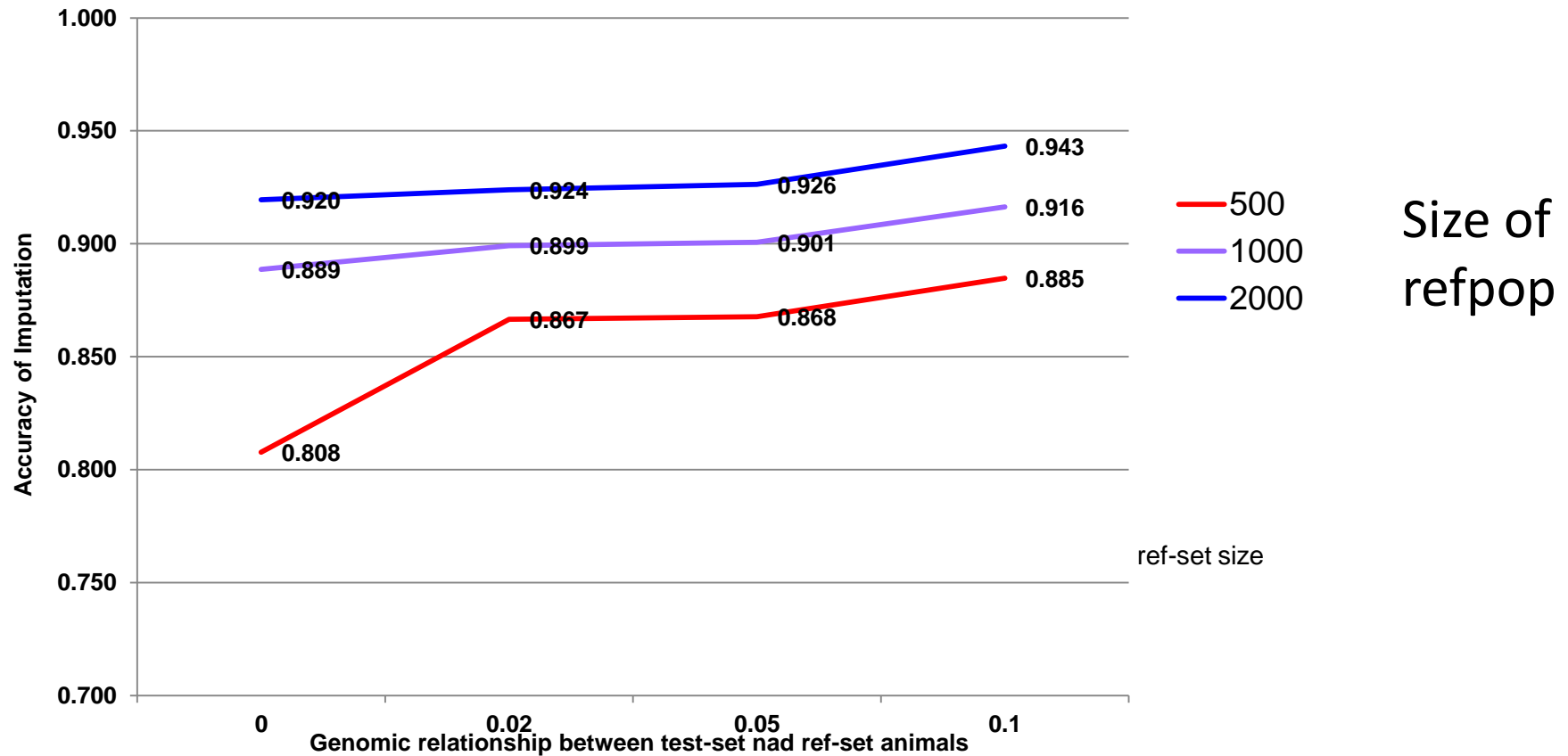
# Accuracy of genomic prediction for PW-Fat

Reference Population		Accuracy	
Type	Size	G1	
		BL	Merino
(1) = Purebred Merino	1000	0.00 <sup>a</sup>	0.31 <sup>c</sup>
(2) = Purebred Merino	2000	-0.01 <sup>a</sup>	0.40 <sup>d</sup>
(3) = Purebred Merino	3000	-0.01 <sup>a</sup>	0.48 <sup>e</sup>
BL*Merino	1606	0.23 <sup>c</sup>	0.17 <sup>a</sup>
BL*Merino + (1)	2606	0.22 <sup>c</sup>	0.24 <sup>b</sup>
BL*Merino + (2)	3606	0.19 <sup>bc</sup>	0.32 <sup>c</sup>
BL*Merino + (3)	4606	0.16 <sup>b</sup>	0.40 <sup>d</sup>
	<b>Size</b>	<b>PD</b>	<b>Merino</b>
PD*Merino	1891	0.26 <sup>a</sup>	0.17 <sup>a</sup>
PD*Merino + (1)	2891	0.26 <sup>a</sup>	0.32 <sup>b</sup>
PD*Merino + (2)	3891	0.28 <sup>a</sup>	0.38 <sup>c</sup>
PD*Merino + (3)	4891	0.28 <sup>a</sup>	0.43 <sup>d</sup>
	<b>Size</b>	<b>WS</b>	<b>Merino</b>
WS*Merino	1258	0.14 <sup>b</sup>	0.17 <sup>a</sup>
WS*Merino + (1)	2258	0.13 <sup>b</sup>	0.35 <sup>b</sup>
WS*Merino + (2)	3258	0.11 <sup>b</sup>	0.42 <sup>c</sup>
WS*Merino + (3)	4258	0.07 <sup>a</sup>	0.45 <sup>c</sup>

# Conclusions:

- Using haplotypes from different breeds seemed to have a zero to negative impact on accuracy of within breed genomic prediction.
- Potential Reasons are:
  - Lack of LD between breeds
  - QTL effects differ between breeds
- Breed specific GRM does not have much impact
- Need to consider more breed specific reference populations with 50k GBLUP

# Accuracy of imputation (12>50k)

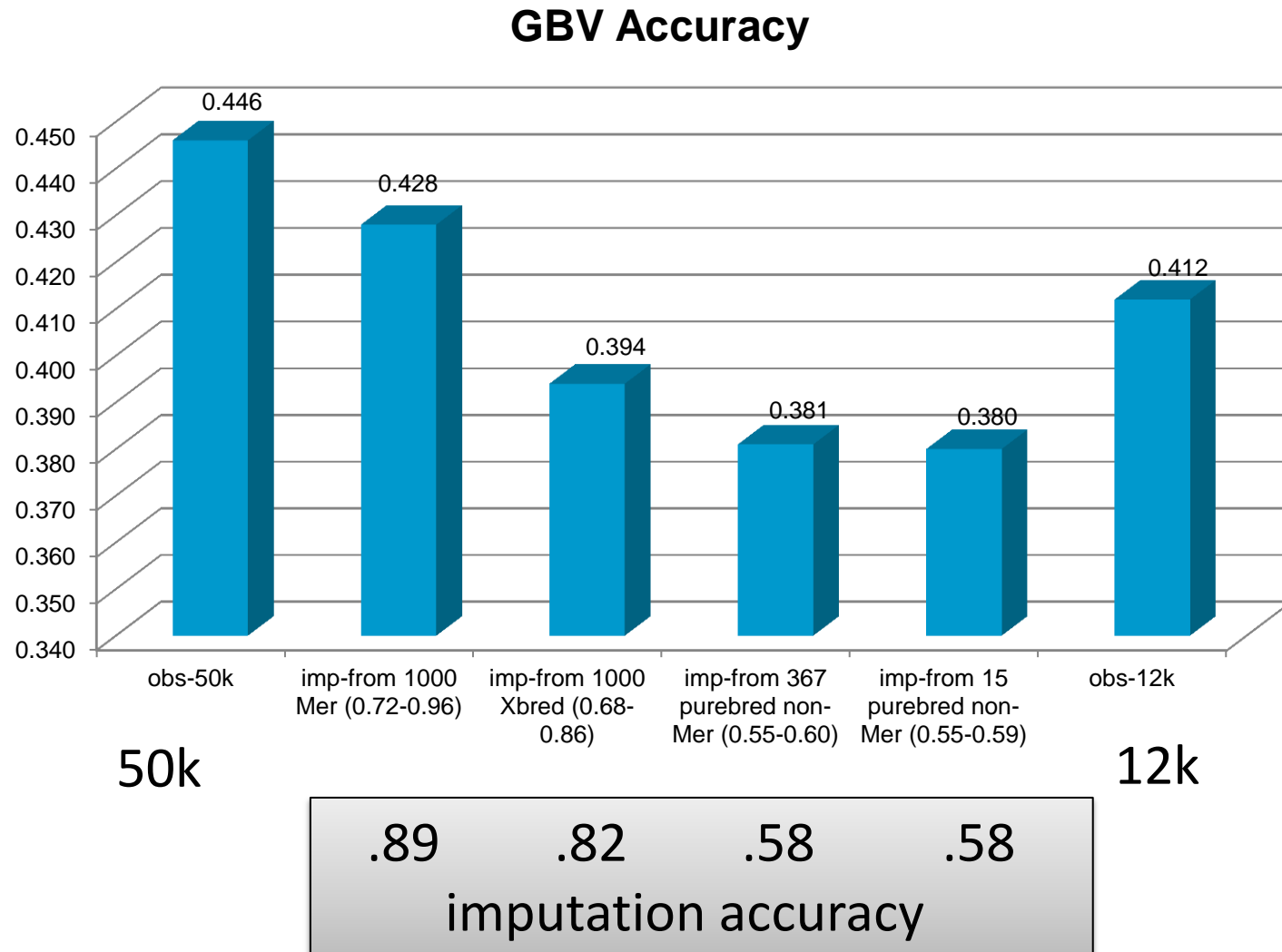


Test Set: 1328 crossbred

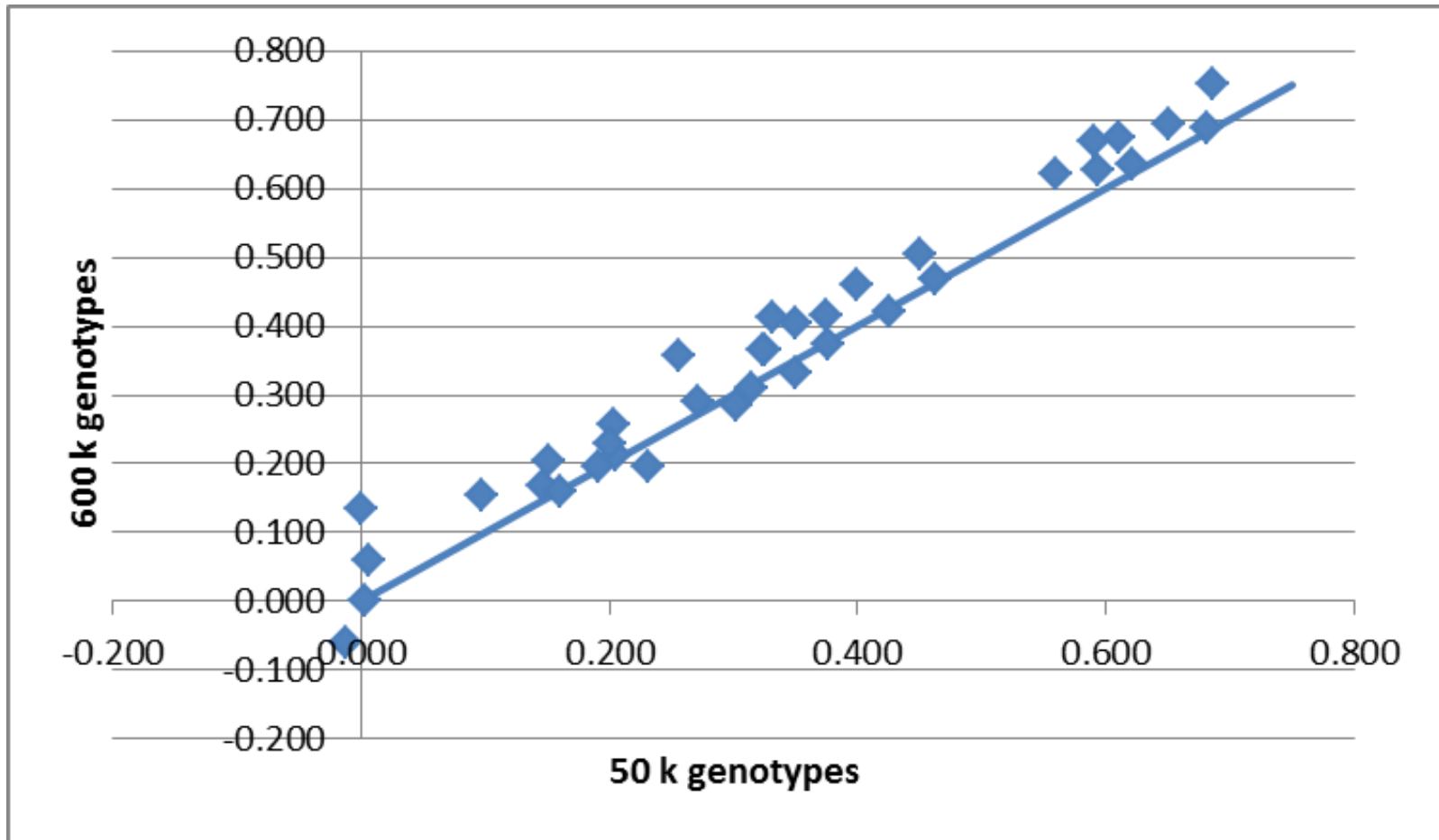
Ref Set: 500, 1000, 2000 crossbreds with 0%, 2%, 5% and 10% GRM

# Accuracy of GEBV from imputed genotypes

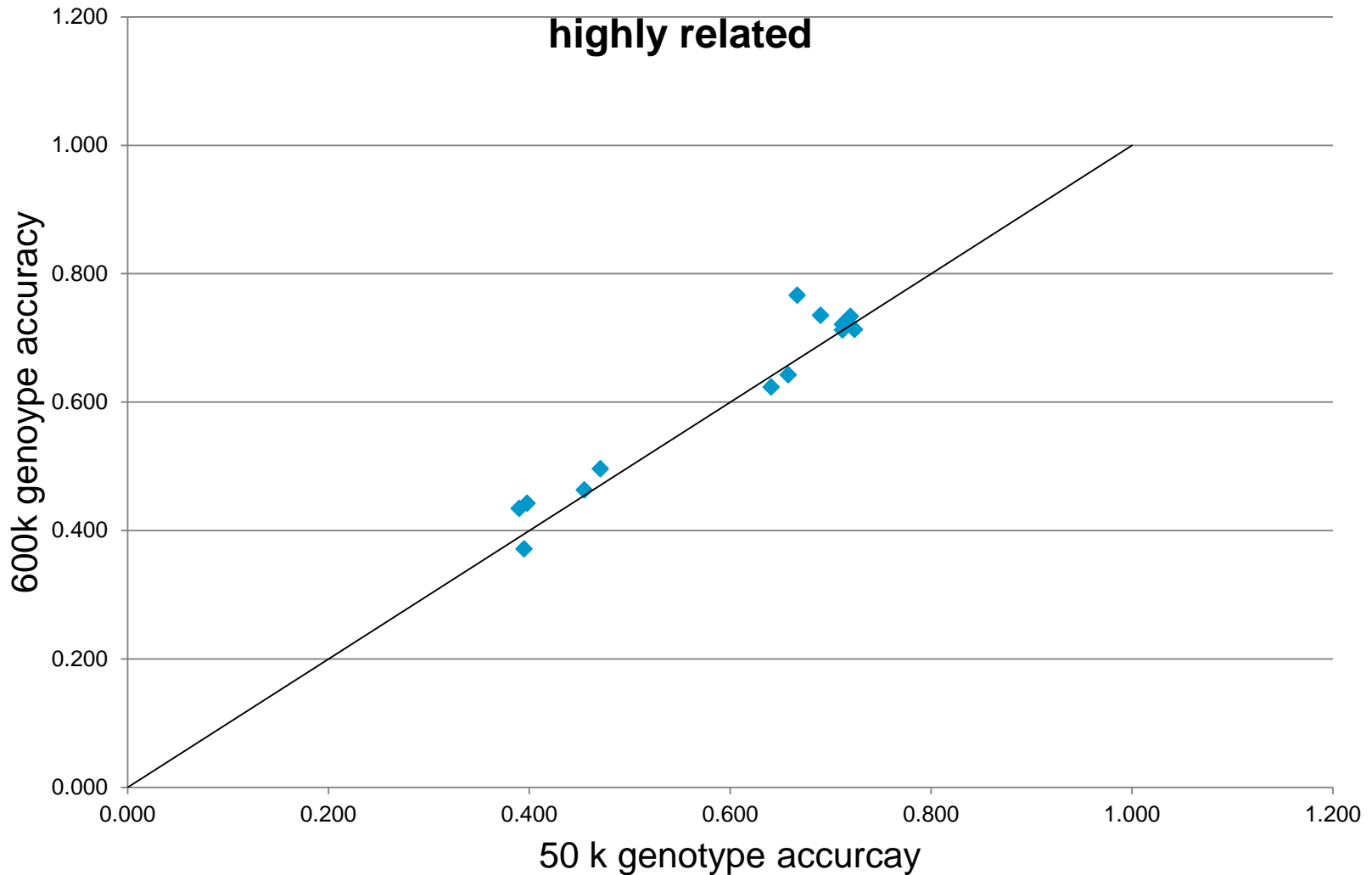
Moghaddar et al 2014



# Higher accuracy with high density markers

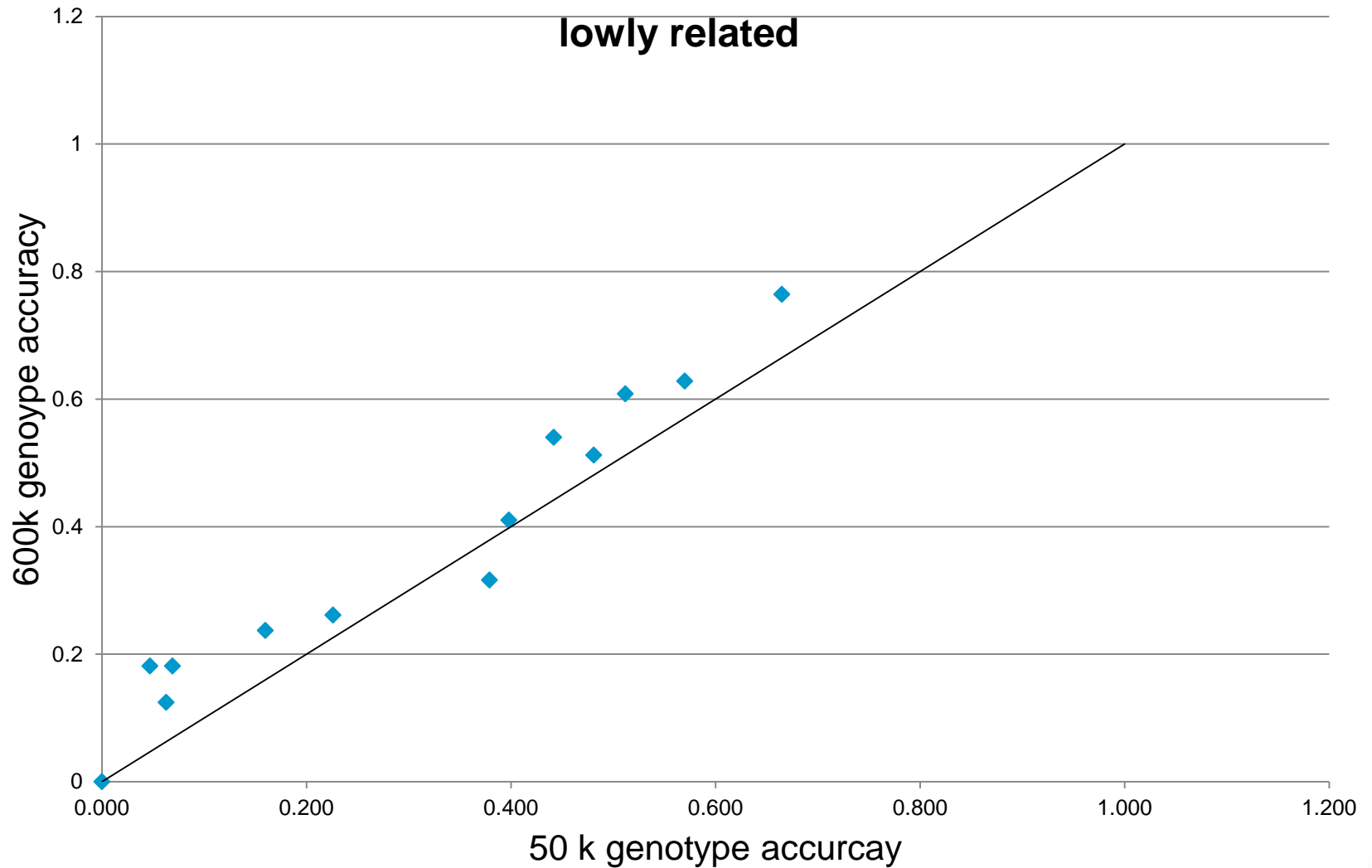


# Higher accuracy with high density markers



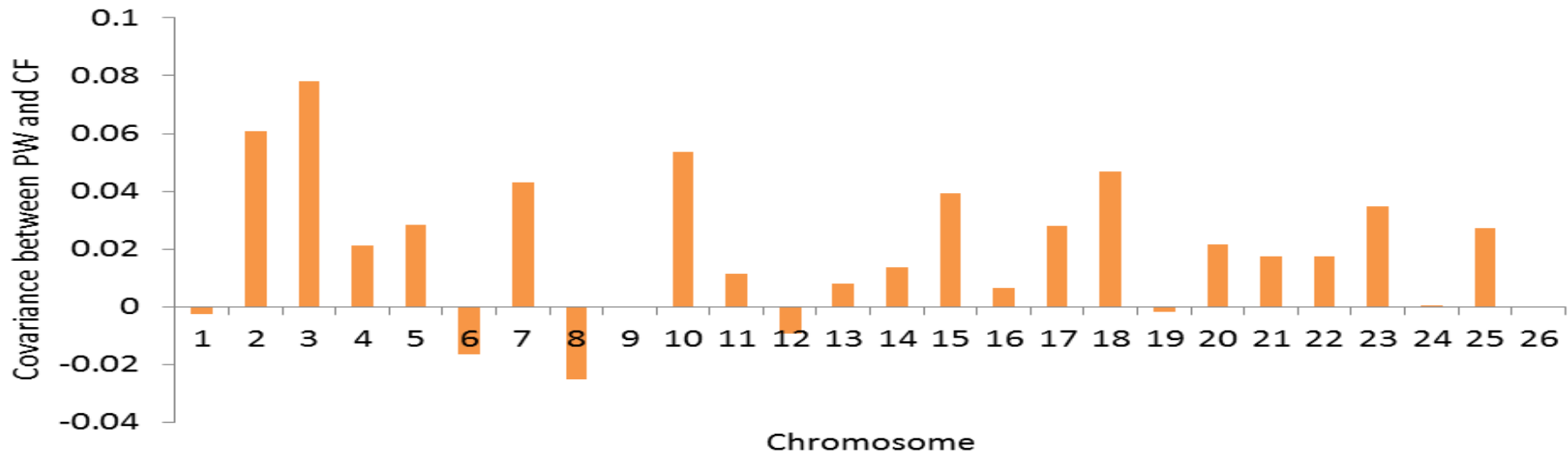
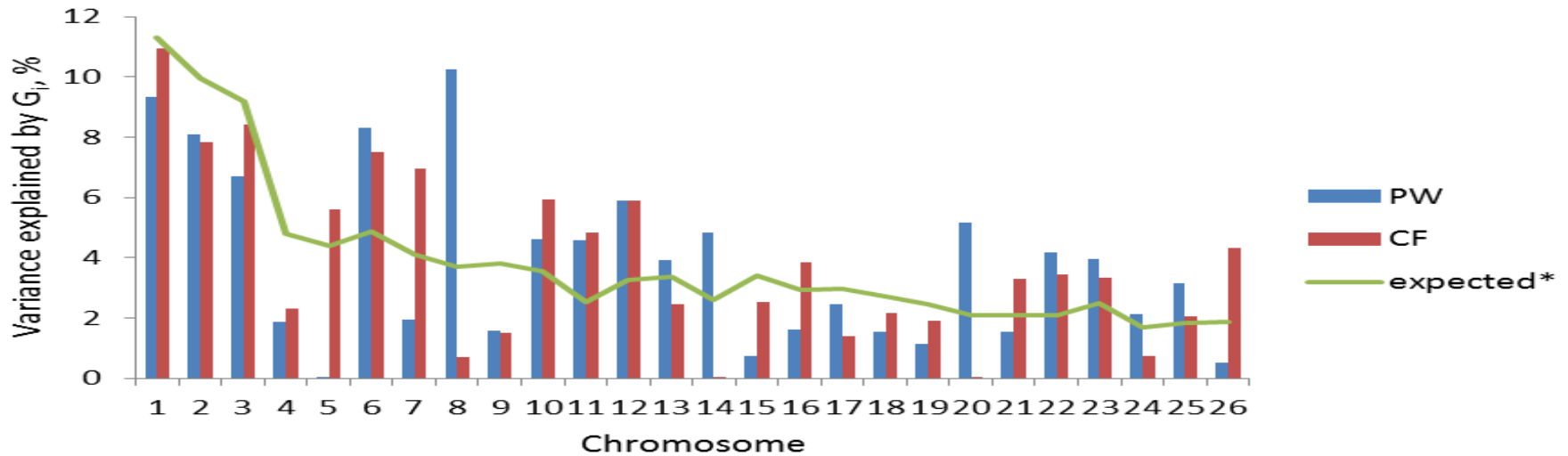


# Higher accuracy with high density markers



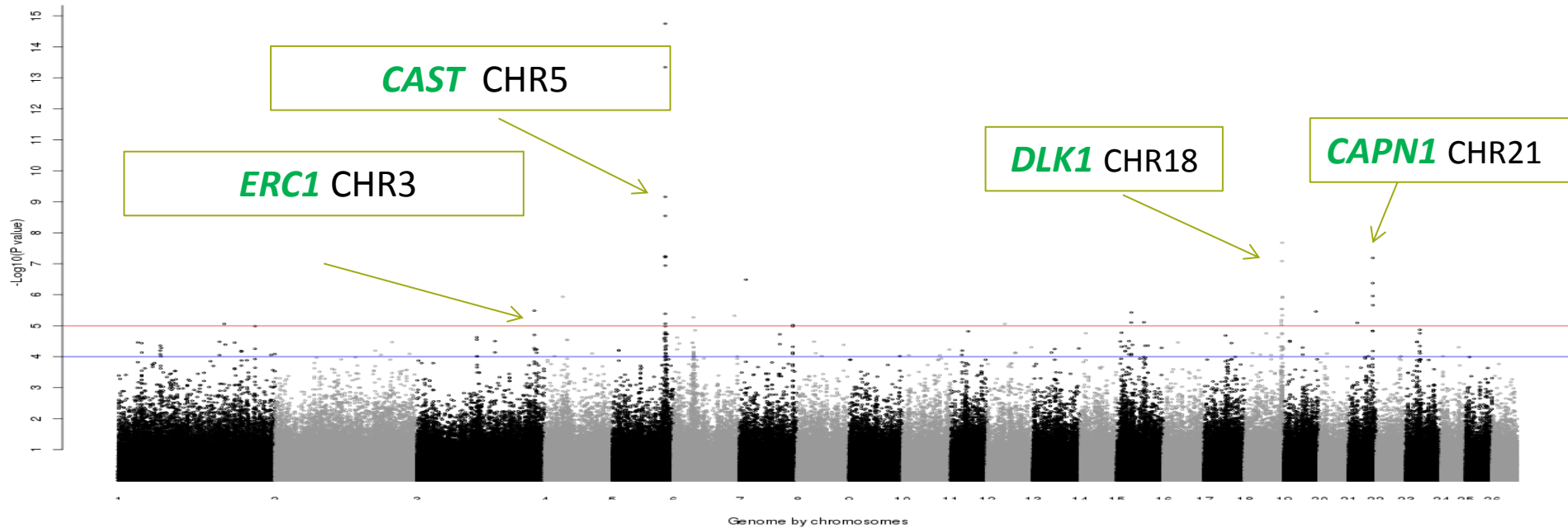
# Breaking unfavourable correlations?

Esquivelzeta-Rabell et al



# Genome Wide Association Studies

## SHEARF5



# Optimizing use of technologies

Proportion Captured	AI	MOET	JIVET	Dams Used	G/yr (\$)	L
0.06	0.95	0.00	0.05	261	\$2.26	1.87
0.32	0.77	0.04	0.19	221	\$2.82	1.46
0.64	0.36	0.10	0.54	136	\$3.96	1.21

# Conclusions

- A number of challenges related to implementing genomic selection in sheep, but there are clear benefits
- We need to increase the accuracy and across breed prediction



# Armidale Animal Breeding

