

Indirect genomic predictions of milk yield for crossbred dairy cattle

Yvette Steyn, D. Gonzalez-Pena, N. Vukasinovic, S.K. DeNise, D.A.L. Lourenco, I. Misztal

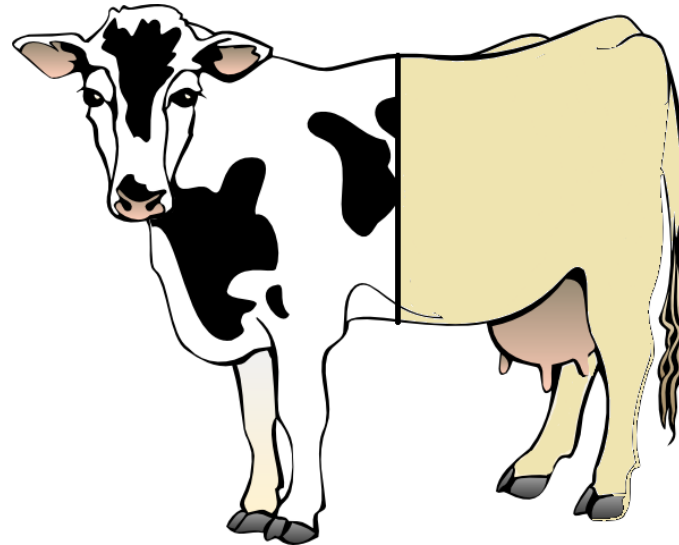
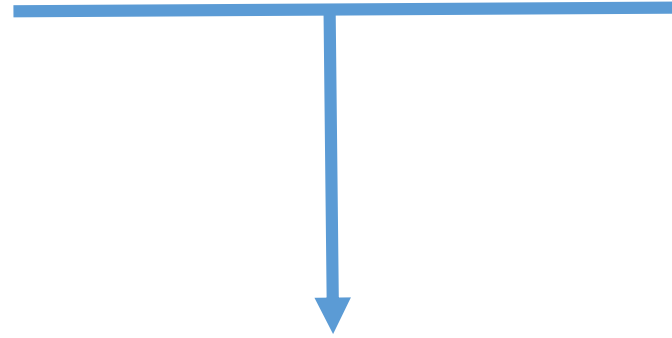


Why crossbreeding in dairy?

- Beef on dairy
- Maintain optimal mixed-breed composition
- Capitalize on heterosis
- Transform herd to another breed

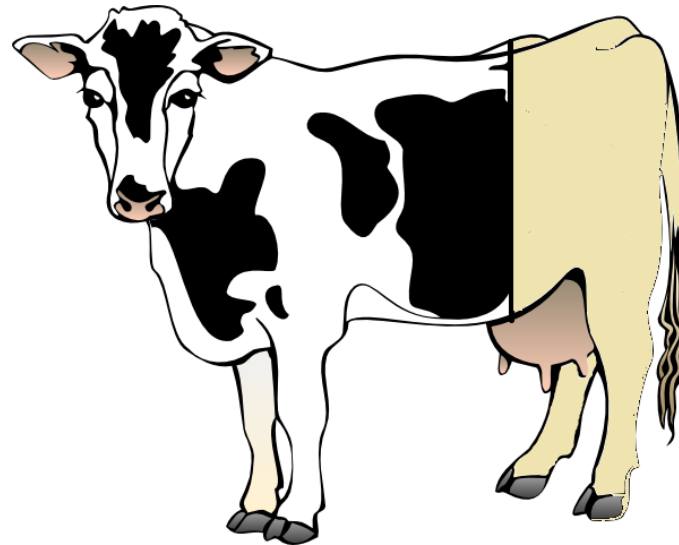
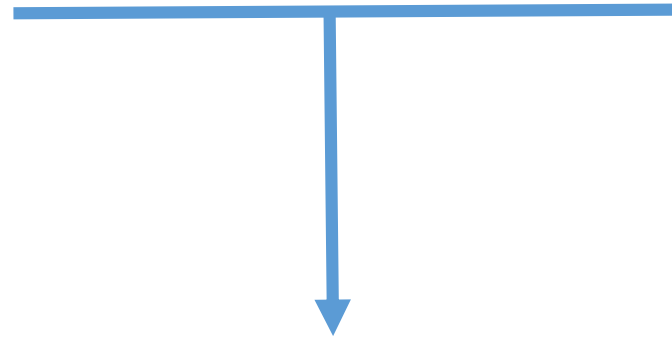
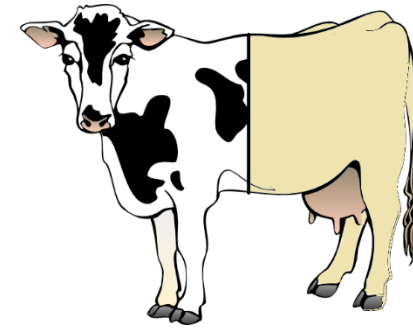
VanRaden *et al.* 2020

Upgrading mating system



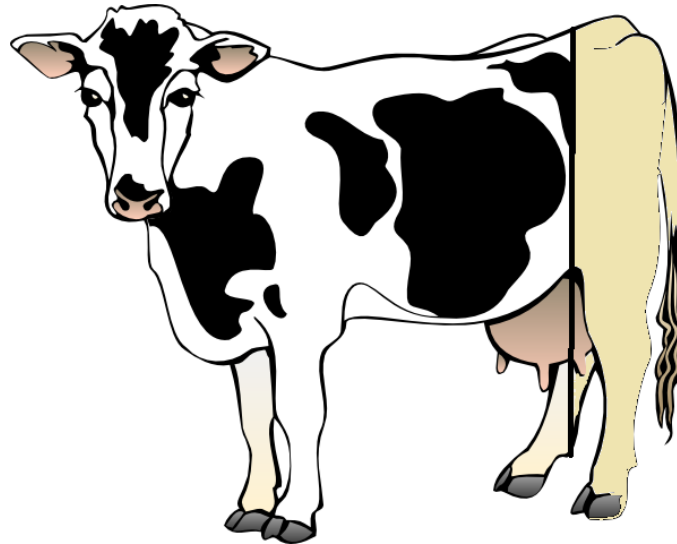
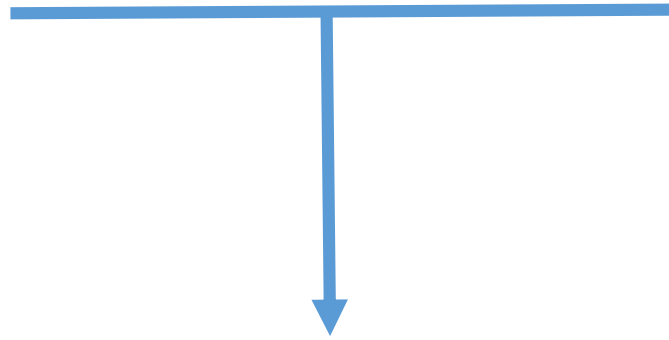
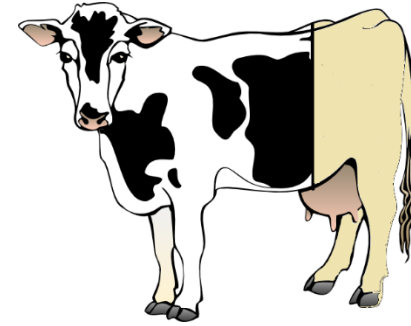
F1

Upgrading mating system



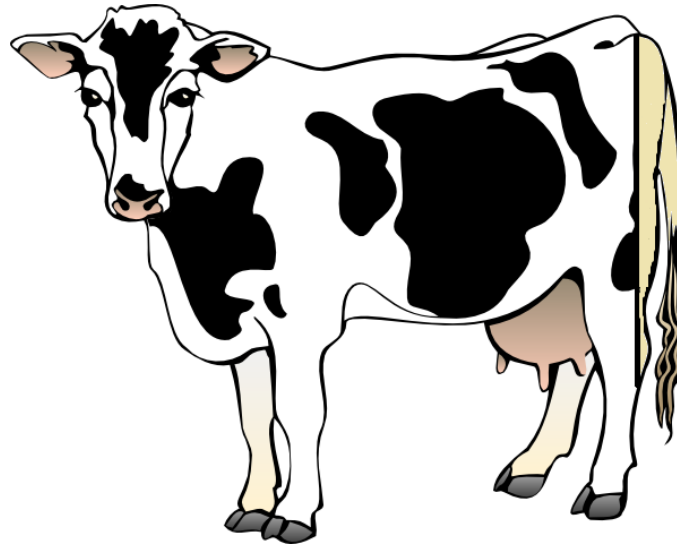
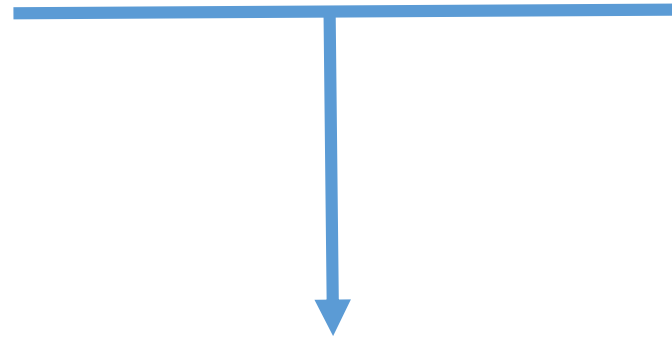
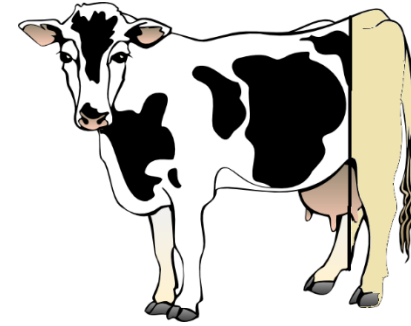
F2

Upgrading mating system



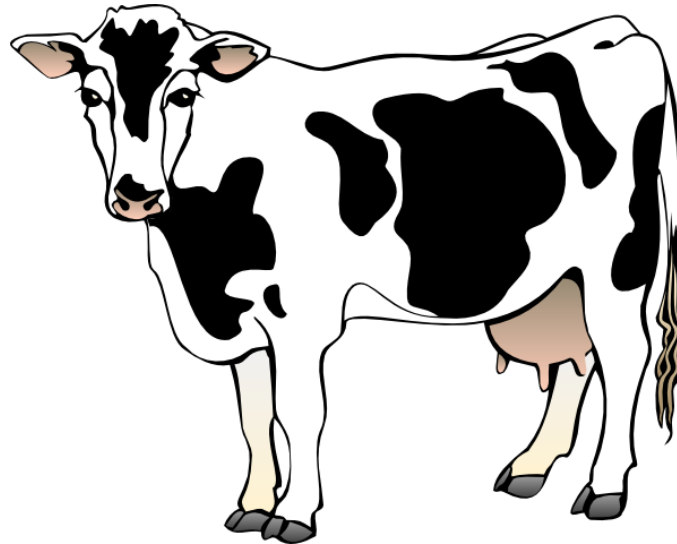
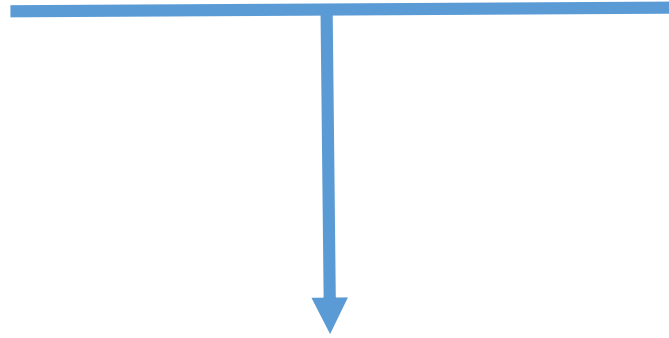
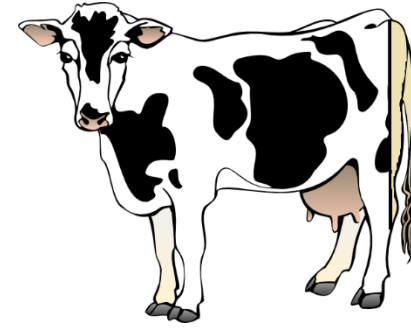
F3

Upgrading mating system



F4

Upgrading mating system



F5

How to evaluate crossbreds

- Breed origin of alleles (Christensen et al. 2014, Lopes et al. 2017, Esfandyari et al. 2015)
- Combine all in a single G-matrix (Lourenco et al. 2016)
- Breed proportions (VanRaden et al. 2020)

Objective

Evaluate the predictive ability and inflation of indirect genomic breeding values for crossbred animals using SNP marker effects from different reference groups, or breed proportions

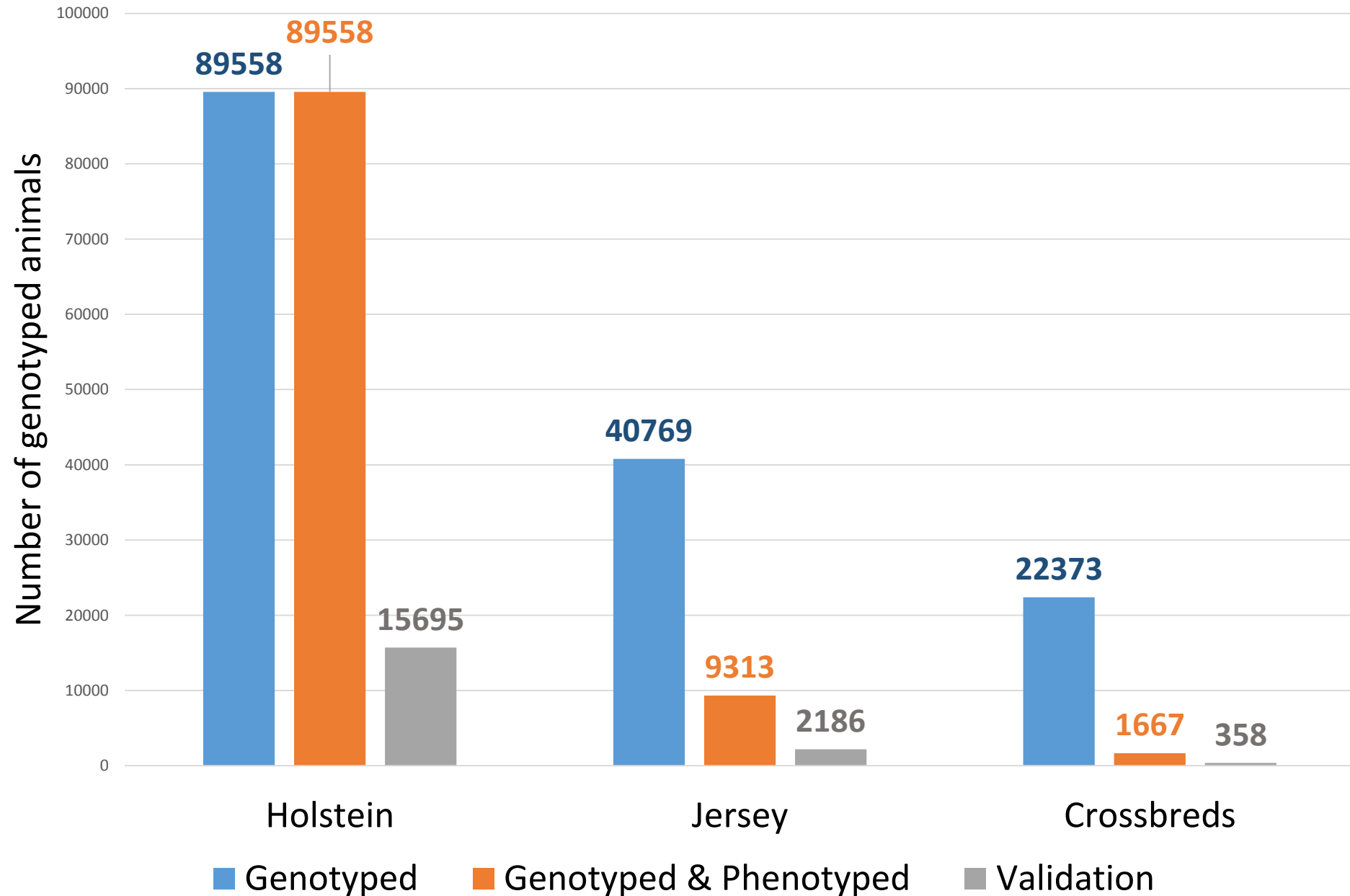
Materials and methods

- 13 880 217 milk yield measurements on 6 830 415 animals
- 19 787 413 in pedigree
- ~45k SNP markers
- Genotyped animals:

Breed	Genotyped animals
Holstein	375 487
Jersey	40 769
Cross	22 373

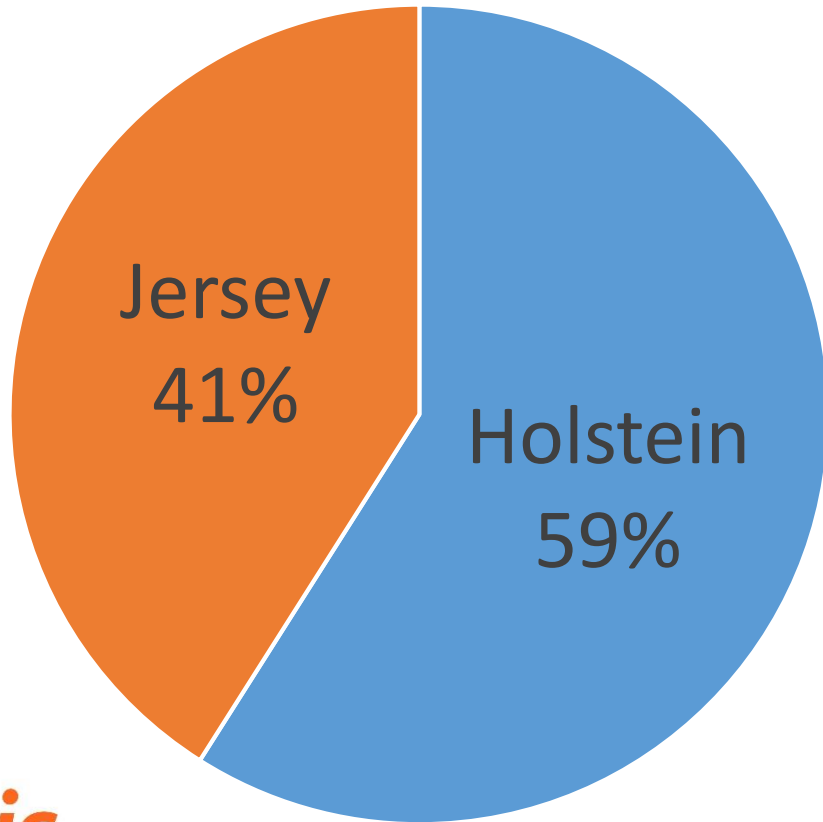
Didn't use all of the Holstein due to computational demand

Data for genotyped animals

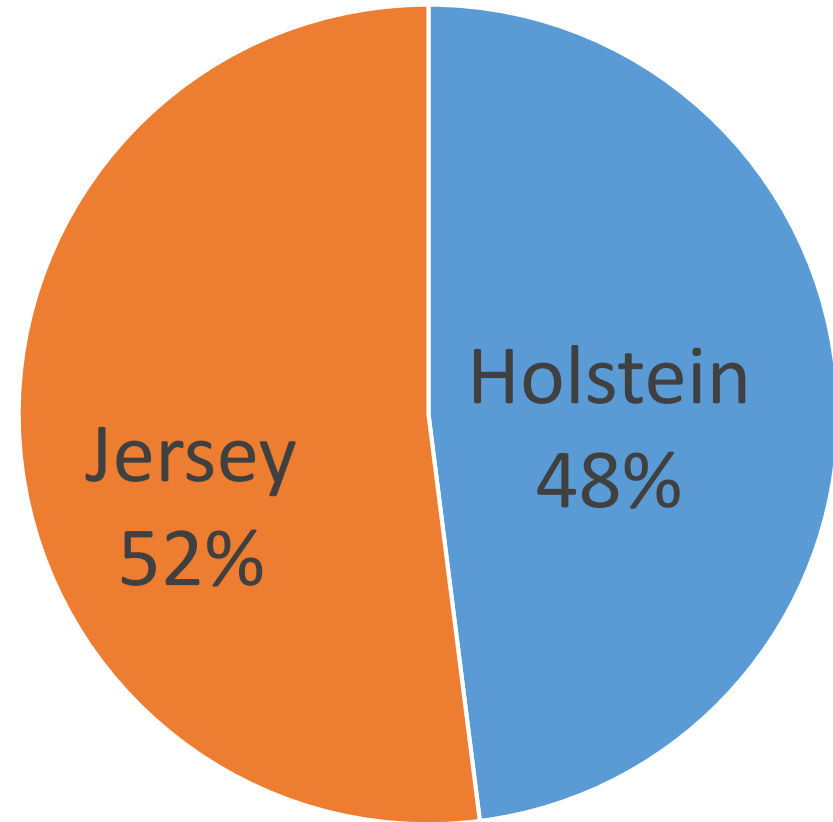


Breed proportions

All crossbreds



Validation crossbreds



Evaluation

- ssGBLUP
- Algorithm for Proven and Young (APY)
- SNP effects from GEBV
- Indirect prediction (DGV) from SNP effects
- Predictive ability: Pearson correlation between adjusted y and DGV

Scenarios to estimate SNP effects

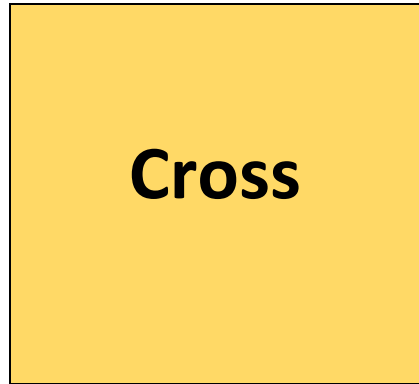
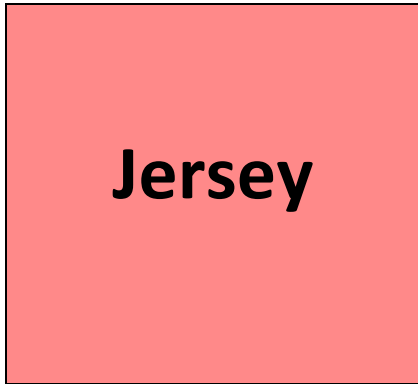
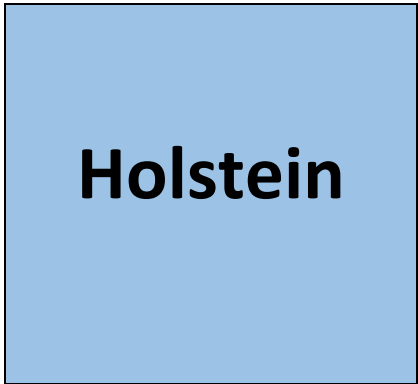
JERSEY	HOLSTEIN	CROSS
<ul style="list-style-type: none">- All Jersey- APY : random 15k	<ul style="list-style-type: none">- All Holstein- APY : random 22k	<ul style="list-style-type: none">- All crossbreds

JERSEY & HOLSTEIN	MIX
<ul style="list-style-type: none">- All Jersey and Holstein- APY : random 25k	<ul style="list-style-type: none">- All crossbreds- Random Holstein and Jersey genotypes to equal 22k each- APY : random 25k

Training



Validation



Training

Holstein

SNP effects



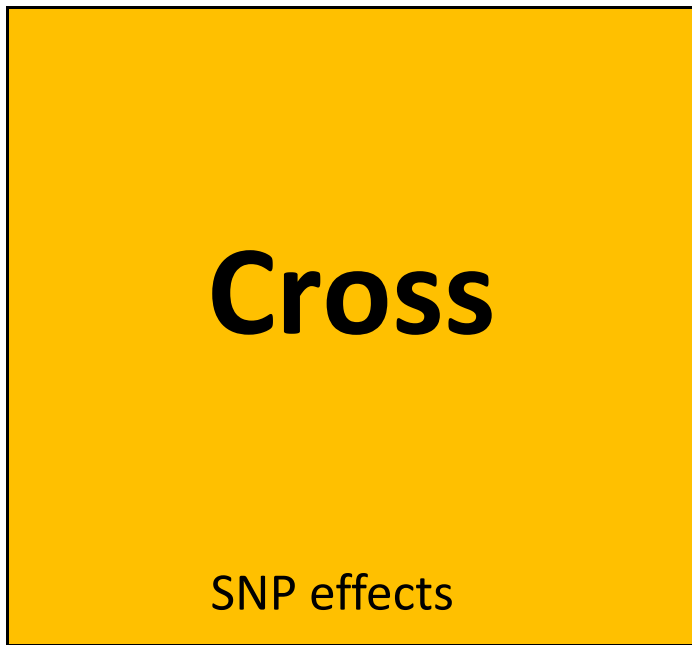
Validation

Holstein

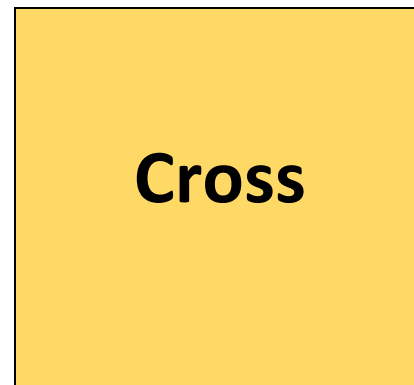
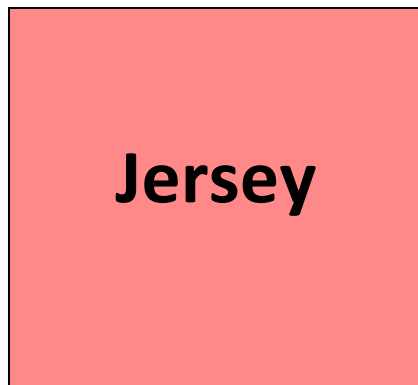
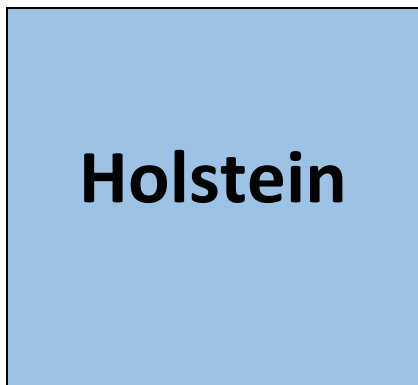
Jersey

Cross

Training



Validation



Training

**Jersey &
Holstein**

SNP effects



Validation

Holstein

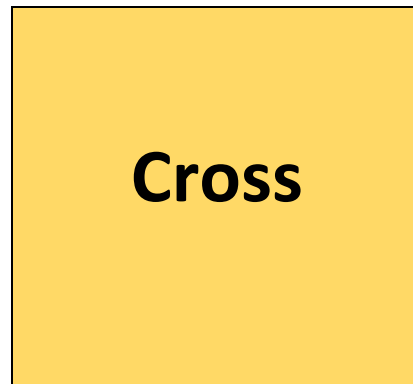
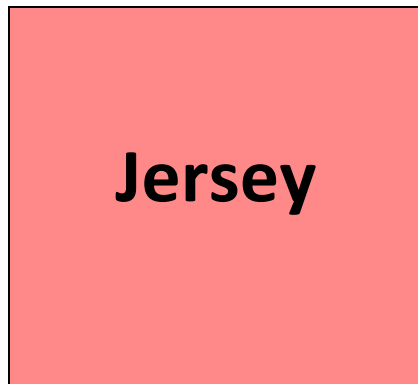
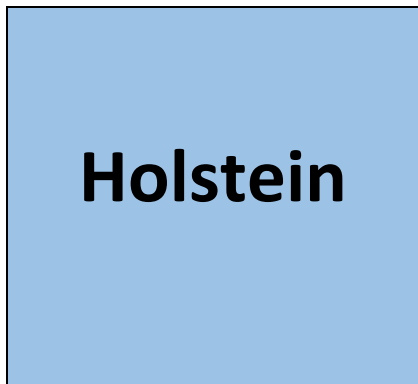
Jersey

Cross

Training



Validation



Proportions

$$\text{DGV}_H \times (\text{Holstein proportion}) + \text{DGV}_J \times (\text{Jersey proportion})$$

Animal 1	% Holstein	80	20	% Jersey
Animal 2		40	60	
Animal 3		48	52	
Animal 4		75	25	
Animal 5		20	80	
Animal 6		42	58	
Animal 7		90	10	

Predictive ability

Breed used	Breed predicted		
	Jersey	Holstein	Cross
Cross	0.24	0.26	0.50

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Jersey	0.48	0.13	0.50
Holstein	0.09	0.45	0.47

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Jersey	0.48	0.13	0.50
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Jersey & Holstein	0.45	0.44	0.50

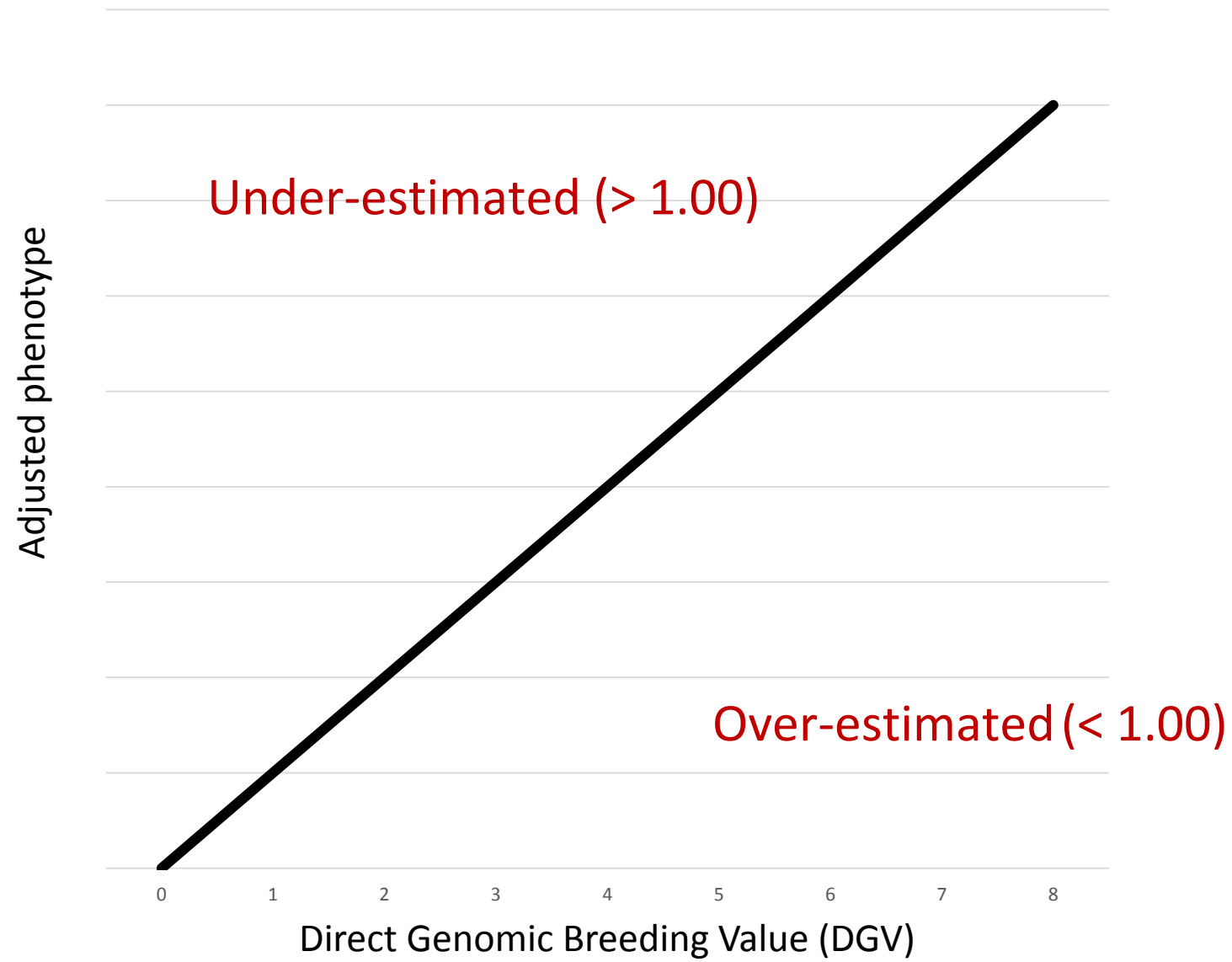
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Mix	0.46	0.40	0.46

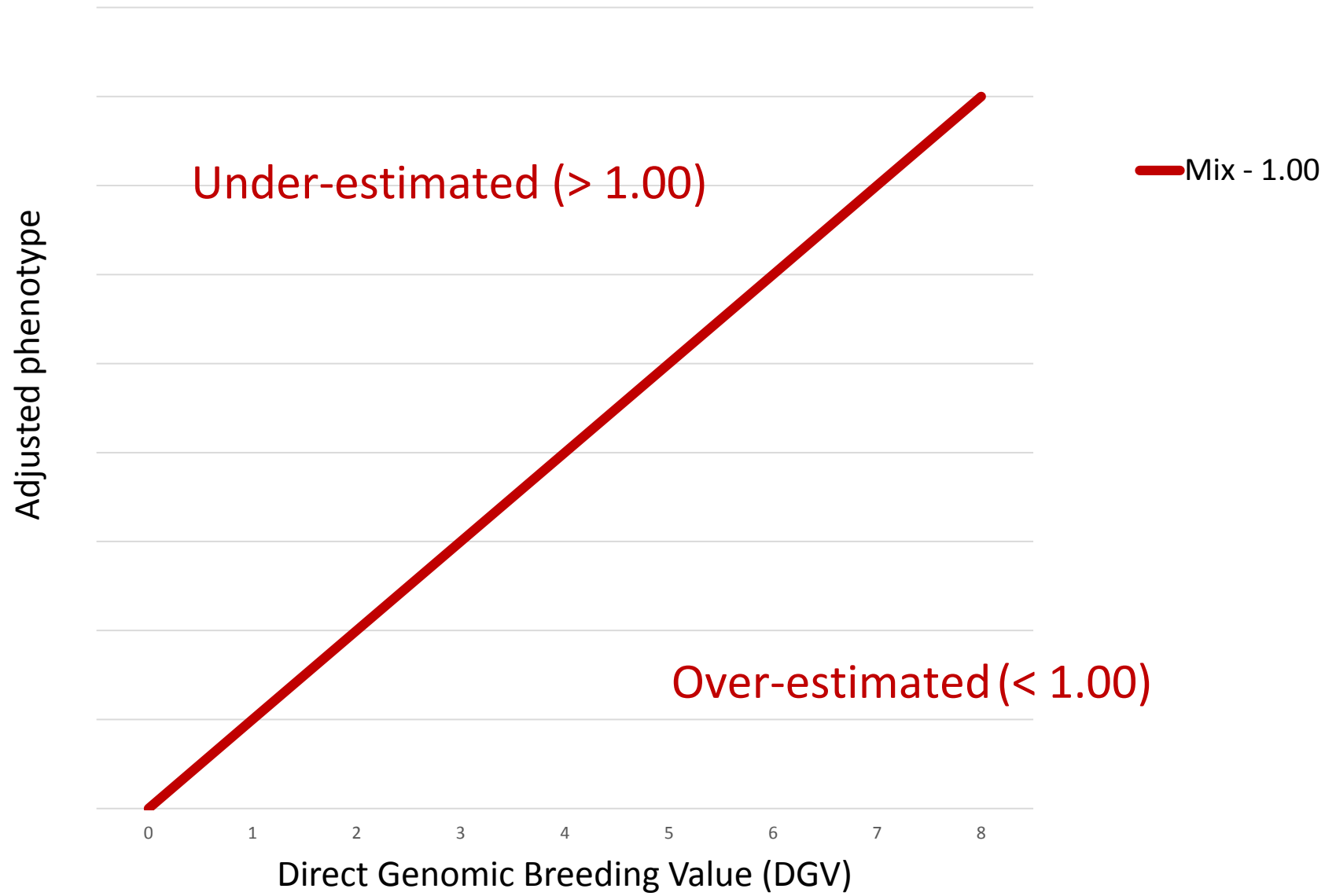
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Proportions	-	-	0.32

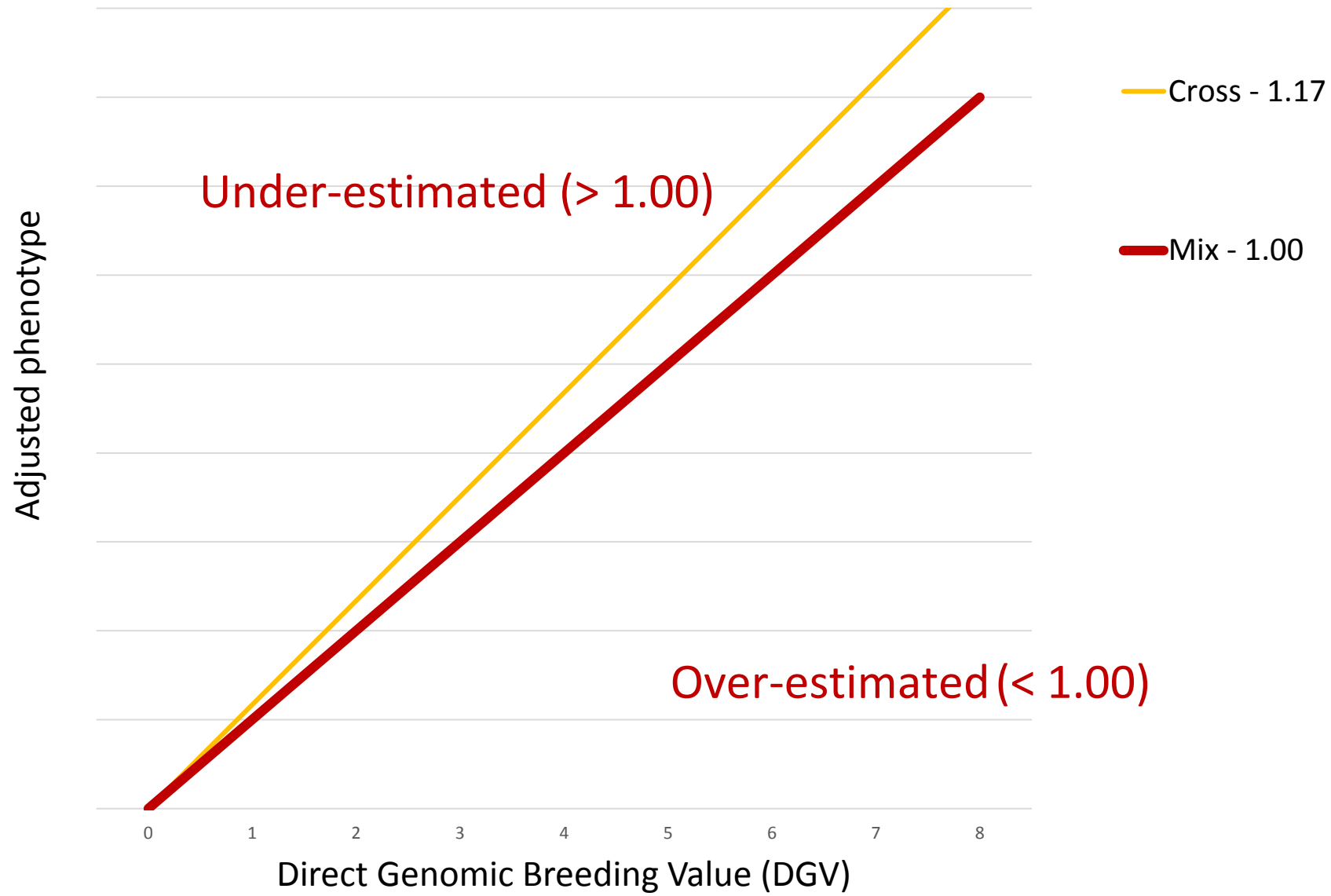
Inflation



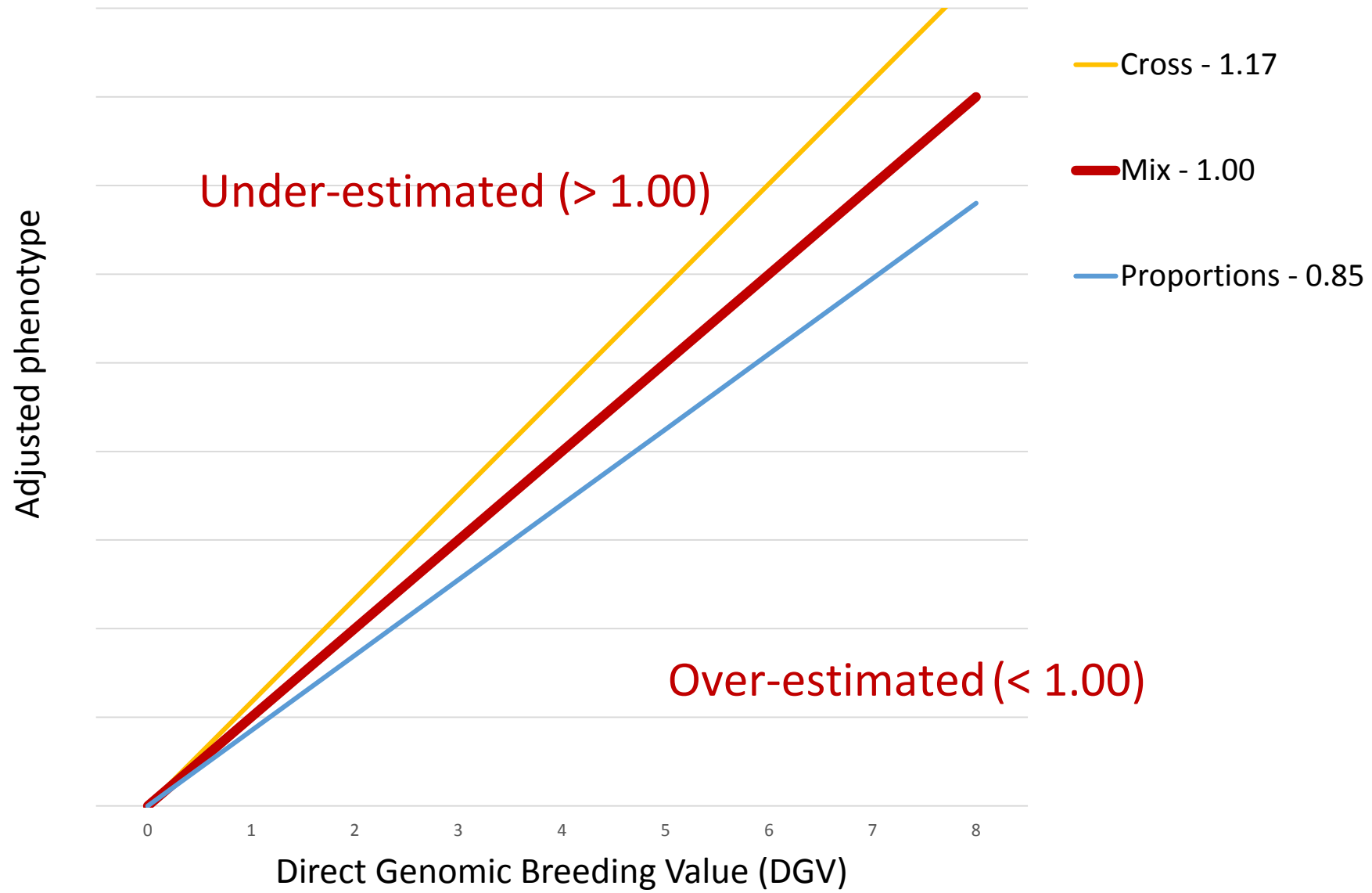
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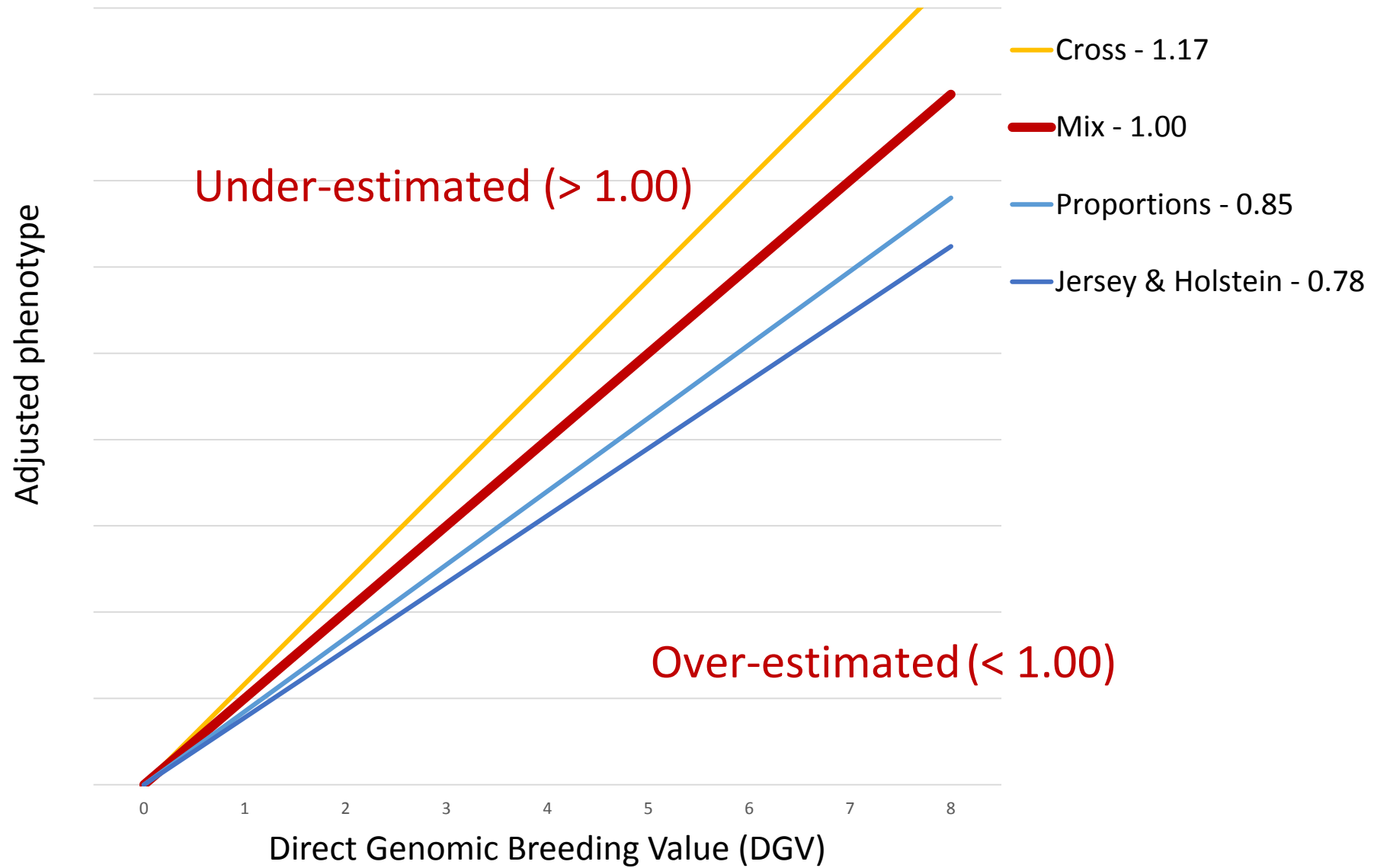
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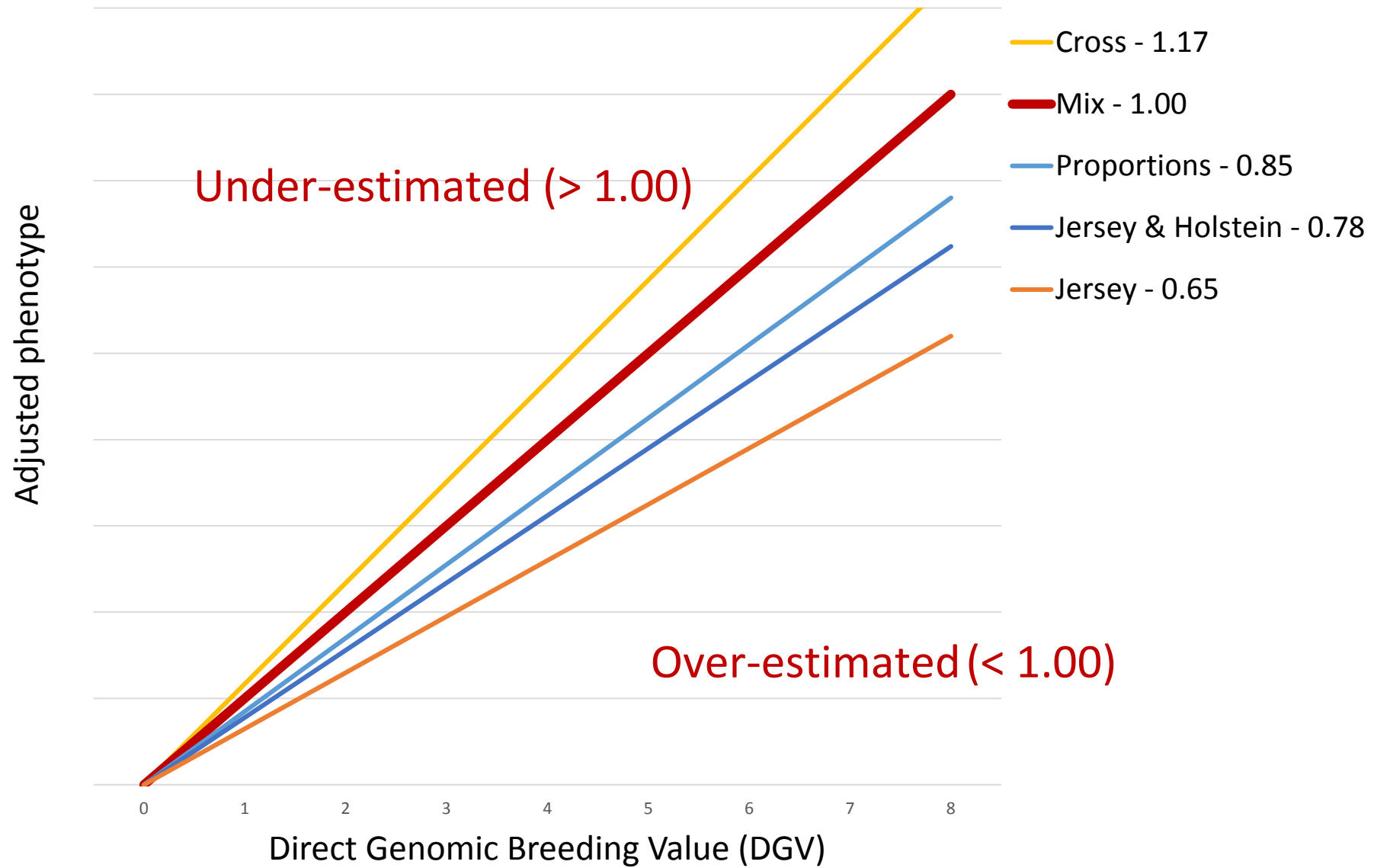
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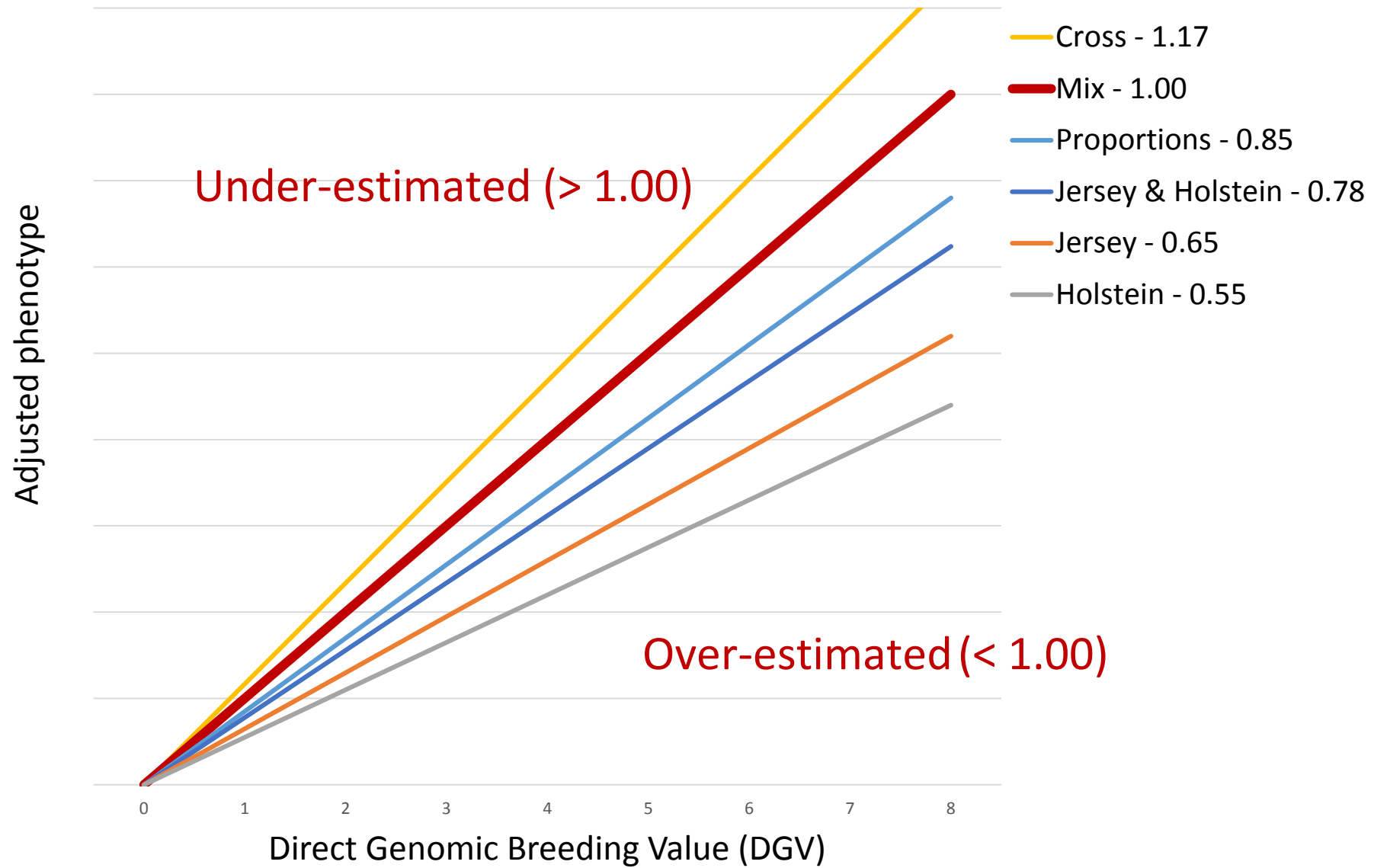
Inflation



Inflation



Inflation



Conclusion

- Accounting for breed proportions is not necessary
- Using mix scenario was slightly less accurate but without inflation
- Breeding objectives are important
- Could possibly use SNP effects of the desired pure breed
- Small validation populations

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