

**Accuracy of DGVs for Original  
Braunvieh: across breed evaluation  
using phenotypes and genotypes of  
Original Braunvieh and Brown-Swiss  
cattle**

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# Background

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- 2 Breeds: Brown Swiss (BSW) / Original Braunvieh (OB)

	Characterization	No. of cows with milk recording	Routine genomic evaluation
BSW	Dairy breed	157,647	Since 2009
OB	Dual purpose	7,189	not yet started

- BSW descends from OB, but has been upgraded by crossbreeding with BSW since 1970s
- One common traditional genetic evaluation
- OB failed validation of genomics in 2009 with 50K data
- Changes since 2009:
  - OB genotype pool has been enlarged
  - HD genotyped pool BSW / OB
  - HD-genotyping of cows from back-cross population

# Objective

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- (Re)evaluate the accuracy of genomic prediction for OB
- applying a multi-breed approach (BSW / OB)
- Genomic prediction based on 50K / HD genotype data
- Traits:
  - Milk yield (MY)
  - Fat yield (FY)
  - Protein Yield (PY)
  - Lactation persistency (PER)
  - Somatic cell score (SCS)

# Data: Genotypes / Phenotypes

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Chip	No. of BSW males	No. of BSW females	No. of males > 50%OB	No. of females > 50%OB	Total
LD	194	143	11	8	356
50K	7,838	688	127	15	8,668
HD	536	870	161	113	1,680
<b>Total</b>	<b>8,568</b>	<b>1,701</b>	<b>299</b>	<b>136</b>	<b>10,704</b>

Trait (EBVs)	No. of BSW males	No. of BSW females	No. of males > 50%OB	No. Of females > 50%OB
MY, FY, PY	5,729	1,188	215	136
Per	2,227	1,188	213	136
SCS	5,173	1,188	215	136

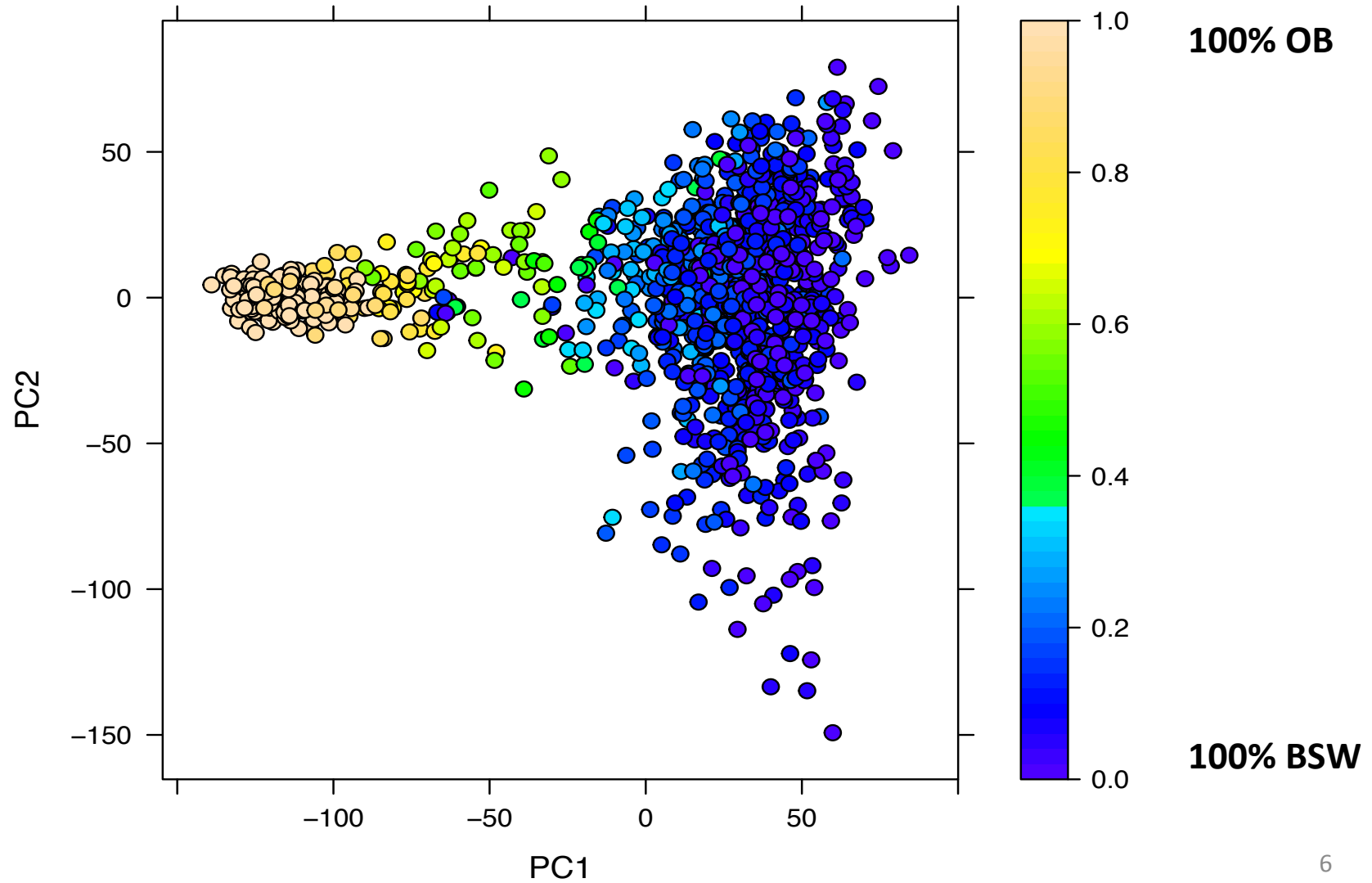
- Evaluation Model BayesC GenSel (Fernando and Garrick, 2009)

$$y_i = \mu + \sum_{j=1}^k X_{ij} \alpha_j + e_j$$

- Phenotype: deregressed EBVs (Garrick et al. 2009)
- Imputation: 2-step imputation (LD/50K, 50K/HD) using FImpute (Sargolzaei et al. 2011)
- Imputation accuracy: Gredler et al. EAAP 2013, Nantes
- Accuracy criteria for genomic prediction of OB:  
r(DGV,EBV), b1

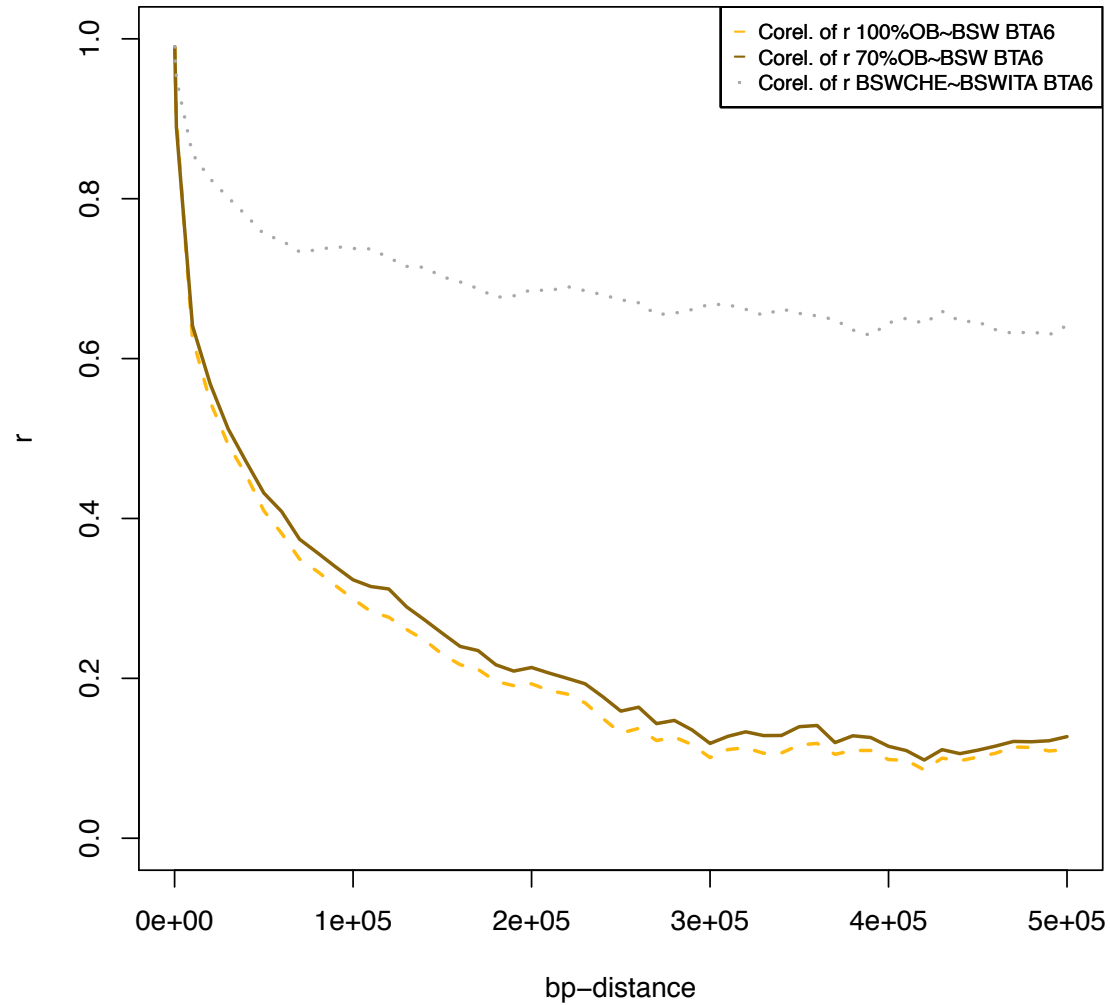
# Population structure: PCA

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# Population structure: Conservation of LD pattern

Correlation of  $r$  between populations as function of genomic distance



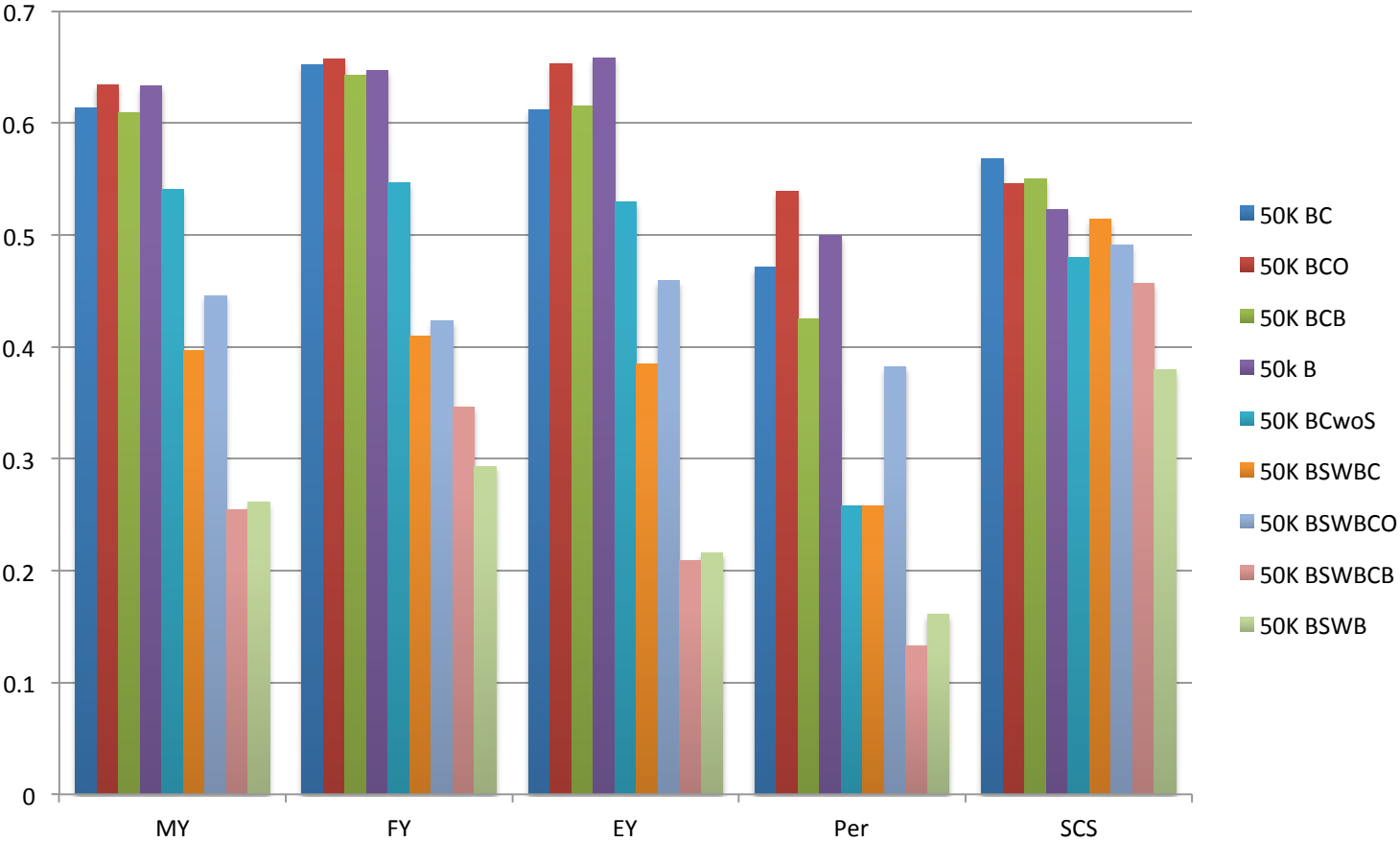
# Validation design

- Validation strategy:
  - OB sires
  - high accurate EBVs (mean acc. MY 0.90)
  - without offspring in reference population
  - n = 79
- Predicted using different reference datasets

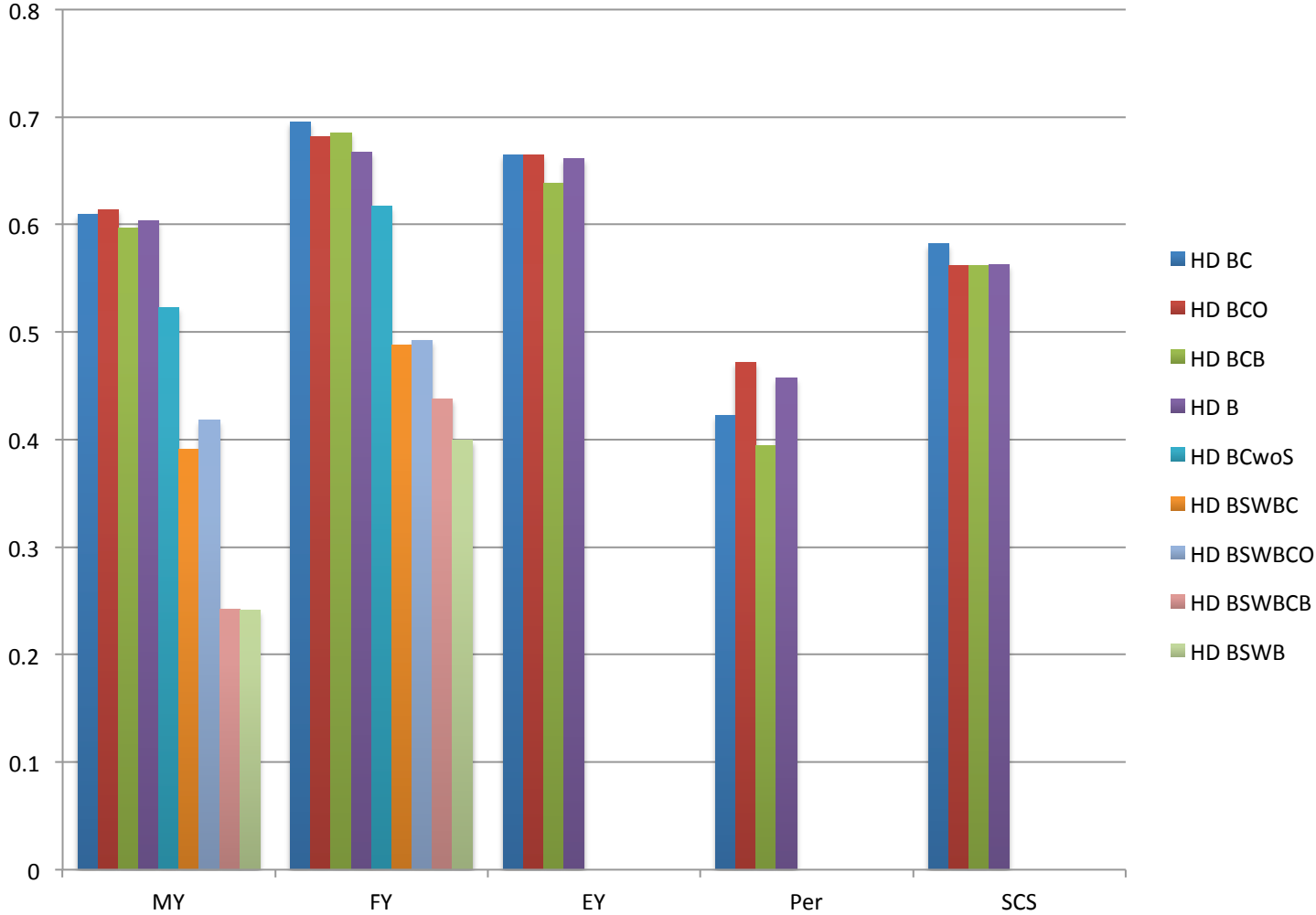
Run	Reference dataset
BC	Bulls + cows
BCO	Bulls + cows if > 50% OB
BCB	Bulls + cows if < 50% OB
B	Bulls only
BCwoS	Bulls + cows, but without sires from validation animals
BSWBC	BSW bulls + all cows
BSWBCO	BSW bulls + cows if > 50% OB
BSWBCB	BSW bulls + cows if < 50% OB
BSWB	BSW bulls



# Results 50K r(EBV,DGV)

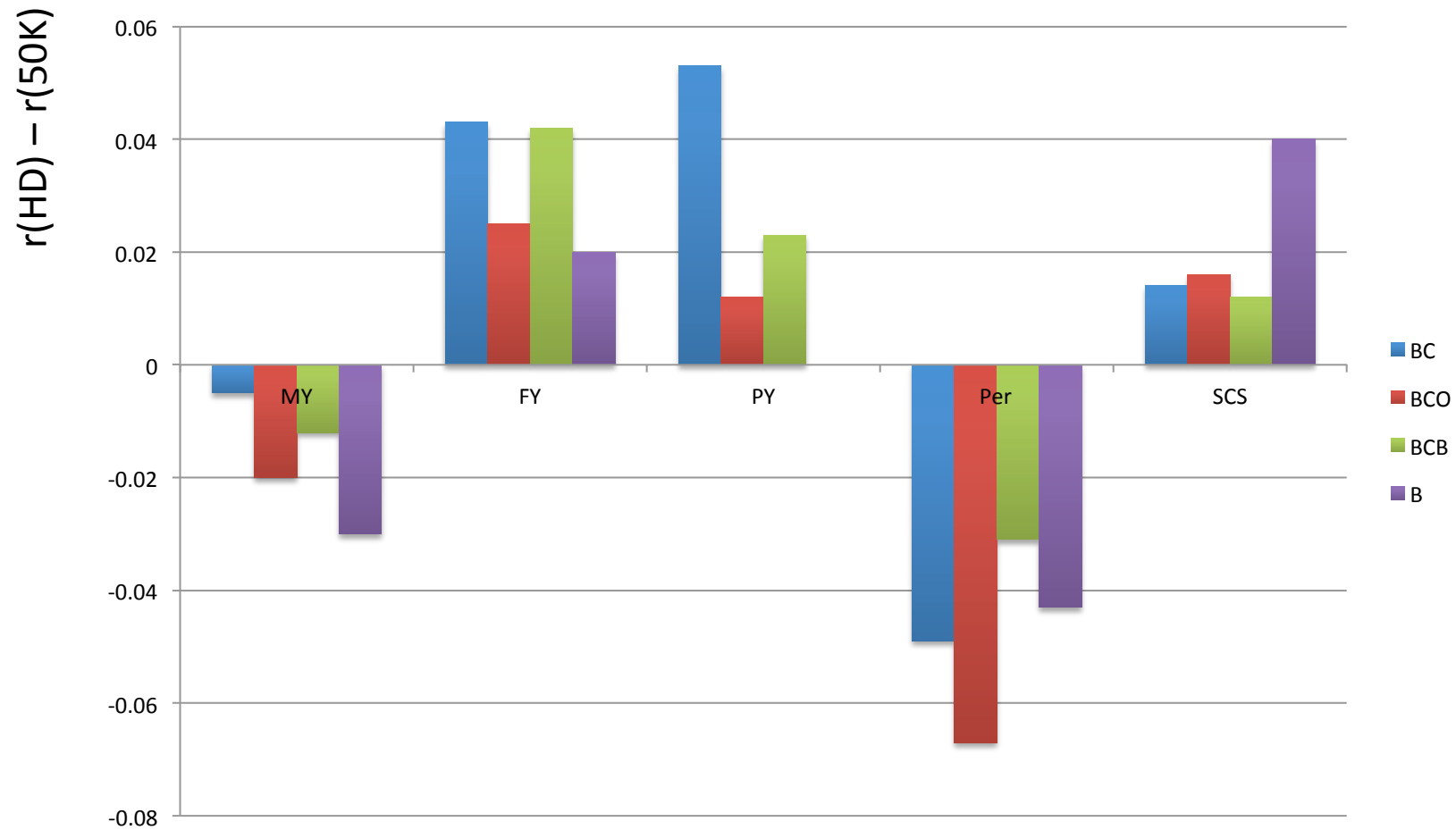


# Results HD $r(EBV,DGV)$

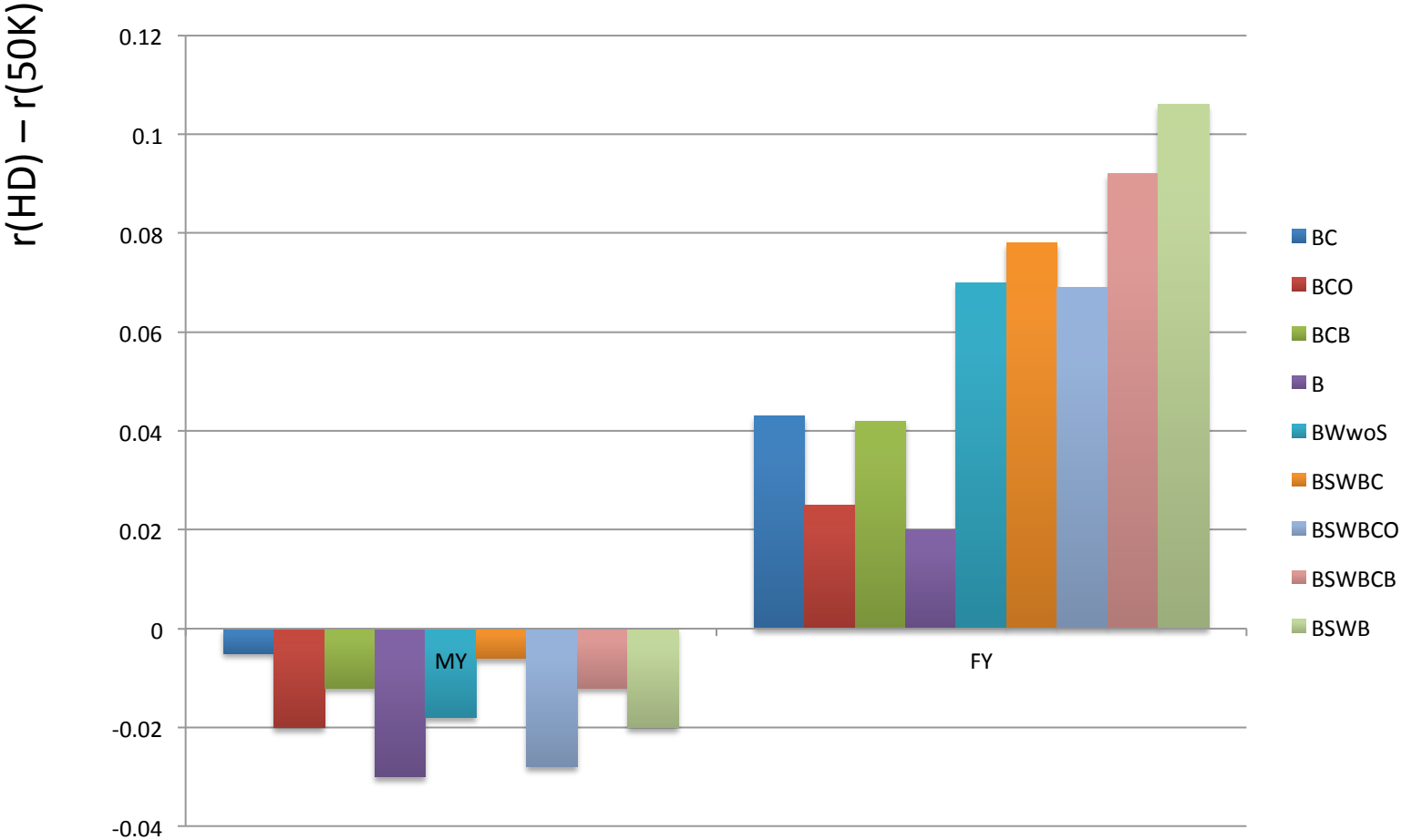


# Accuracy gain with HD

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# Accuracy gain with HD



# Conclusions

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- OB and BSW: different populations
- Conservation of LD was increased by genotyping of high OB% cows
- 50K Genomic prediction is most accurate with high OB-females in reference population with more over/under dispersed DGVs
- Additional gain with HD data is marginal and depending on trait



A photograph of a brown cow with a bell around its neck, grazing in a green field. The cow is the central focus, facing left. The background shows a grassy hillside with a wooden fence and some trees under a blue sky with light clouds. The overall scene is a typical rural landscape.

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Thank you!

We acknowledge

BRAUNVIEH 

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