

**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

- 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

- (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
Total	8,568	1,701	299	136	10,704

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

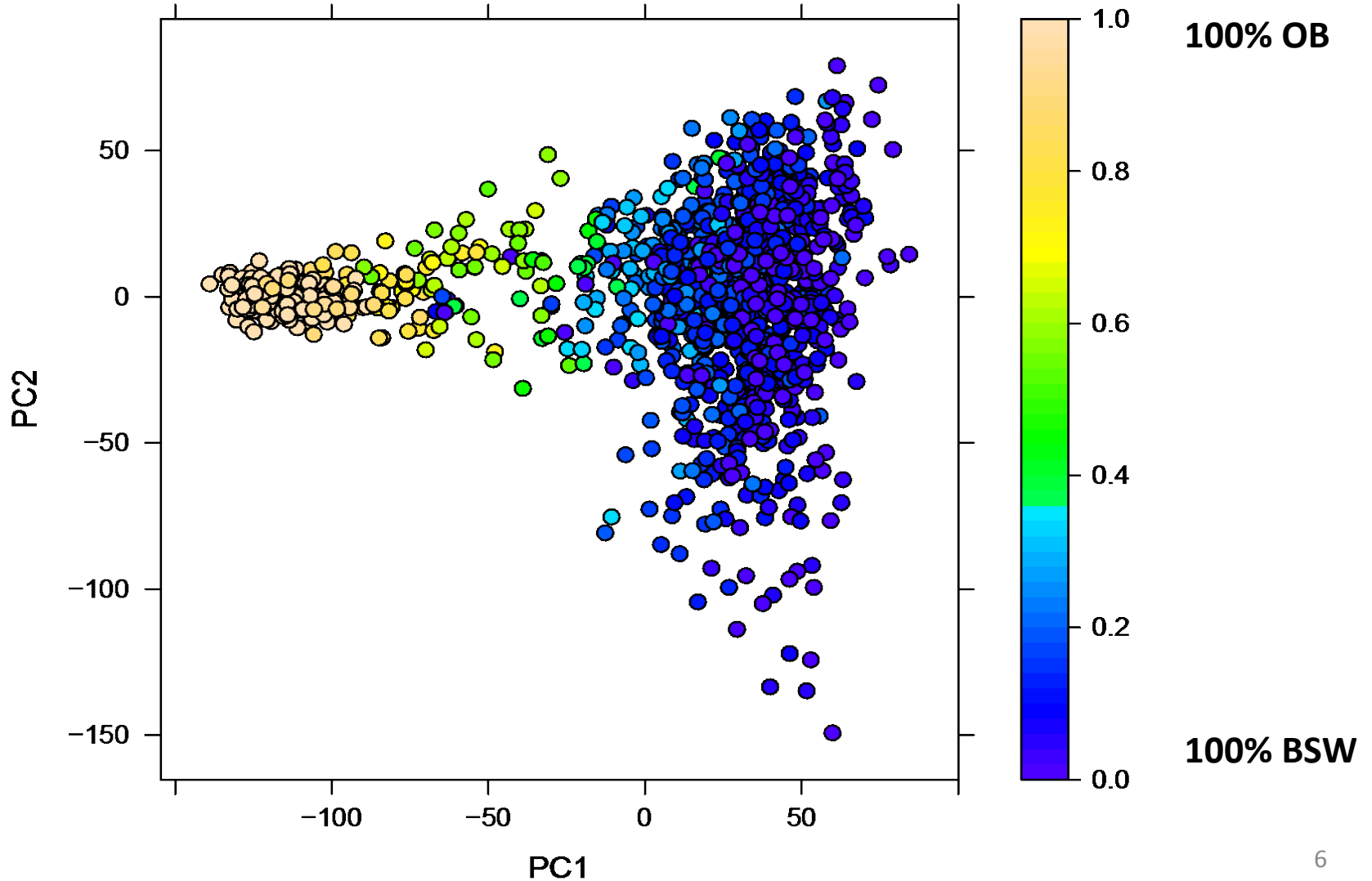
- Evaluation Model BayesC GenSel (Fernando and Garrick, 2009)

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

- 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)

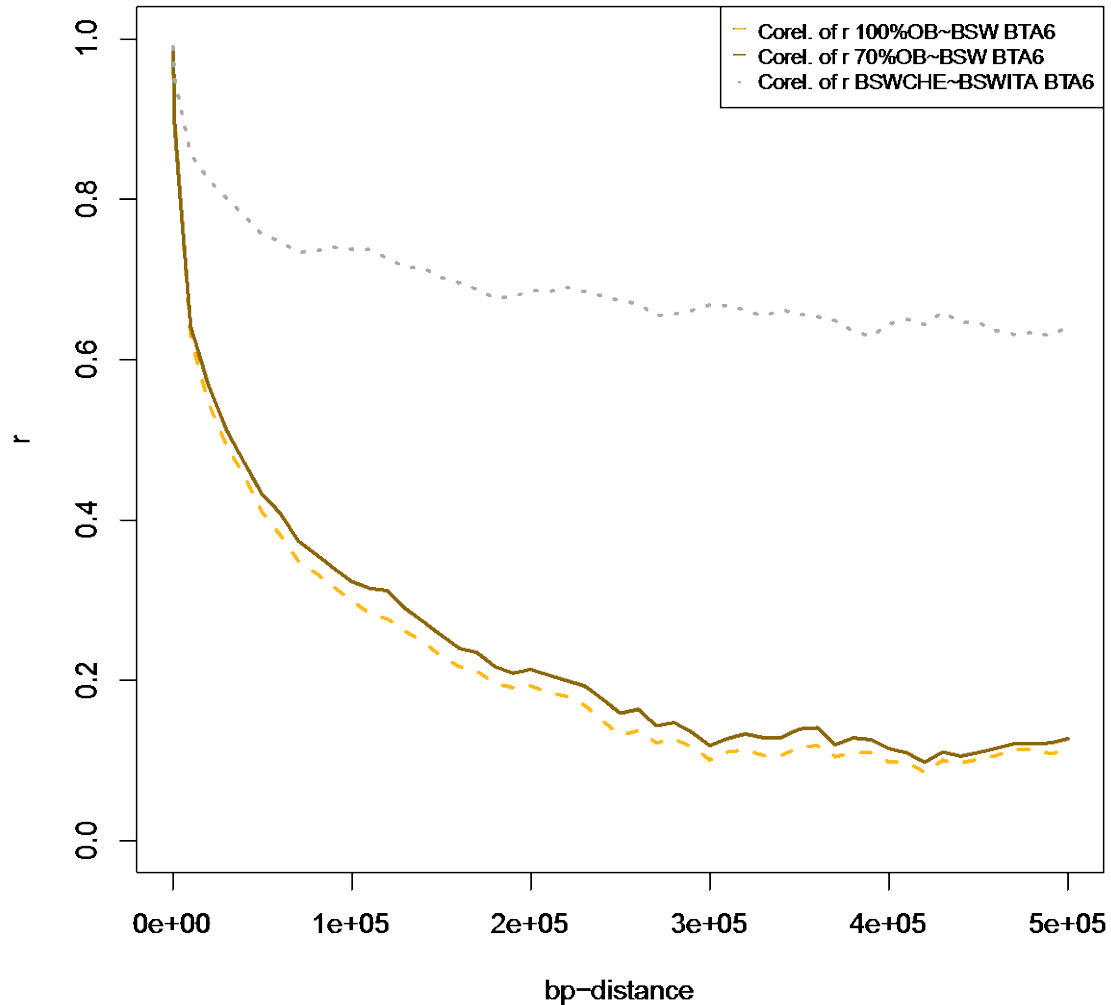
Population structure: PCA

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Population structure: Conservation of LD pattern

Correlation of r between populations as function of genomic distance

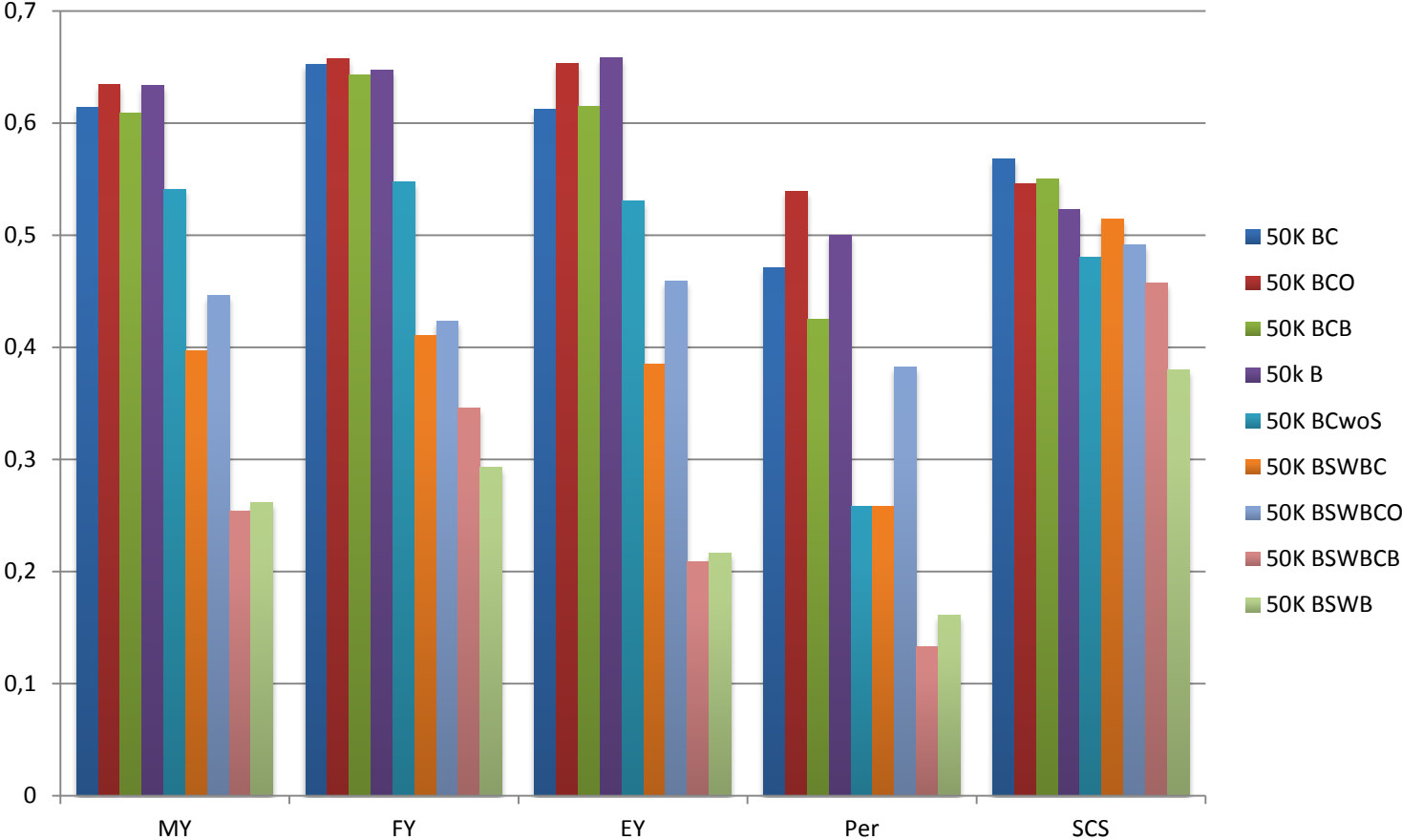


Validation design

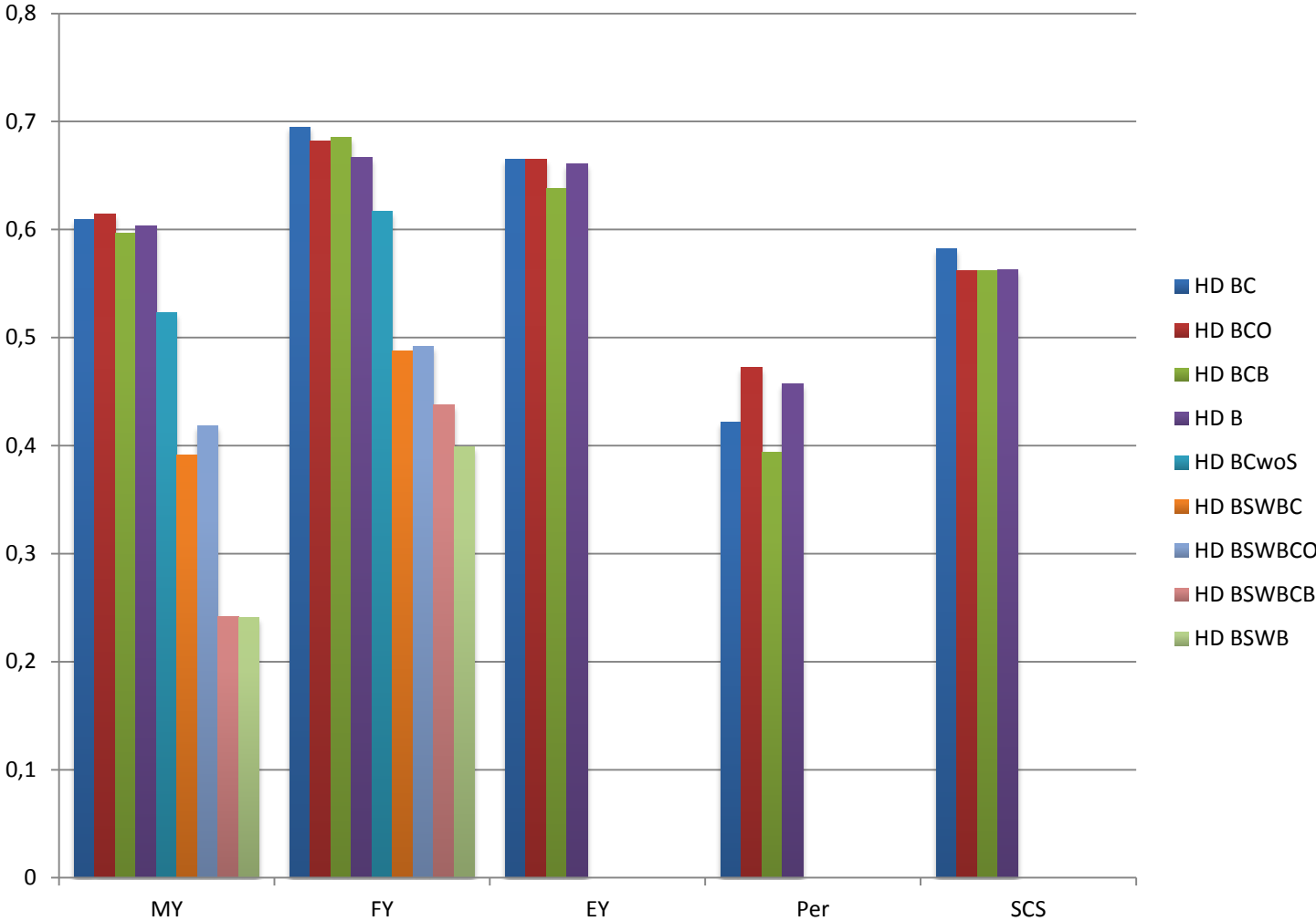
- Validation strategy:
 - OB sires
 - high accurate EBVs (mean acc. MY 0.90)
 - without offspring in reference population
 - n = 79
- Predicted using different reference datasets

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

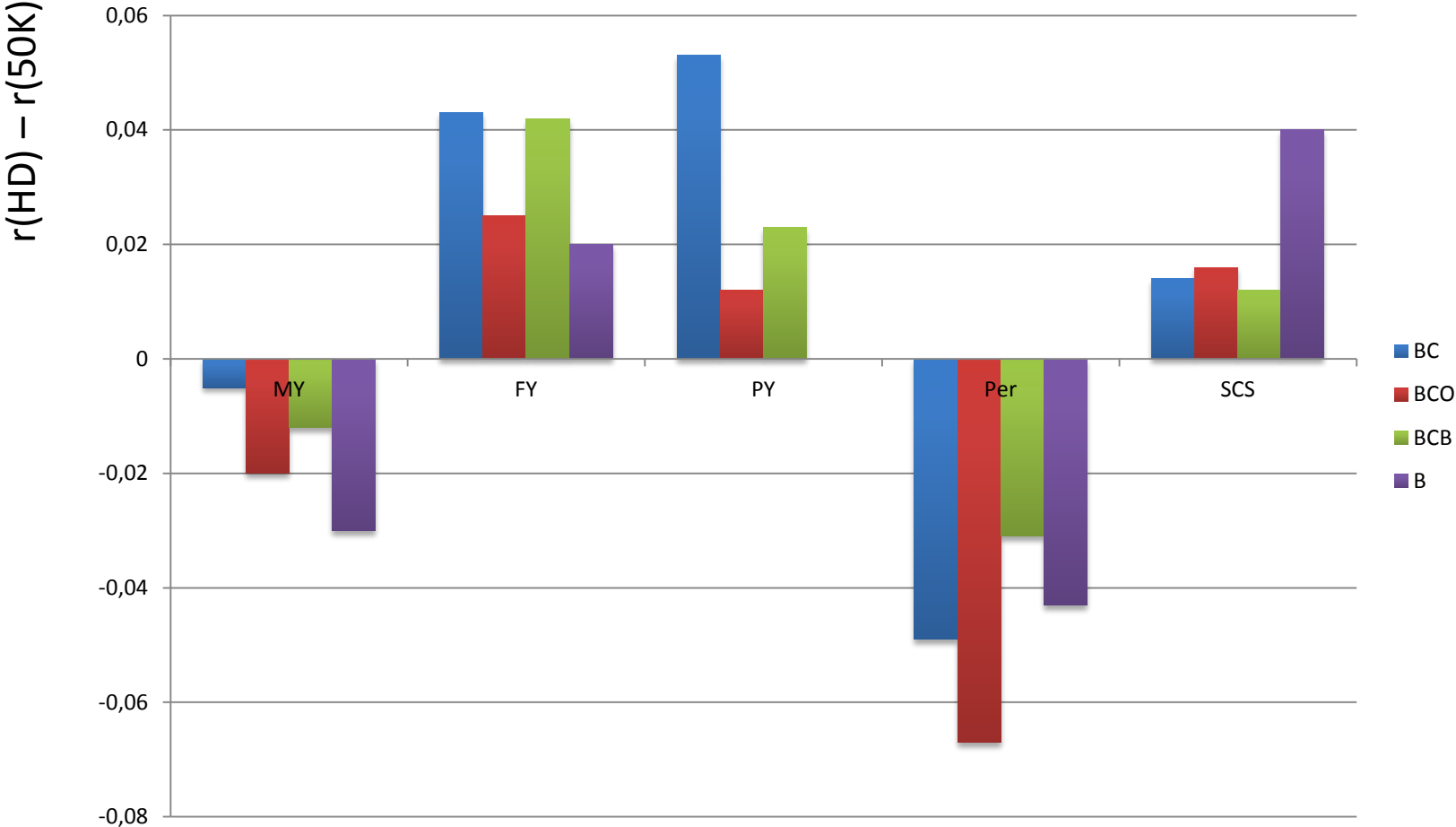
Results 50K r(EBV,DGV)



Results HD r(EBV,DGV)



Accuracy gain with HD




Conclusions

- 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
- Accuracy gain with HD data is marginal and depending on trait
- Implementation of Genomic prediction in OB is feasible provided that ancestors of selection candidates are in reference population

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Thank you!

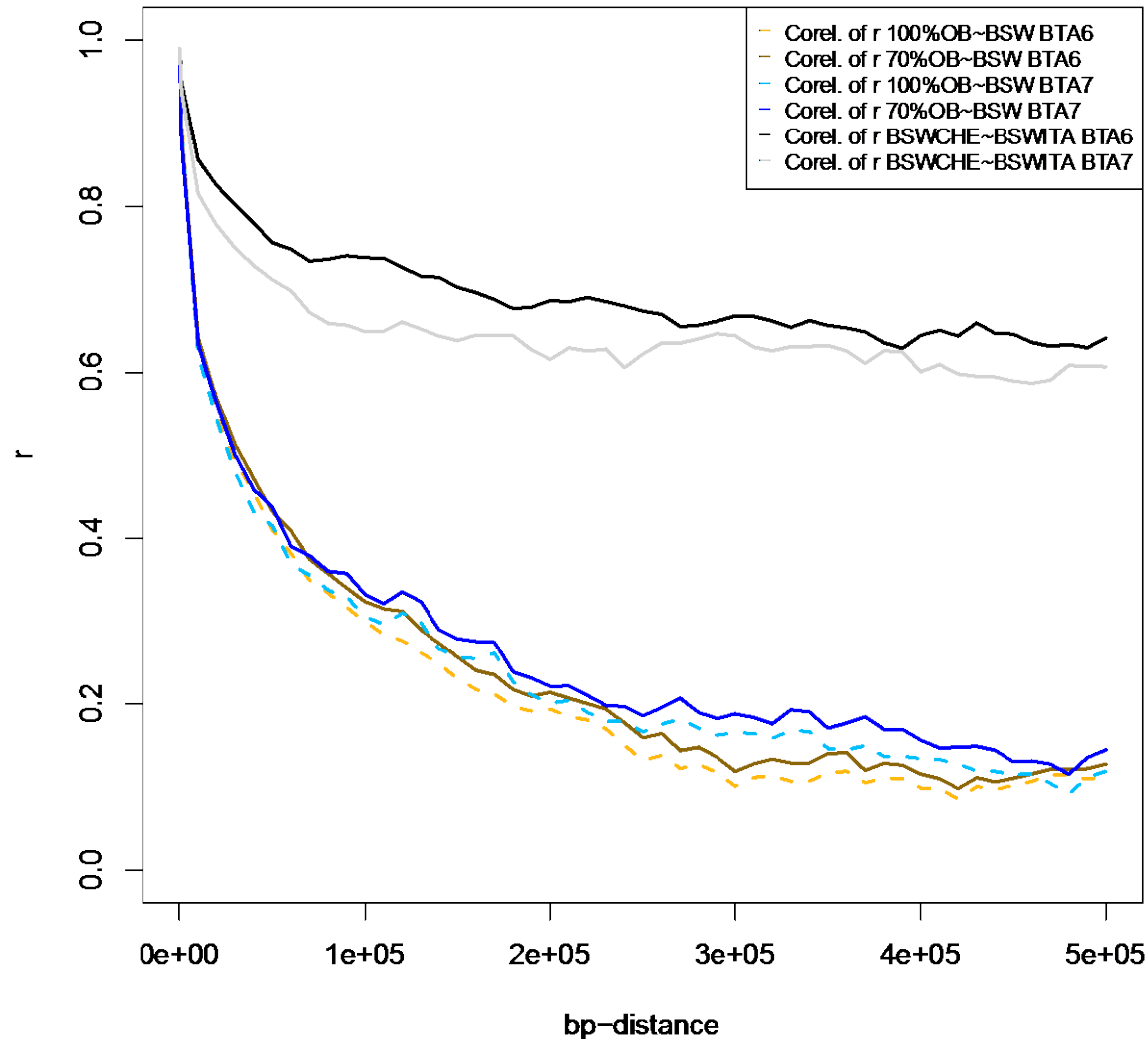
We acknowledge

BRAUNVIEH 

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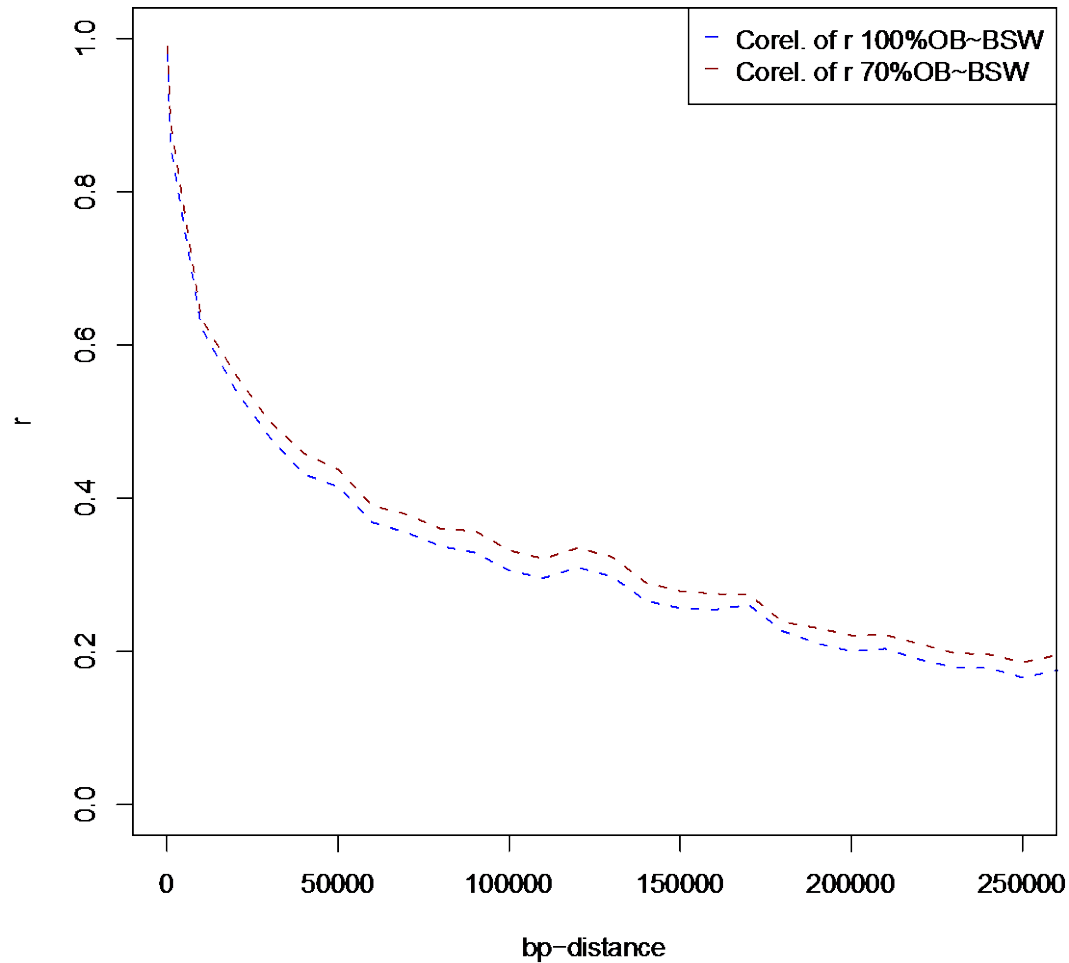
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