Bavarian State Research Center
for Agriculture

How do imputation errors affect genomic breeding values?

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Institute of Animal Breeding

Motivation / Objective

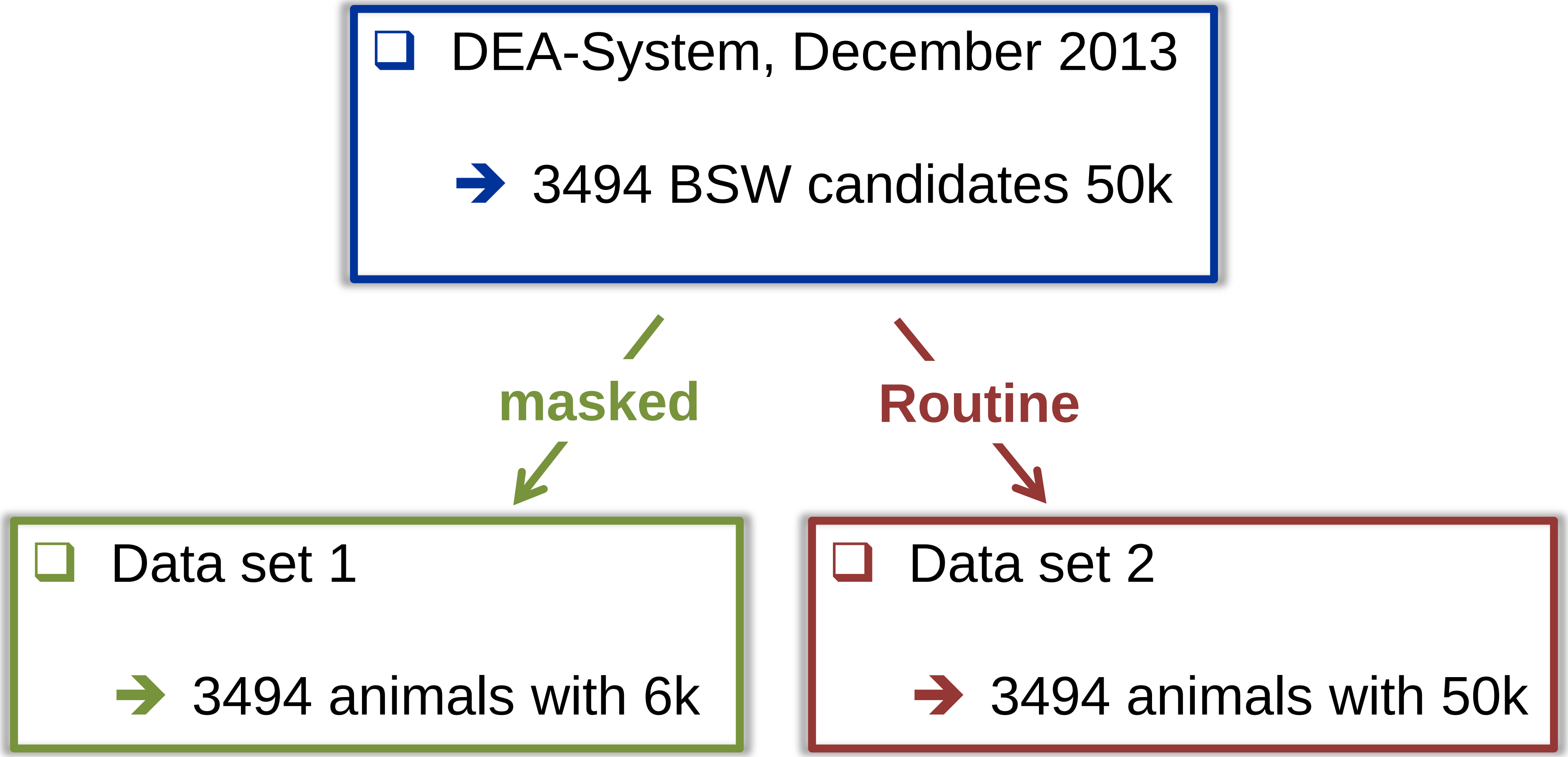
❑ Most studies about the effects of imputation report:

➔ overall correlations between GEBV

➔ comparisons between software

❑ Further investigate the causes and patterns underlying the bias in GEBV due to imputation errors

Material and Methods



□ DEA-System, December 2013

→ 3494 BSW candidates 50k

masked

Routine

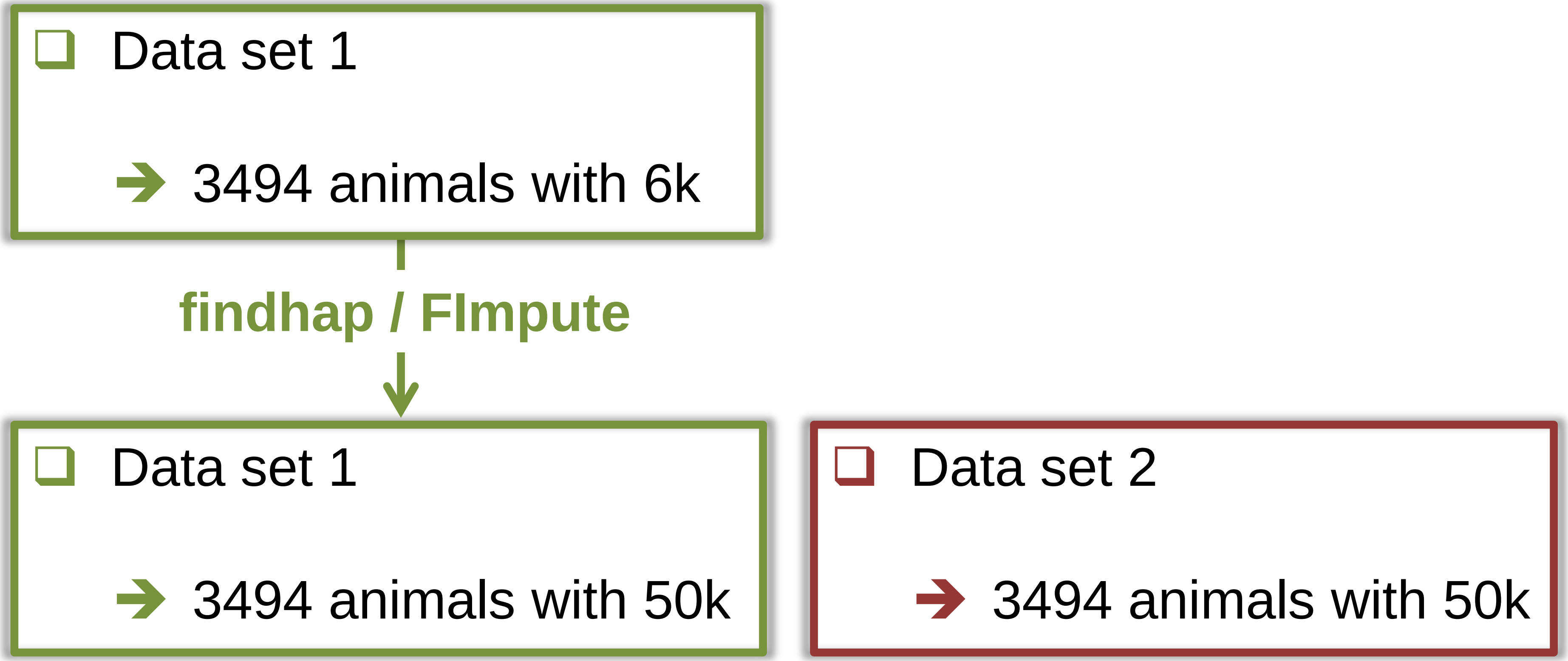
□ Data set 1

→ 3494 animals with 6k

□ Data set 2

→ 3494 animals with 50k

Material and Methods



- □ Data set 1

  → 3494 animals with 6k

findhap / FImpute

- □ Data set 1

  → 3494 animals with 50k

- □ Data set 2

  → 3494 animals with 50k

→ Prediction of GEBV for 37 traits

→ Comparison between GEBV from observed 50k with GEBV from imputed 50k

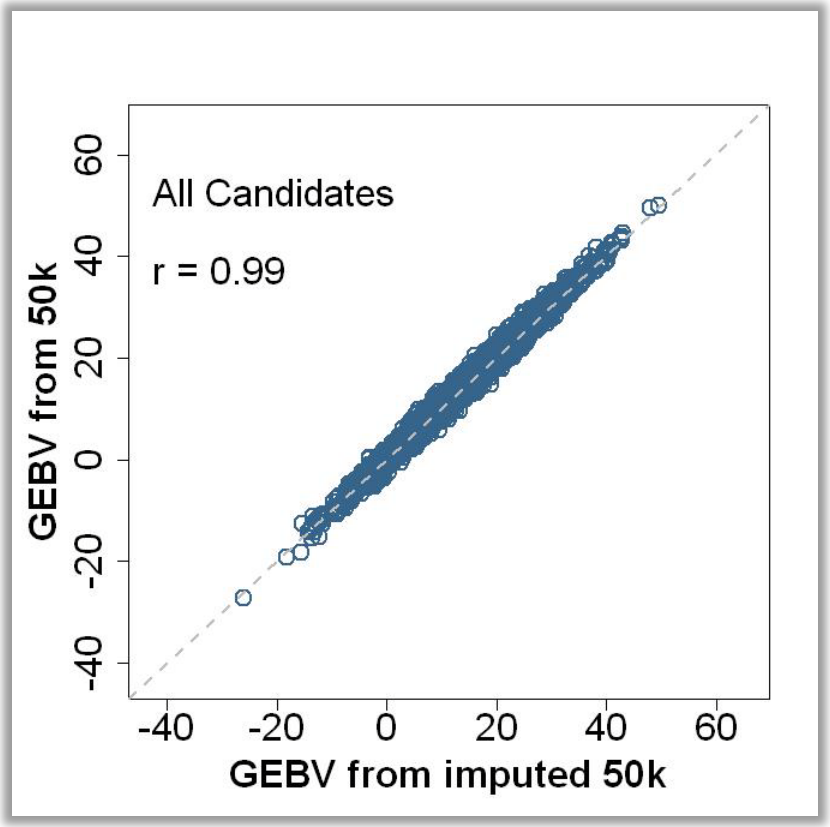
LfL Tierzucht

Changes in ranking within TOP 50 candidates

Trait	Rank correlation		Also top 50 in imputed set	
	findhap	FImpute	findhap	FImpute
Milk (kg)	0.82	0.90	42	44
Fat (kg)	0.90	0.91	42	46
Protein (kg)	0.82	0.91	42	43
SCS	0.79	0.87	43	41
Workability	0.71	0.88	40	44
Udder depth	0.89	0.89	42	40
Feet & legs	0.89	0.93	45	44
Udder	0.80	0.84	44	42
Overall score	0.86	0.89	44	43
Average (n=37)	**0.84**	**0.88**	**44**	**43**

Impact of Imputation errors on GEBV

Protein (kg) / FImpute



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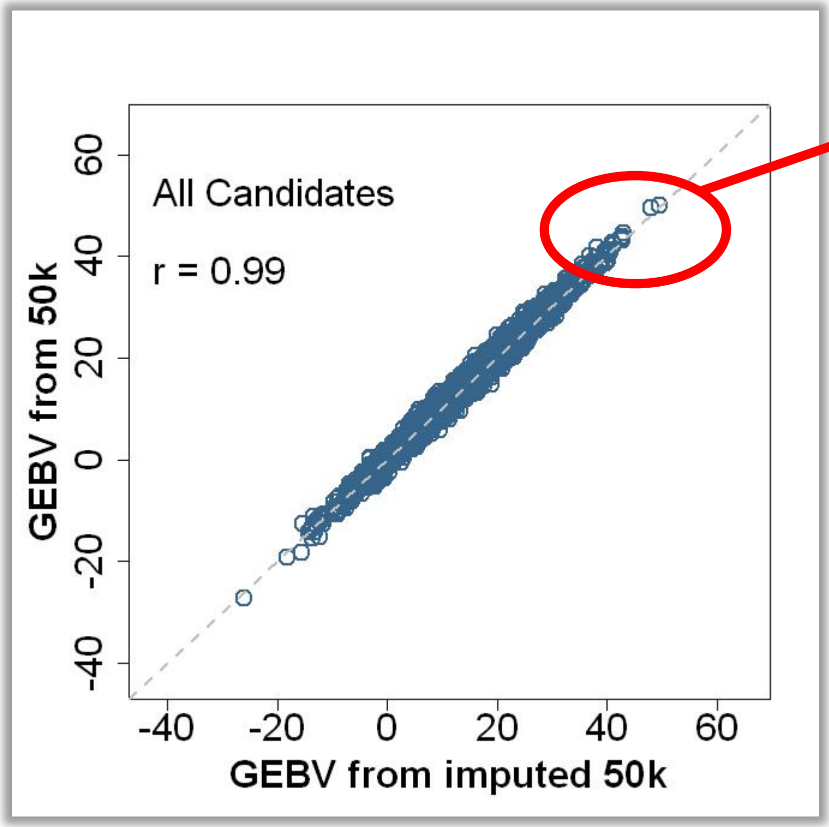

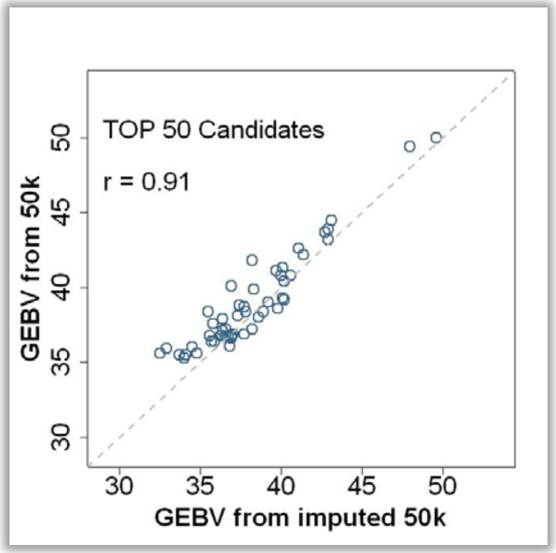

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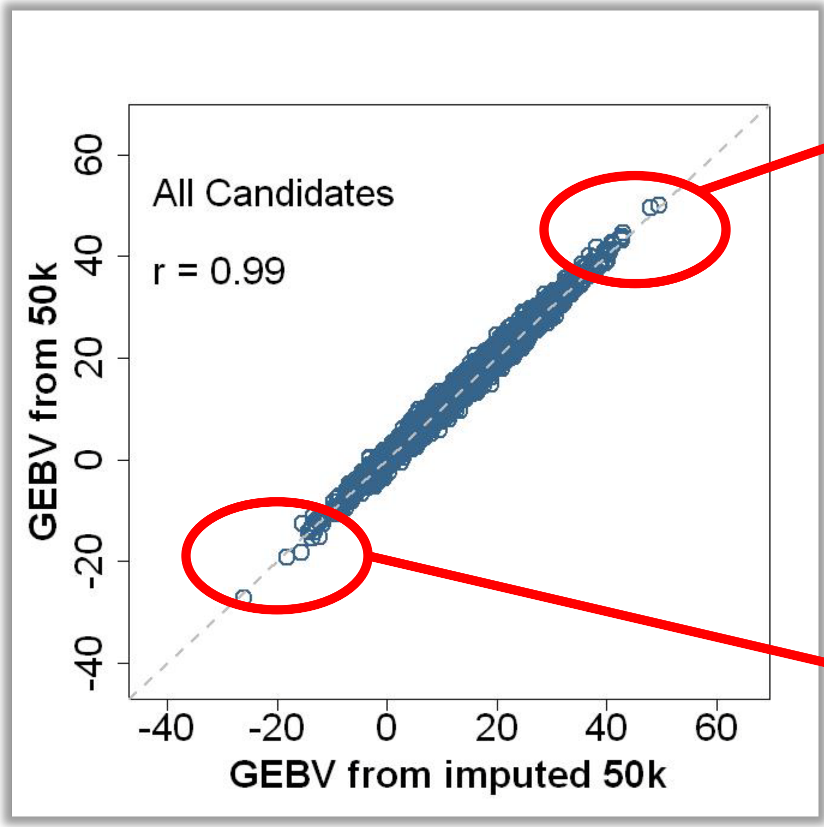

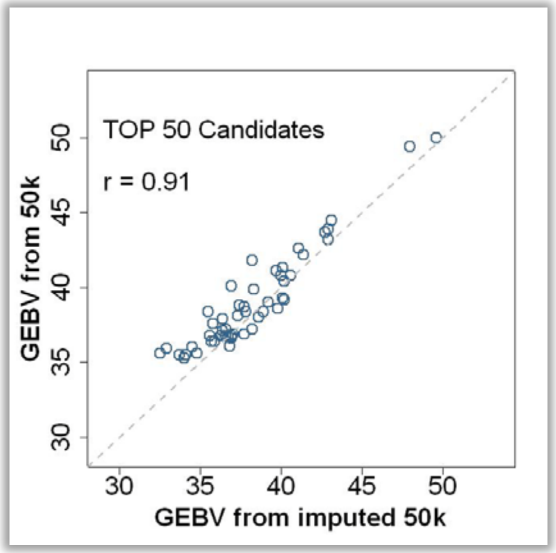

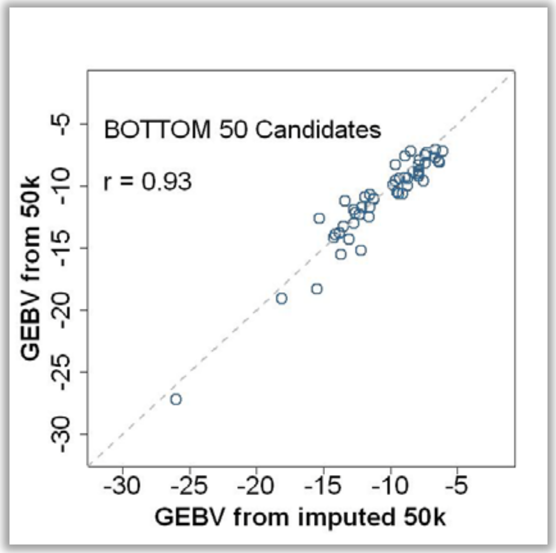

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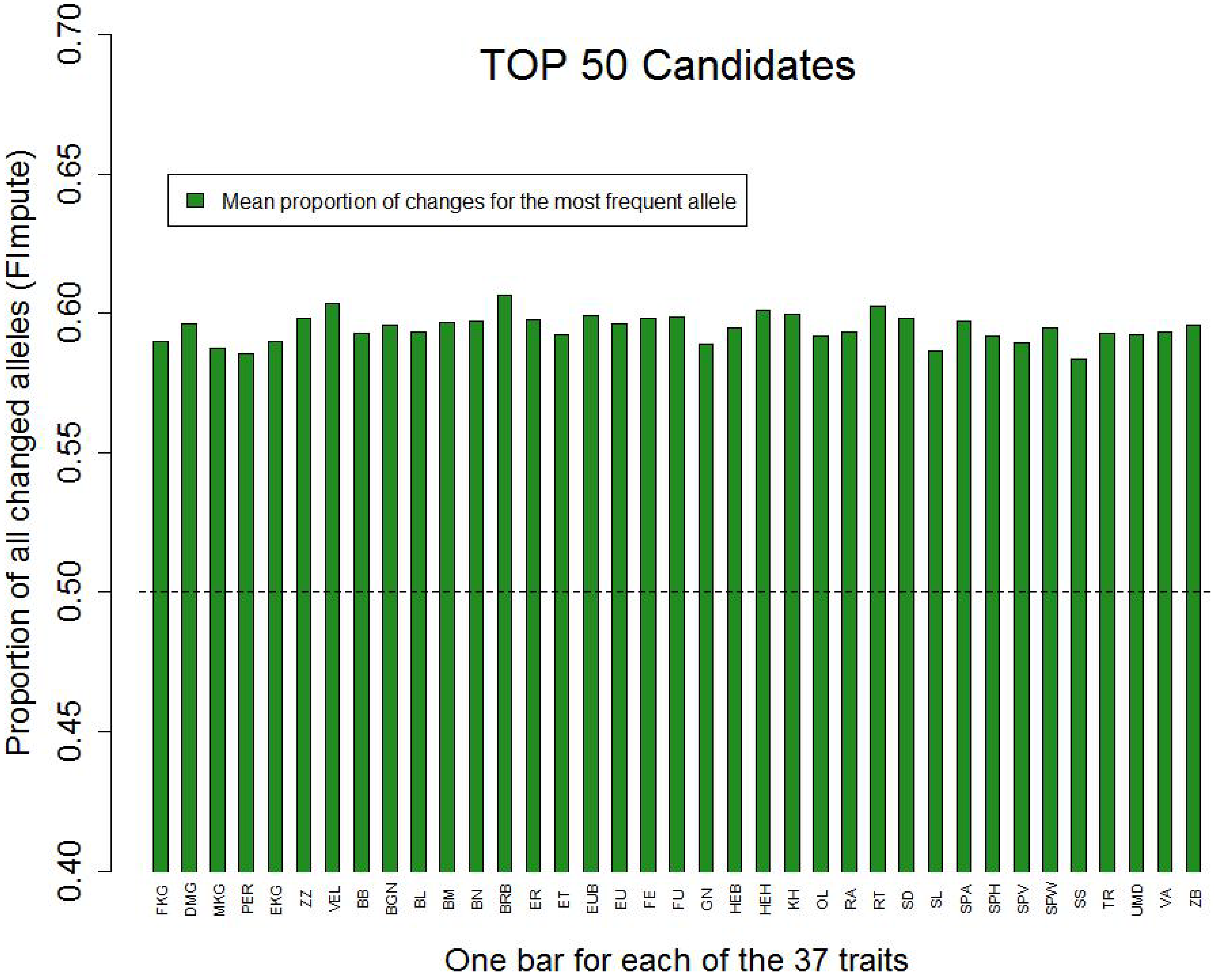

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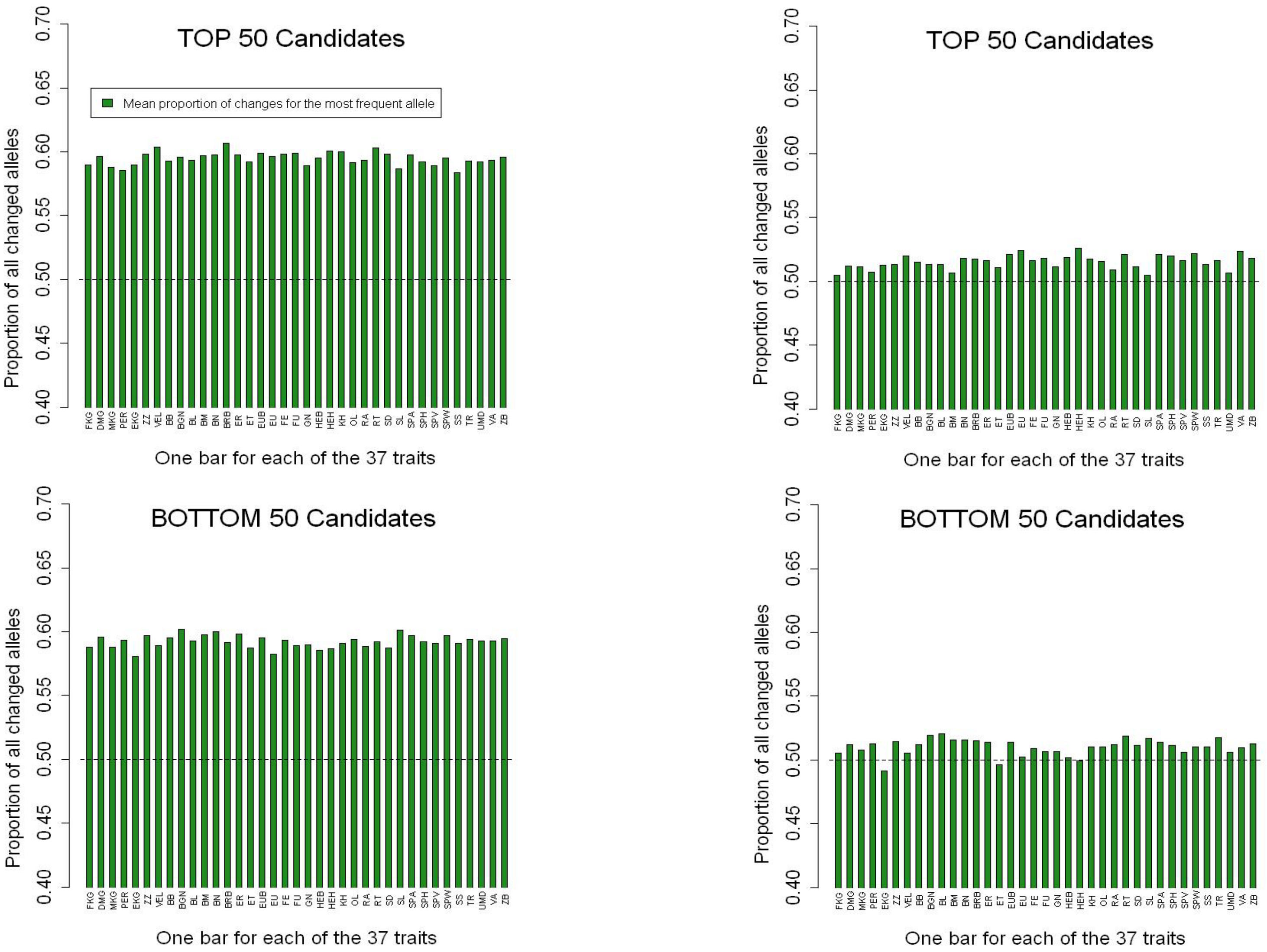
FImpute | findhap



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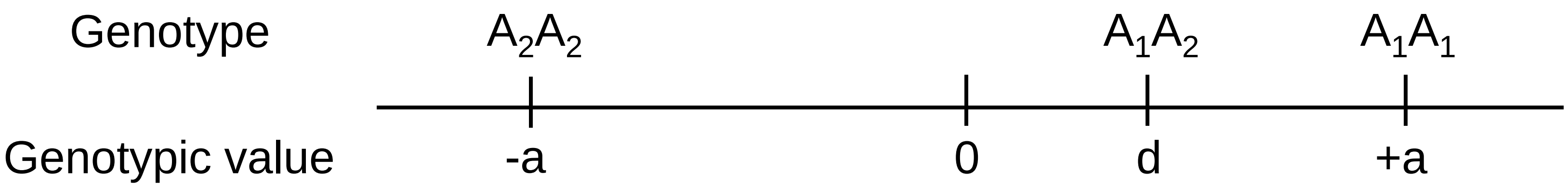

Genotype	A_2A_2		A_1A_2	A_1A_1
Genotypic value	-a	0	d	+a

Assuming Hardy-Weinberg equilibrium:

$$\begin{cases} f(A_1A_1) = p^2 \\ f(A_1A_2) = 2pq \\ f(A_2A_2) = q^2 \end{cases}$$

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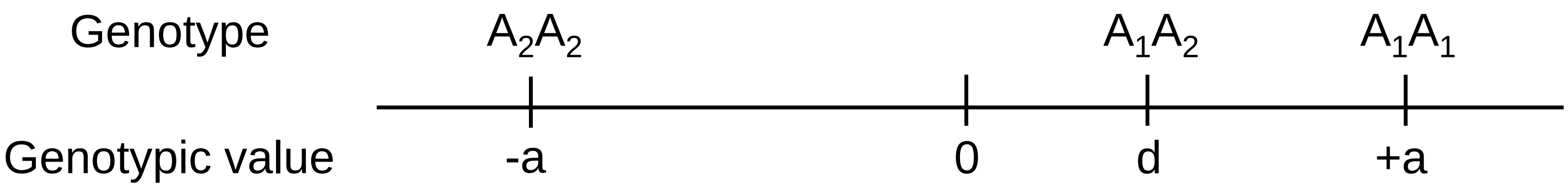

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Population mean: $M = a(p - q) + 2pqd$

*Average effect of A_1: $\alpha_1 = q[a + d(q - p)]$

*Average effect of A_2: $\alpha_2 = -p[a + d(q - p)]$

*as deviation from the population mean

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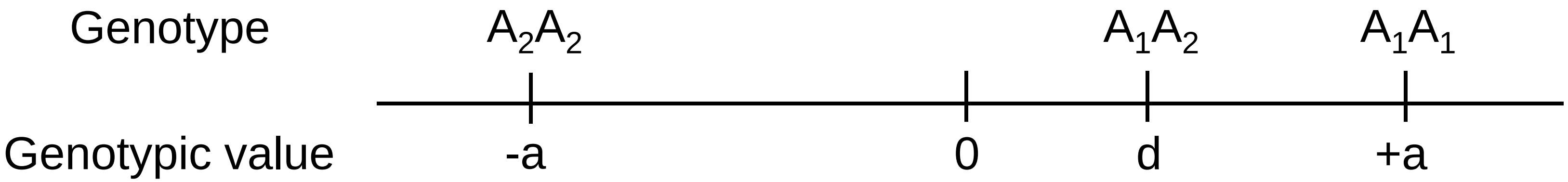

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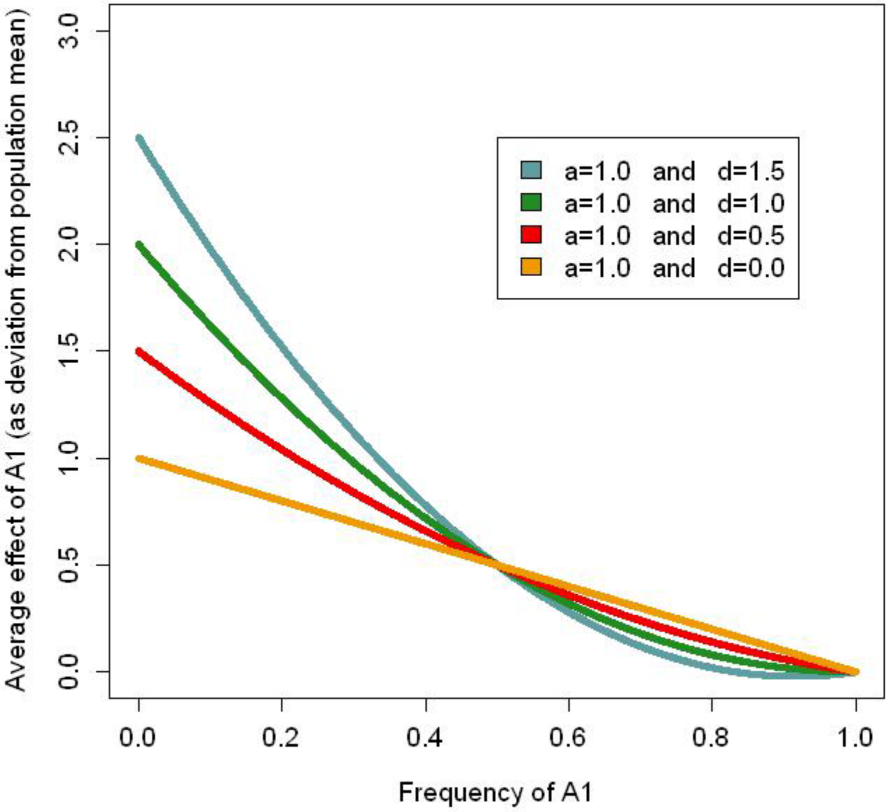

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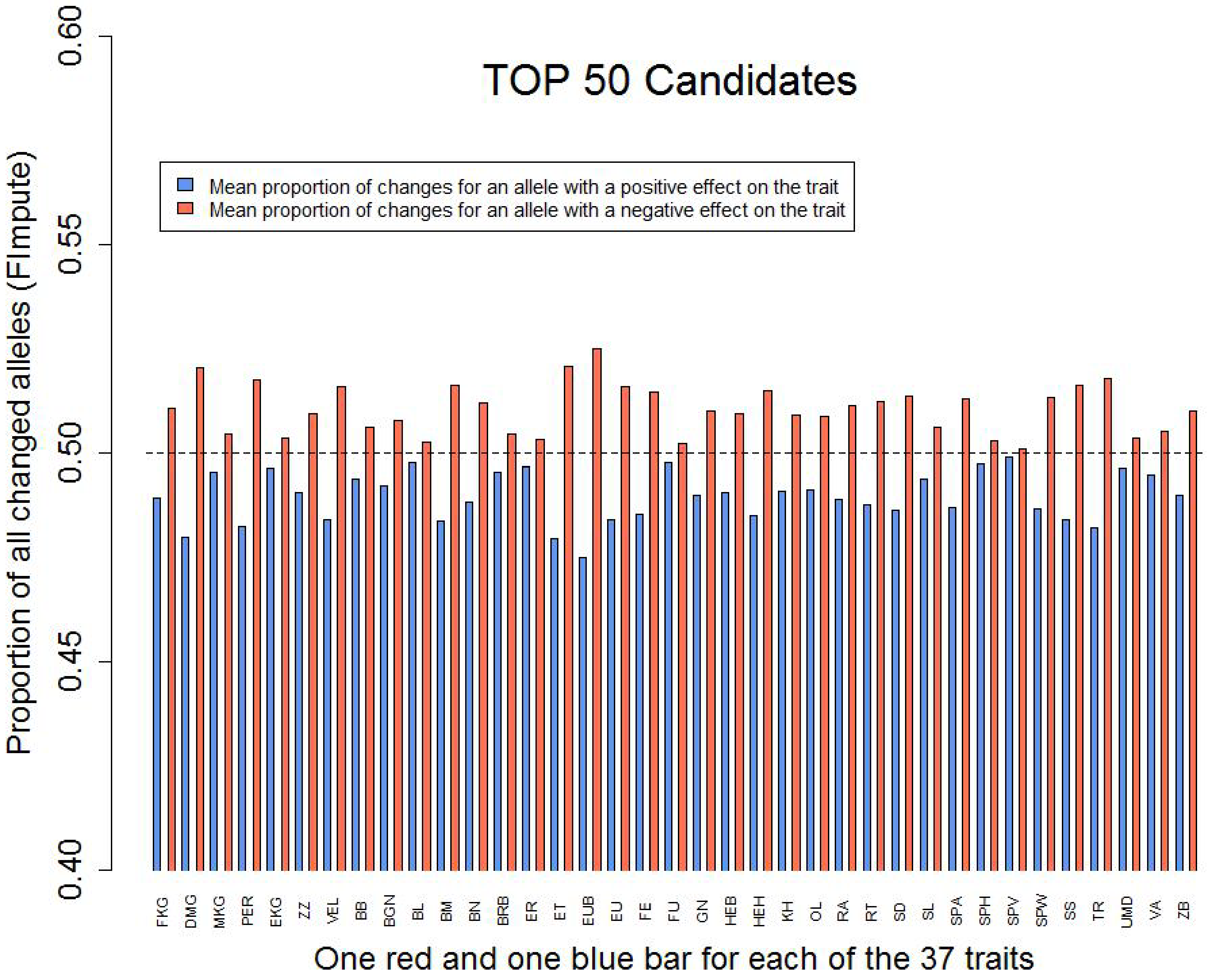

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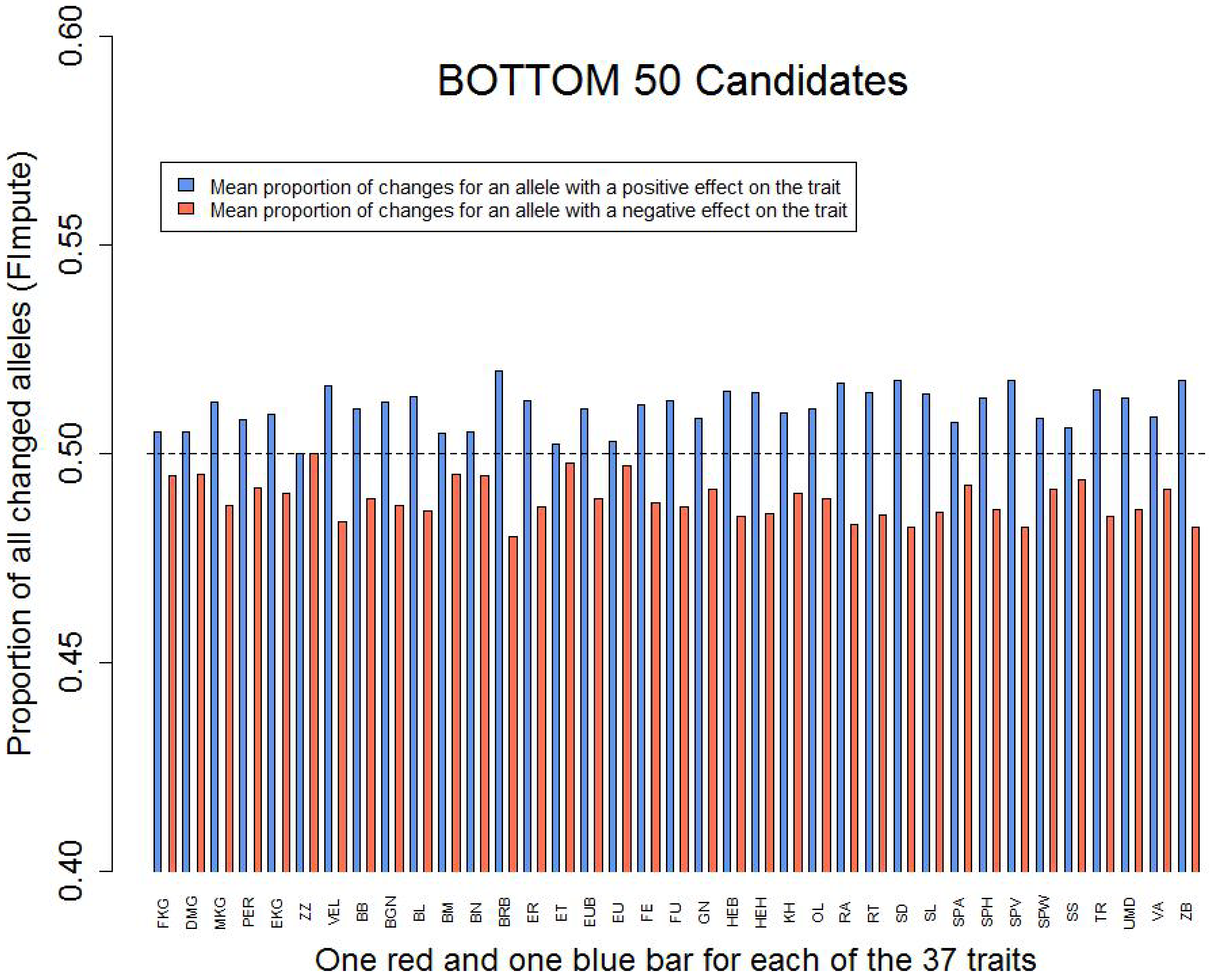

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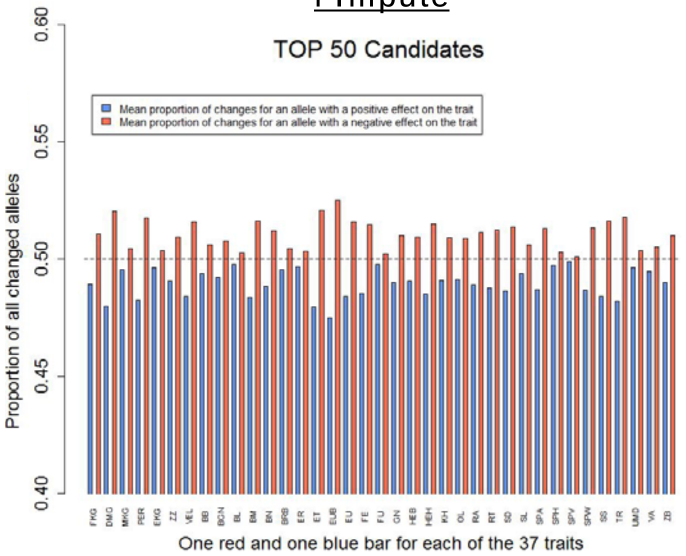
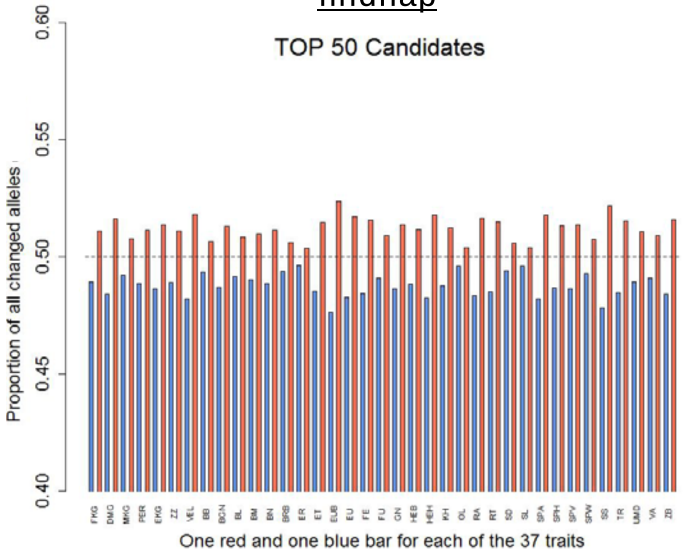
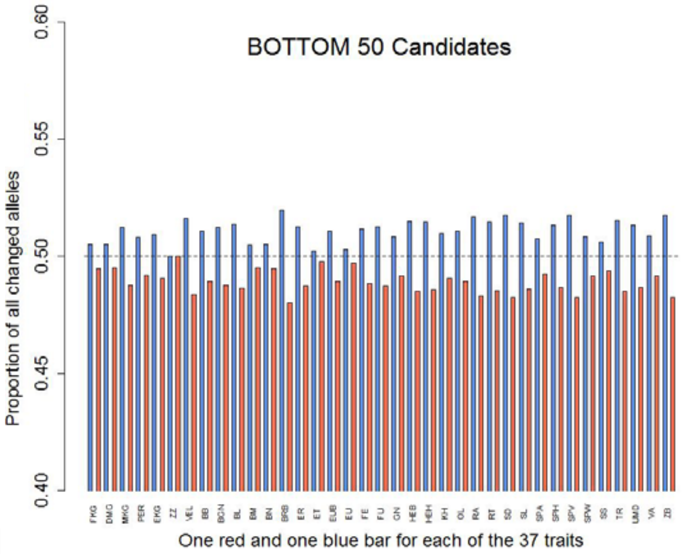
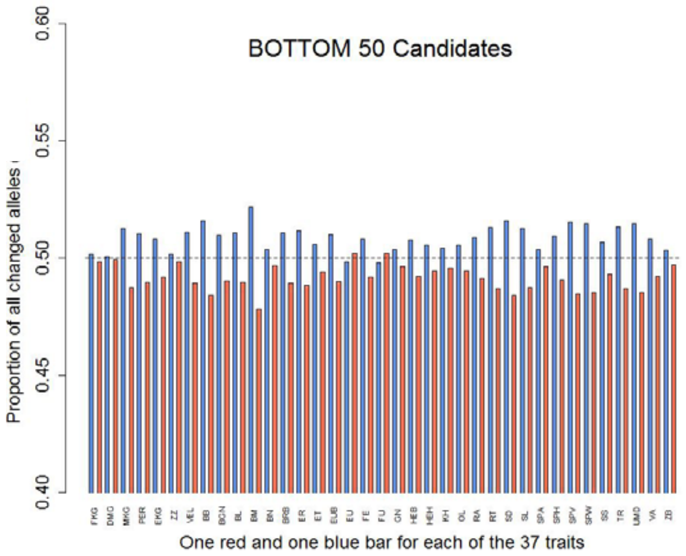
FImpute



findhap







Conclusions

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❑ Bias in GEBV due to imputation errors

➔ downwards in top and upwards in bottom segment

❑ Imputation algorithms usually suggest haplotypes with higher frequency and more neutral effects

➔ disadvantage for top and advantage for bottom animals

❑ Might have implications, especially for mixed pools of candidates genotyped at different densities

Aknowledgements

- Paul VanRaden (findhap)
- Mehdi Sargolzaei (FImpute)
- intergenomics

Thanks!

LfL
Tierzucht