Bavarian State Research Center
for Agriculture

Strategic genotyping of cow groups to improve reliability of genomic predictions

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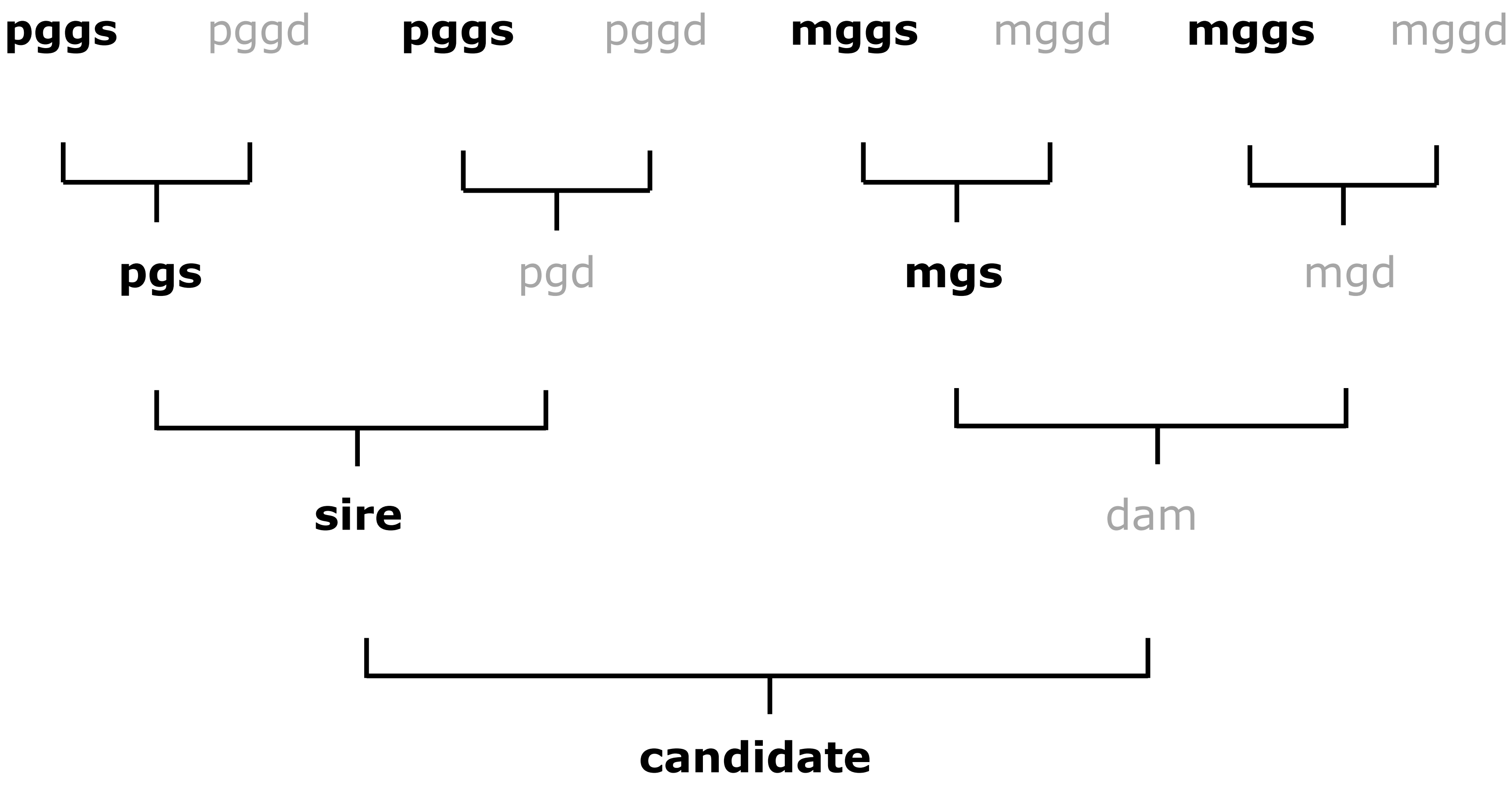
Preliminary study: Leading question

- ☐ Routinely genotyping a random sample of the female offspring of each AI bull and …
- ☐ including the genotypes and phenotypes into the reference population:
- ☐ What is the benefit with respect to the accuracy of selection of a young bull?

Deterministic approach on ‚nuclear pedigrees'

Nuclear pedigree (nucped):

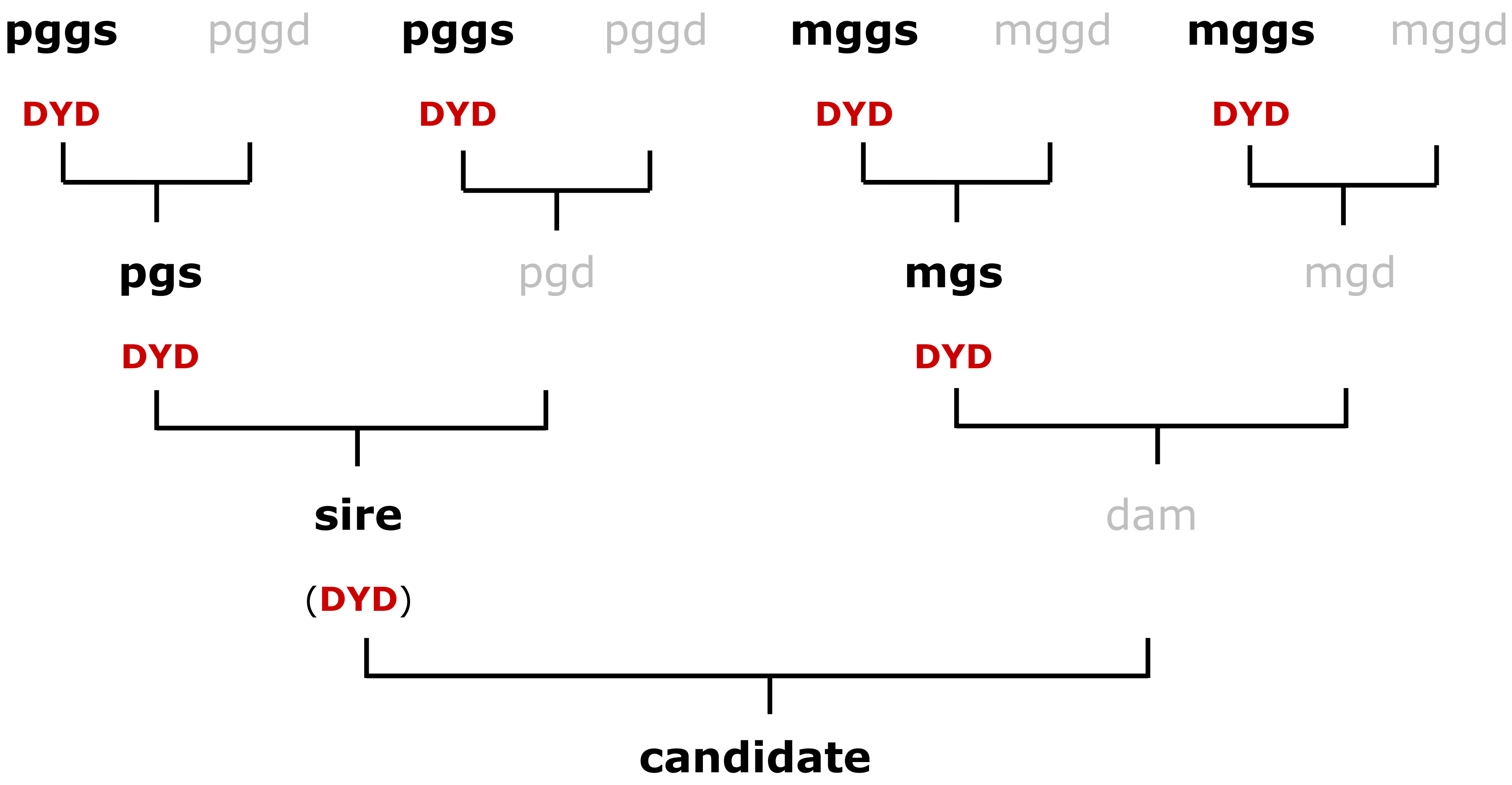


Methods

- From several thousand nucpeds identified in FV database:
  - Randomly selected 100
- Step 1: With extracted genotypes from data-base
  - Calculated ‘mini‘ G-matrix for each nucped
  - Made assumptions about information content of DYD
  - Solved for model reliability of the candidate
  - Averaged over 100 nucpeds: R^2 of base design (R^2_b)

Deterministic approach on ‚nuclear pedigrees‘

Base design:



pggs pggd **pggs** pggd **mggs** mggd **mggs** mggd

DYD **DYD** **DYD** **DYD**

pgs pgd **mgs** mgd

DYD **DYD**

sire dam

(**DYD**)

candidate

Methods

☐ Step 2: Generation of daughter genotypes (S/GS/GGS)

  - ✓ Sampling paternal haplotypes from sires‘s haplotypes
  - ✓ Sampling maternal haplotypes from haplotype library

- Calculated extended G-matrix
- Made assumptions about number of daughters now gt/pt (adjusted ‚residual‘ DYD)
- Solved for model reliability of the candidate
- Averaged over 100 nucpeds: R^2 of extended design (R^2_e)

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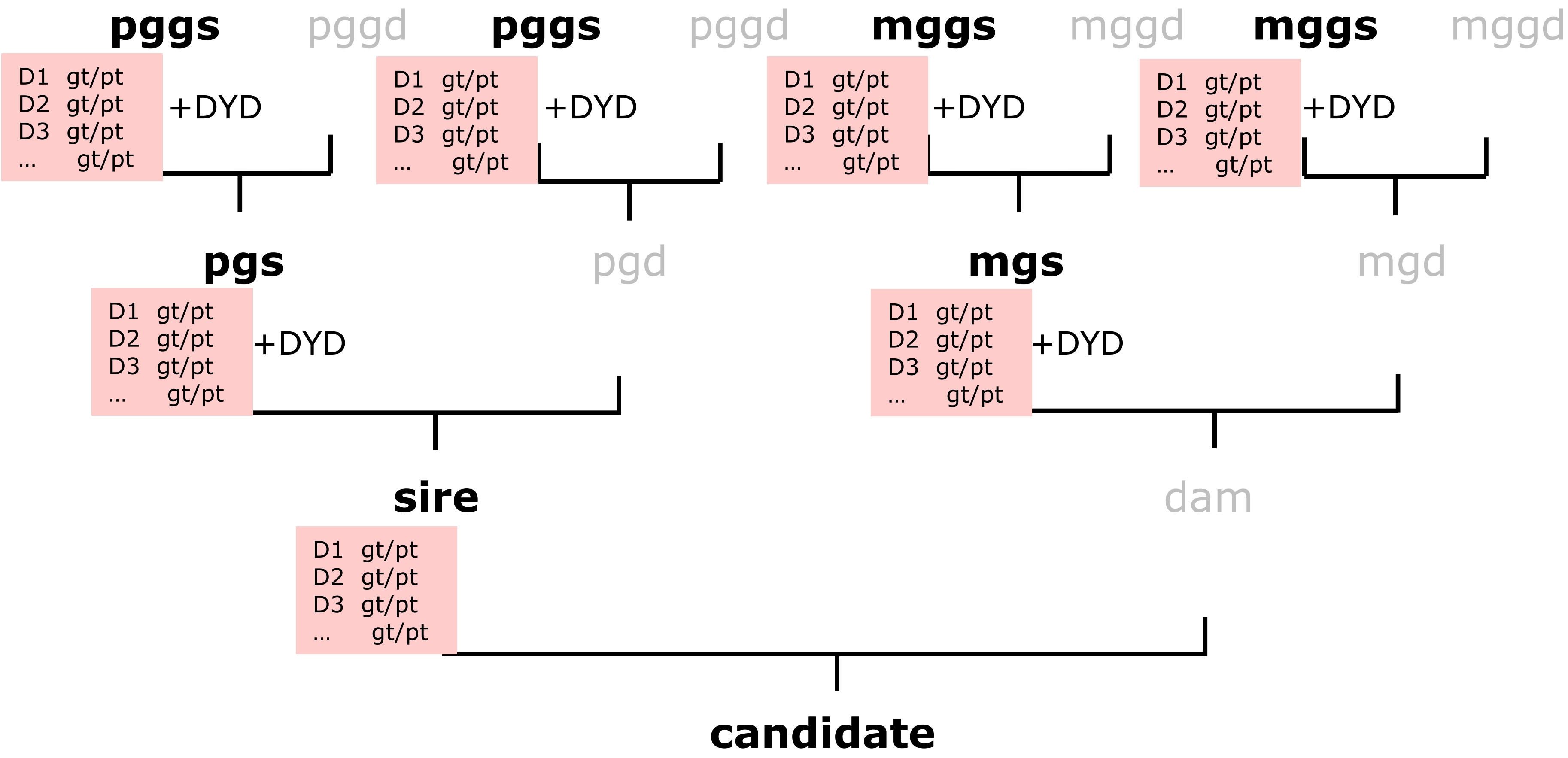
Deterministic approach on ‚nuclear pedigrees‘

Extended design:



pggs pggd **pggs** pggd **mggs** mggd **mggs** mggd

D1 gt/pt
D2 gt/pt
D3 gt/pt
… gt/pt
+DYD

D1 gt/pt
D2 gt/pt
D3 gt/pt
… gt/pt
+DYD

D1 gt/pt
D2 gt/pt
D3 gt/pt
… gt/pt
+DYD

D1 gt/pt
D2 gt/pt
D3 gt/pt
… gt/pt
+DYD

pgs pgd **mgs** mgd

D1 gt/pt
D2 gt/pt
D3 gt/pt
… gt/pt
+DYD

D1 gt/pt
D2 gt/pt
D3 gt/pt
… gt/pt
+DYD

sire dam

D1 gt/pt
D2 gt/pt
D3 gt/pt
… gt/pt

candidate

Methods

- Calculating of the marginal reliability contribution:

$$R_m^2 = \frac{R_e^2 - R_b^2}{R_e^2 R_b^2 + 1 - 2R_b^2}$$

(Harris & Johnson, 1998)

- Makes reliability contribution independent of level of base R^2

- Simplifies comparability of R^2 contributions

Designs investigated

			gs/ggs generation		**sire generation**	
Design	**scenario**	**h^2**	**nDau**	**nGeno**	**snDau**	**snGeno**
D_P	S	.35	1000	0	50/100/200/500	50/100/200/500
	S-GS-GGS	.35	1000	50/100/200/500	50/100/200/500	50/100/200/500
	GS-GGS	.35	1000	50/100/200/500	0	0
D_F	like **D_P** except h^2 = .05					
D_{CM}	S	.25	200	0	50/100	50/100
	S-GS-GGS	.25	200	50/100	50/100	50/100
	GS-GGS	.25	200	50/100	0	0
D_{CL}	like **D_{CM}** except h^2 = .10					

D_P: production trait design **D_F**: fitness trait design

D_{CM}: conformation trait design (moderate h^2)

D_{CL}: conformation trait design (low h^2)

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	S-GS-GGS	.35	1000	50/100/200/500	50/100/200/500	50/100/200/500
	GS-GGS	.35	1000	50/100/200/500	0	0
D_F						
D_{CM}	S					0/100
	S-GS-GGS					0/100
	GS-GGS					
D_{CL}	like **D_{CM}** except h^2 = .10					

All comparrissons were drawn extended design vs. corresponding base design

D_P: production trait design **D_F**: fitness trait design

D_{CM}: conformation trait design (moderate h^2)

D_{CL}: conformation trait design (low h^2)

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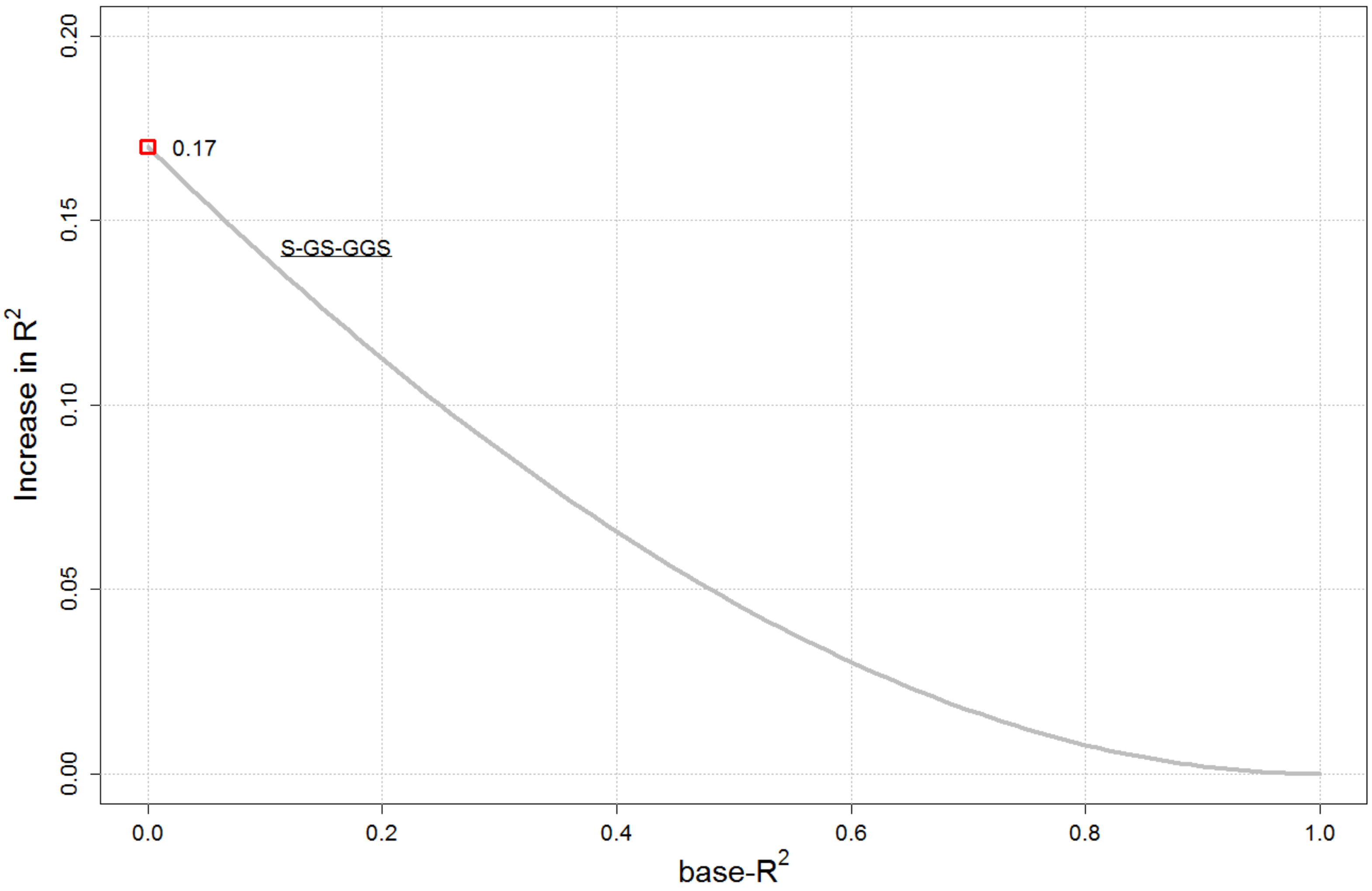
Results

Example for the effect of adding marginal R^2: design D_P with 100 daughters genotyped



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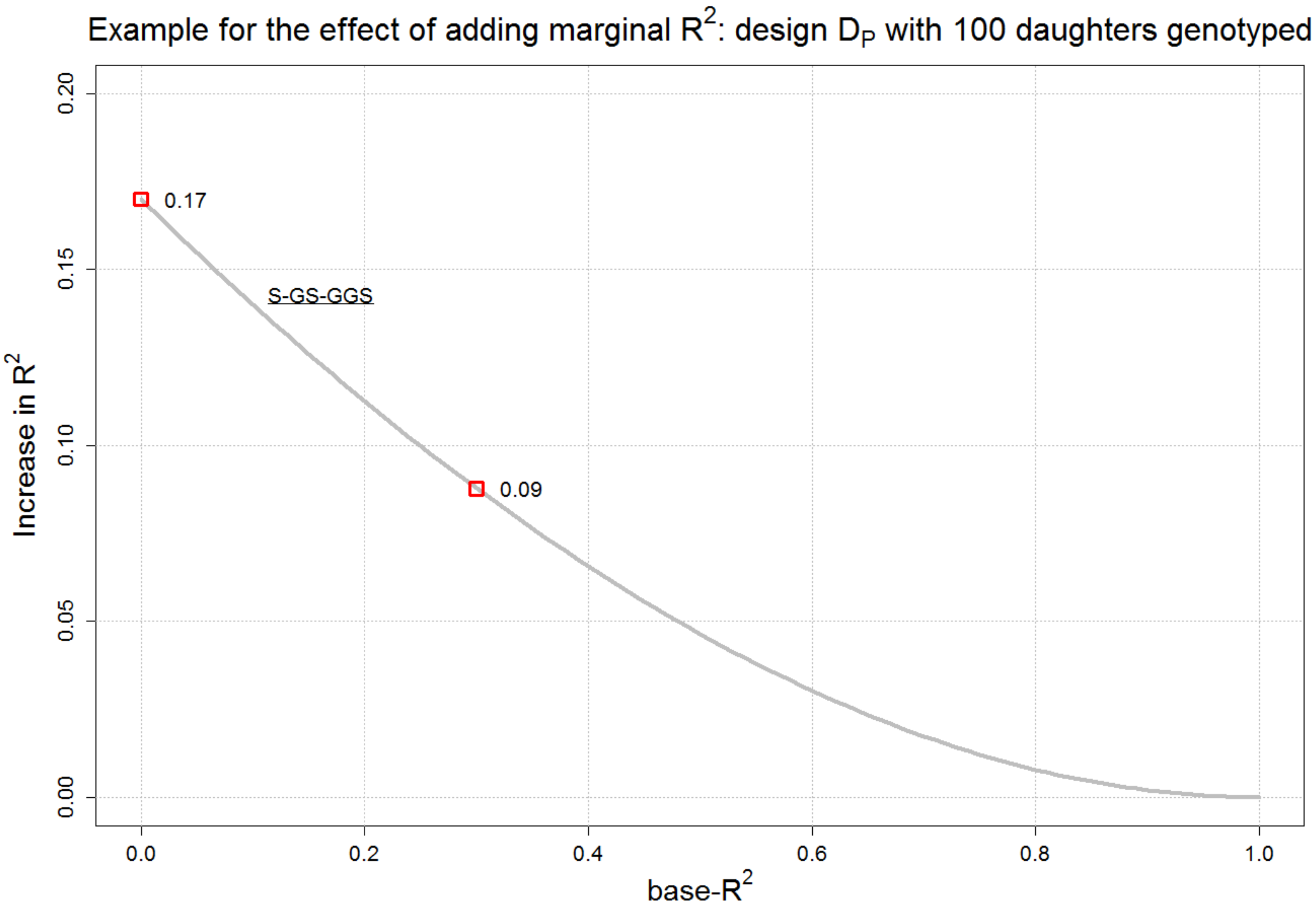
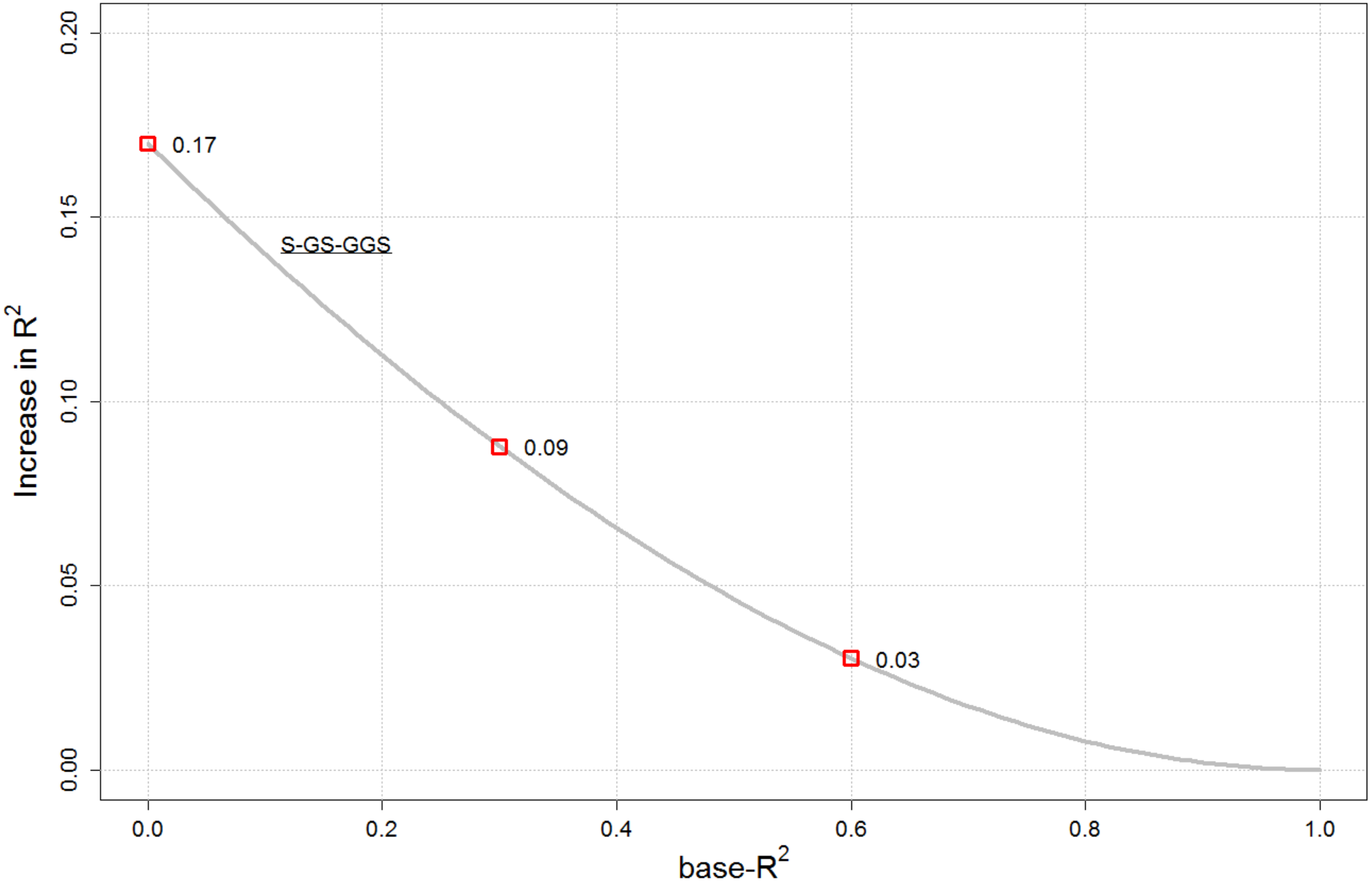
Results


Example for the effect of adding marginal R²: design D_P with 100 daughters genotyped
Increase in R²
0.00
0.05
0.10
0.15
0.20
base-R²
0.0
0.2
0.4
0.6
0.8
1.0
0.17
S-GS-GGS
0.09

Results

Example for the effect of adding marginal R^2: design D_P with 100 daughters genotyped



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Results

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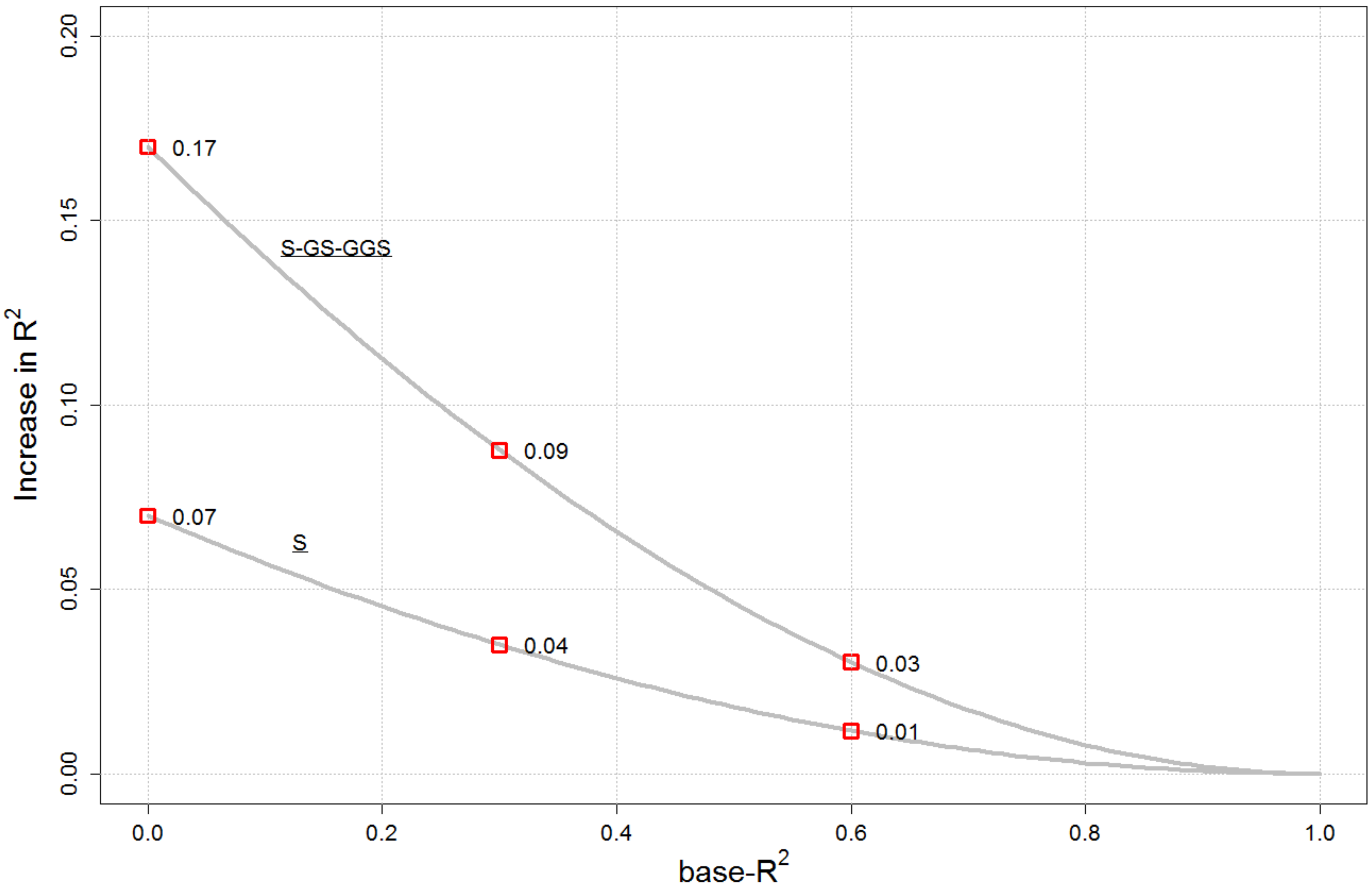

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Results

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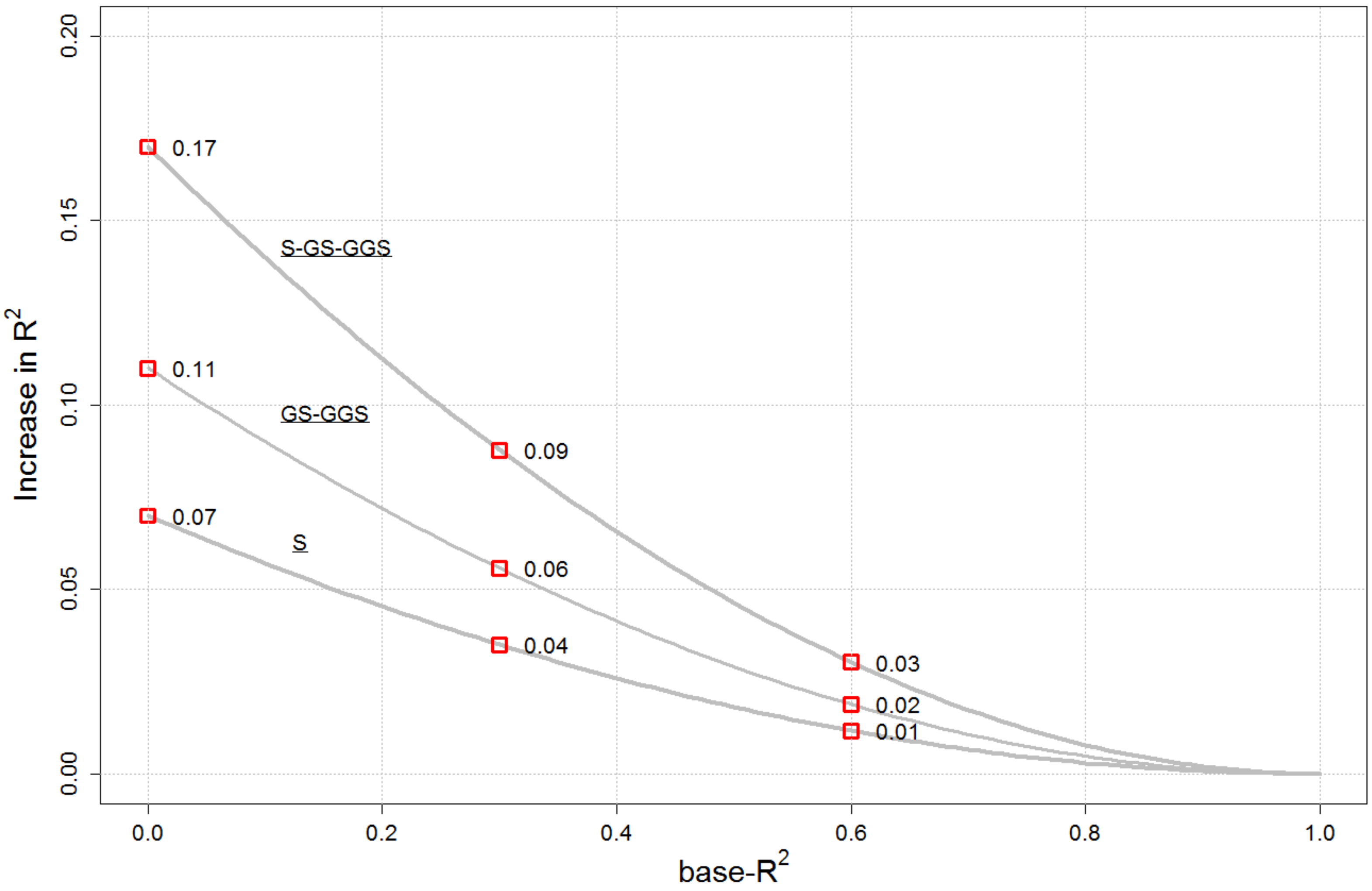

Results

		D_P (h^2 =.35)			D_F (h^2 =.05)	
	genotyped daughters for			**genotyped daughters for**		
nGeno	**S**	**S-GS-GGS**	**GS-GGS**	**S**	**S-GS-GGS**	**GS-GGS**
50	4 (0/9)	10 (5/24)	7 (4/15)	1 (0/2)	2 (1/4)	1 (1/2)
100	**7 (3/12)**	**17 (12/33)**	**11 (7/21)**	2 (0/4)	4 (2/7)	2 (1/5)
200	12 (7/27)	26 (17/38)	17 (11/27)	3 (1/6)	6 (4/9)	4 (2/6)
500	19 (12/28)	40 (28/55)	29 (19/43)	5 (3/9)	12 (7/17)	8 (5/14)

Results

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Results

	D_{CM} (h^2 = .25)			D_{CL} (h^2 = .10)		
nGeno	**S**	**S-GS-GGS**	**GS-GGS**	**S**	**S-GS-GGS**	**GS-GGS**
50	3 (0/11)	8 (2/18)	5 (3/15)	2 (0/5)	4 (1/7)	3 (1/7)
100	**6 (2/13)**	**12 (8/22)**	**9 (6/16)**	3 (1/7)	6 (3/10)	5 (3/9)

Results

	D_{CM} (h^2 = .25)			D_{CL} (h^2 = .10)		
nGeno	**S**	**S-GS-GGS**	**GS-GGS**	**S**	**S-GS-GGS**	**GS-GGS**
50	3 (0/11)	8 (2/18)	5 (3/15)	2 (0/5)	4 (1/7)	3 (1/7)
100	6 (2/13)	12 (8/22)	9 (6/16)	**3 (1/7)**	**6 (3/10)**	**5 (3/9)**

Conclusion

- Genotyping a random sample of daughters of every AI bull can increase the accuracy of selection of young bulls.

- The magnitude of the contribution is a function of
  - the number of meioses between the animals providing the information and the candidates
  - the heritability of the trait (e.g. Hayes et al., 2009)

Conclusion

- Considerable contributions will be achieved
  - with higher heritabilities
  - with a large amount of genotyped daughters
- Strategy lends itself to broad genotyping with lower densities
- But: The effective contribution does depend on the magnitude of reliability already achieved with the existing design
  - Small reference population or high N_e (e.g. Thomasen et al., 2014)

Outlook

- Aspects currently under investigation:
  - Impact on validation reliability in forward prediction
  - Cumulative effects in a population (→ R^2 from LD?)
  - Benefits in other paths of selection
  - Increased relative importance in scenarios with strong selection (→ selection within families)
  - Potential surplus: bias-control

Outlook

- Aspects currently under investigation:
  - Impact on validation reliability in forward prediction
  - Cumulative effects in a population (→ R^2 from LD?)
  - Benefits in other paths of selection
  - **Increased relative importance in scenarios with strong selection (→ selection within families)**
  - Potential surplus: bias-control

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Thank you for your attention

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