

Accuracy of genomic prediction in a commercial perennial ryegrass breeding program.

Dario Fè *, Bilal H. Ashraf, Morten G. Pedersen, Luc Janss, Stephen Byrne,
Niels Roulund, Ingo Lenk, Thomas Didion, Torben Asp, Christian S. Jensen,
Just Jensen

Number of figures: 2

Number of tables: 1

Supplemental Figure captions

Supplemental Figure S1. Construction of the design matrices for PPs.

F_{2_j} = F_2 families; SYN_j = synthetic families; PP_i = parent populations.

Supplemental Figure S2. Off-diagonals within and between different sets.

Supplemental Tables

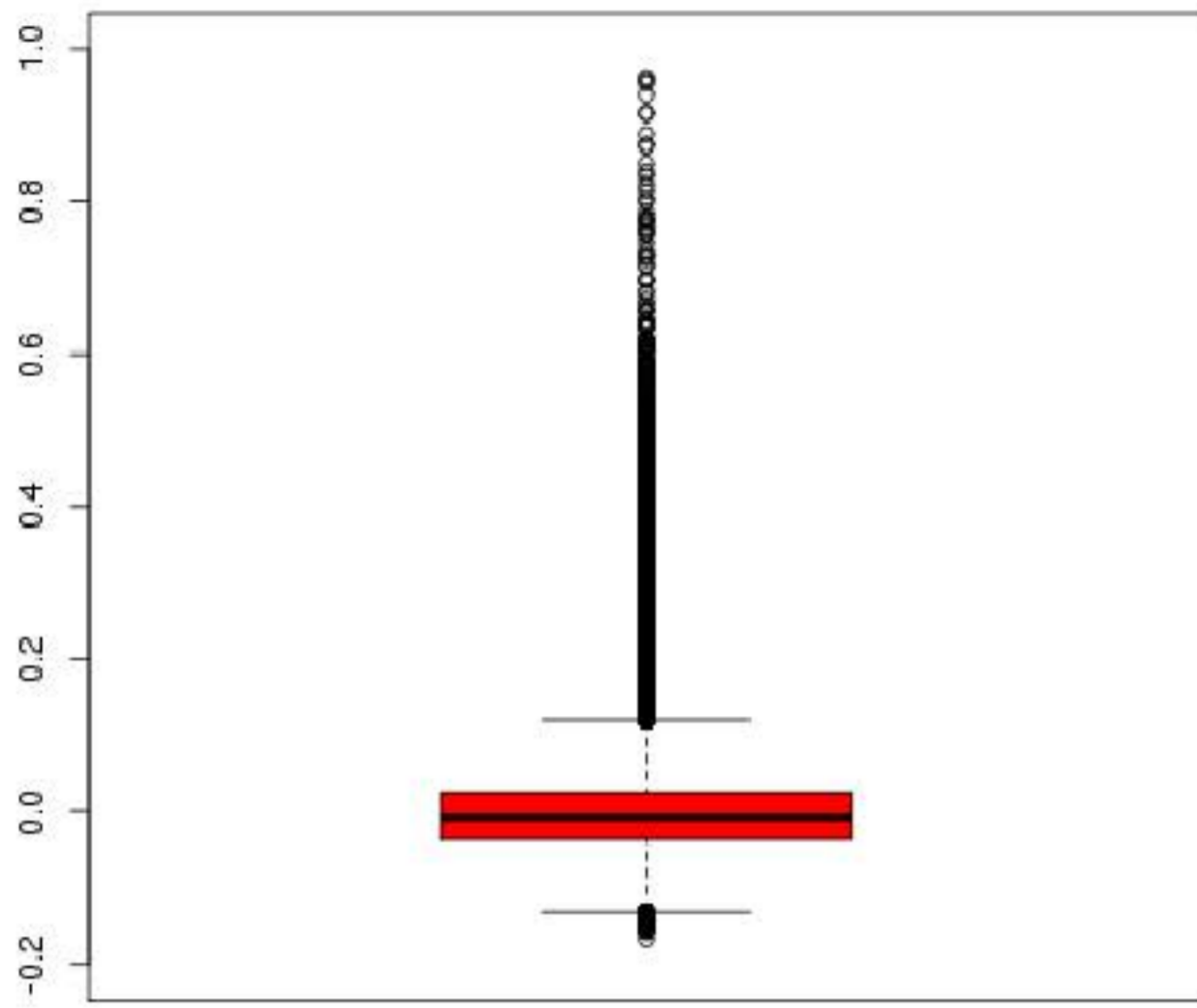
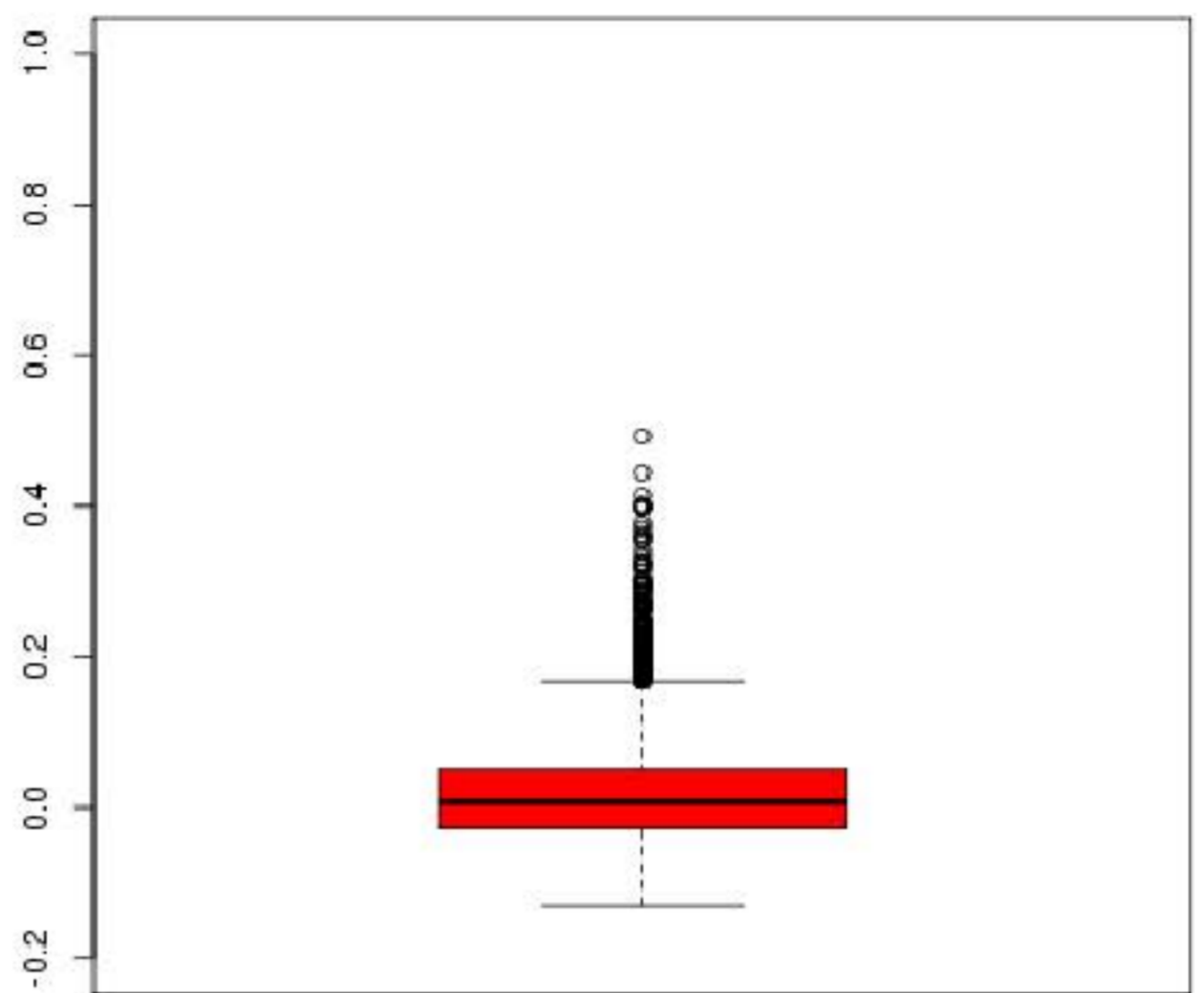
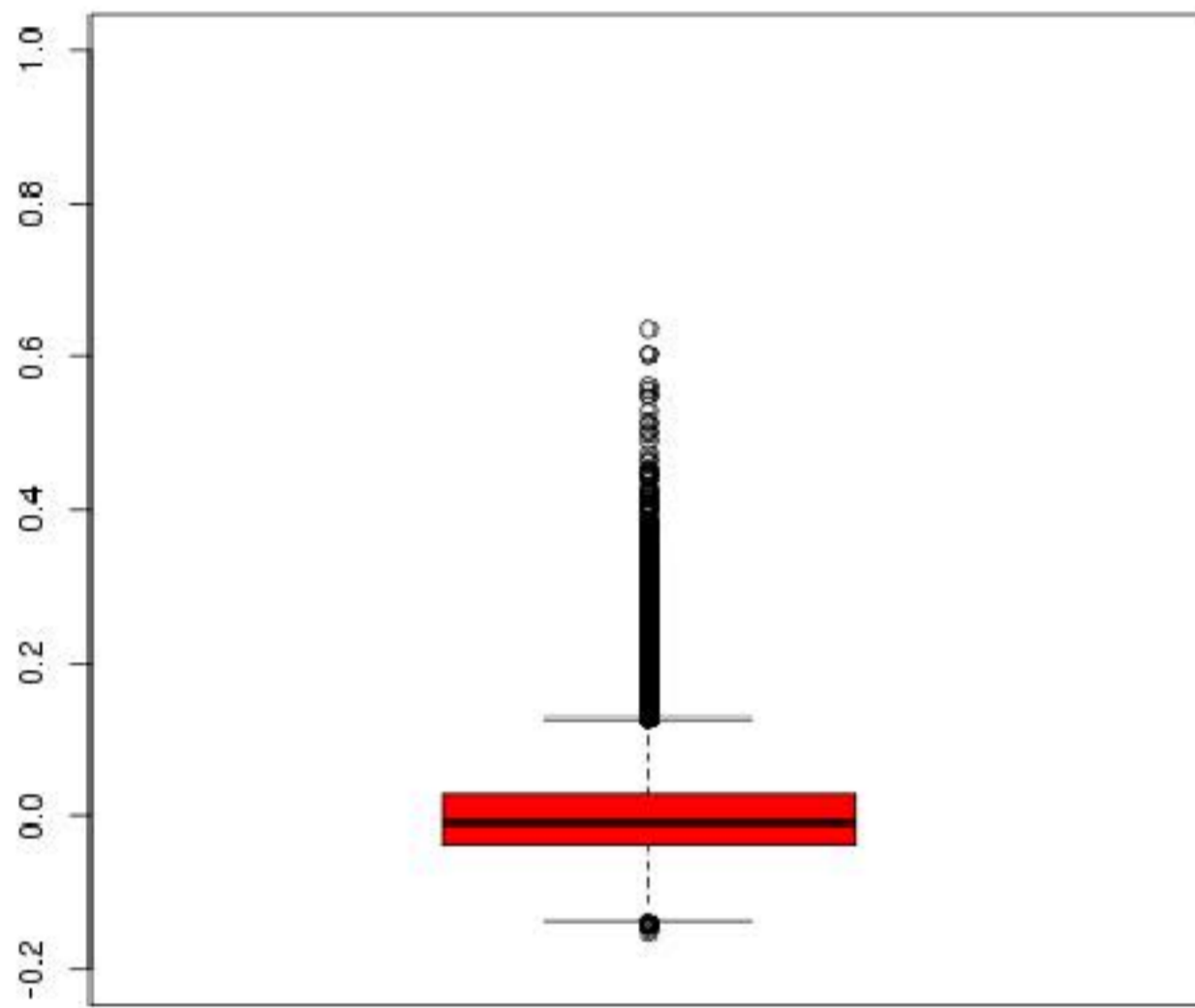
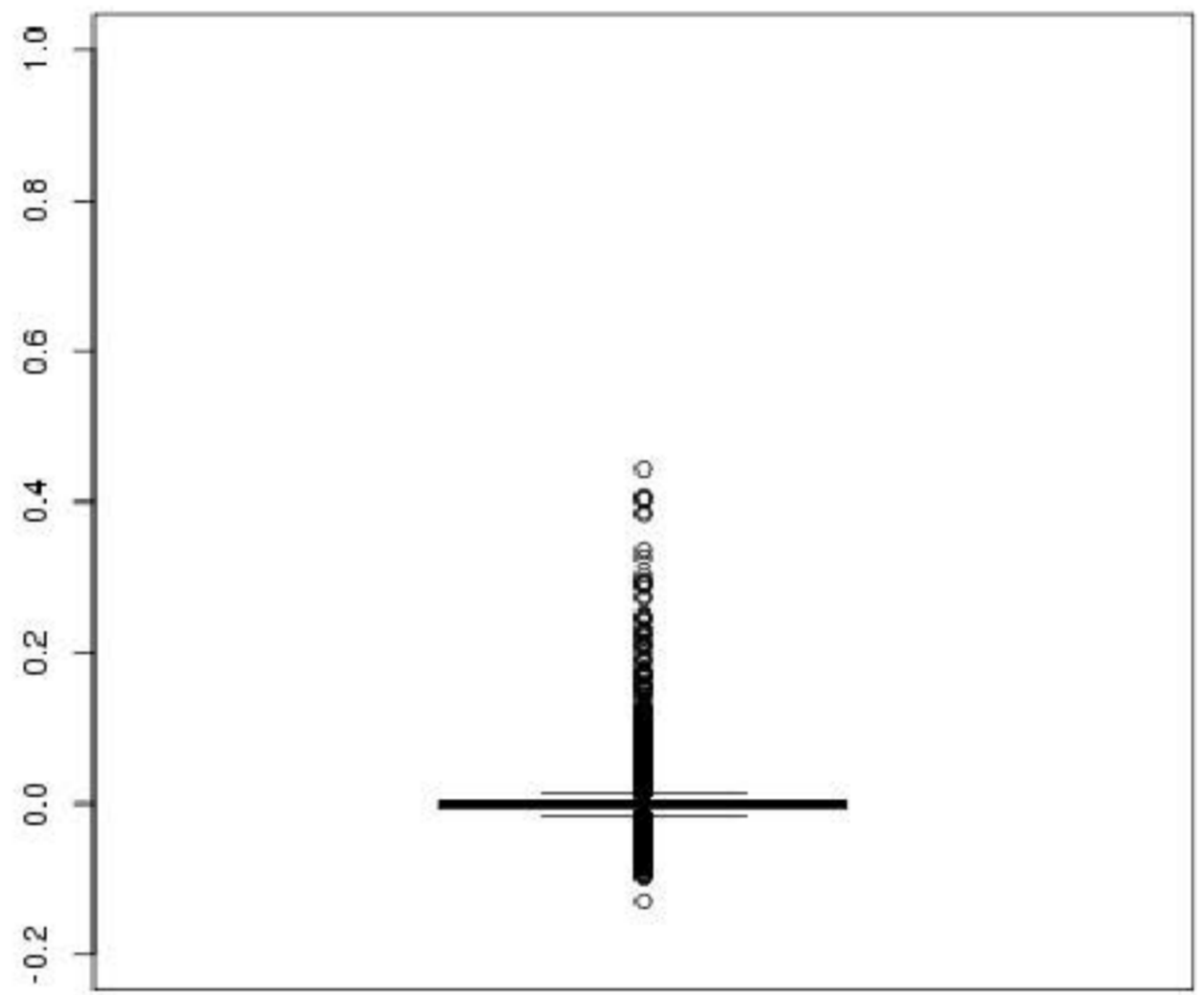
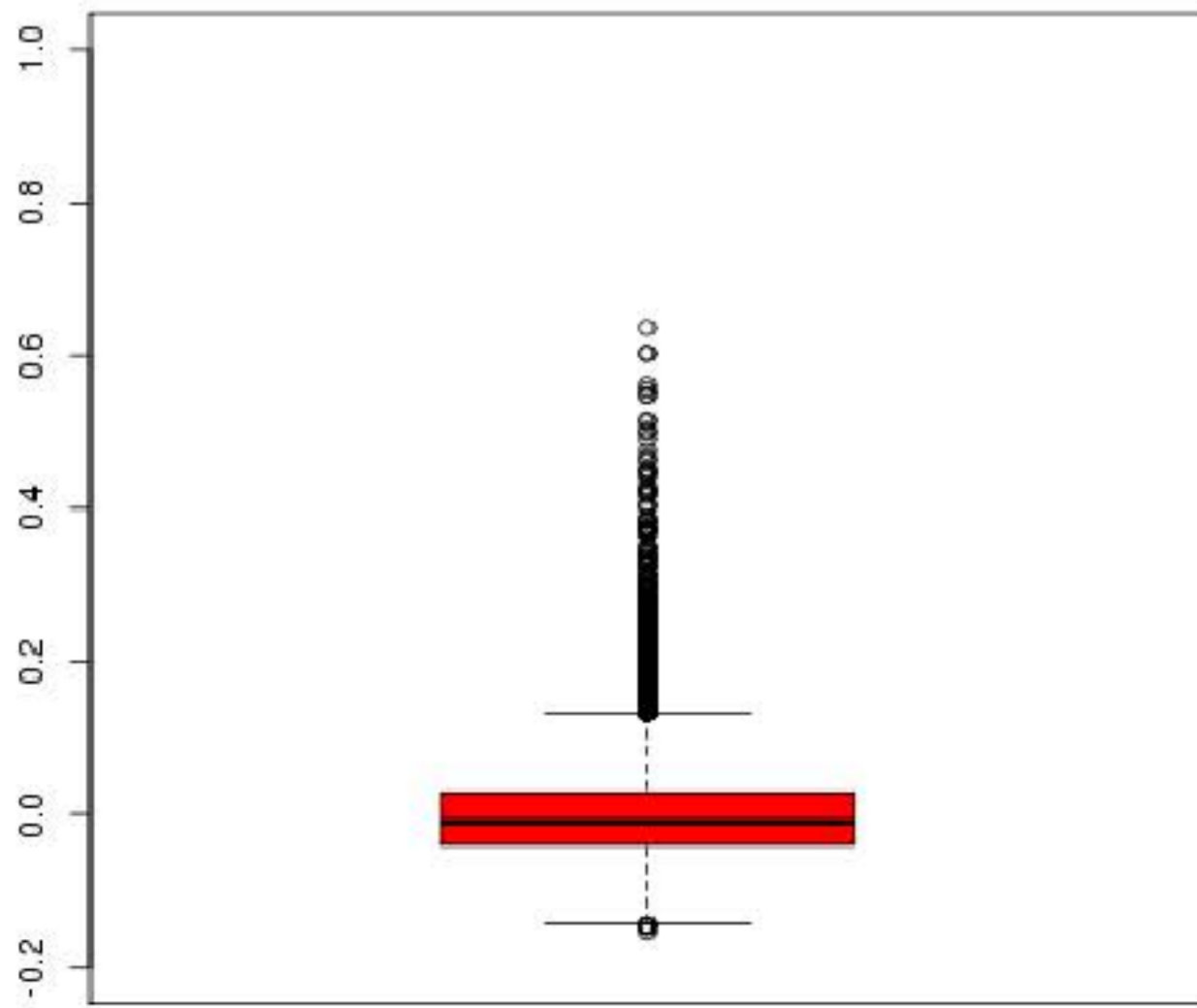
Supplemental Table S1. Variance components for all traits.

Variance components‡	Traits†				
	CRR	SY	TKW	NDF	FR
σ^2_i	0.4677	164.5786	0.0176	3.4771	1.9125
σ^2_p	0.0462	35.6401	0.0073	2.2594	0.3601
σ^2_{il}	0.1067				
σ^2_{ily}	0.0641	40.9365			
σ^2_{ply}	0.1175				
σ^2_{ilys}	0.2245				
σ^2_{plys}	0.0677				
σ^2_{pp}		26.8926			
σ^2_c		32.3697	0.0056	0.2544	0.1854
σ^2_{cs}	0.1109				
σ^2_o	0.2143				
σ^2_e	0.4944	176.7344	0.0229	4.6937	3.1902

†CRR = crown rust resistance; SY = seed yield; TKW = thousand kernel weight; NDF = neutral detergent fiber; FR = fructan.

‡ σ^2_i = additive genetic variance within PPs; σ^2_p = additive genetic variance among PPs; σ^2_{il} = G × location variance; σ^2_{ily} = G × location × year variance; σ^2_{ply} = G × location × year variance among PPs; σ^2_{ilys} = G × location × year × score variance; σ^2_{plys} = G × location × year × score variance among PPs; σ^2_{pp} = variance among PPs combinations; σ^2_c = variance among sub-trials within YLTs; σ^2_{cs} = variance among sub-trials within YLST; σ^2_o = environmental variance within plots and across scores; σ^2_e = residual variance.

	PP₁	PP₂	PP₃	...	PP_i
F_{2_1}	1	0	0	...	1
F_{2_2}	1	1	0	...	0
F_{2_3}	0	1	1	...	0
...
SYN₁	0.50	1	0.50	...	0
SYN₂	0.67	0	0.67	...	0.67
...

F2s**SYNs****F2s - SYNs****PPs****F2s - SYNs(a)****F2s - SYNs(b)**