

Genomic prediction in hybrid breeding: II. Reciprocal recurrent genomic selection with full-sib and half-sib families

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Supplementary Tables and Figures

Table S1: Survey for estimates of general combining ability (GCA, σ_{gca}^2) and specific combining ability (SCA, σ_{sca}^2) variances for hybrids of (partially-)autogamous species for important agronomic traits reported in the literature.

Species	Trait	σ_{gca}^2 †	σ_{sca}^2 ‡	τ	Source
Barley	Yield	0.36	0.04	10.0%	Philipp et al. (2016)
Rapeseed	Yield	546720	14833	2.7%	Hu et al. (2021)
Rice	Yield	0.430	0.347	43.0%	Beukert et al. (2017)
	Yield	14.81	11.79	44.3%	Gramaje et al. (2020)
	Plant height	0.61	8.44	93.3%	Gramaje et al. (2020)
Triticale	Yield	63.85	1.28	2.0%	Oettler et al. (2003)
	Plant height	58.23	0.07	1.2%	Oettler et al. (2003)
Wheat	Yield	0.058	0.028	32.6%	Longin et al. (2013)
	Plant height	17.86	1.16	6.1%	Longin et al. (2013)
	Heading date	2.05	0.05	2.4%	Longin et al. (2013)
	Yield	0.200	0.082	29.1%	Gowda et al. (2012)
	Yield	0.03	0.02	50.0%	Zhao et al. (2015)

† Sum of σ_{gcaF}^2 and σ_{gcaM}^2 if presented separately in the reference

‡ $\tau = 100\% \times \frac{\sigma_{sca}^2}{\sigma_{gcaF}^2 + \sigma_{gcaM}^2 + \sigma_{sca}^2}$ is the proportion of SCA variance in the total genetic variance among hybrids

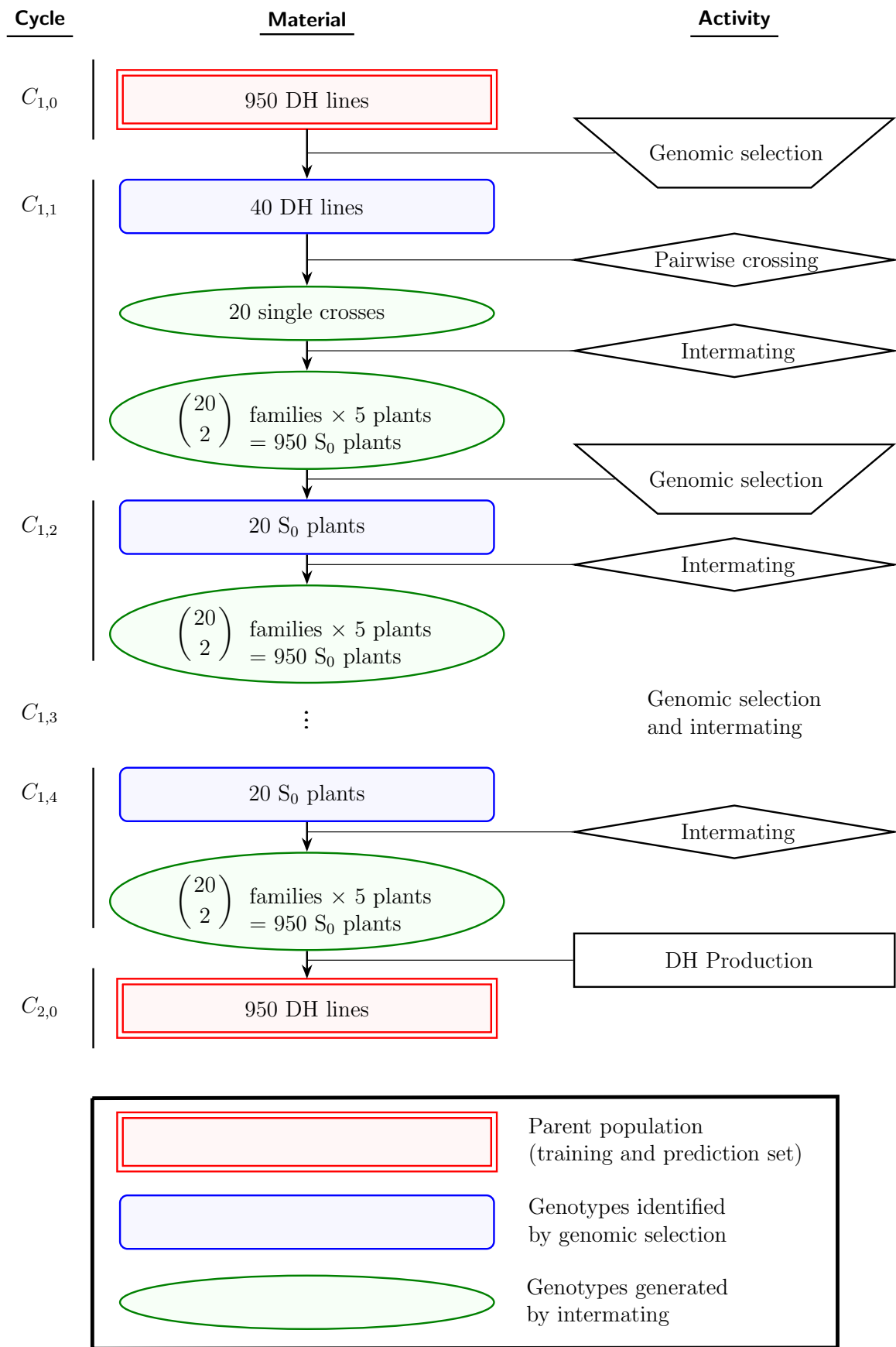


Figure S1: Schematic representation of selection cycle C_1 with (i) model training and genomic selection ($C_{1,0}$), (ii) subsequent subcycles $C_{1,1}$ to $C_{1,4}$ of genomic selection, and (iii) generating in sub-cycle $C_{1,4}$ the material used for re-training the model in cycle $C_{2,0}$.

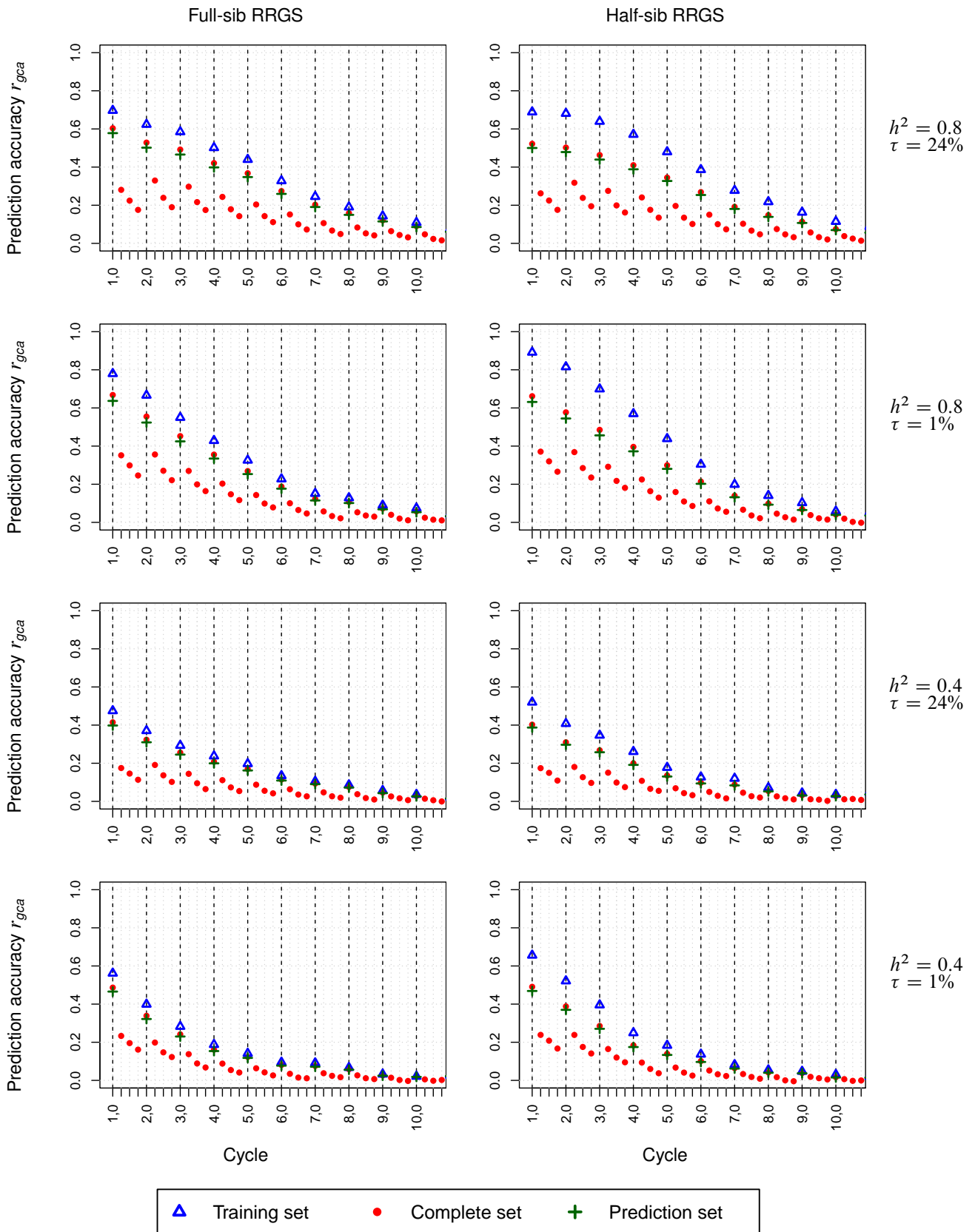


Figure S2: Prediction accuracy r_{gca} for GCA averaged over populations Π_F and Π_M for full-sib and half-sib reciprocal recurrent genomic selection (RRGS). Results for 10 selection cycles, each consisting of four subcycles, based on SNP data from maize. Scenarios differed in the heritability h^2 and the proportion $\tau = 100\% \times \sigma_{sca}^2 : \sigma_G^2$ of the trait. The training set size was $N_{TS} = 190$.

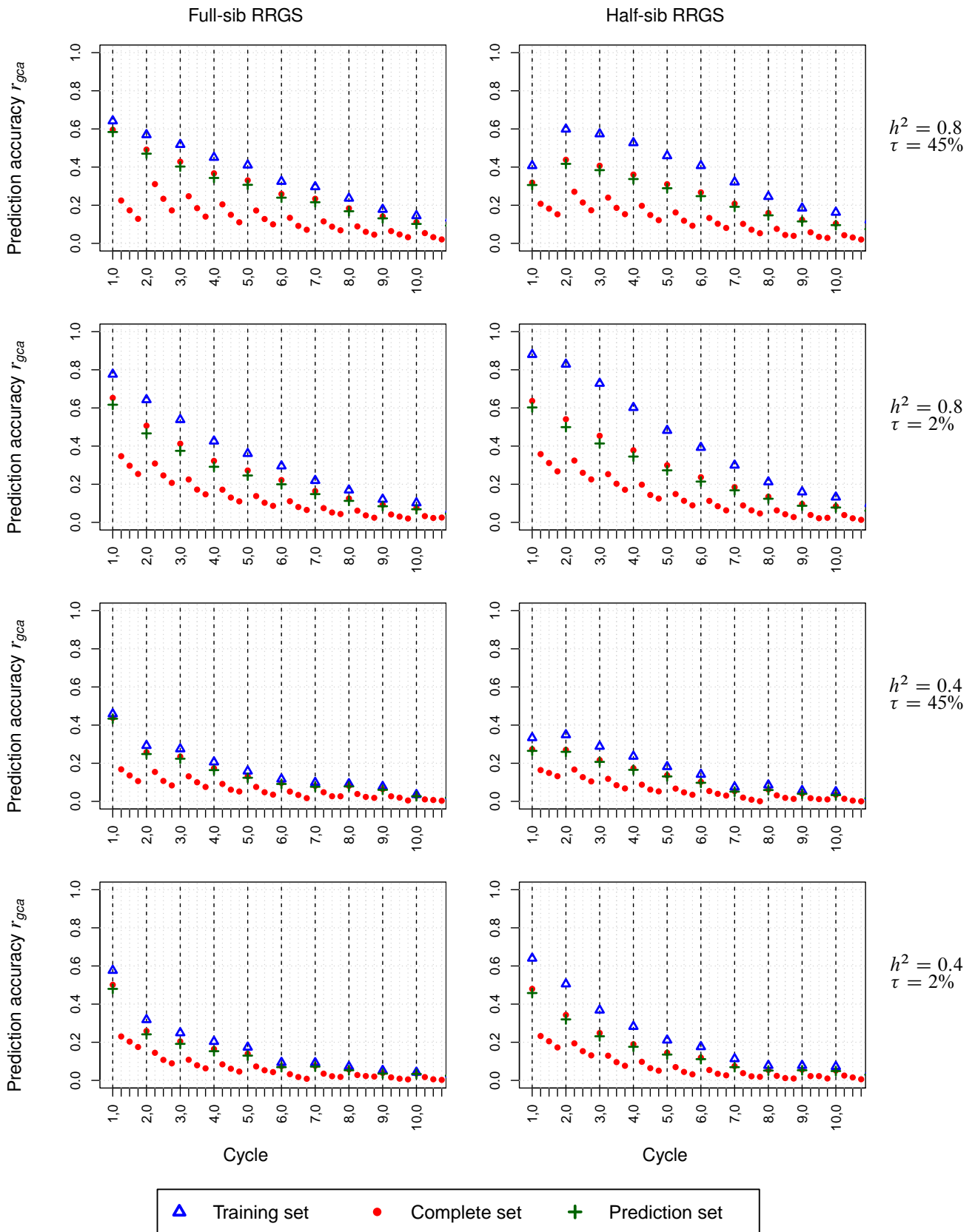


Figure S3: Prediction accuracy r_{gca} for GCA averaged over populations Π_F and Π_M for full-sib and half-sib reciprocal recurrent genomic selection (RRGS). Results for 10 selection cycles, each consisting of four subcycles, based on SNP data from wheat. Scenarios differed in the heritability h^2 and the proportion $\tau = 100\% \times \sigma_{sca}^2 : \sigma_G^2$ of the trait. The training set size was $N_{TS} = 190$.

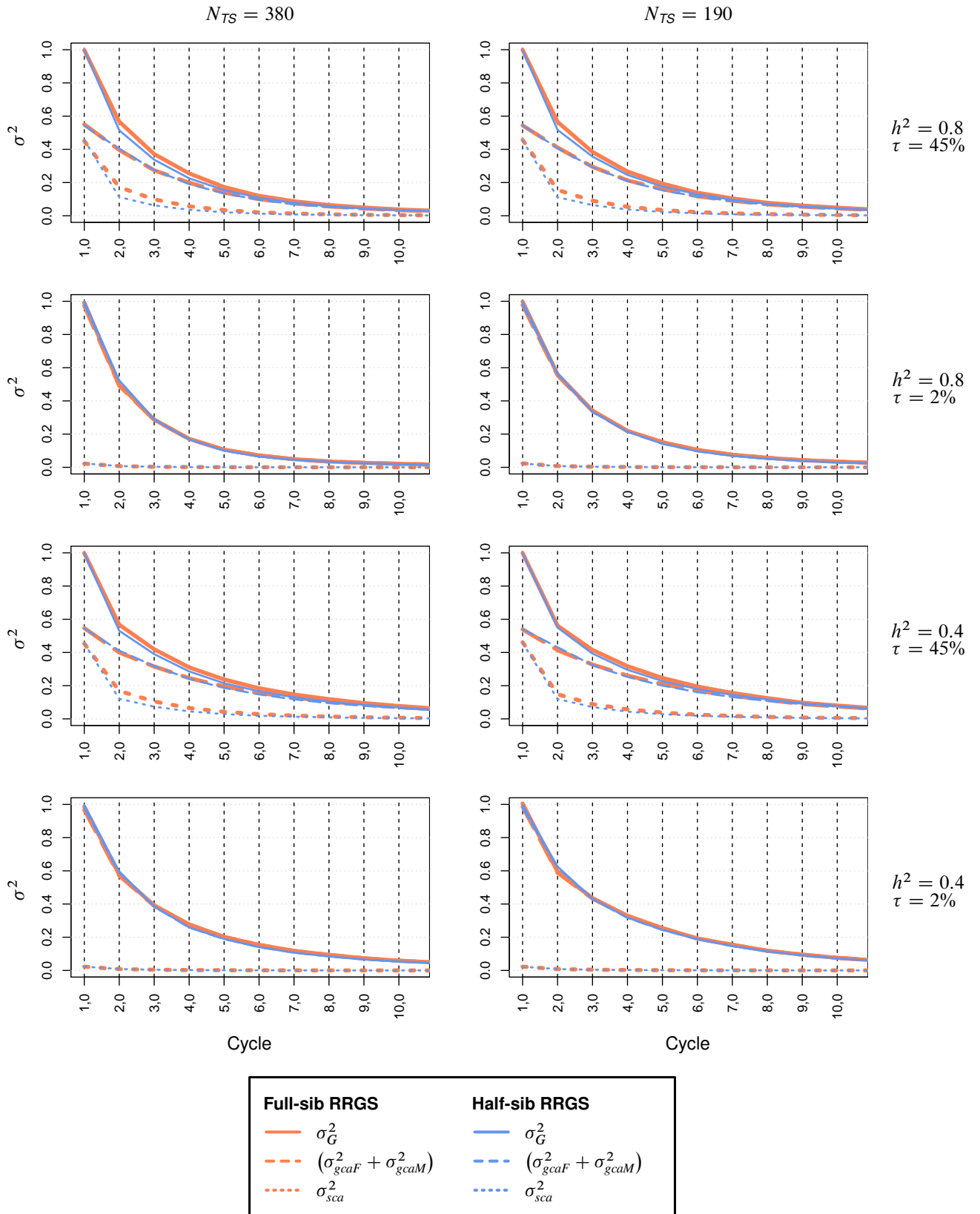


Figure S4: Genetic variances σ_G^2 , GCA variances $\sigma_{gcaF}^2 + \sigma_{gcaM}^2$, and SCA variances σ_{sca}^2 among hybrids for full-sib and half-sib reciprocal recurrent genomic selection (RRGS). Results for 10 selection cycles based on SNP data from wheat. Scenarios differed for the training set size N_{TS} , heritability h^2 , and proportion $\tau = 100\% \times \sigma_{sca}^2 : \sigma_G^2$ of the trait.

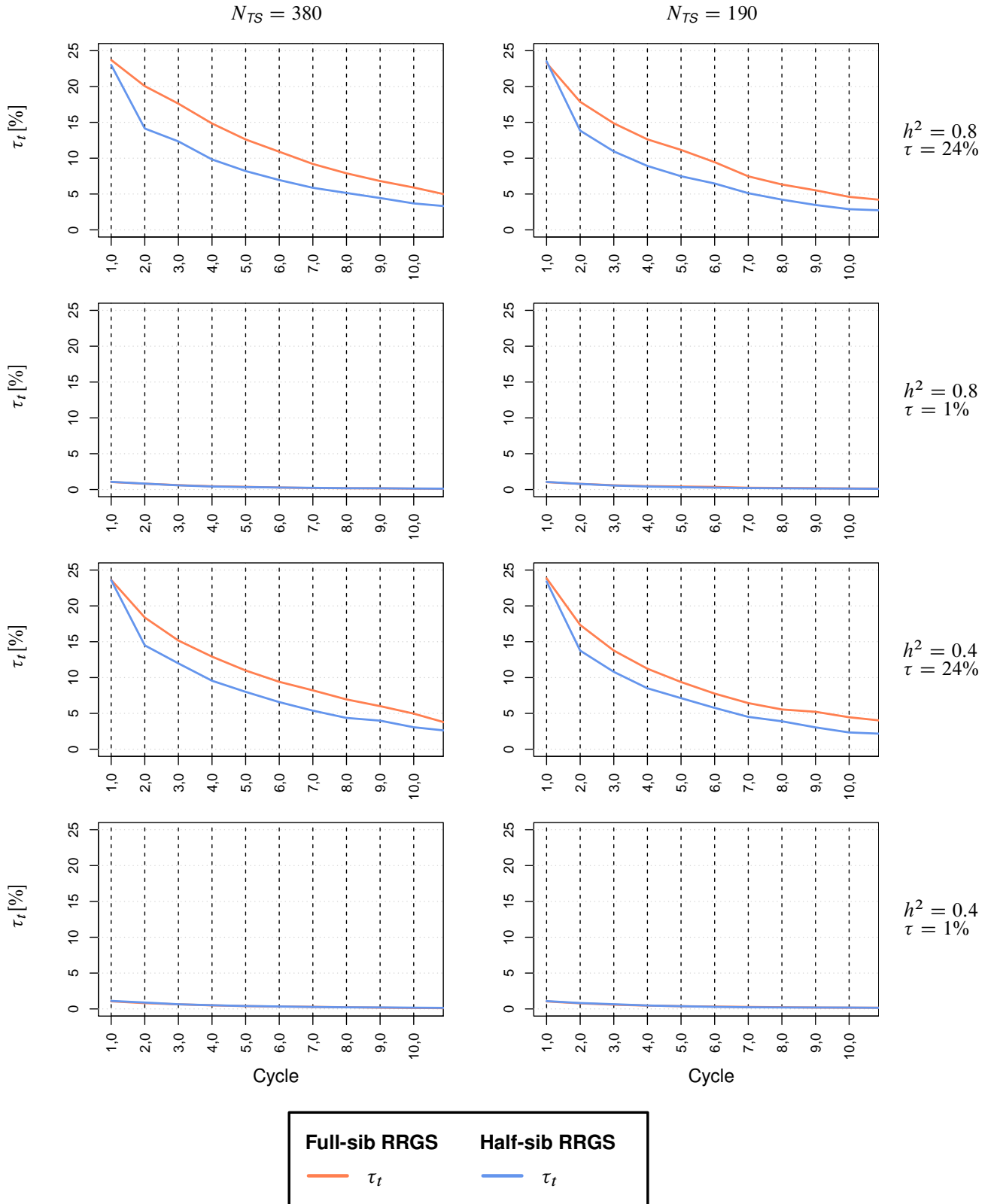


Figure S5: Proportion $\tau_t = 100\% \times \sigma_{sca}^2 : \sigma_G^2$ for full-sib and half-sib reciprocal recurrent genomic selection (RRGS). Results for 10 selection cycles based on SNP data from maize. Scenarios differed for the training set size N_{TS} , heritability h^2 , and proportion $\tau = 100\% \times \sigma_{sca}^2 : \sigma_G^2$ of the trait.

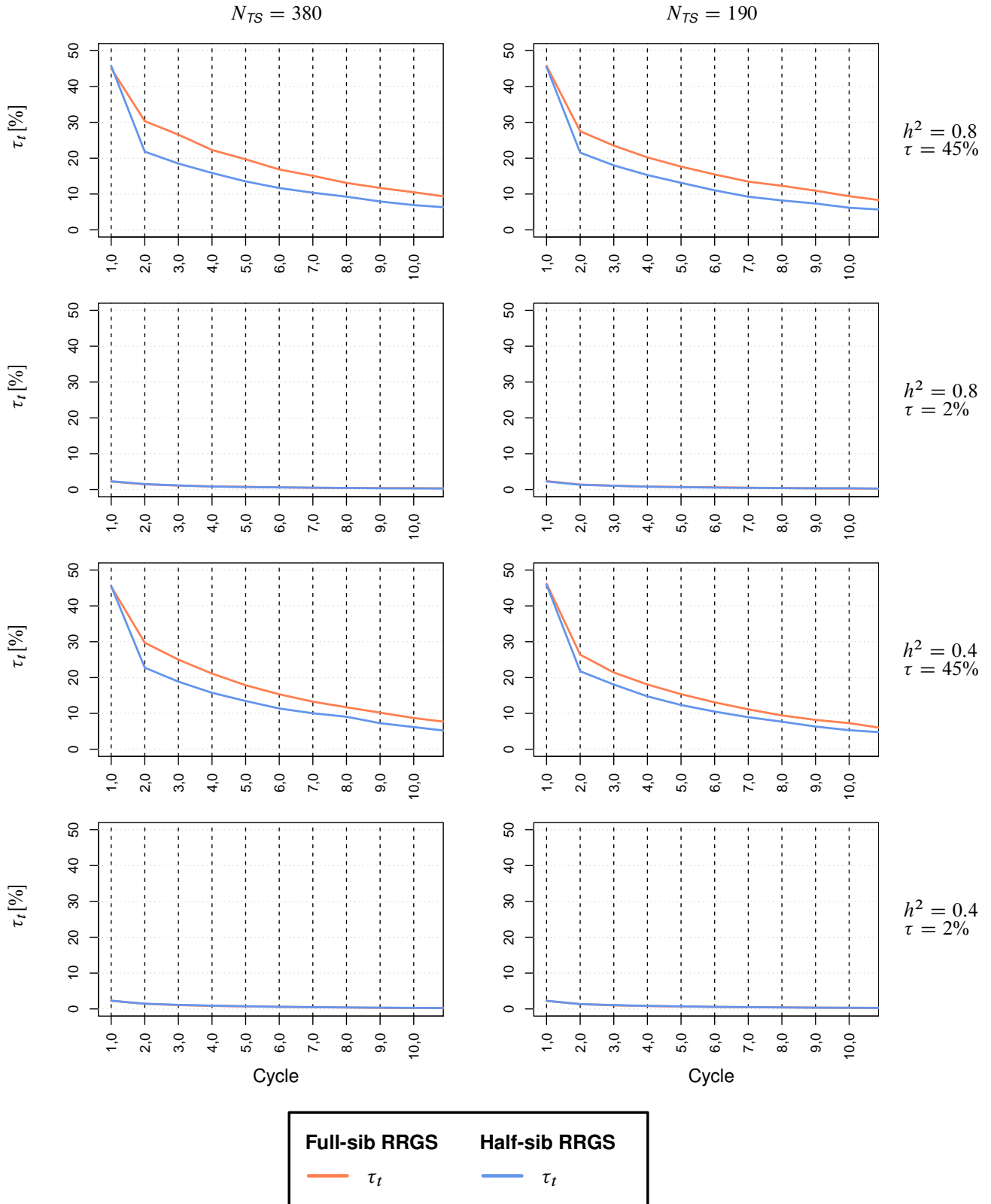


Figure S6: Proportion $\tau_t = 100\% \times \sigma_{sca}^2 : \sigma_G^2$ for full-sib and half-sib reciprocal recurrent genomic selection (RRGS). Results for 10 selection cycles based on SNP data from wheat. Scenarios differed for the training set size N_{TS} , heritability h^2 , and proportion $\tau = 100\% \times \sigma_{sca}^2 : \sigma_G^2$ of the trait.

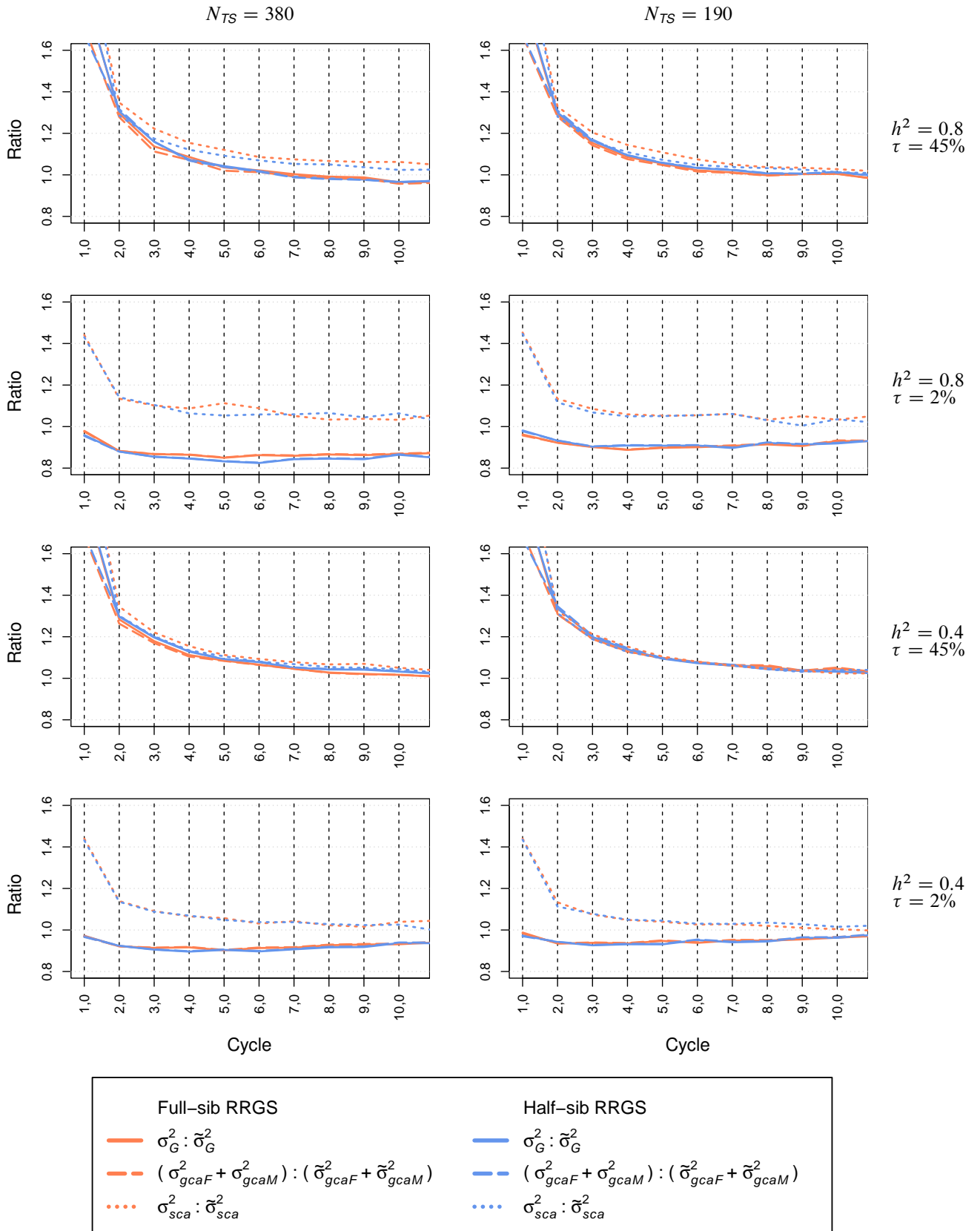


Figure S7: Ratio of genetic to genic variances $\sigma_G^2 : \tilde{\sigma}_G^2$, of genetic to genic GCA variances $(\sigma_{gcaF}^2 + \sigma_{gcaM}^2) : (\tilde{\sigma}_{gcaF}^2 + \tilde{\sigma}_{gcaM}^2)$, and genetic to genic SCA variances $\sigma_{sca}^2 : \tilde{\sigma}_{sca}^2$ among hybrids for full-sib and half-sib reciprocal recurrent genomic selection (RRGS). Results for 10 selection cycles based on SNP data from wheat. Scenarios differed for the training set size N_{TS} , heritability h^2 , and proportion $\tau = 100\% \times \sigma_{sca}^2 : \sigma_G^2$ of the trait.

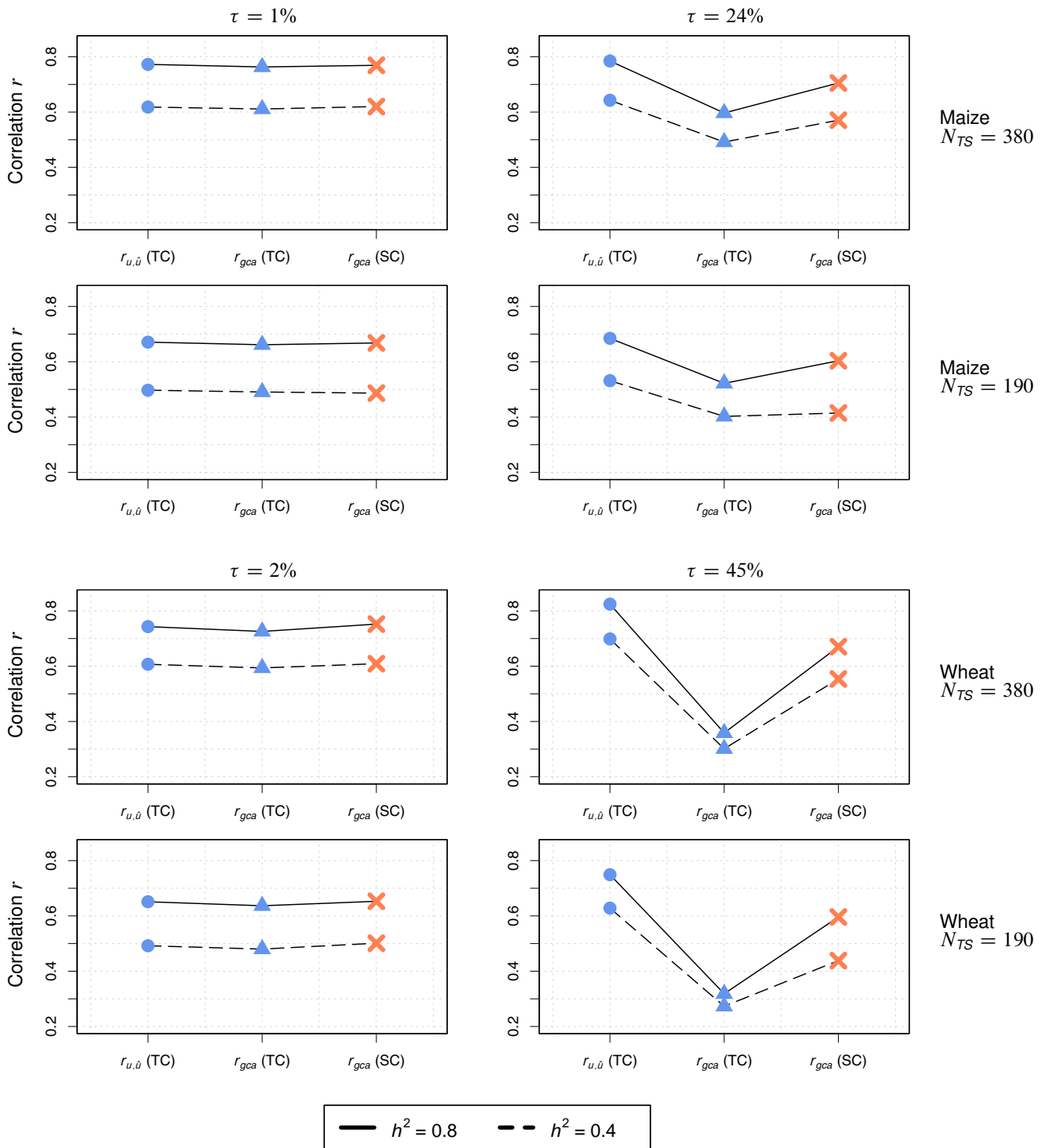


Figure S8: Prediction accuracy for testcross performance $r_{u,\hat{u}}(\text{TC})$ and for GCA $r_{gca}(\text{TC})$ in half-sib reciprocal recurrent genomic selection, and for GCA in full-sib reciprocal recurrent genomic selection $r_{gca}(\text{SC})$. Results for selection cycle $C_{1,0}$. Scenarios differed for the training set size N_{TS} , heritability h^2 , proportion $\tau = 100\% \times \sigma_{sca}^2 : \sigma_G^2$ of the trait, and the crop from which the SNP data were used for the simulations.

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