

Supplementary Material of "Estimation of Molecular Pairwise Relatedness in Autopolyploid Crops"

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Supplementary Table S1

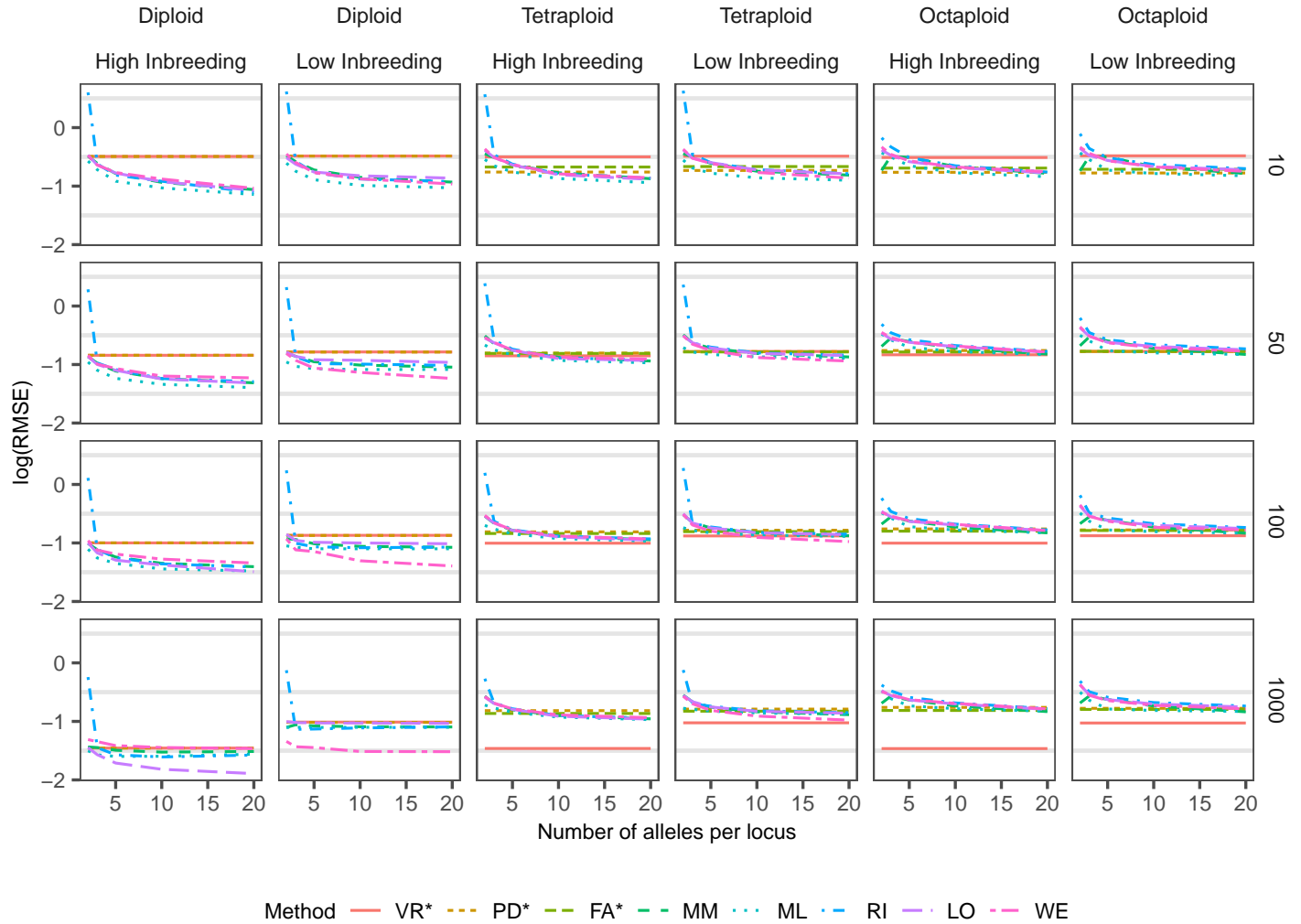
Mendelian sampling mean (Mean) and standard deviation (SD) based on 10,000 loci for different cytotypes considering a genome with 10 chromosomes with 100 cM each.

Cytotype	Relationship	Mean ^a	SD	Mean ^b	SD
2n = 2x	Full-sibs	0.5001	0.0663		
2n = 2x	Half-sibs	0.2472	0.0457		
2n = 2x	Grandparent-grandoffspring	0.2534	0.0574		
2n = 2x	Uncle-nephew	0.1210	0.0370		
2n = 2x	Granduncle-grandnephew	0.0611	0.0277		
2n = 4x	Full-sibs	0.5042	0.0397	0.4911	0.0380
2n = 4x	Half-sibs	0.2508	0.0258	0.2476	0.0290
2n = 4x	Grandparent-grandoffspring	0.2520	0.0315	0.2509	0.0362
2n = 4x	Uncle-nephew	0.1281	0.0276	0.1257	0.0292
2n = 4x	Granduncle-grandnephew	0.0652	0.0220	0.0645	0.0219
2n = 6x	Full-sibs	0.4963	0.0266	0.4975	0.0320
2n = 6x	Half-sibs	0.2469	0.0213	0.2442	0.0256
2n = 6x	Grandparent-grandoffspring	0.2480	0.0265	0.2499	0.0305
2n = 6x	Uncle-nephew	0.1215	0.0193	0.1249	0.0236
2n = 6x	Granduncle-grandnephew	0.0602	0.0159	0.0636	0.0198
2n = 8x	Full-sibs	0.4985	0.0234	0.4900	0.0262
2n = 8x	Half-sibs	0.2471	0.0168	0.2423	0.0205
2n = 8x	Grandparent-grandoffspring	0.2513	0.0213	0.2519	0.0234
2n = 8x	Uncle-nephew	0.1257	0.0169	0.1201	0.0187
2n = 8x	Granduncle-grandnephew	0.0640	0.0140	0.0608	0.0149

^a Simulation considered bivalent pairing.

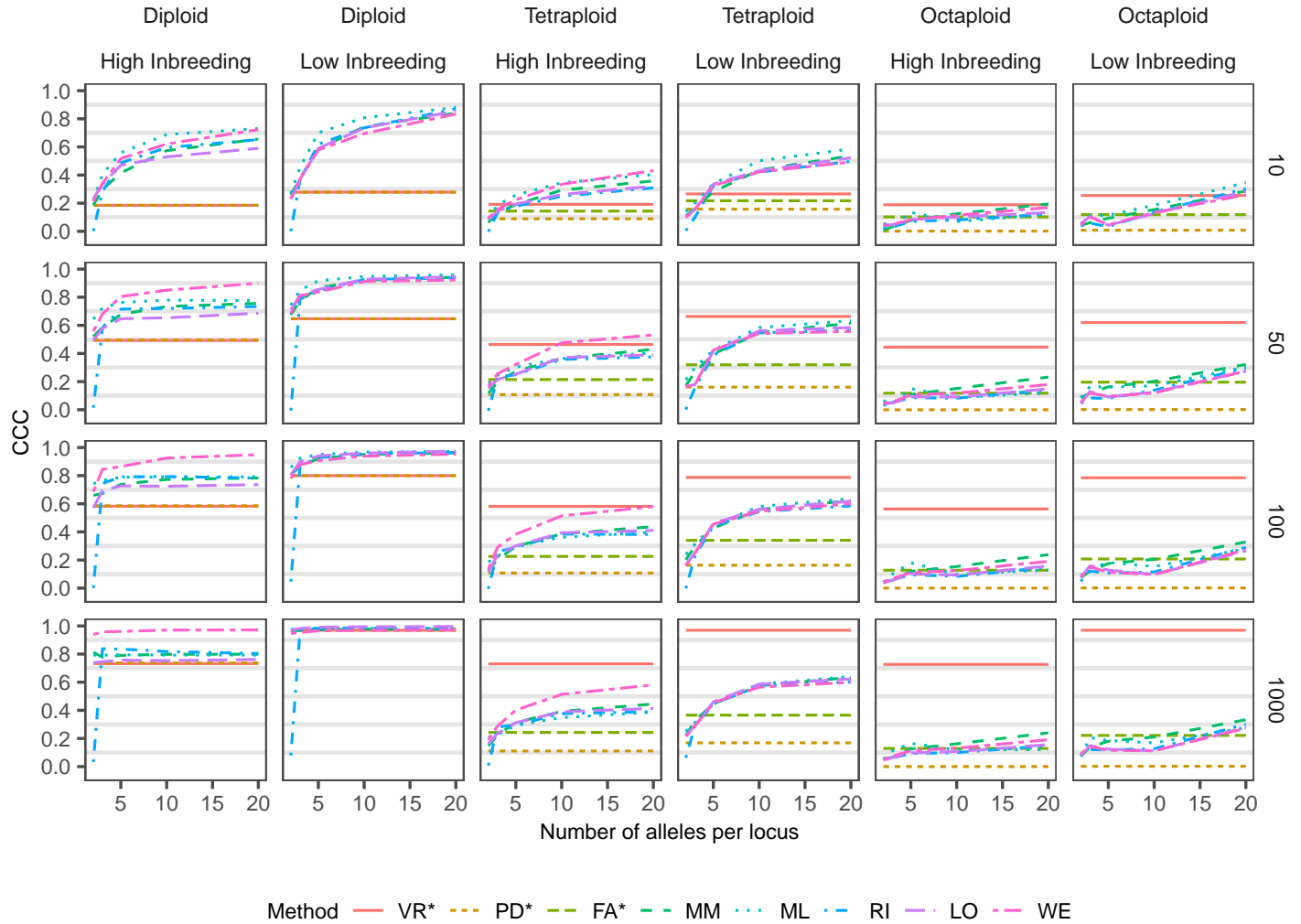
^b Simulation considered multivalent pairing (allows double-reduction).

Supplementary Figure S1



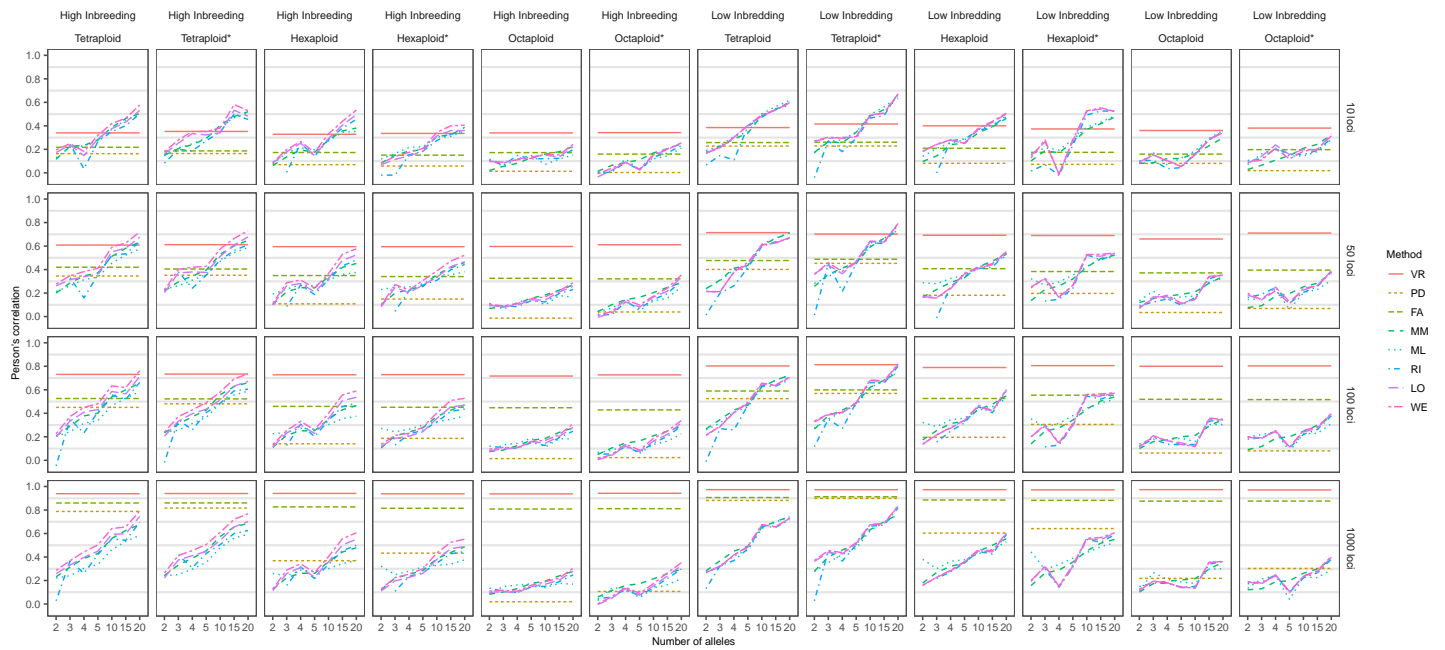
Root mean square error expressed as the logarithm base 10 between observed (lower the better) and estimated \hat{p} based on 100 replicates across numbers of loci and alleles on different ploidies based on simulated genotypes of two pedigrees with high and low inbreeding assuming uniform distribution of ancestral alleles. * meiosis with multivalent pairing (double-reduction); without * meiosis with only bivalent formation. Methods: VR (extended Van Raden), PD (pseudo-diploid), FA (full-autopolyploid) MM (method-of-moments), ML (maximum-likelihood), RI (extended Ritland), LO (extended Loiselle), and WE (extended Weir). Biallelic methods (VR, PD, and FA) considered only two alleles scenarios, plotted line extended to better comparison.

Supplementary Figure S2



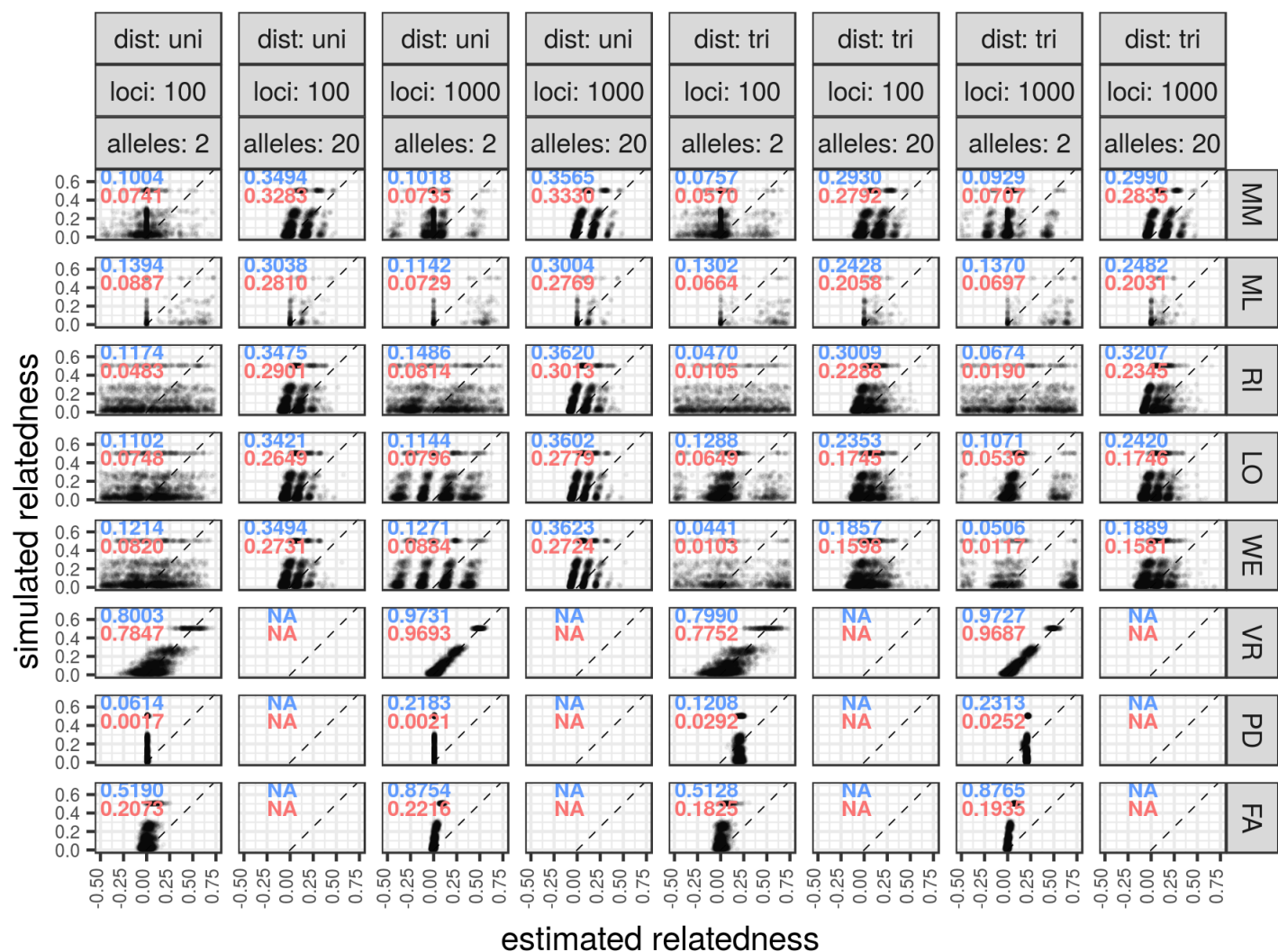
Lin's concordance correlation coefficient (closer to one, the better) between observed and estimated \hat{r} based on 100 replicates across numbers of loci and alleles on different ploidies based on simulated genotypes of two pedigrees with high and low inbreeding assuming uniform distribution of ancestral alleles. * meiosis with multivalent pairing (double-reduction); without * meiosis with only bivalent formation. Methods: VR (extended Van Raden), PD (pseudo-diploid), FA (full-autopolyploid) MM (method-of-moments), ML (maximum-likelihood), RI (extended Ritland), LO (extended Loiselle), and WE (extended Weir). Biallelic methods (VR, PD, and FA) considered only two alleles scenarios, plotted line extended to better comparison.

Supplementary Figure S3



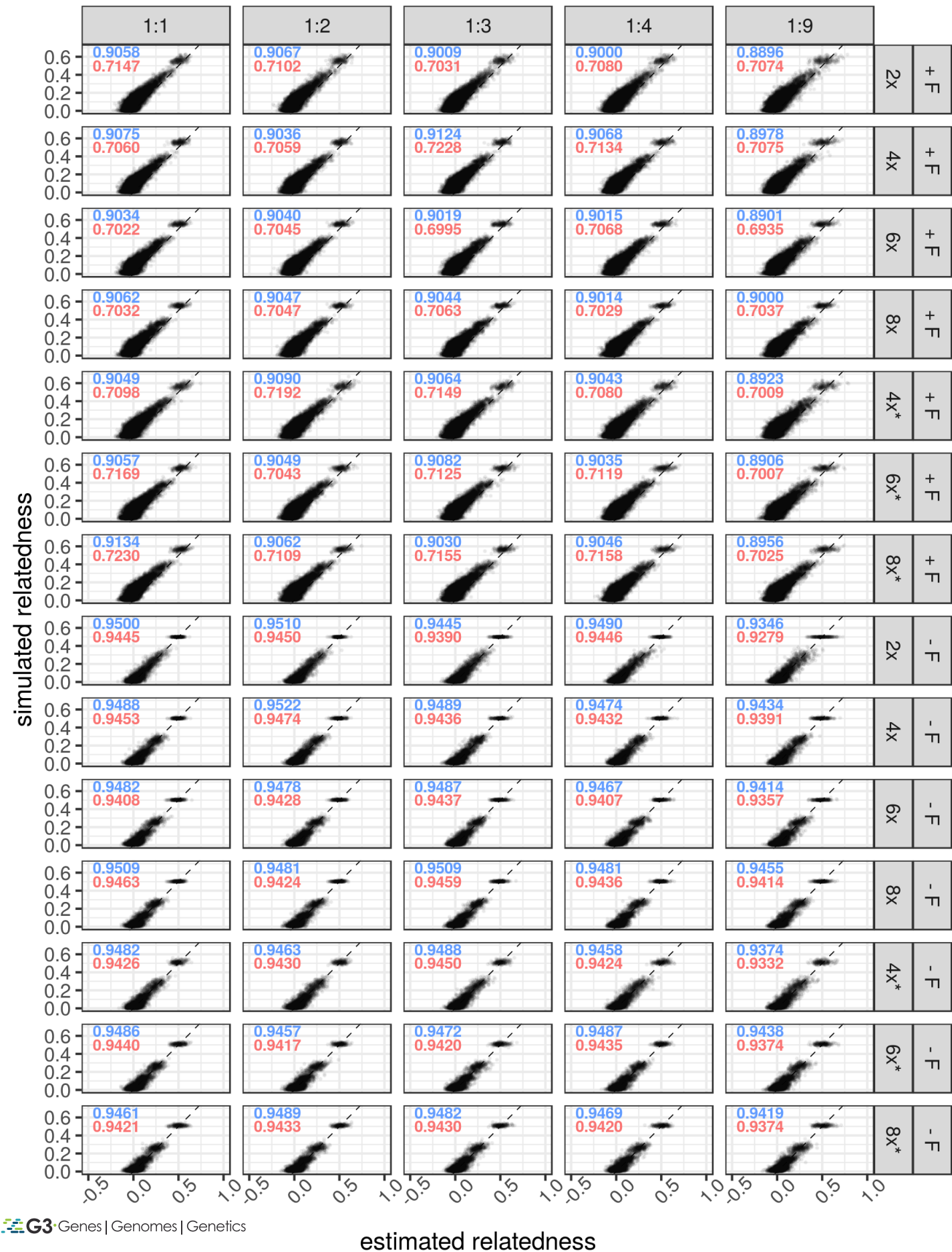
Correlation between observed and estimated \hat{p} based on 100 replicates across numbers of loci and alleles on different ploidies based on simulated genotypes of two pedigrees with high and low inbreeding assuming uniform distribution of ancestral alleles. * meiosis with multivalent pairing (double-reduction); without * meiosis with only bivalent formation. Methods: VR (extended Van Raden), PD (pseudo-diploid), FA (full-autopolyploid) MM (method-of-moments), ML (maximum-likelihood), RI (extended Ritland), LO (extended Loiselle), and WE (extended Weir). Biallelic methods (VR, PD, and FA) considered only two alleles scenarios, plotted line extended to better comparison.

Supplementary Figure S4

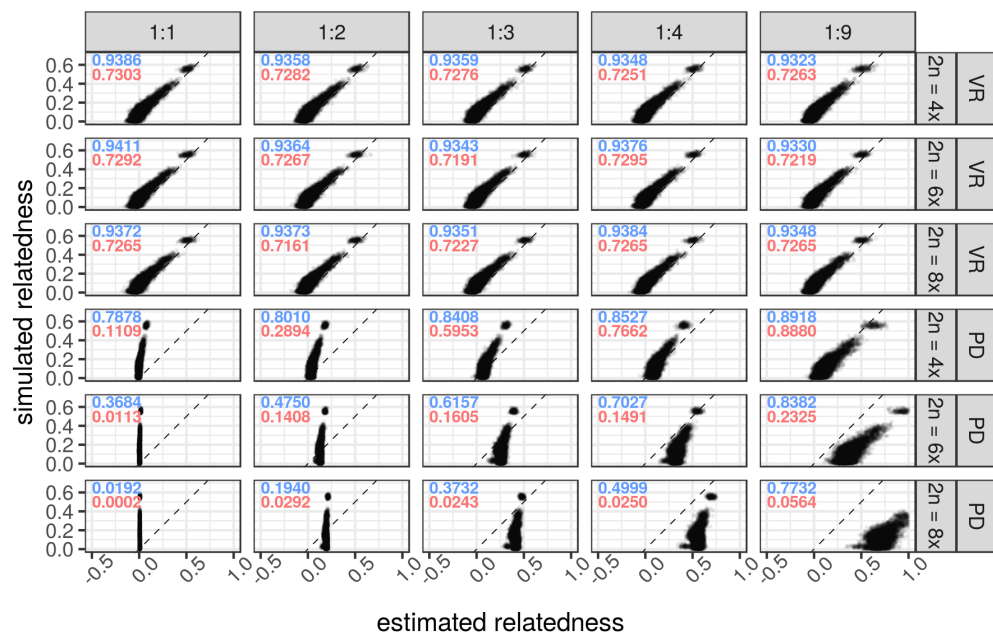


Observed relatedness (\hat{r}_{obs}) and estimated relatedness (\hat{r}_{method} computed with VR (Van Raden based) and PD (pseudo-diploid) methods comparing different allele frequencies distribution in high-inbreeding genealogy with 1,000 loci assuming different ploidies ($2n = 4x$, $2n = 6x$, and $2n = 8x$). Proportion of minor to major alleles in the ancestral genotypes are 1:1, 1:2, 1:3, and 1:9. Concordance correlation coefficient (blue) and Pearson's correlation (red) statistics values between \hat{r} 's. Dashed line at indicates perfect concordance between observed and estimates (45° line).

Supplementary Figure S5



Supplementary Figure S6



Observed relatedness (\hat{r}_{obs}) and estimated relatedness (\hat{r}_{VR}) computed with the VR (Van Raden based) method comparing different biallelic frequencies distribution in the population with 500 loci. Proportion of minor to major alleles in the ancestral genotypes are 1:1, 1:2, 1:3, and 1:9. Concordance correlation coefficient (blue) and Pearson's correlation (red) statistics values between \hat{r} 's. Based on simulated genotypes of high-inbreeding pedigree (+F) and the low-inbreeding pedigree (-F). * meiosis with multivalent pairing (double-reduction); without * meiosis with only bivalent formation. Dashed line at indicates perfect concordance between observed and estimates (45° line).