

Appendix B

Supplementary figures

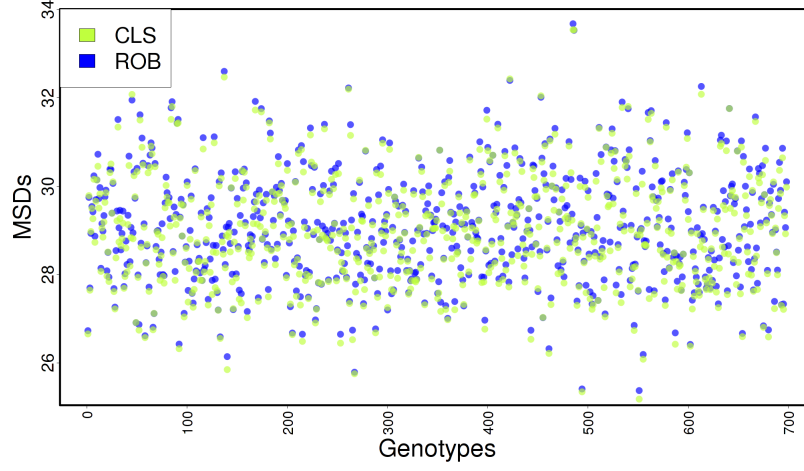


Figure S1. Plot of the classical and robust $\text{MSD}_{\mu}^i = \sum_{l=1}^{1000} \frac{(\hat{\mu}_{il} - \mu_{il})^2}{1000}$ for each of the 698 genotypes for the **null** scenario (1st stage)

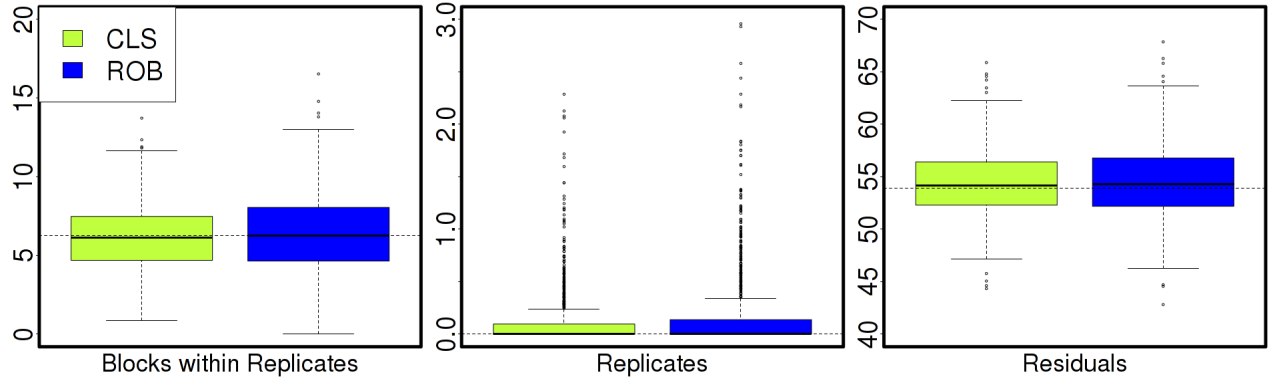


Figure S2. Boxplots of the 1000 classical and robust estimated *block* ($\sigma_{r,b}^2$), *replicate* (σ_r^2) and *residual* variances (σ_e^2) for the **null** scenario (1st stage)

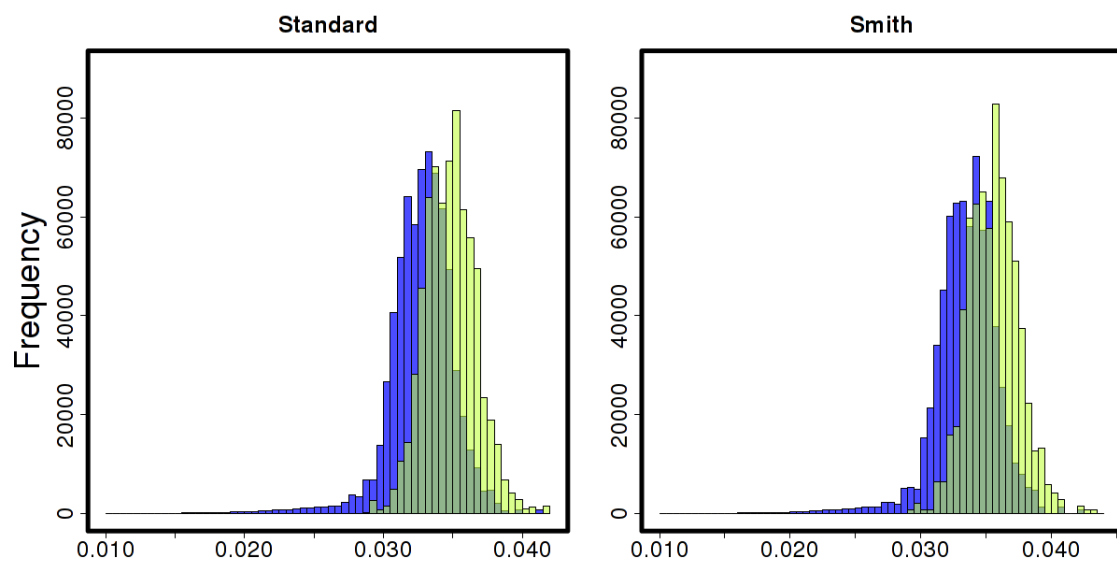


Figure S3: Histograms of the classical and robust Standard and Smith's weights for the **null** scenario (1st stage)

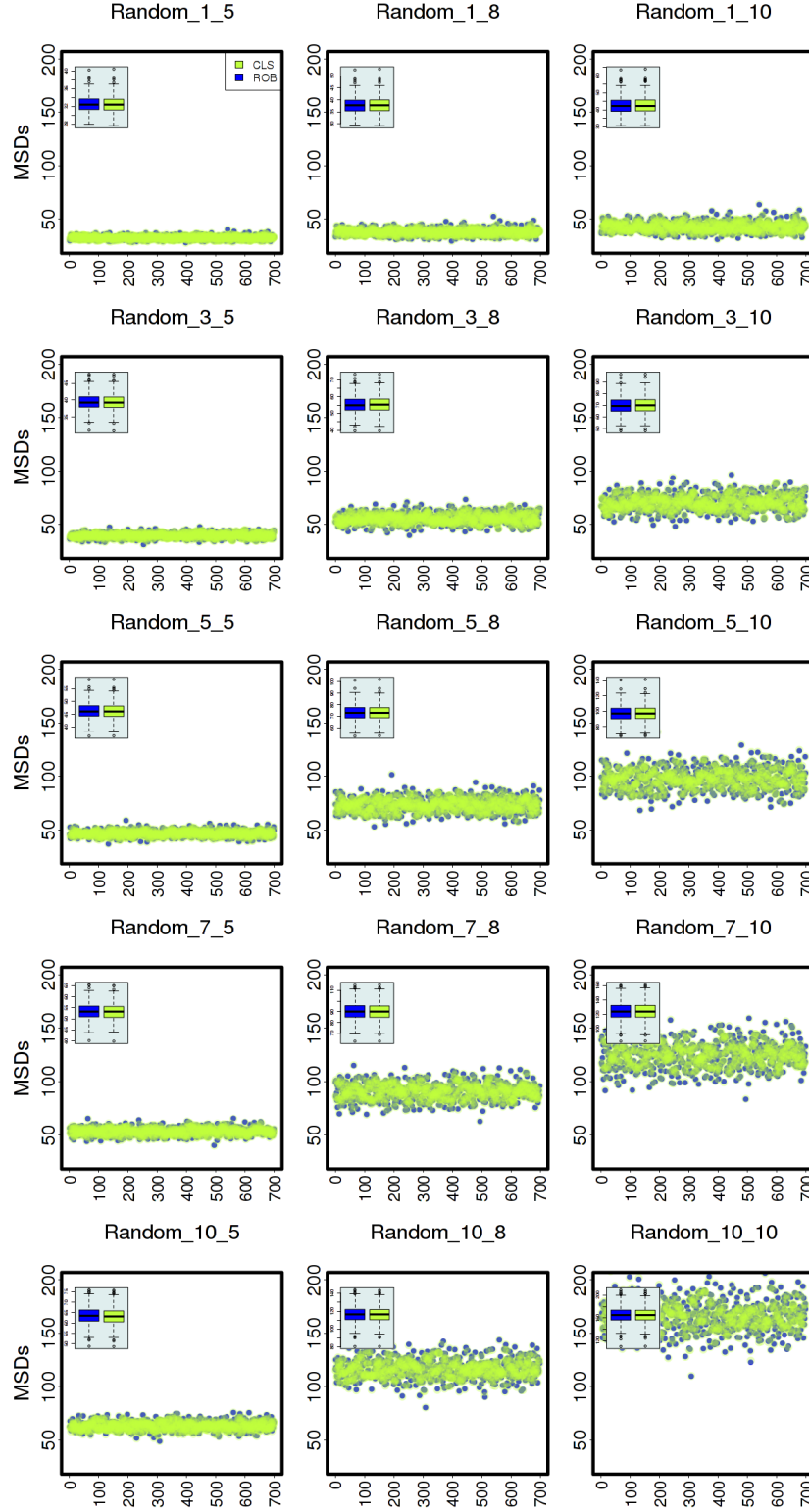


Figure S4. Plots of classical and robust $\text{MSD}_{\mu}^i = \sum_{l=1}^{1000} \frac{(\hat{\mu}_{il} - \mu_{il})^2}{1000}$ for each of the 698 genotypes for the **random** contamination scenarios (1st stage)

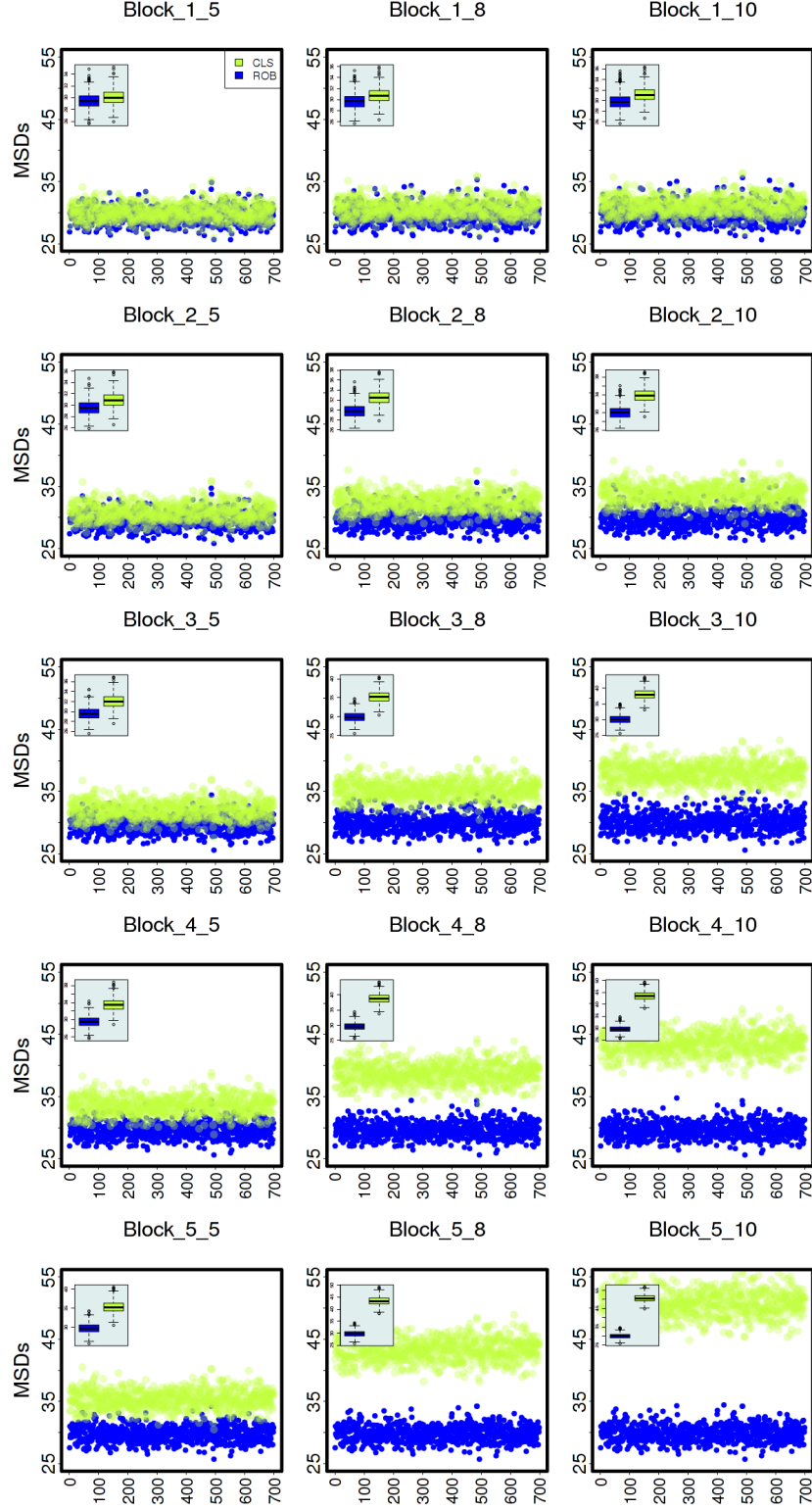


Figure S5. Plots of classical and robust $\text{MSD}_{\mu}^i = \sum_{l=1}^{1000} \frac{(\hat{\mu}_{il} - \mu_{il})^2}{1000}$ for each of the 698 genotypes for the **block** contamination scenarios (1st stage)

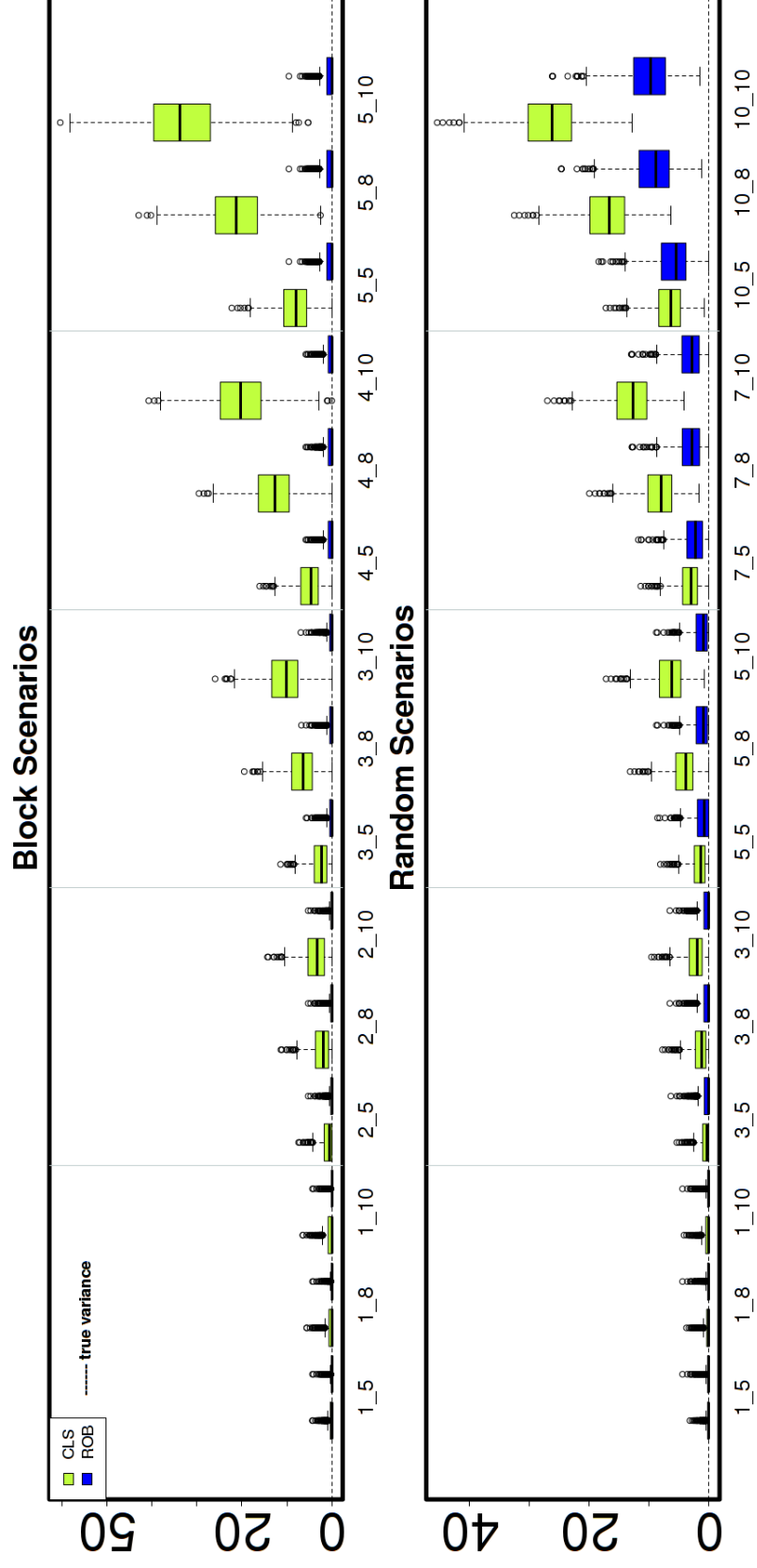


Figure S6. Boxplots of the 1000 classical and robust estimated variances for *replicates* (σ_r^2) for the **block** and **random** contamination scenarios (1st stage)

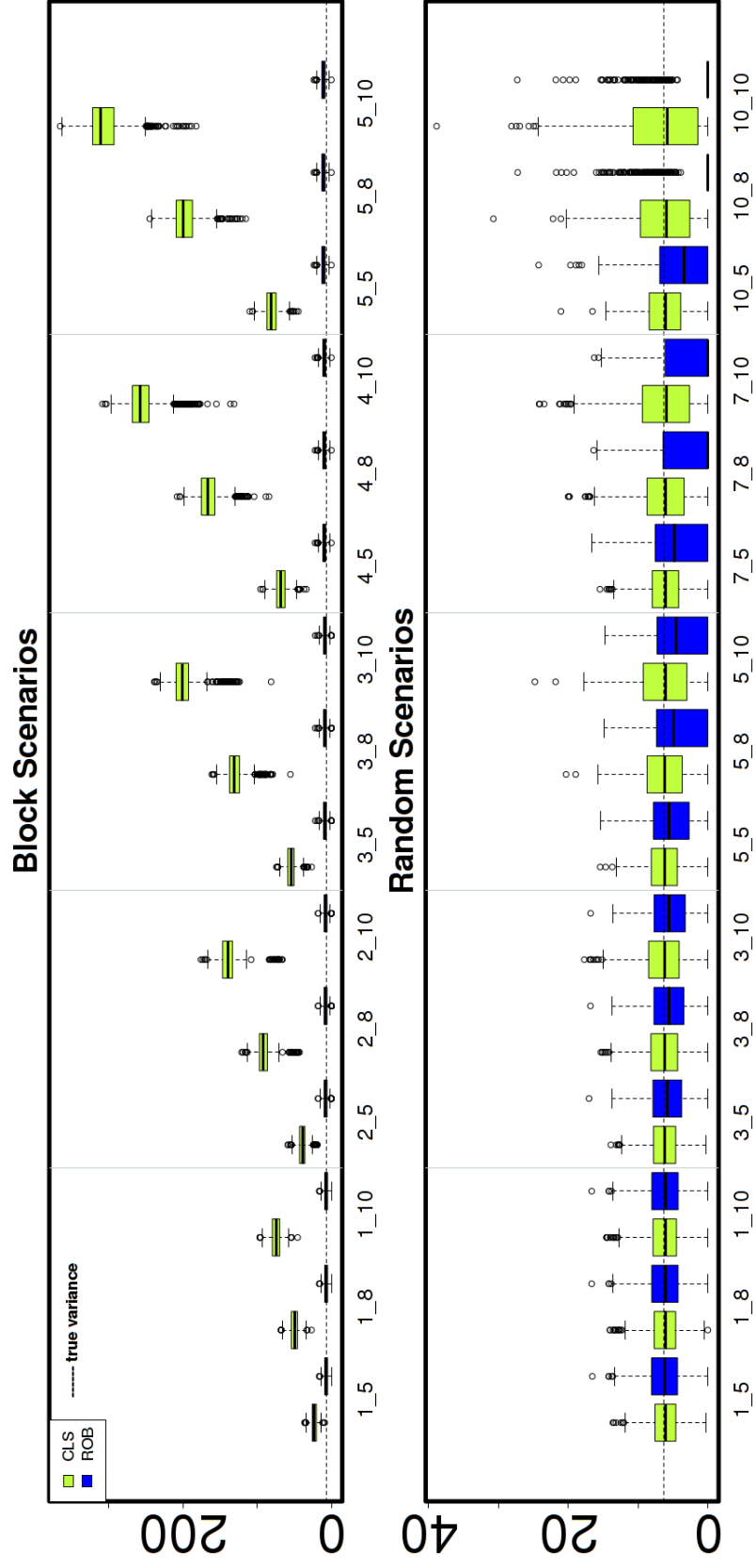


Figure S7: Boxplots of the 1000 classical and robust estimated variances for *block nested within replicates* ($\sigma_{r;b}^2$) for the **block** and **random** contamination scenarios (1st stage)

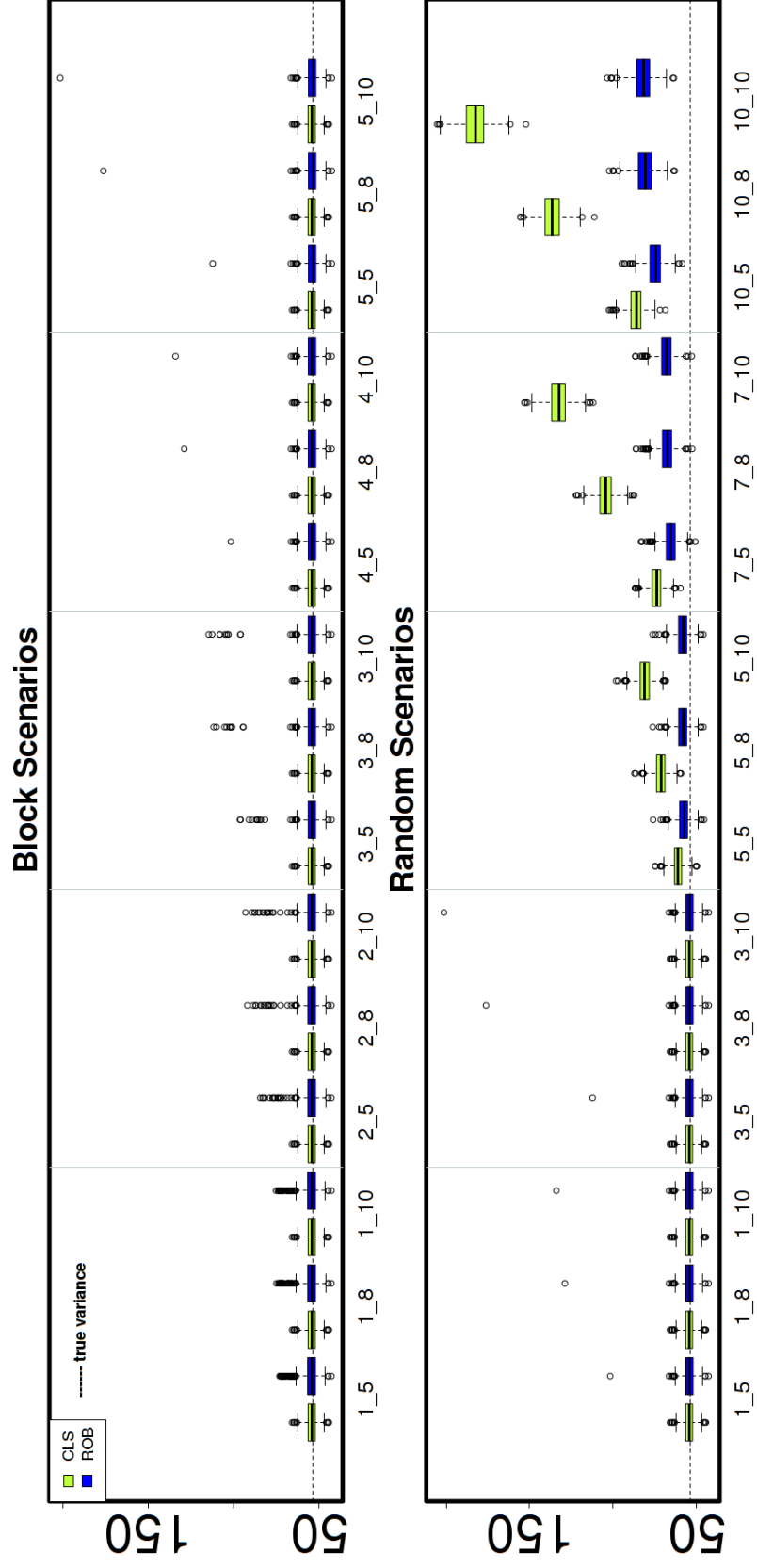


Figure S8: Boxplots of the 1000 classical and robust estimated variances for *residuals* (σ_e^2) for the **block** and **random** contamination scenarios (1st stage)

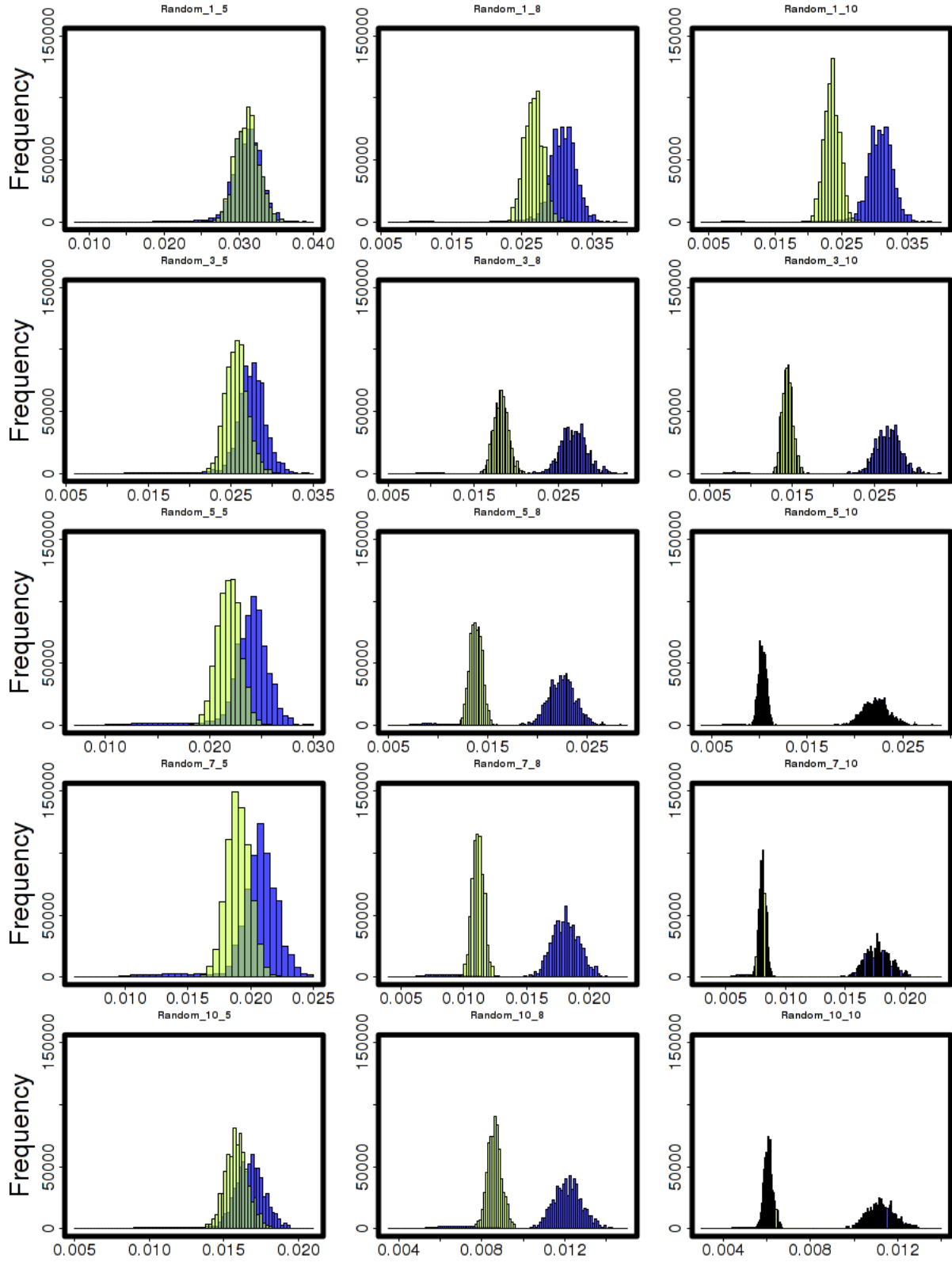


Figure S9. Histograms of the classical and robust Standard's weights for the **random** contamination scenarios (1st stage)

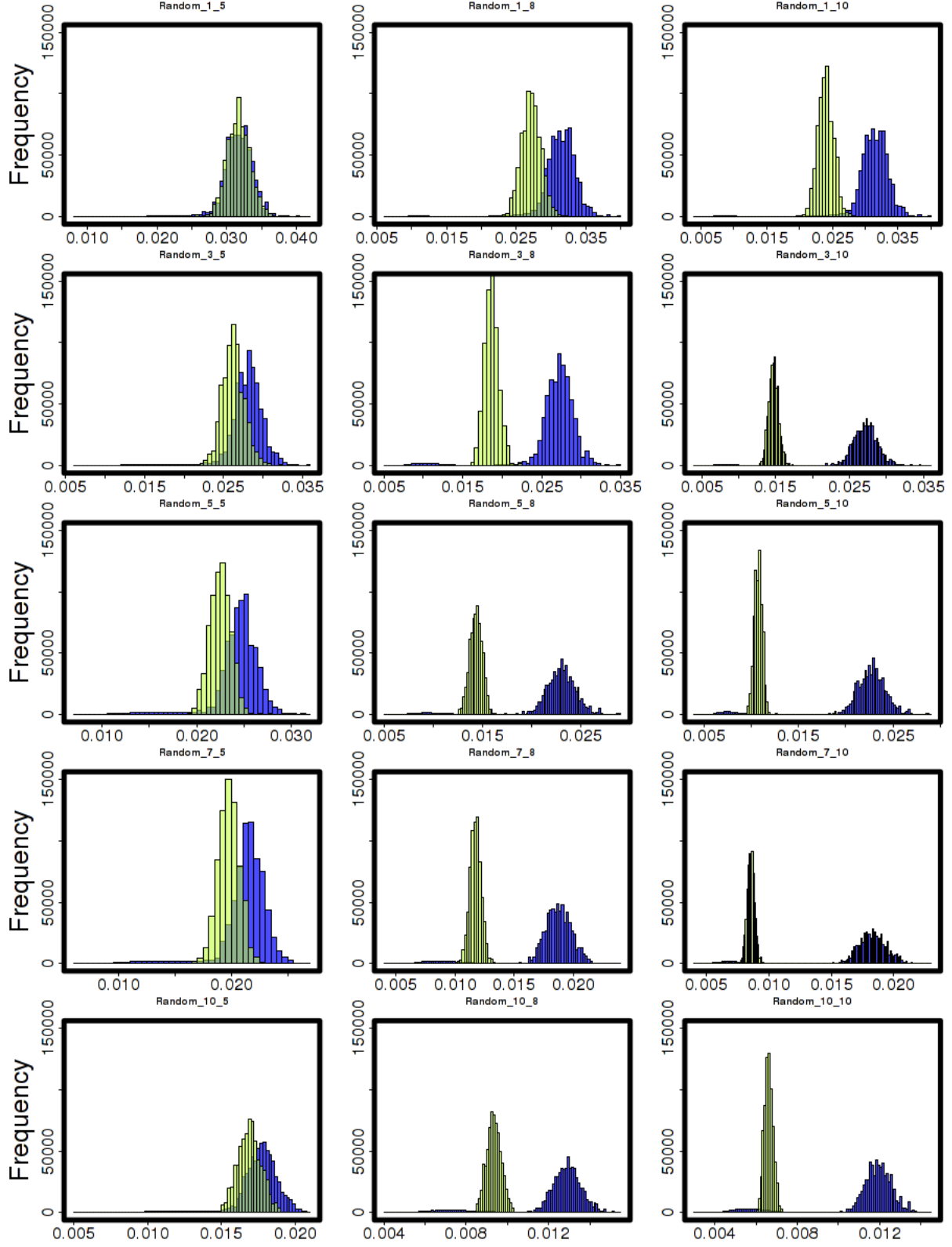


Figure S10. Histograms of the classical and robust Smith's weights for the **random** contamination scenarios (1st stage)

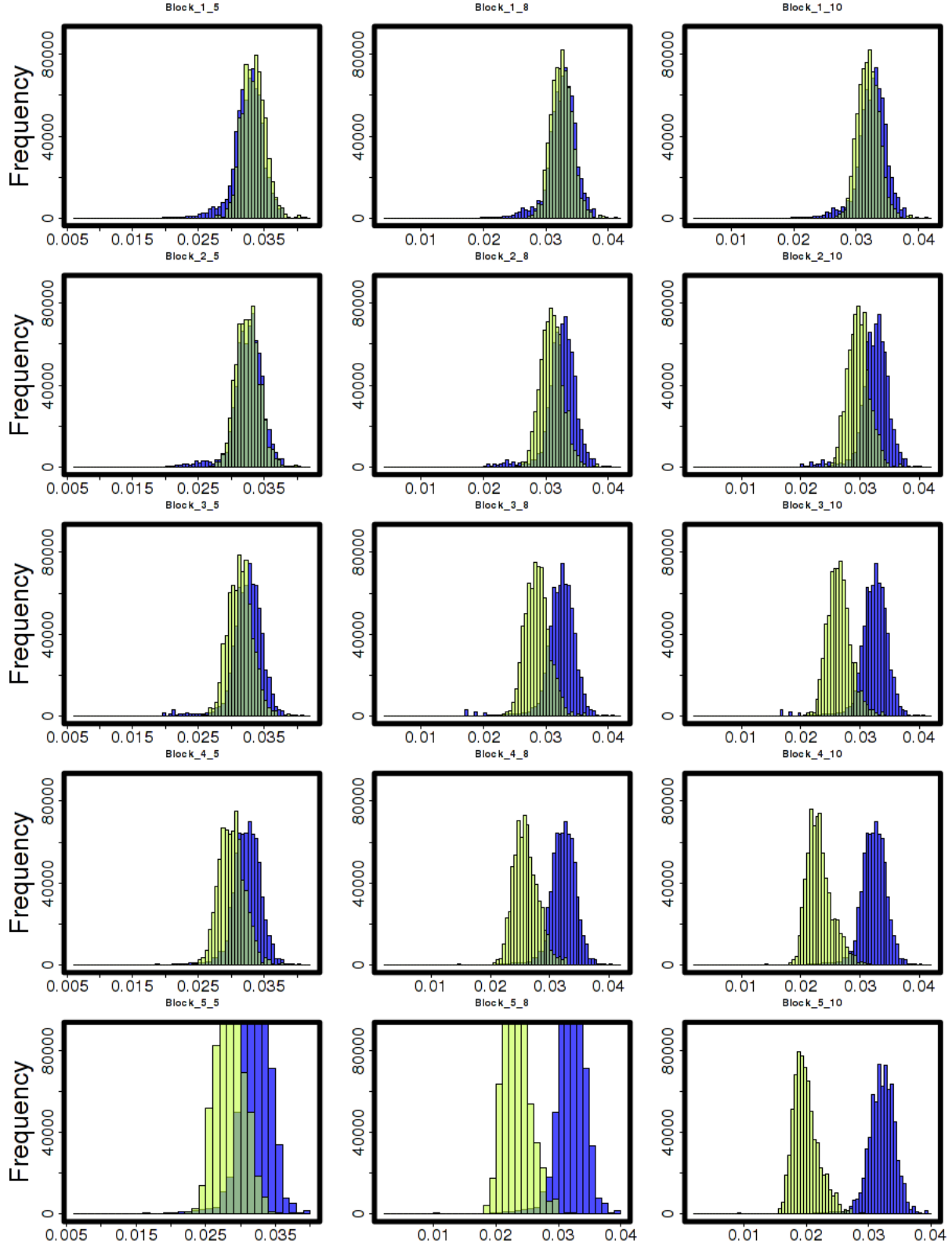


Figure S11. Histograms of the classical and robust Standard's weights for the **block** contamination scenarios (1st stage)

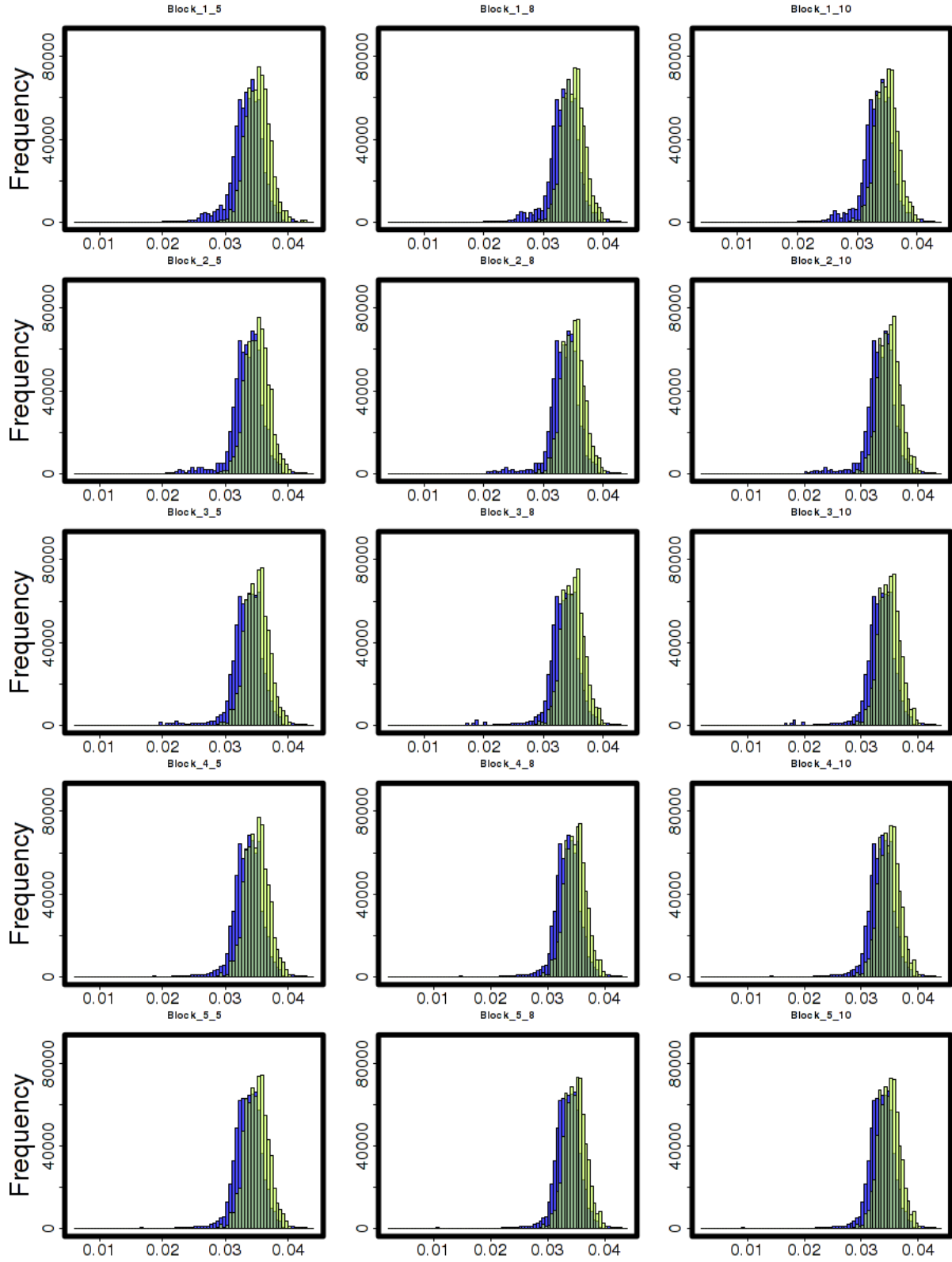


Figure S12. Histograms of the classical and robust Smith's weights for the **block** contamination scenarios (1st stage)

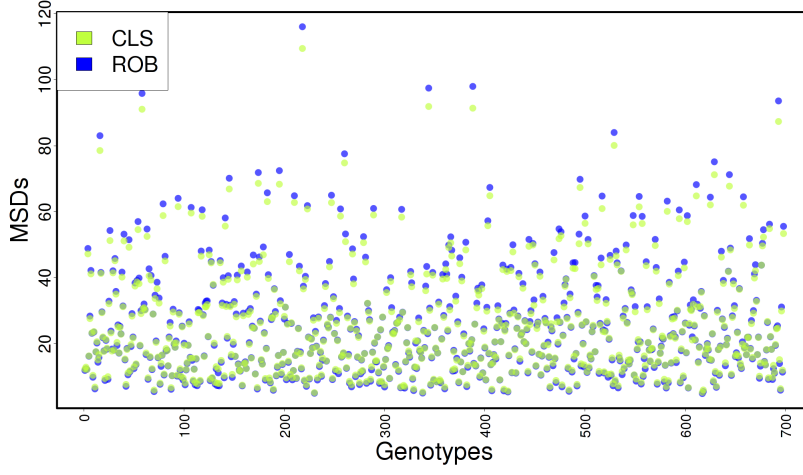


Figure S13. Plot of the classical and robust $\text{MSD}_g^i = \sum_{j=1}^{1000} \frac{(\hat{g}_{ij} - g_{ij})^2}{1000}$ for each of the 698 genotypes for the **null** scenario (2nd stage)

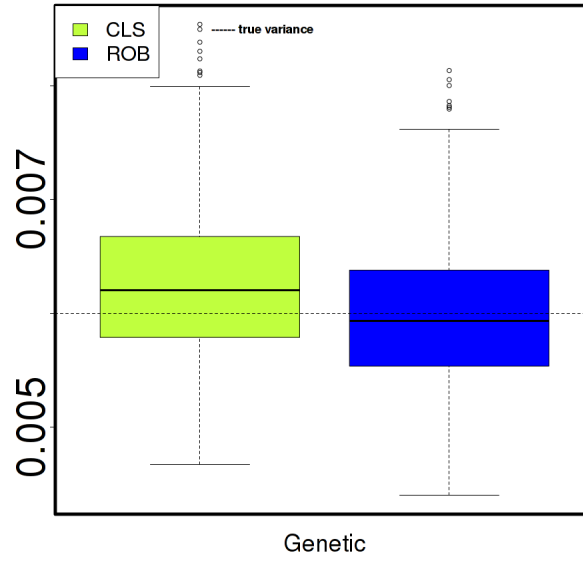


Figure S14. Boxplots of the 1000 classical and robust estimated *marker-effect* (σ_s^2) variances for the **null** scenario (2nd stage)

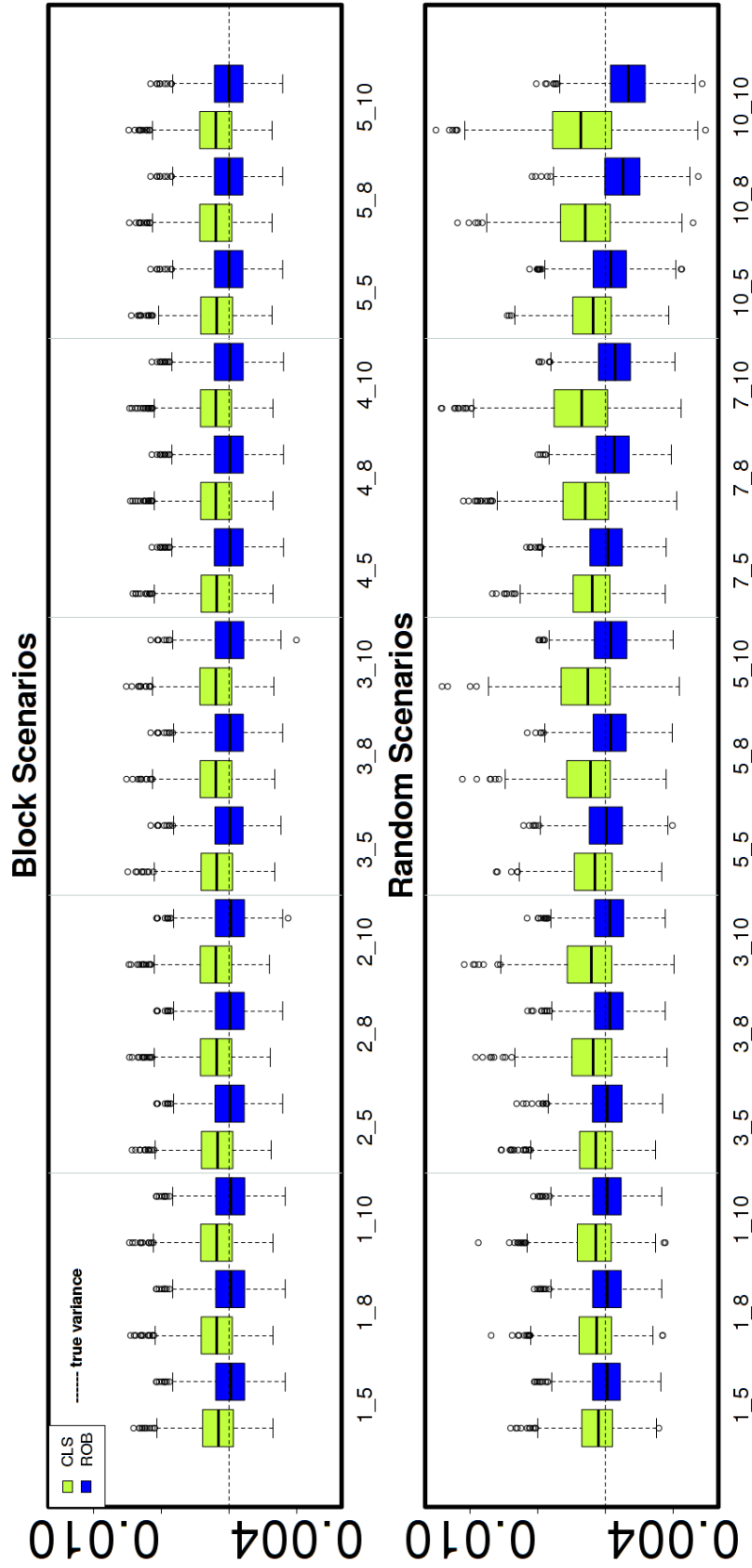


Figure S15: Boxplots of the 1000 classical and robust estimated *marker-effect* variances (σ_s^2) for the **block** and **random** contamination scenarios (2nd stage)

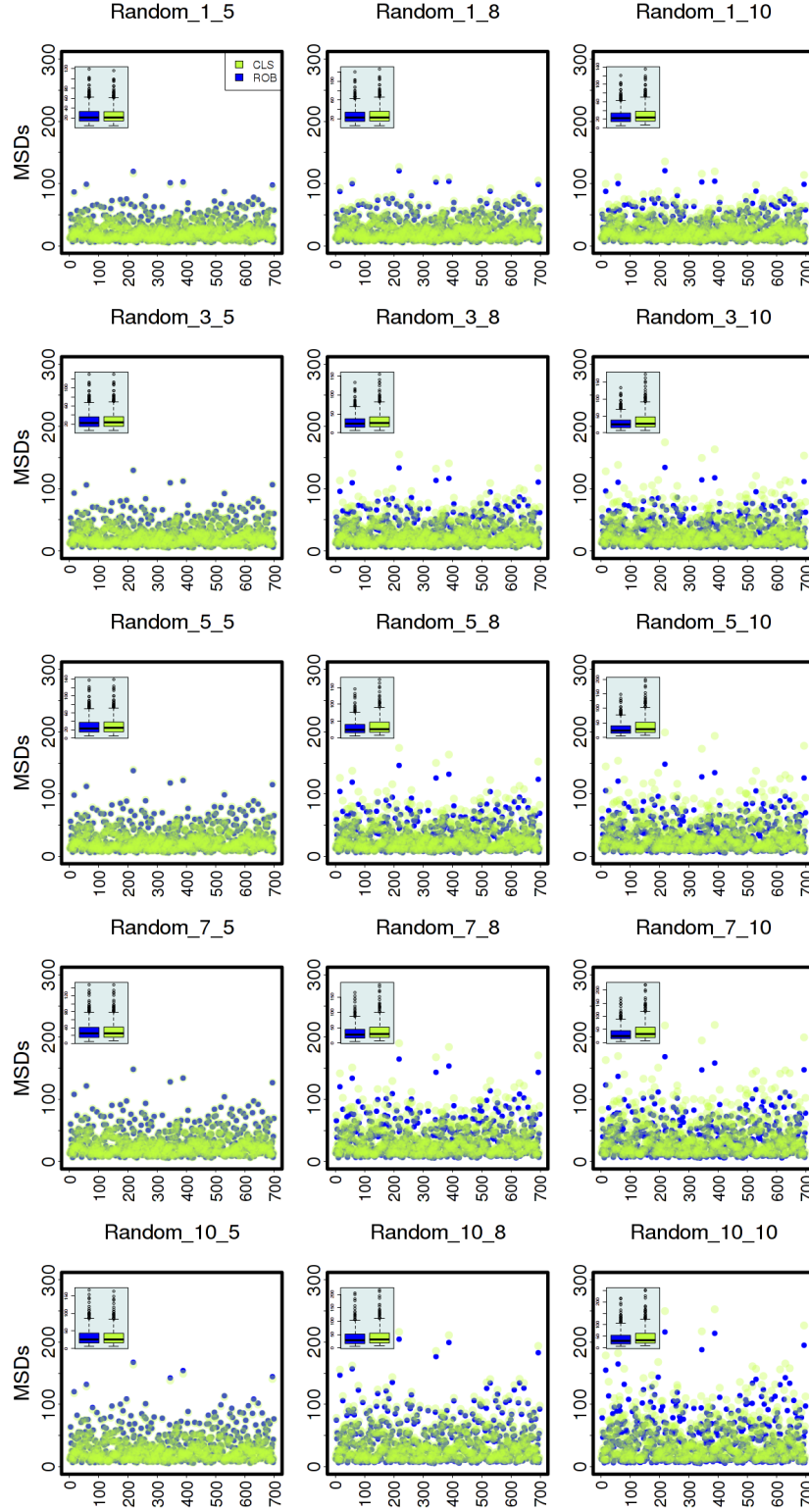


Figure S16. Plots of the classical and robust $\text{MSD}_g^i = \sum_{l=1}^{1000} \frac{(\hat{g}_{il} - g_{il})^2}{1000}$ for each of the 698 genotypes for the **random** contamination scenarios (2nd stage)

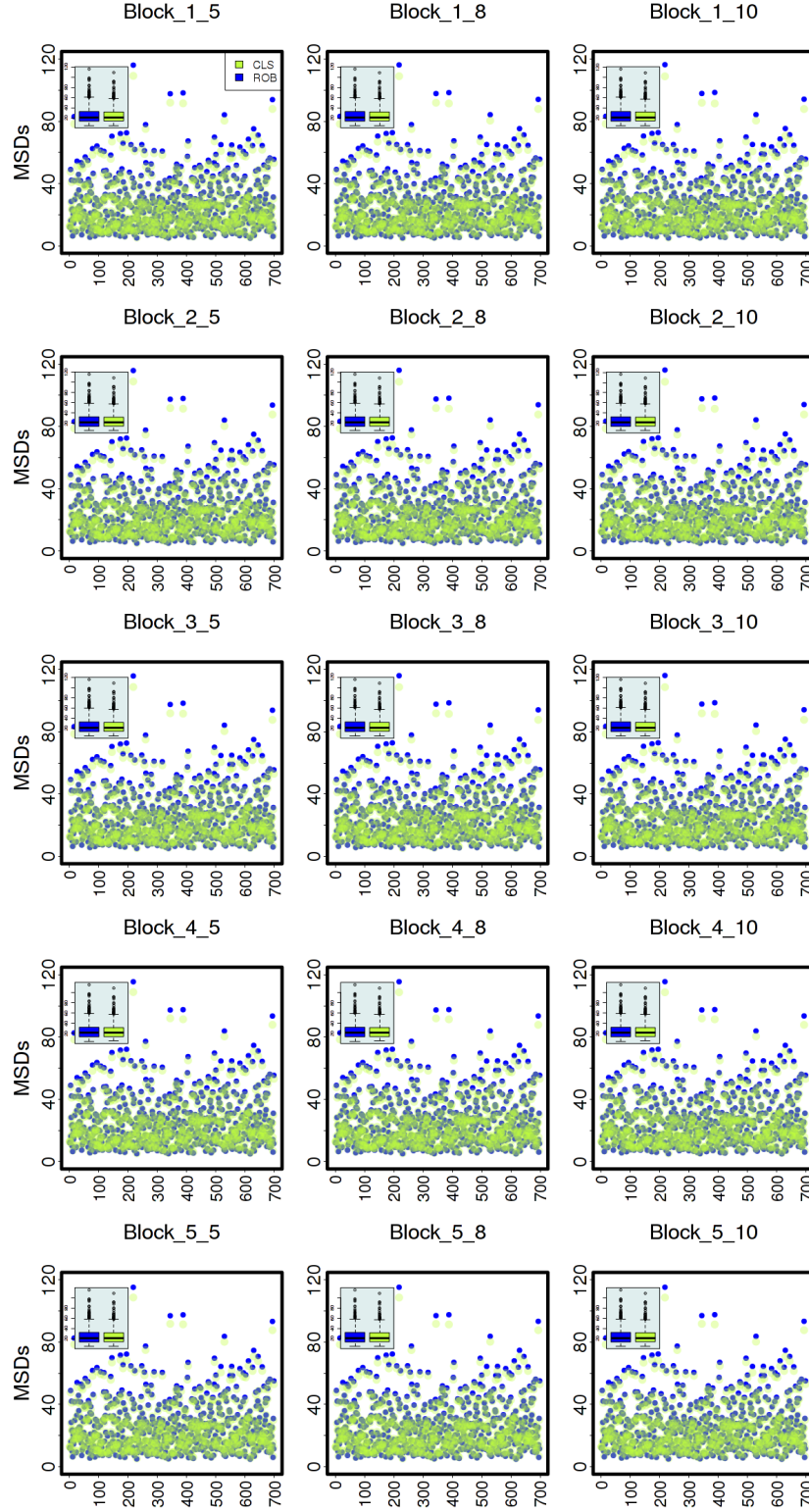


Figure S17. Plots of the classical and robust $\text{MSD}_g^i = \sum_{l=1}^{1000} \frac{(\hat{g}_{il} - g_{il})^2}{1000}$ for each of the 698 genotypes for the **block** contamination scenarios (2nd stage)

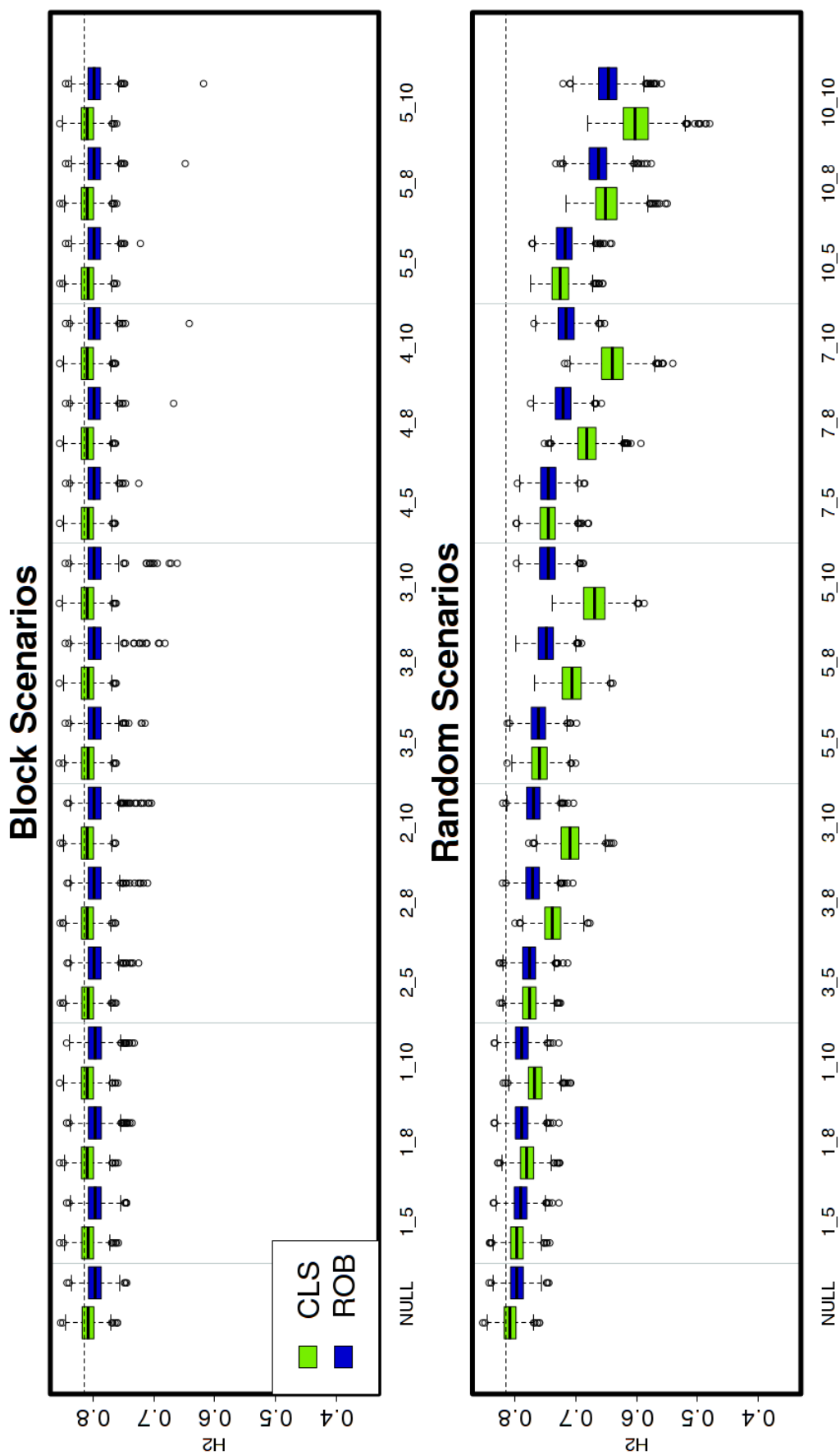


Figure S18. Boxplots of estimated heritabilities (H^2) computed by method M5 for the **block** and **random** contamination scenarios (3rd stage)

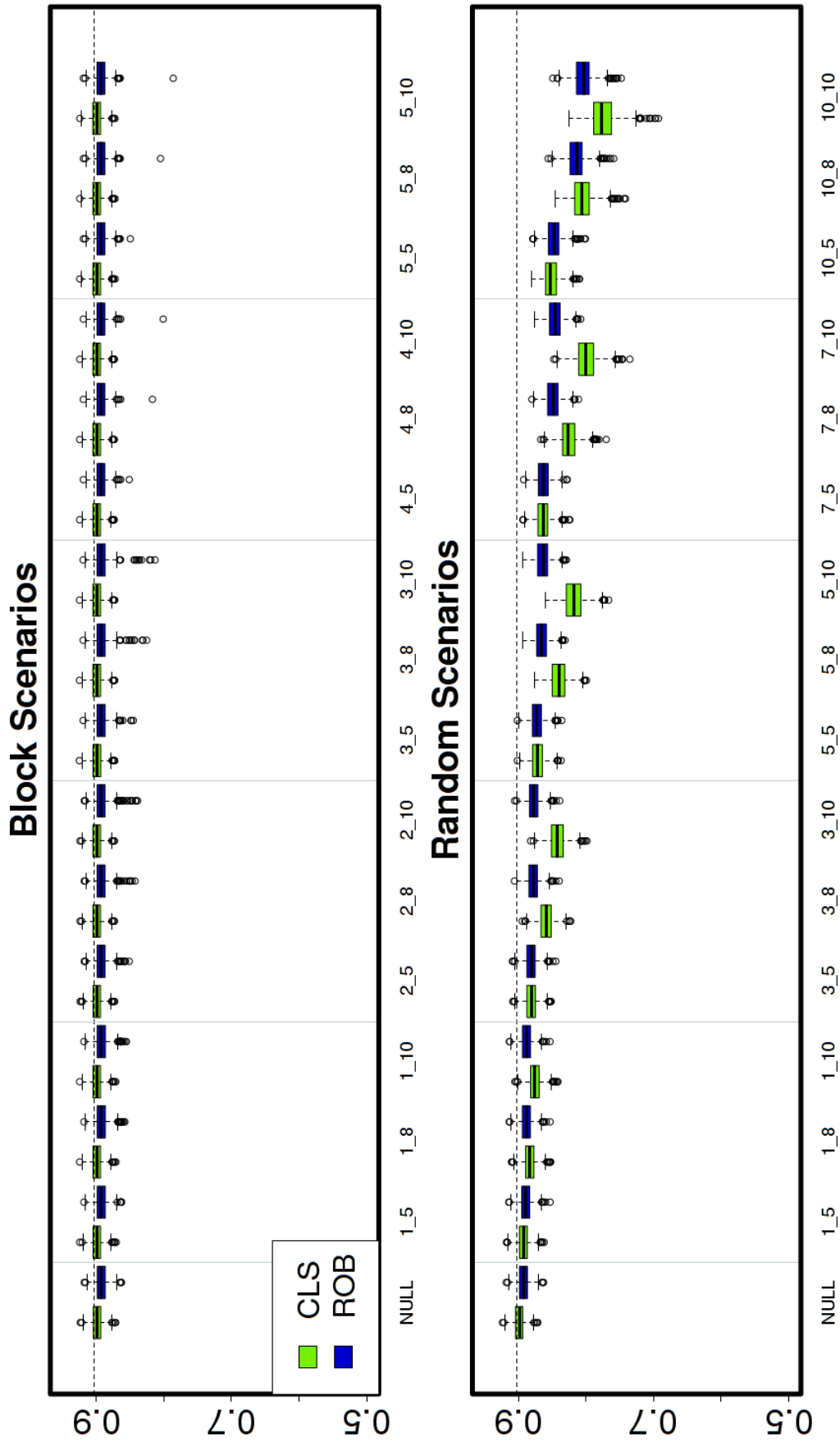


Figure S19. Boxplots of estimated predictive accuracies (PA) computed by method M5 for the **block** and **random** contamination scenarios (3rd stage)

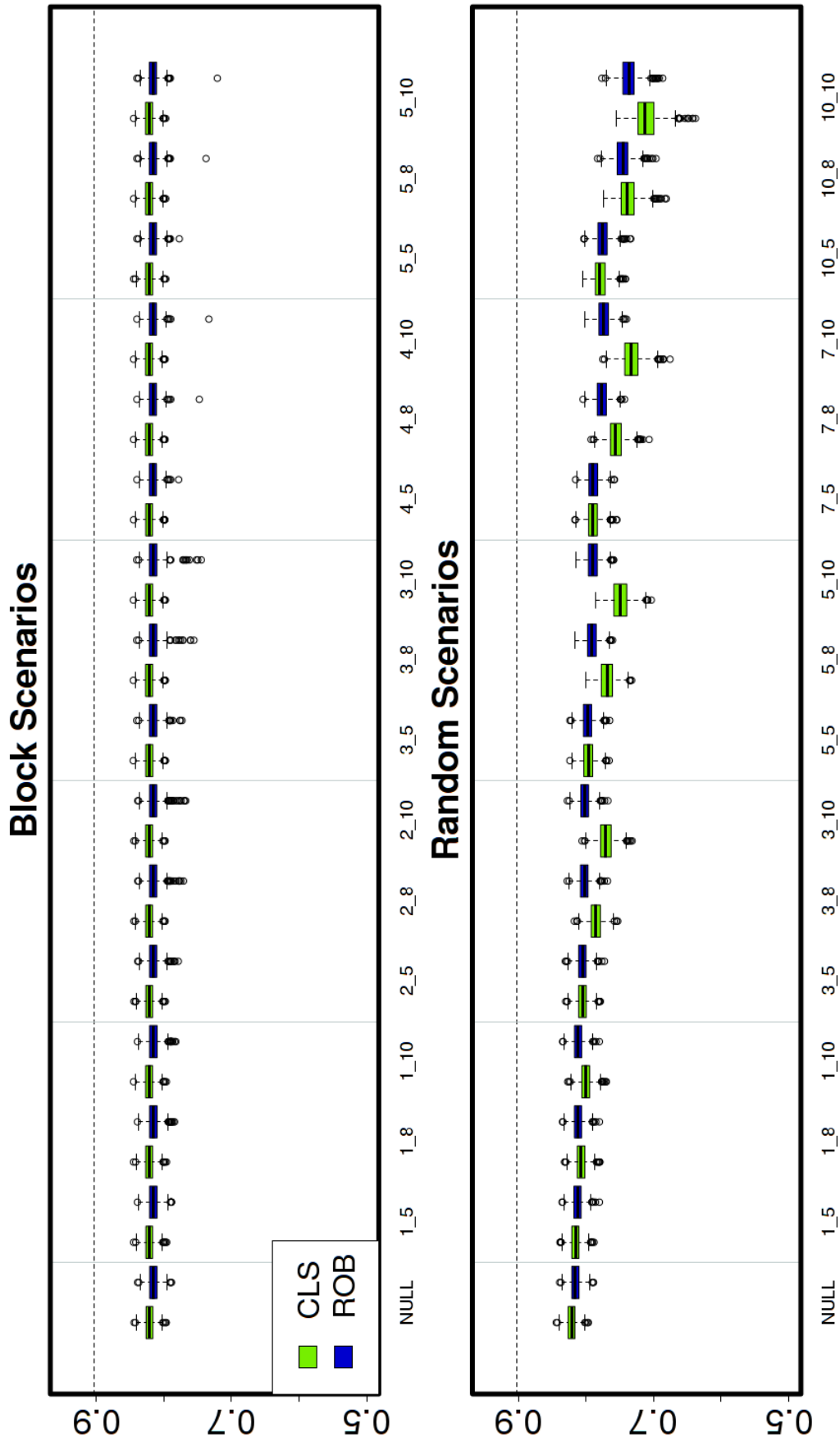


Figure S20. Boxplots of estimated predictive accuracies (PA) computed by method **M7** for the **block** and **random** contamination scenarios (3rd stage)