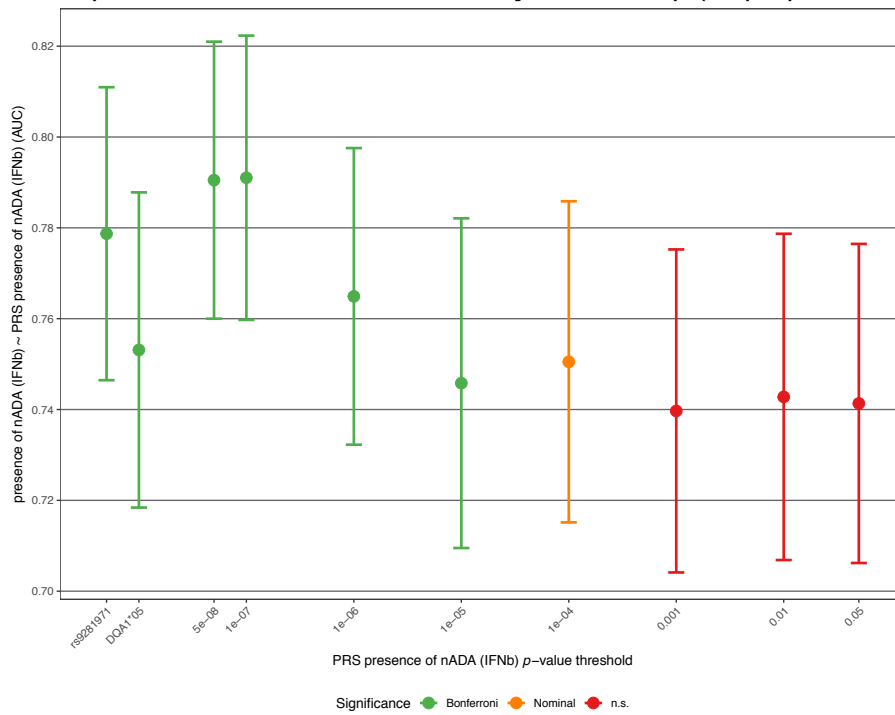


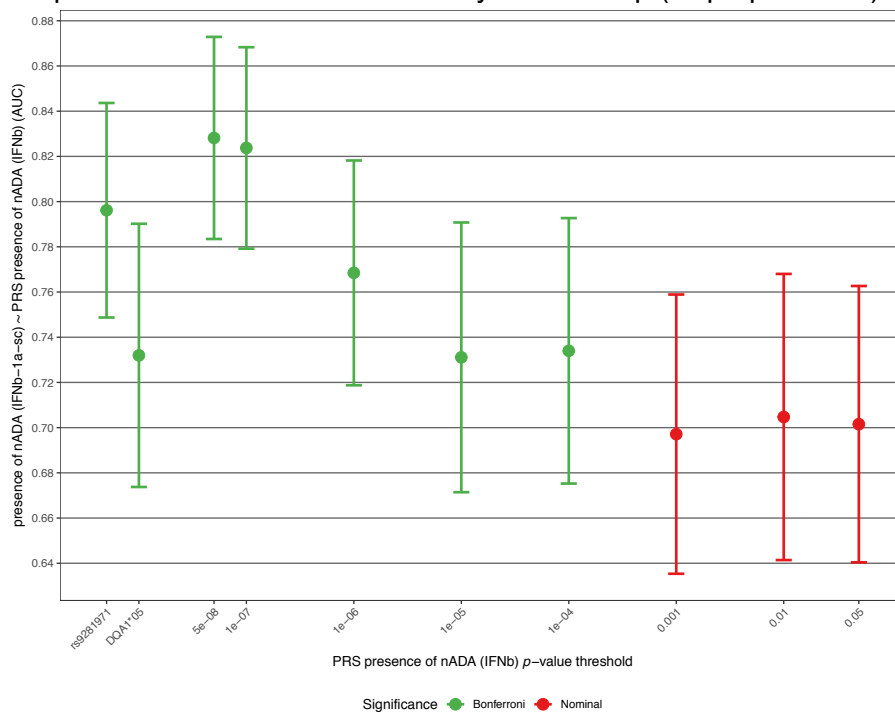
**Treatment-specific prediction of the presence of nADA in the replication data: performance of single models.**

Eight PRS, the top single GWAS variant, and the top *HLA* allele from the discovery stage. Covariates: sex, age, treatment duration, titration site, and ancestry components. The plots show the area under the receiver operating characteristic curve (AUC) and its 95 % confidence interval (CI). Bonferroni = significant after Bonferroni correction for multiple testing; nominal = nominally significant ( $p < 0.05$ ); n.s. = not significant.

**A:** AUC for the prediction of the presence of nADA across all treatment preparations using all ten prediction models based on analyses for IFN $\beta$  (all preparations) in the discovery data.

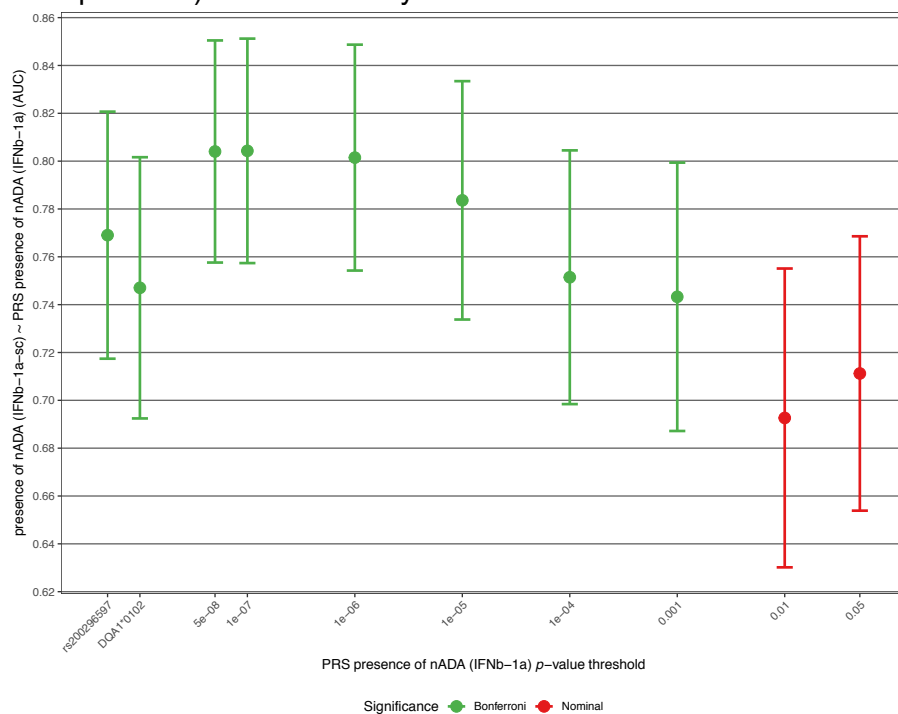


**B:** AUC for the prediction of the presence of nADA in IFN $\beta$ -1a s.c.-treated patients using all ten prediction models based on analyses for IFN $\beta$  (all preparations) in the discovery data.

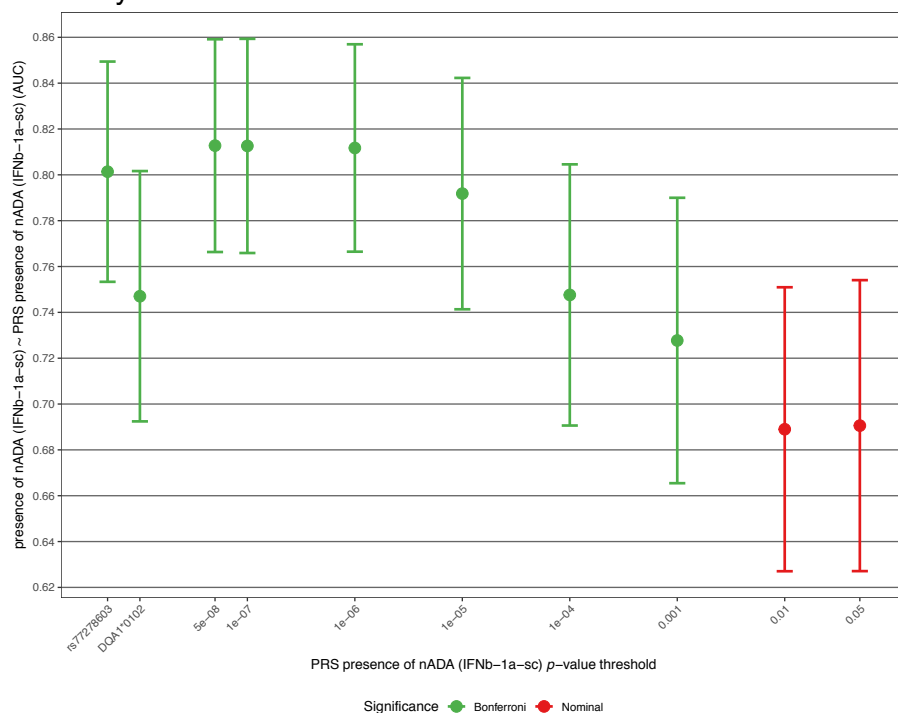


## Genetic risk for anti-drug antibodies against interferon-beta – Prediction results

**C:** AUC for the prediction of the presence of nADA in IFN $\beta$ -1a s.c.-treated patients from the replication data using all ten prediction models based on analyses for IFN $\beta$ -1a (IFN $\beta$ -1a s.c. + IFN $\beta$ -1a *i.m.*) in the discovery data.

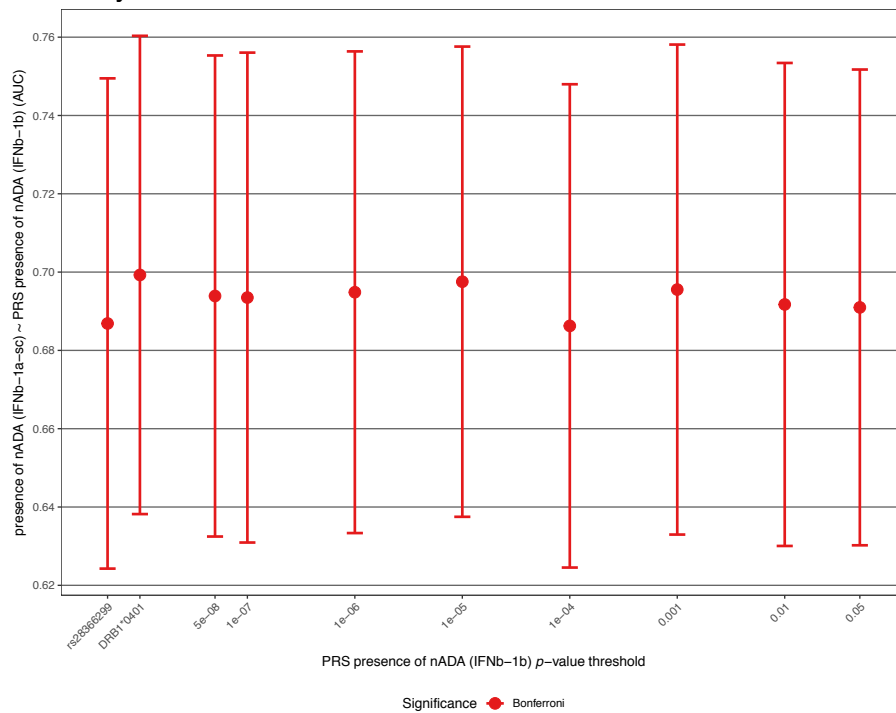


**D:** AUC for the prediction of the presence of nADA in IFN $\beta$ -1a s.c.-treated patients from the replication data using all ten prediction models based on analyses for IFN $\beta$ -1a s.c. in the discovery data.

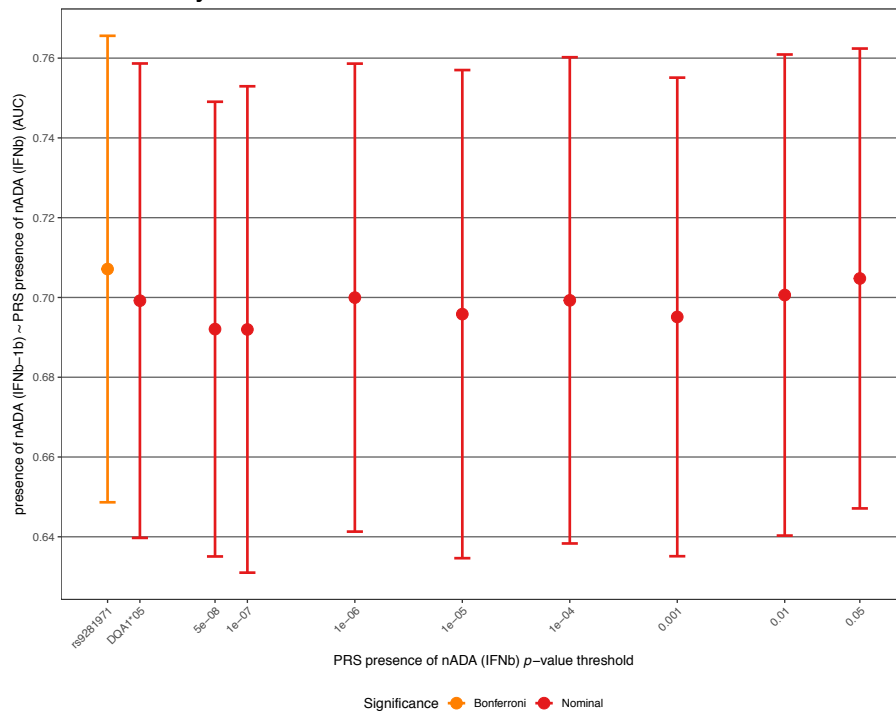


## Genetic risk for anti-drug antibodies against interferon-beta – Prediction results

**E:** AUC for the prediction of the presence of nADA in IFN $\beta$ -1a s.c.-treated patients from the replication data using all ten prediction models based on analyses for IFN $\beta$ -1b s.c. in the discovery data.

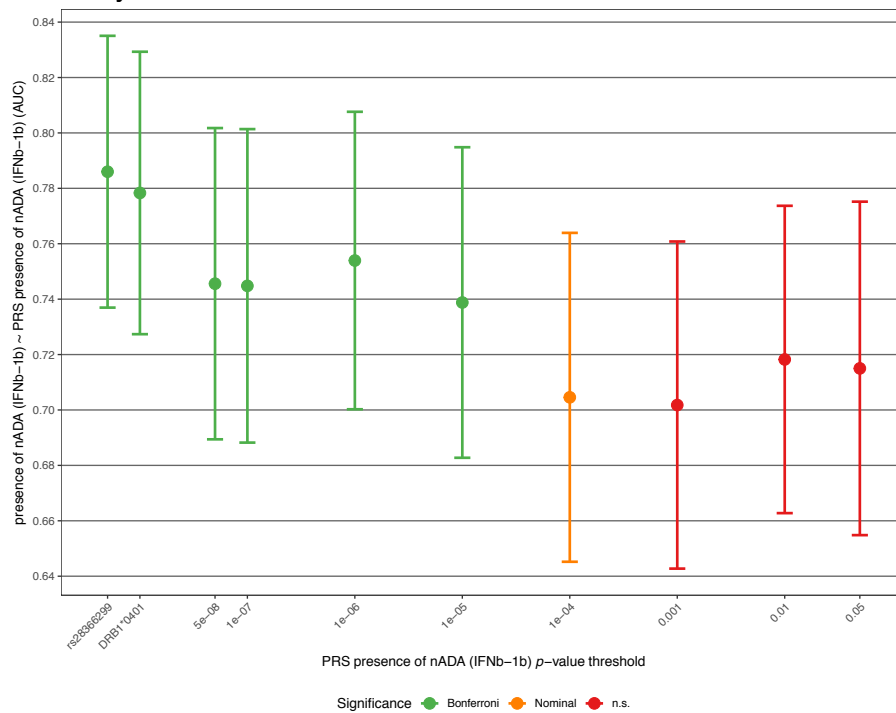


**F:** AUC for the prediction of the presence of nADA in IFN $\beta$ -1b s.c.-treated patients from the replication data using all ten prediction models based on analyses for IFN $\beta$  (all preparations) in the discovery data.

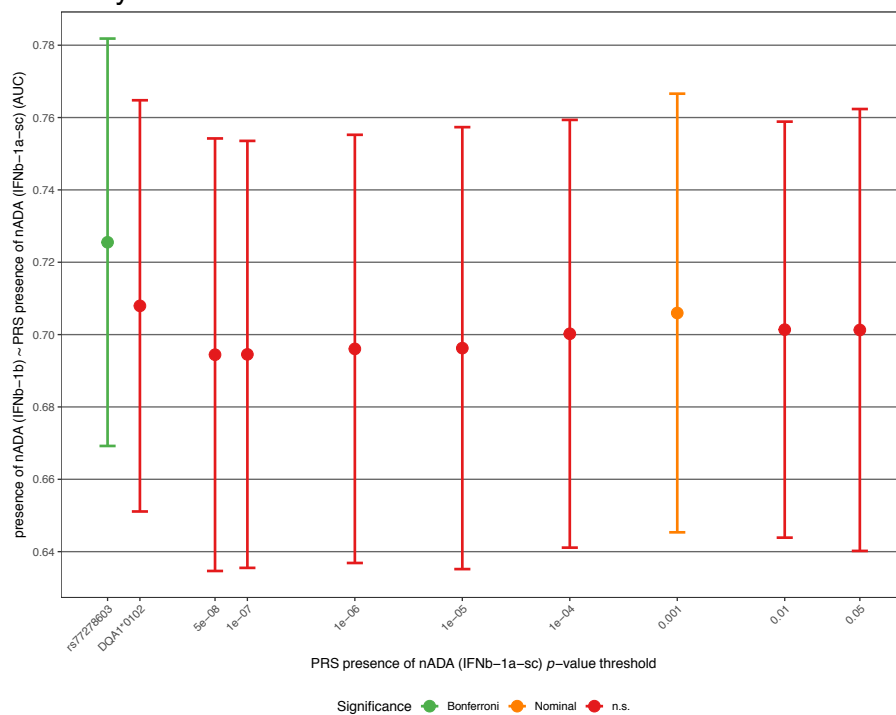


## Genetic risk for anti-drug antibodies against interferon-beta – Prediction results

**G:** AUC for the prediction of the presence of nADA in IFN $\beta$ -1b s.c.-treated patients from the replication data using all ten prediction models based on analyses for IFN $\beta$ -1b s.c. in the discovery data.



**H:** AUC for the prediction of the presence of nADA in IFN $\beta$ -1b s.c.-treated patients from the replication data using all ten prediction models based on analyses for IFN $\beta$ -1a s.c. in the discovery data.



## Genetic risk for anti-drug antibodies against interferon-beta – Prediction results

I: AUC for the prediction of the presence of nADA in IFN $\beta$ -1b s.c.-treated patients from the replication data using all ten prediction models based on analyses for IFN $\beta$ -1a (IFN $\beta$ -1a s.c. + IFN $\beta$ -1a *i.m.*) in the discovery data.

