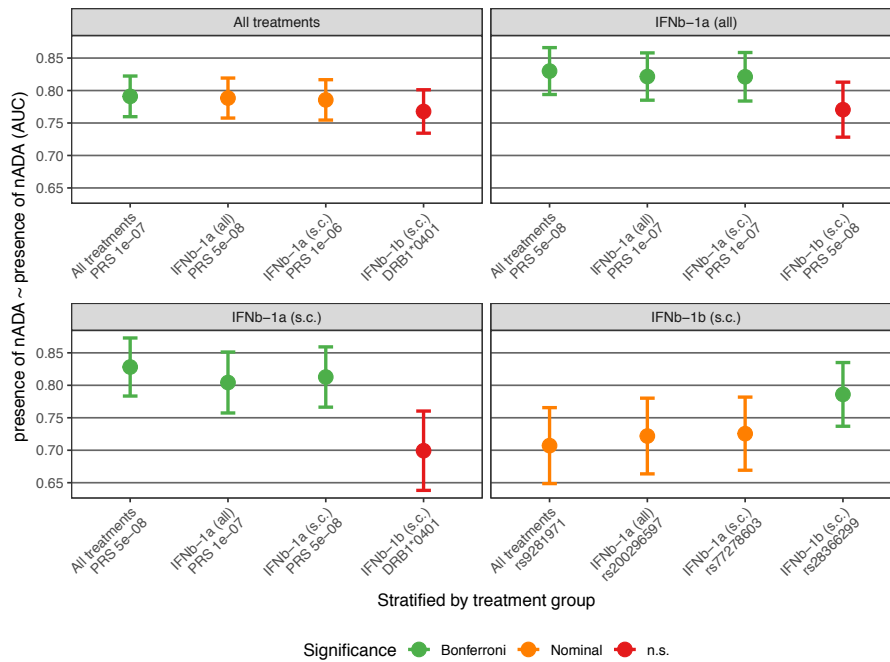


Genetic risk for anti-drug antibodies against interferon-beta – **Top prediction models**

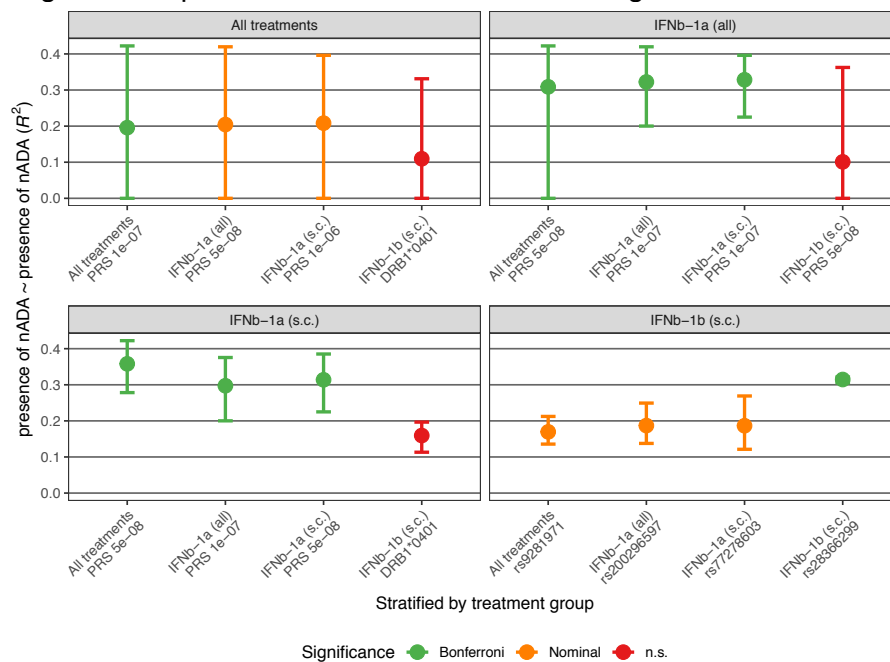
Treatment-specific prediction of the presence of nADA in the replication data: comparison of top models.

For each top model, the plots show either the AUC and its 95 % CI or Nagelkerke’s pseudo- R^2 and its 95 % CI. Boxes show the prediction groups (replication data) and columns within each box the training data groups (discovery data). Bonferroni = significant after Bonferroni correction for multiple testing; nominal = nominally significant ($p < 0.05$); n.s. = not significant.

A: Prediction of the presence of nADA using analyses on the presence of nADA. AUC of the model with the highest AUC for each treatment preparation.

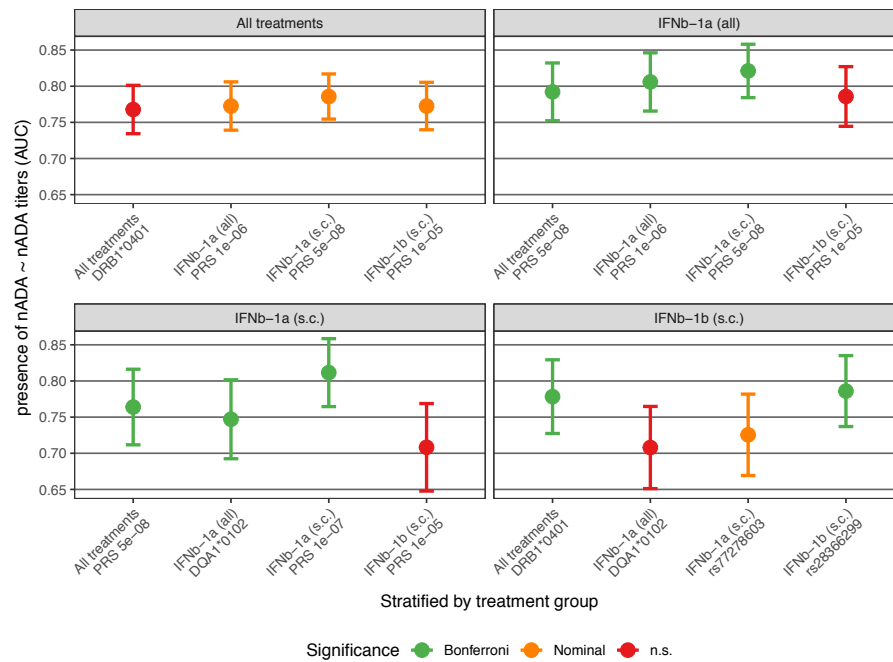


B: Prediction of the presence of nADA using analyses on the presence of nADA. Nagelkerke’s pseudo- R^2 of the model with the highest AUC for each treatment preparation.

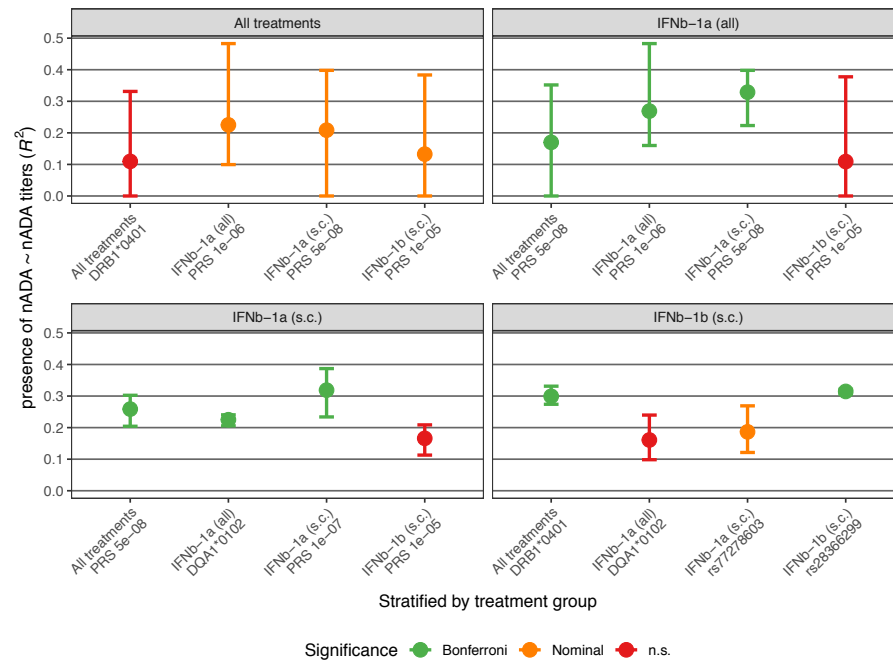


Genetic risk for anti-drug antibodies against interferon-beta – Top prediction models

C: Prediction of the presence of nADA using analyses of nADA titers. AUC of the model with the highest AUC for each treatment preparation.

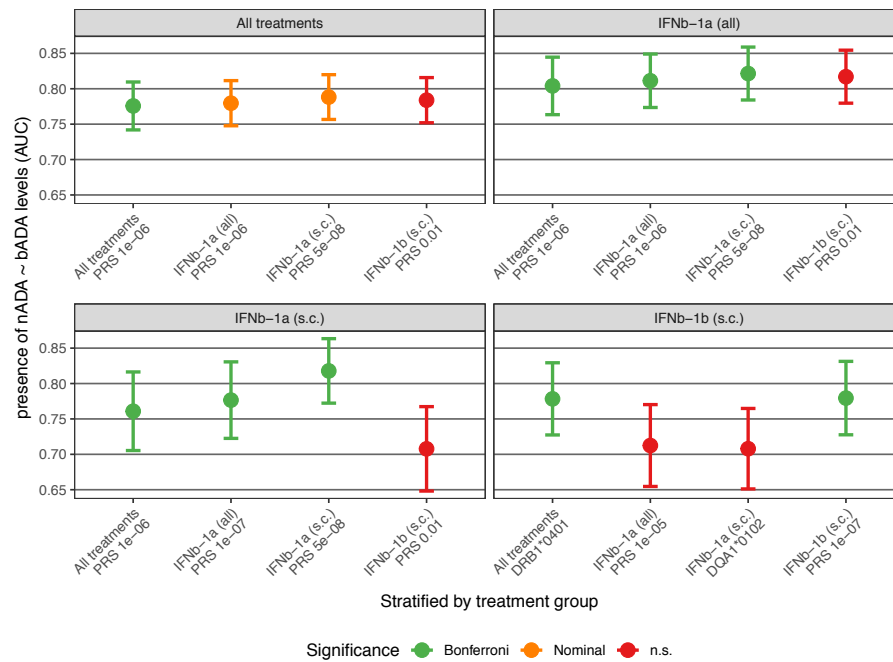


D: Prediction of the presence of nADA using analyses of nADA titers. Nagelkerke's pseudo- R^2 of the model with the highest AUC for each treatment preparation.



Genetic risk for anti-drug antibodies against interferon-beta – Top prediction models

E: Prediction of the presence of nADA using analyses of bADA levels. AUC of the model with the highest AUC for each treatment preparation.



F: Prediction of the presence of nADA using analyses of bADA levels. Nagelkerke's pseudo- R^2 of the model with the highest AUC for each treatment preparation.

