

Supplementary Data.

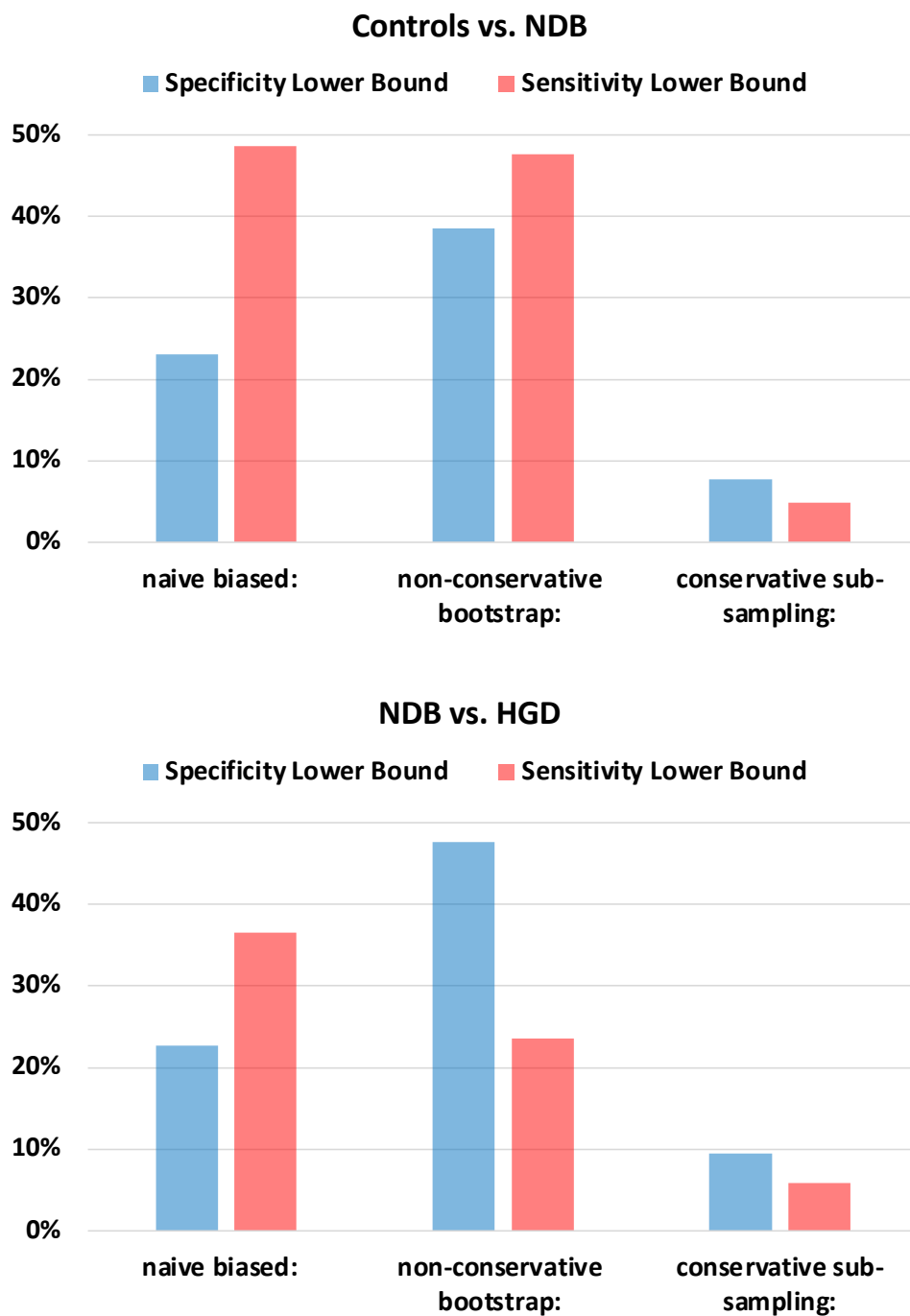


Figure S1. Standard nested cross validation: naive biased, non-conservative bootstrap, and *conservative* sub-sampling per sample derived prediction probability 95% confidence interval lower bounds for the estimates of specificity and sensitivity. **Blue bars** are 95% confidence interval lower bounds on the Specificity, and **red bars** are 95% confidence interval lower bounds on the Sensitivity.

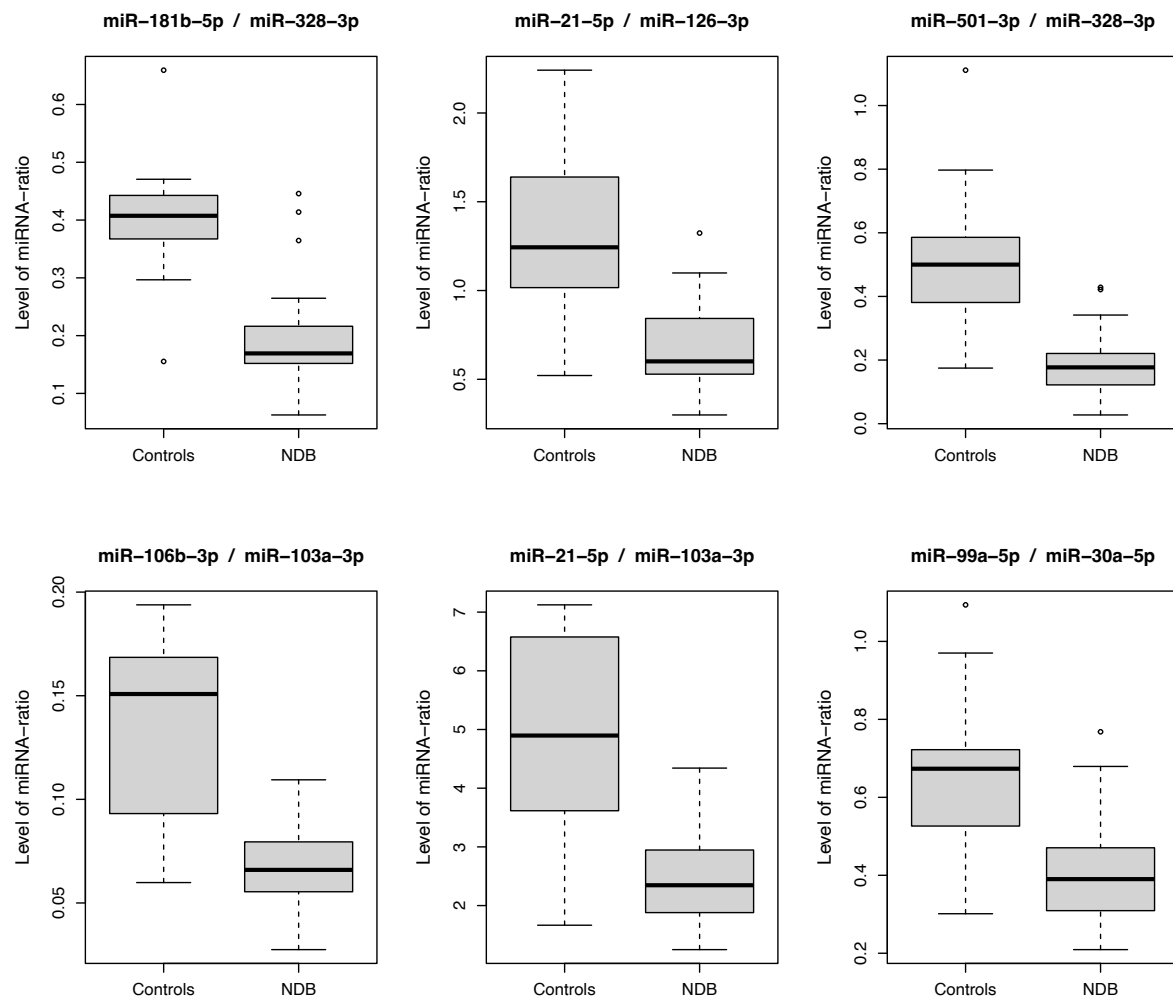


Figure S2. Controls vs. NDB: boxplots for miRNA-ratios in final models.
 Box (25th – 75th percentiles) and whisker (5th and 95th percentiles) plots with median values shown by a thick black line. Outlier values are shown by small open circles.

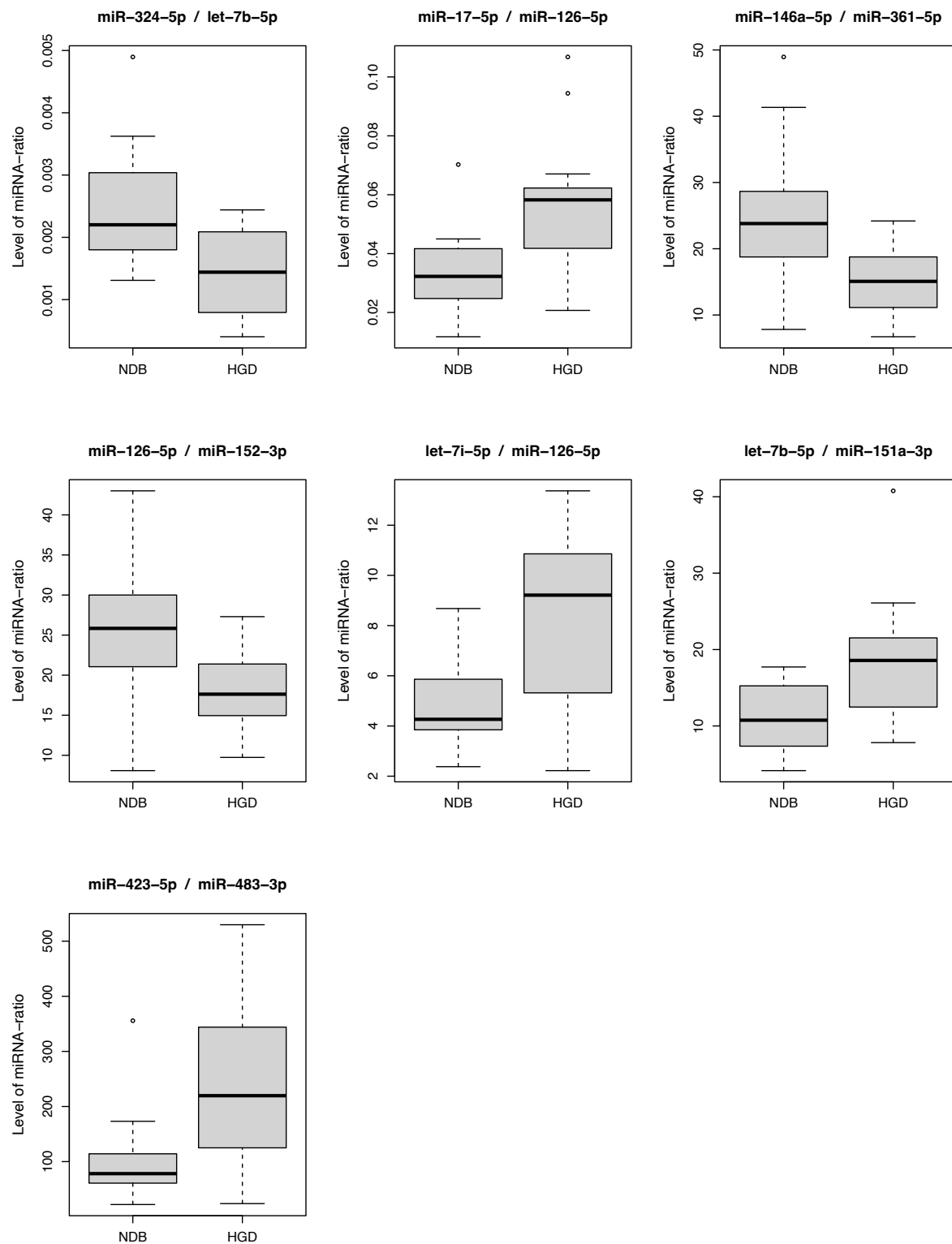
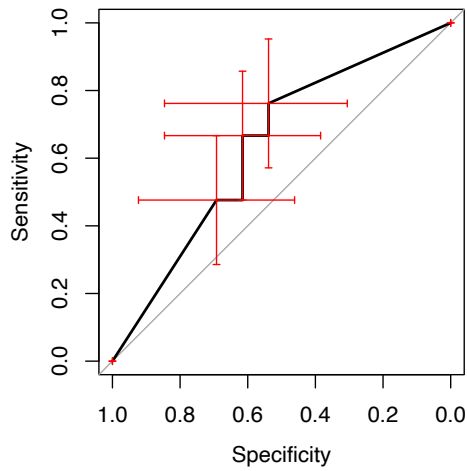


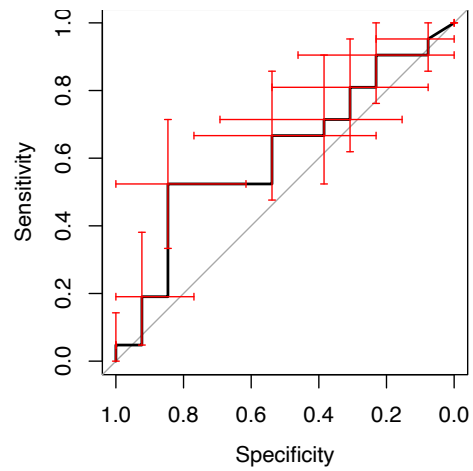
Figure S3. NDB vs. HGD: boxplots for miRNA-ratios in final models.

Box (25th – 75th percentiles) and whisker (5th and 95th percentiles) plots with median values shown by a thick black line. Outlier values are shown by small open circles.

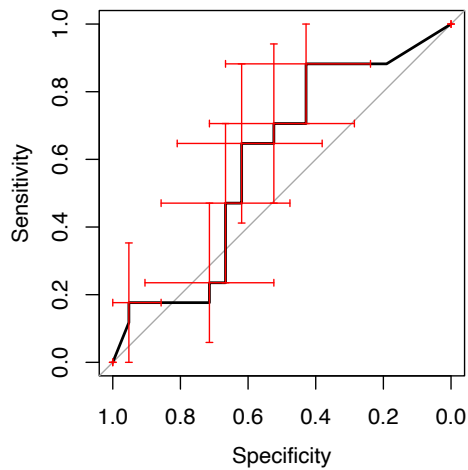
a. Non-conservative: Controls vs. NDB
lambda.min



b. Non-conservative: Controls vs. NDB
lambda.1se



c. Non-conservative: NDB vs. HGD
lambda.min



d. Non-conservative: NDB vs. HGD
lambda.1se

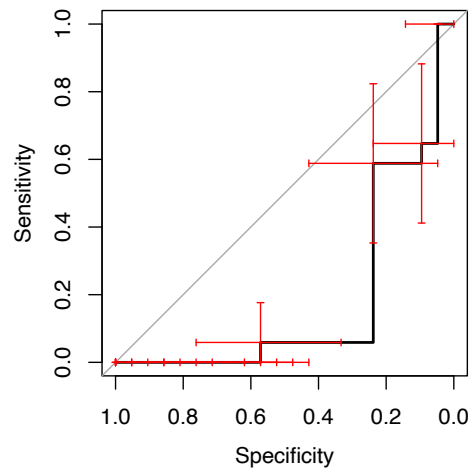


Figure S4. Effects of increased regularisation on predictive capacity.

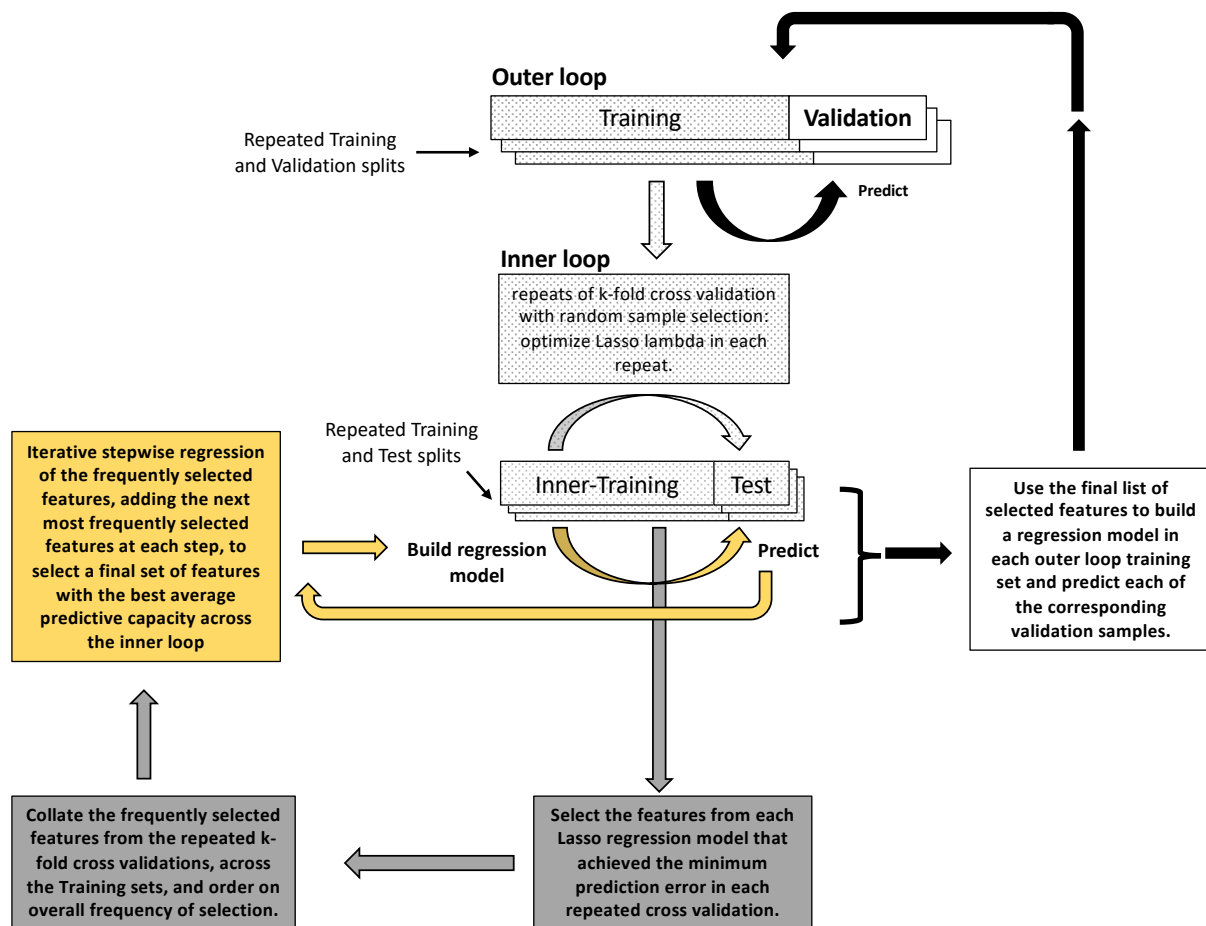
Lambda.min refers to the optimum level of penalisation for LASSO regression that minimises the prediction error. **Lambda.1se** refers to an increased level of penalisation for LASSO regression that lies within one standard error of λ_{\min} . ROC curve error bars (red) are non-conservative bootstrapped 95% confidence intervals.

Supplementary Table S1. Details of miRNAs in final model miRNA-ratios for Controls vs. NDB.

	miRBase v22 ID	miRBase v22 mature sequence	miRbase Accession
1	hsa-miR-181b-5p	AACAUUCAUUGCUGUCGGUGGGU	MIMAT0000257
2	hsa-miR-328-3p	CUGGCCUCUCUGCCCUUCCGU	MIMAT0000752
3	hsa-miR-21-5p	UAGCUUAUCAGACUGAUGUUGA	MIMAT0000076
4	hsa-miR-126-3p	UCGUACCGUGAGUAAUAAUGCG	MIMAT0000445
5	hsa-miR-501-3p	AAUGCACCCGGGCAAGGAUUCU	MIMAT0004774
6	hsa-miR-106b-3p	CCGCACUGUGGGUACUUGCUGC	MIMAT0004672
7	hsa-miR-103a-3p	AGCAGCAUUGUACAGGGCUAUGA	MIMAT0000101
8	hsa-miR-99a-5p	AACCCGUAGAUCCGAUCUUGUG	MIMAT0000097
9	hsa-miR-30a-5p	UGUAAACAUCCUCGACUGGAAG	MIMAT0000087

Supplementary Table S2. Details of miRNAs in final model miRNA-ratios for NDB vs. HGD.

	miRBase v22 ID	miRBase v22 mature sequence	miRbase Accession
1	hsa-miR-324-5p	CGCAUCCCCUAGGGCAUUGGUG	MIMAT0000761
2	hsa-let-7b-5p	UGAGGUAGUAGGUUGUGUGGUU	MIMAT0000063
3	hsa-miR-17-5p	CAAAGUGCUUACAGUGCAGGUAG	MIMAT0000070
4	hsa-miR-126-5p	CAUUAUUACUUUUGGUACGCG	MIMAT0000444
5	hsa-miR-146a-5p	UGAGAACUGAAUUGCAUGGGUU	MIMAT0000449
6	hsa-miR-361-5p	UUAUCAGAAUCUCCAGGGGUAC	MIMAT0000703
7	hsa-miR-152-3p	UCAGUGCAUGACAGAACUUGG	MIMAT0000438
8	hsa-let-7i-5p	UGAGGUAGUAGUUUGUGCUGUU	MIMAT0000415
9	hsa-miR-151a-3p	CUAGACUGAAGCUCCUUGAGG	MIMAT0000757
10	hsa-miR-423-5p	UGAGGGGCAGAGAGCGAGACUUU	MIMAT0004748
11	hsa-miR-483-3p	UCACUCCUCUCCUCCCGUCUU	MIMAT0002173



Supplementary Schema: Stable nested cross validation (StaVarSel) scheme: In the inner loop the level of regularisation (λ) for the regression model was optimised via repeated 10-fold cross validation. The miR-ratios derived from applying lasso regression with the optimised λ to each training set were collated, ranked according to frequency of selection, and then subjected to a form of stepwise forward regression to determine the optimum model with the least prediction error. The miR-ratios selected from the inner loop cross validation were used to build regression models in each training set, and these models were then used to make predictions for the held-out samples.