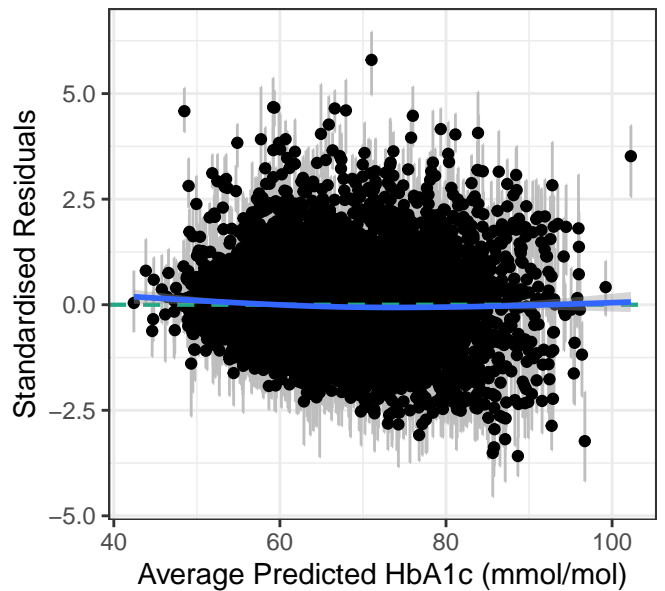
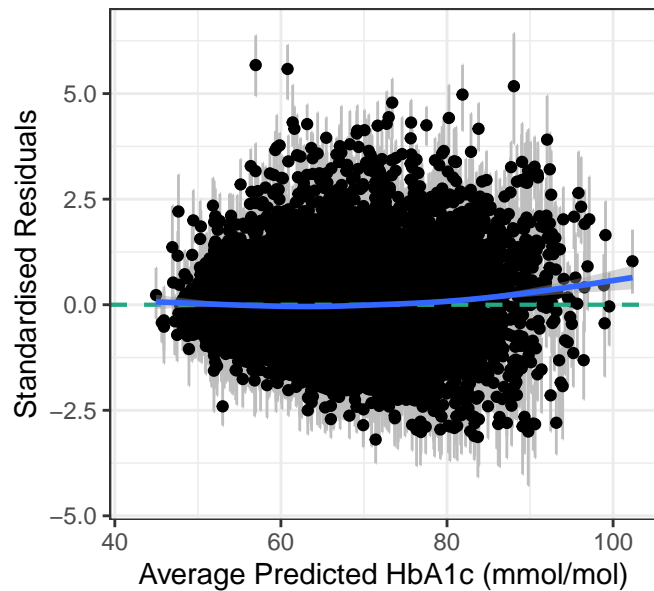
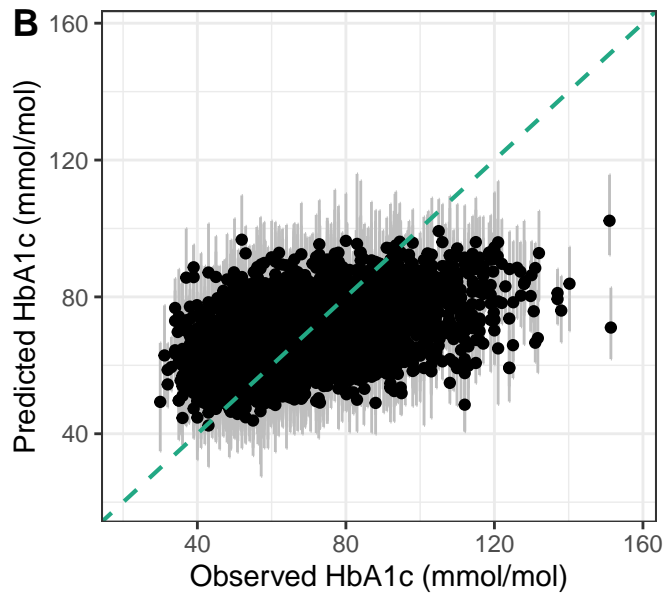
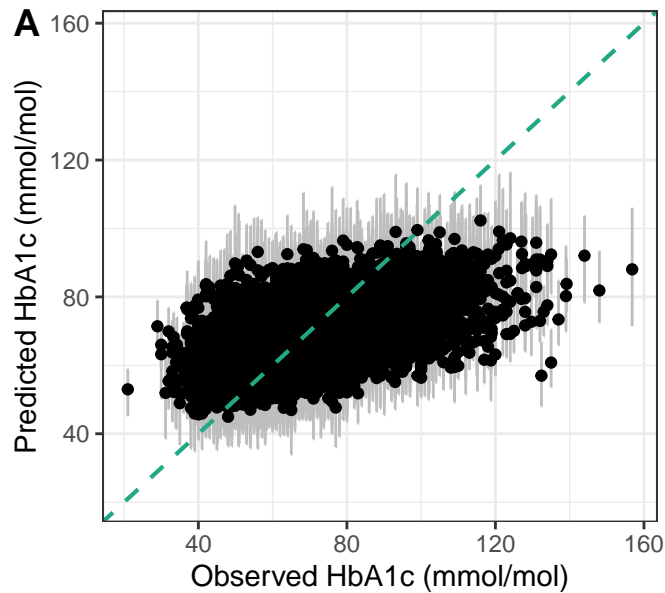


Residuals of Model 4



Model

R2 (bigger is better)

0.26

0.28

0.30

0.32

Model

RMSE (smaller is better)

13.4

13.6

13.8

Model

RSS (smaller is better)

1300000

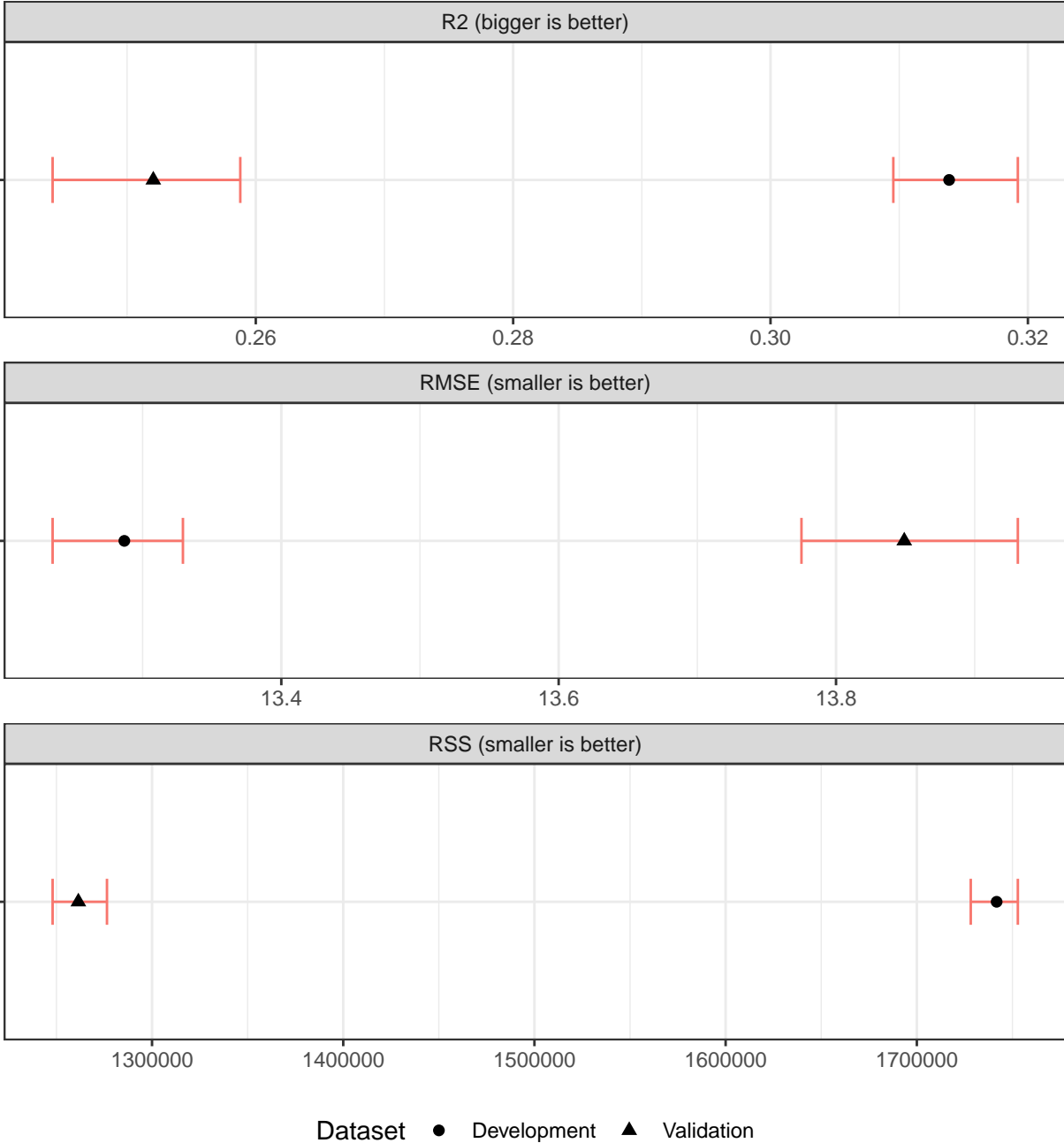
1400000

1500000

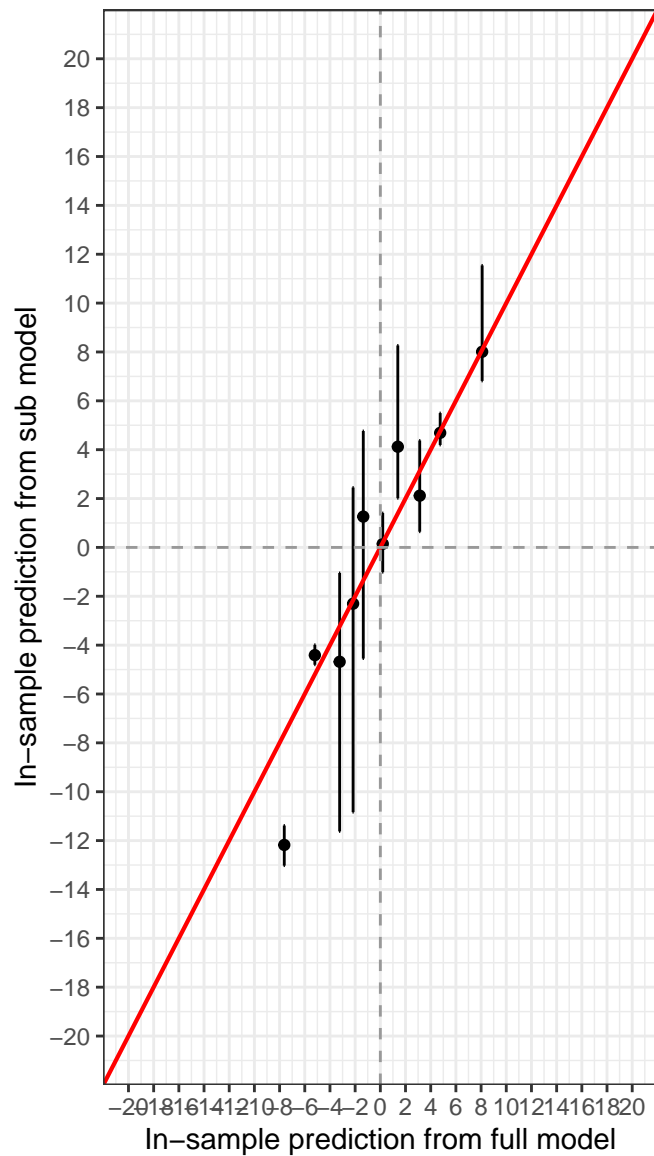
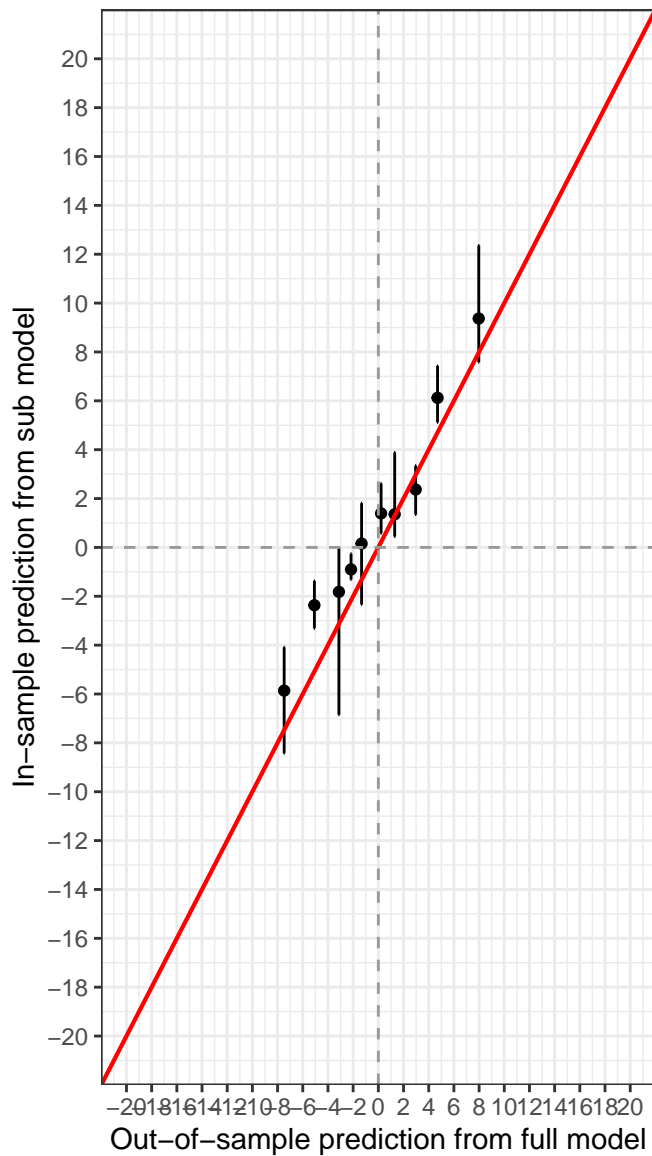
1600000

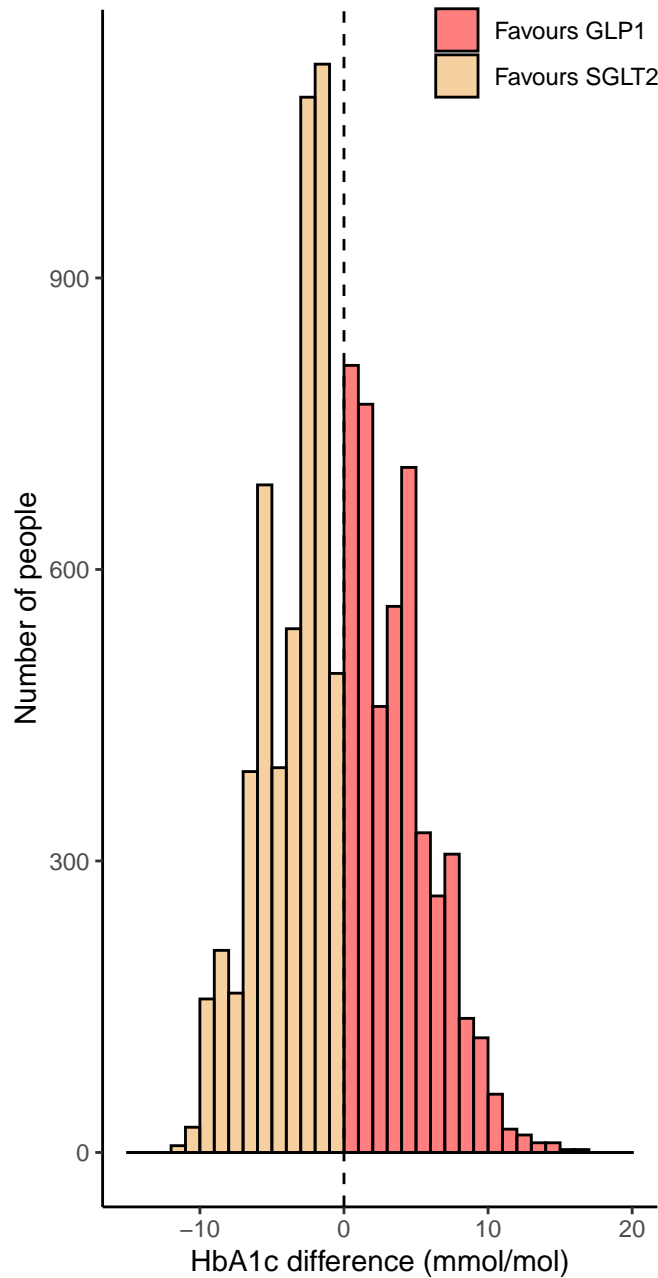
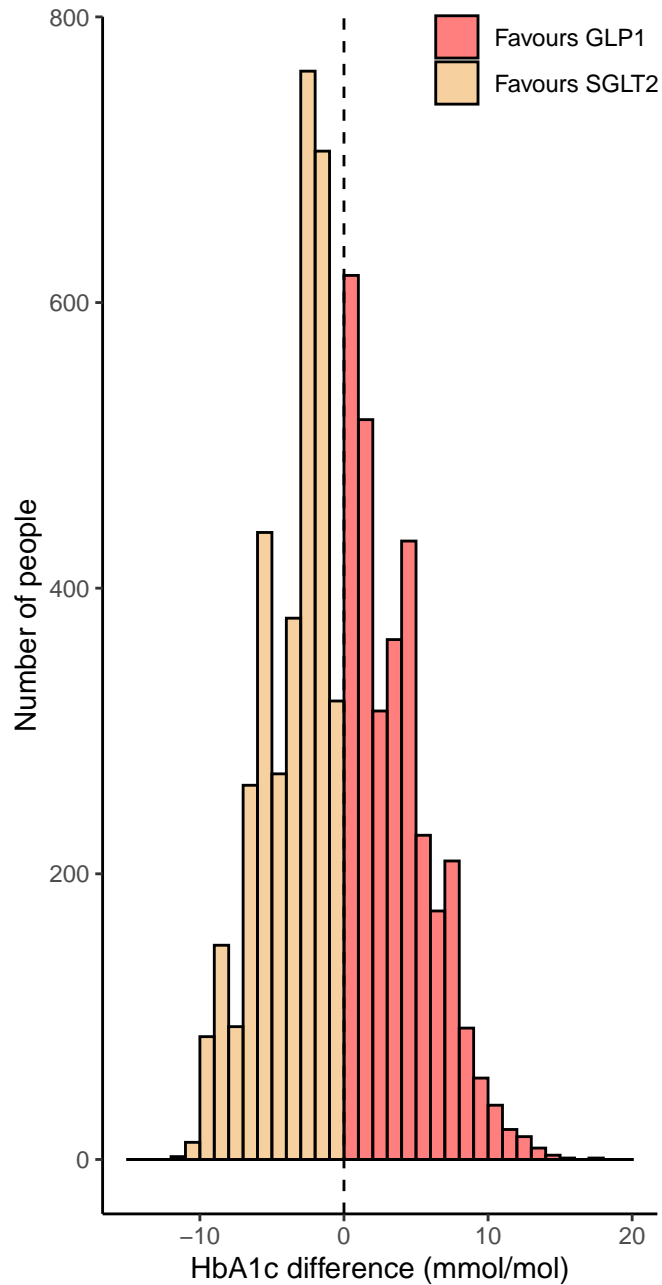
1700000

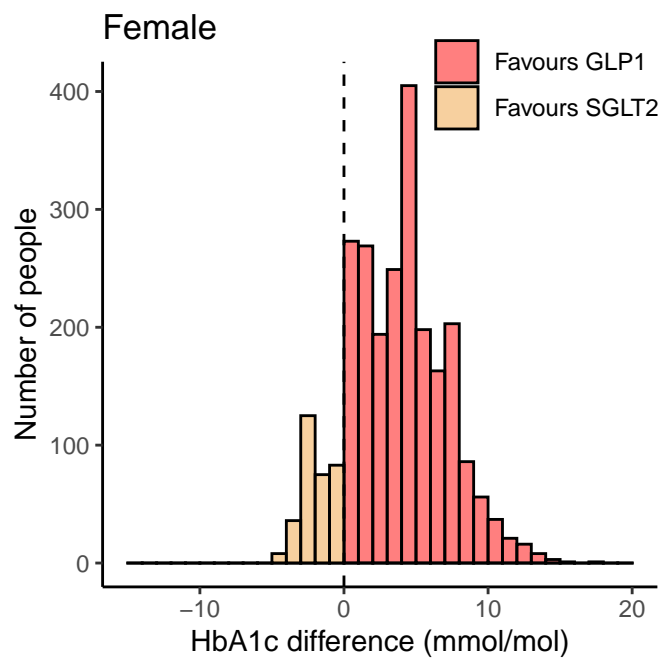
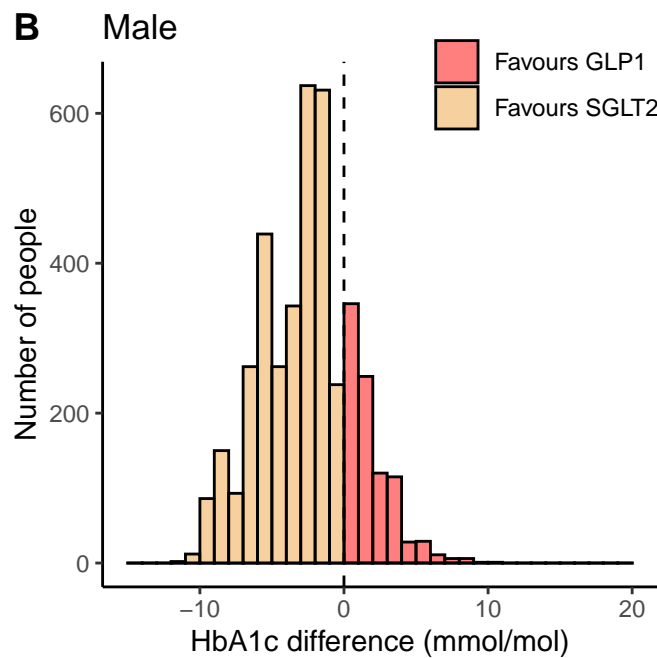
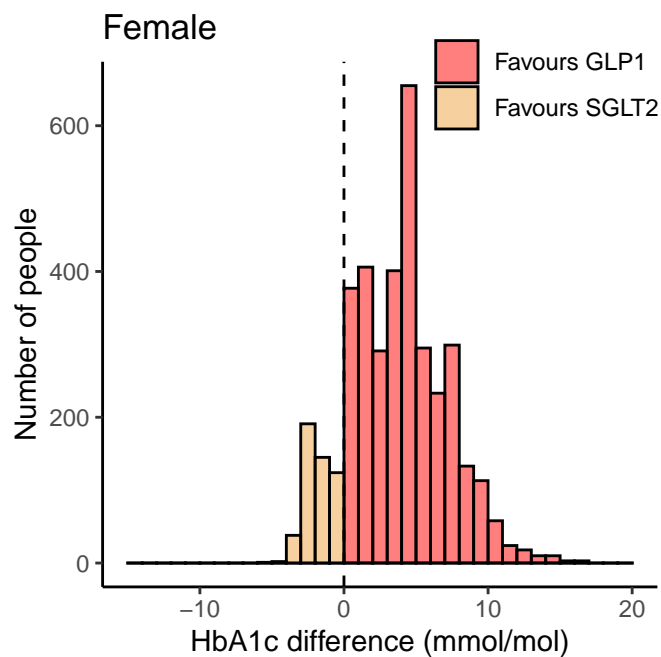
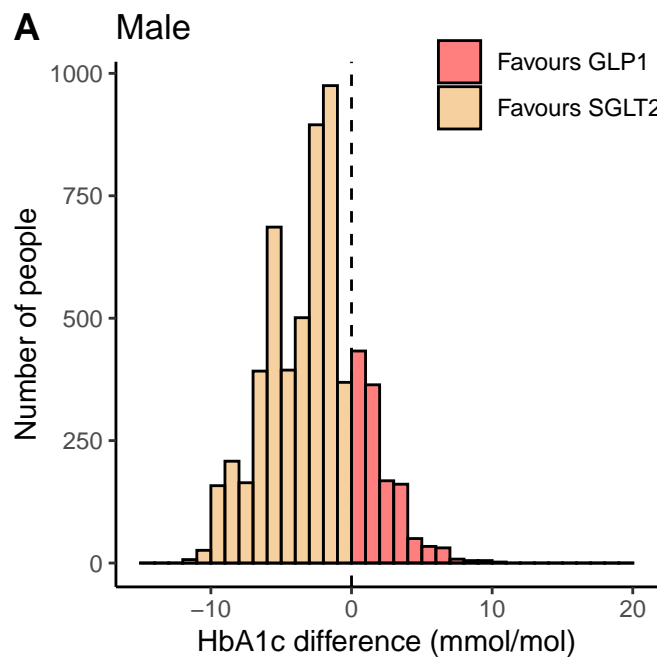
Dataset ● Development ▲ Validation



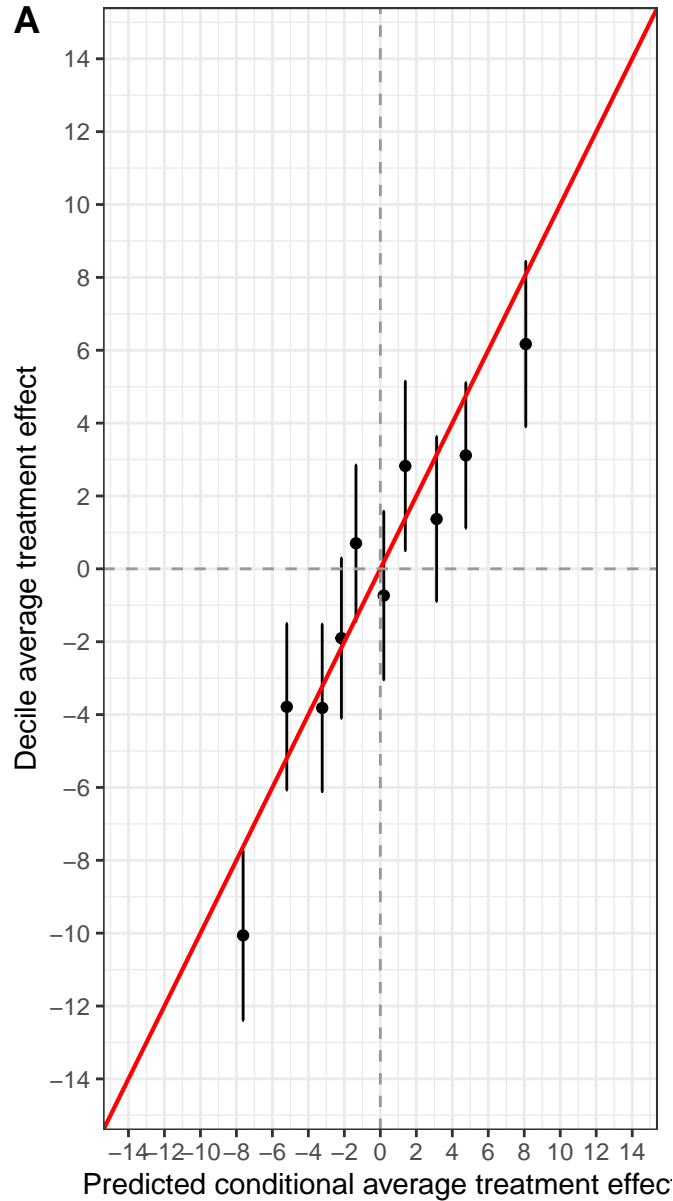
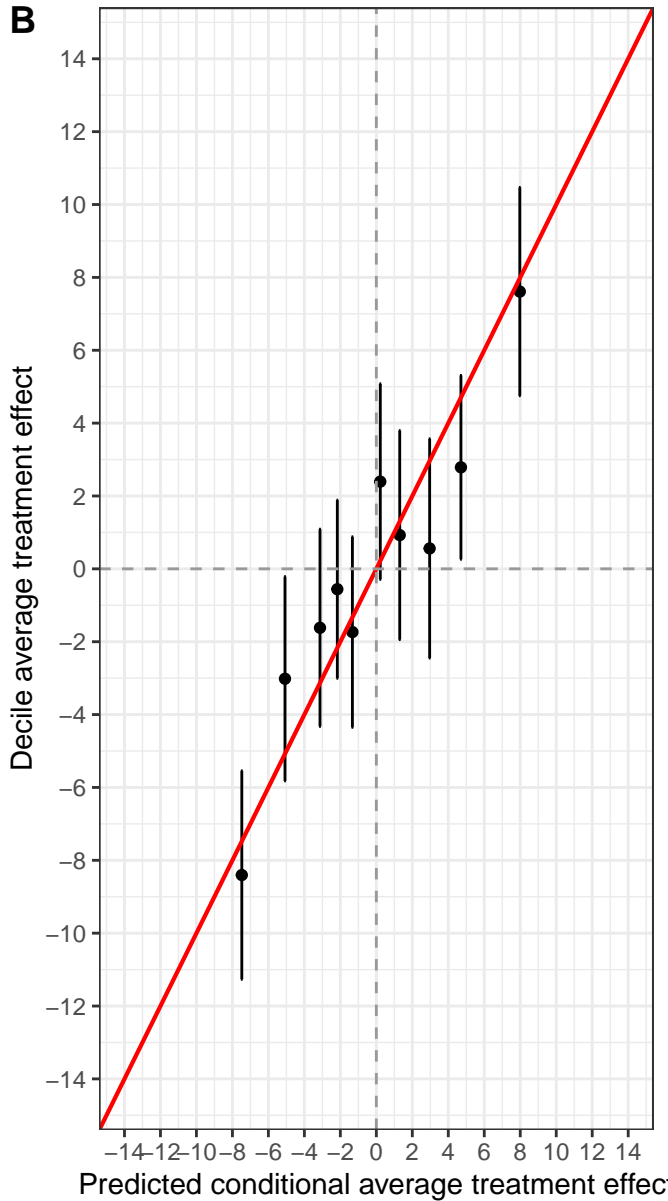
Effect submodels

A**B**

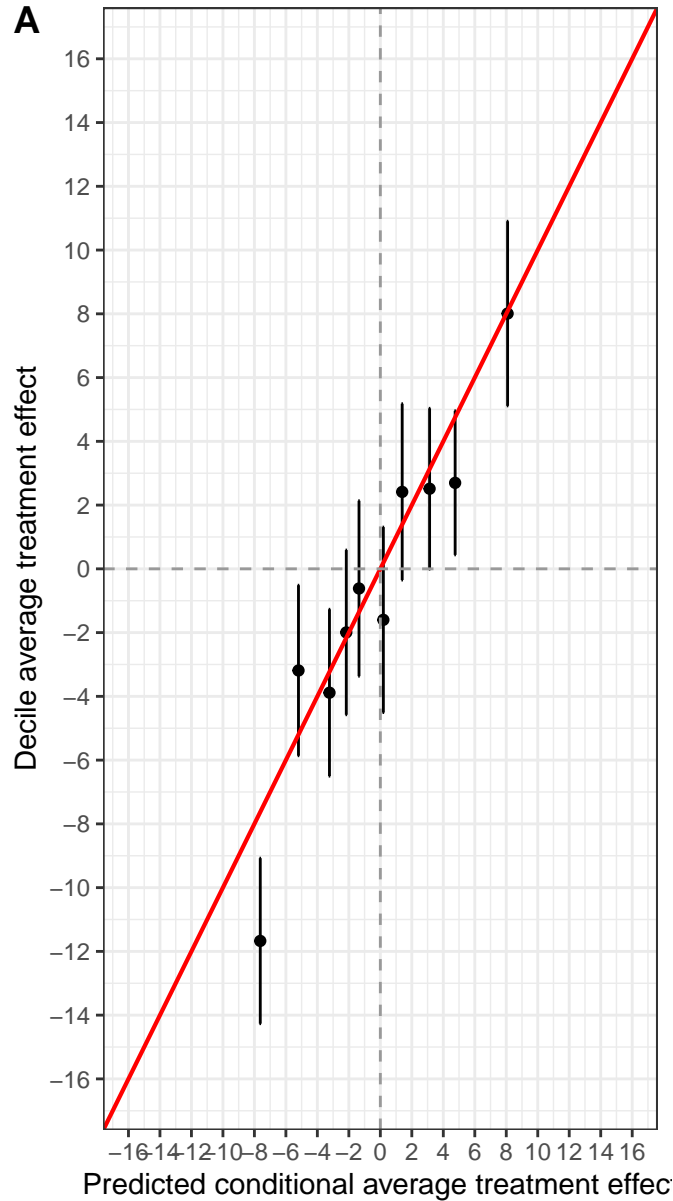
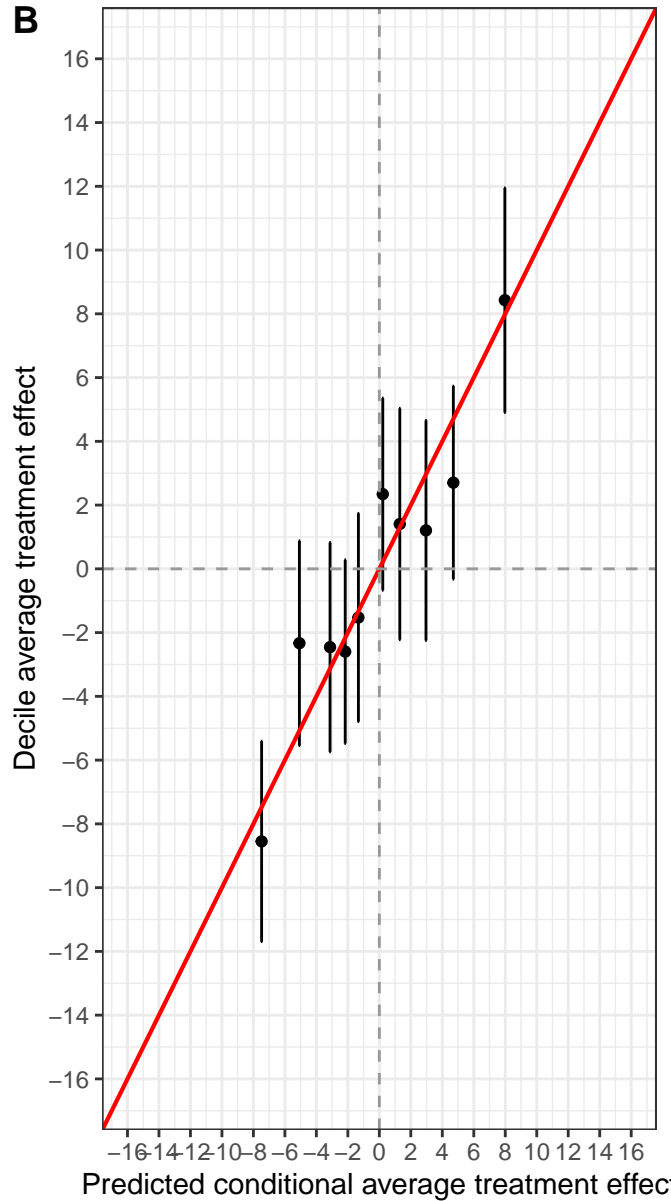
A**B**



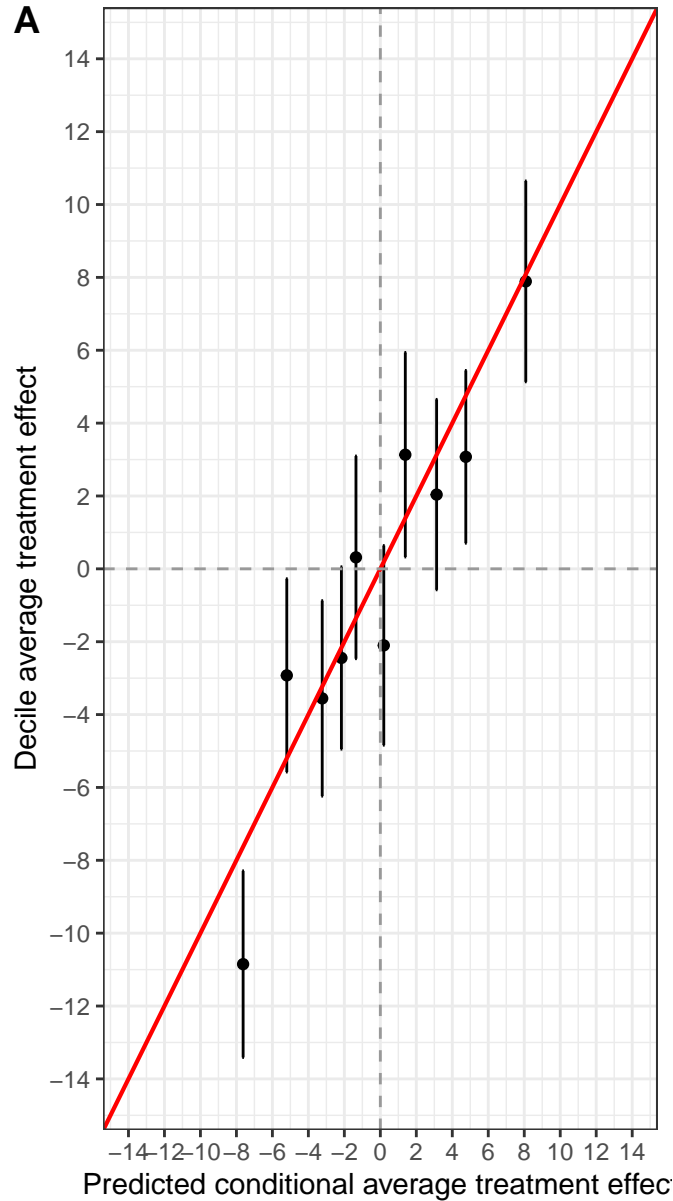
Effects validation $\text{lm}(\text{hba1c} \sim \text{drugclass} + \text{prop_score})$

A**B**

Effects validation prop score matching

A**B**

Effects validation prop score inverse weighting

A**B**