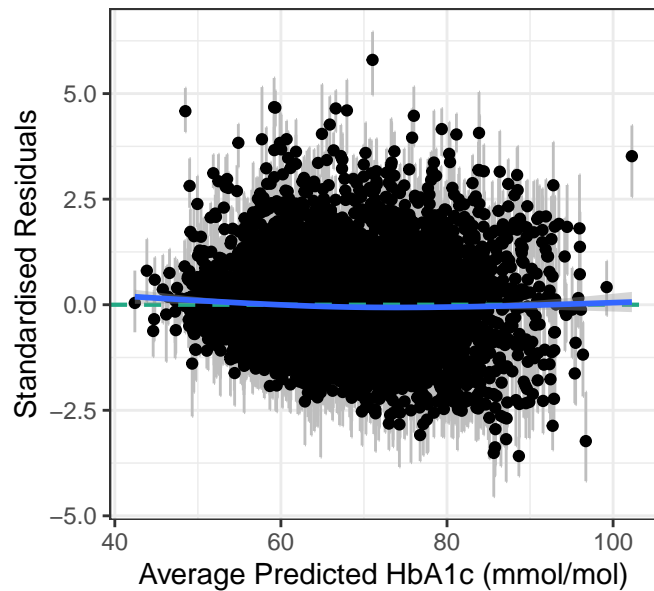
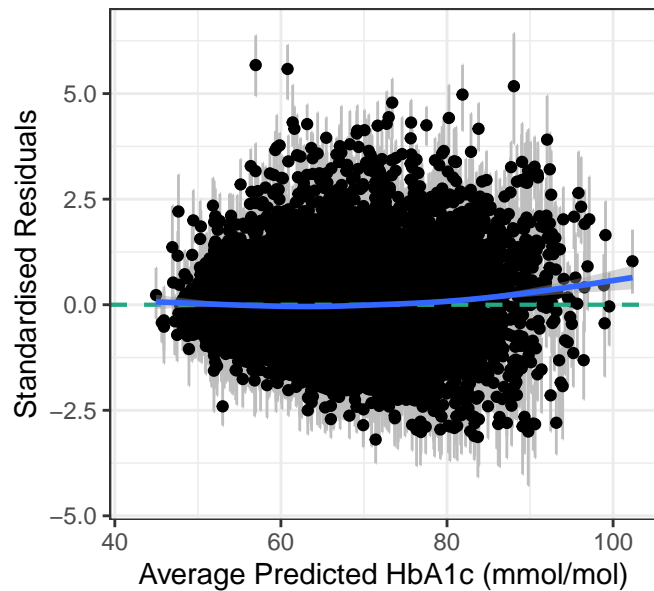
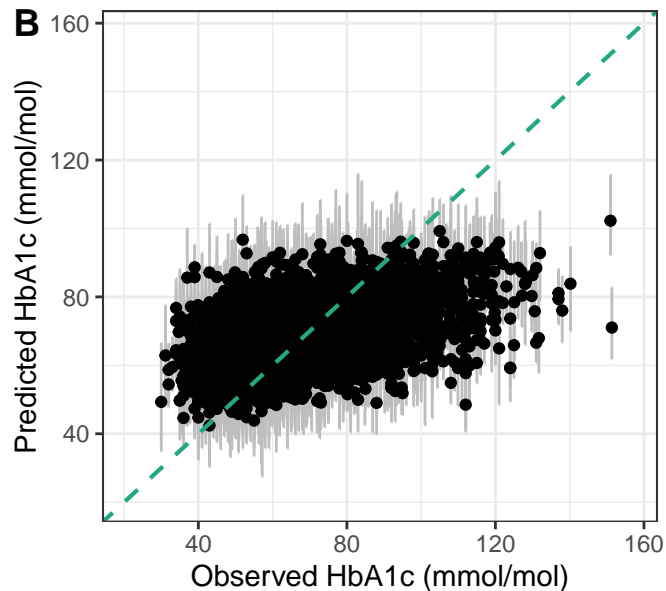
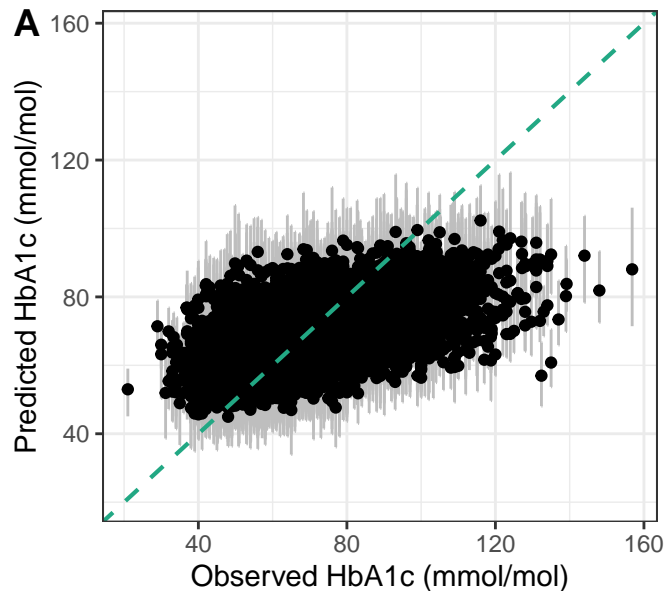


## Residuals of Model 4



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

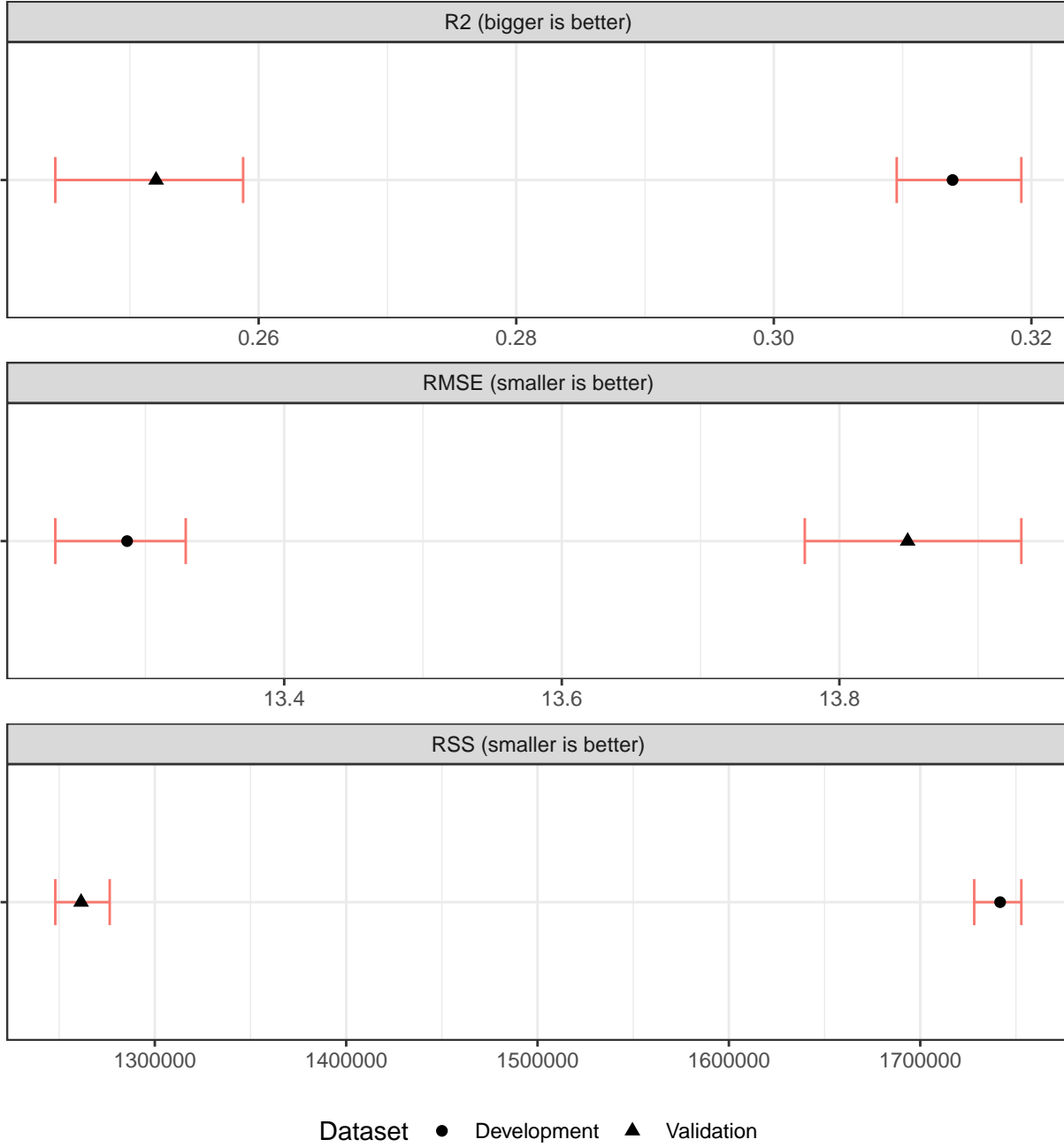
1400000

1500000

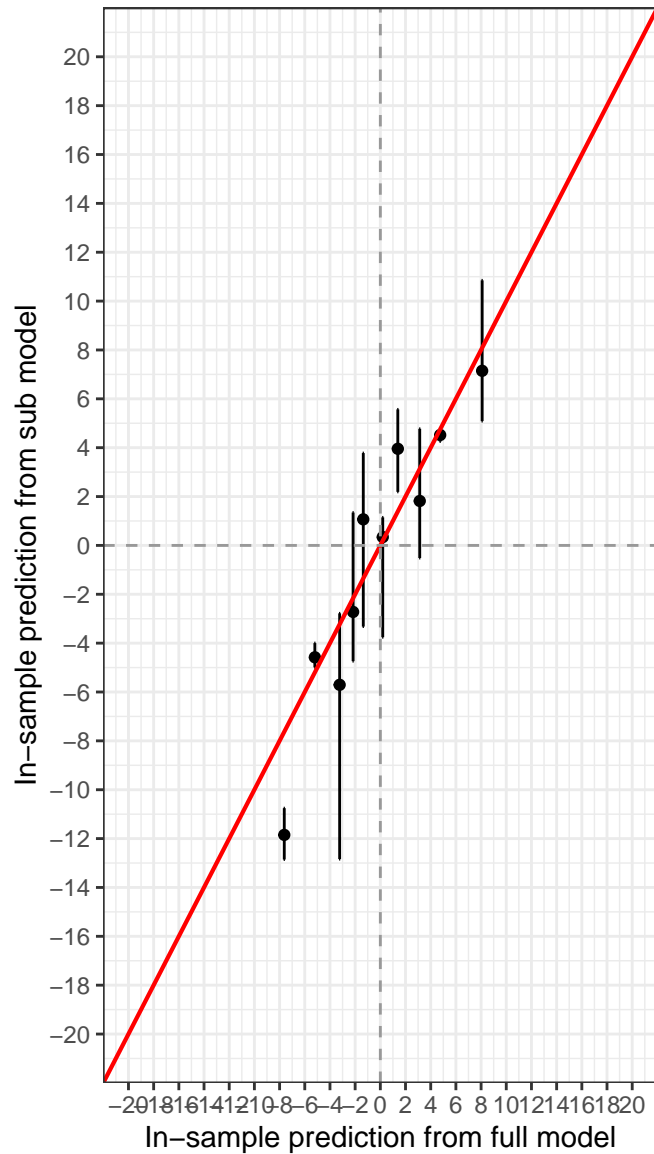
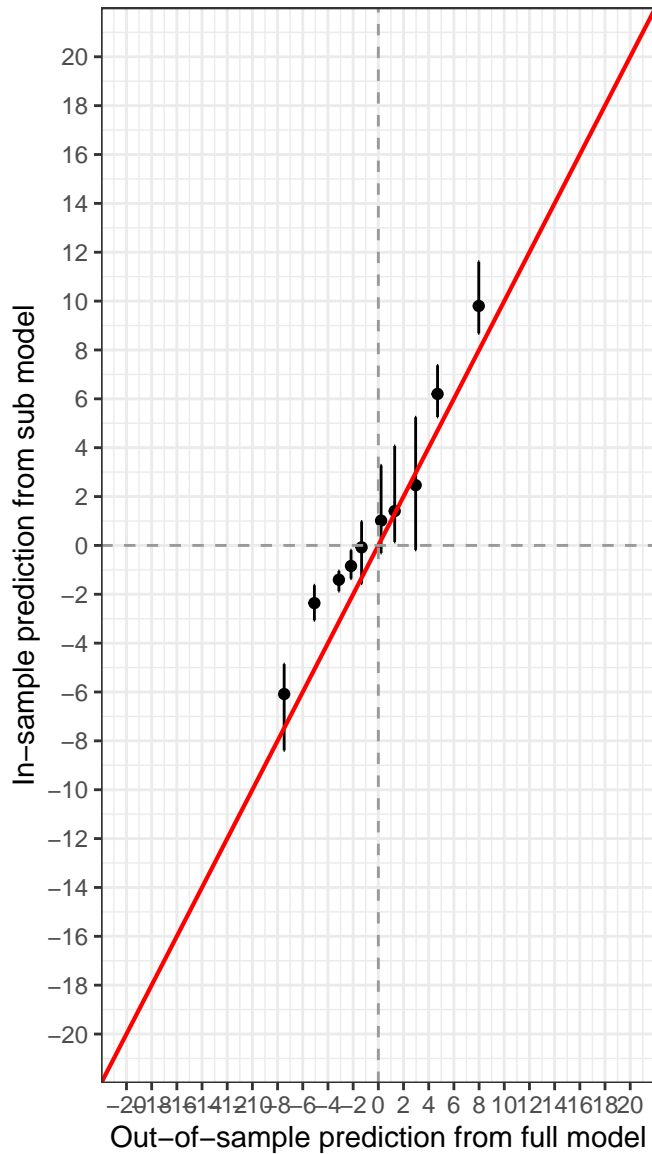
1600000

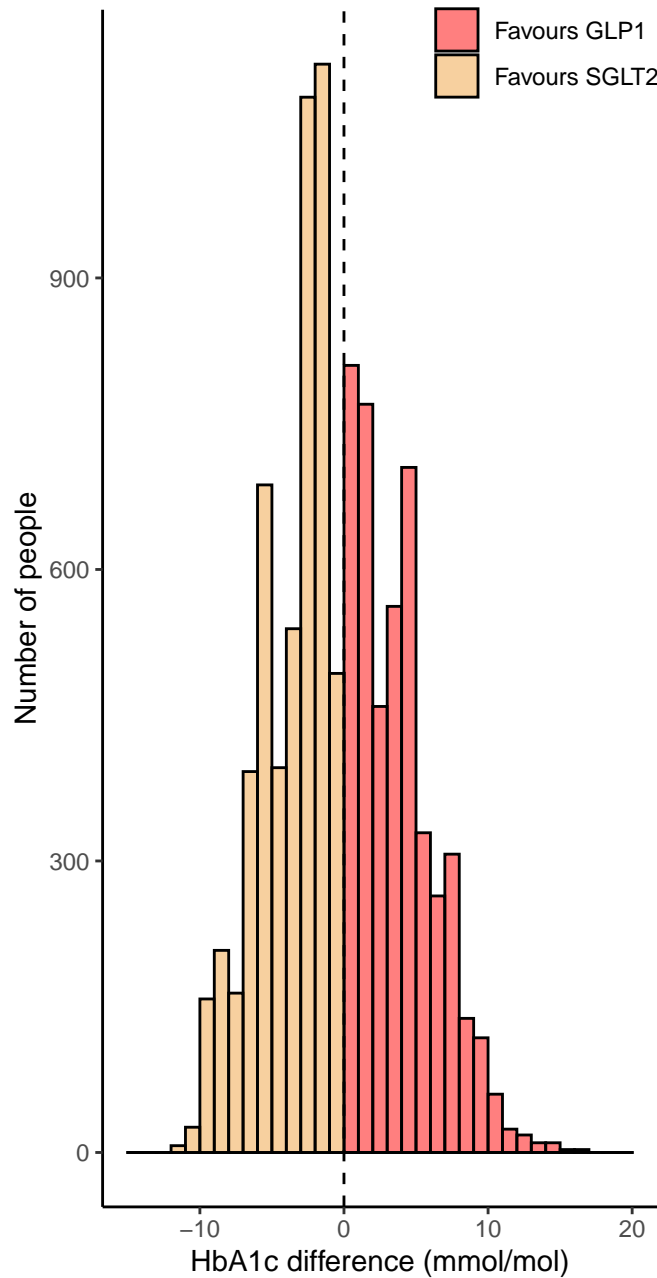
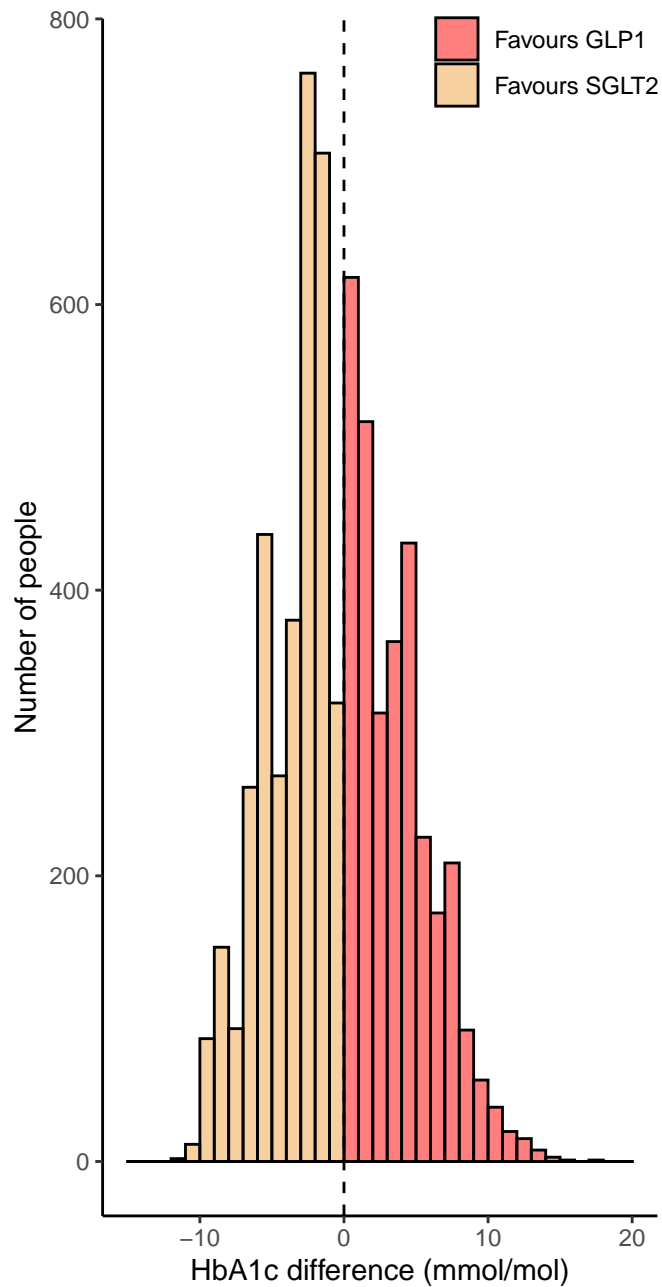
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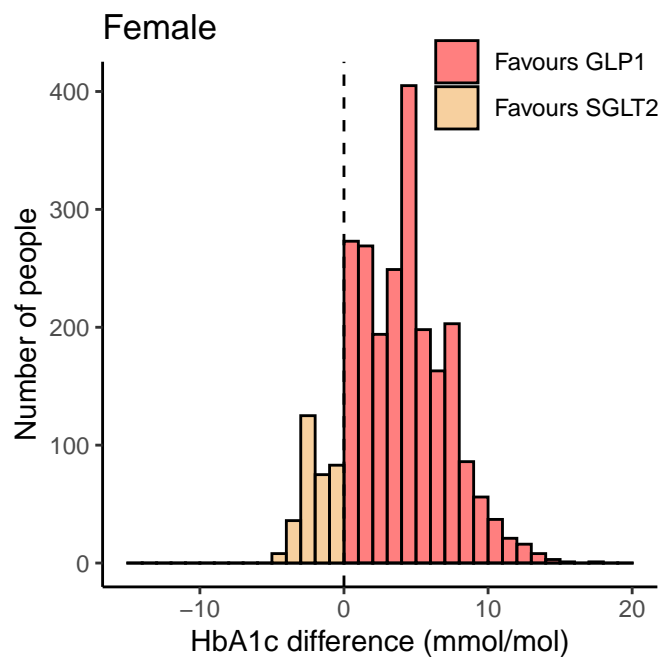
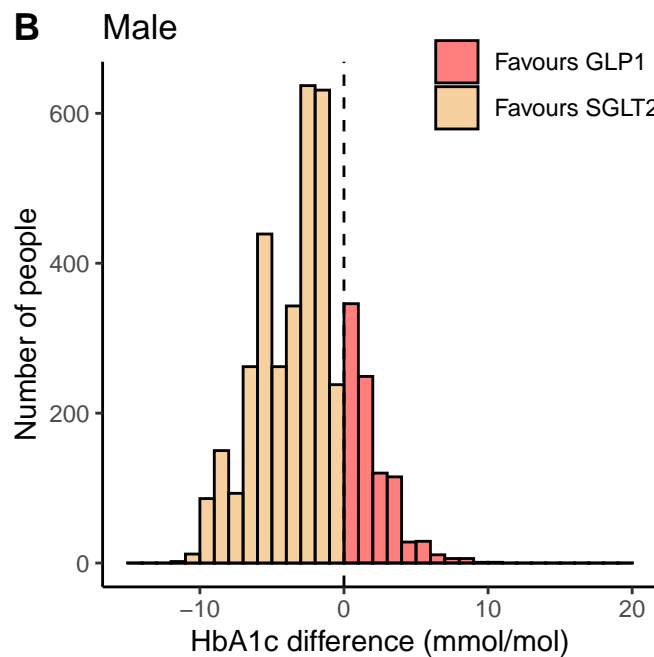
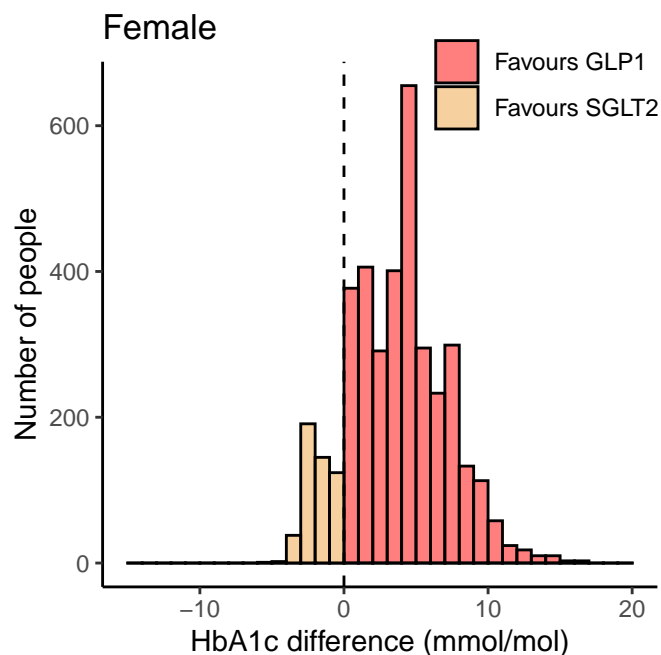
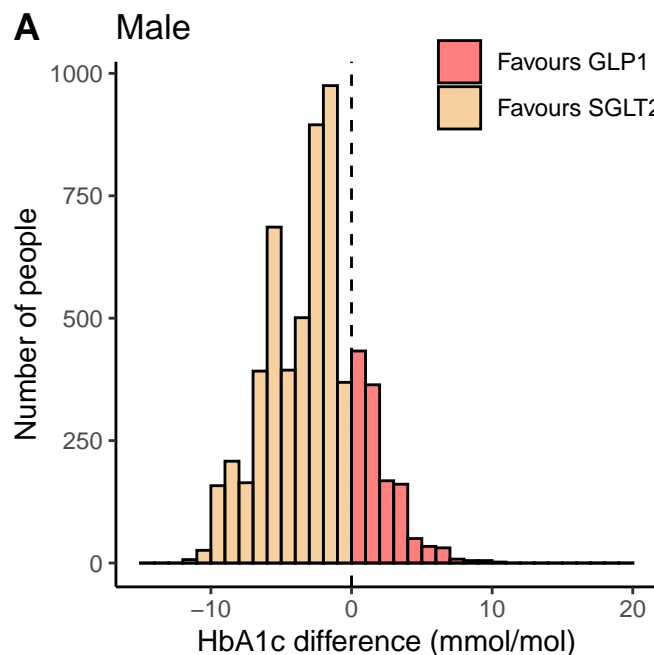
Dataset ● Development ▲ Validation



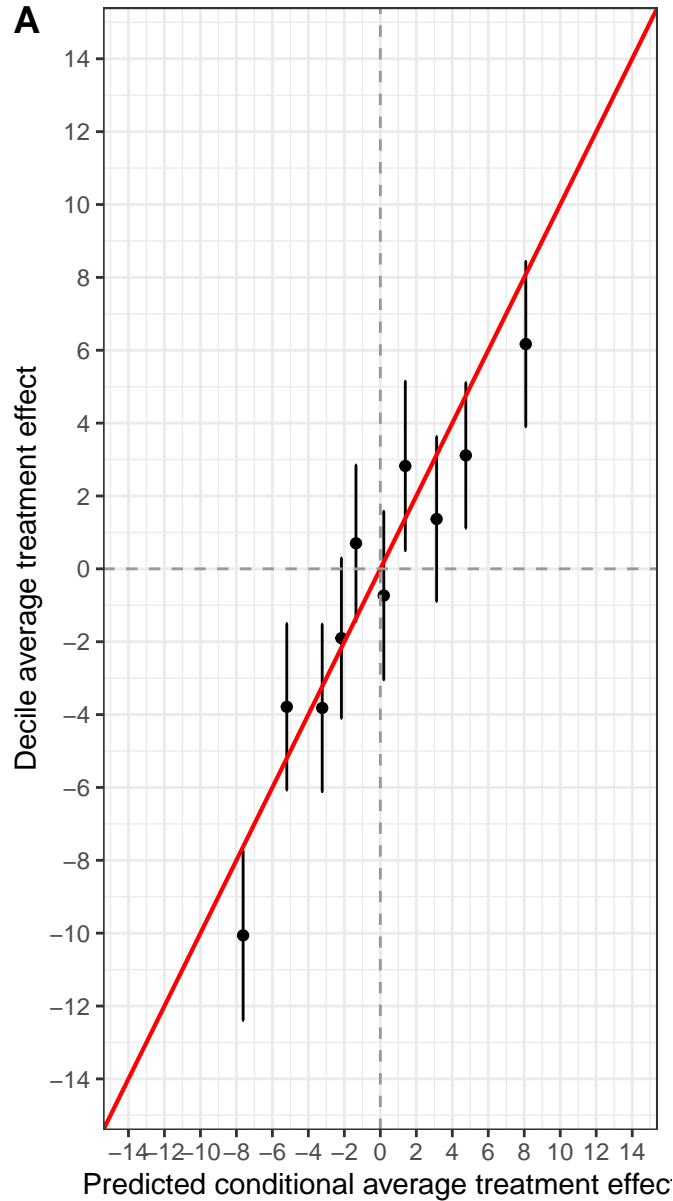
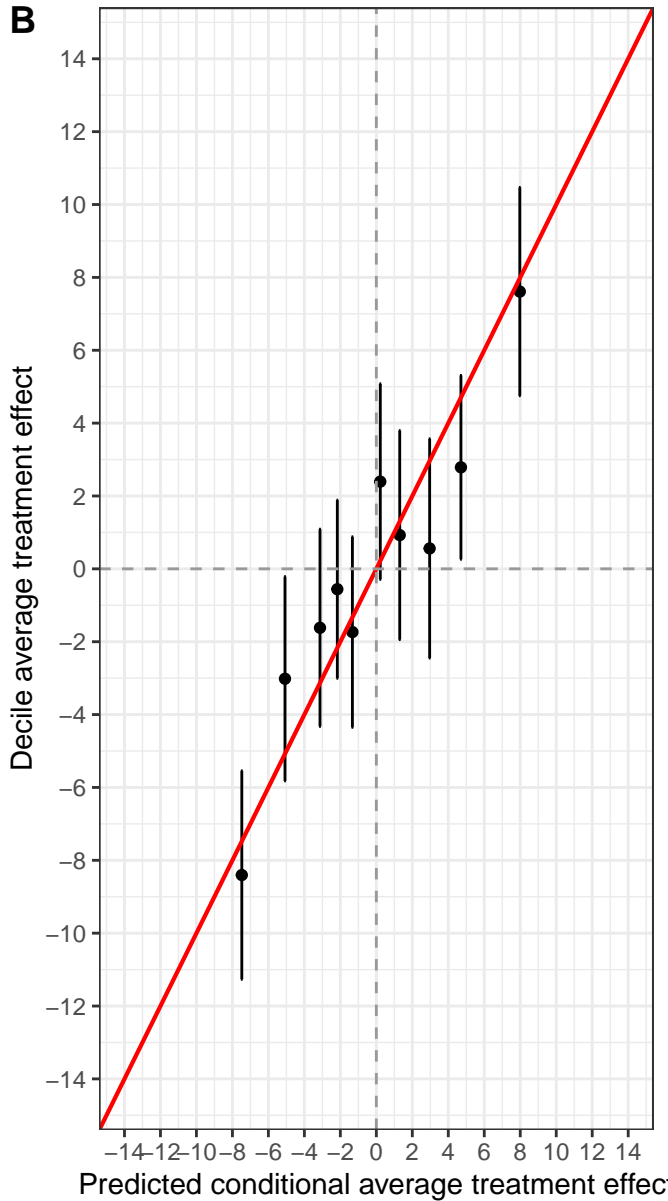
# Effect submodels

**A****B**

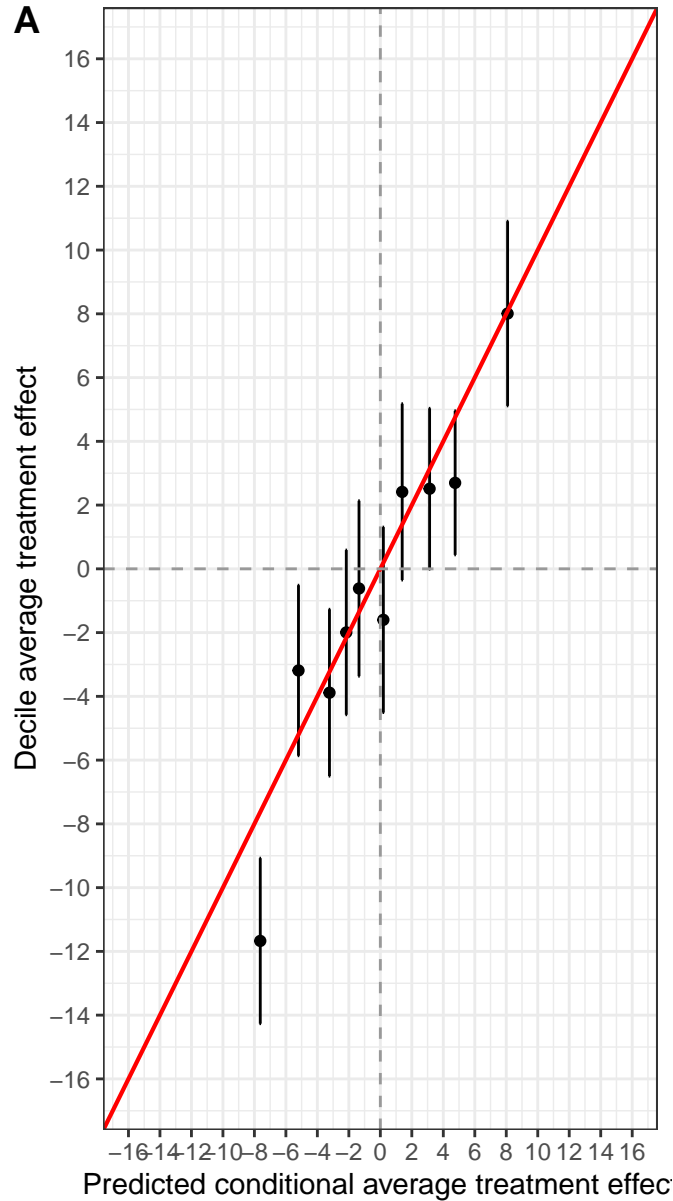
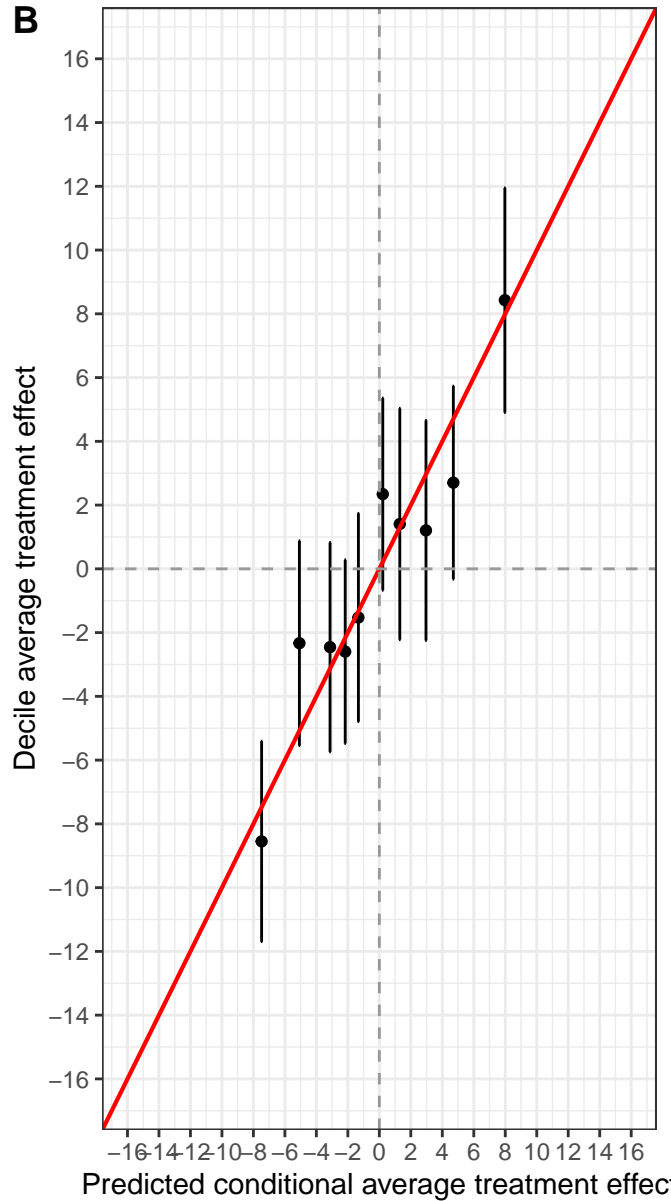
**A****B**



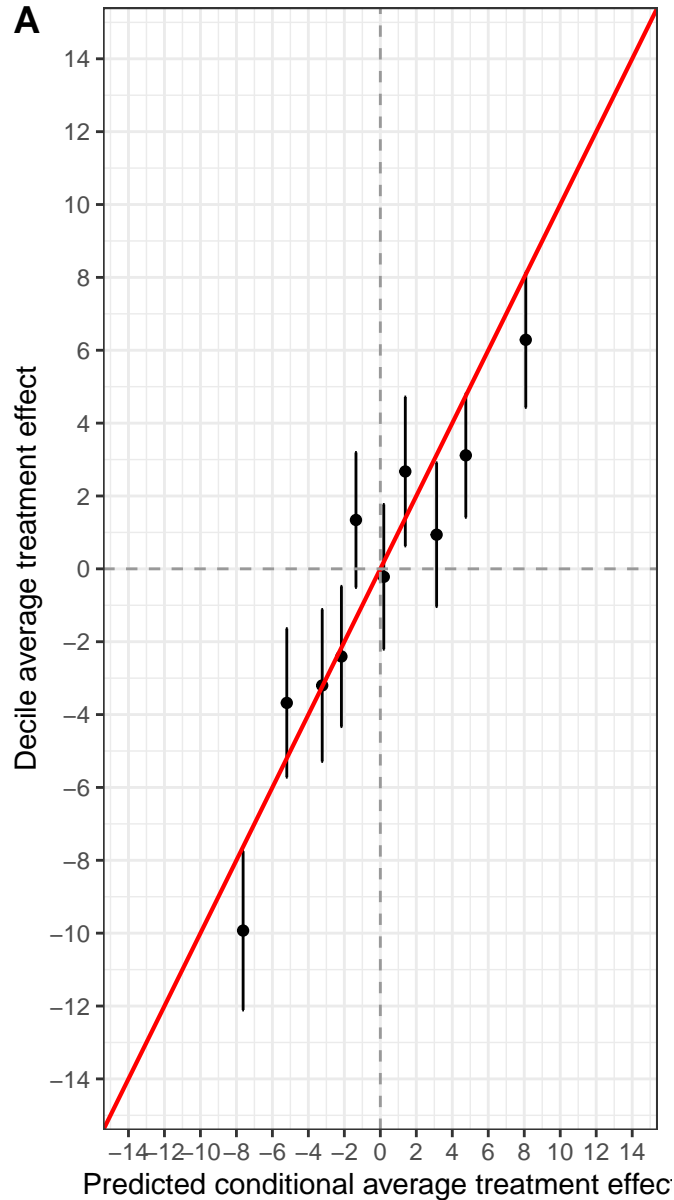
# Effects validation $\text{lm}(\text{hba1c} \sim \text{drugclass} + \text{prop\_score})$

**A****B**

# Effects validation prop score matching

**A****B**

# Effects validation prop score inverse weighting

**A****B**