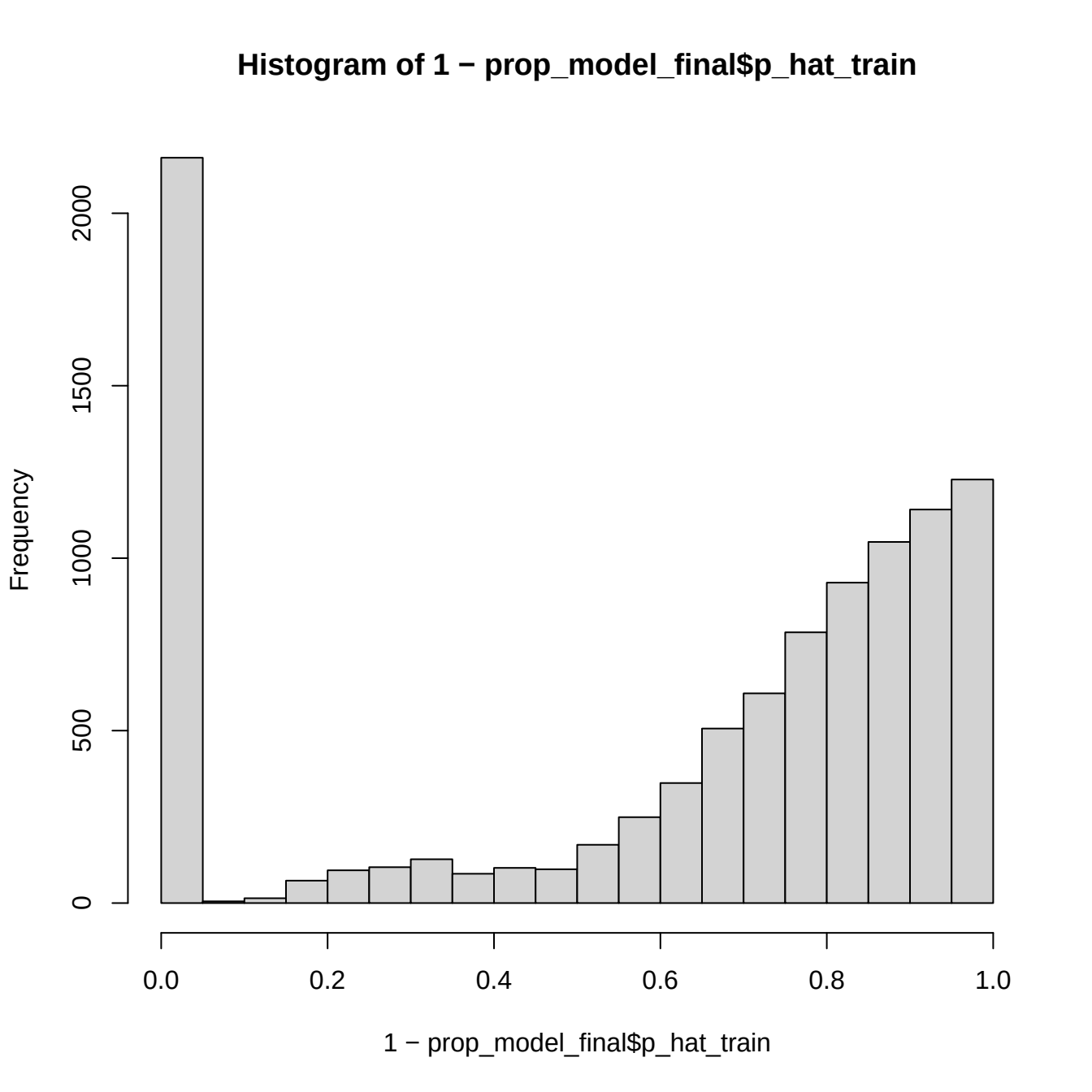
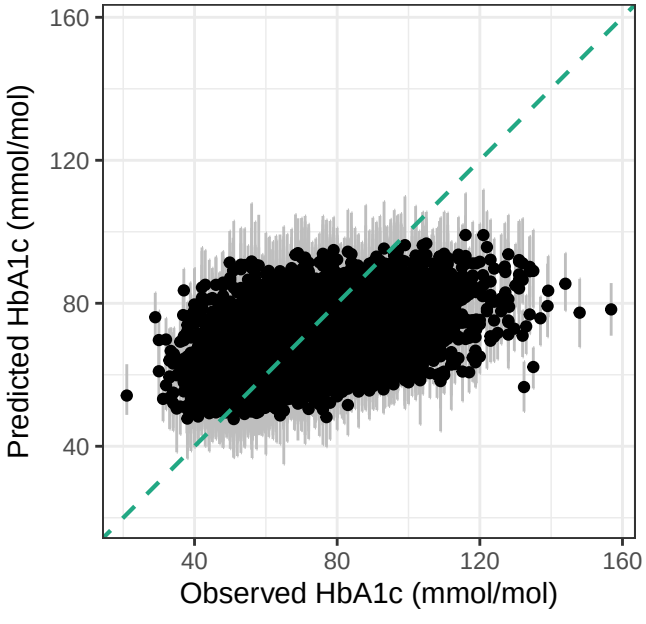
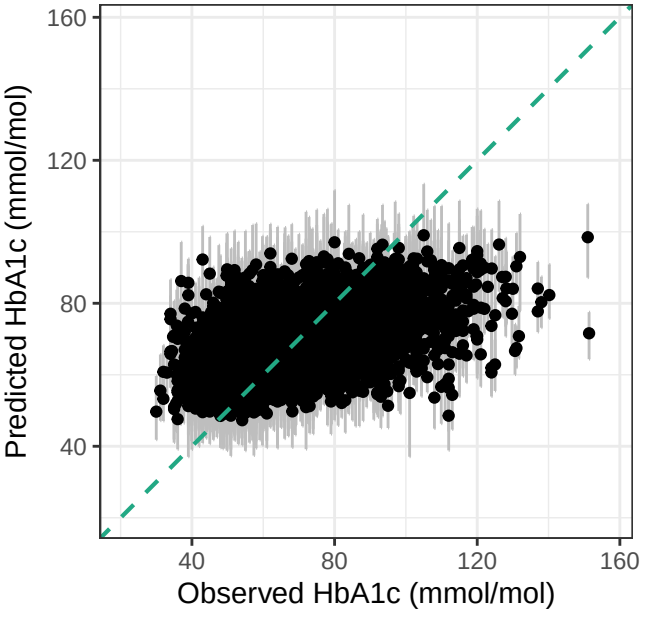
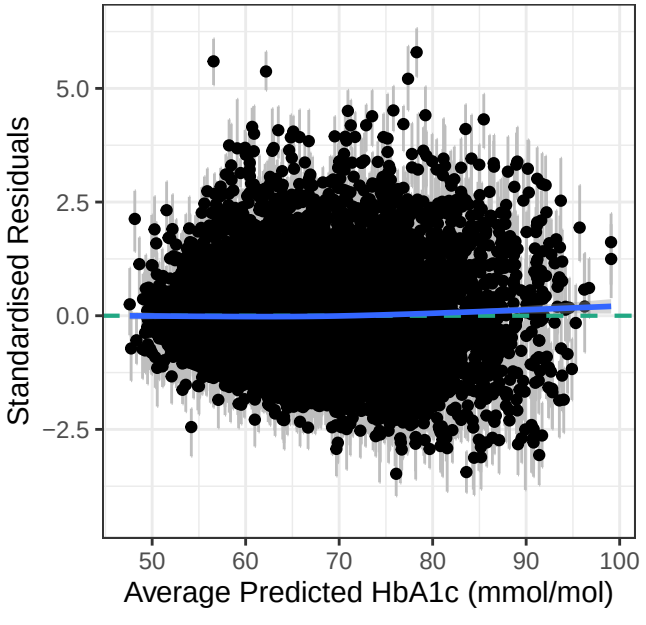
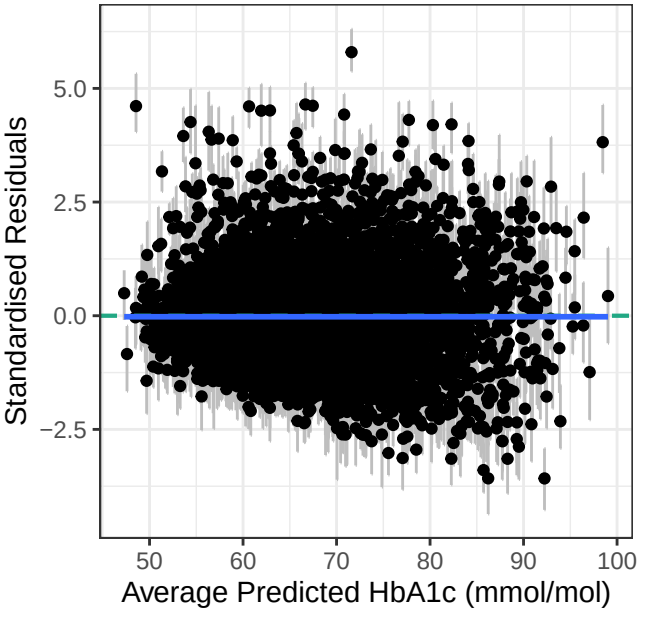

Histogram of 1 − prop_model_final$p_hat_train
Frequency
0
500
1000
1500
2000
0.0
0.2
0.4
0.6
0.8
1.0
1 − prop_model_final$p_hat_train

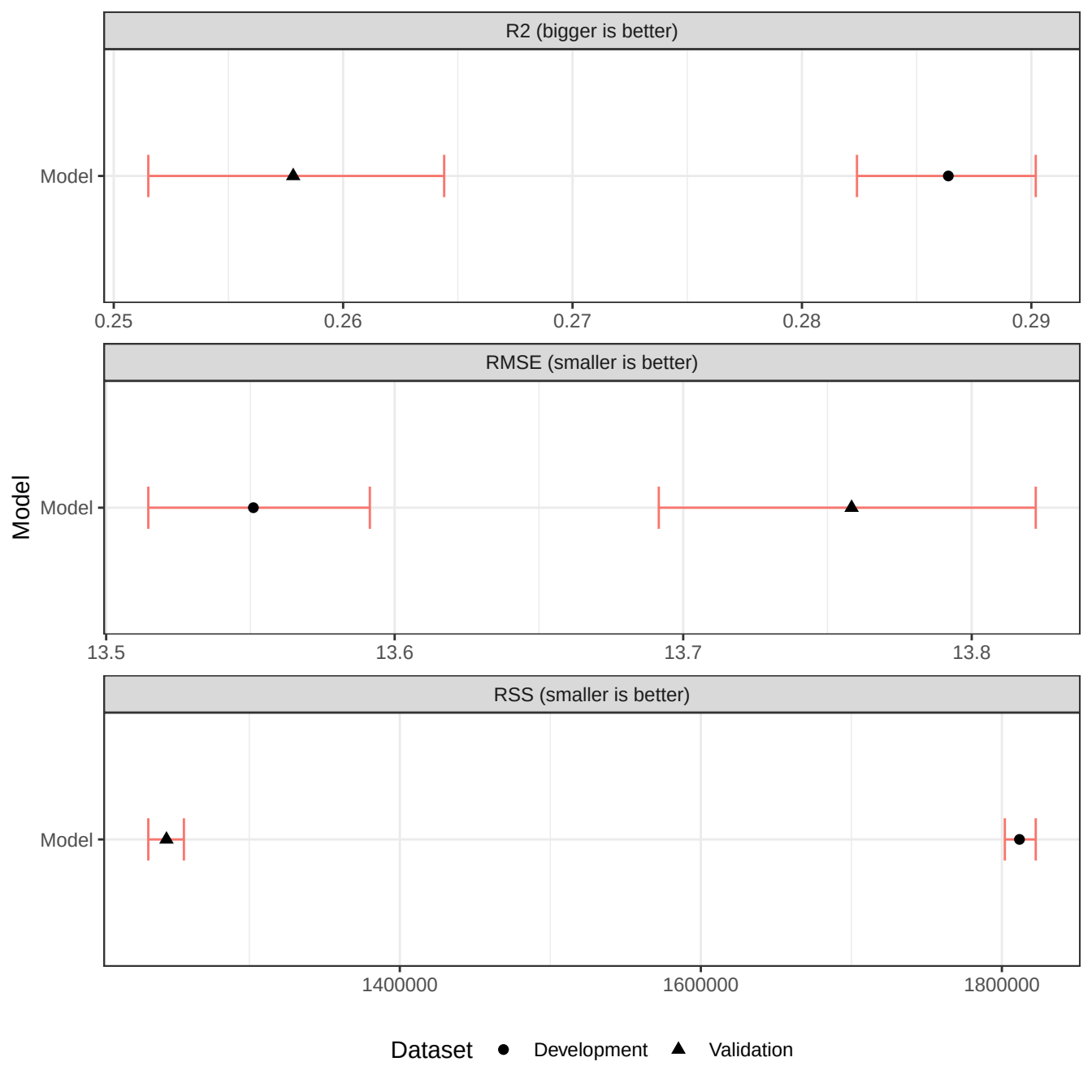
Residuals of Model 1

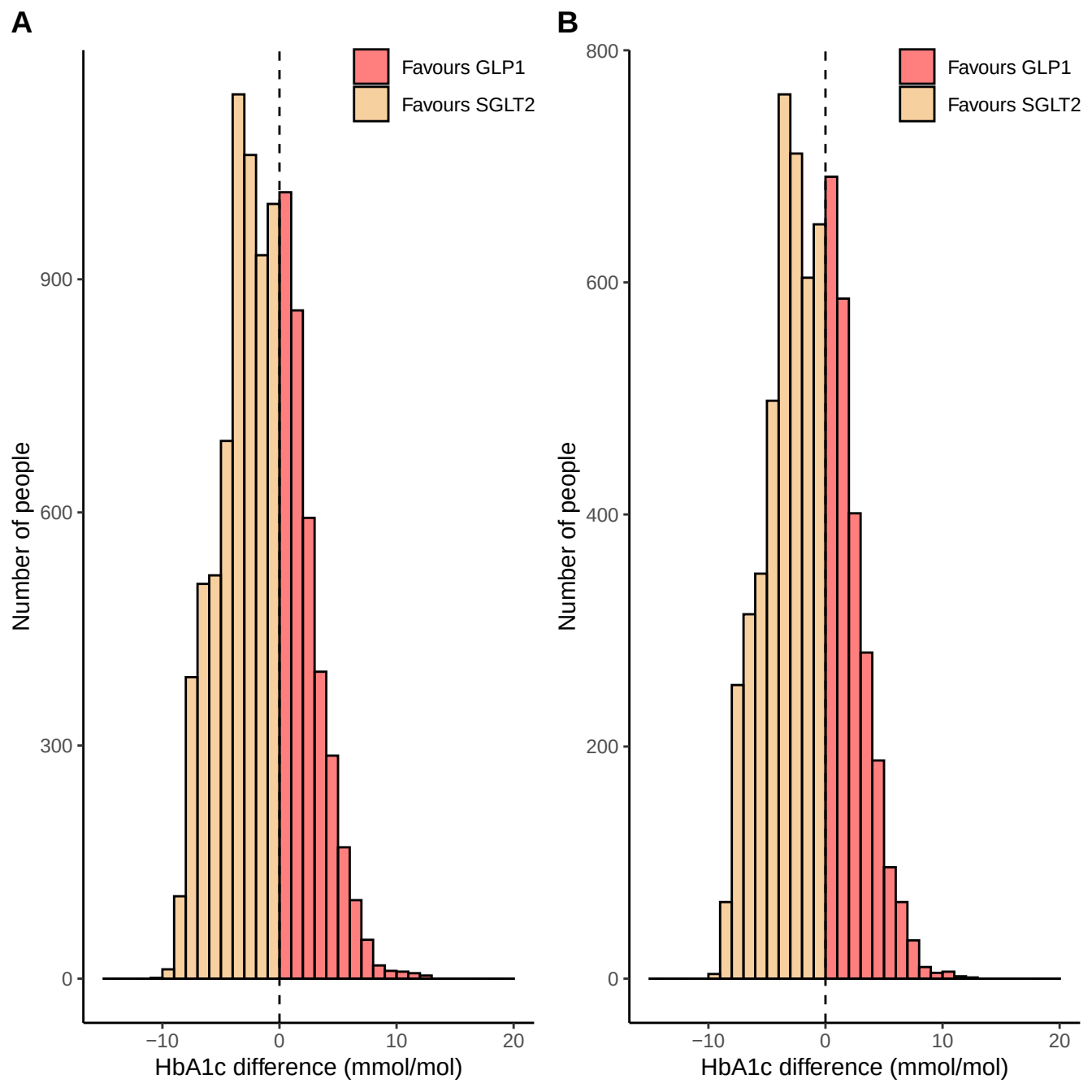


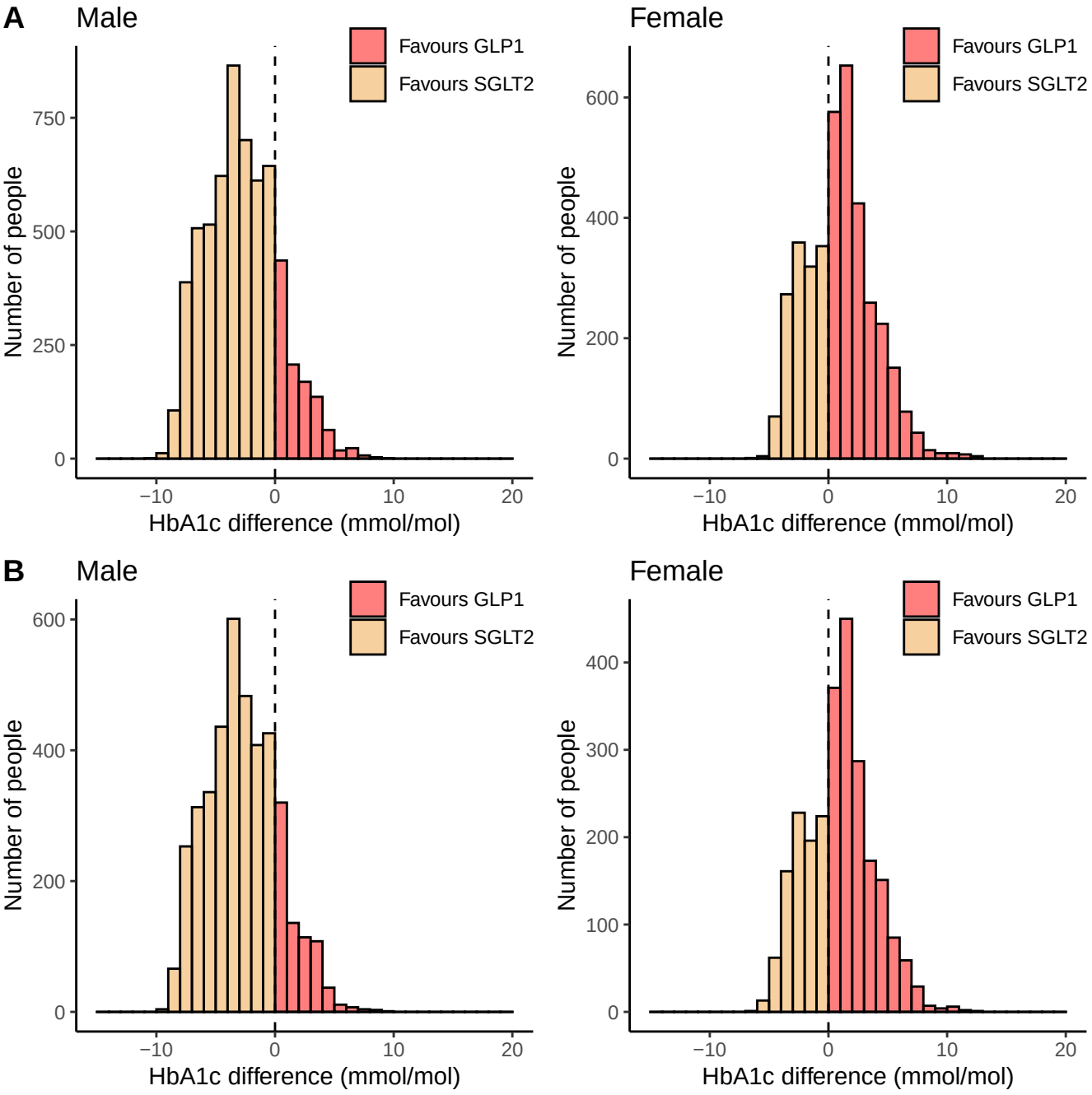


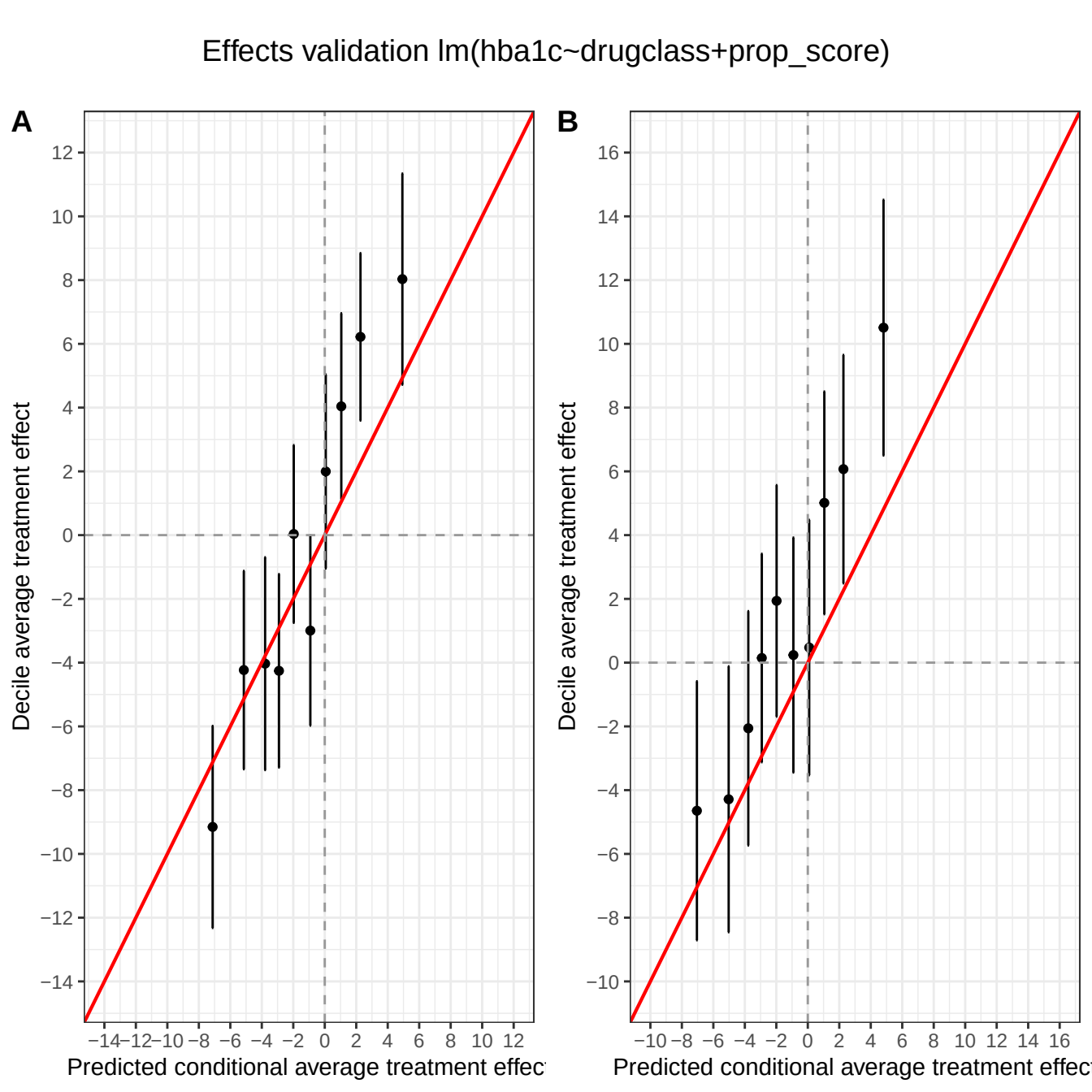


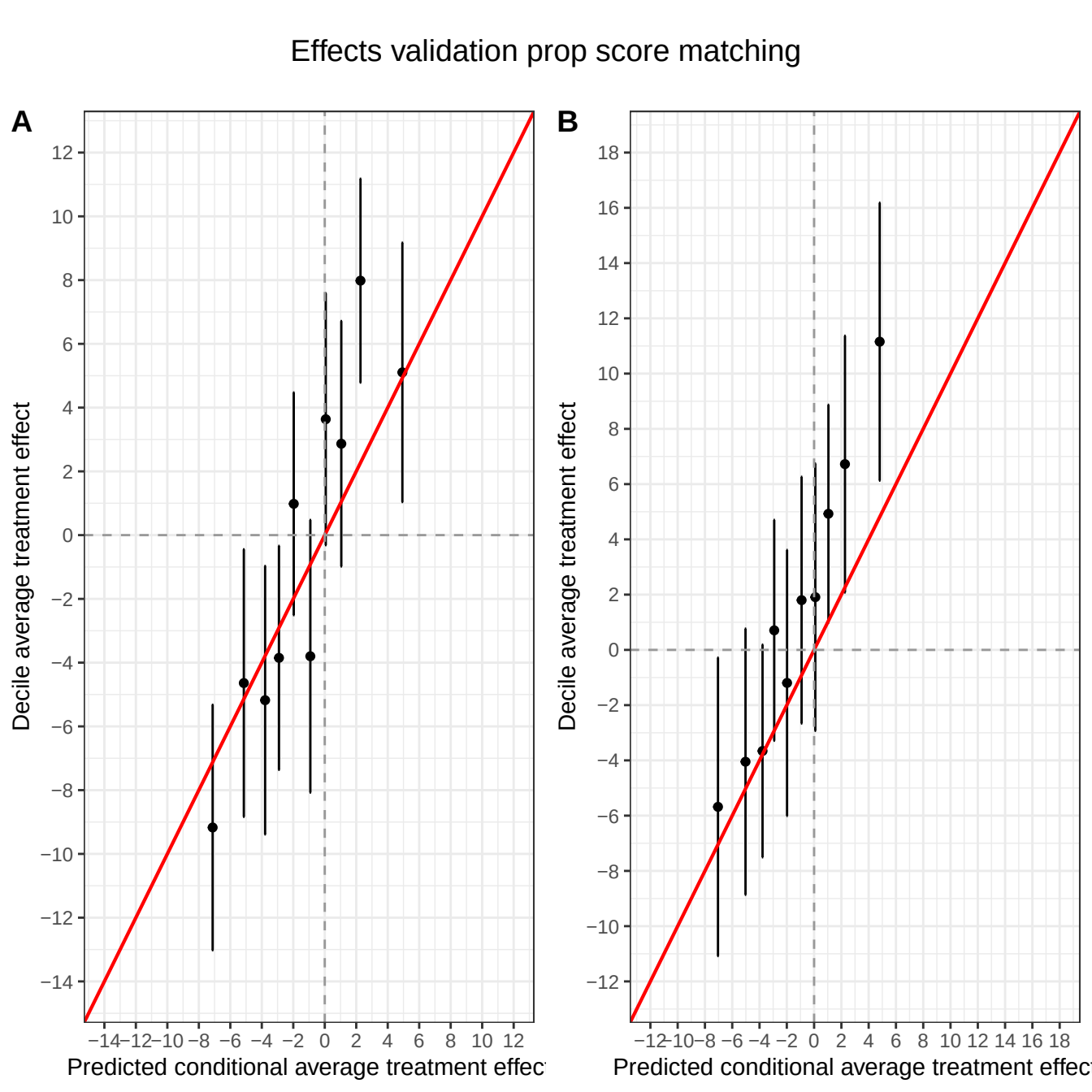


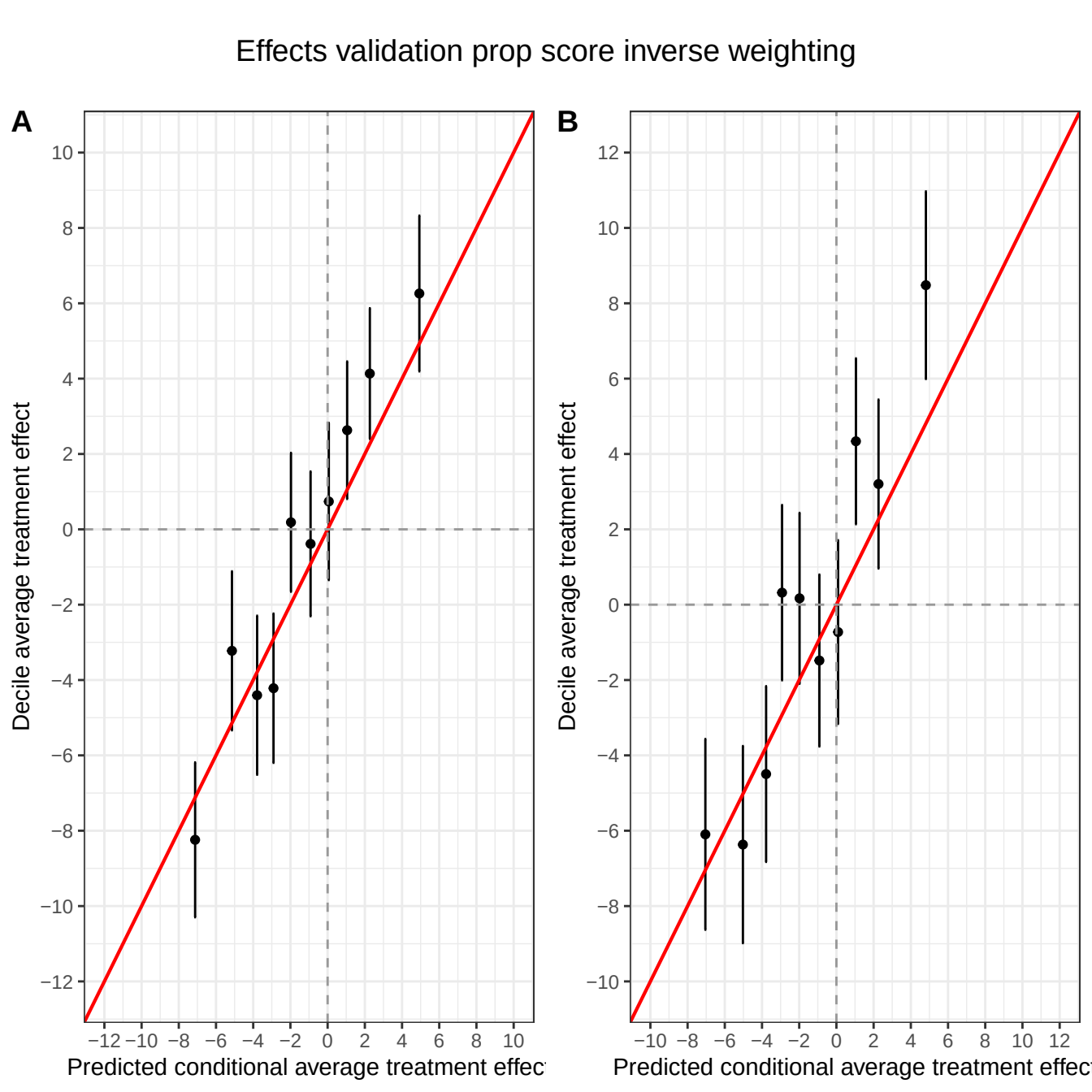

R2 (bigger is better)
Model
0.25
0.26
0.27
0.28
0.29
RMSE (smaller is better)
Model
13.5
13.6
13.7
13.8
RSS (smaller is better)
Model
1400000
1600000
1800000
Model
Dataset
Development
Validation


A
B
Favours GLP1
Favours SGLT2
Number of people
HbA1c difference (mmol/mol)
0
300
600
900
200
400
800
−10
0
10
20


A
Male
Favours GLP1
Favours SGLT2
Number of people
HbA1c difference (mmol/mol)
Female
B
Male
Female


Effects validation lm(hba1c~drugclass+prop_score)
A
B
Decile average treatment effect
Predicted conditional average treatment effec
Decile average treatment effect
Predicted conditional average treatment effec


Effects validation prop score matching
A
B
Decile average treatment effect
Predicted conditional average treatment effec
Decile average treatment effect
Predicted conditional average treatment effec


Effects validation prop score inverse weighting
A
B
Decile average treatment effect
Predicted conditional average treatment effec
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12
12