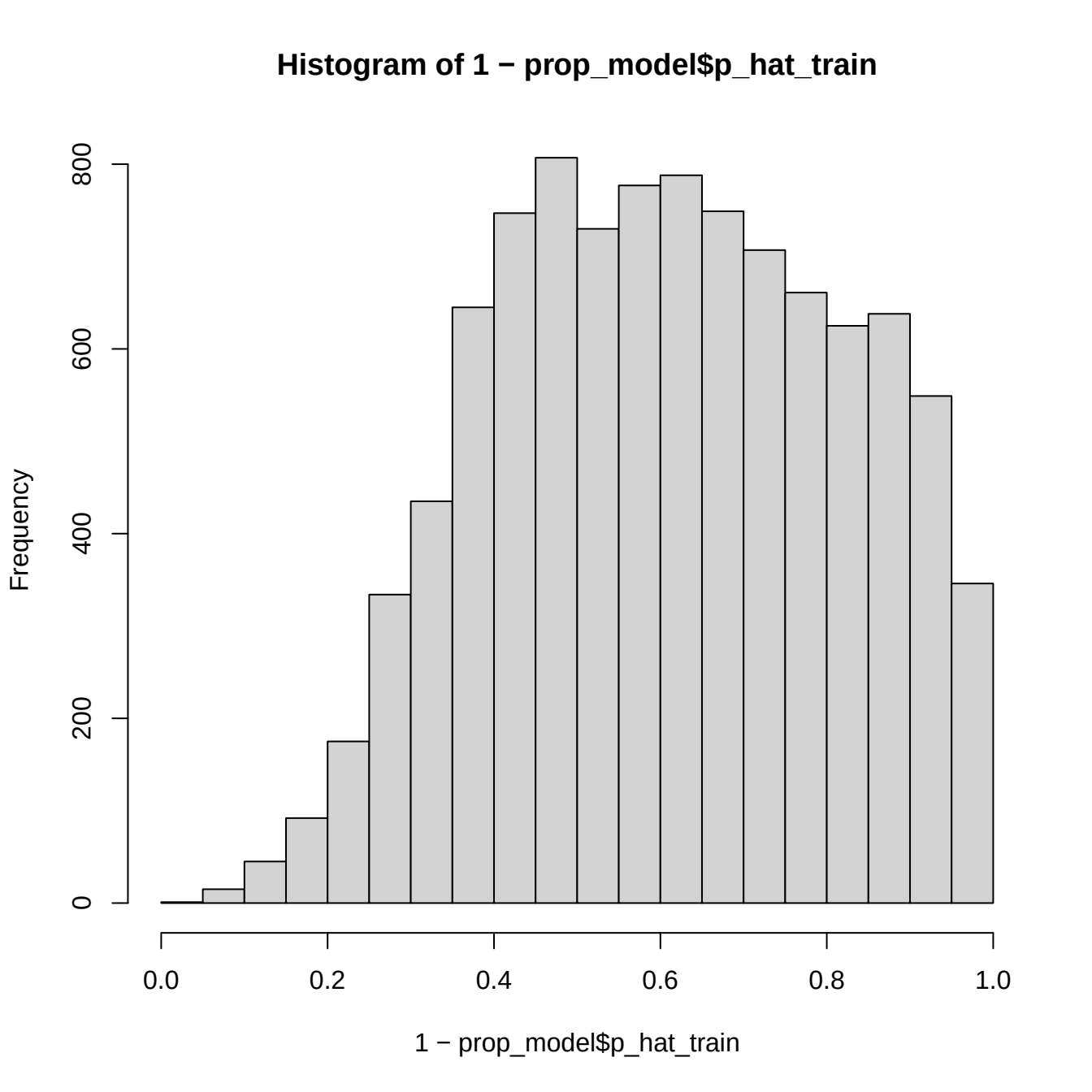
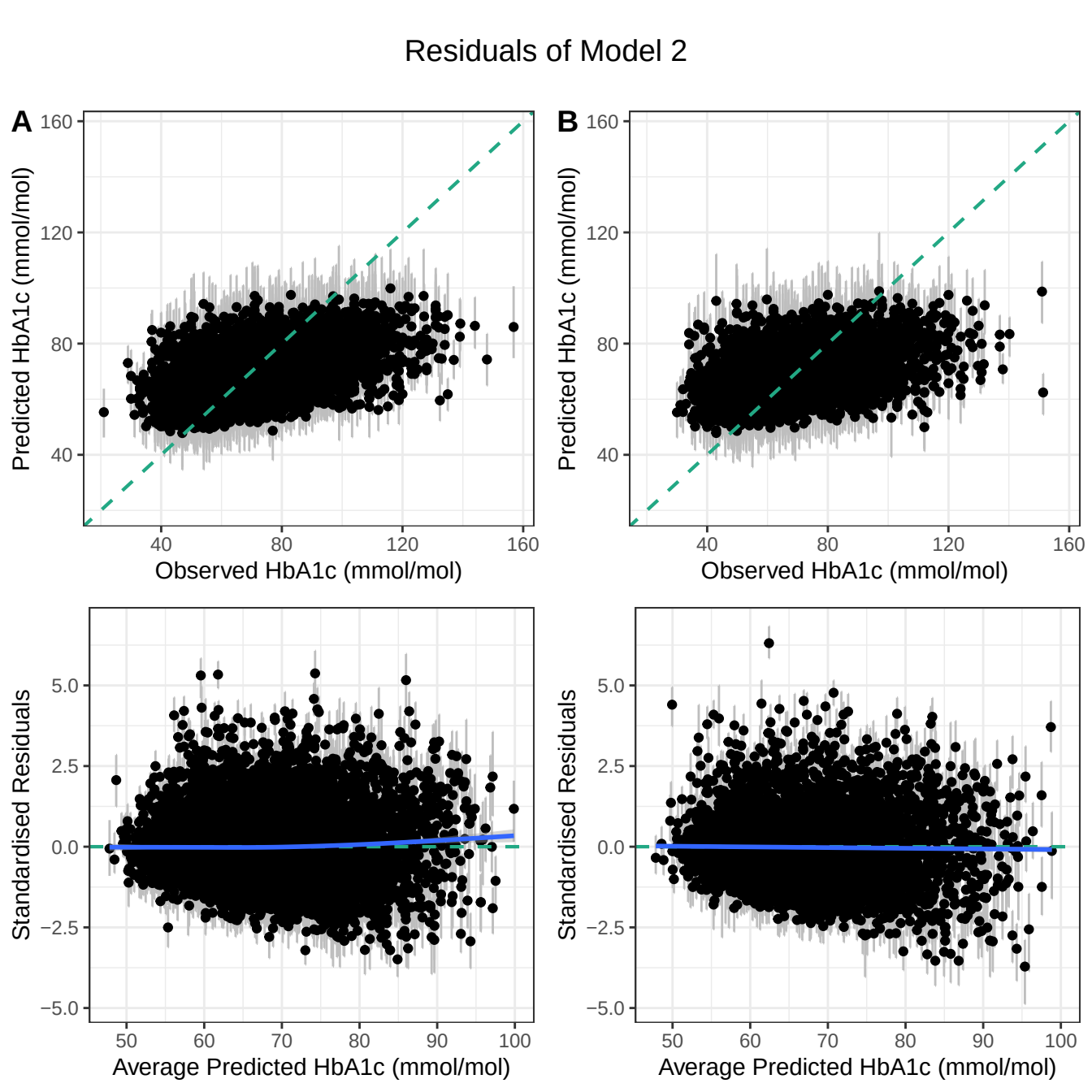
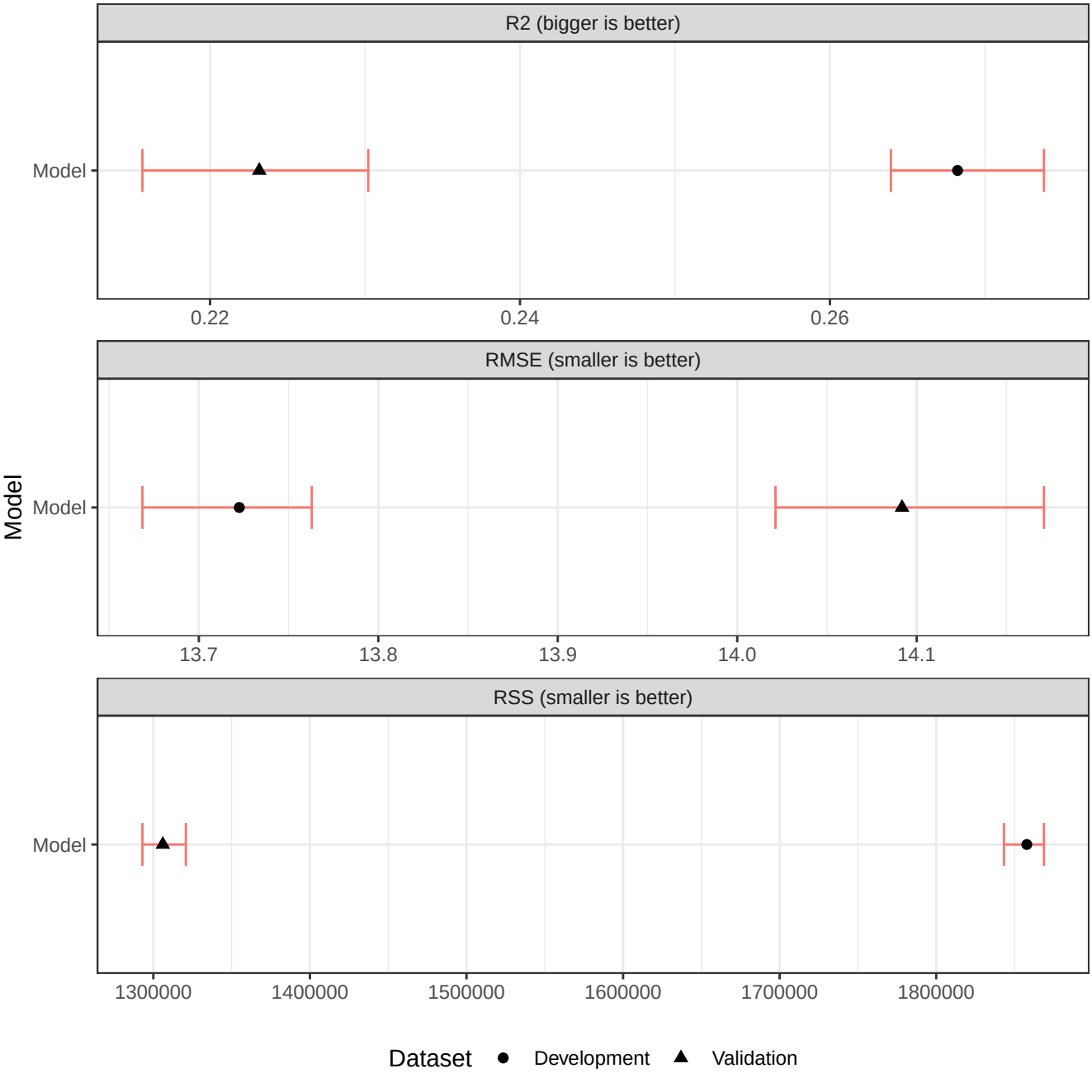
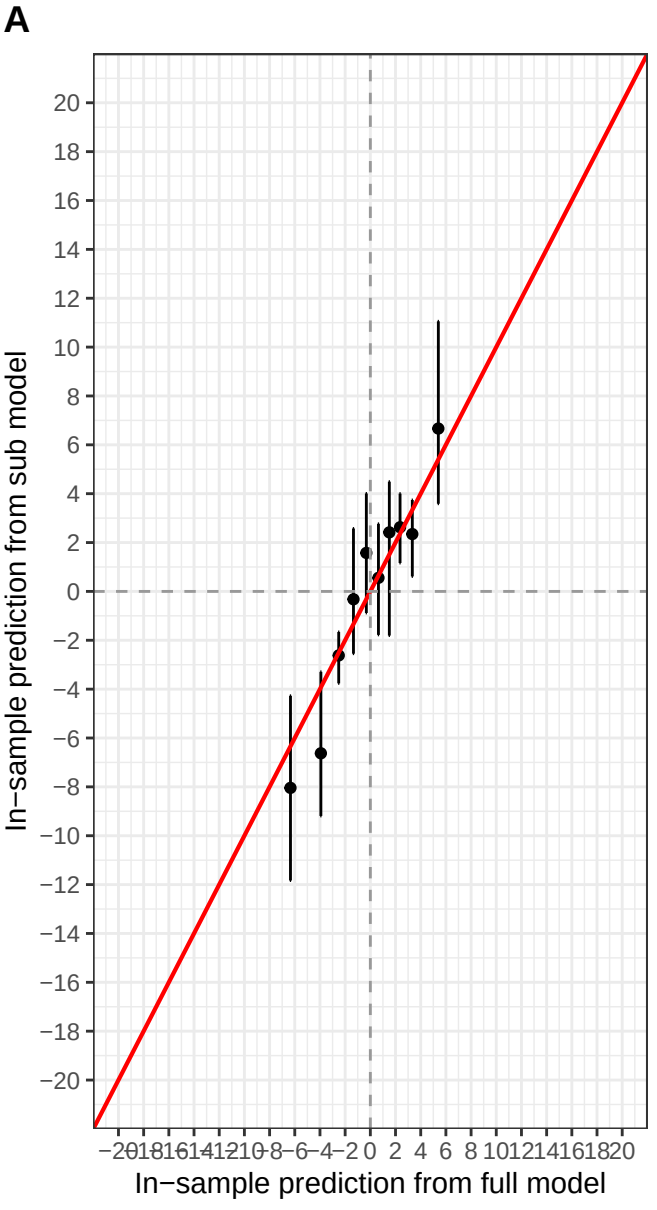
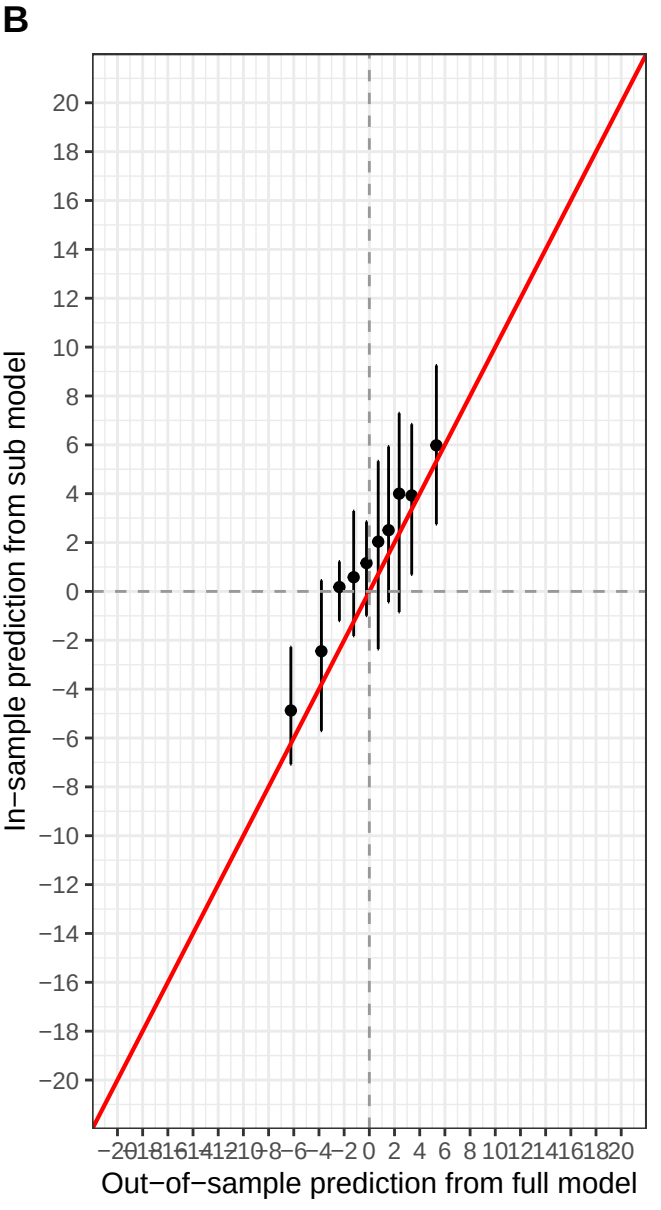

Histogram of 1 − prop_model$p_hat_train
Frequency
0
200
400
600
800
0.0
0.2
0.4
0.6
0.8
1.0
1 − prop_model$p_hat_train

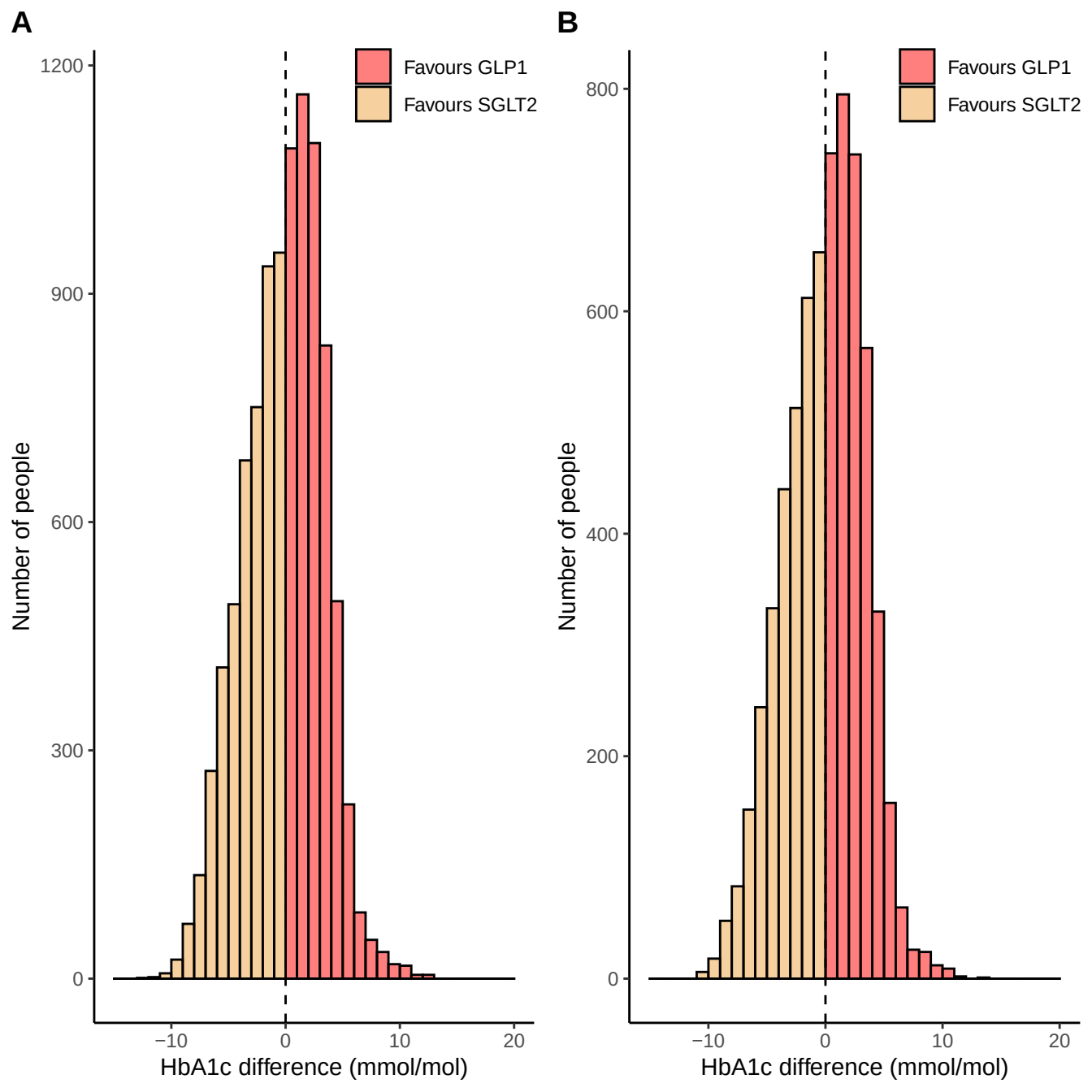

Residuals of Model 2
A
B
Predicted HbA1c (mmol/mol)
Observed HbA1c (mmol/mol)
Standardised Residuals
Average Predicted HbA1c (mmol/mol)
40
80
120
160
−5.0
0.0
2.5
5.0
50
60
70
90
100

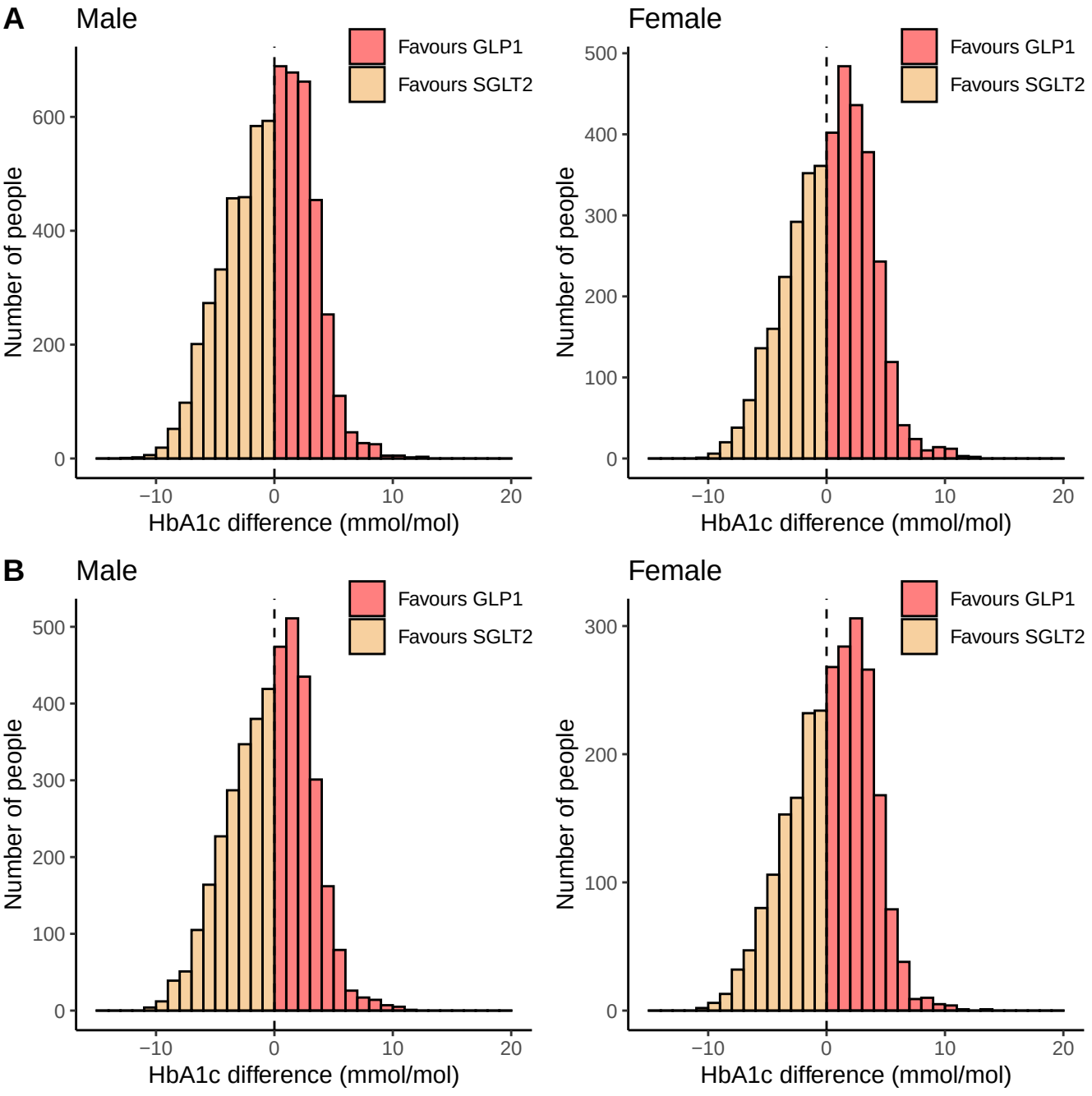

R2 (bigger is better)
Model
0.22
0.24
0.26
RMSE (smaller is better)
Model
13.7
13.8
13.9
14.0
14.1
RSS (smaller is better)
Model
1300000
1400000
1500000
1600000
1700000
1800000
Model
Dataset
Development
Validation

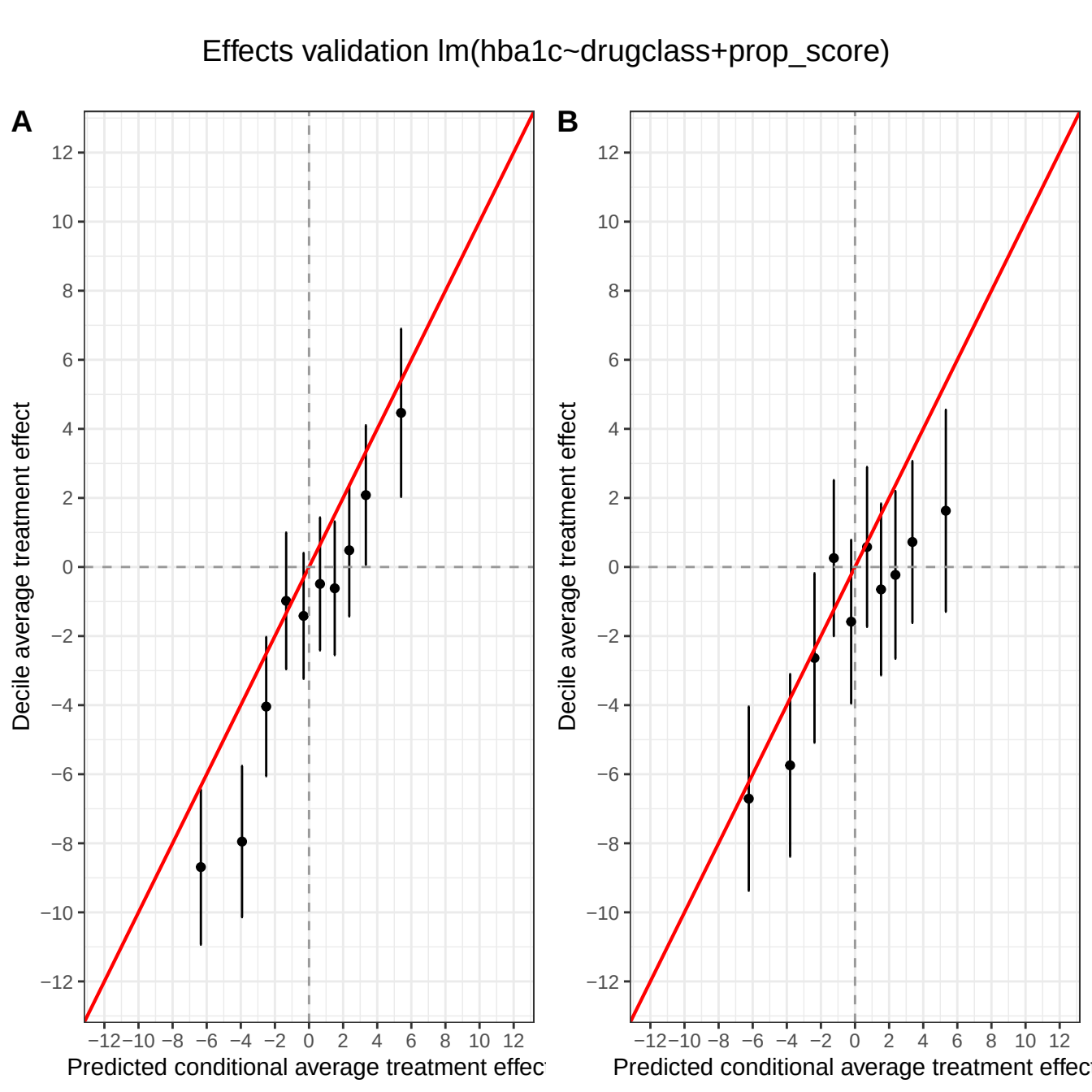
Effect submodels

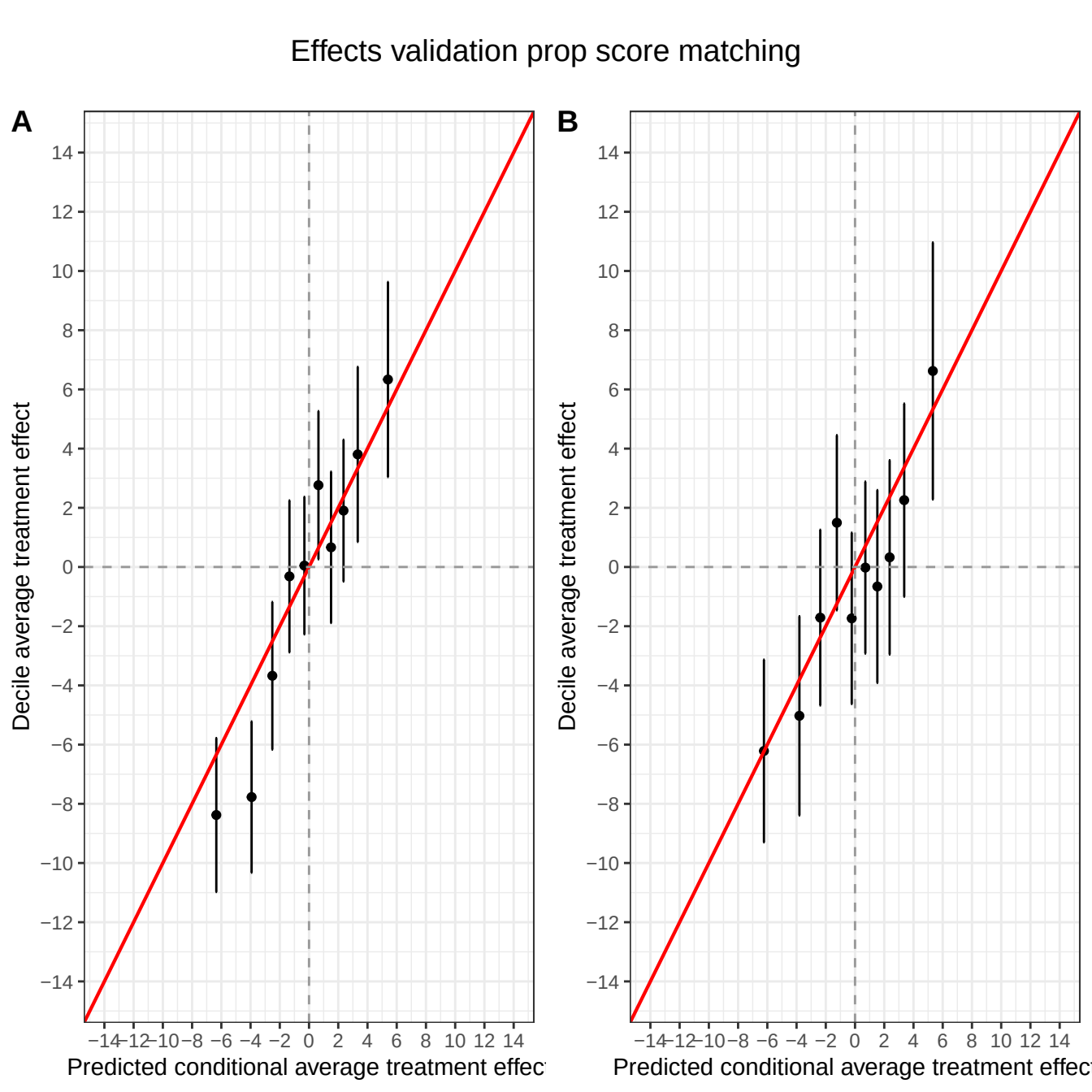


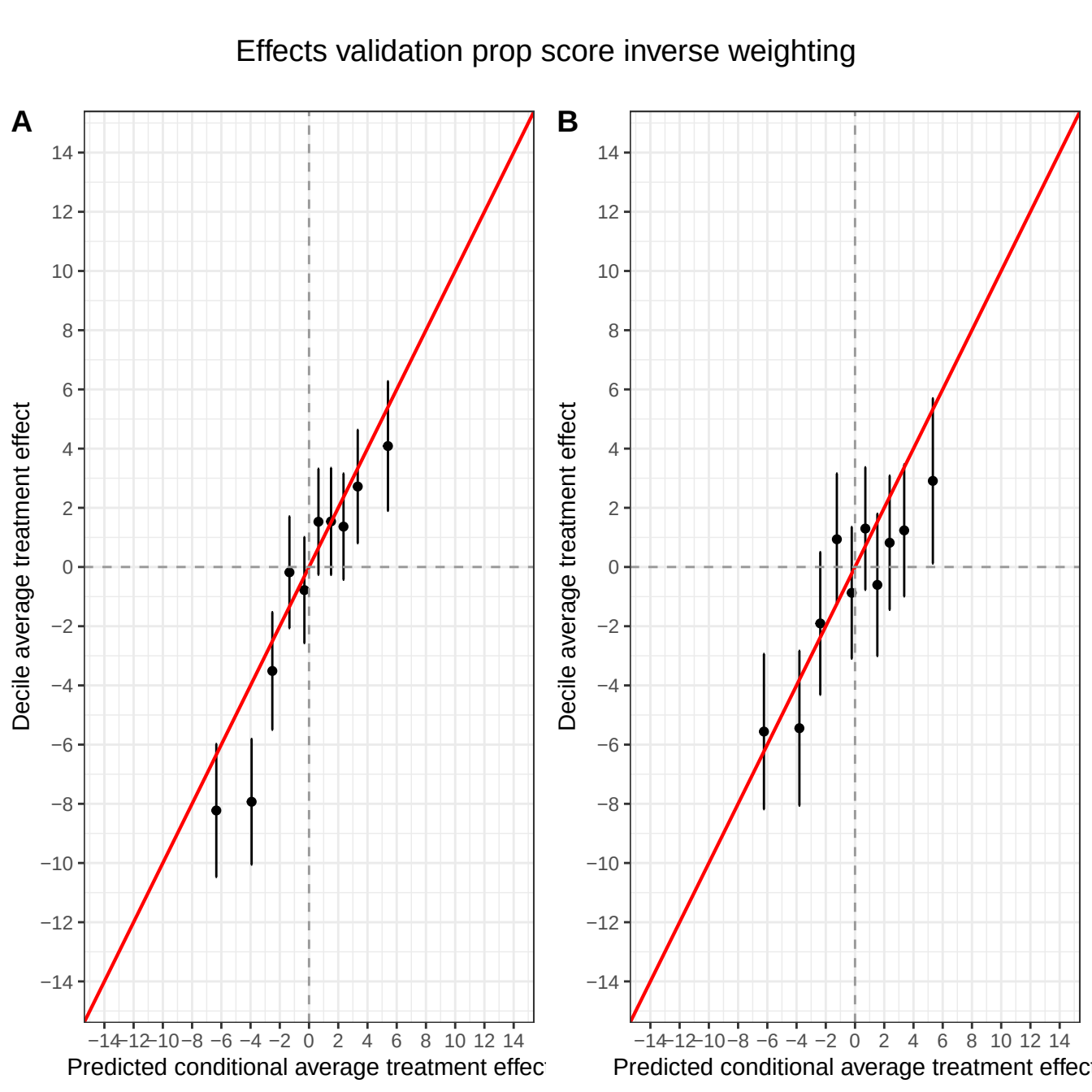



A
B
Favours GLP1
Favours SGLT2
Number of people
HbA1c difference (mmol/mol)
1200
900
600
300
0
800
400
200
−10
0
10
20


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
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12


Effects validation prop score matching
A
B
Decile average treatment effect
Predicted conditional average treatment effec
14
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12
−14


Effects validation prop score inverse weighting
A
B
Decile average treatment effect
Predicted conditional average treatment effec
14
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12
−14