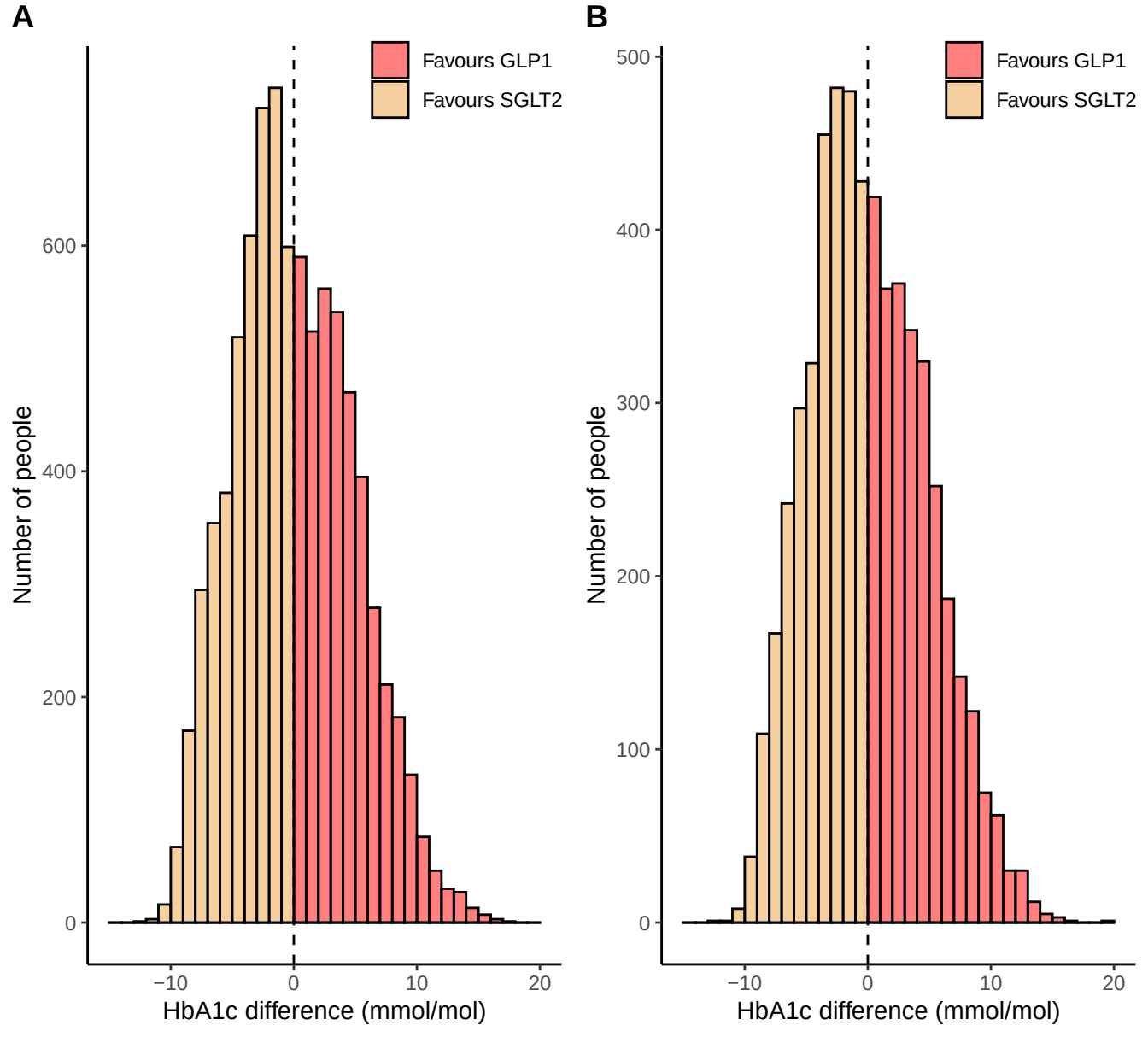
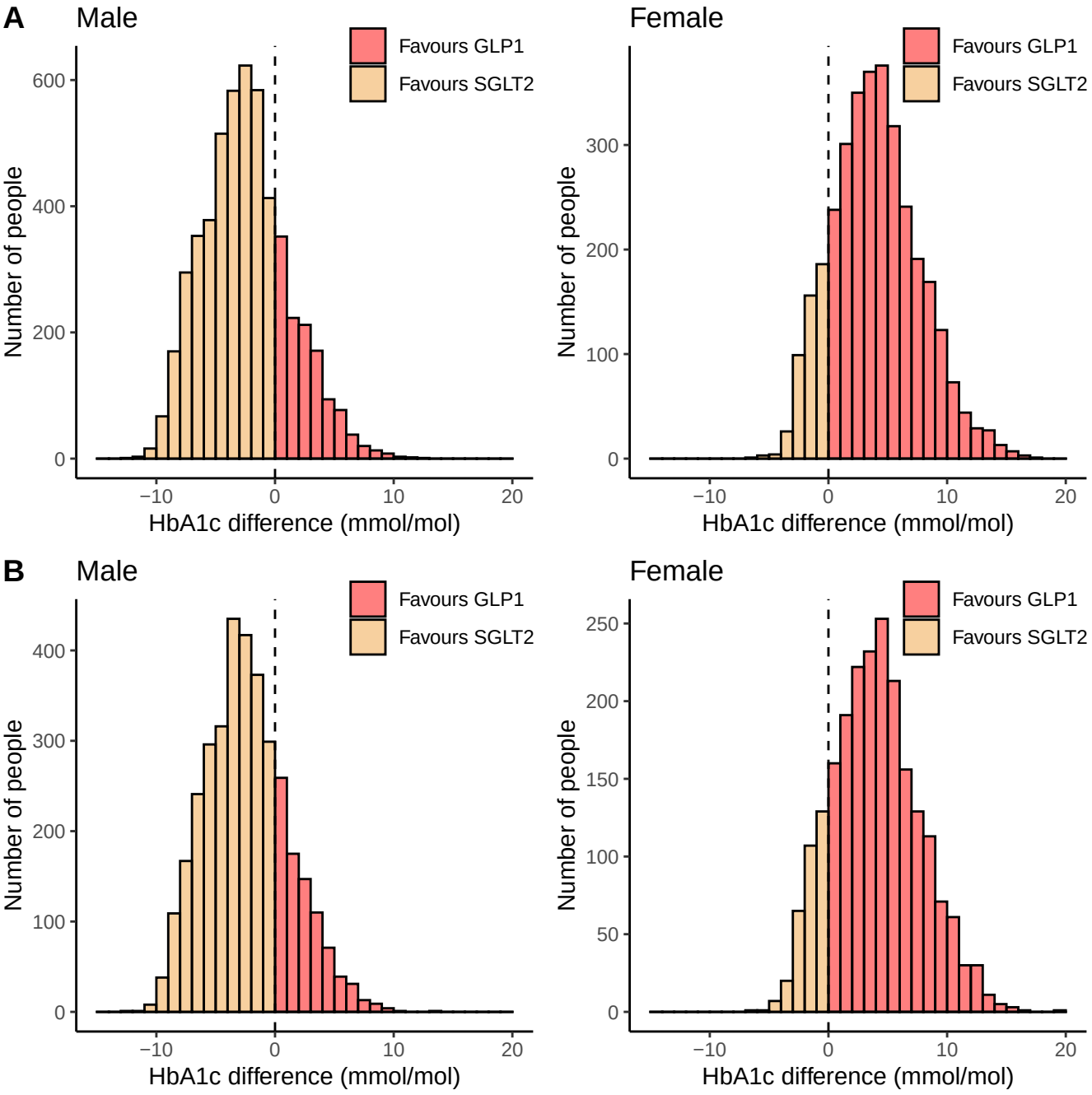
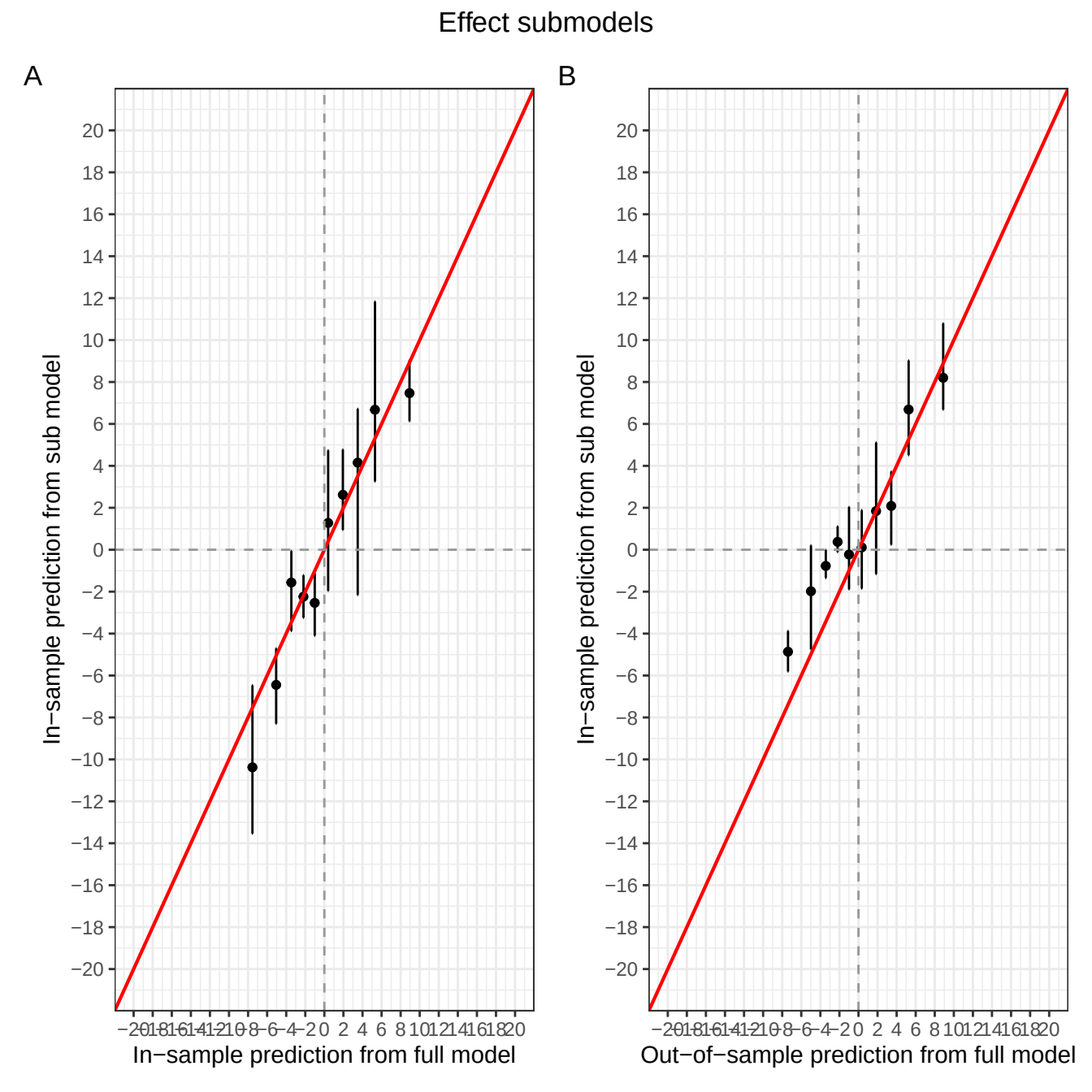
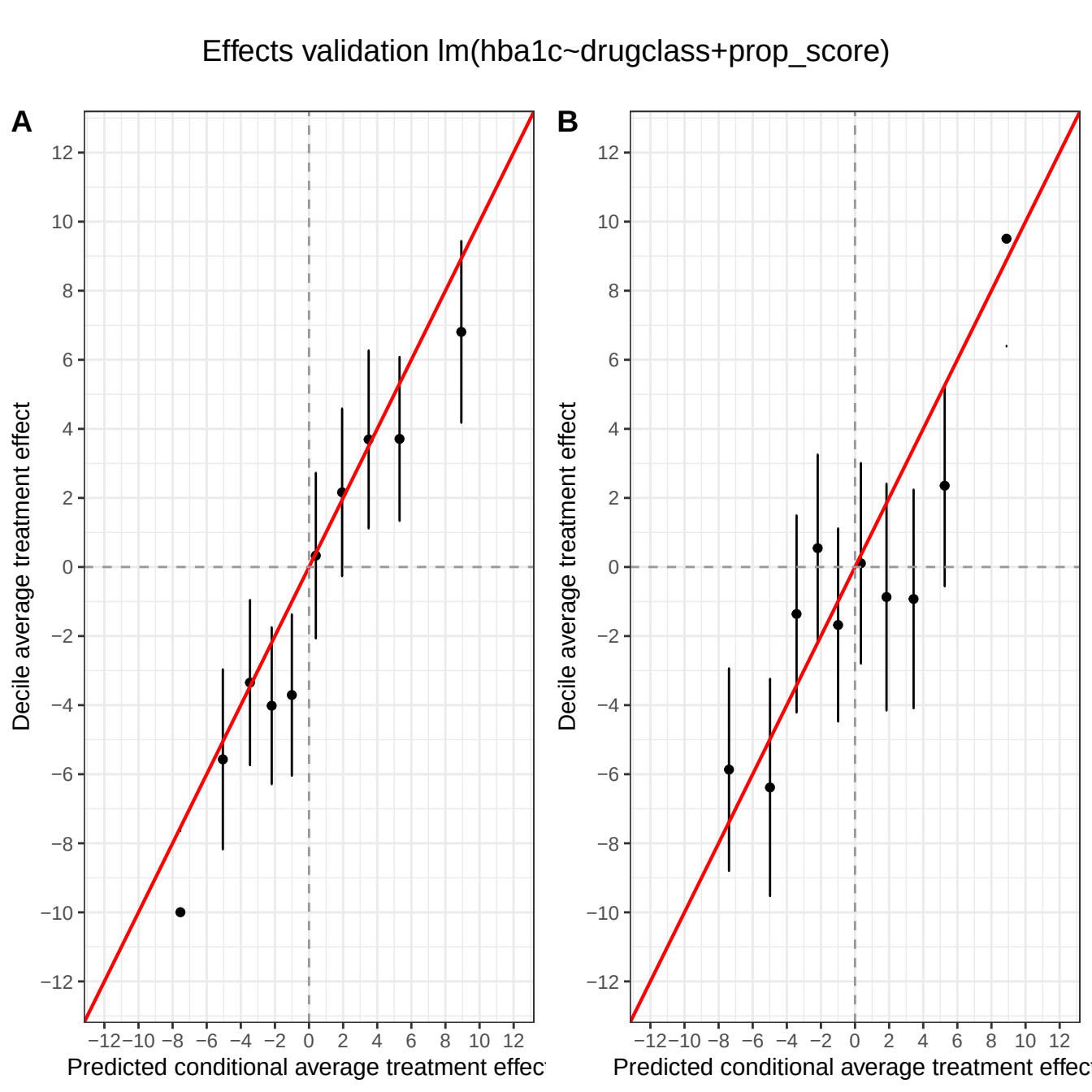
Model fitting: Complete data (Routine/No propensity score)

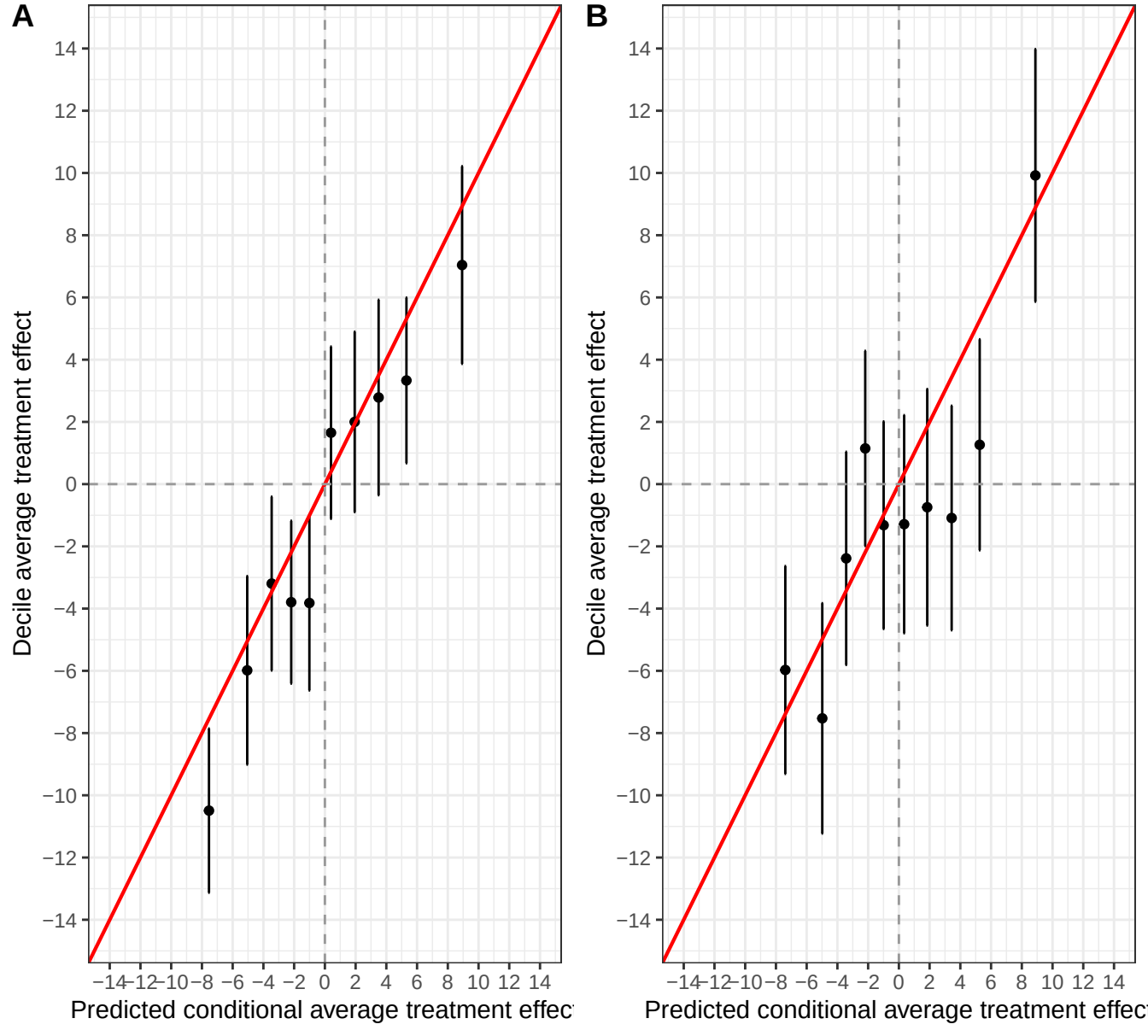



A
Male
Favours GLP1
Favours SGLT2
Number of people
HbA1c difference (mmol/mol)
Female
B
Male
Female

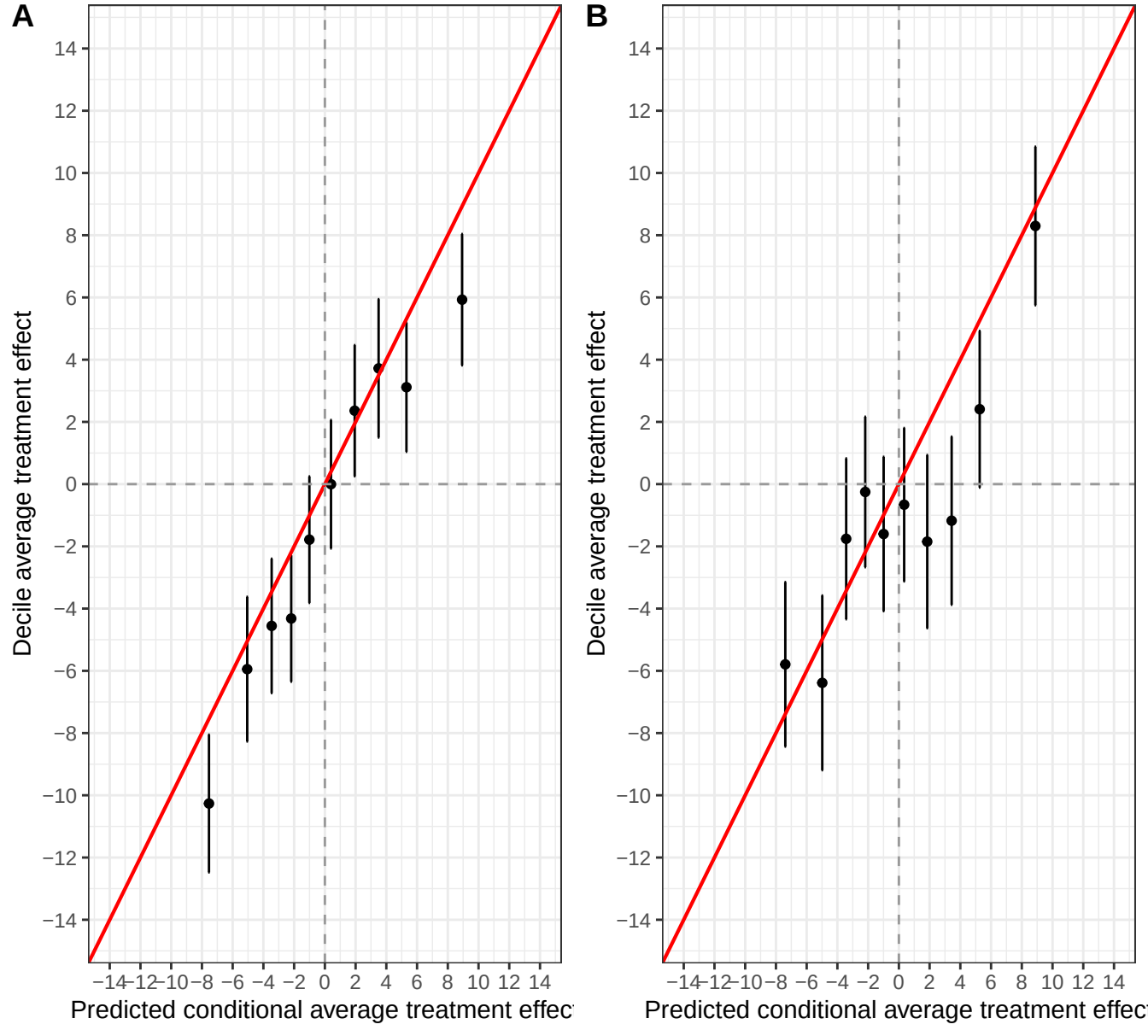

Effect submodels
A
B
In−sample prediction from sub model
In−sample prediction from full model
Out−of−sample prediction from full model


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

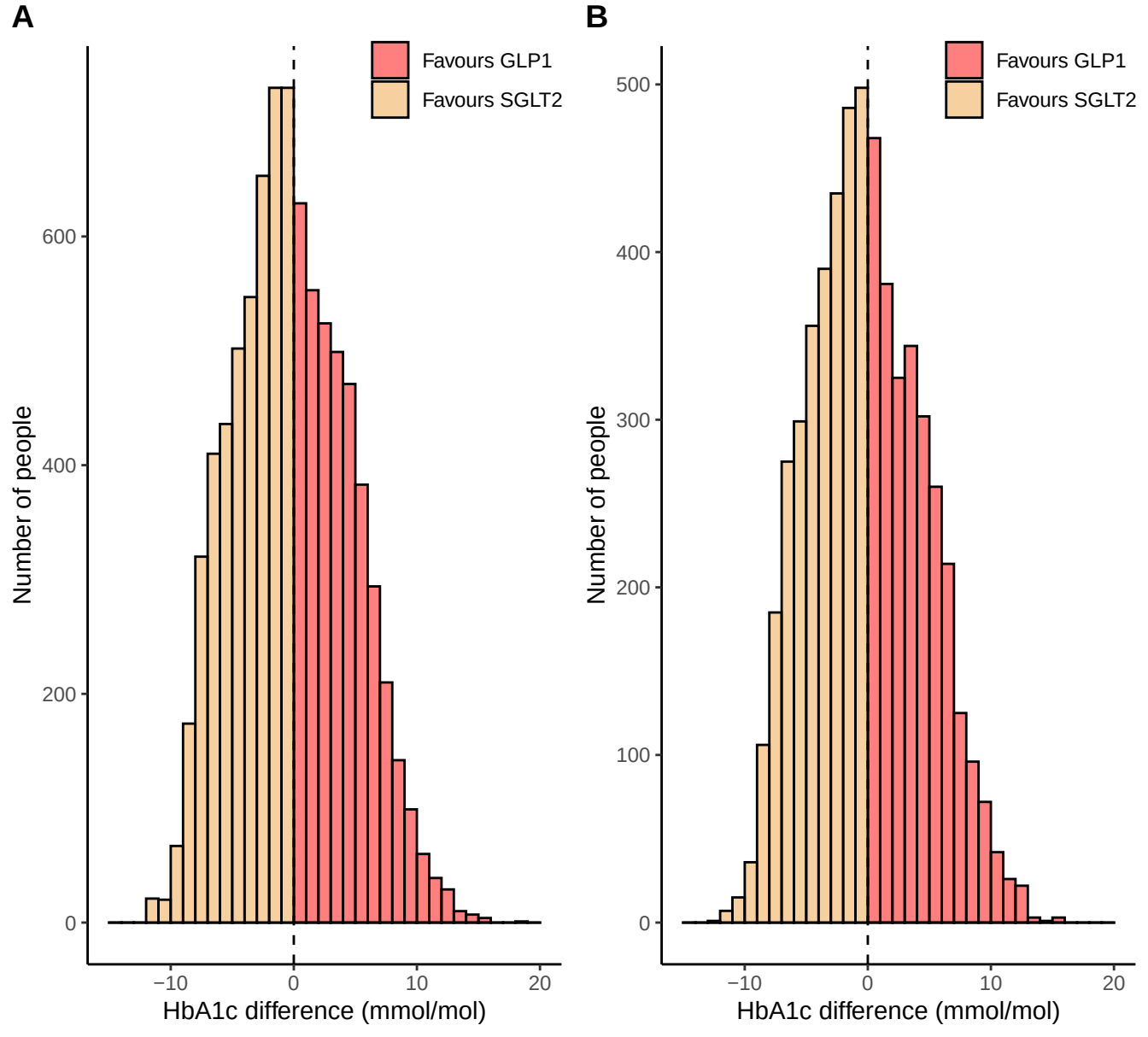
Effects validation prop score matching

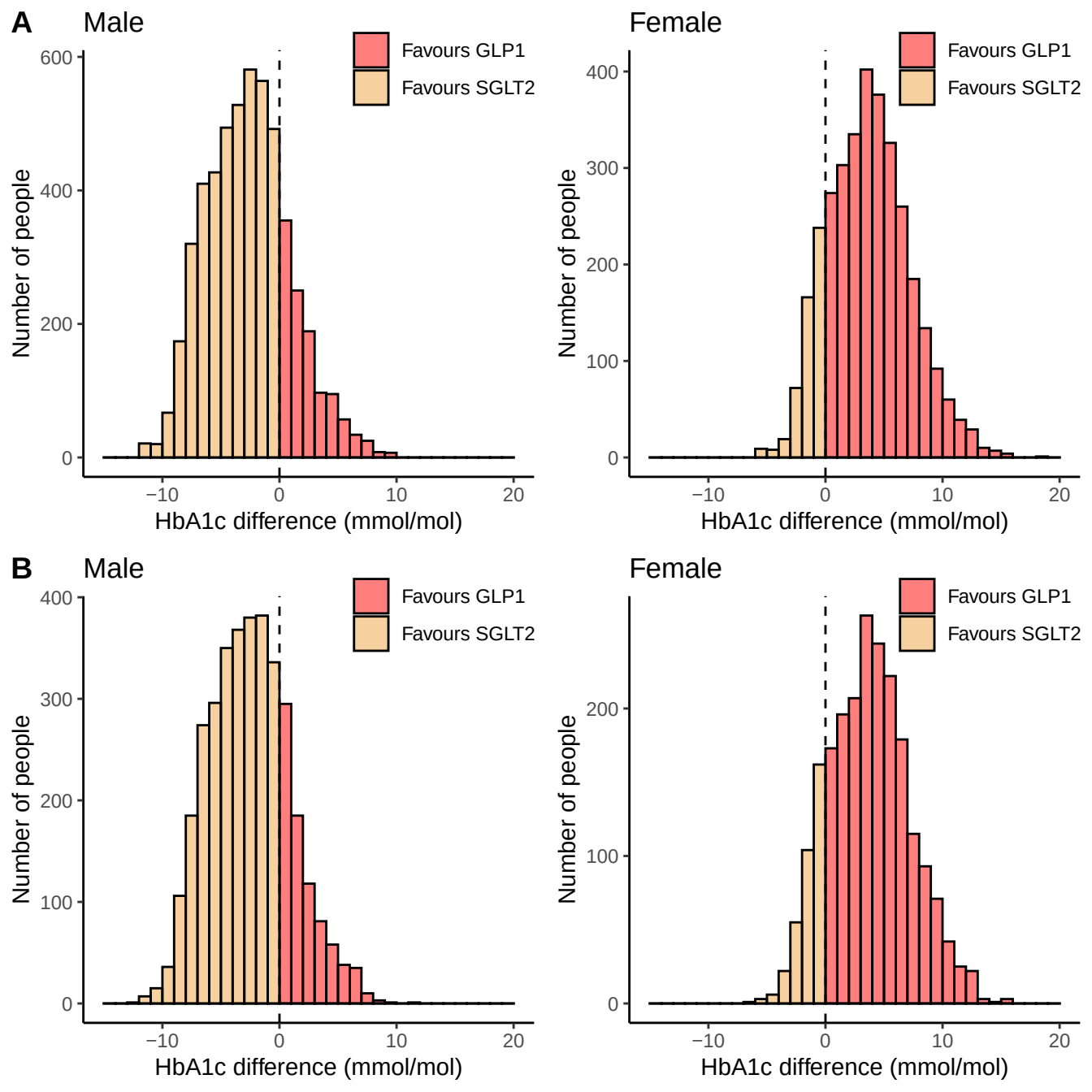


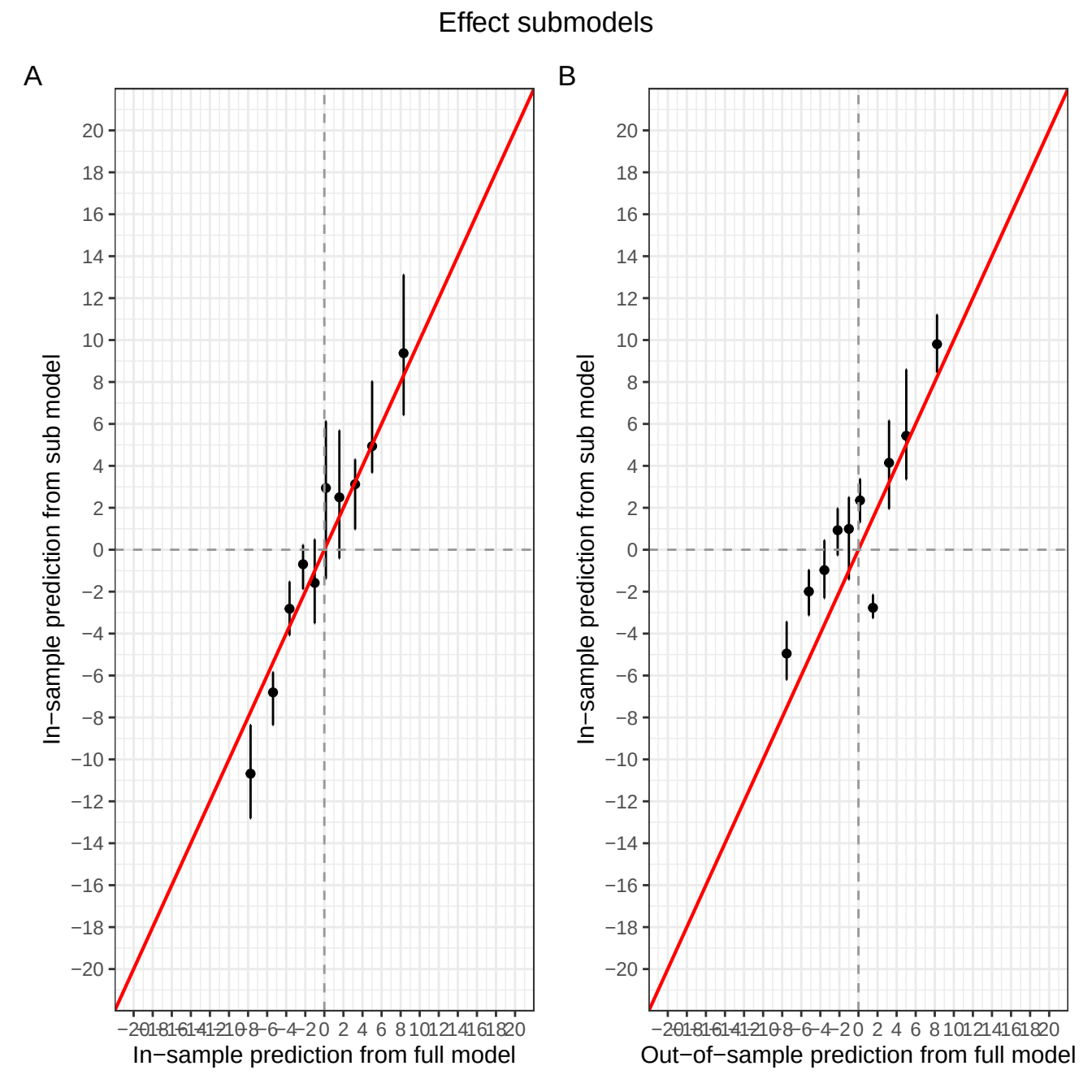
Effects validation prop score inverse weighting



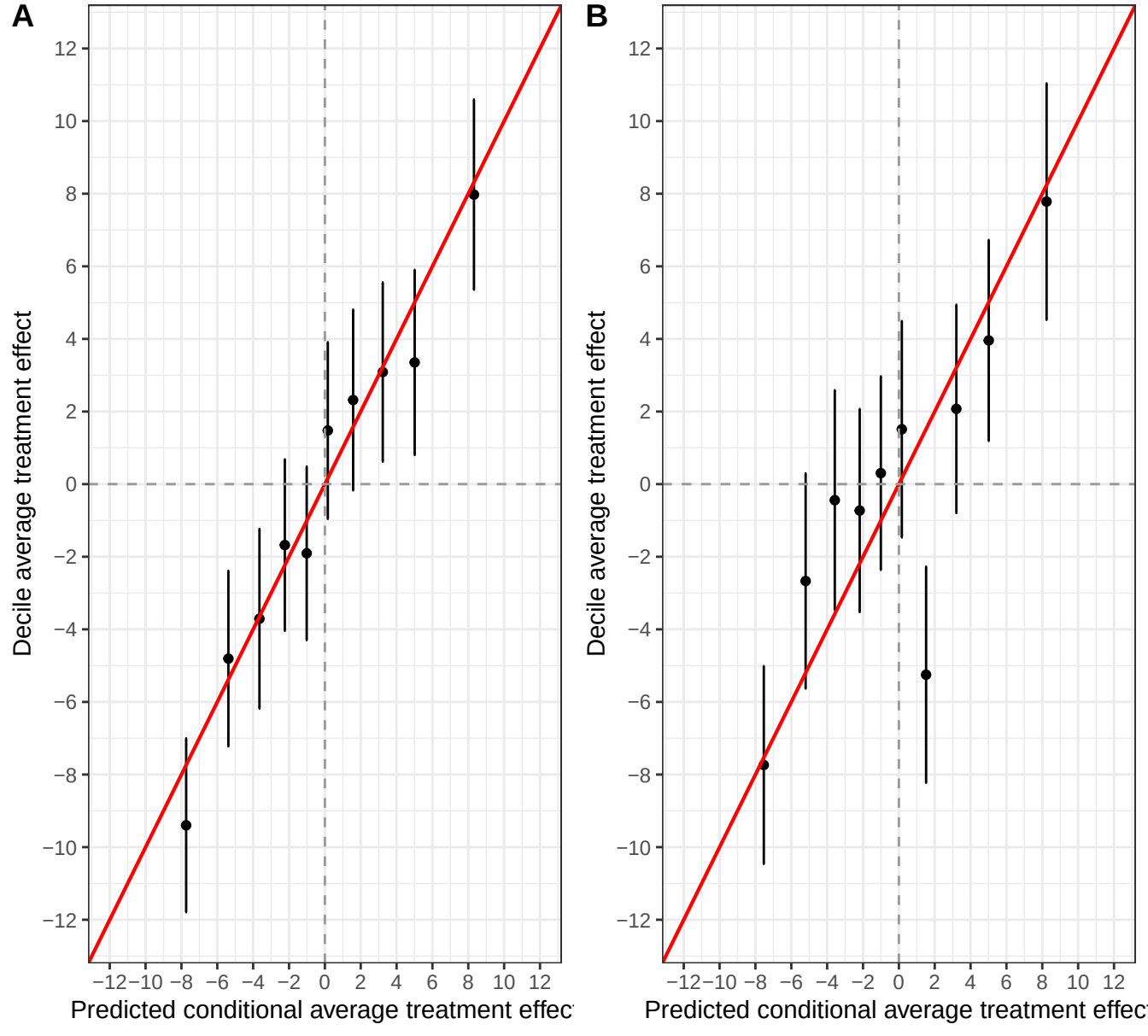
Model fitting: Complete data (Routine/Propensity score)



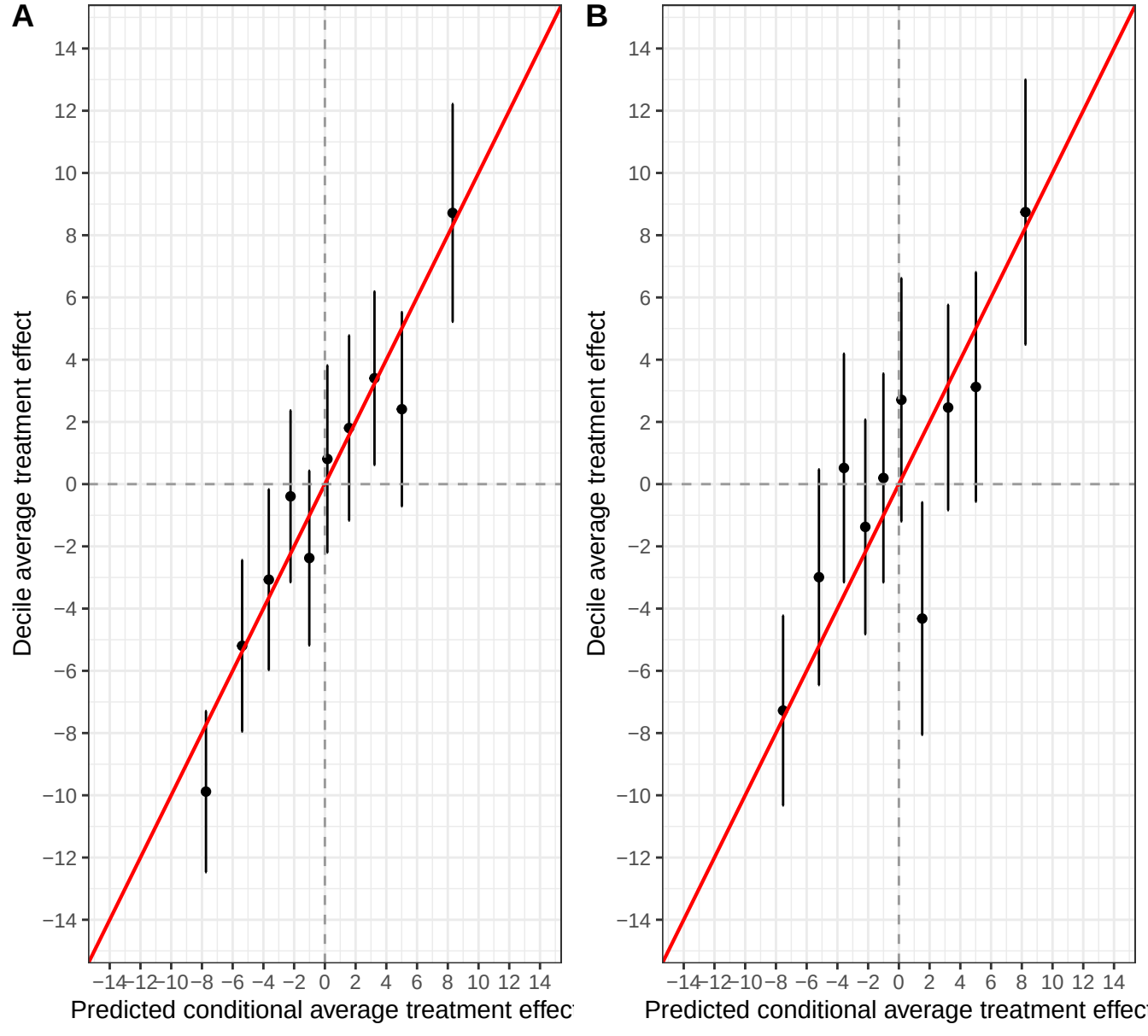

A
Male
Favours GLP1
Favours SGLT2
Number of people
HbA1c difference (mmol/mol)
Female
B
Male
Female

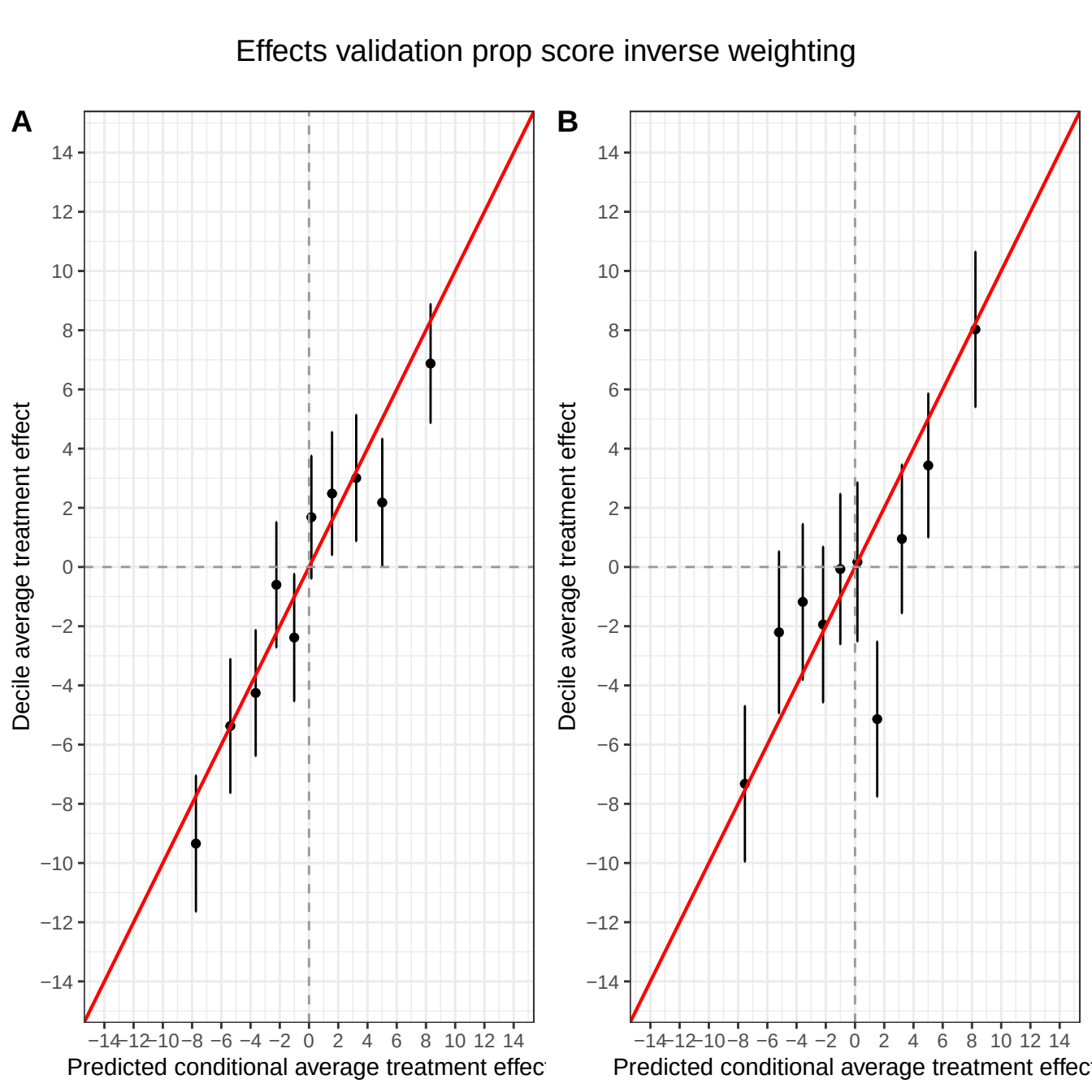

Effect submodels
A
B
In−sample prediction from sub model
In−sample prediction from full model
Out−of−sample prediction from full model

Effects validation lm(hba1c~drugclass+prop_score)

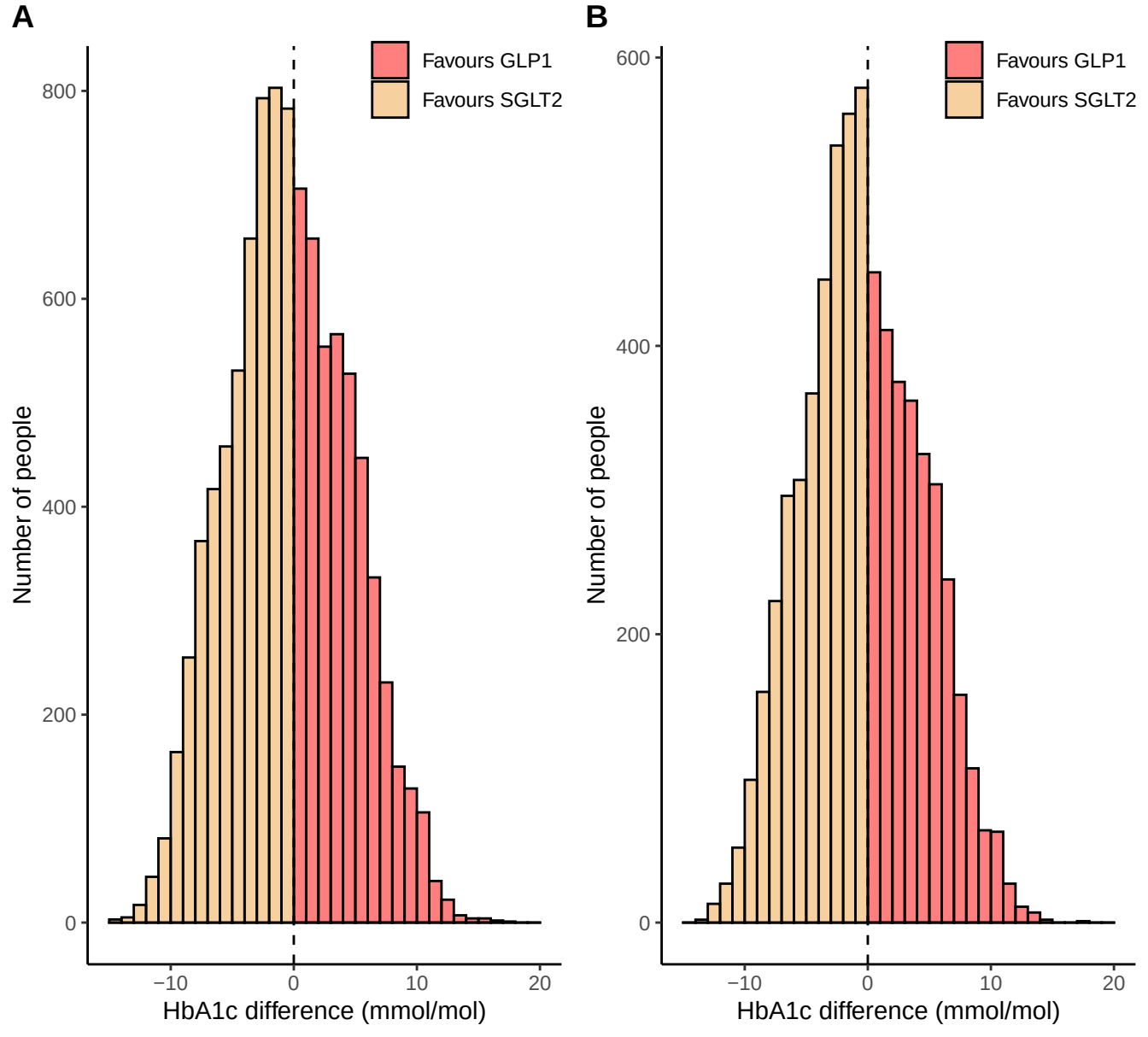


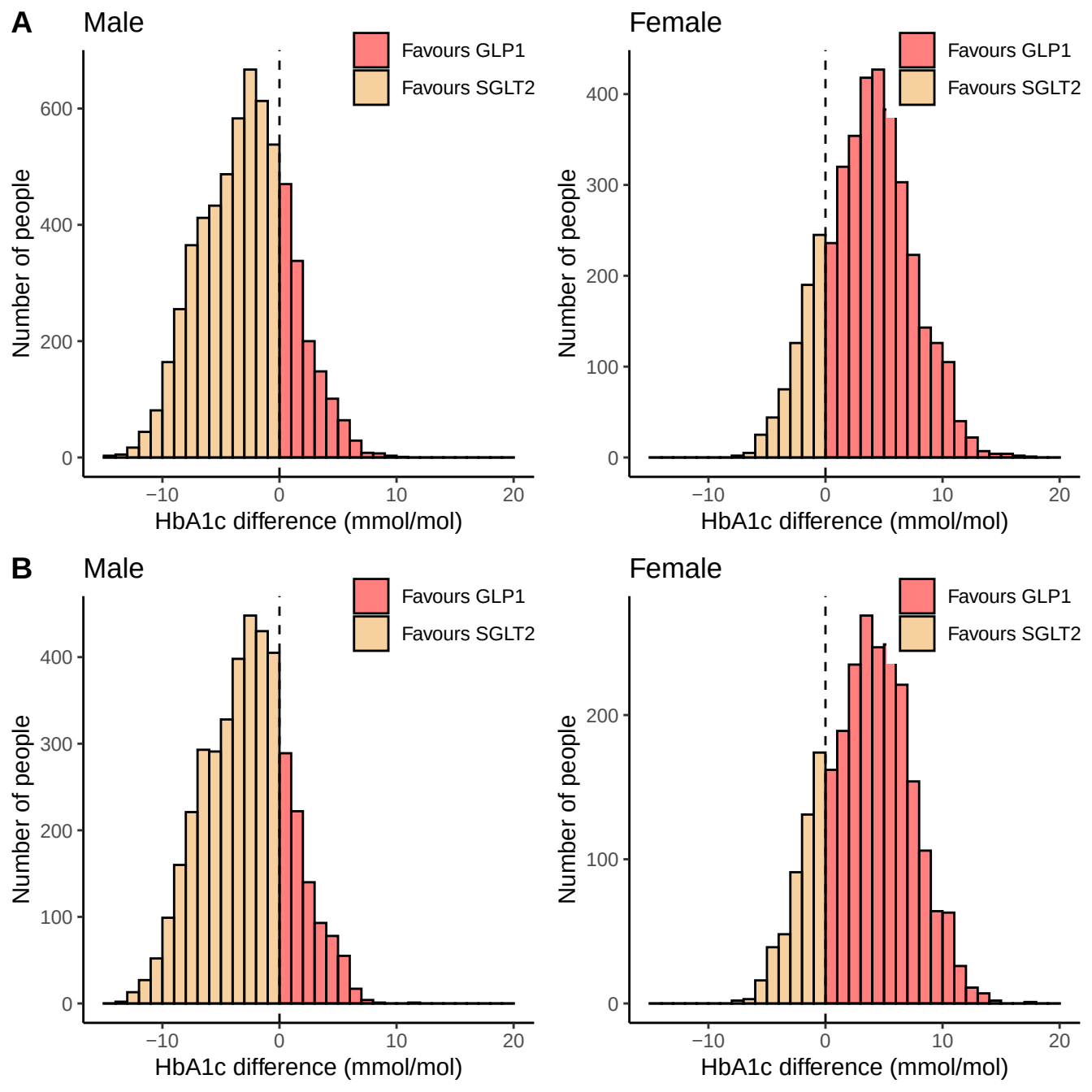
Effects validation prop score matching

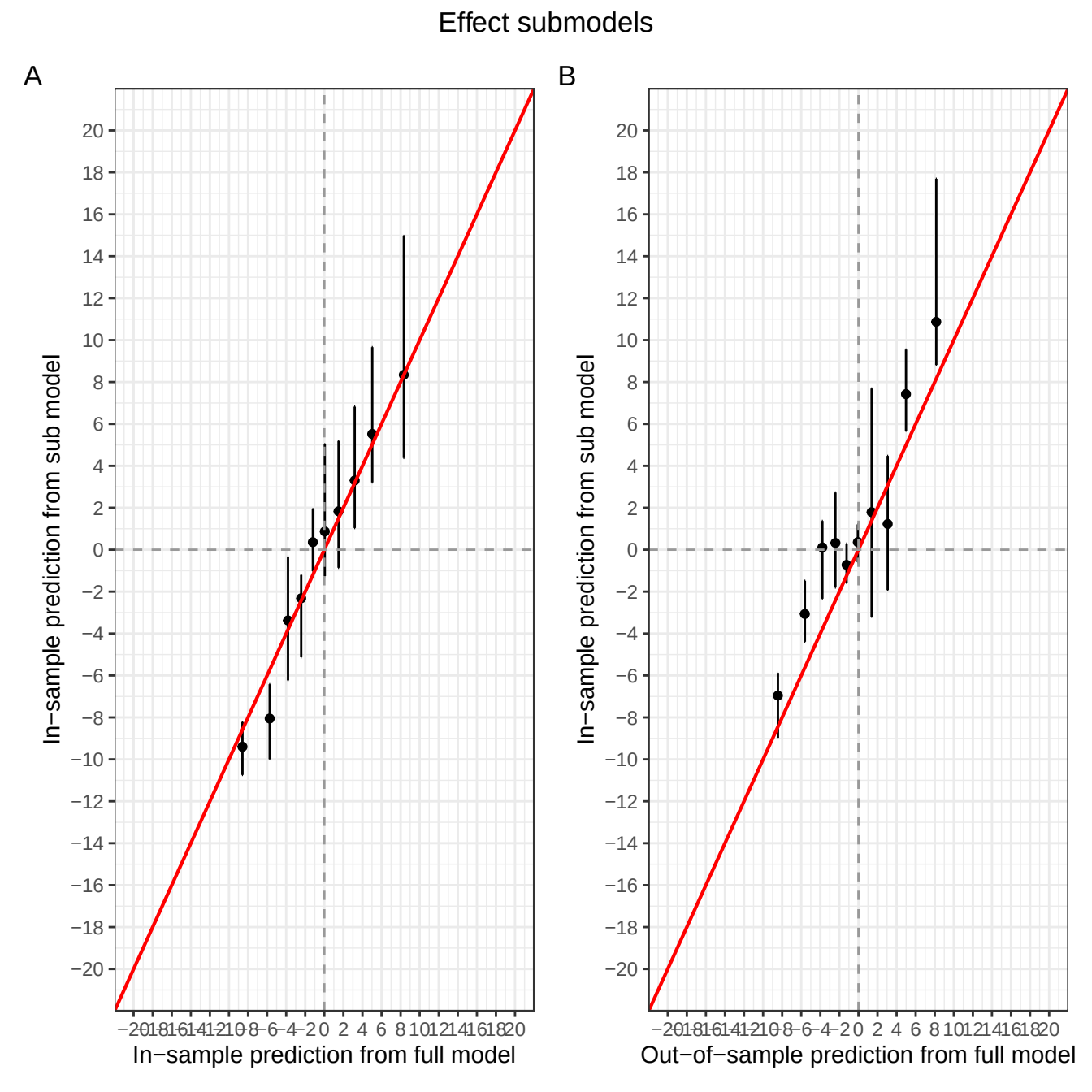


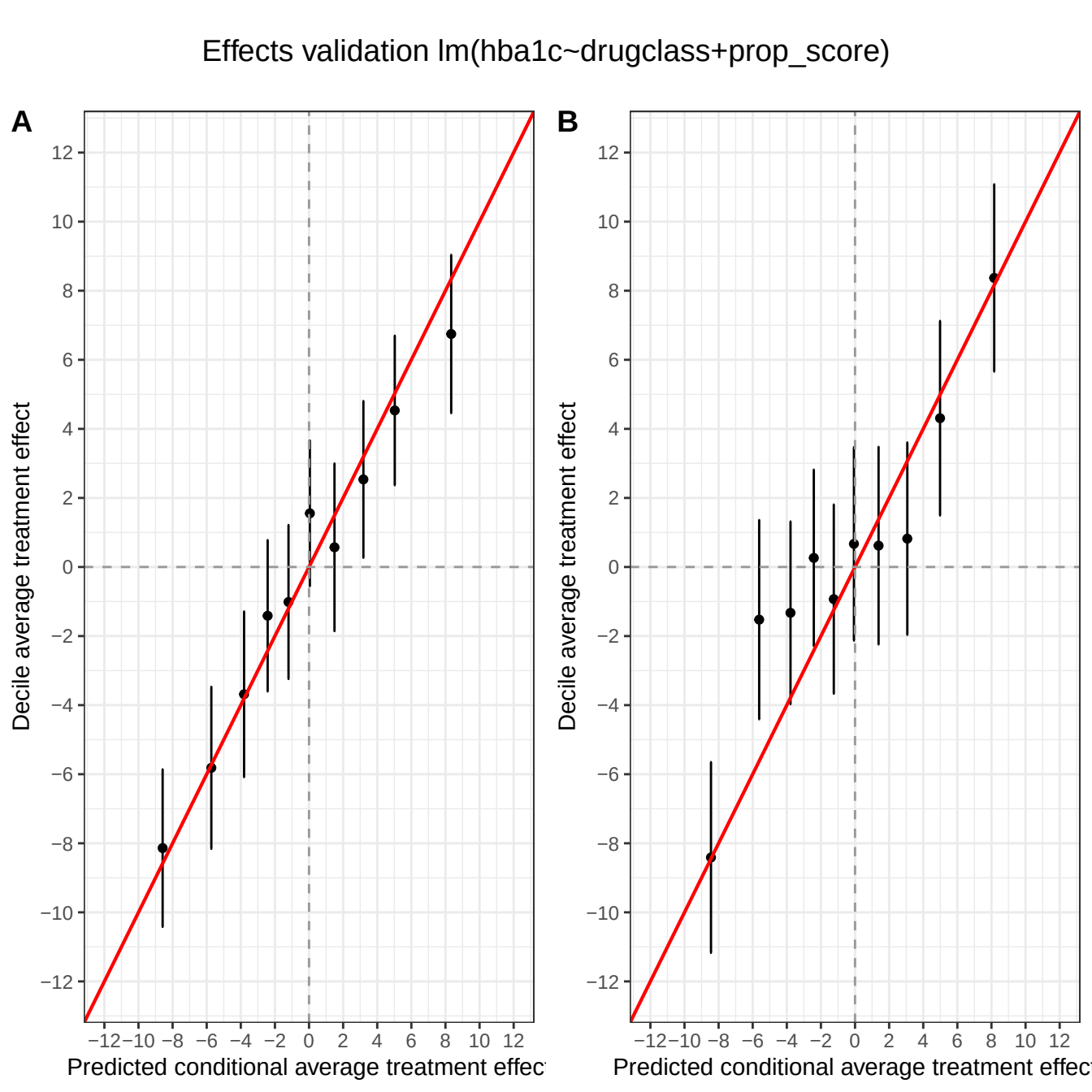

Effects validation prop score inverse weighting
A
B
Decile average treatment effect
Predicted conditional average treatment effec
14
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12
−14

Model fitting: Incomplete data (Routine/No propensity score)

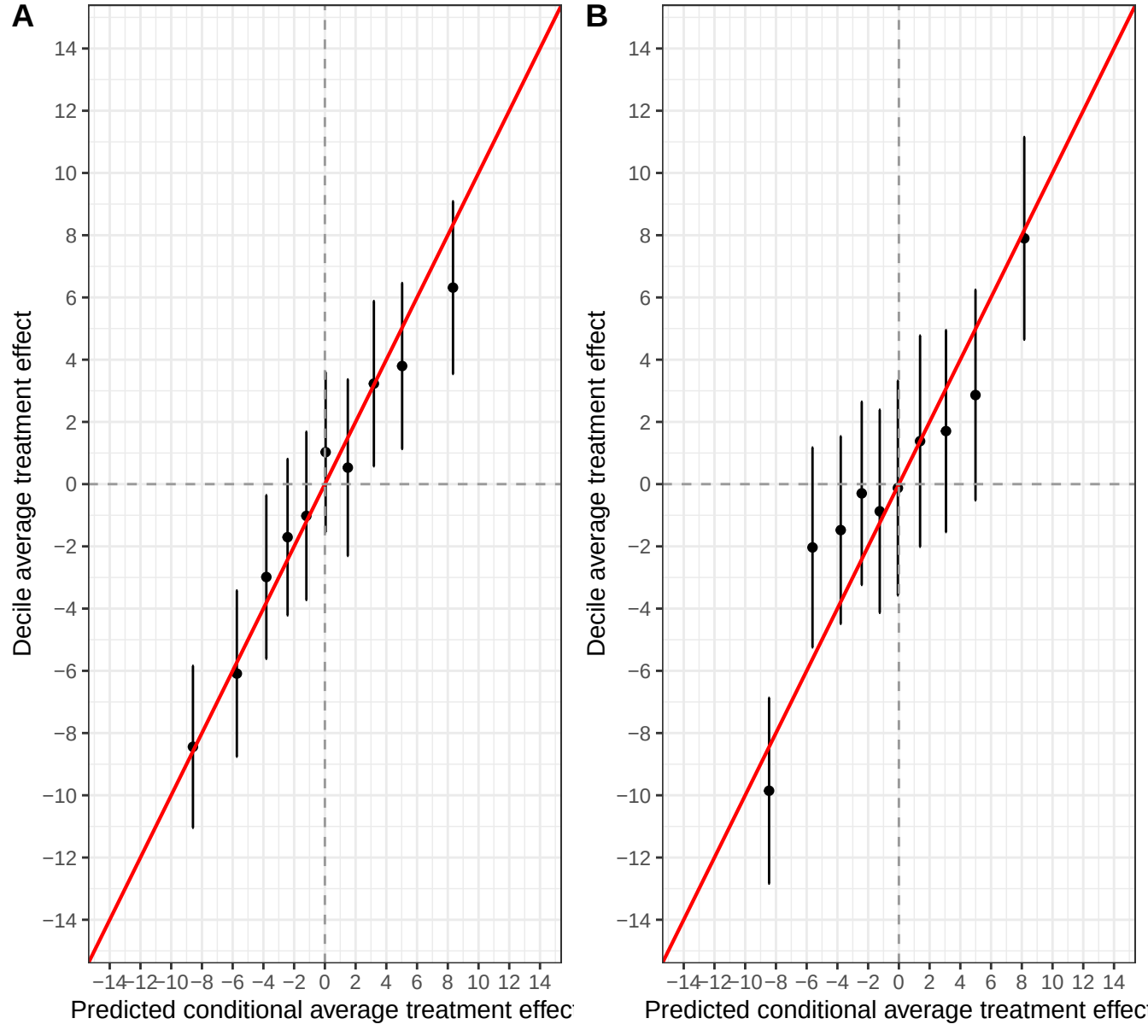


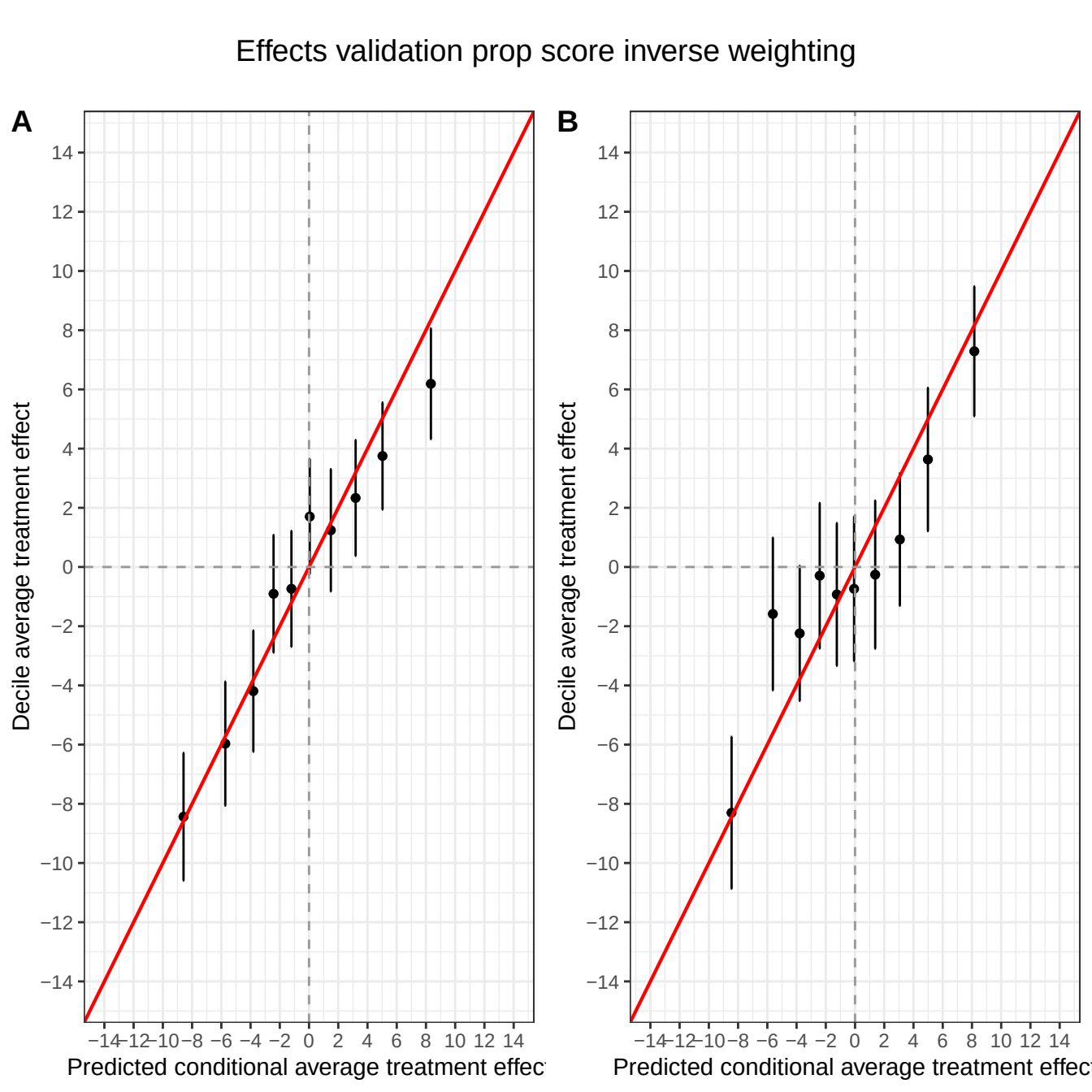

A
Male
Favours GLP1
Favours SGLT2
Number of people
HbA1c difference (mmol/mol)
Female
B
Male
Female


Effect submodels
A
B
In−sample prediction from sub model
In−sample prediction from full model
Out−of−sample prediction from full model

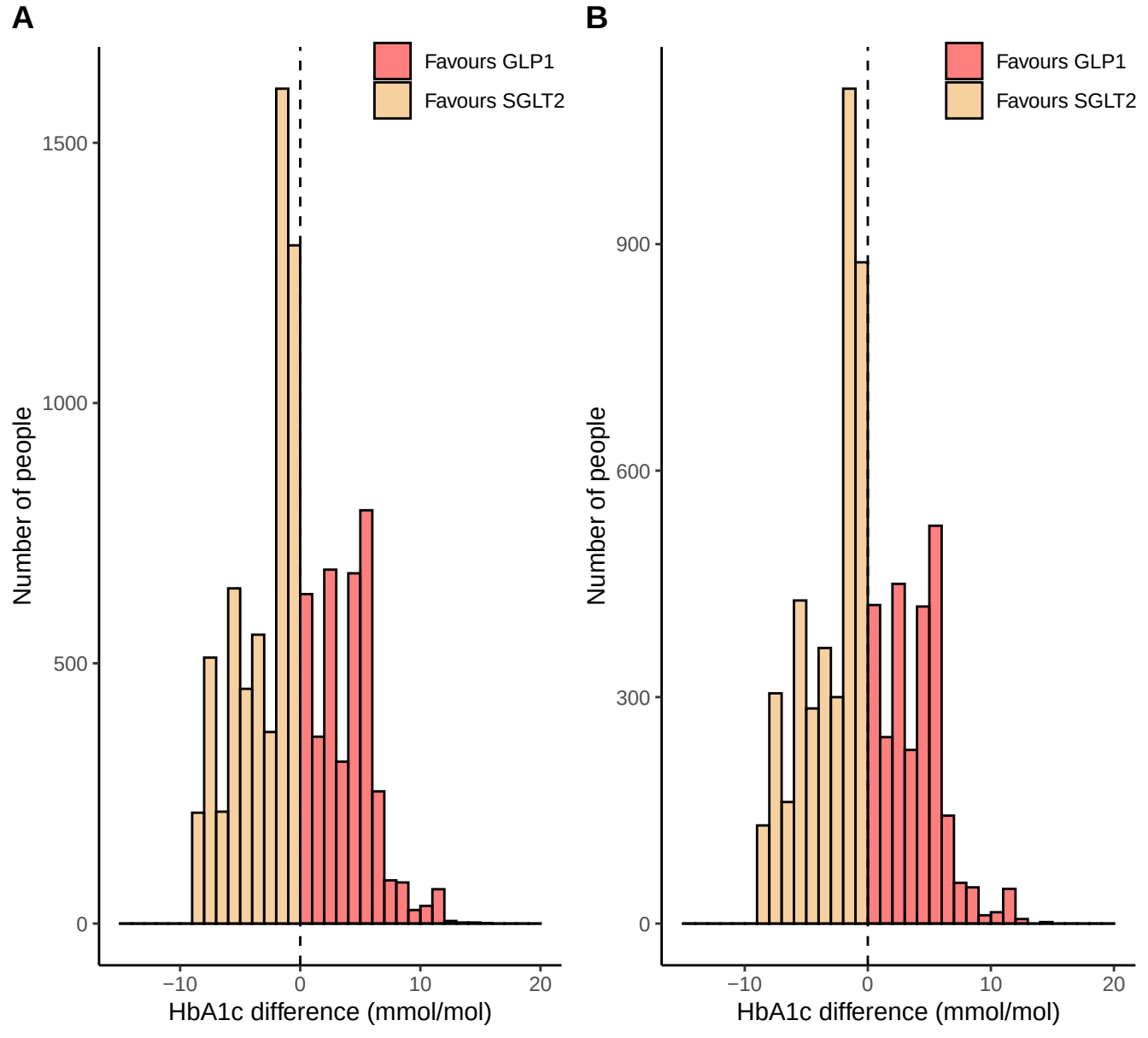

Effects validation lm(hba1c~drugclass+prop_score)
A
B
Decile average treatment effect
Predicted conditional average treatment effec
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12

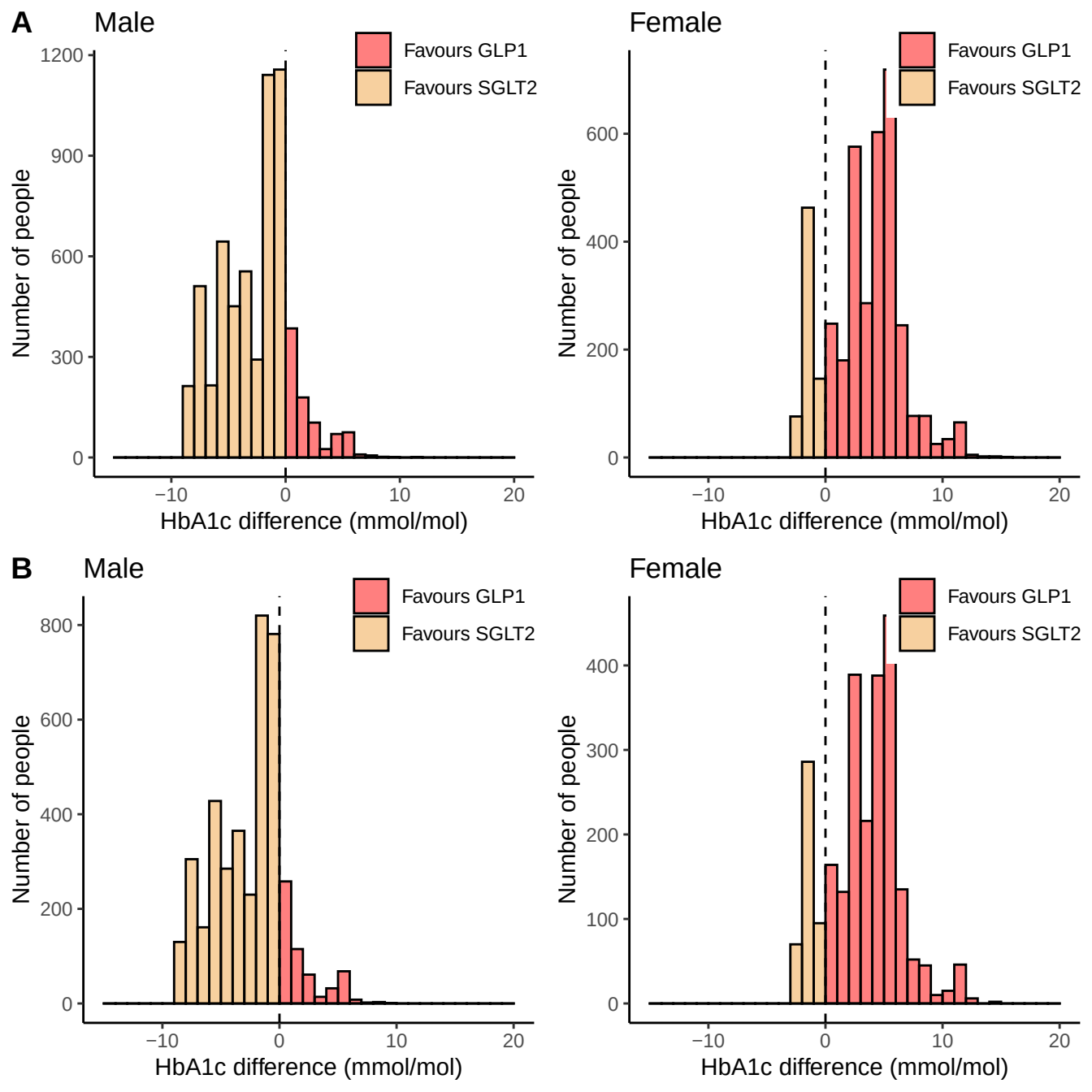
Effects validation prop score matching

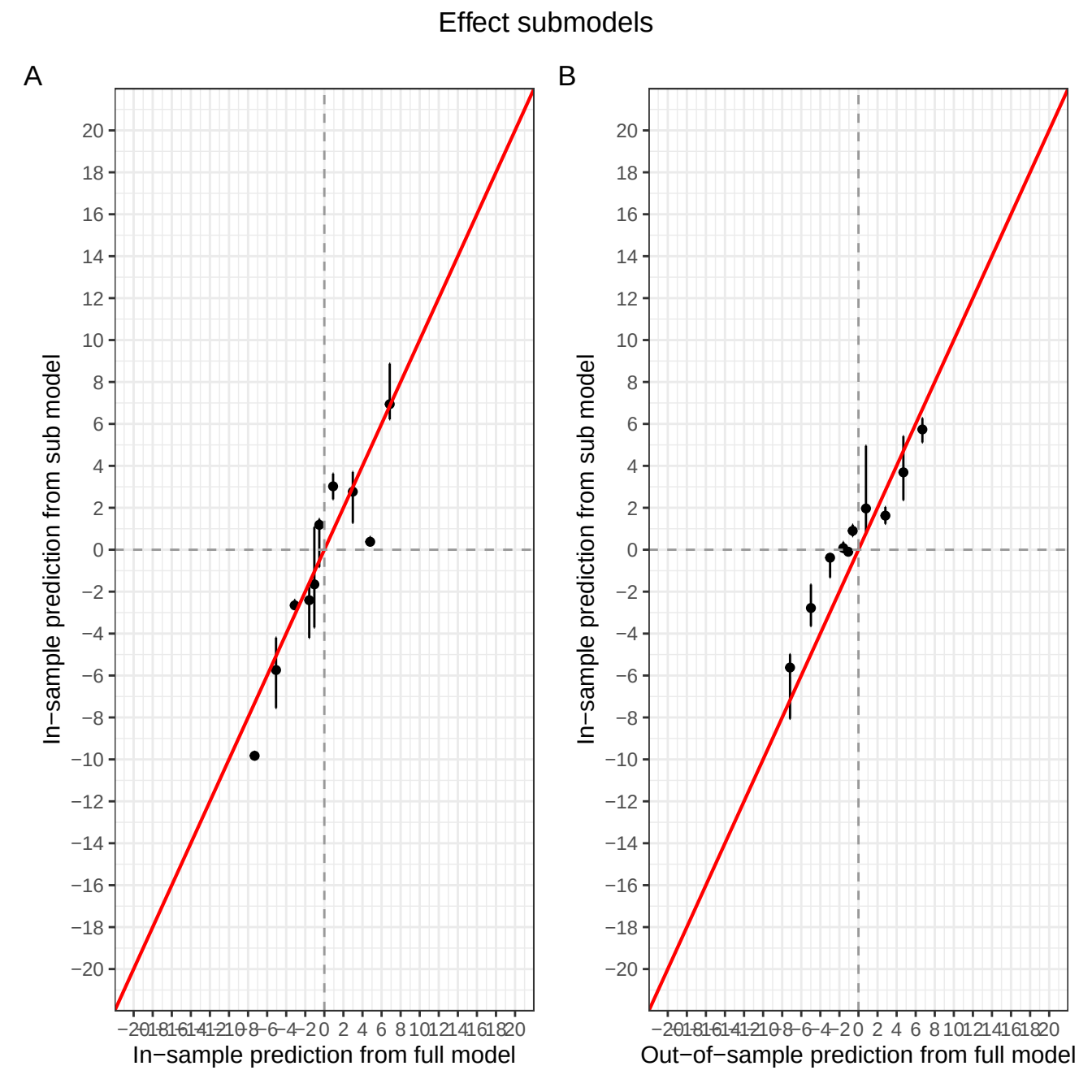


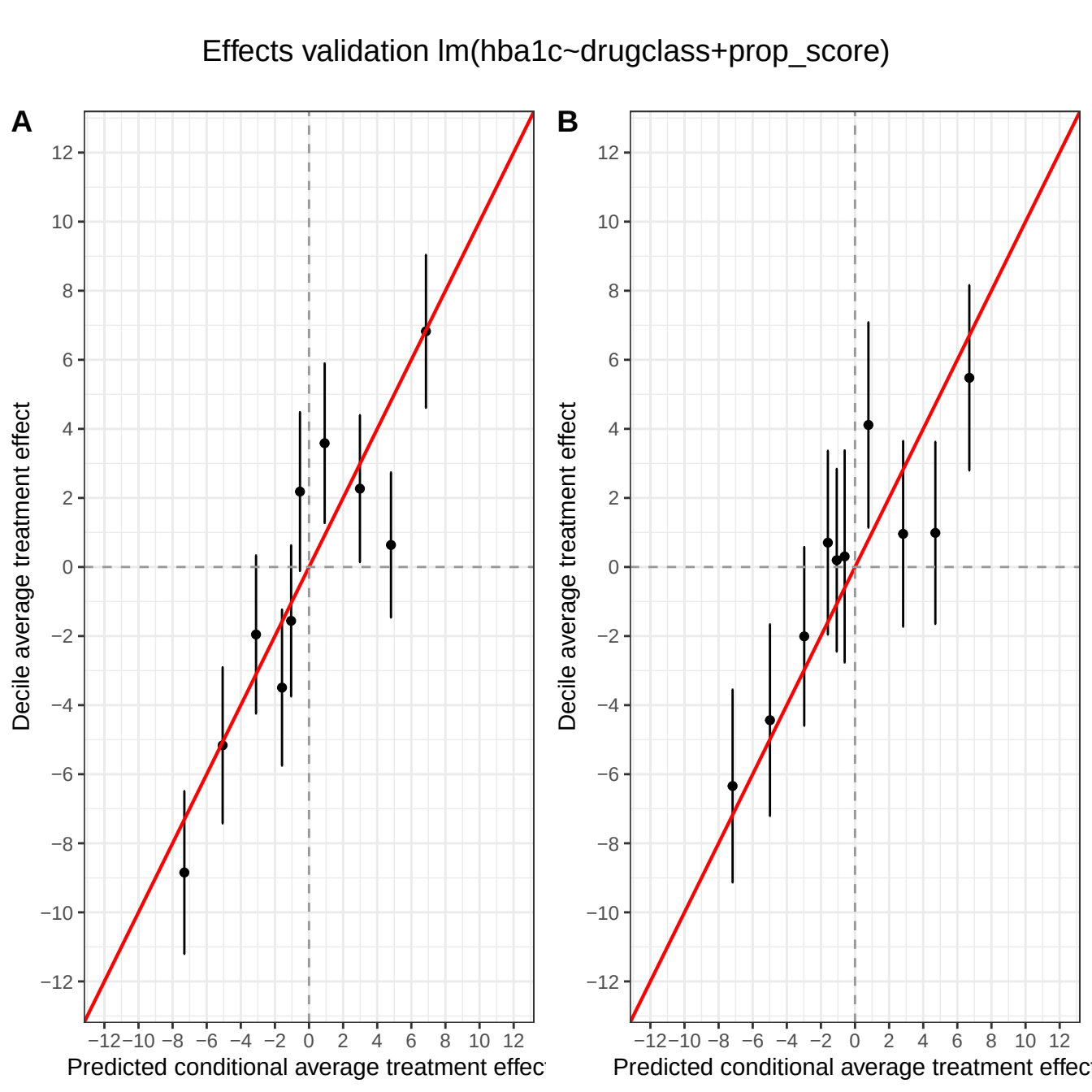

Effects validation prop score inverse weighting
A
B
Decile average treatment effect
Predicted conditional average treatment effec
14
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12
−14

Model fitting: Incomplete data (No propensity score)

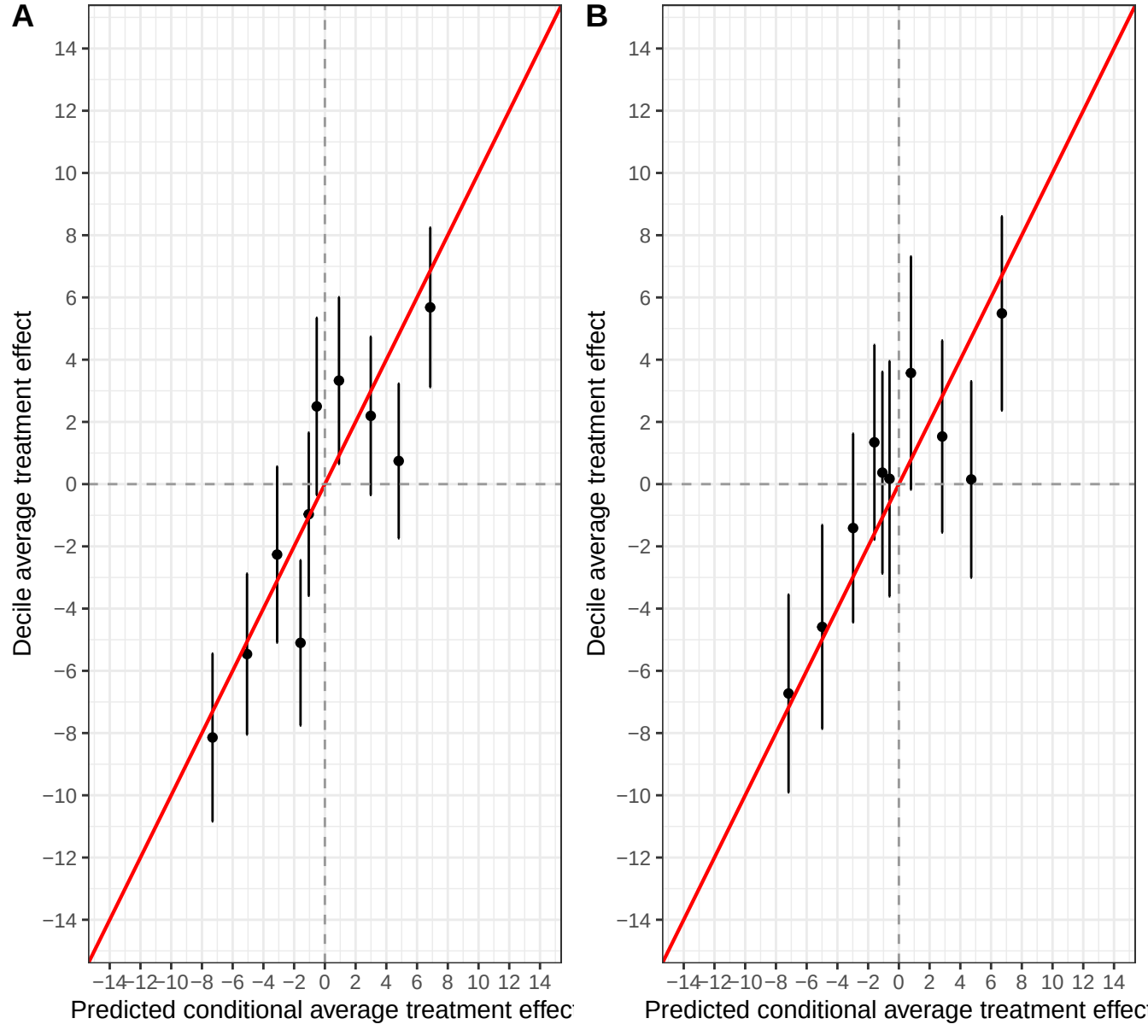



A
Male
Female
Favours GLP1
Favours SGLT2
Number of people
HbA1c difference (mmol/mol)
B
Male
Female
Favours GLP1
Favours SGLT2
Number of people
HbA1c difference (mmol/mol)

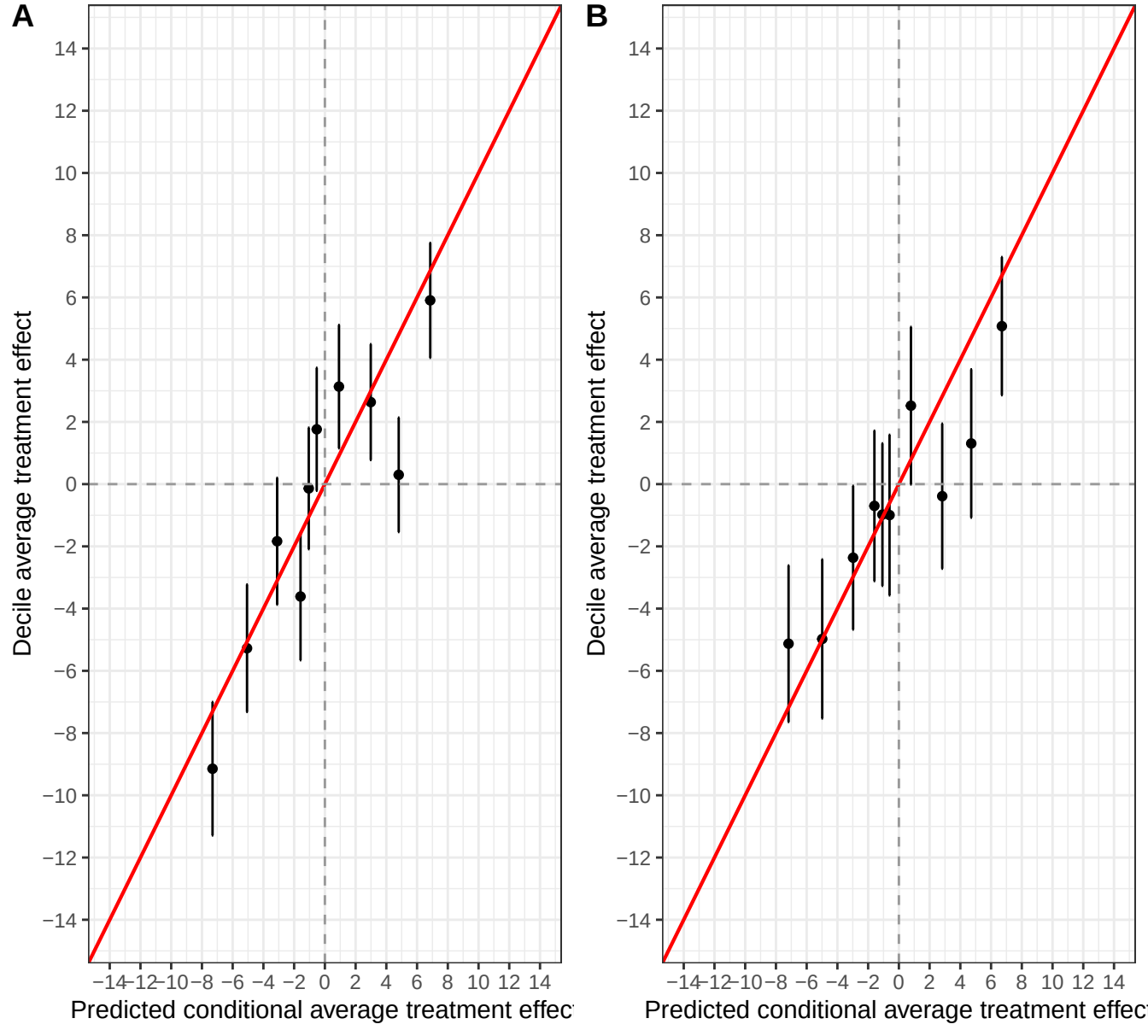

Effect submodels
A
B
In−sample prediction from sub model
In−sample prediction from full model
Out−of−sample prediction from full model


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

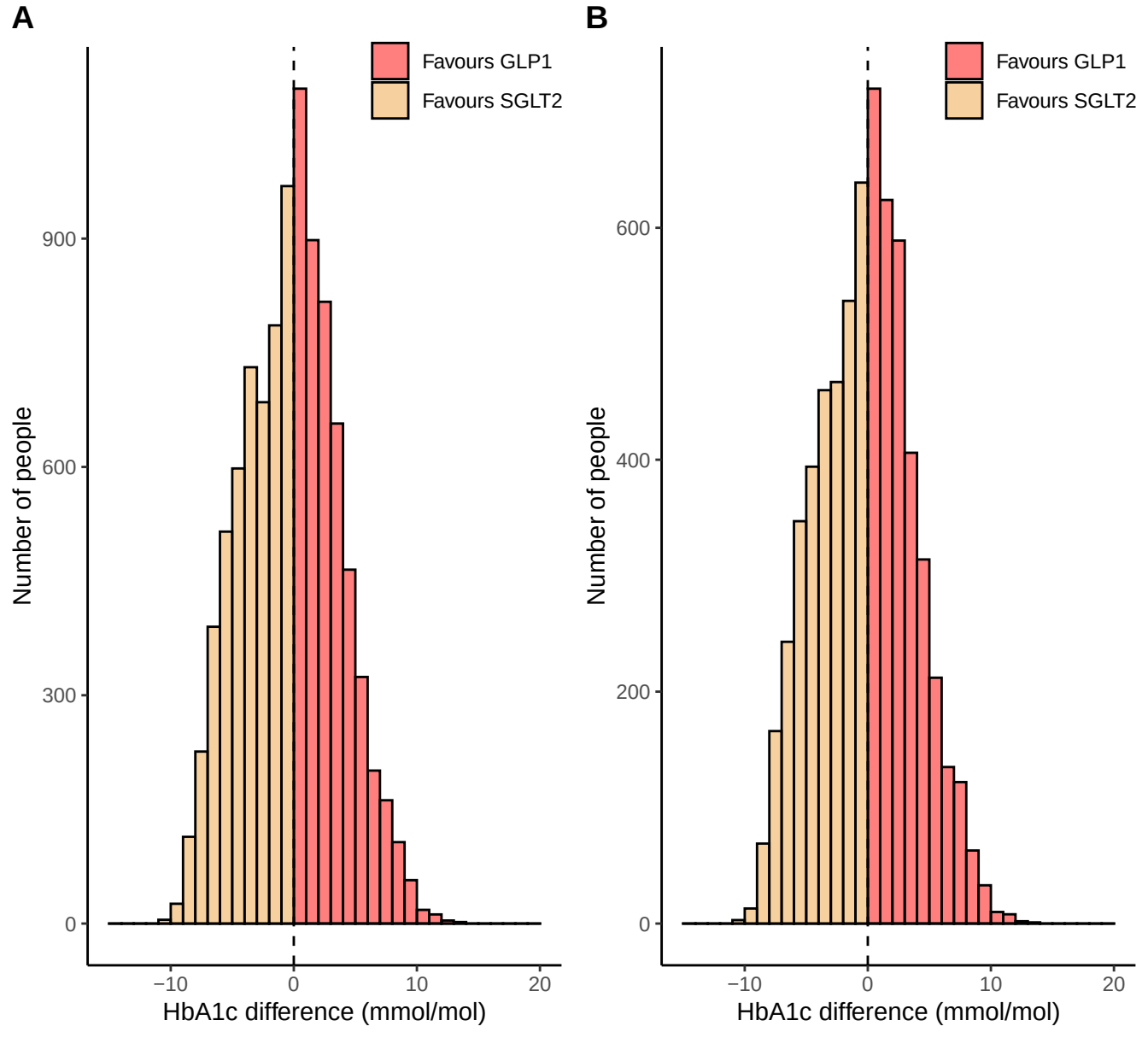
Effects validation prop score matching

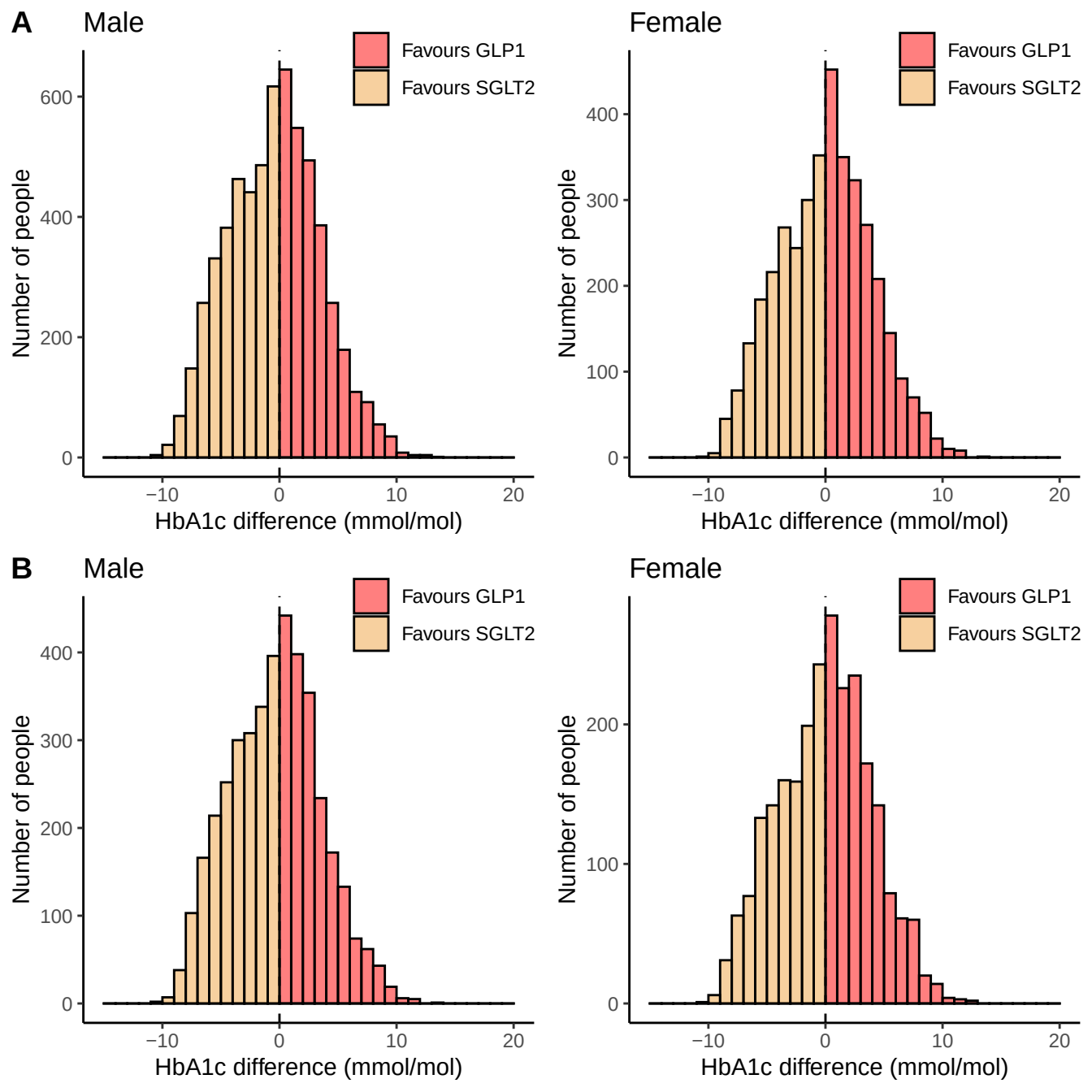


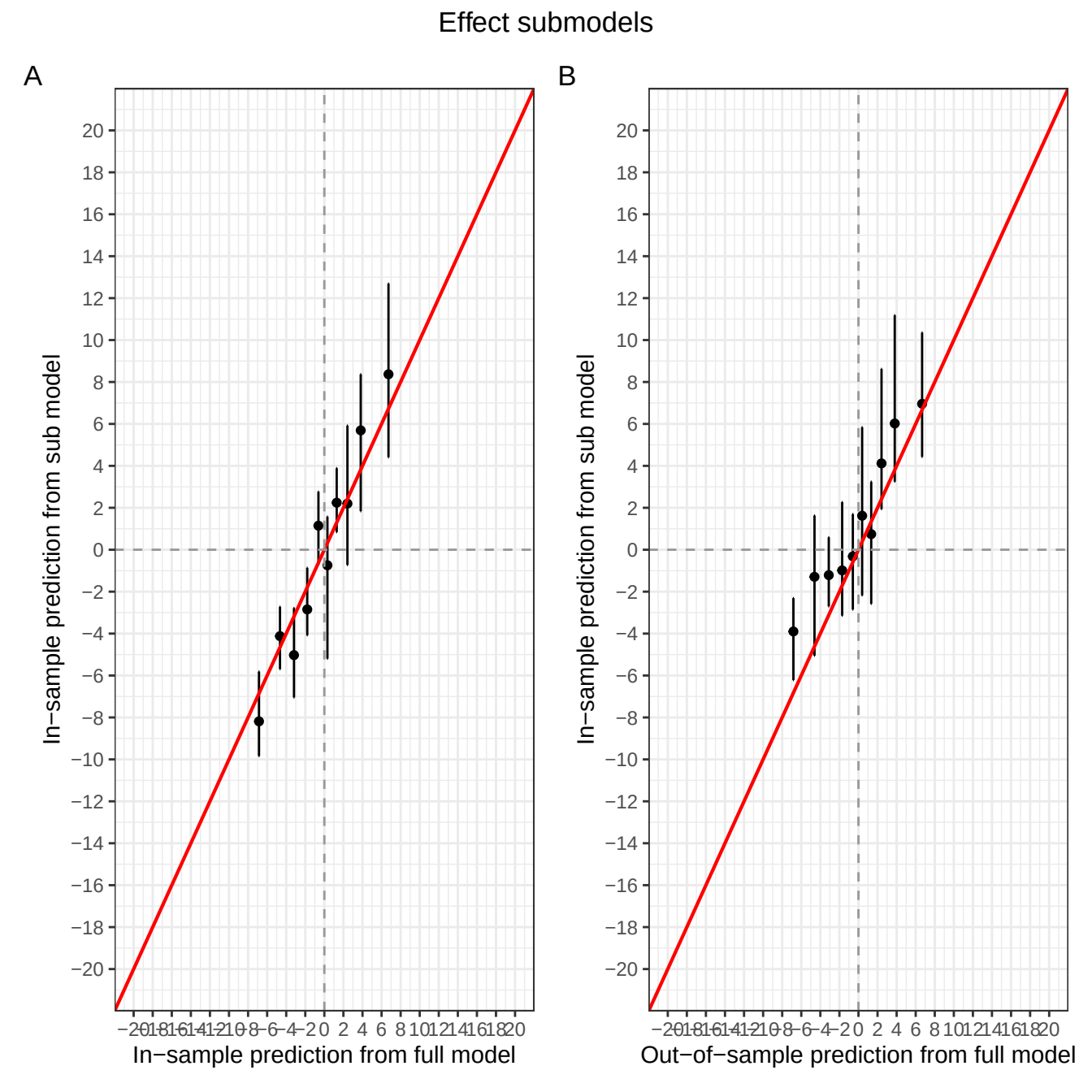
Effects validation prop score inverse weighting

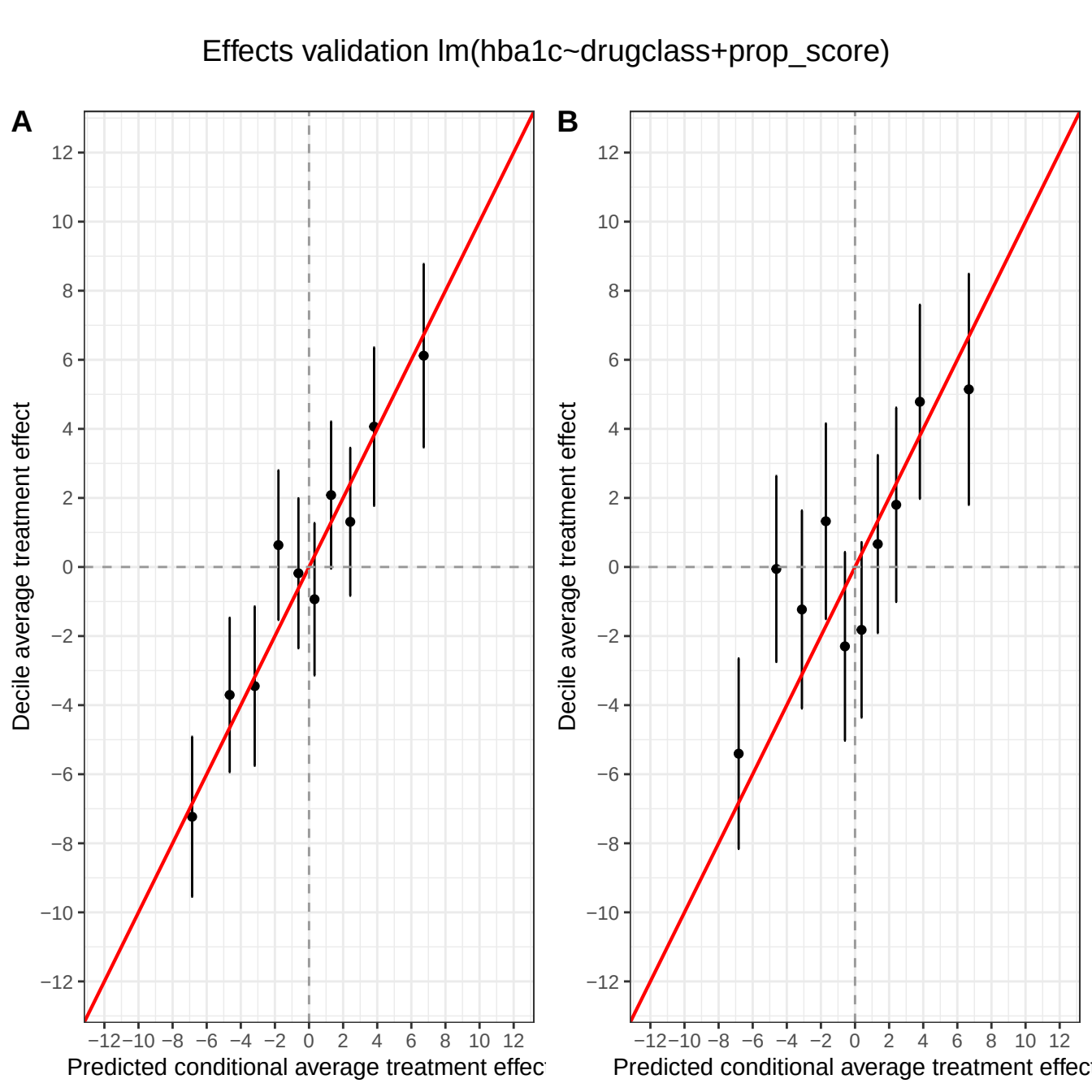


Model fitting: Variable Selection 1, Incomplete data (No propensity score)

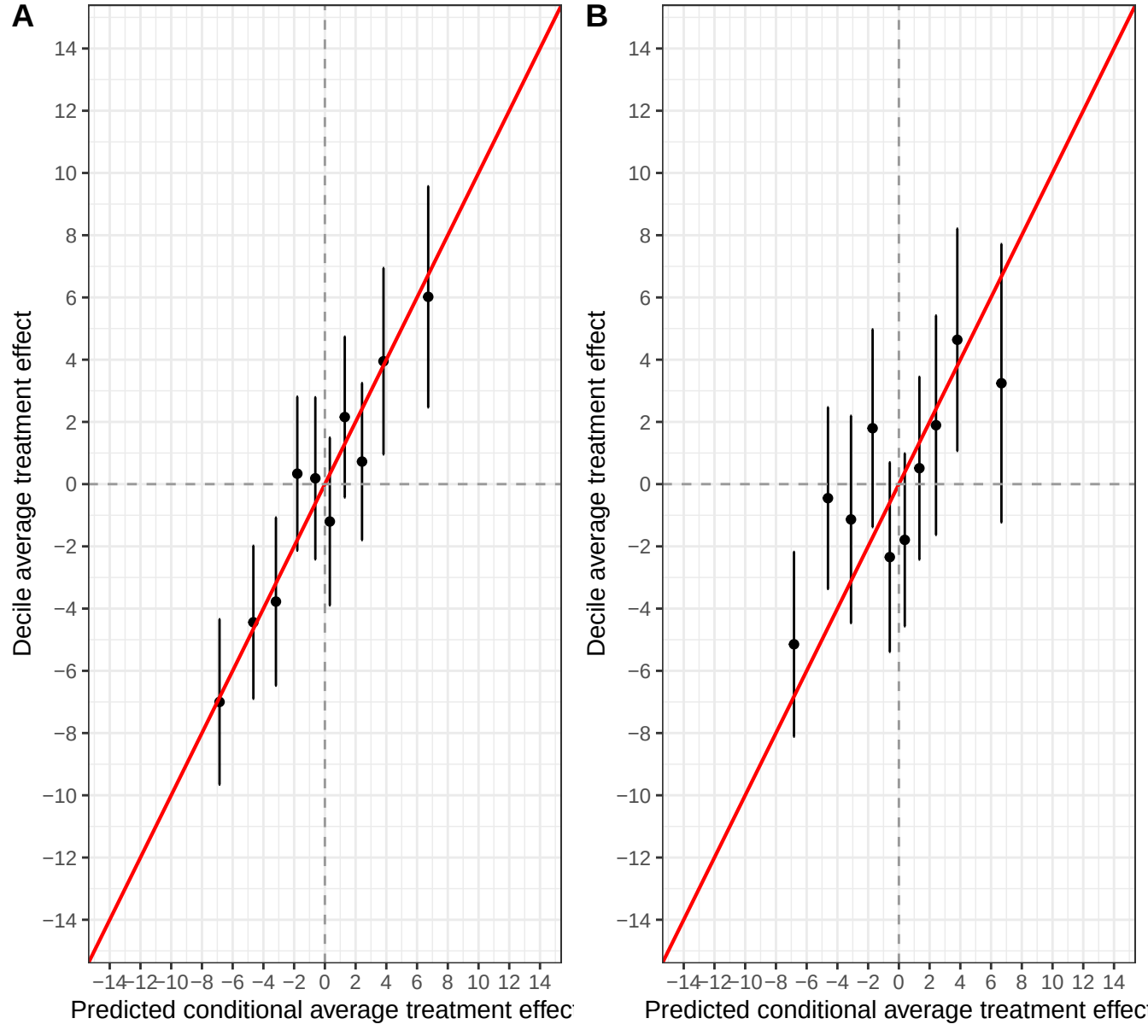


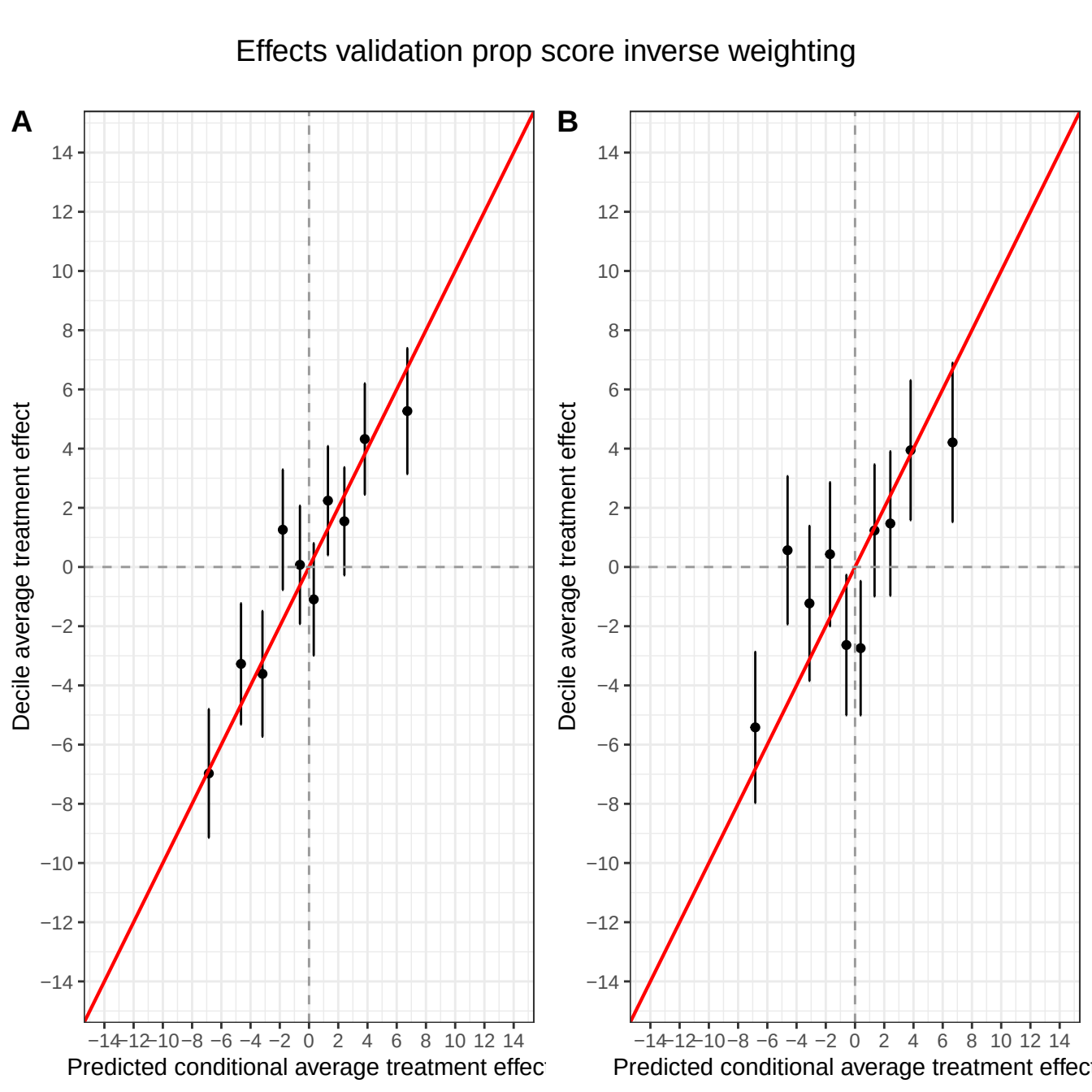

A
Male
Favours GLP1
Favours SGLT2
Number of people
HbA1c difference (mmol/mol)
Female
B
Male
Female

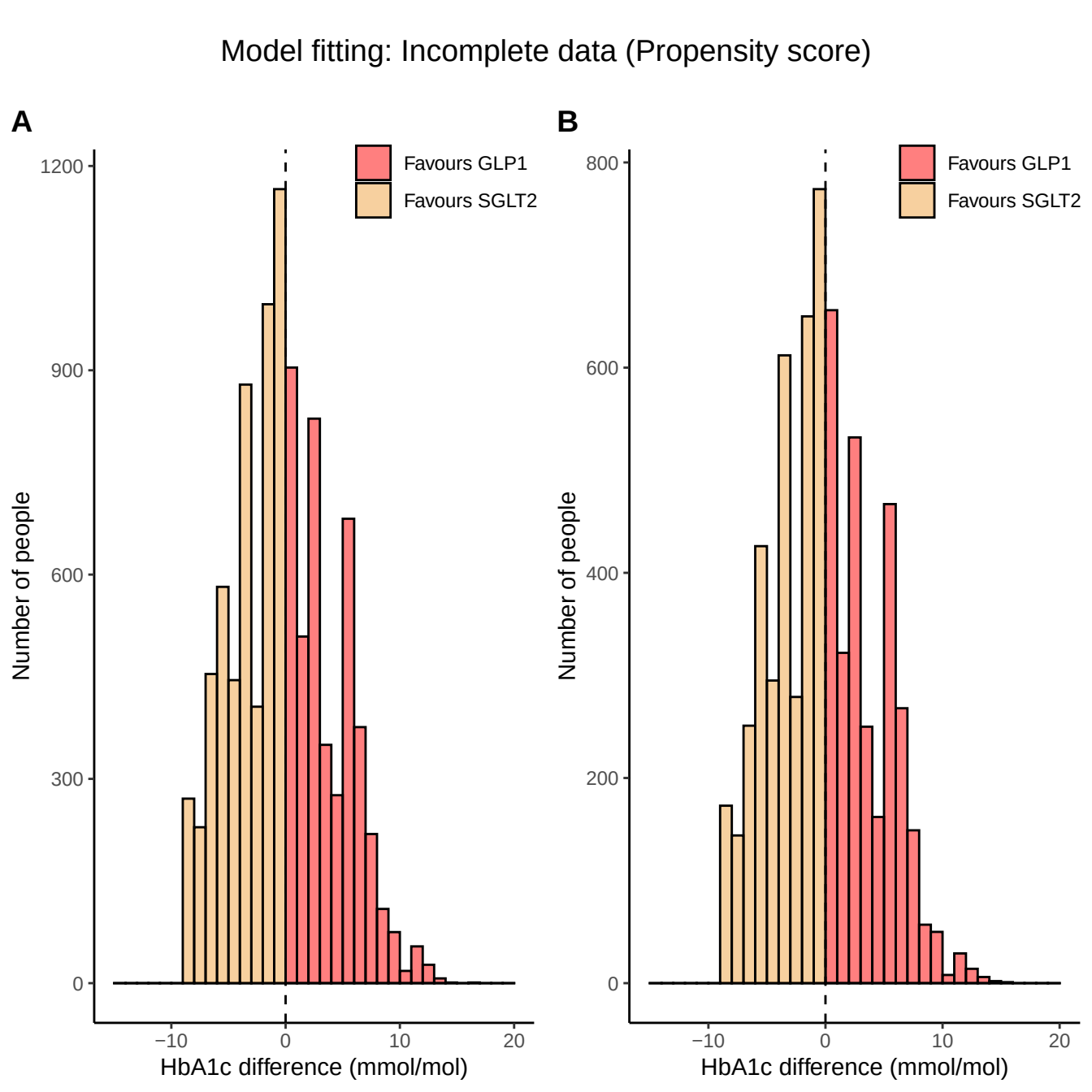

Effect submodels
A
B
In−sample prediction from sub model
In−sample prediction from full model
Out−of−sample prediction from full model
20
18
16
14
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12
−14
−16
−18
−20
−20 −18 −16 −14 −12 −10 −8 −6 −4 −2 0 2 4 6 8 10 12 14 16 18 20

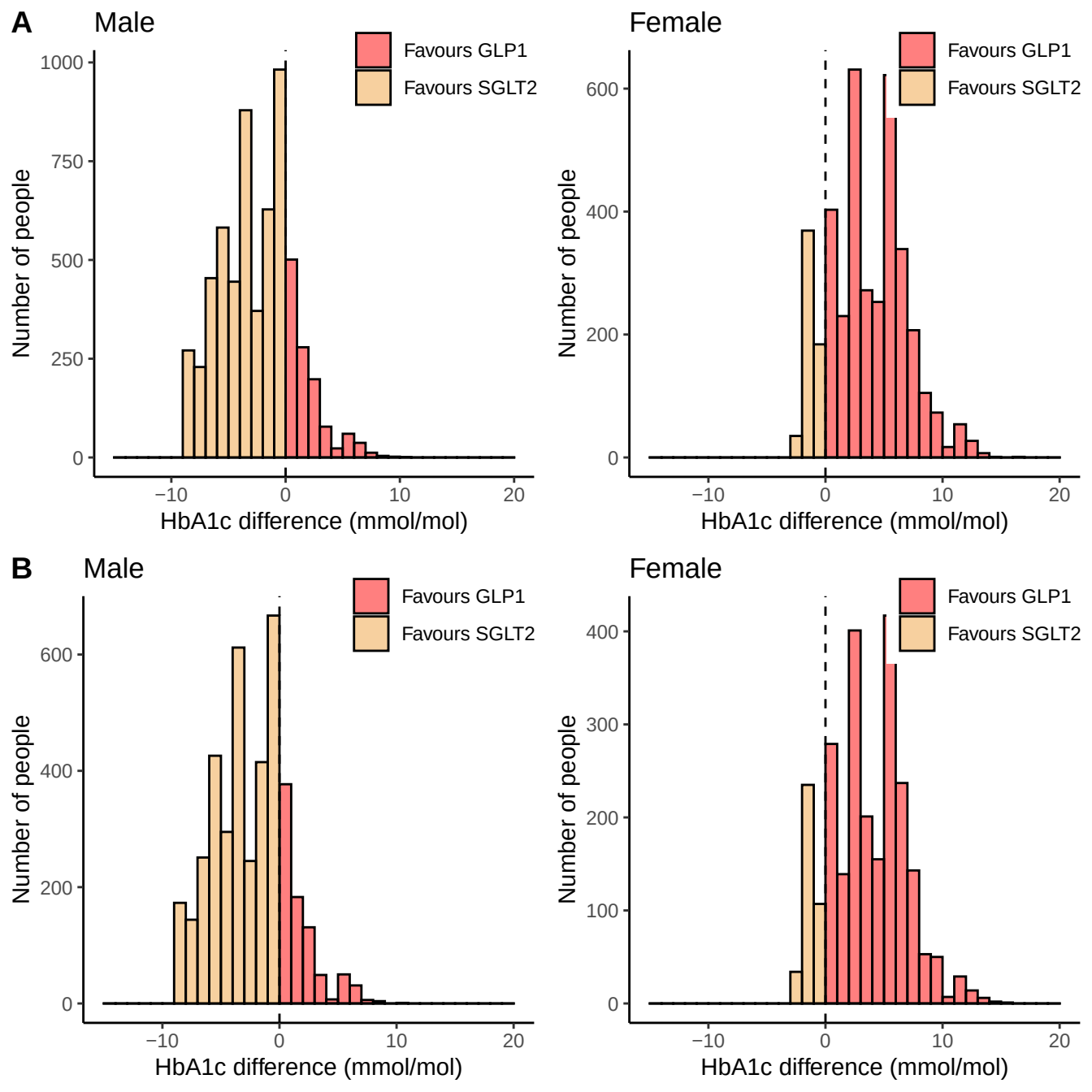

Effects validation lm(hba1c~drugclass+prop_score)
A
B
Decile average treatment effect
Predicted conditional average treatment effec
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12

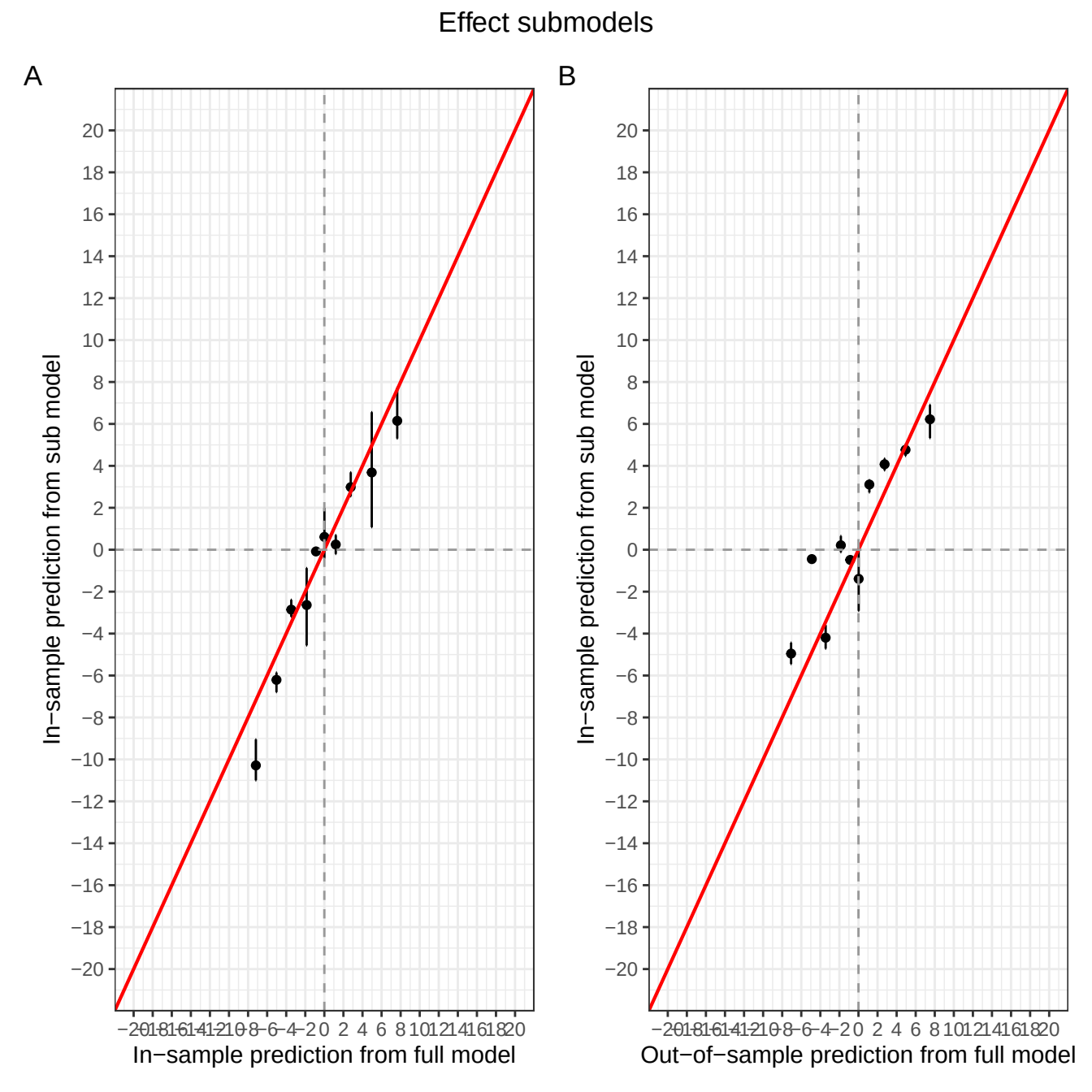
Effects validation prop score matching

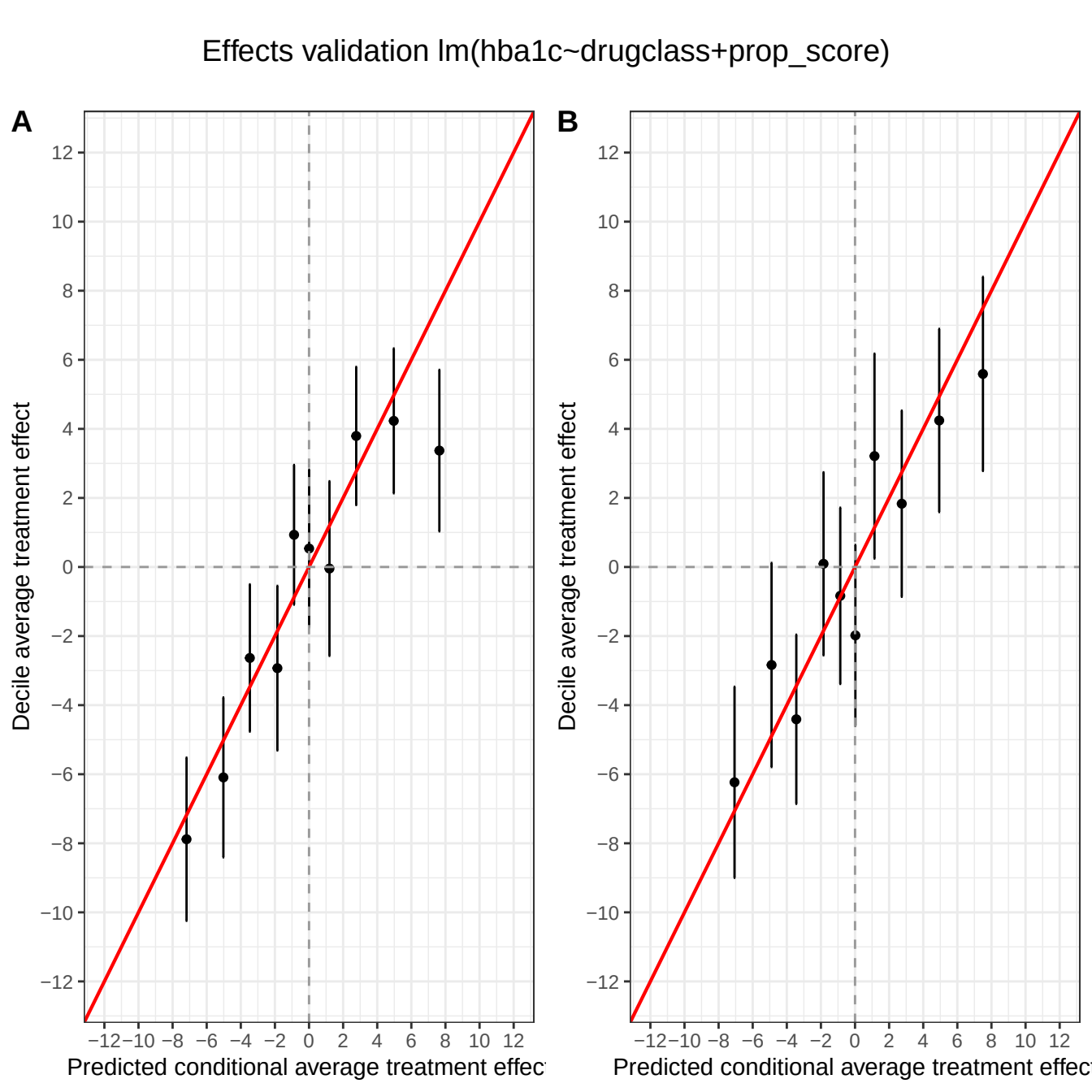


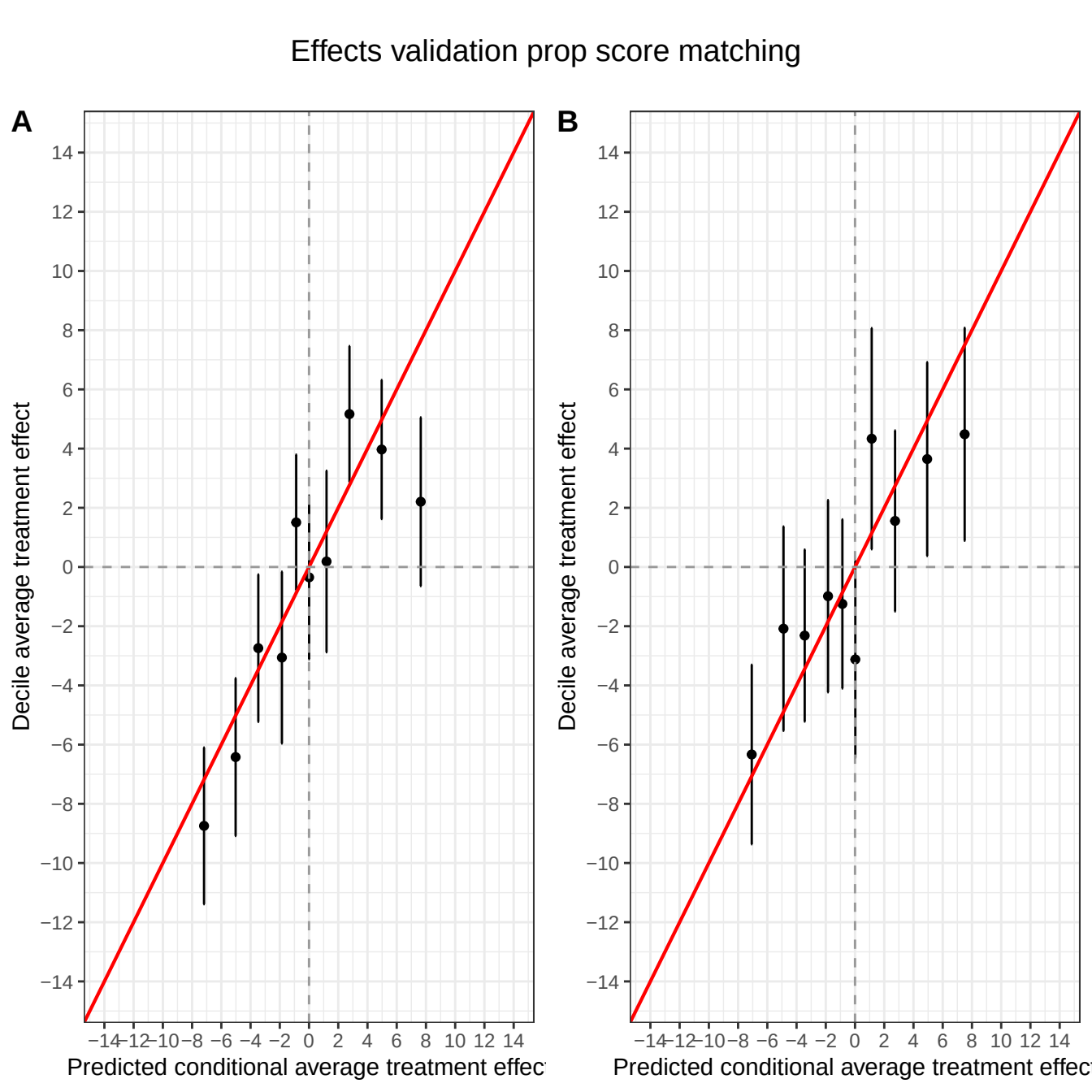

Effects validation prop score inverse weighting
A
B
Decile average treatment effect
Predicted conditional average treatment effec
14
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12
−14

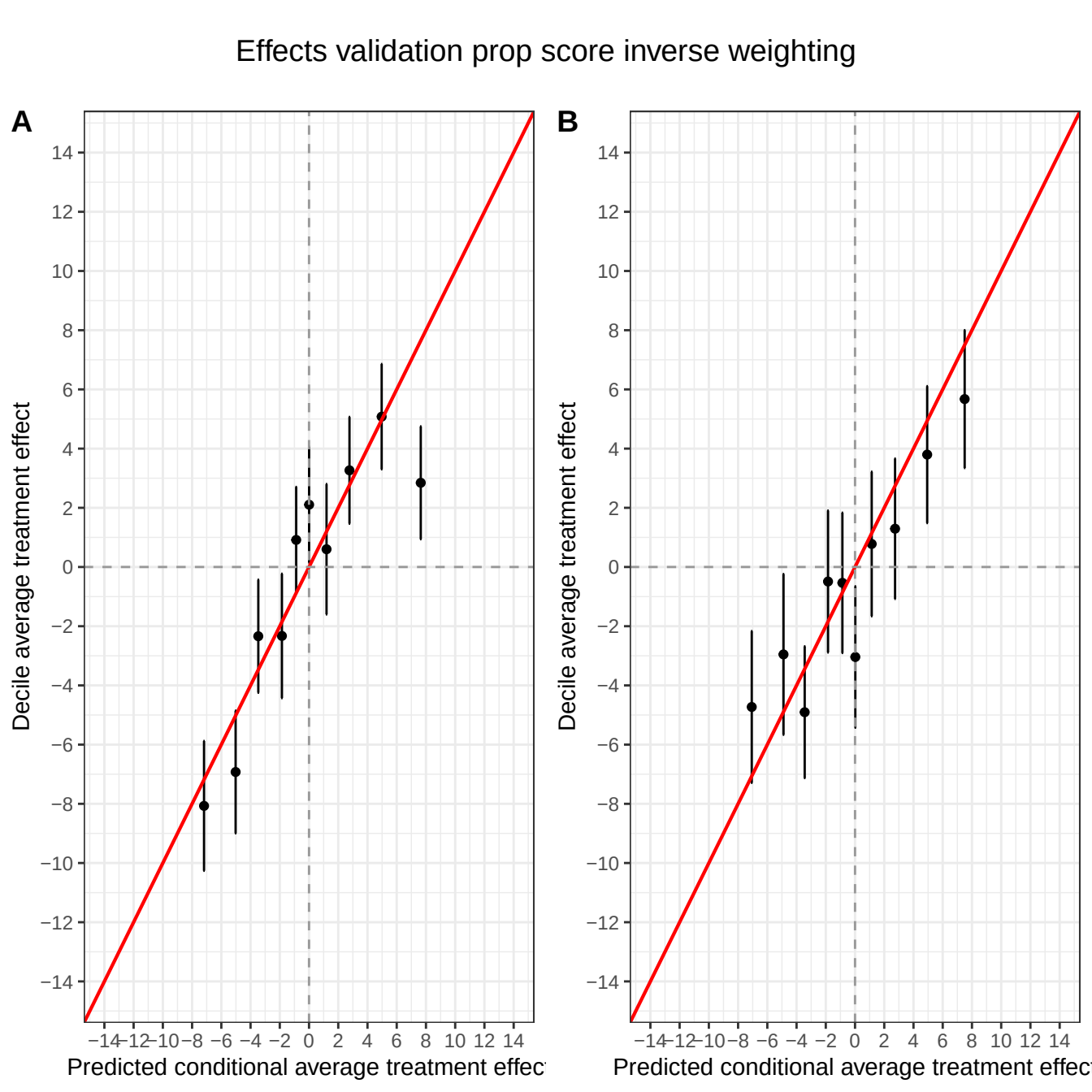

Model fitting: Incomplete data (Propensity score)
A
B
Favours GLP1
Favours SGLT2
Number of people
HbA1c difference (mmol/mol)
1200
900
600
300
0
800
400
200
−10
0
10
20


A
Male
Favours GLP1
Favours SGLT2
Number of people
1000
750
500
250
0
−10
0
10
20
HbA1c difference (mmol/mol)
Female
Favours GLP1
Favours SGLT2
Number of people
600
400
200
0
−10
0
10
20
HbA1c difference (mmol/mol)
B
Male
Favours GLP1
Favours SGLT2
Number of people
600
400
200
0
−10
0
10
20
HbA1c difference (mmol/mol)
Female
Favours GLP1
Favours SGLT2
Number of people
400
300
200
100
0
−10
0
10
20
HbA1c difference (mmol/mol)

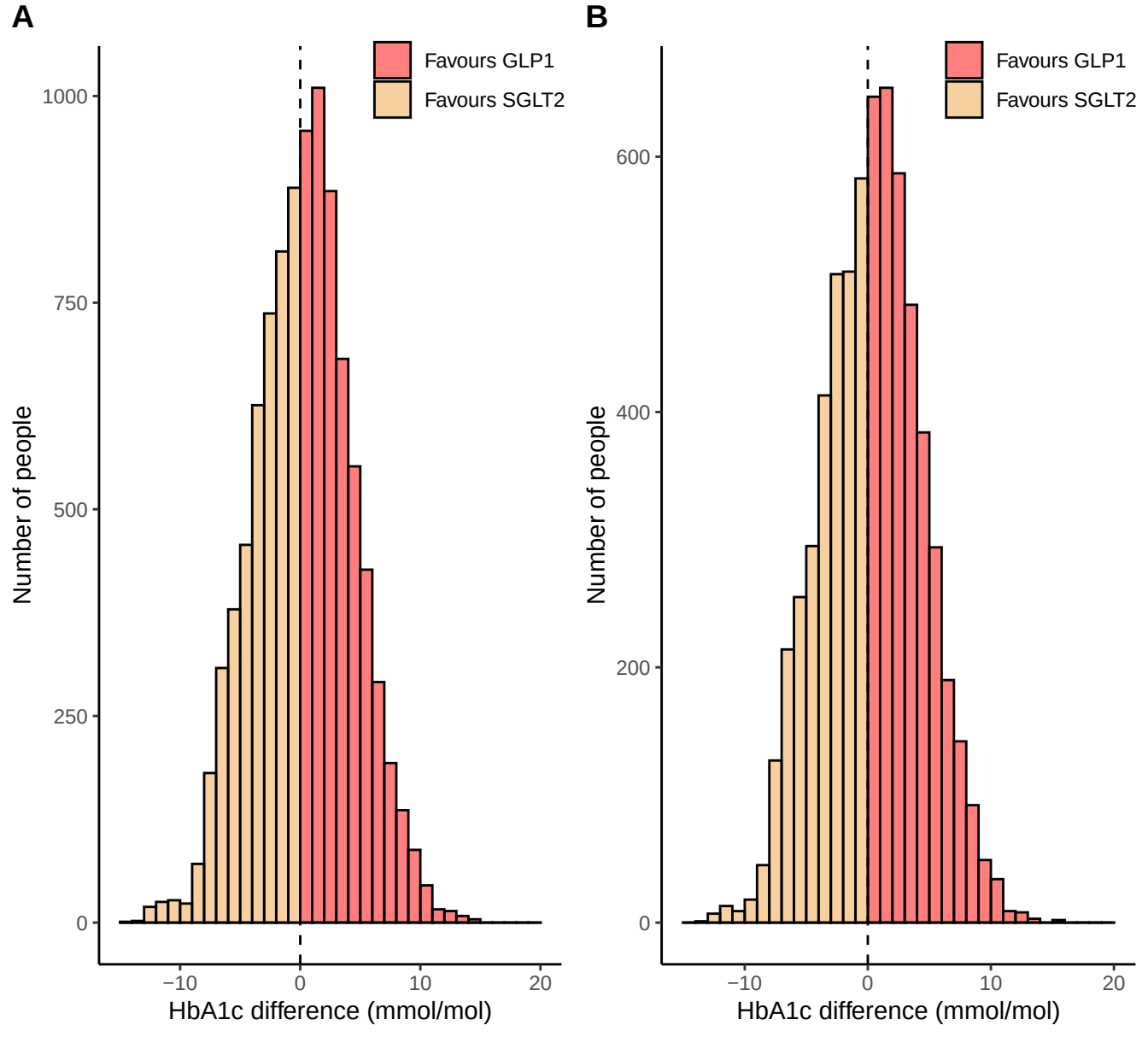

Effect submodels
A
B
In−sample prediction from sub model
In−sample prediction from full model
Out−of−sample prediction from full model
20
18
16
14
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12
−14
−16
−18
−20
−20 −18 −16 −14 −12 −10 −8 −6 −4 −2 0 2 4 6 8 10 12 14 16 18 20

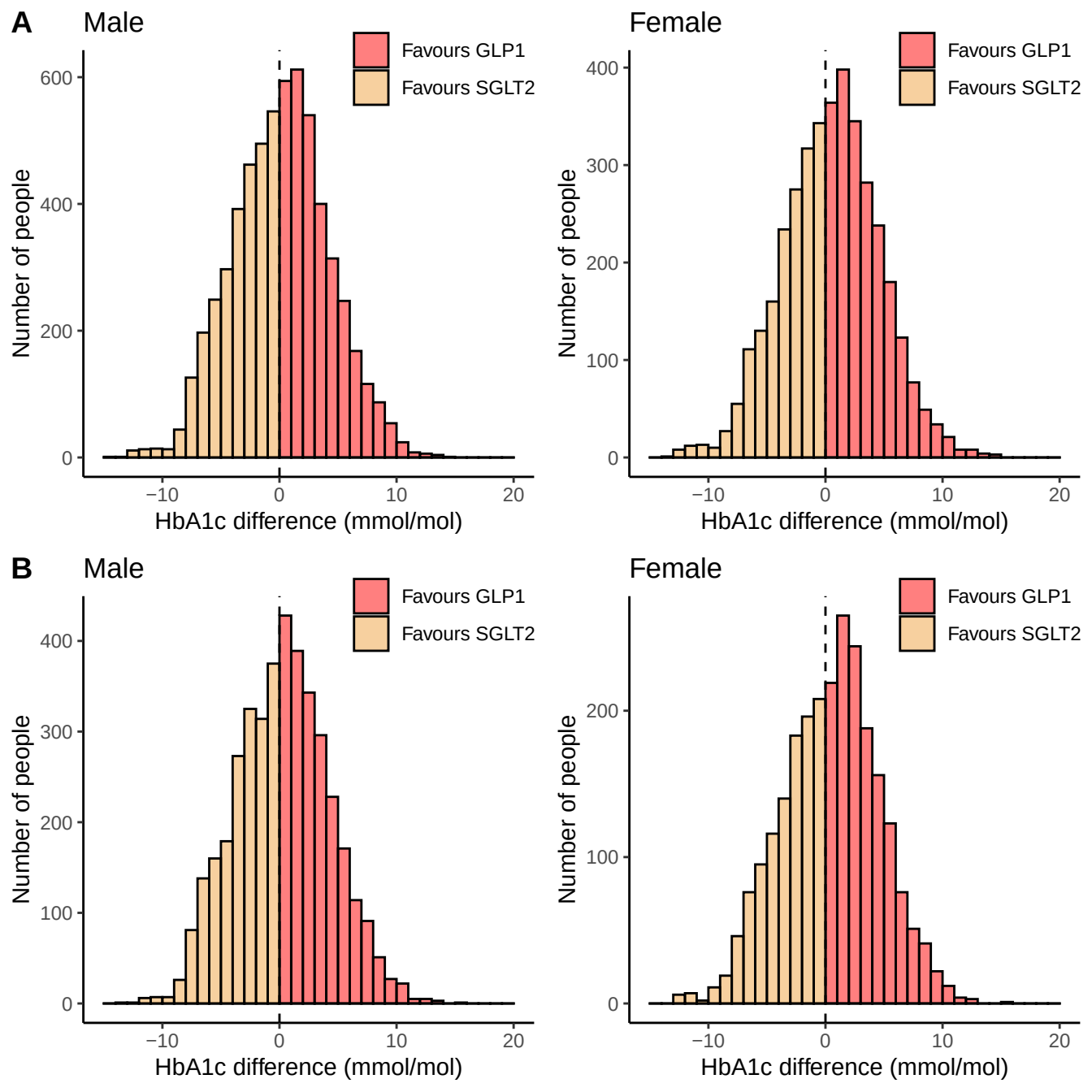

Effects validation lm(hba1c~drugclass+prop_score)
A
B
Decile average treatment effect
Predicted conditional average treatment effec
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12

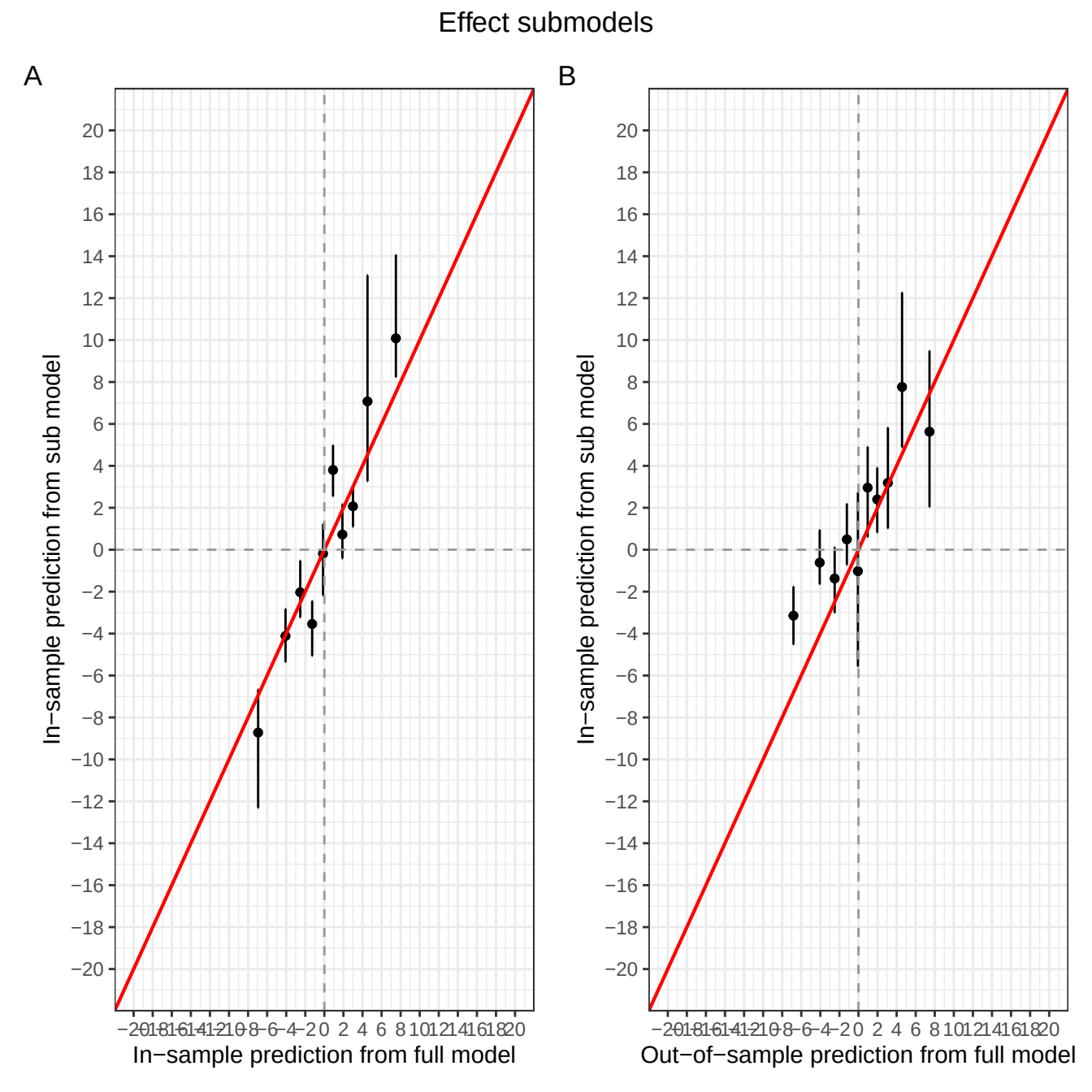

Effects validation prop score matching
A
B
Decile average treatment effect
Predicted conditional average treatment effec
14
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12
−14

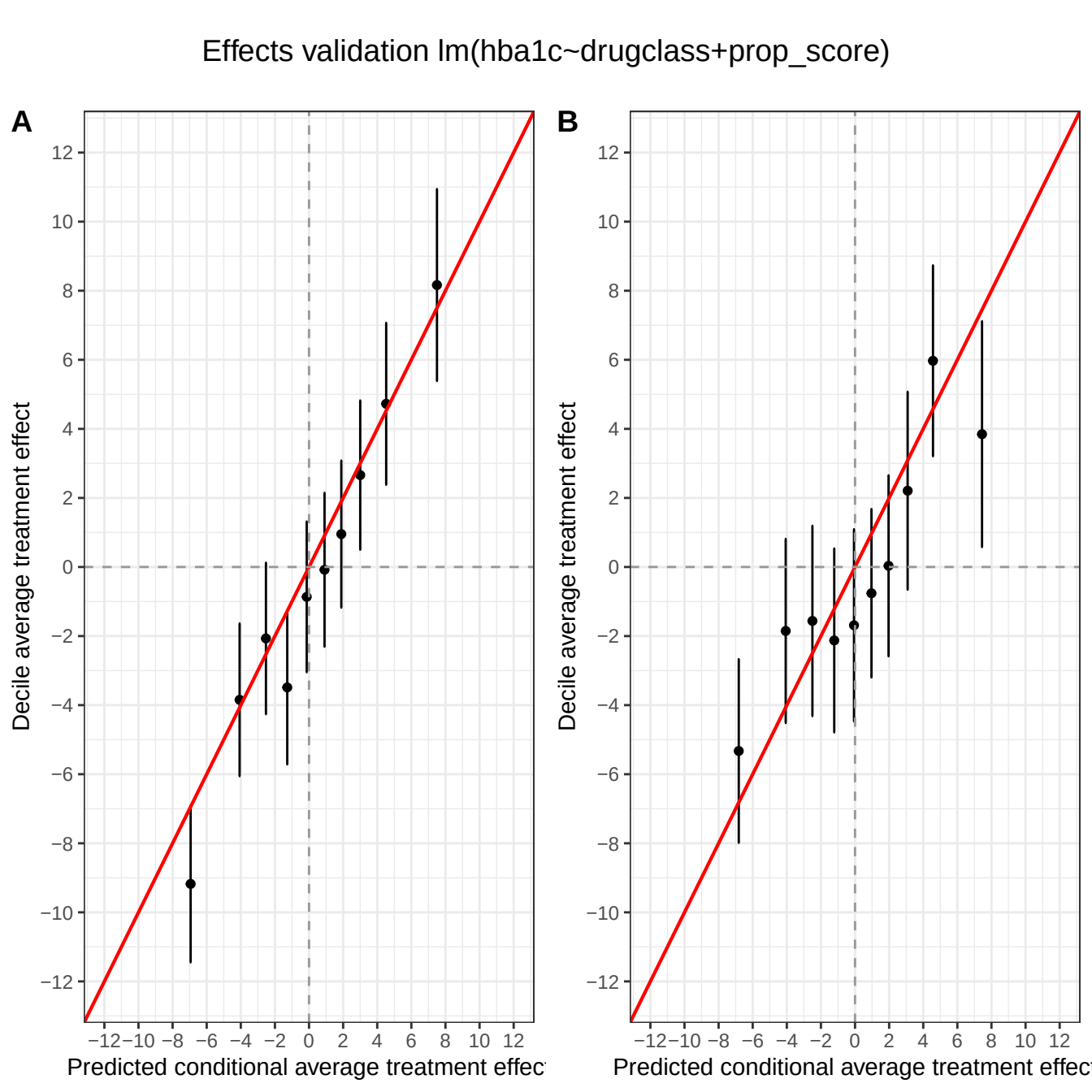

Effects validation prop score inverse weighting
A
B
Decile average treatment effect
Predicted conditional average treatment effec
14
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12
−14

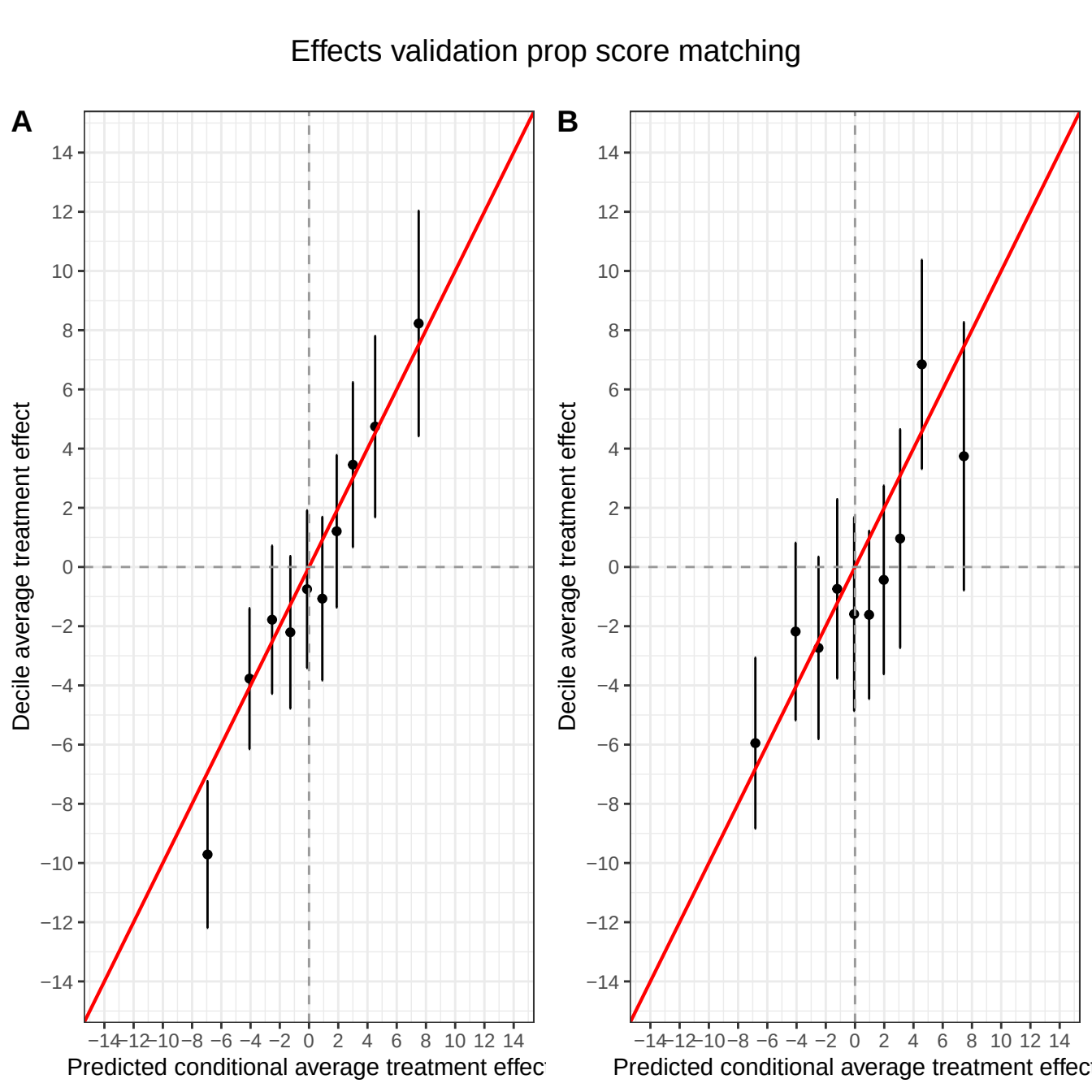
Model fitting: Variable Selection 1, Incomplete data (Propensity score)

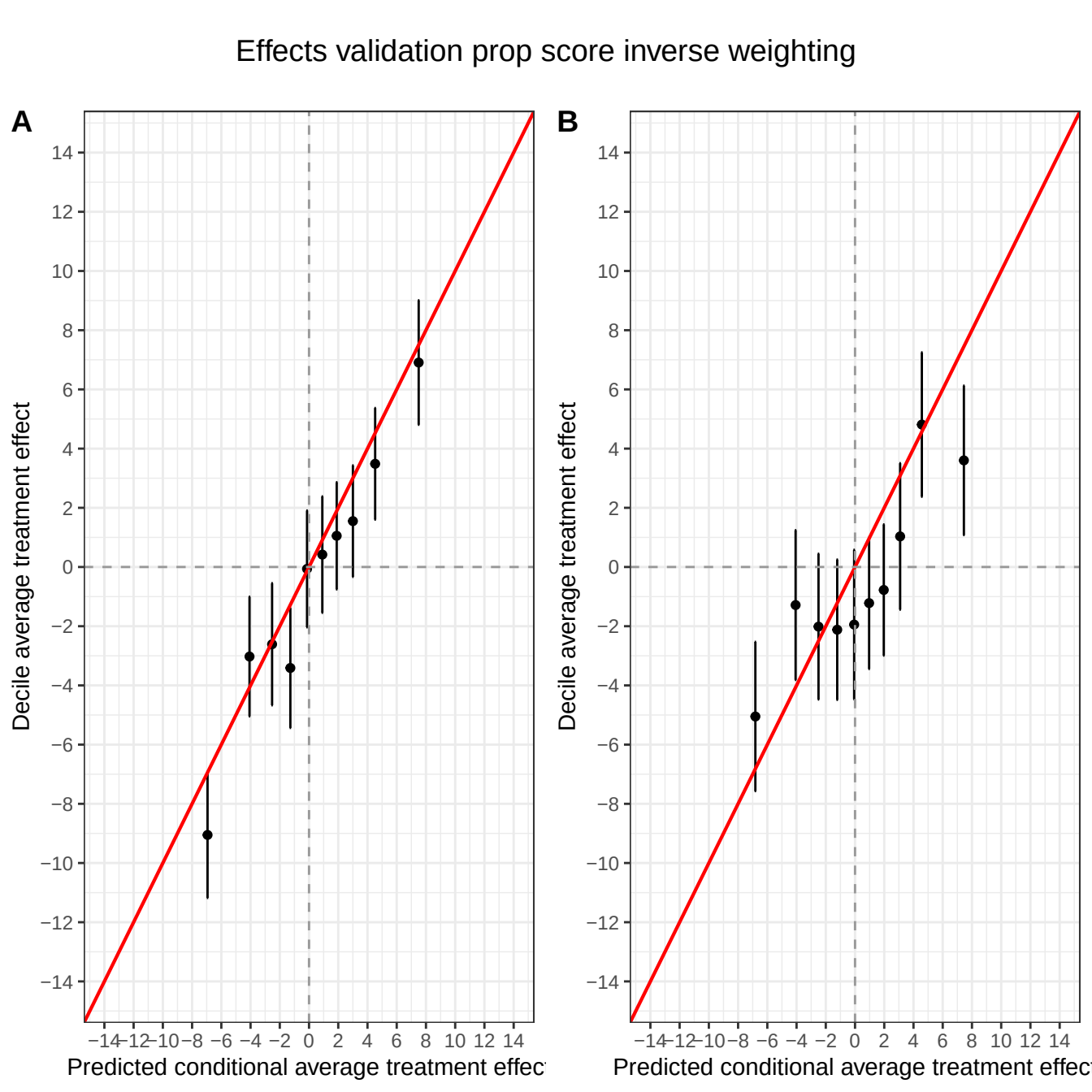



A
Male
Favours GLP1
Favours SGLT2
Number of people
HbA1c difference (mmol/mol)
Female
B
Male
Female

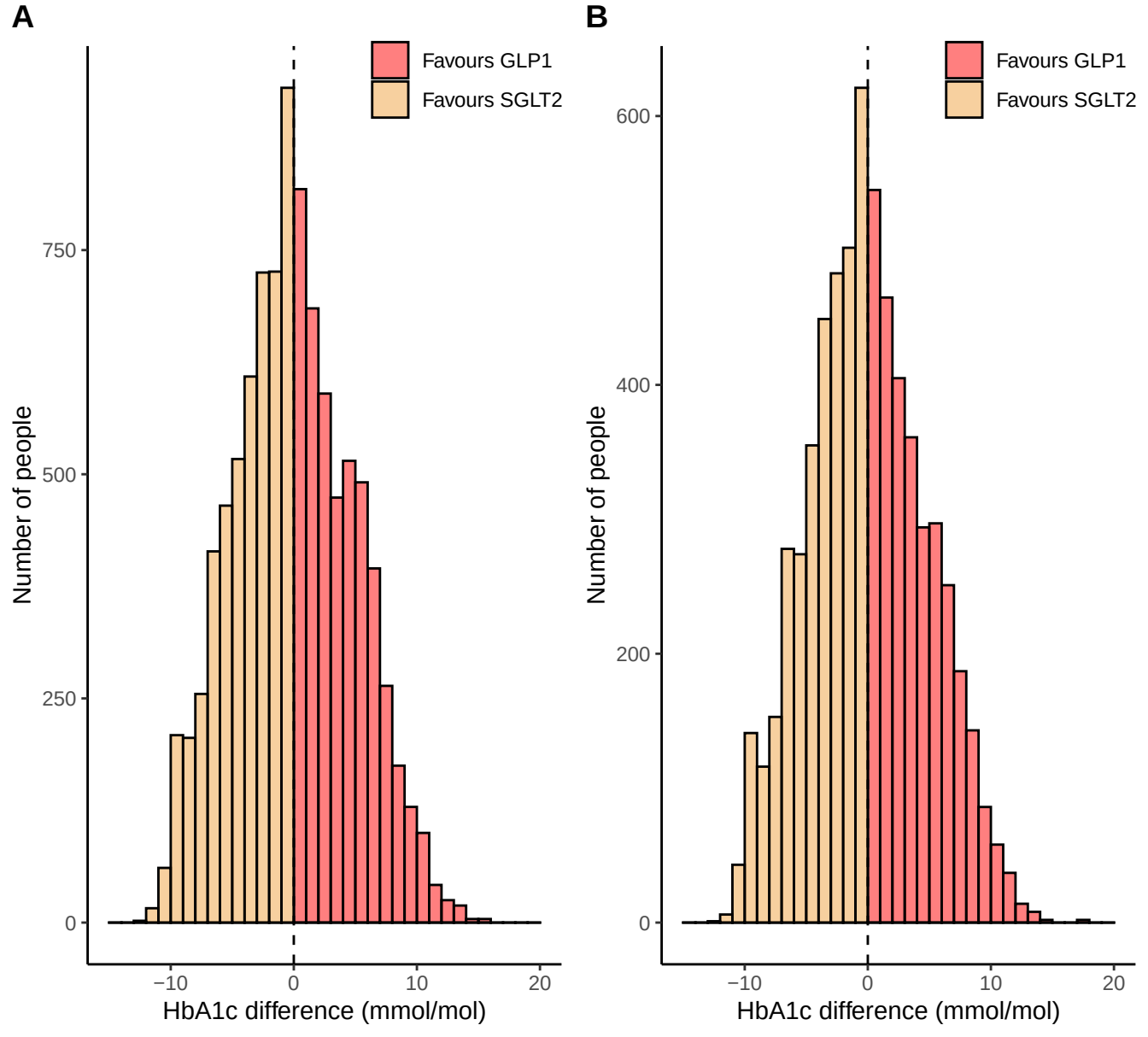

Effect submodels
A
B
In−sample prediction from sub model
In−sample prediction from full model
Out−of−sample prediction from full model

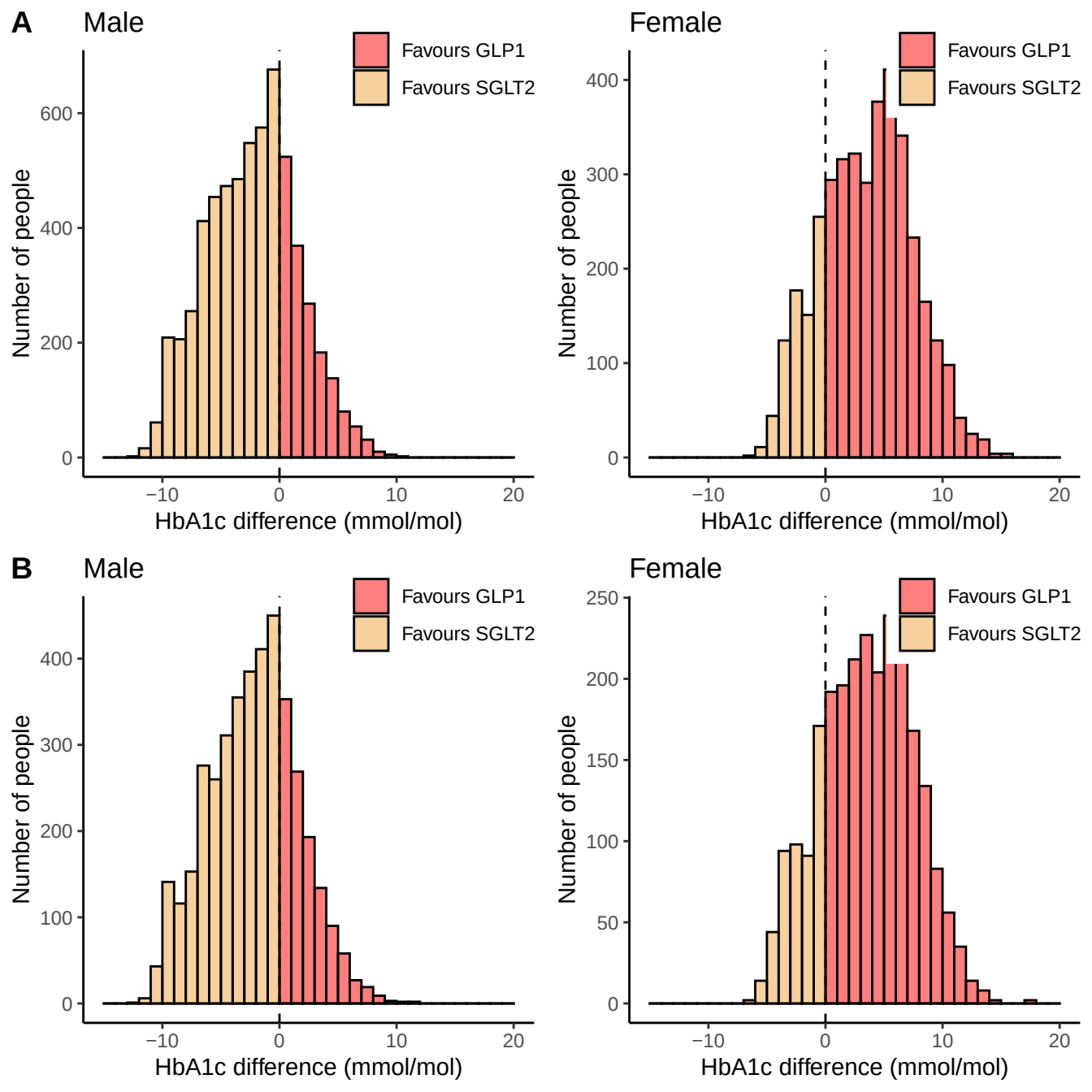

Effects validation lm(hba1c~drugclass+prop_score)
A
B
Decile average treatment effect
Predicted conditional average treatment effec
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12

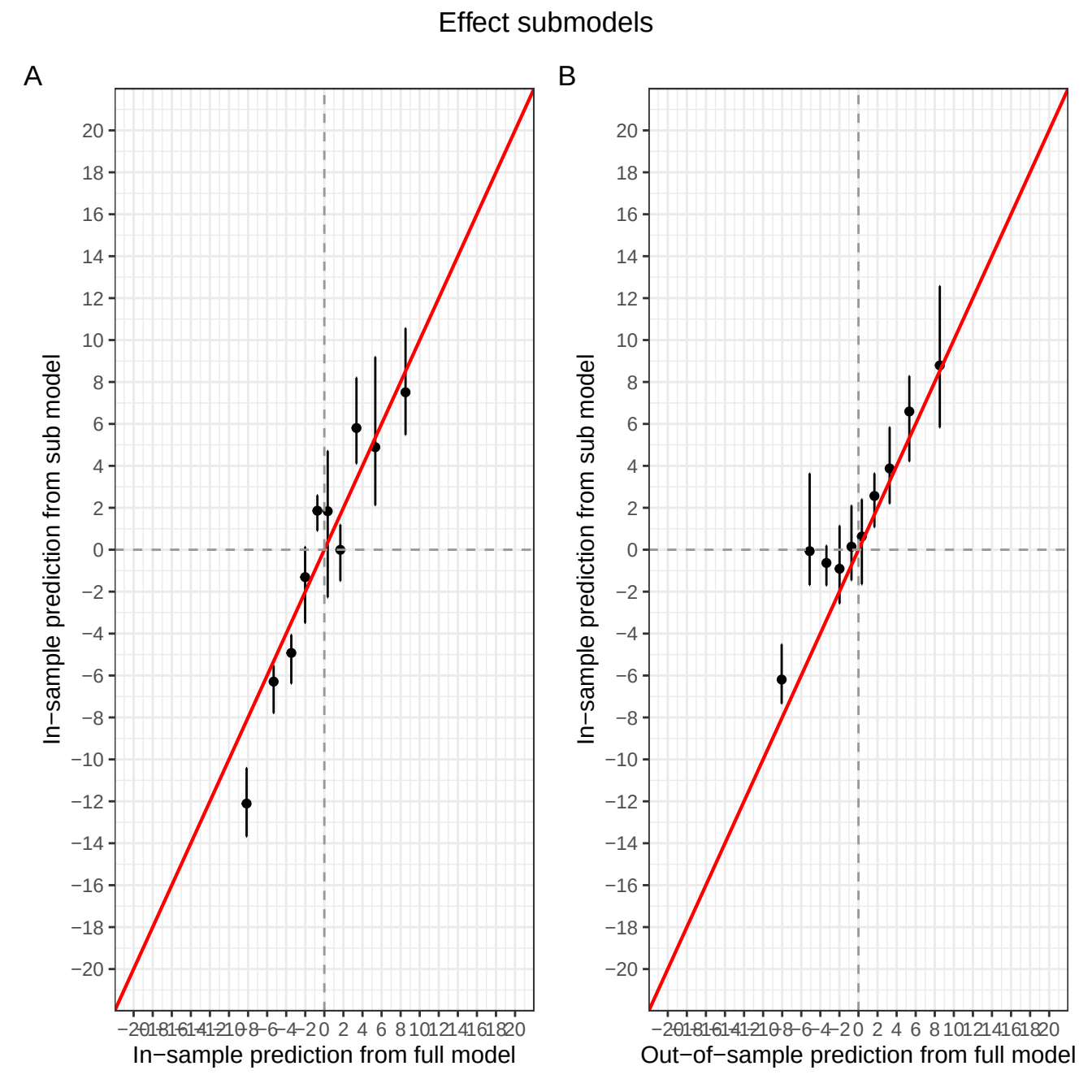

Effects validation prop score matching
A
B
Decile average treatment effect
Predicted conditional average treatment effec
14
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12
−14

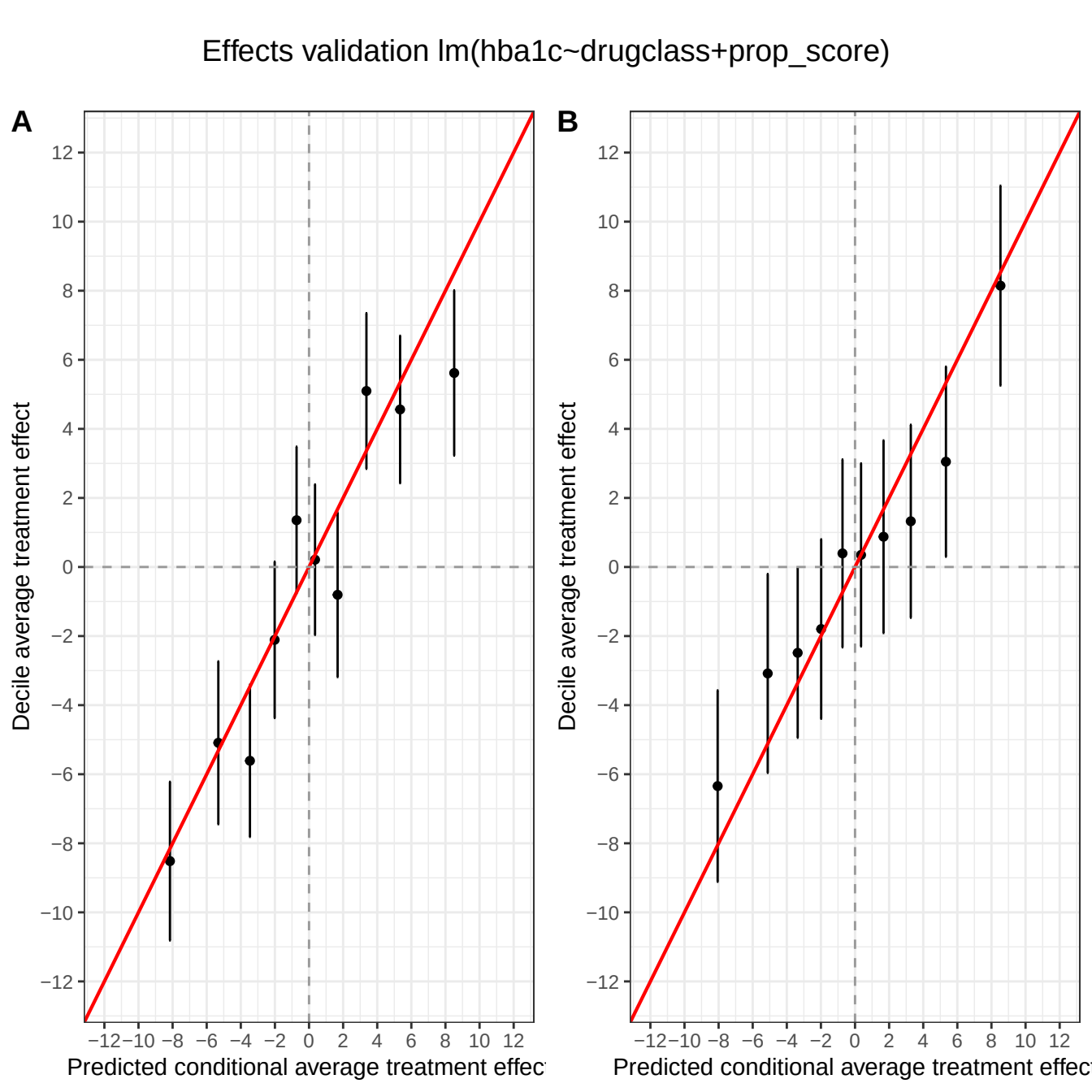

Effects validation prop score inverse weighting
A
B
Decile average treatment effect
Predicted conditional average treatment effec
14
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12
−14

Model fitting: Variable Selection 2, Incomplete data (Propensity score)

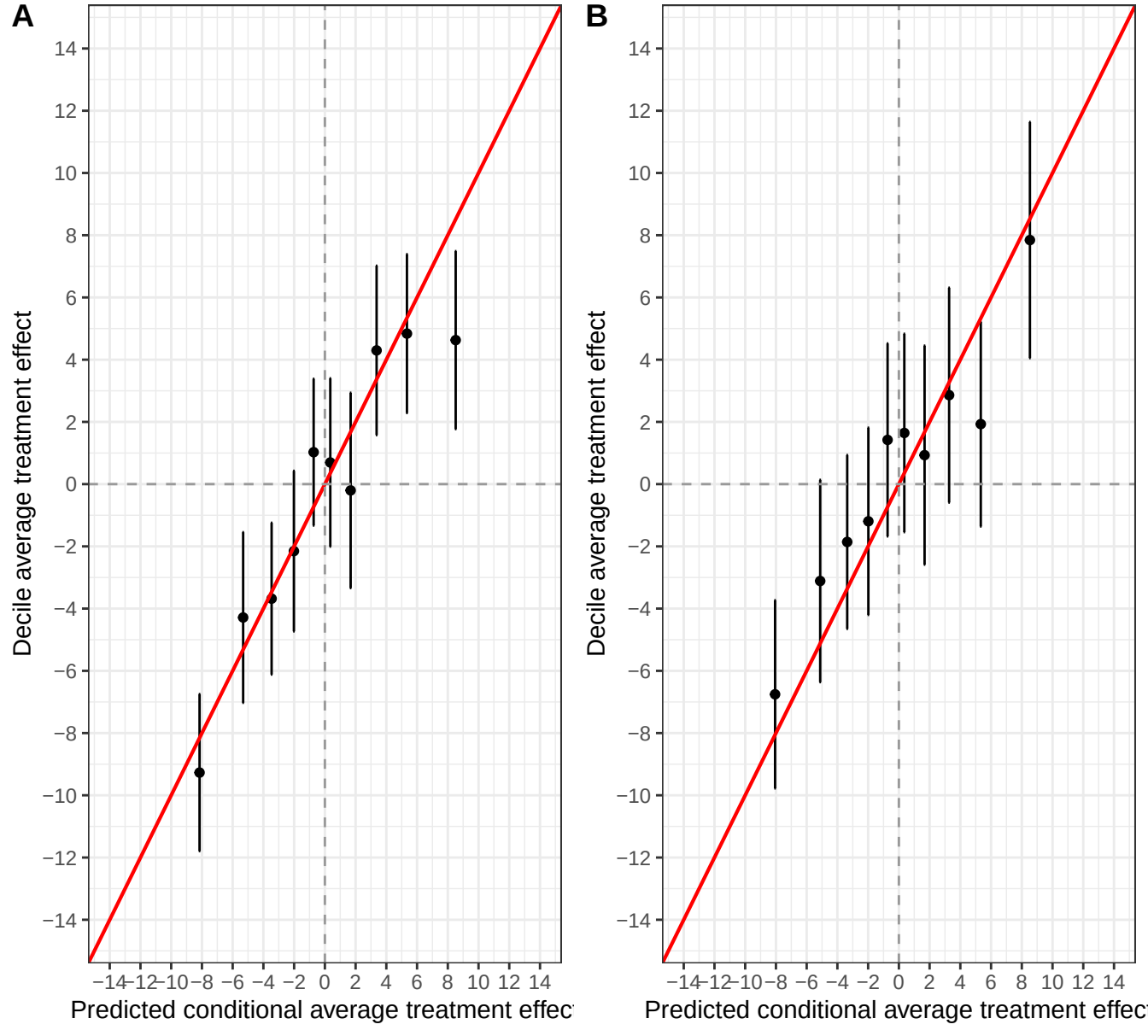


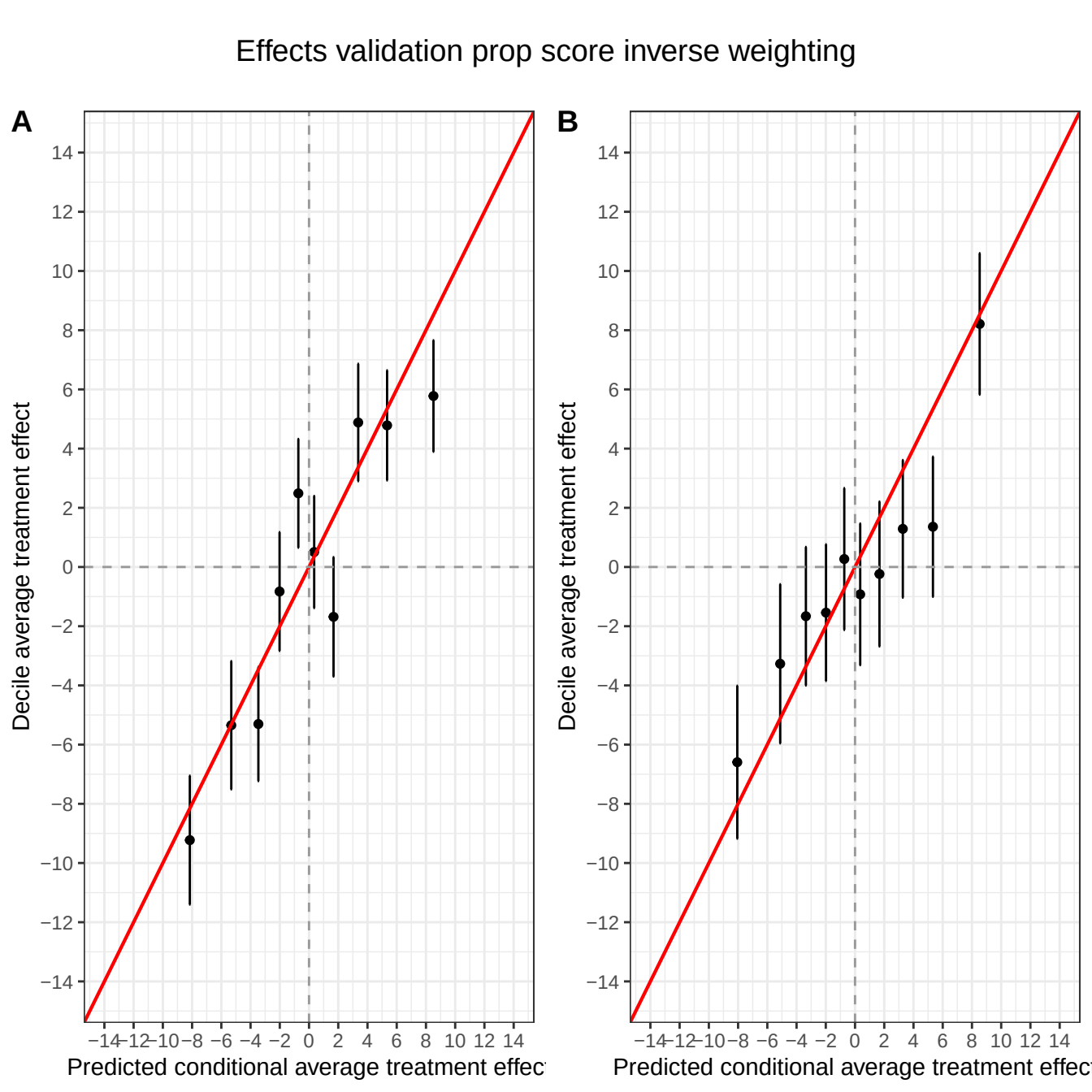

A
Male
Favours GLP1
Favours SGLT2
Number of people
HbA1c difference (mmol/mol)
Female
B
Male
Female


Effect submodels
A
B
In−sample prediction from sub model
In−sample prediction from full model
Out−of−sample prediction from full model
20
18
16
14
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12
−14
−16
−18
−20

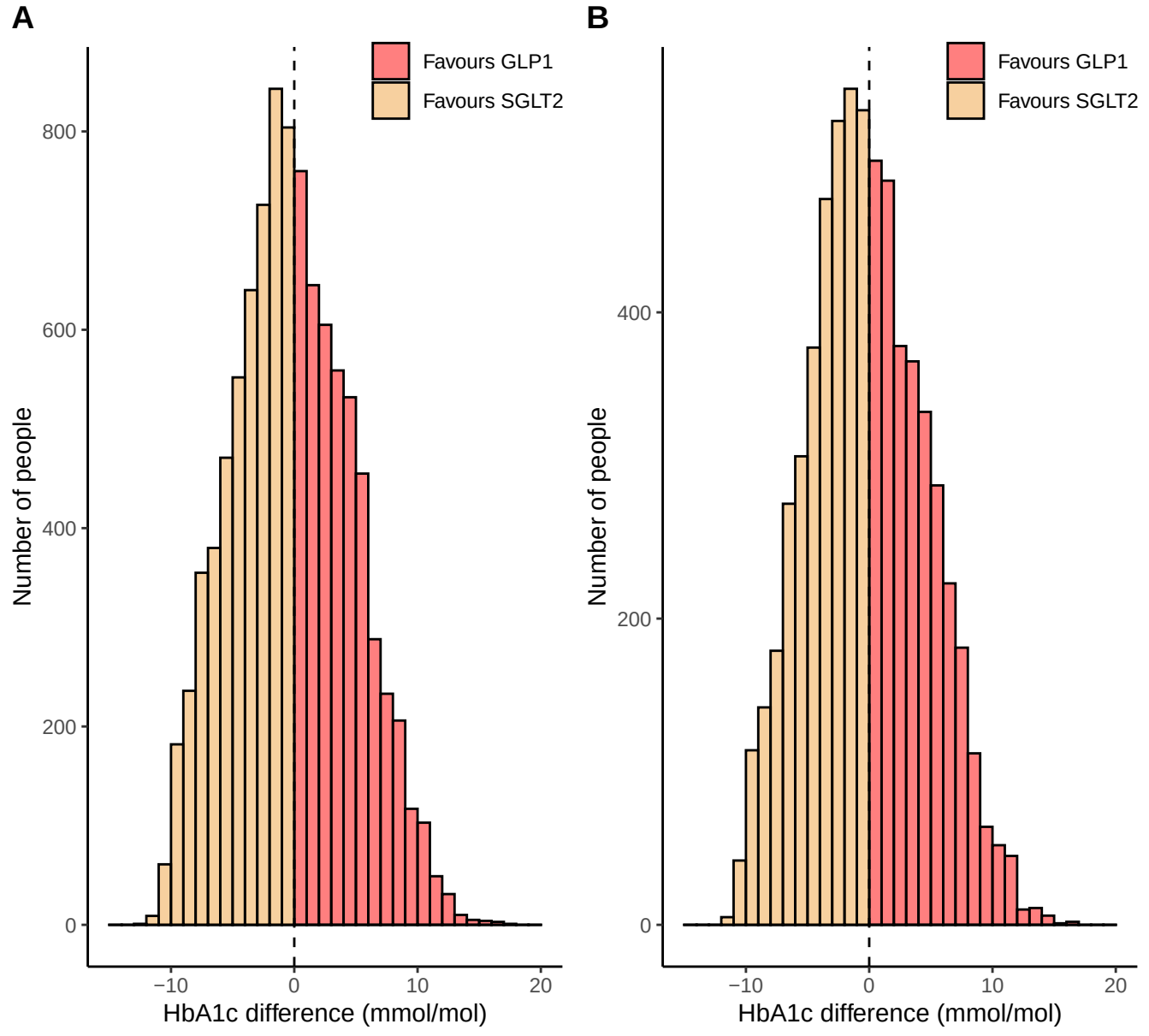

Effects validation lm(hba1c~drugclass+prop_score)
A
B
Decile average treatment effect
Predicted conditional average treatment effec
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12

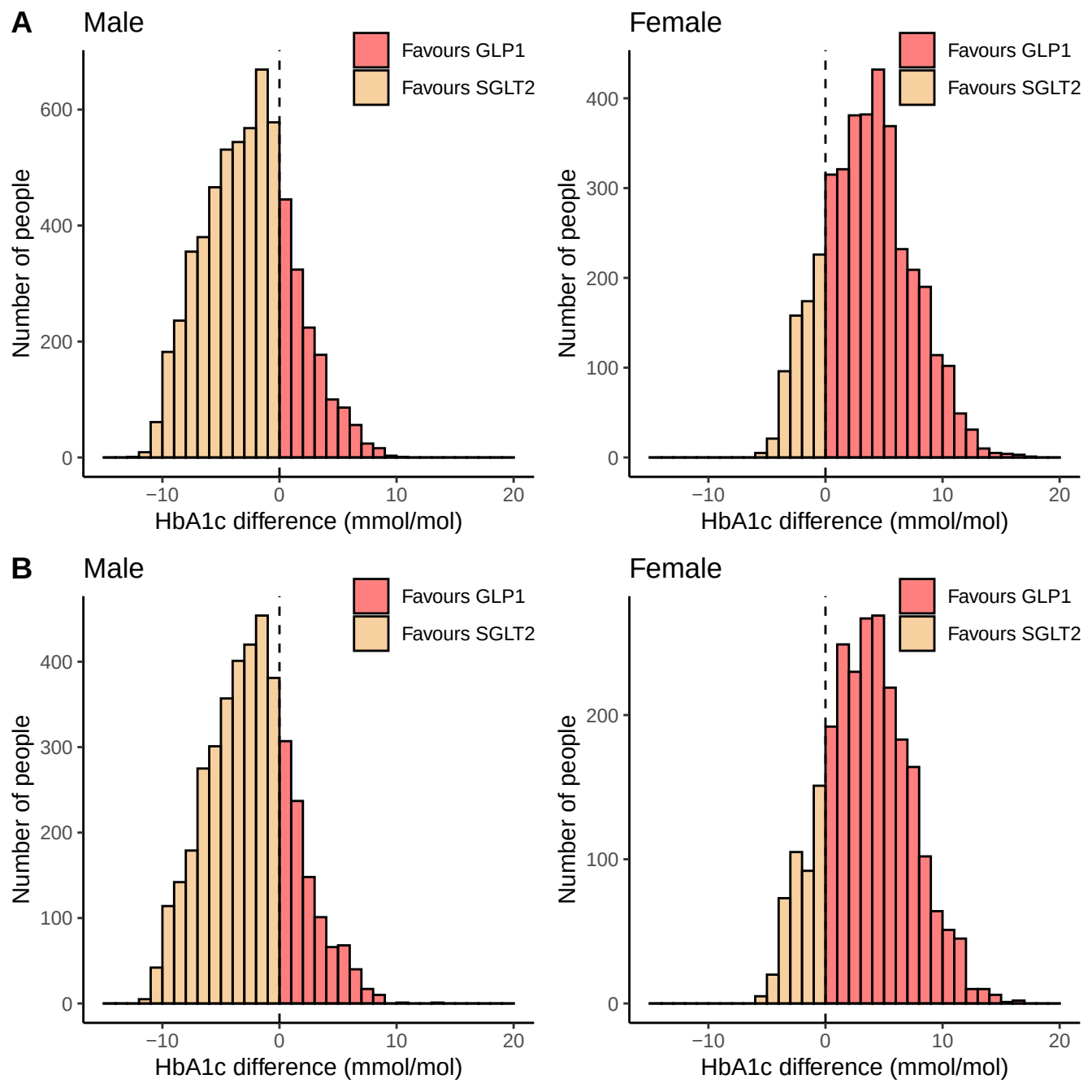
Effects validation prop score matching

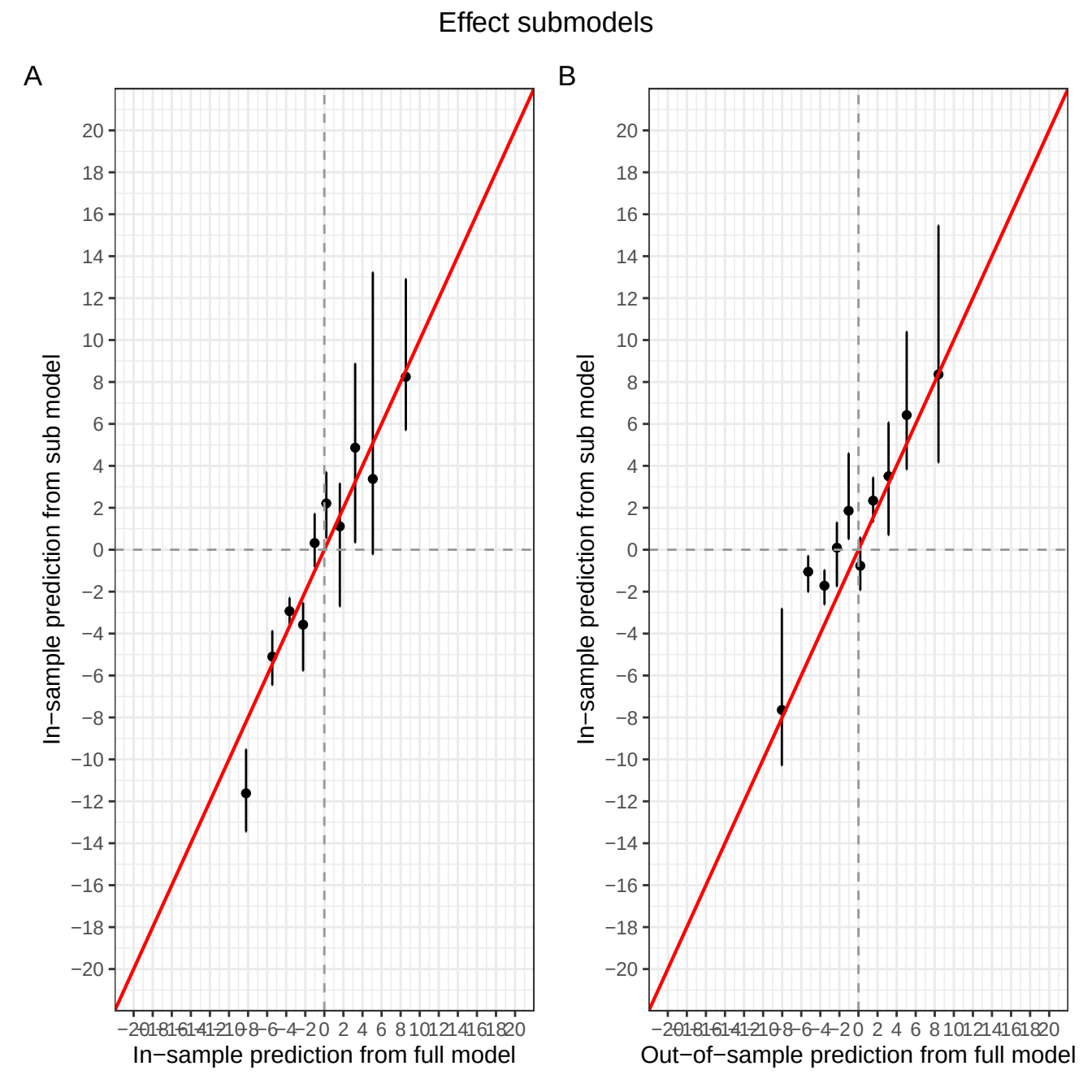


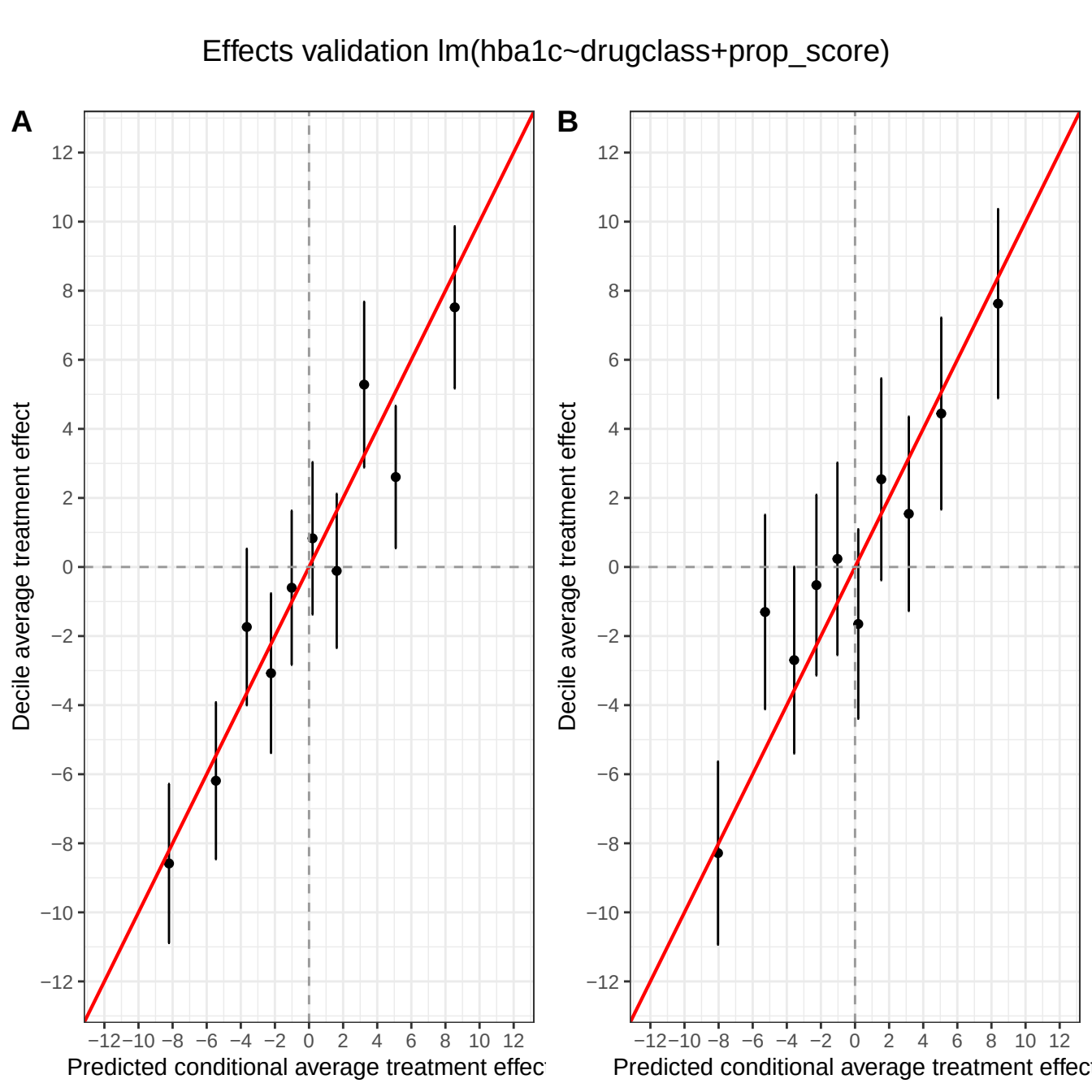

Effects validation prop score inverse weighting
A
B
Decile average treatment effect
Predicted conditional average treatment effec
14
12
10
8
6
4
2
0
−2
−4
−6
−8
−10
−12
−14

Model fitting: Variable Selection 2, Incomplete data (no propensity score)

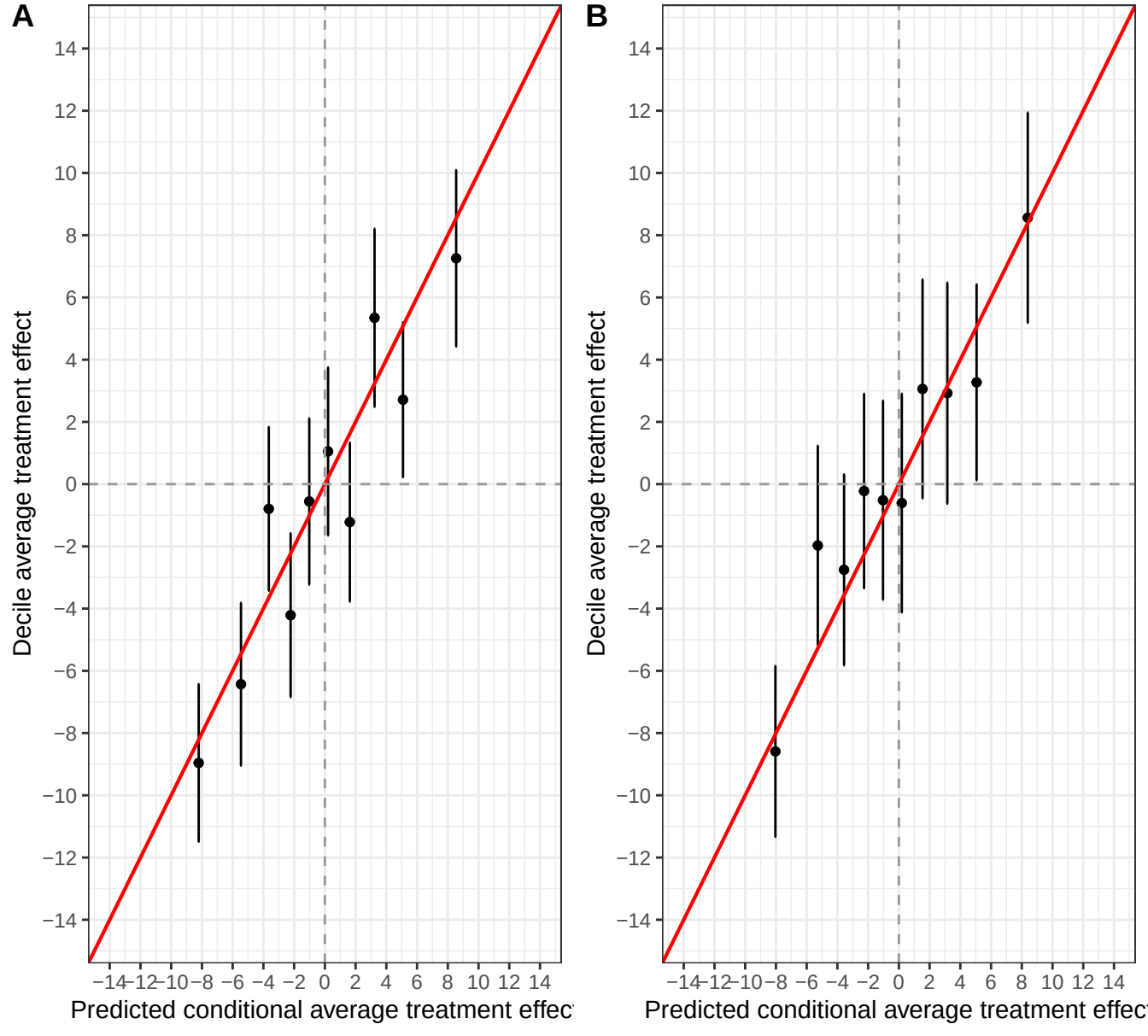


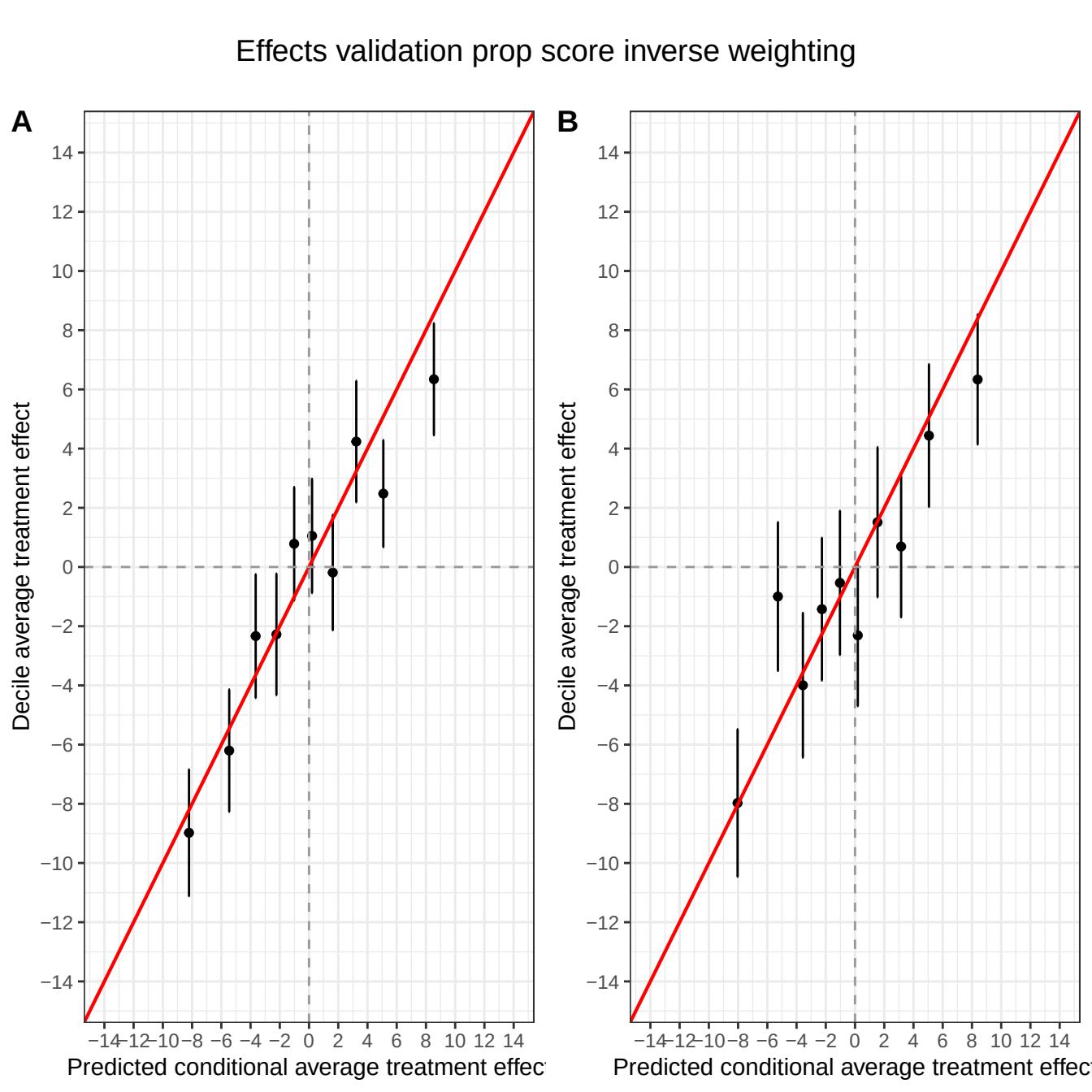

A
Male
Favours GLP1
Favours SGLT2
Number of people
HbA1c difference (mmol/mol)
Female
B
Male
Female


Effect submodels
A
B
In−sample prediction from sub model
In−sample prediction from full model
Out−of−sample prediction from full model


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




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