Supplemental Datafile 1: Analyses related to Main Text Figure 1

Data S1.1: Hierarchical clustering of genetic architecture across eight neuropsychiatric disorders.

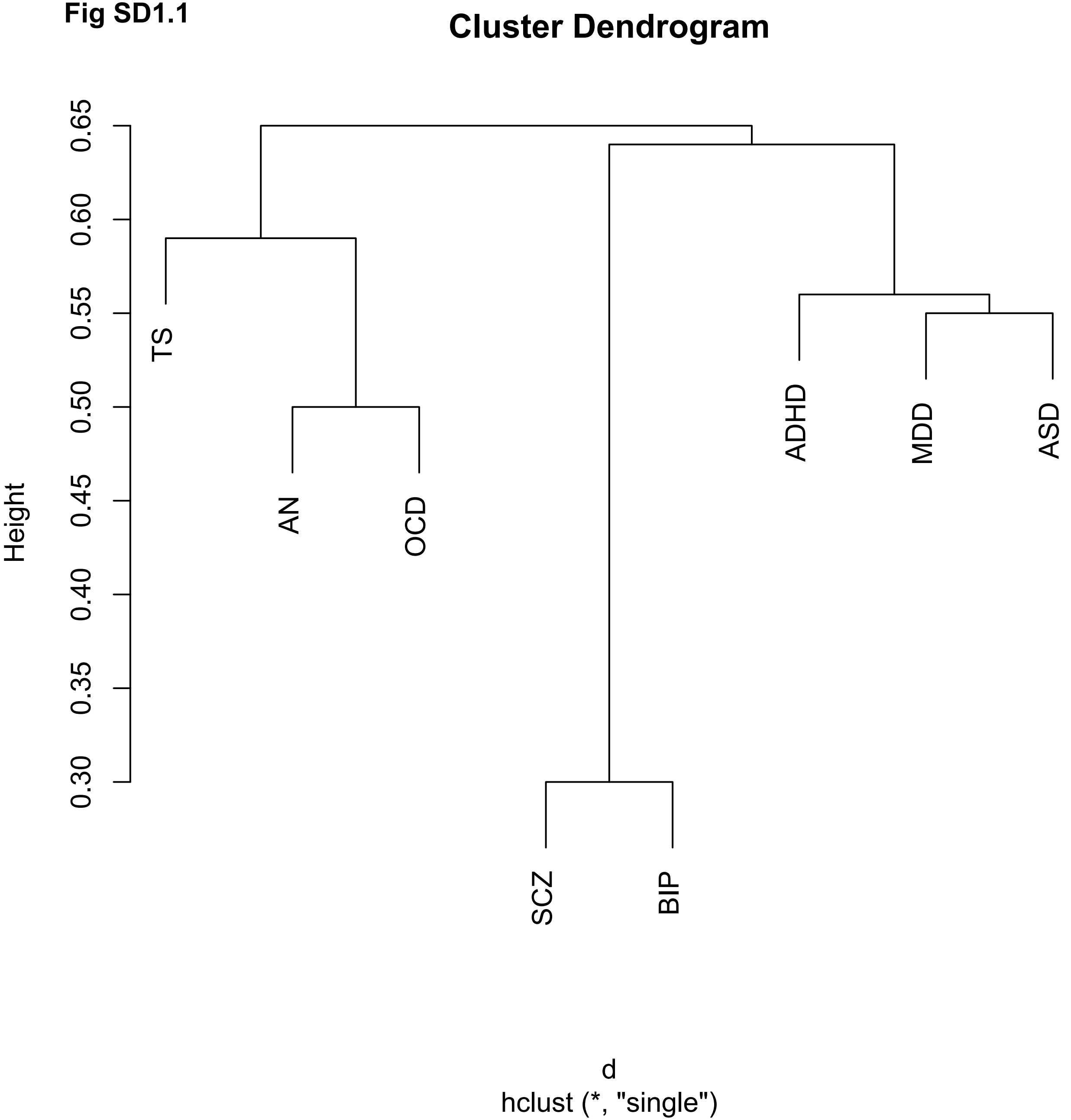
Data S1.2: Relationship between the estimated genetic correlation and the effective sample sizes for each pair of disorders.

Data S1.3: Relationship between the estimated genetic correlation and the effective sample sizes for MD and four other disorders, SCZ, BIP, ADHD, and ASD, in three studies.

Data S1.4: Genomic SEM analysis result using a Weighted Least Squares (WLS) estimator on top (A) and that based on a Maximum Likelihood (ML) estimator (B).

Data S1.5: Distribution of the number of cross-disorder loci identified in meta-analysis of chromosome 1 across 100 simulation replicates.

Fig SD1.1


Cluster Dendrogram
Height
0.65
0.60
0.55
0.50
0.45
0.40
0.35
0.30
TS
AN
OCD
SCZ
BIP
ADHD
MDD
ASD
d
hclust (*, "single")

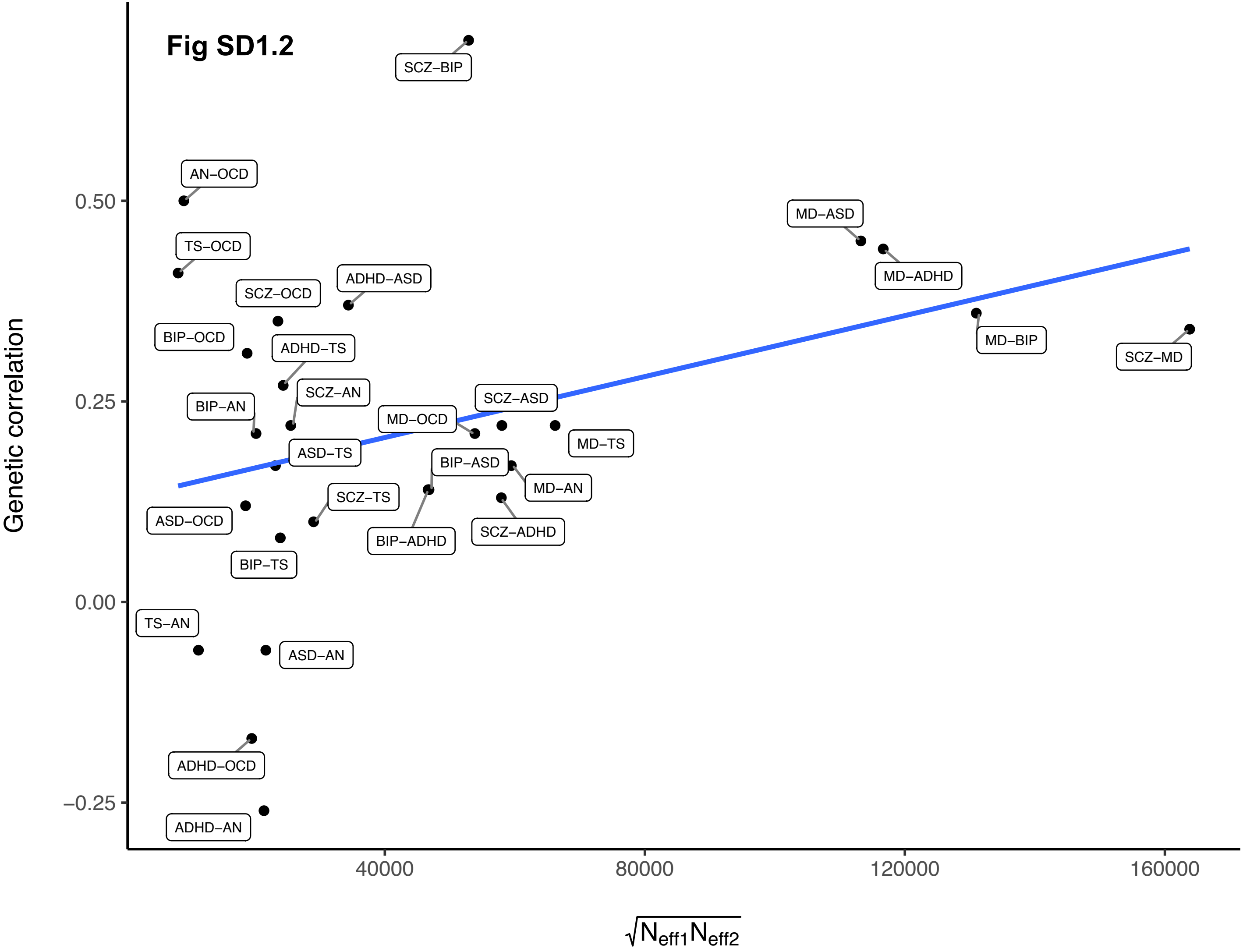


Fig SD1.2

SCZ–BIP
AN–OCD
TS–OCD
SCZ–OCD
ADHD–ASD
BIP–OCD
ADHD–TS
SCZ–AN
BIP–AN
MD–OCD
SCZ–ASD
MD–TS
ASD–TS
BIP–ASD
MD–AN
SCZ–TS
ASD–OCD
BIP–ADHD
SCZ–ADHD
BIP–TS
TS–AN
ASD–AN
ADHD–OCD
ADHD–AN
MD–ASD
MD–ADHD
MD–BIP
SCZ–MD
0.50
0.25
0.00
–0.25
40000
80000
120000
160000
Genetic correlation
$\sqrt{N_{eff1}N_{eff2}}$

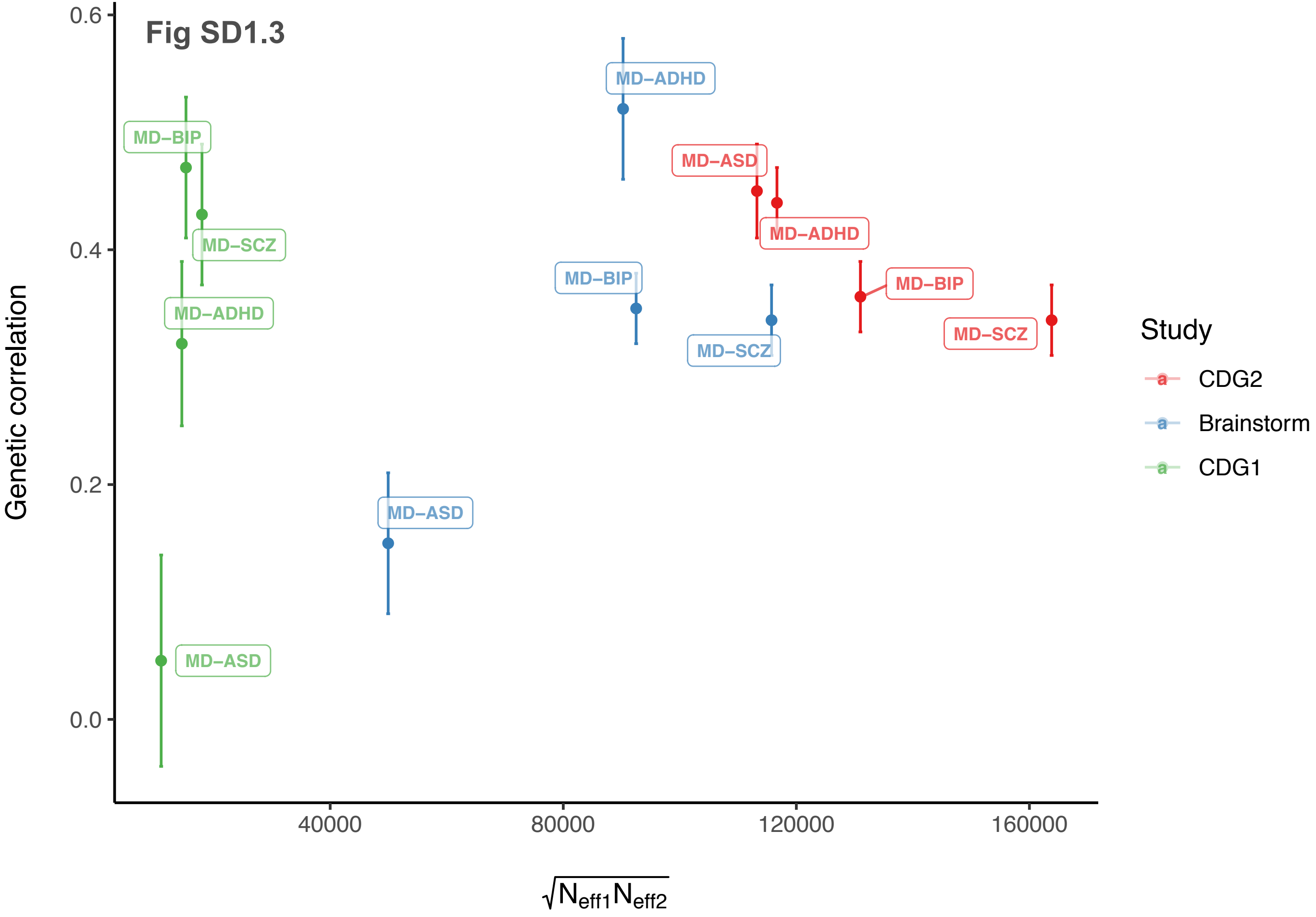


Fig SD1.3

Genetic correlation
0.6
0.4
0.2
0.0
40000
80000
120000
160000
$\sqrt{N_{eff1} N_{eff2}}$
MD–BIP
MD–SCZ
MD–ADHD
MD–ASD
MD–ADHD
MD–BIP
MD–SCZ
MD–ASD
MD–ASD
MD–ADHD
MD–BIP
MD–SCZ
Study
CDG2
Brainstorm
CDG1

Fig SD1.4

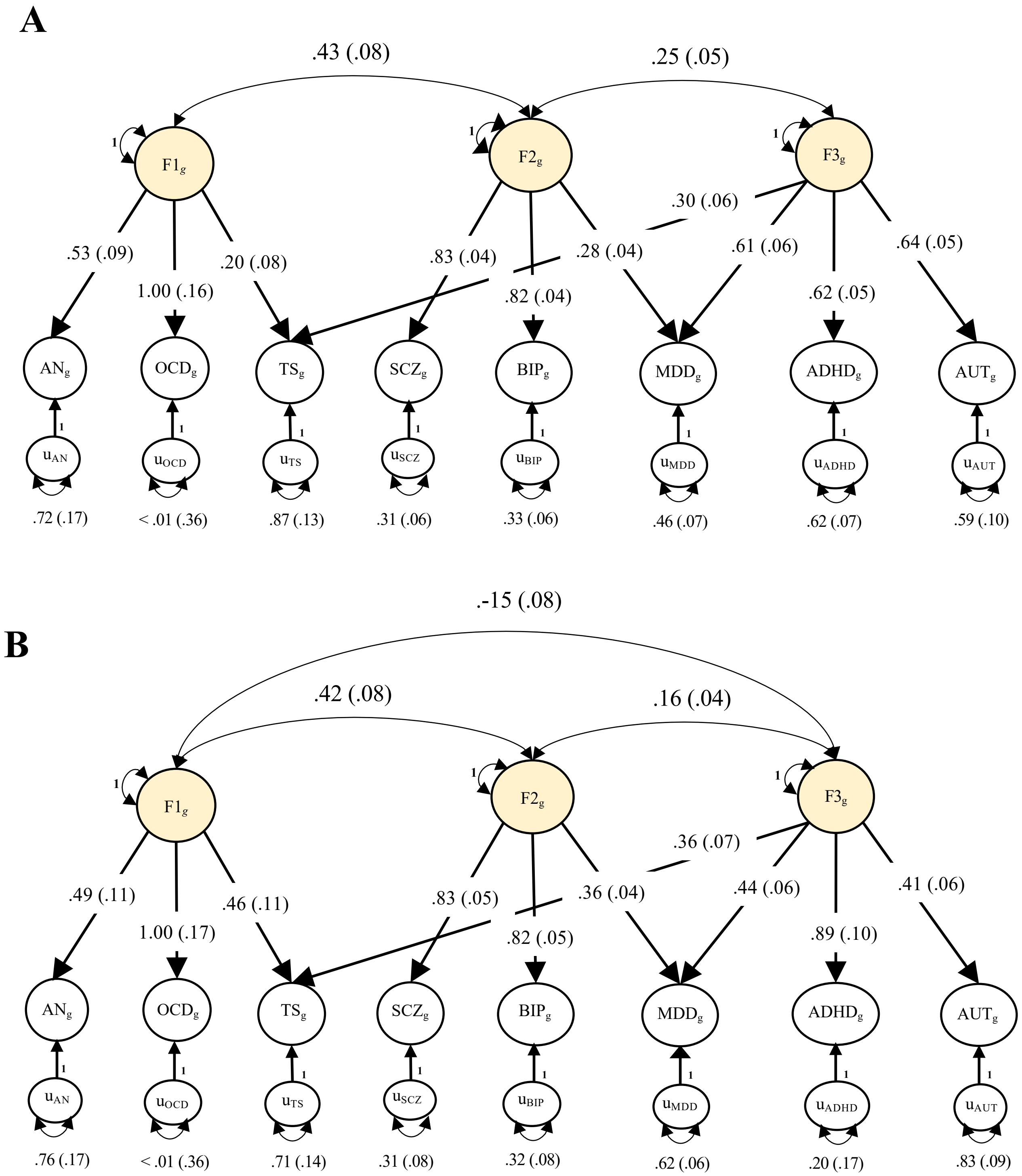
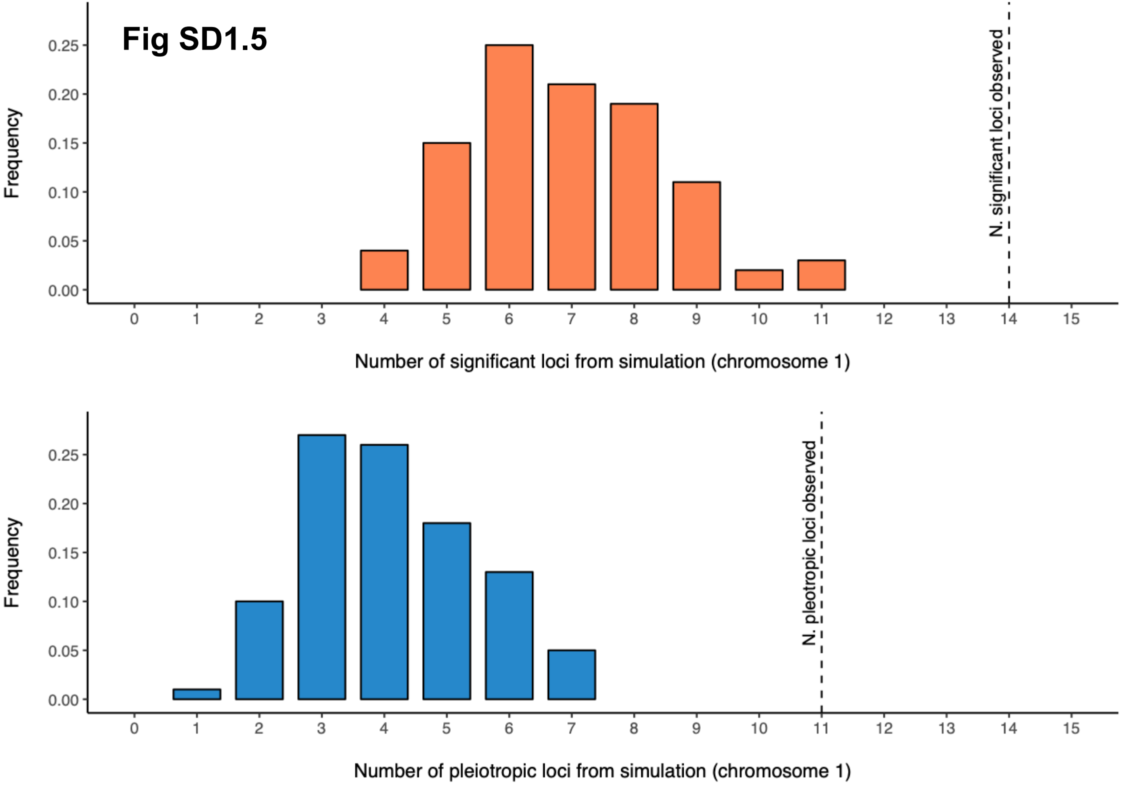

A
.43 (.08)
.25 (.05)
1
F1g
1
F2g
1
F3g
.30 (.06)
.53 (.09)
1.00 (.16)
.20 (.08)
.83 (.04)
.28 (.04)
.61 (.06)
.64 (.05)
.82 (.04)
.62 (.05)
ANg
OCDg
TSg
SCZg
BIPg
MDDg
ADHDg
AUTg
1
uAN
uOCD
uTS
uSCZ
uBIP
uMDD
uADHD
uAUT
.72 (.17)
< .01 (.36)
.87 (.13)
.31 (.06)
.33 (.06)
.46 (.07)
.62 (.07)
.59 (.10)
.-15 (.08)
B
.42 (.08)
.16 (.04)
1
F1g
1
F2g
1
F3g
.36 (.07)
.49 (.11)
1.00 (.17)
.46 (.11)
.83 (.05)
.36 (.04)
.44 (.06)
.41 (.06)
.82 (.05)
.89 (.10)
ANg
OCDg
TSg
SCZg
BIPg
MDDg
ADHDg
AUTg
1
uAN
uOCD
uTS
uSCZ
uBIP
uMDD
uADHD
uAUT
.76 (.17)
< .01 (.36)
.71 (.14)
.31 (.08)
.32 (.08)
.62 (.06)
.20 (.17)
.83 (.09)

Fig SD1.5


Frequency
0.25
0.20
0.15
0.10
0.05
0.00
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
N. significant loci observed
Number of significant loci from simulation (chromosome 1)
Frequency
0.25
0.20
0.15
0.10
0.05
0.00
0
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
N. pleotropic loci observed
Number of pleiotropic loci from simulation (chromosome 1)