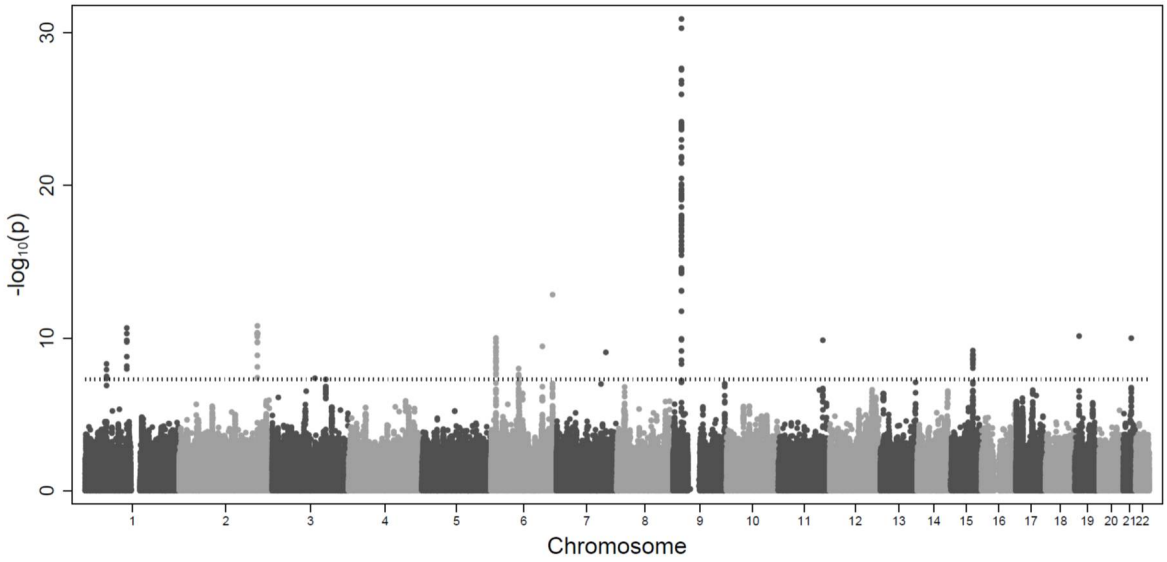
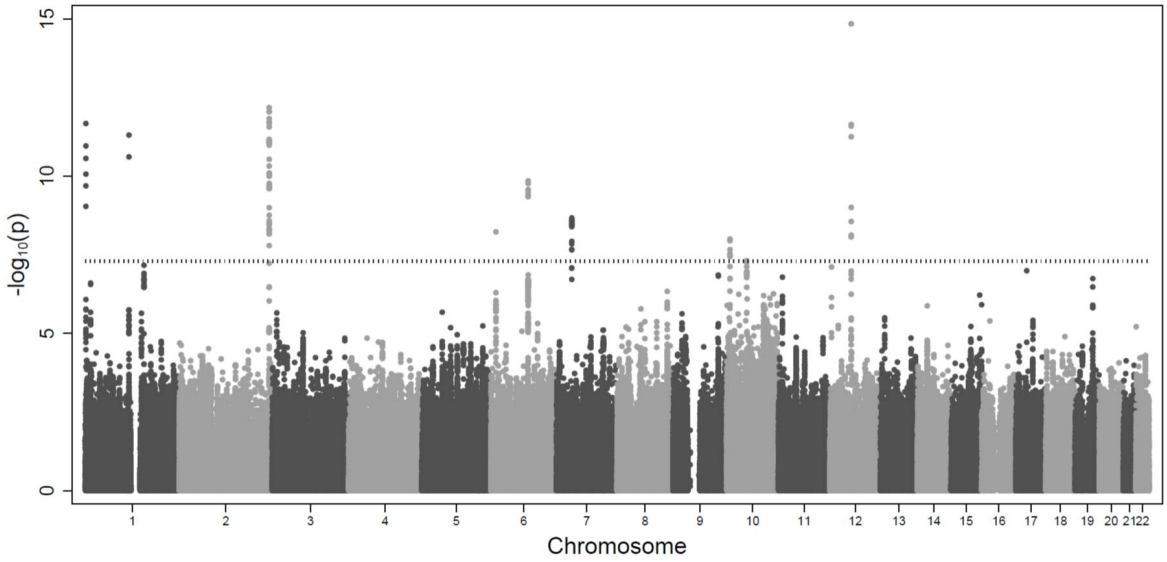
**Figure e1. Manhattan plots for the meta-analyses of genome-wide association data used in the current study.**

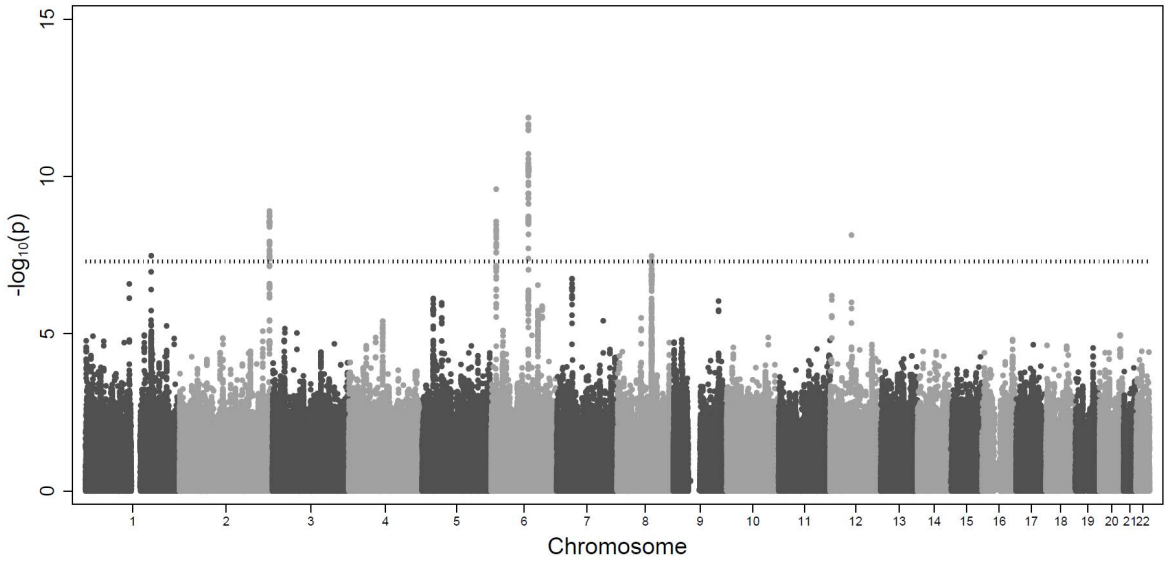
A)



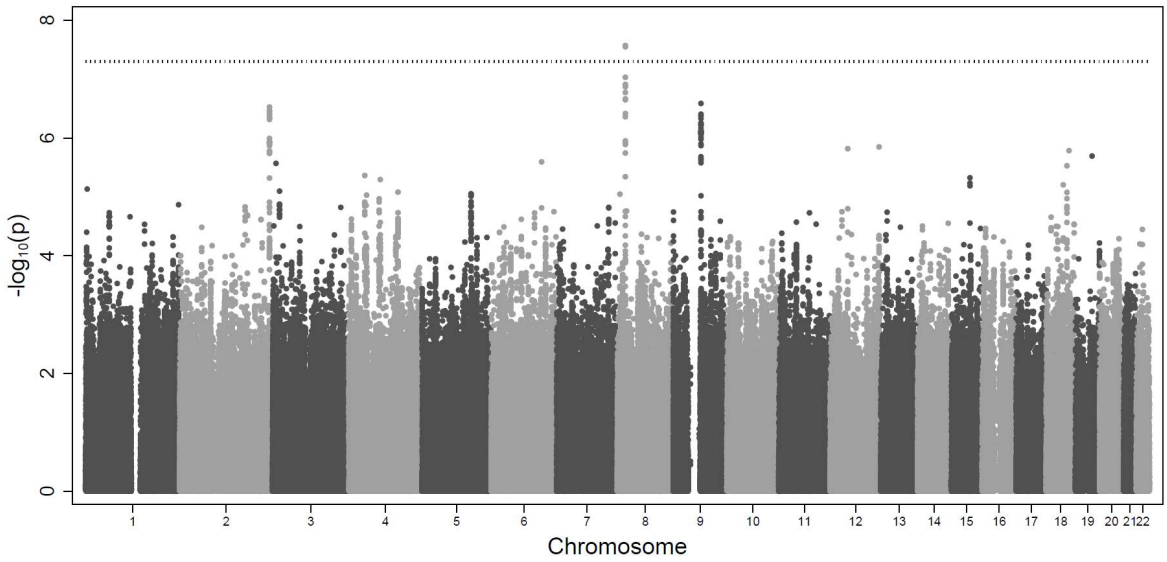

B)



C)

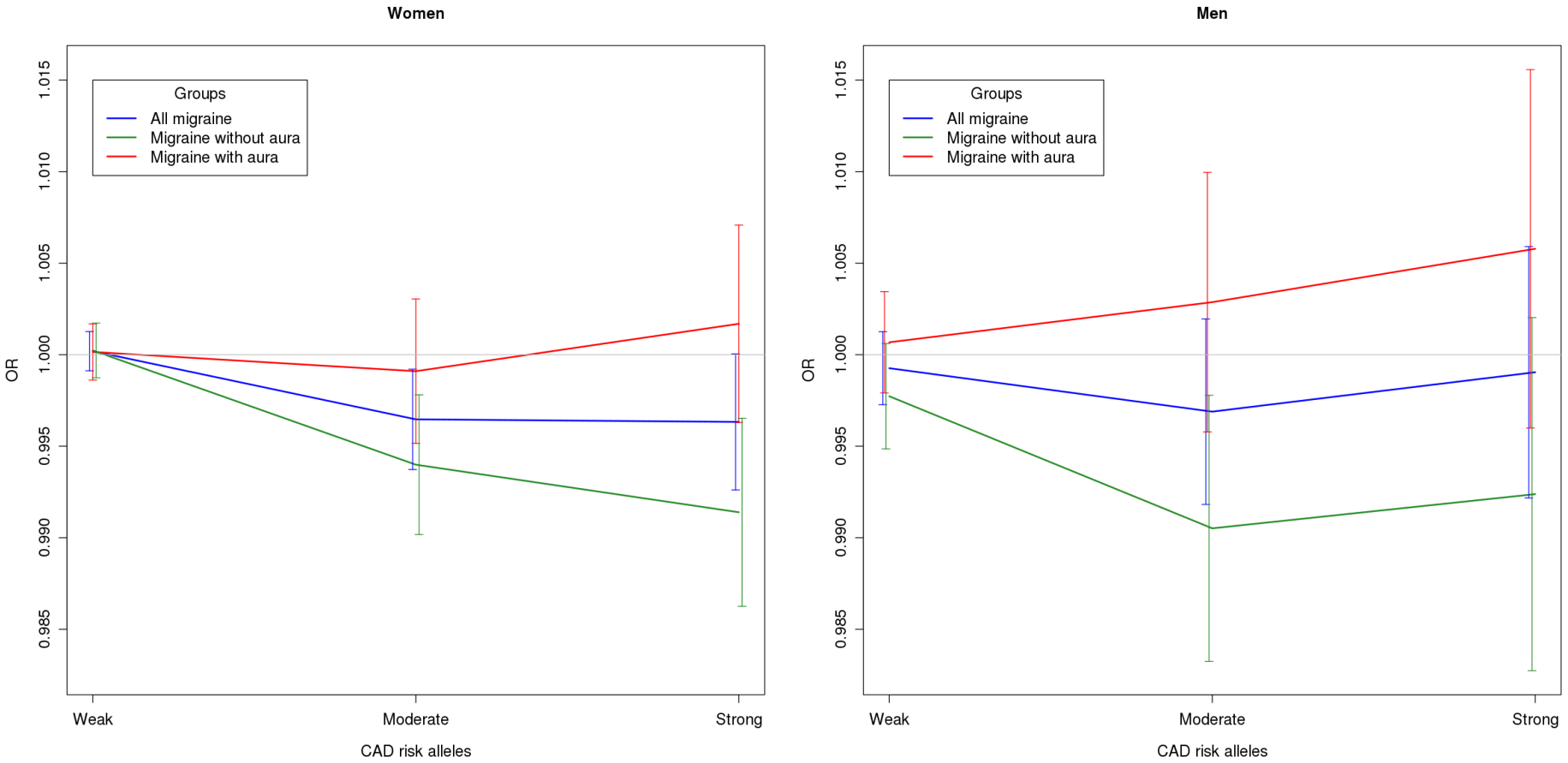



D)




Grey horizontal line indicates genome-wide significance level ($P < 5 \times 10^{-8}$). Separate plots are shown for A) Coronary artery disease (21 076 cases versus 63 014 controls), B) Migraine (19 981 cases versus 56 667 controls), C) Migraine subanalysis: Migraine without aura (6 413 cases versus 32 745 controls), D) Migraine subanalysis: Migraine with aura (4 940 cases versus 37 557 controls).

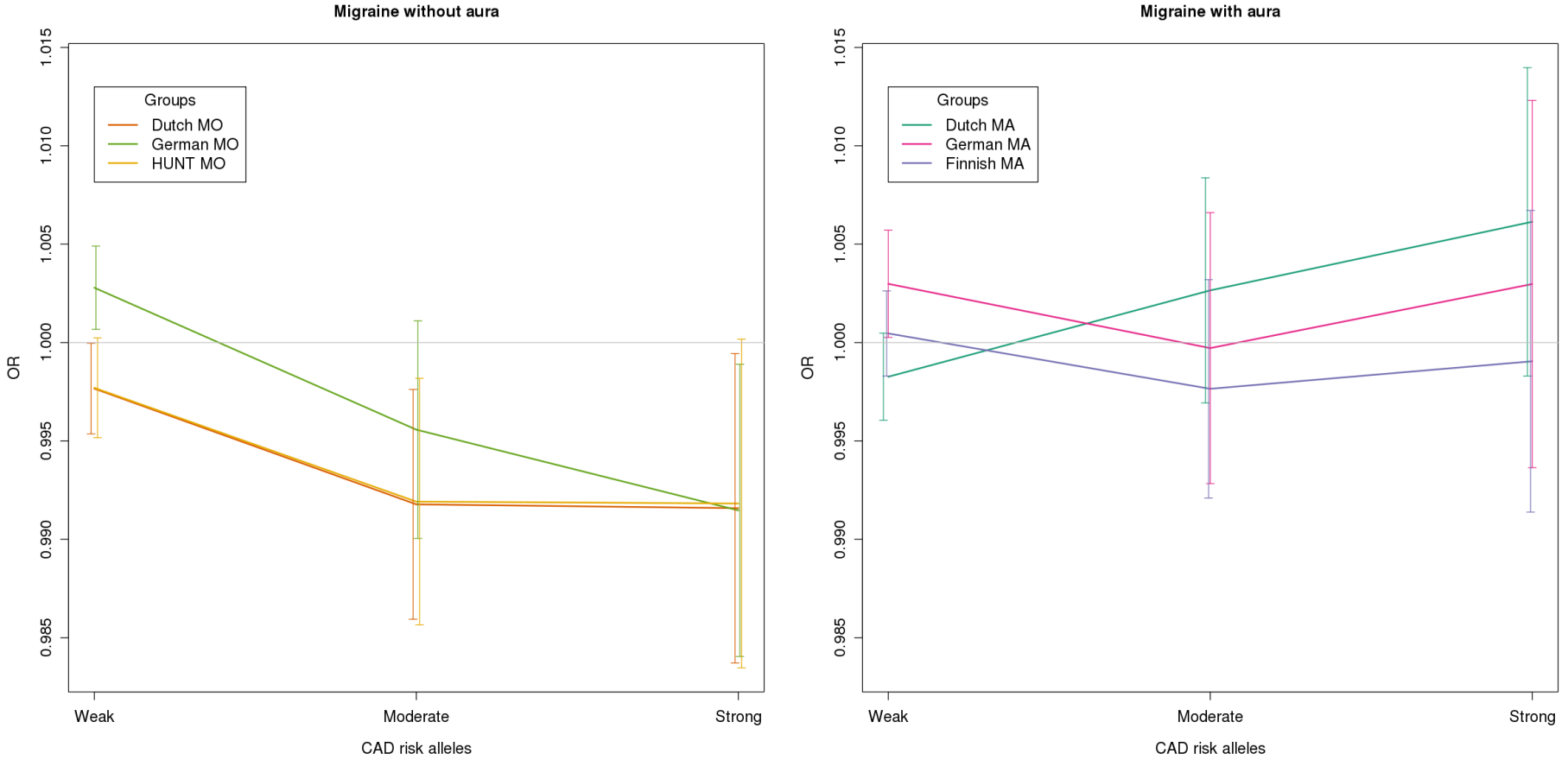
**Figure e2. Association between coronary artery disease polygenic risk score and the presence of migraine, stratified by gender.**




CAD = coronary artery disease.

Results are given as odds ratios (OR) with 95% confidence intervals. Separate plots are shown for women (6 395 females cases versus 9 468 female controls) and men (1 563 male cases versus 6 698 male controls). Separate lines are given for all migraine (blue), migraine without aura (green), and migraine with aura (red). The CAD polygenic risk score was calculated based on SNPs with either weak ($P<1 \times 10^{-2}$), moderate ($P<1 \times 10^{-4}$) or strong ($P<5 \times 10^{-8}$) association to CAD in the CARDIoGRAM study.

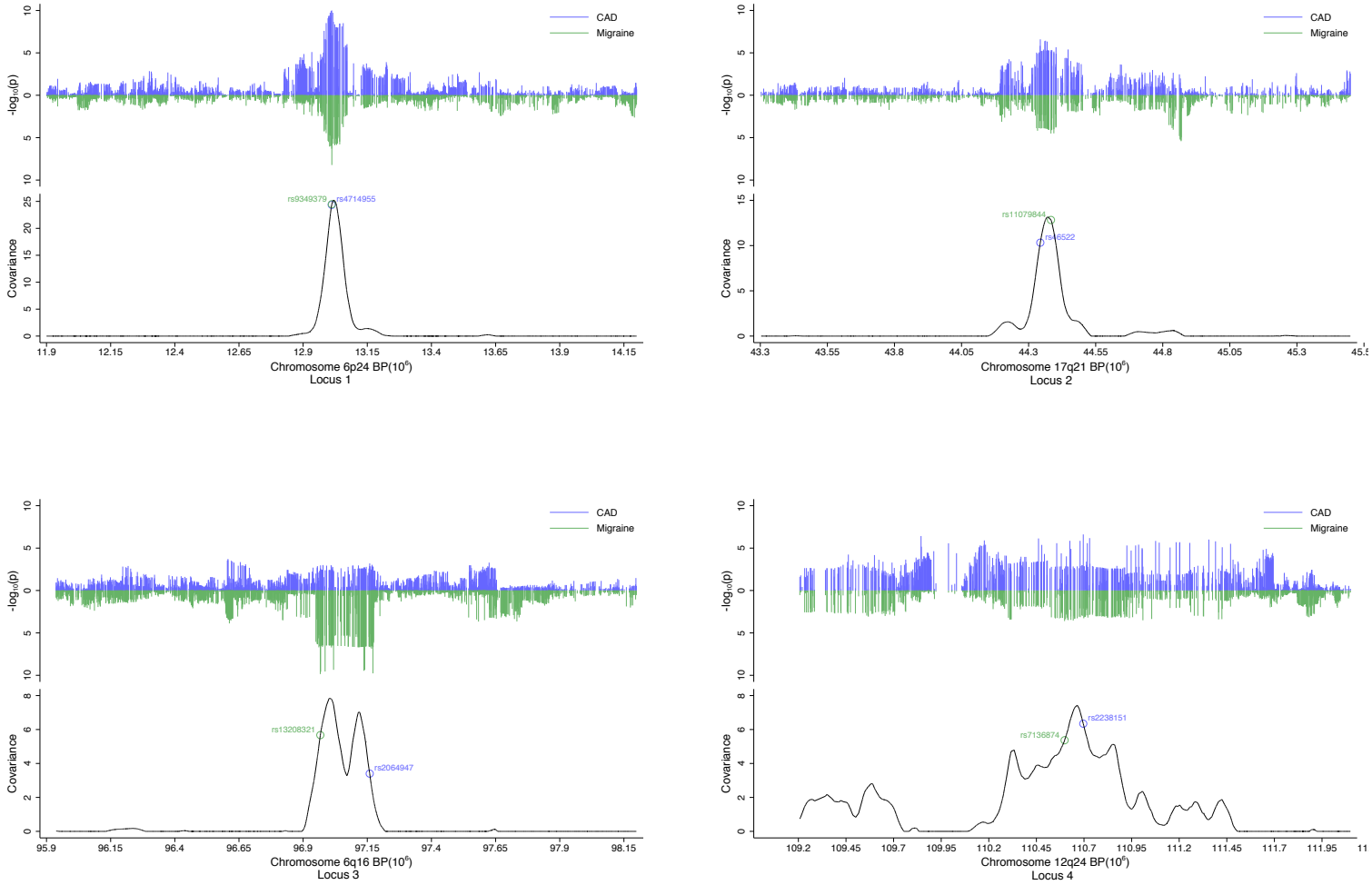
**Figure e3. Association between coronary artery disease polygenic risk score and the presence of migraine, stratified by migraine aura status.**

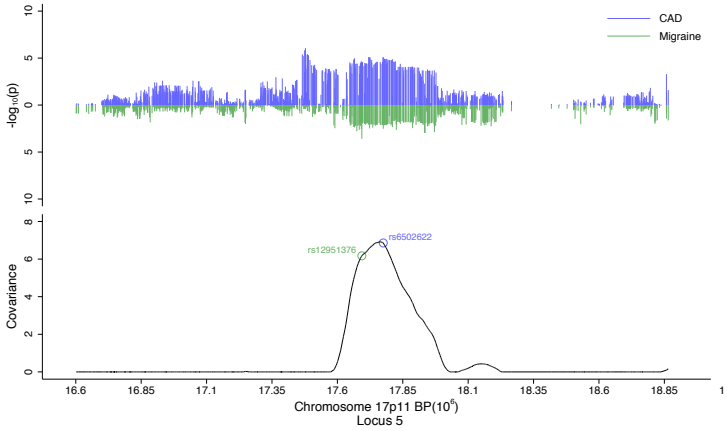


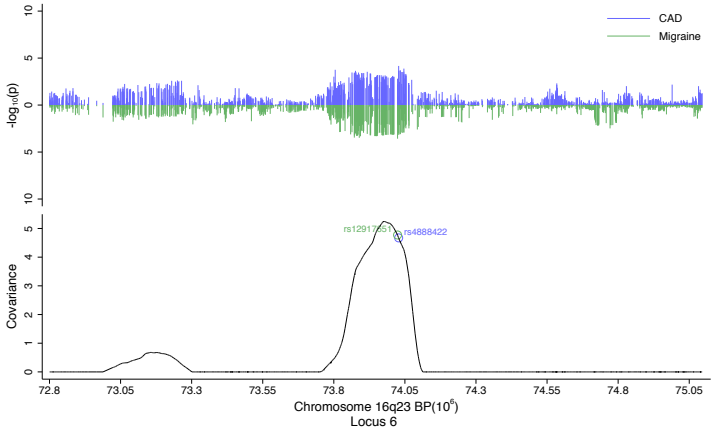

CAD = coronary artery disease.

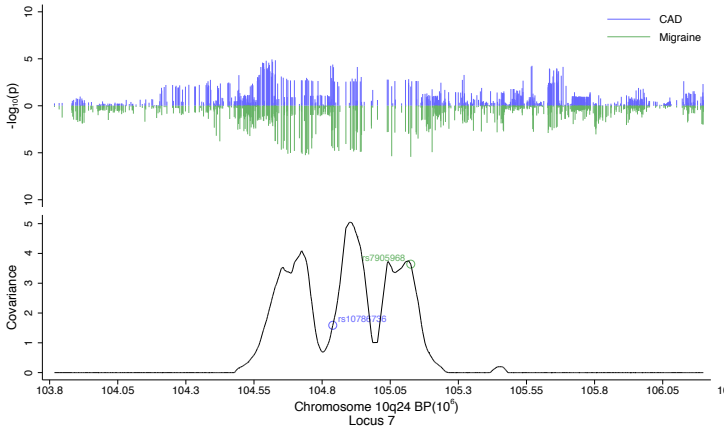
Results are given as odds ratios (OR) with 95% confidence intervals. Separate plots are shown for migraine without aura (3 501 cases versus 5 677 controls) and migraine with aura (2 849 cases versus 9 392 controls). Separate lines are given for each cohort. The CAD polygenic risk score was calculated based on SNPs with either weak ($P<1 \times 10^{-2}$), moderate ($P<1 \times 10^{-4}$) or strong ($P<5 \times 10^{-8}$) association to CAD in the CARDIoGRAM study.

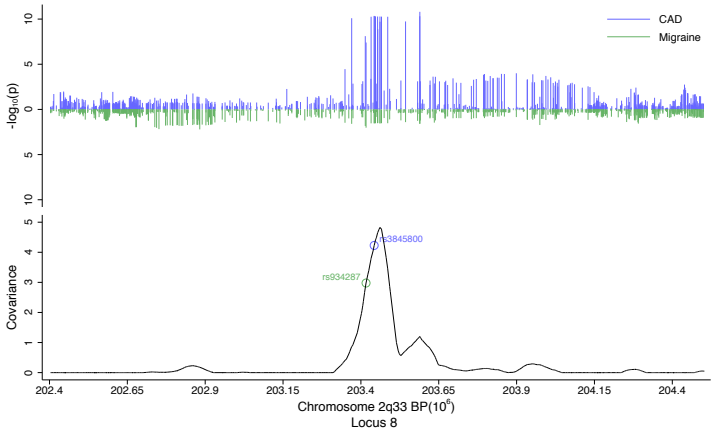
**Figure e4: Local Manhattan plots and covariance signals at the overlapping loci identified by cross-phenotype spatial mapping.**

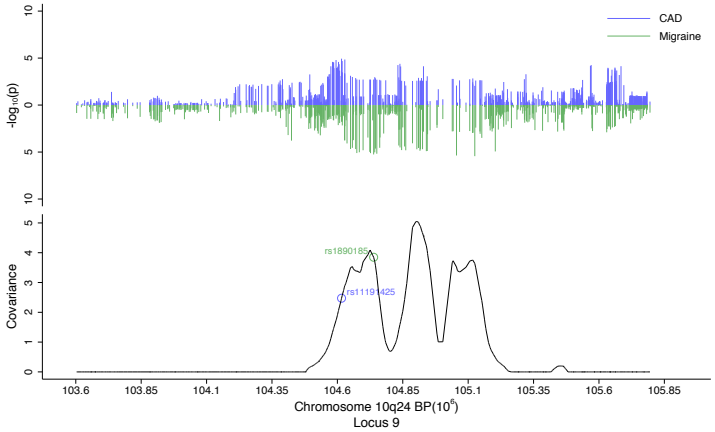


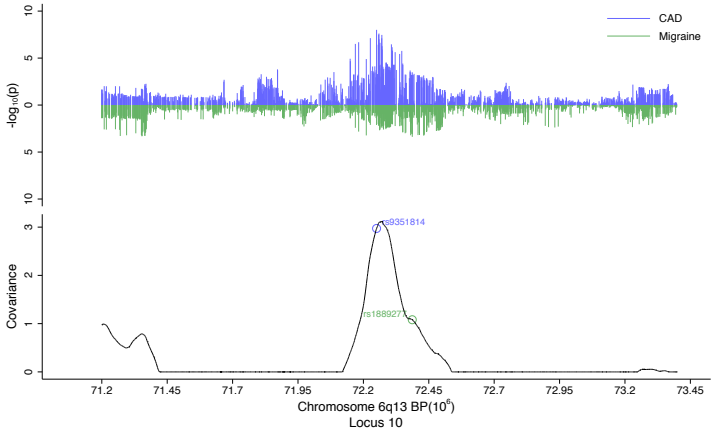

CAD
Migraine
-log10(p)
Covariance
rs12951376
rs6502622
16.6
16.85
17.1
17.35
17.6
17.85
18.1
18.35
18.6
18.85
Chromosome 17p11 BP(10^6)
Locus 5

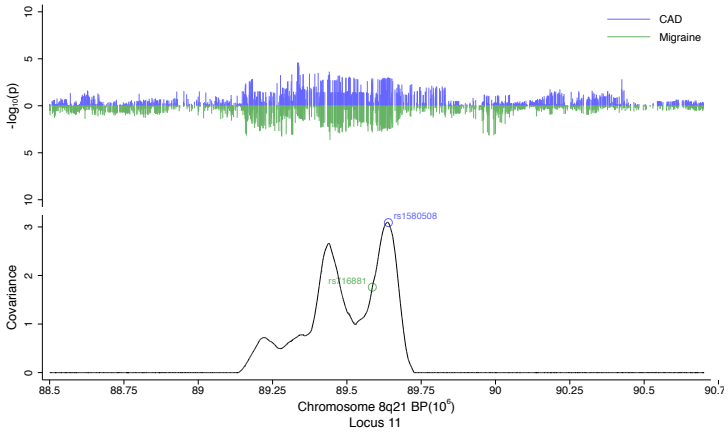

CAD
Migraine
-log10(p)
Covariance
rs12917251
rs4888422
72.8
73.05
73.3
73.55
73.8
74.05
74.3
74.55
74.8
75.05
Chromosome 16q23 BP(10^6)
Locus 6

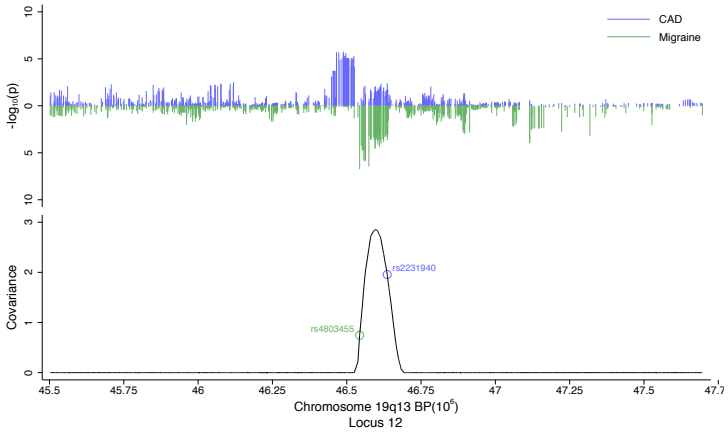

CAD
Migraine
-log10(p)
Covariance
rs7905968
rs10786708
103.8
104.05
104.3
104.55
104.8
105.05
105.3
105.55
105.8
106.05
Chromosome 10q24 BP(10^6)
Locus 7

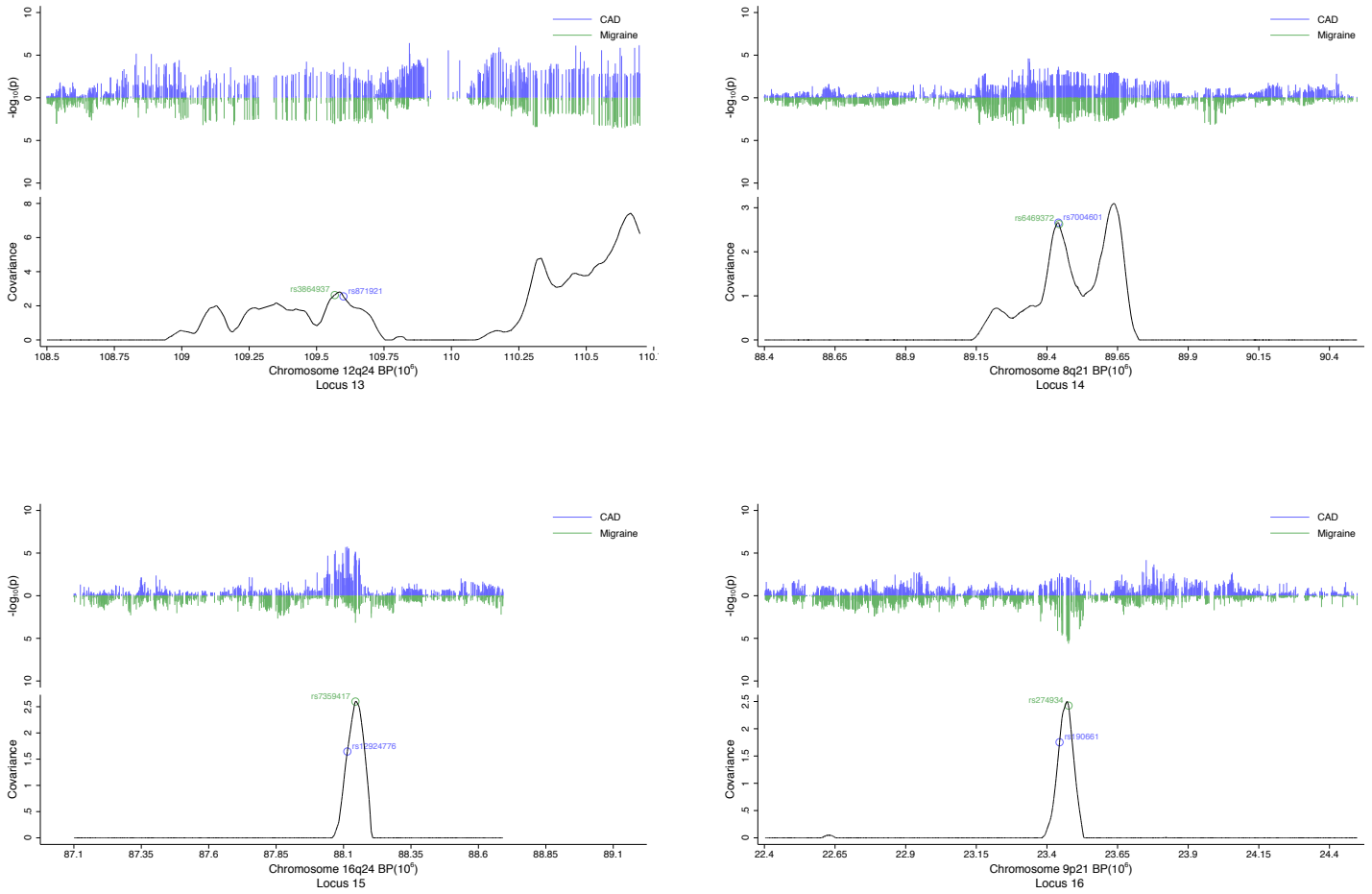

CAD
Migraine
-log10(p)
Covariance
rs3845800
rs934287
202.4
202.65
202.9
203.15
203.4
203.65
203.9
204.15
204.4
Chromosome 2q33 BP(10^6)
Locus 8


CAD
Migraine
-log10(p)
Covariance
rs1890185
rs11191425
103.6
103.85
104.1
104.35
104.6
104.85
105.1
105.35
105.6
105.85
Chromosome 10q24 BP(10^6)
Locus 9


CAD
Migraine
-log10(p)
Covariance
rs9351814
rs1889271
71.2
71.45
71.7
71.95
72.2
72.45
72.7
72.95
73.2
73.45
Chromosome 6q13 BP(10^6)
Locus 10


CAD
Migraine
-log10(p)
Covariance
rs1580508
rs716881
88.5
88.75
89
89.25
89.5
89.75
90
90.25
90.5
90.7
Chromosome 8q21 BP(10^6)
Locus 11


CAD
Migraine
-log10(p)
Covariance
rs2231940
rs4803455
45.5
45.75
46
46.25
46.5
46.75
47
47.25
47.5
47.7
Chromosome 19q13 BP(10^6)
Locus 12




CAD = coronary artery disease.

For each locus $-\log_{10} P$ values are given for both CAD (blue) and migraine (green). In the covariance plots, circles mark the lead SNPs for CAD (blue circle) and migraine (green circle).