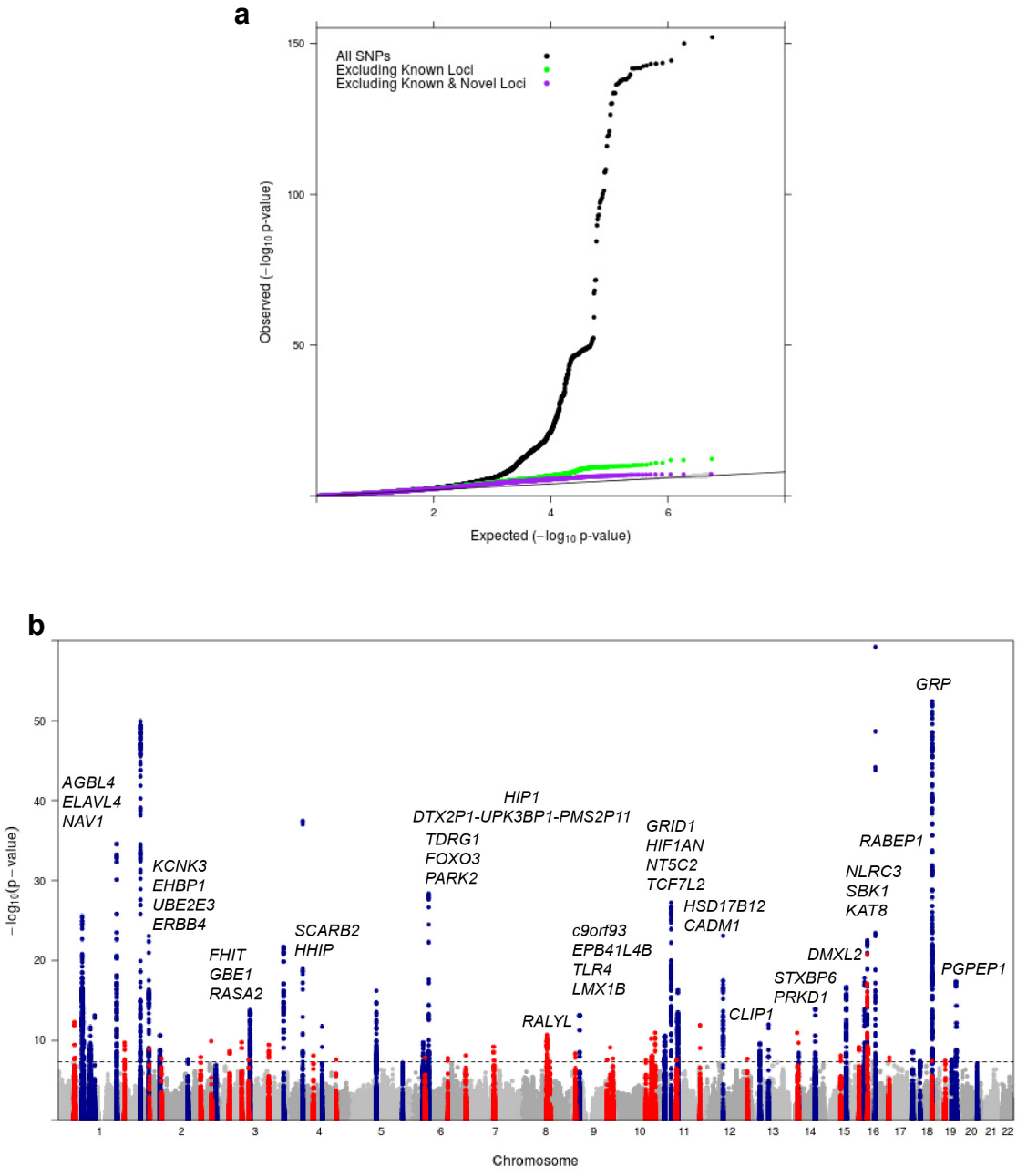
doi:10.1038/nature14177

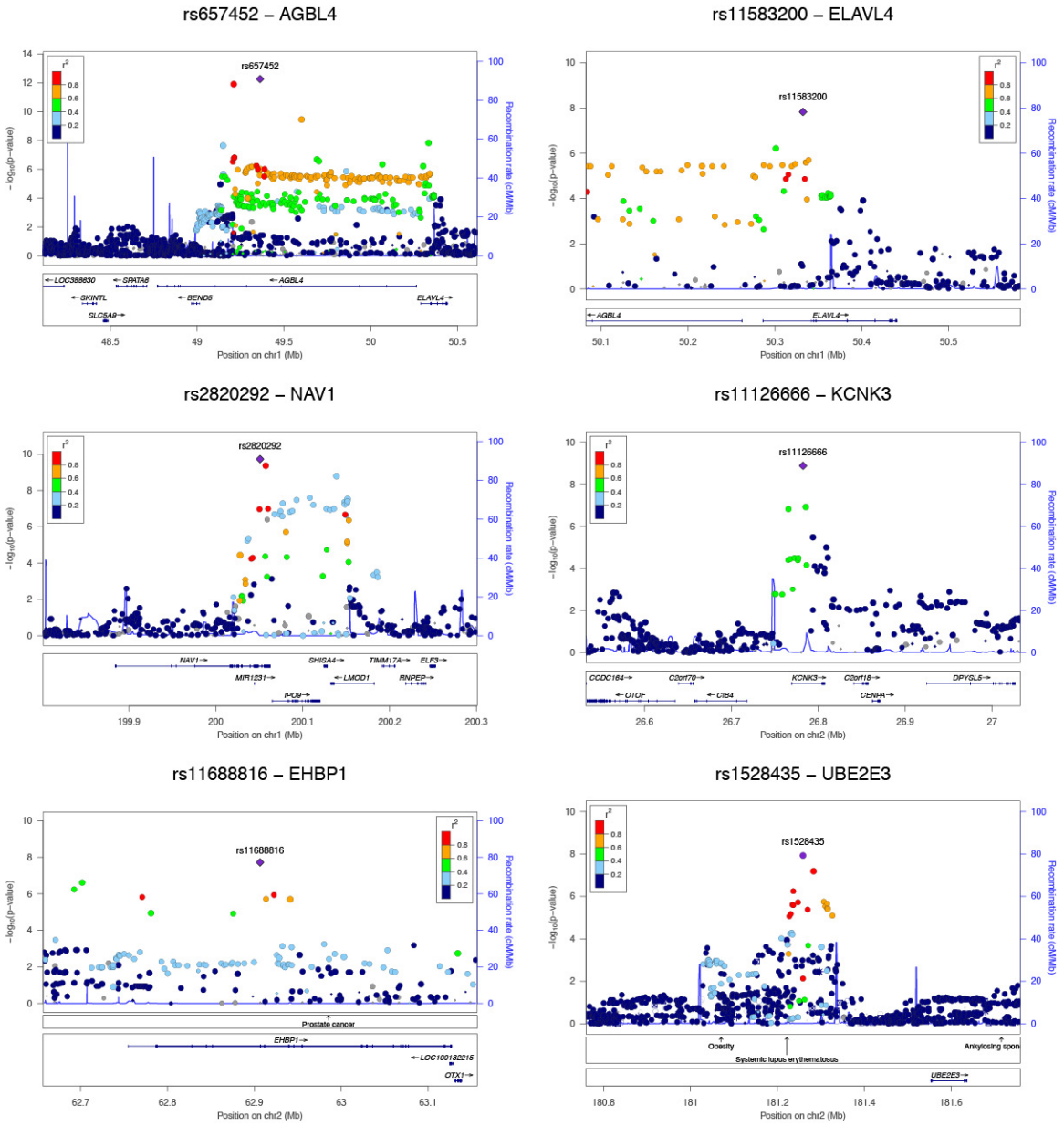
1. Supplementary Figures

Supplementary Figure 1 | Summary plots of European sex-combined meta-analysis. A. Quantile-quantile plot of SNP associations. All SNPs are plotted in black, after excluding previously known loci (±500 kb) in green, and after excluding previously known and novel loci (±500 kb) in purple. B. Manhattan plot showing previously identified loci in blue and novel loci in red. Novel loci are labeled with the nearest gene, and the *y-axis* is truncated to allow easier observation of novel associations. The index SNP near *FTO* reaches $P<10^{-150}$.



Supplementary Figure 2 | Regional association plots for European sex-combined meta-analysis. A. Regional plots for all novel loci. B. Regional plots for all previously identified loci.

a



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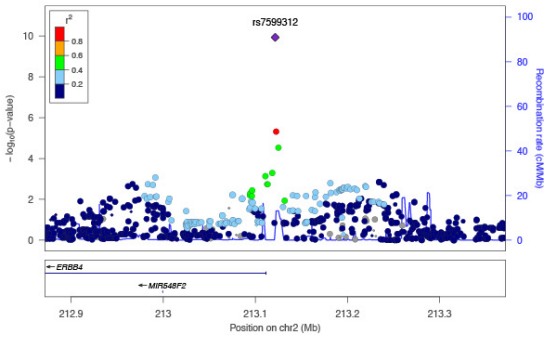

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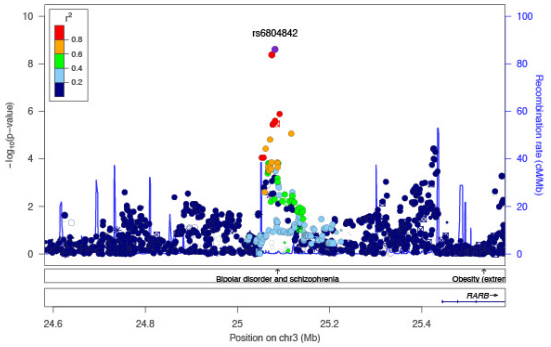

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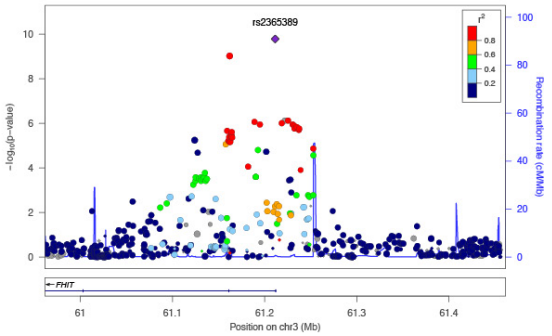

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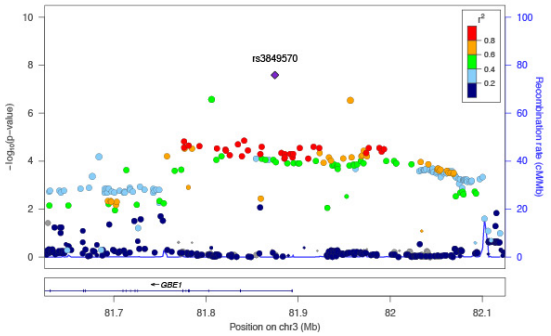

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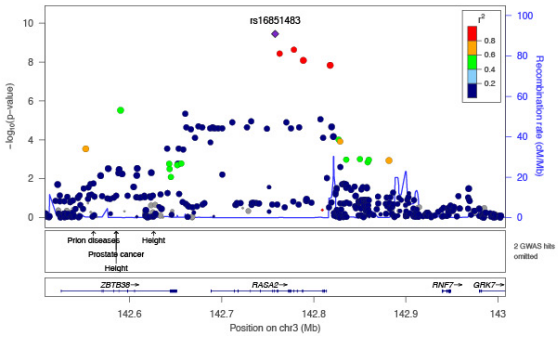

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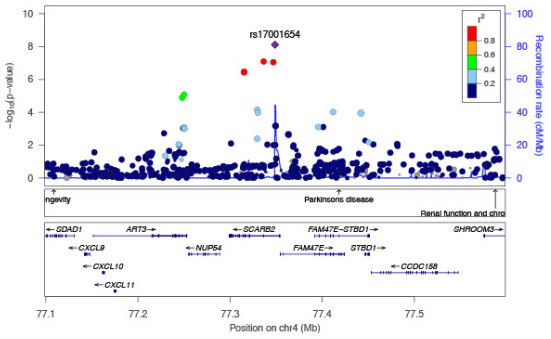

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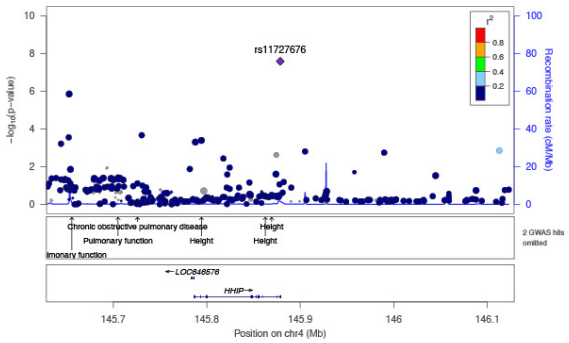

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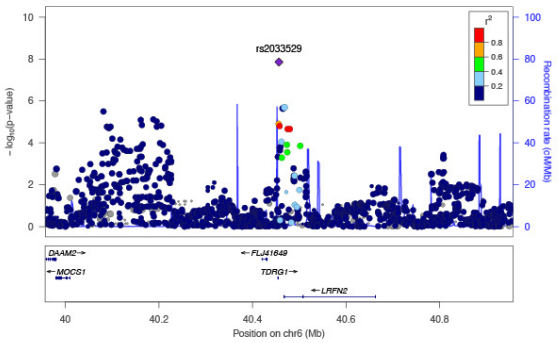

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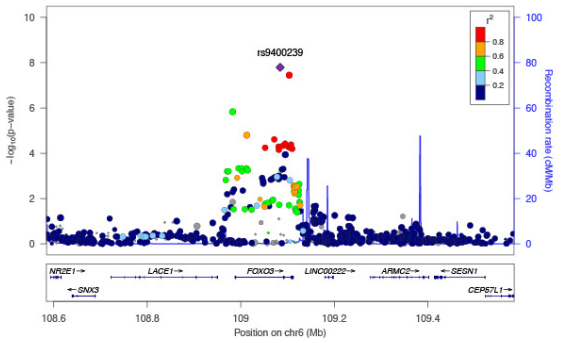

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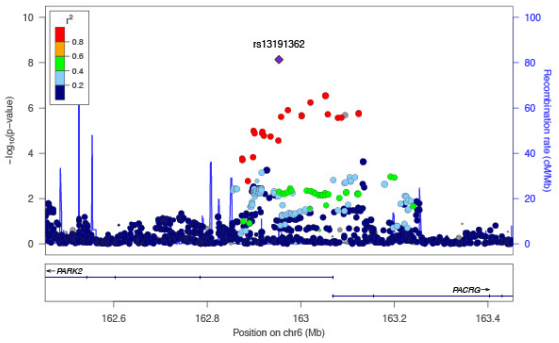

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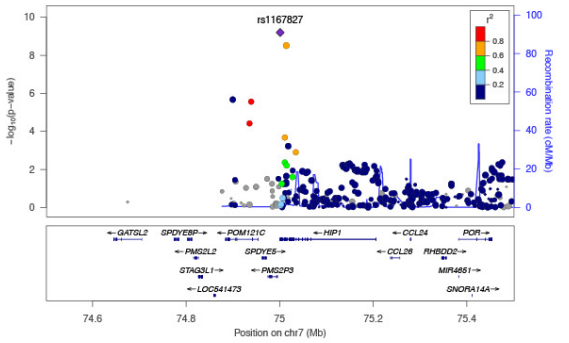

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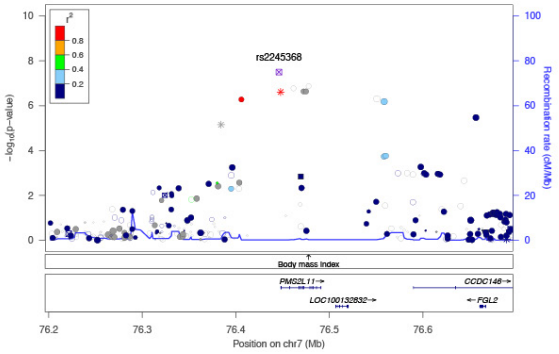

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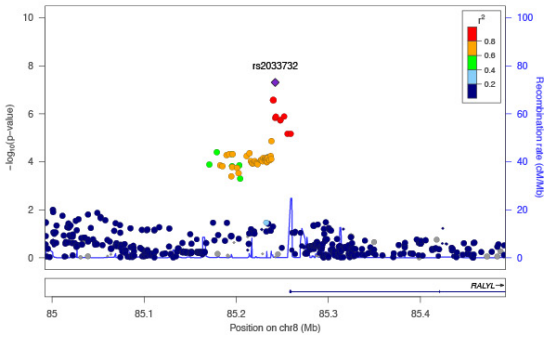

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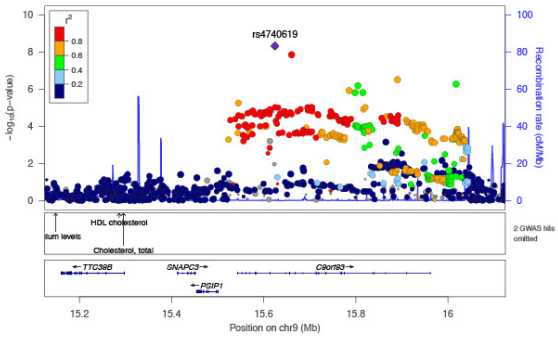

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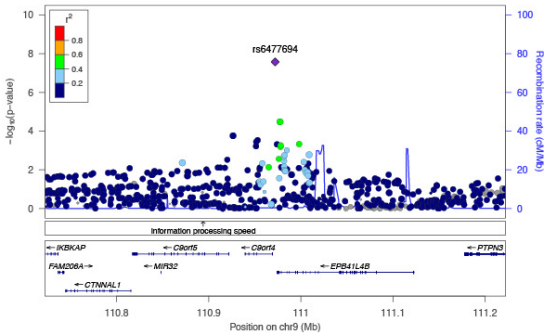

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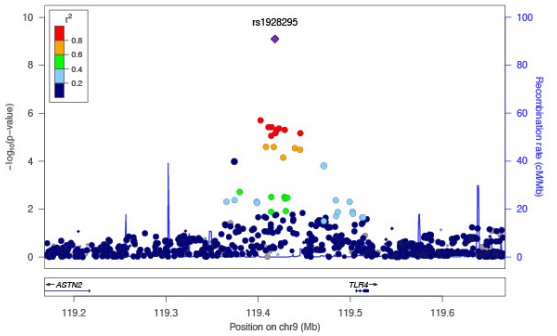

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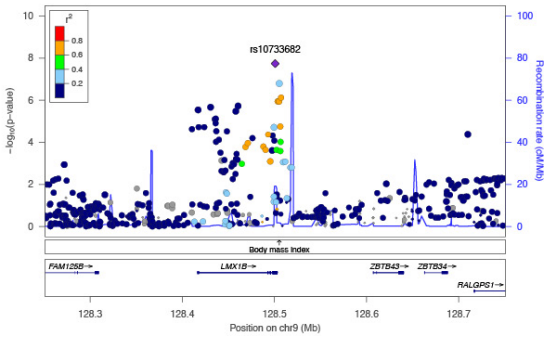

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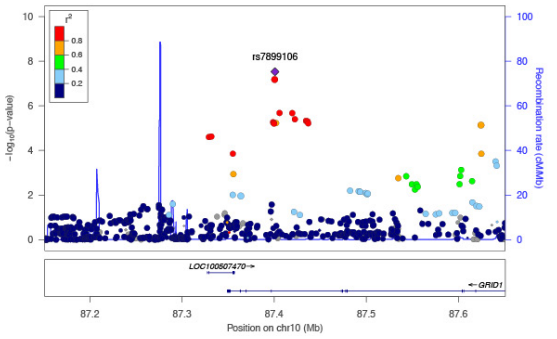

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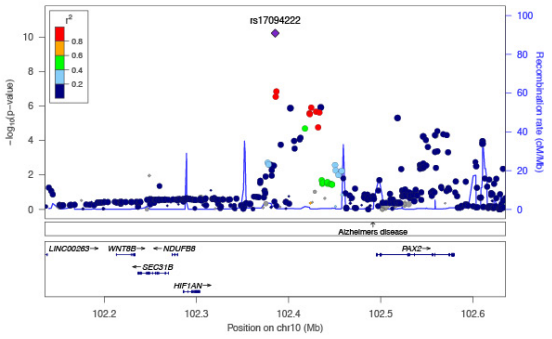

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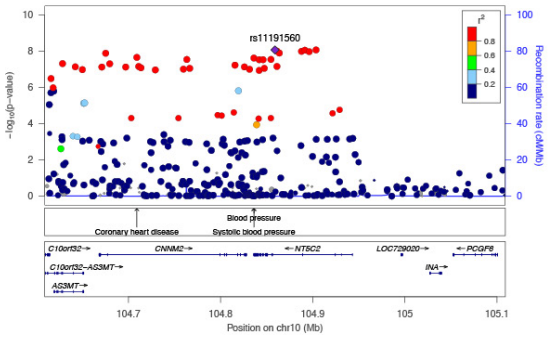

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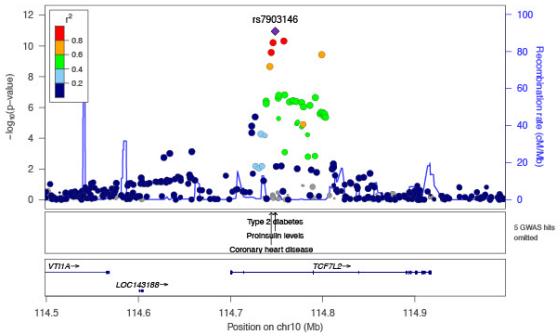

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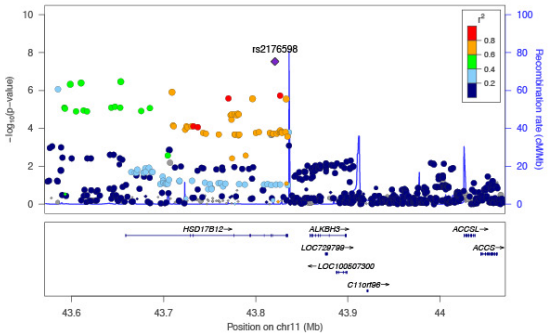

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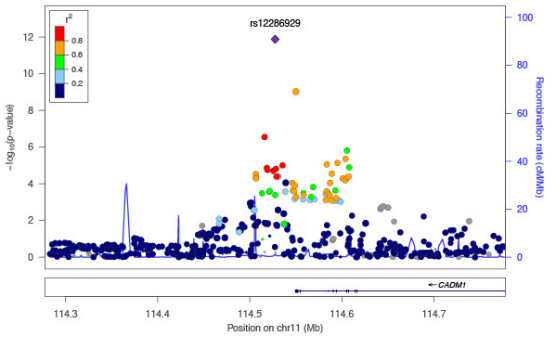

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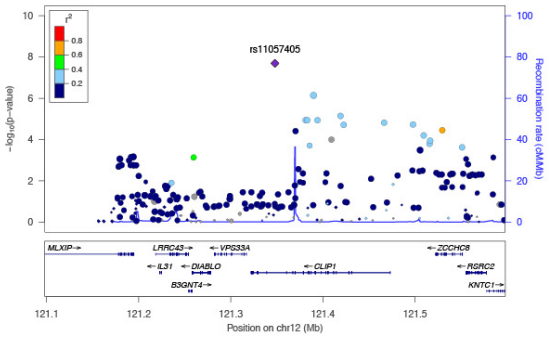

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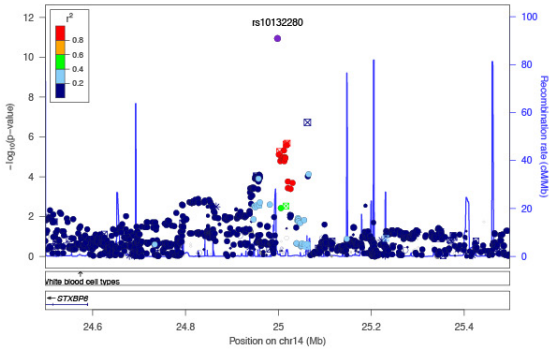

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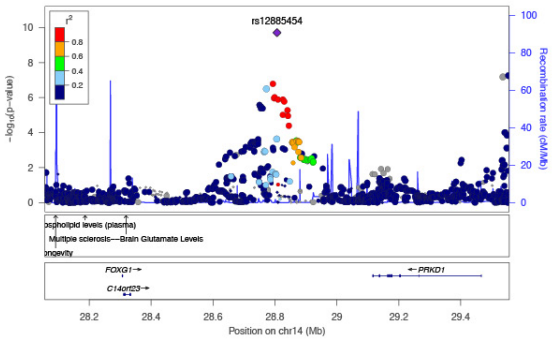

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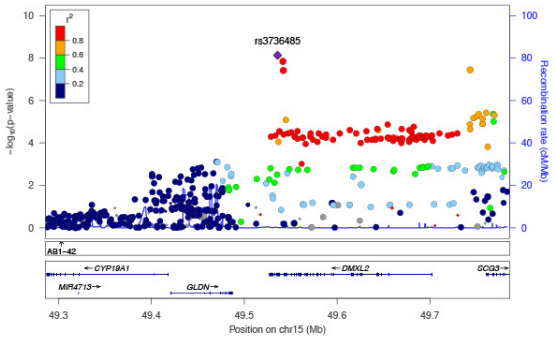

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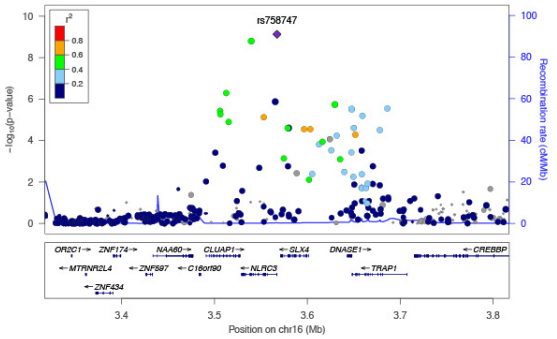

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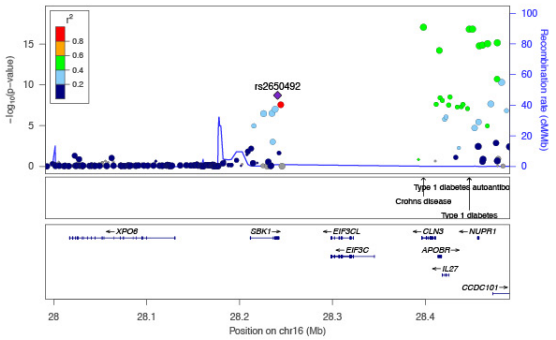

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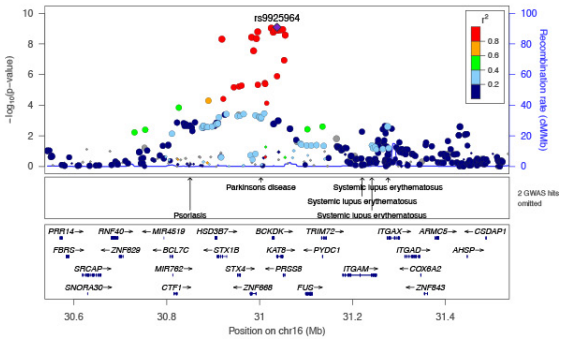

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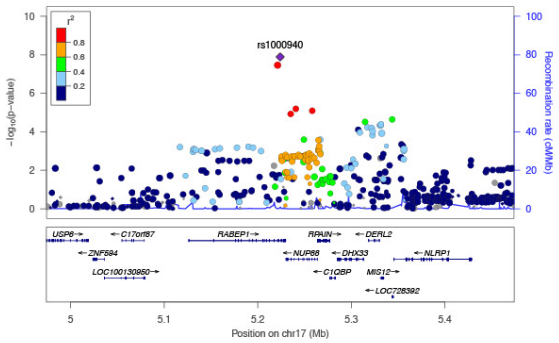

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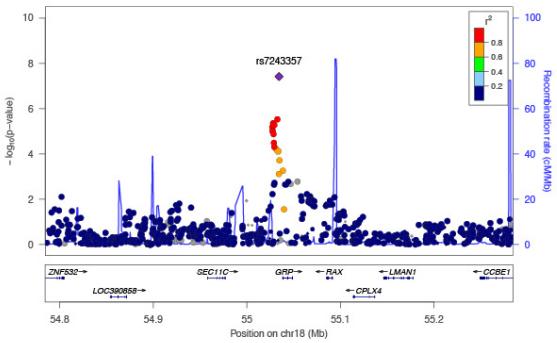

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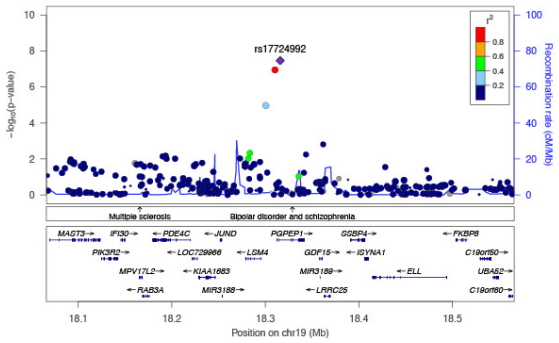

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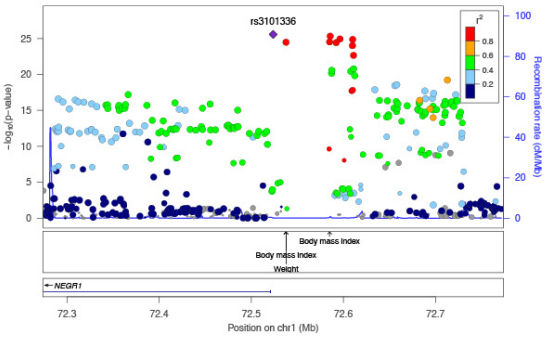

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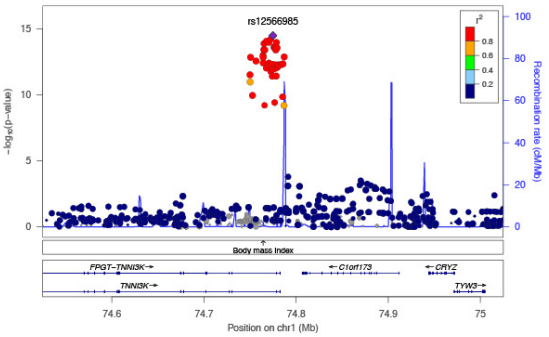

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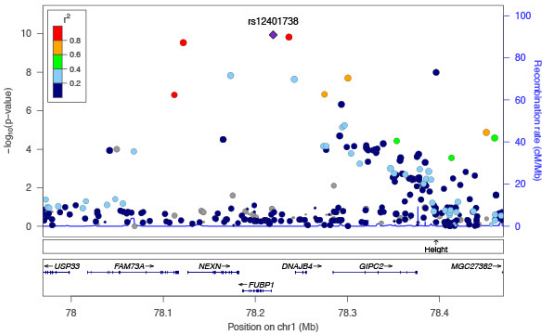

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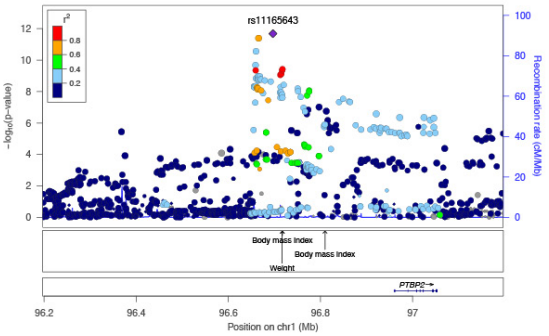

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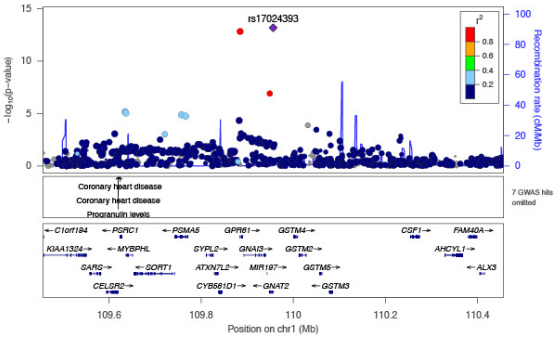

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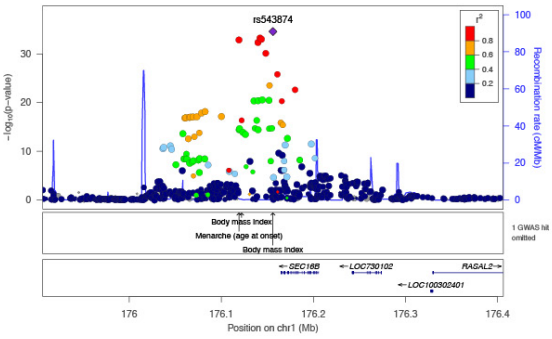

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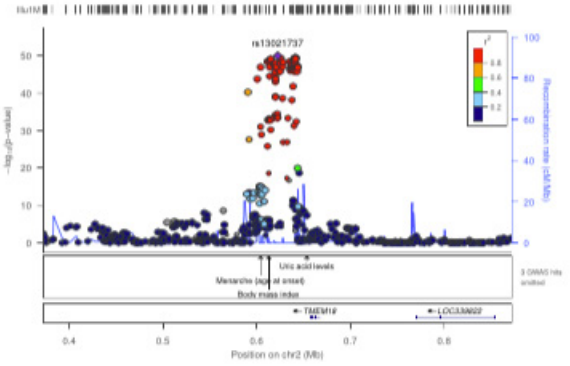

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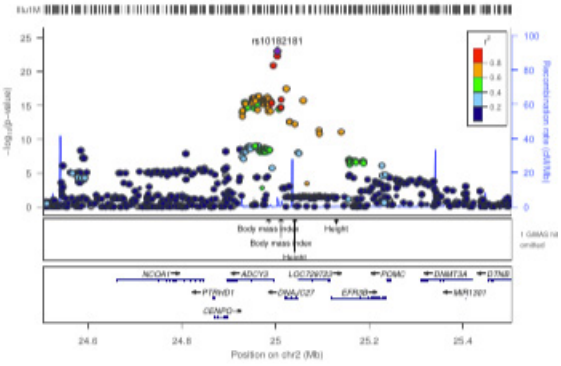

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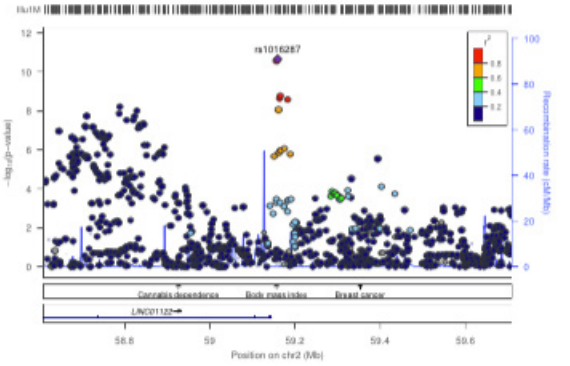

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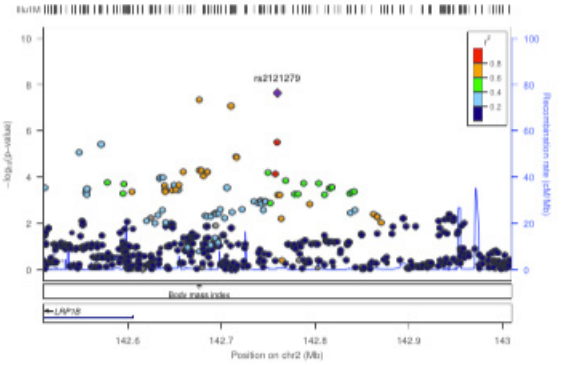

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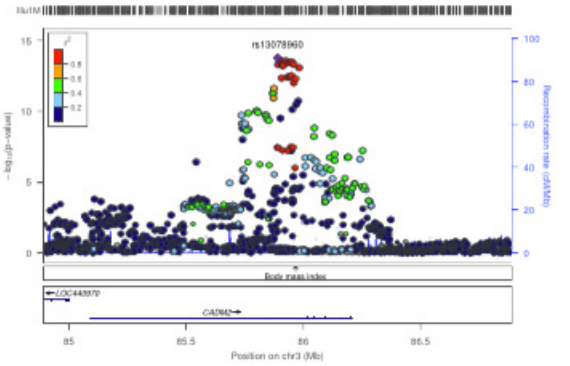

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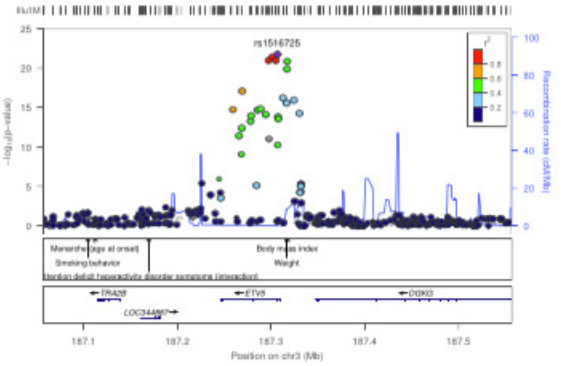

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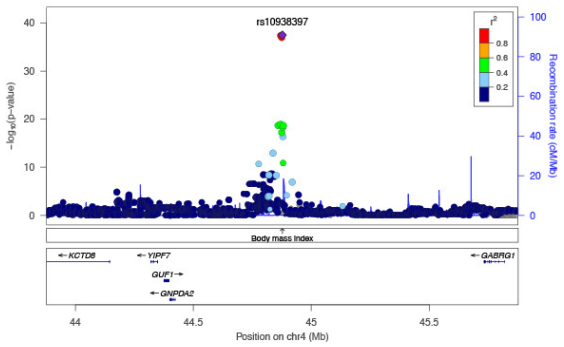

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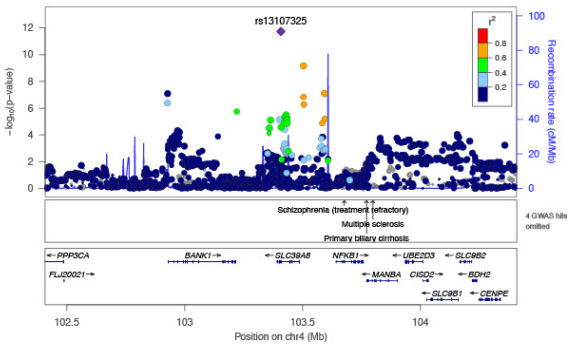

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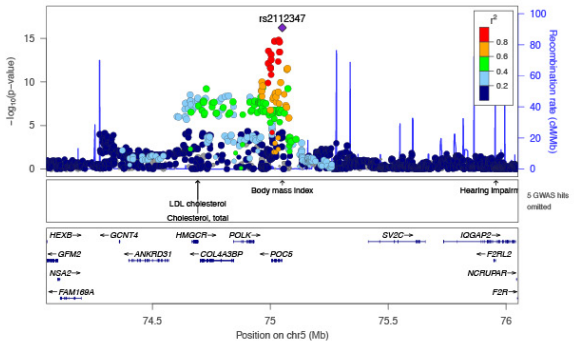

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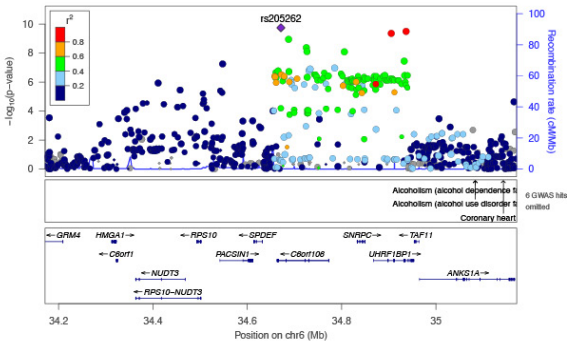

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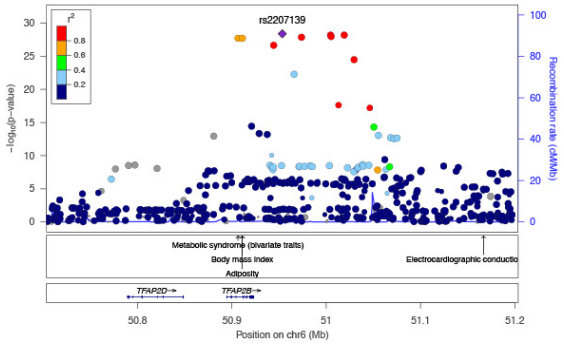

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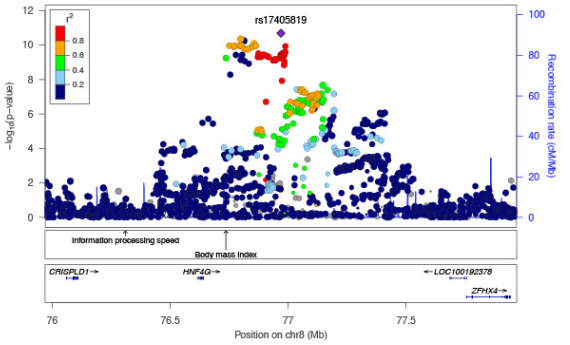

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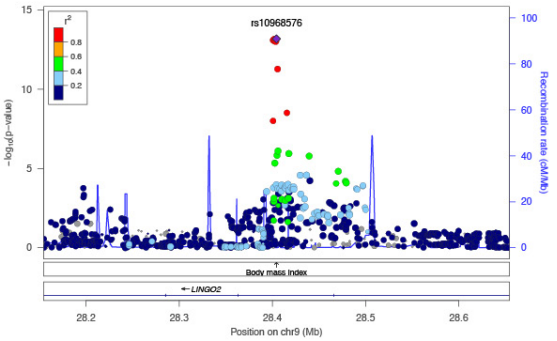

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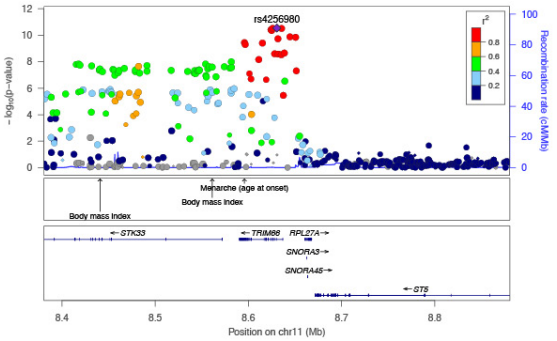

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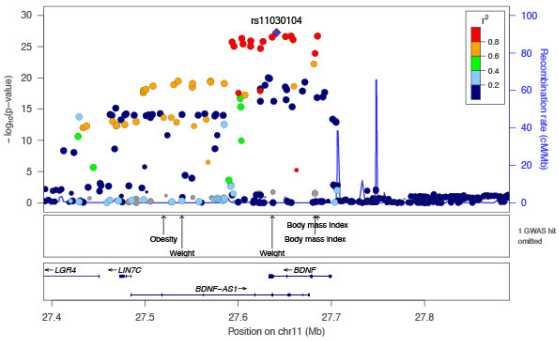

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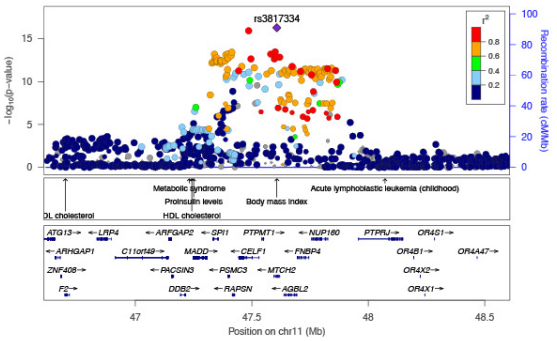

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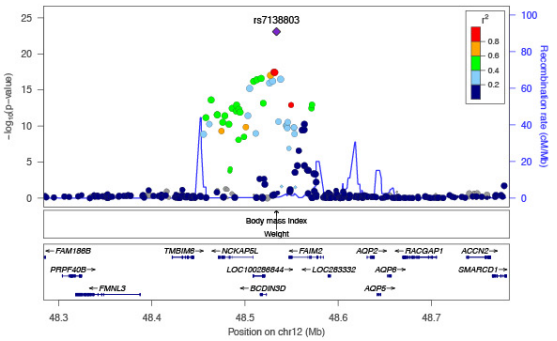

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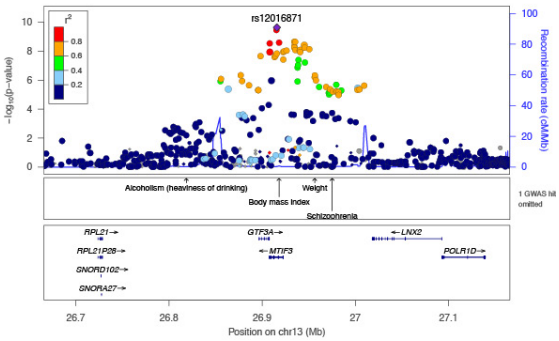

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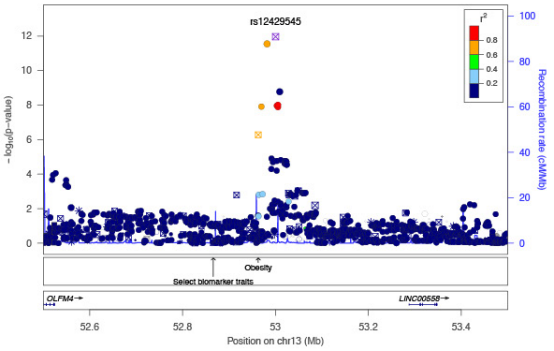

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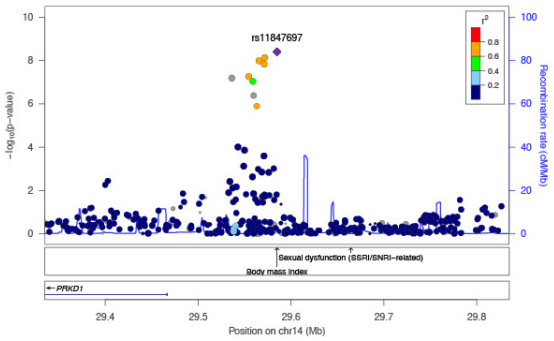

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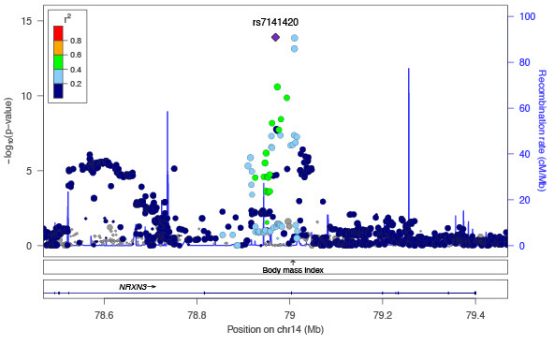

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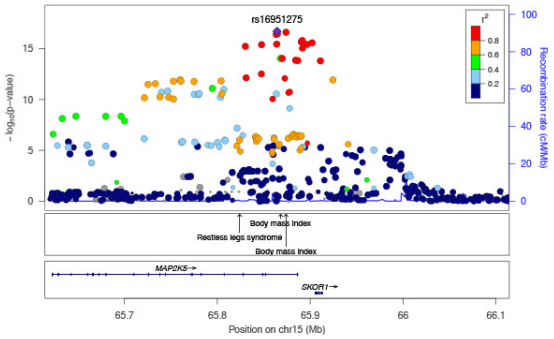

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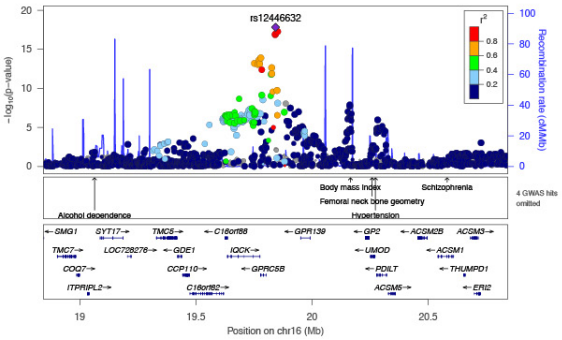

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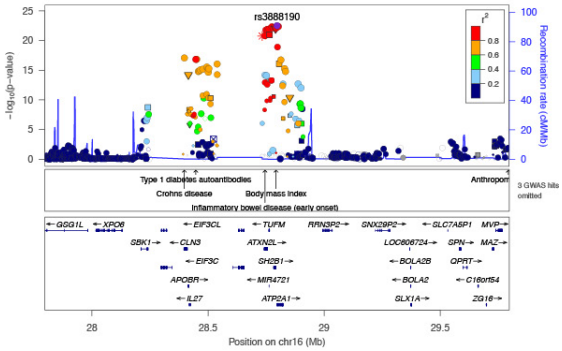

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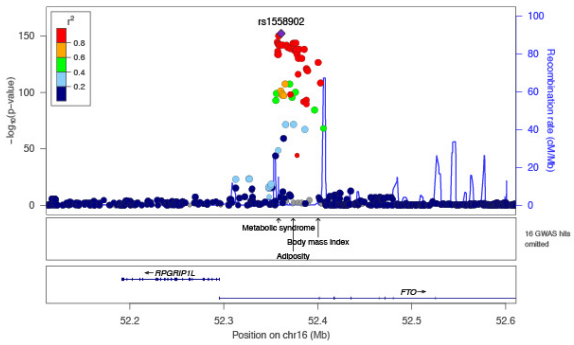

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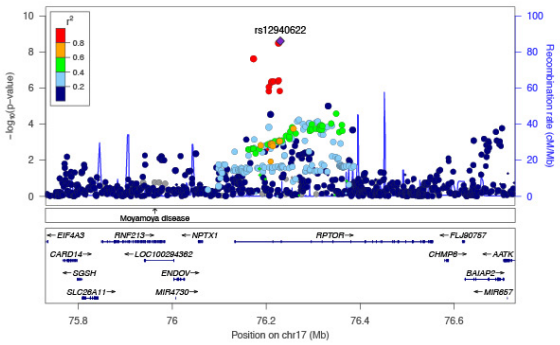

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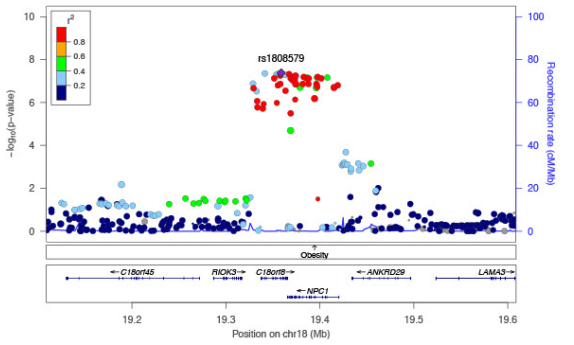

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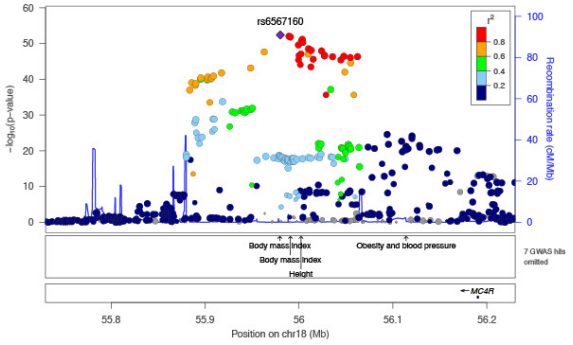

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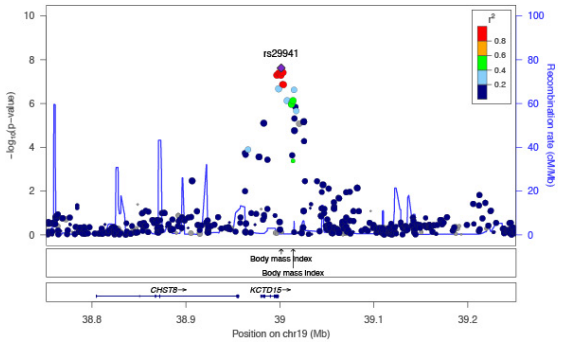

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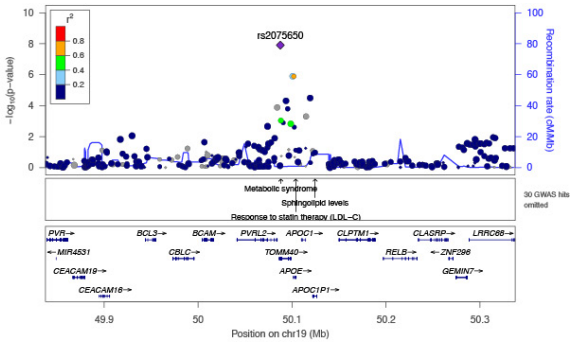

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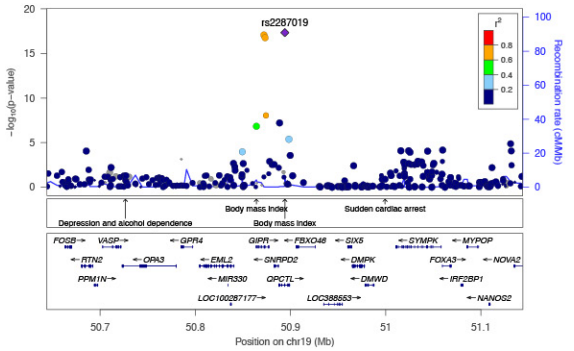

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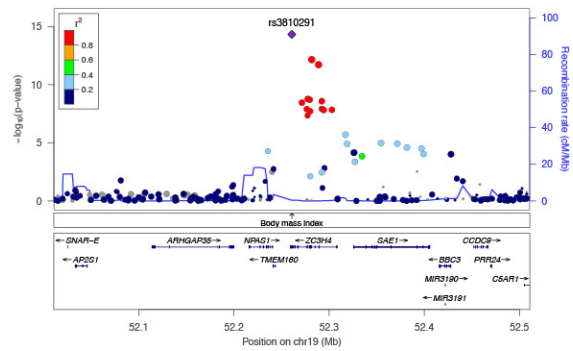
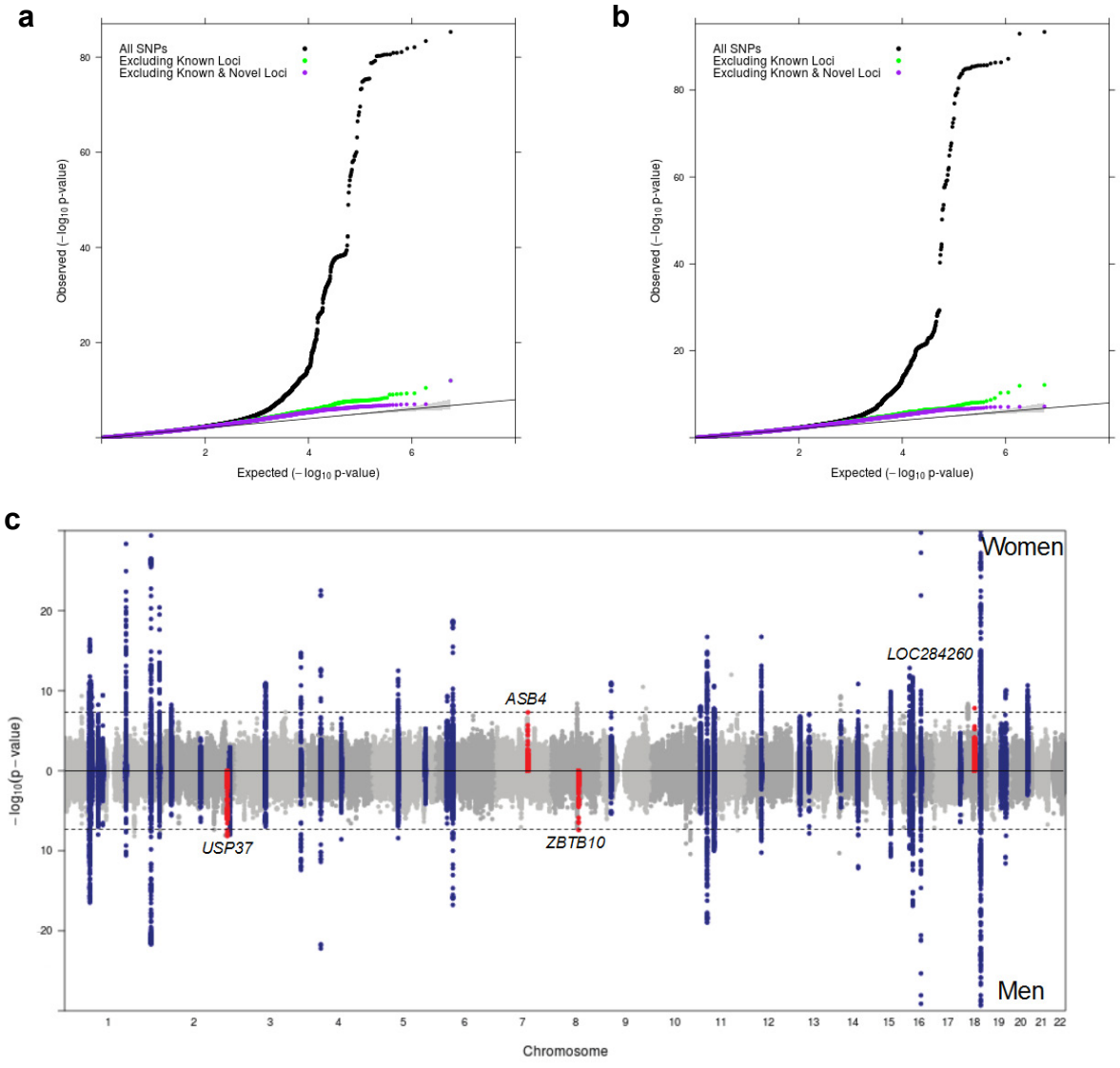


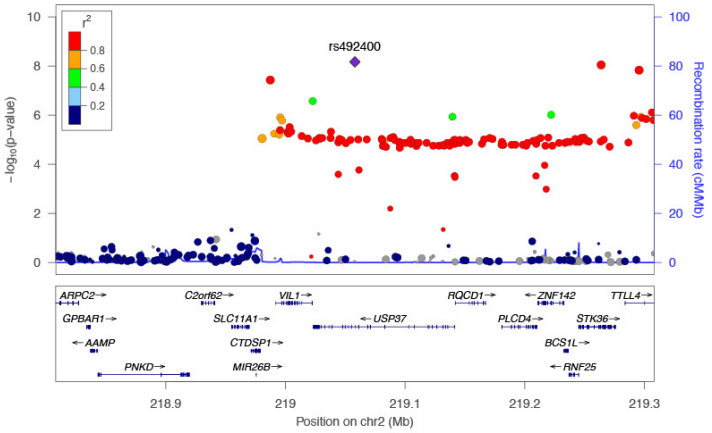
Supplementary Figure 3 | Summary plots of European Sex-specific meta-analyses. A. Quantile-quantile plot of SNP associations for female-specific meta-analsysis. B. Quantile-quantile plot of SNP associations for male-specific meta-analysis. For both plots, all SNPs are plotted in black, after excluding previously known loci (±500 kb) are in green, and after excluding previously known and novel loci (±500 kb) are in purple. C. Chicago plot of association statistics ($-\log_{10}$ (*P* values)) for women on the positive *y-axis* and men on the negative *y-axis*. Previously identified loci are in blue. Novel associations identified in each stratified analysis are in red and are labeled with the nearest gene.



Supplementary Figure 4 | Regional association plots for European male-specific meta-analysis. A. Regional plots for novel loci. B. Regional plots for previously identified loci.

a

rs492400 – USP37 (European Men)



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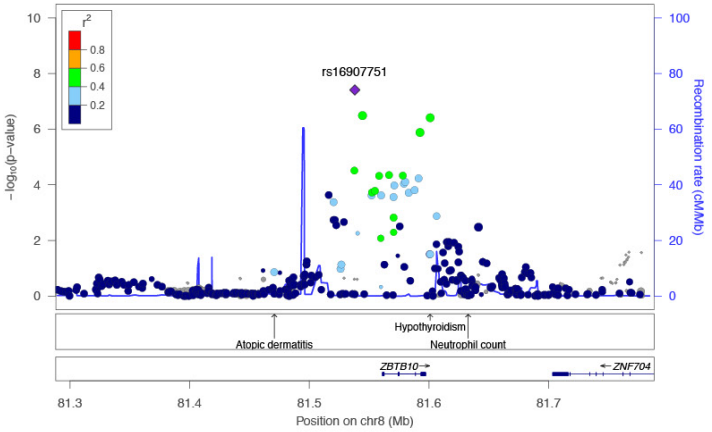

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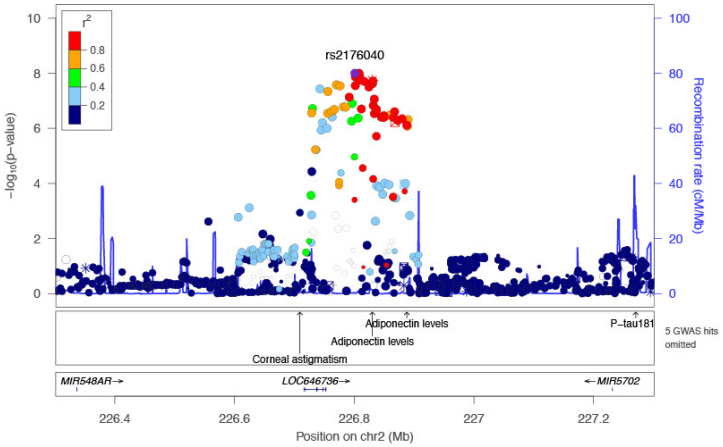
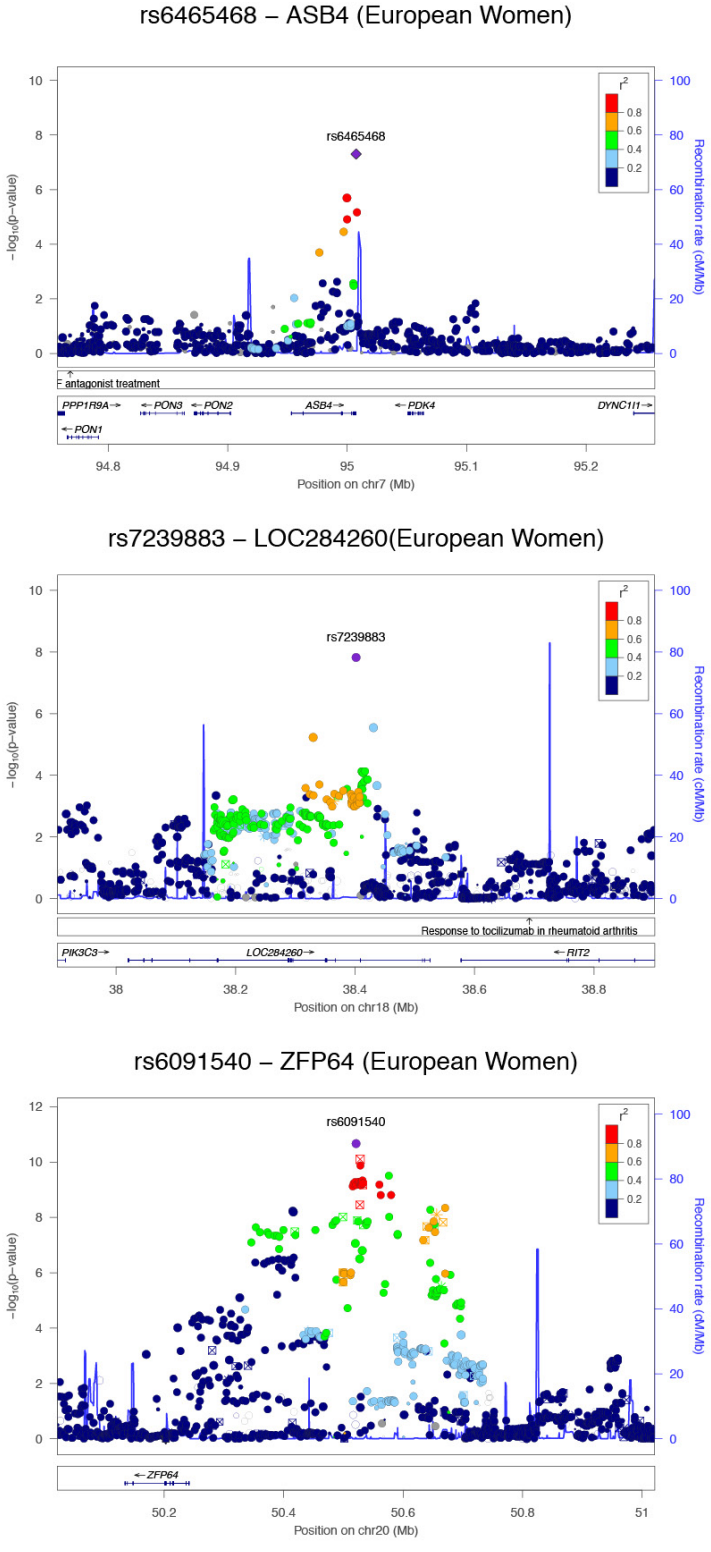
rs2176040 – LOC646736 (European Men)



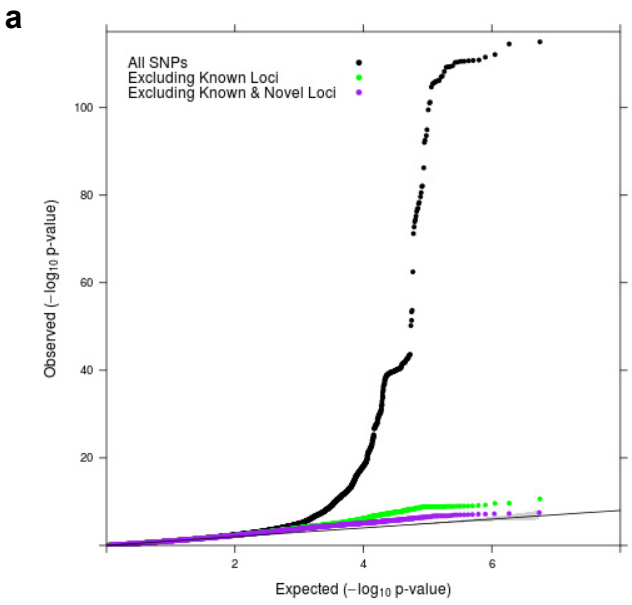
Supplementary Figure 5 | Regional association plots for European female-spcific meta-analysis. A. Regional plots for previously identified loci. B. Regional plots for novel loci.

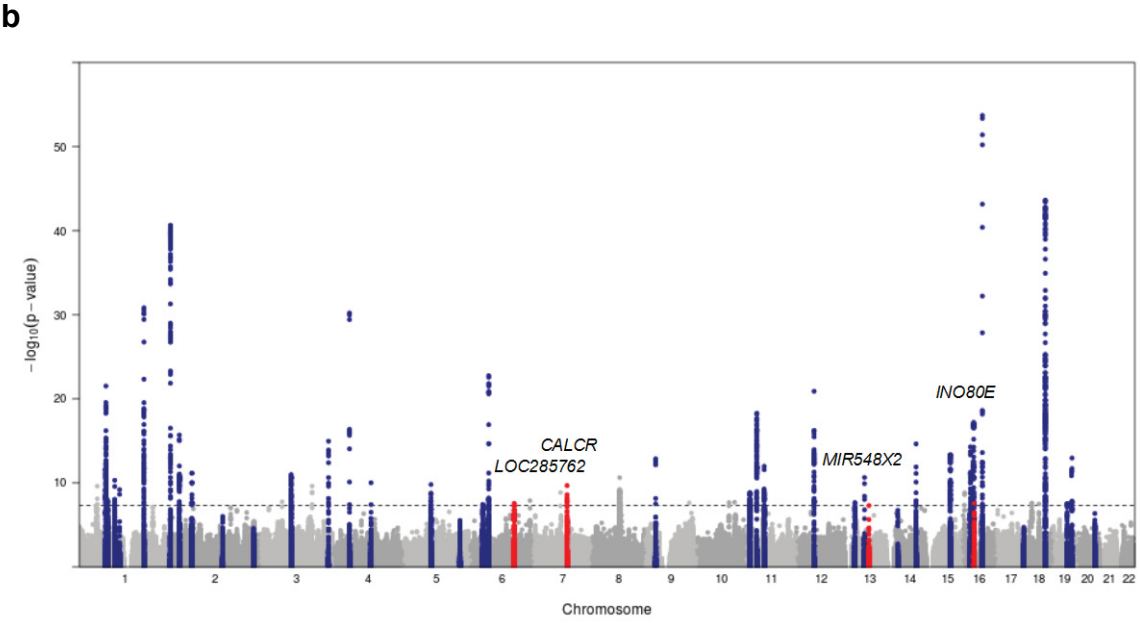
a



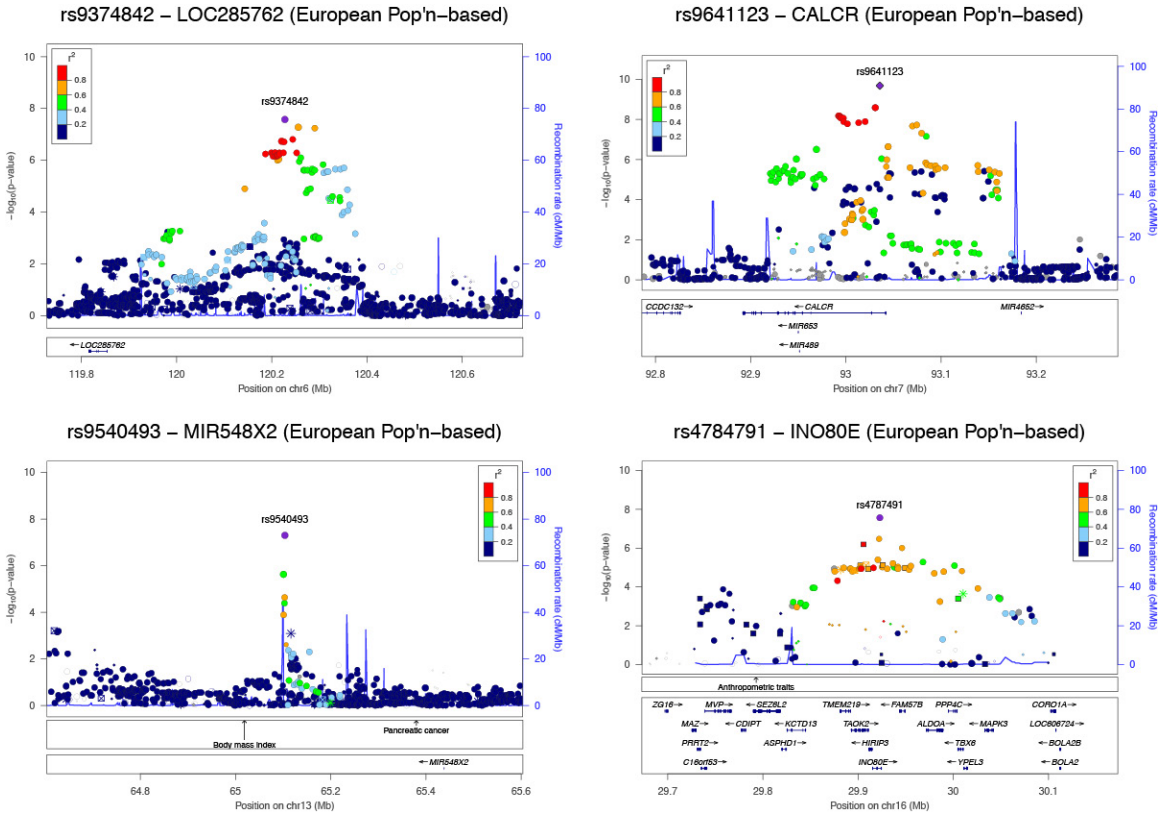
b

Supplementary Figure 6 | Summary plots of European population-based meta-analysis. A. Quantile-quantile of SNPs in meta-analysis. All SNPs are plotted in black, after excluding previously known loci (±500 kb) are in green, and after excluding previously known and novel loci (±500 kb) are in purple. B. Manhattan plot showing previously identified loci in blue and novel loci in red. Novel loci are labeled with the nearest gene.

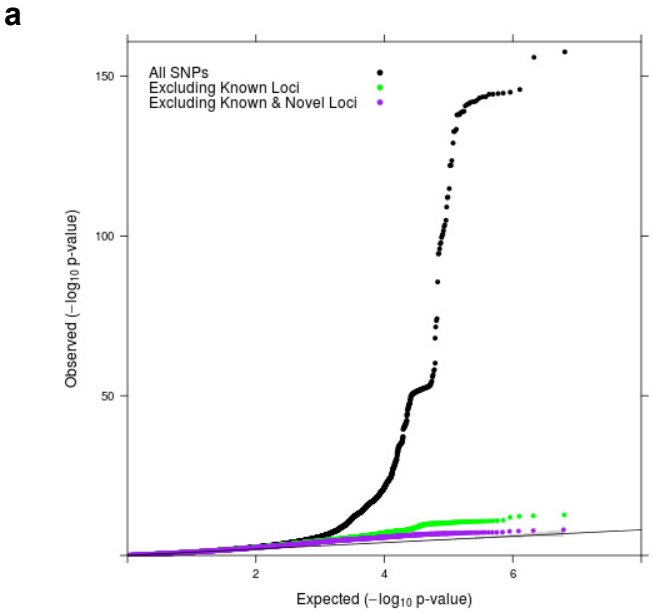


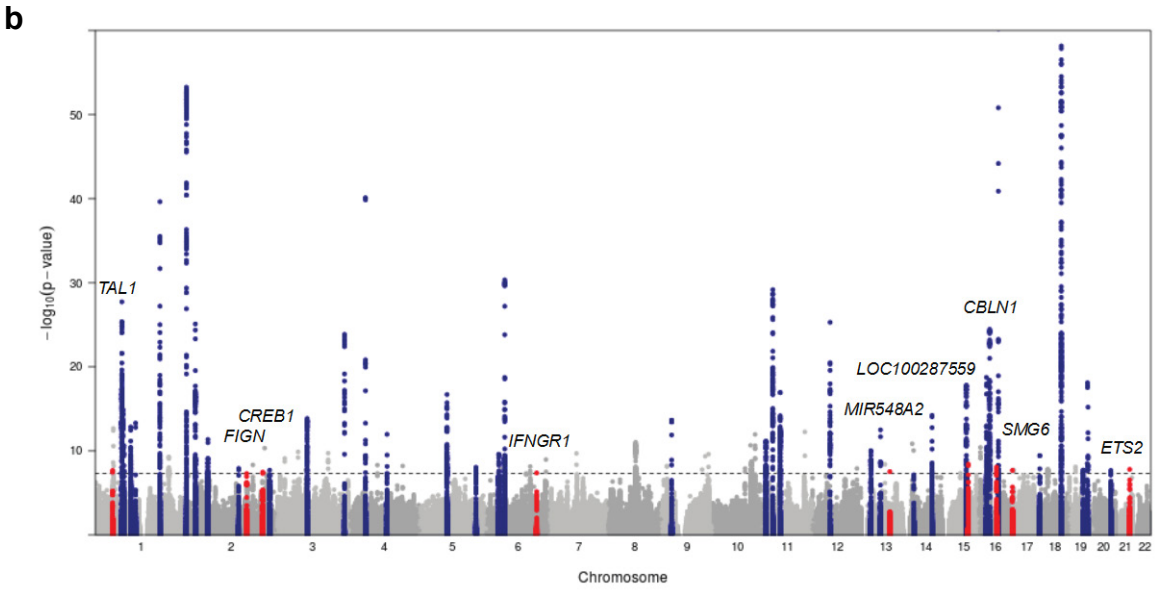


Supplementary Figure 7 | Regional association plots for European population-based meta-analysis. All are novel.

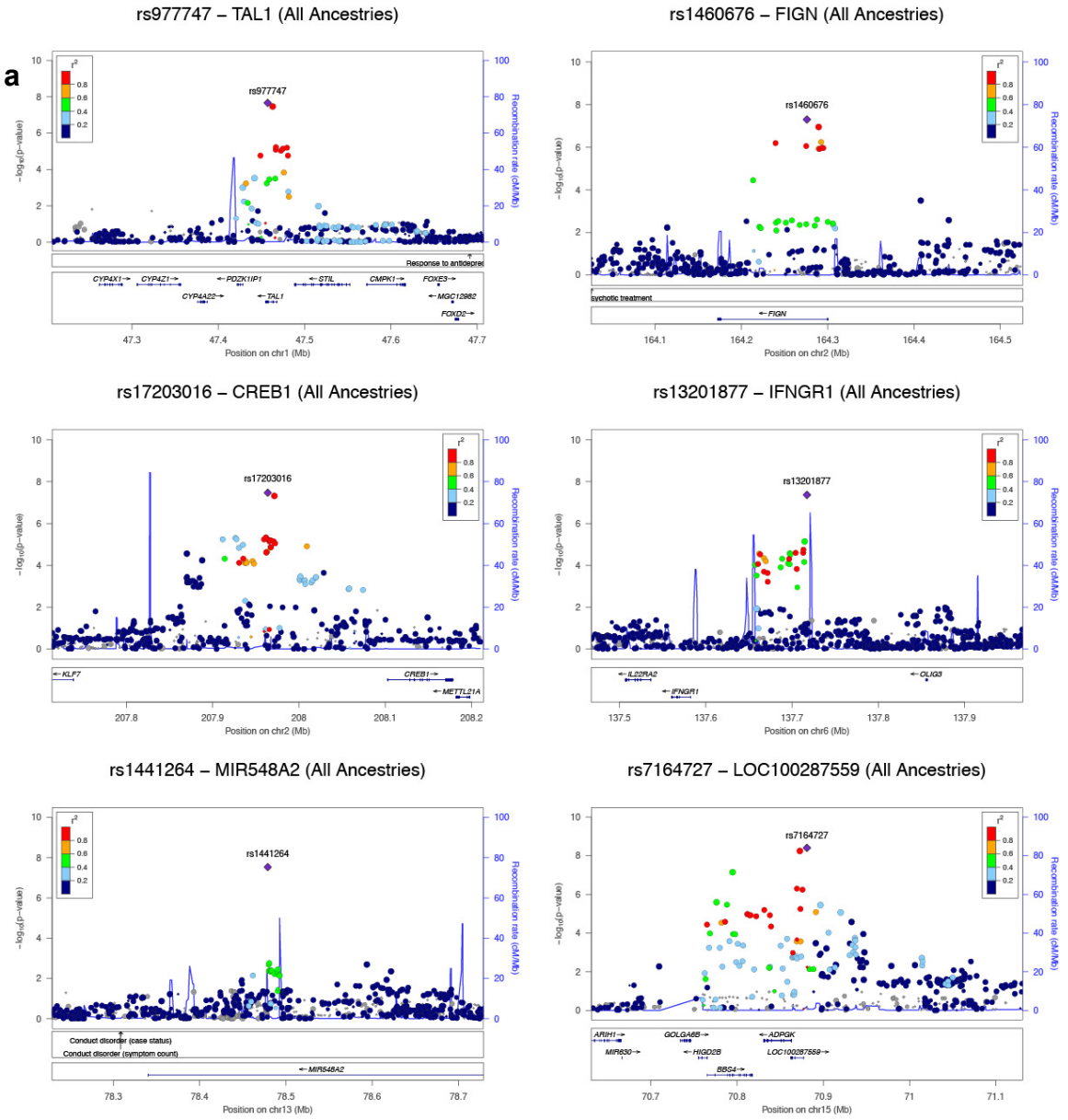


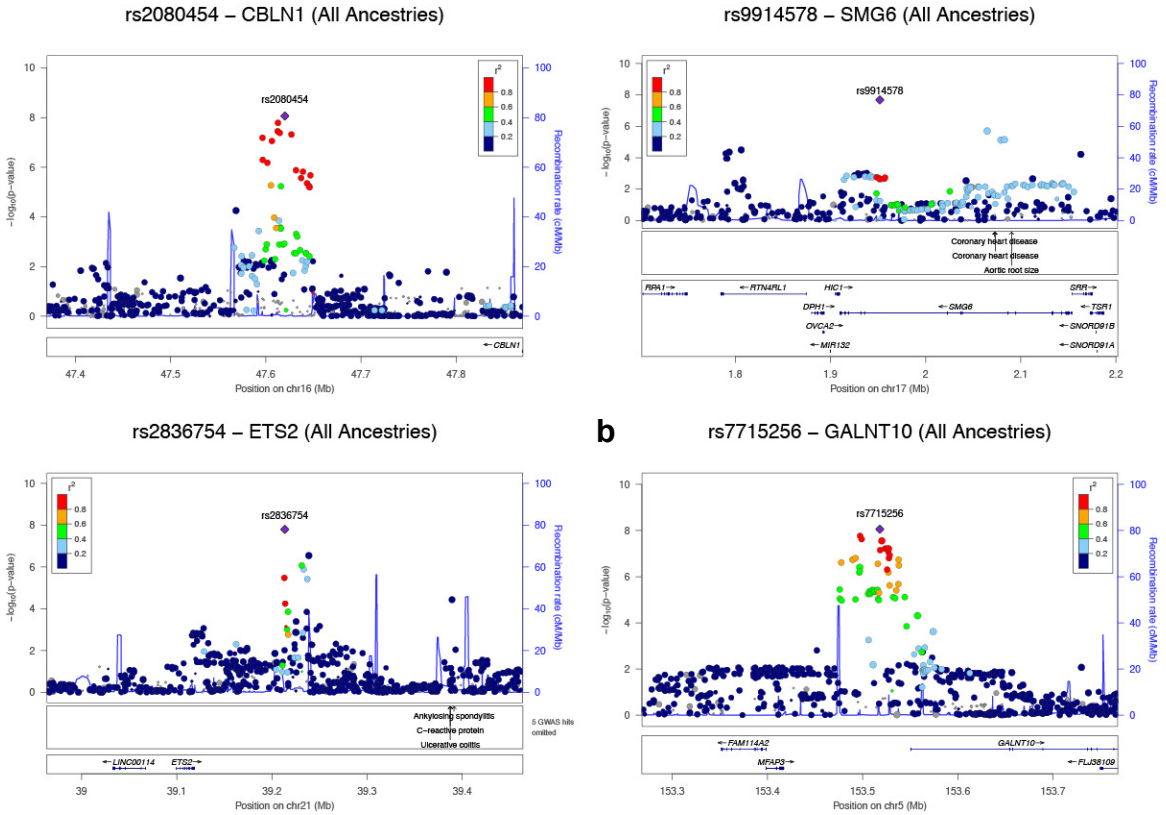
Supplementary Figure 8 | Summary plots of all ancestries sex-combined meta-analysis. A. Quantile-quantile plot of SNP associations. All SNPs are plotted in black, after excluding previously known loci (±500 kb) in green, and after excluding previously known and novel loci (±500 kb) in purple. B. Manhattan plot showing previously identified loci in blue and novel loci in red. Novel loci are labeled with the nearest gene, and the *y-axis* is truncated to allow easier observation of novel associations.





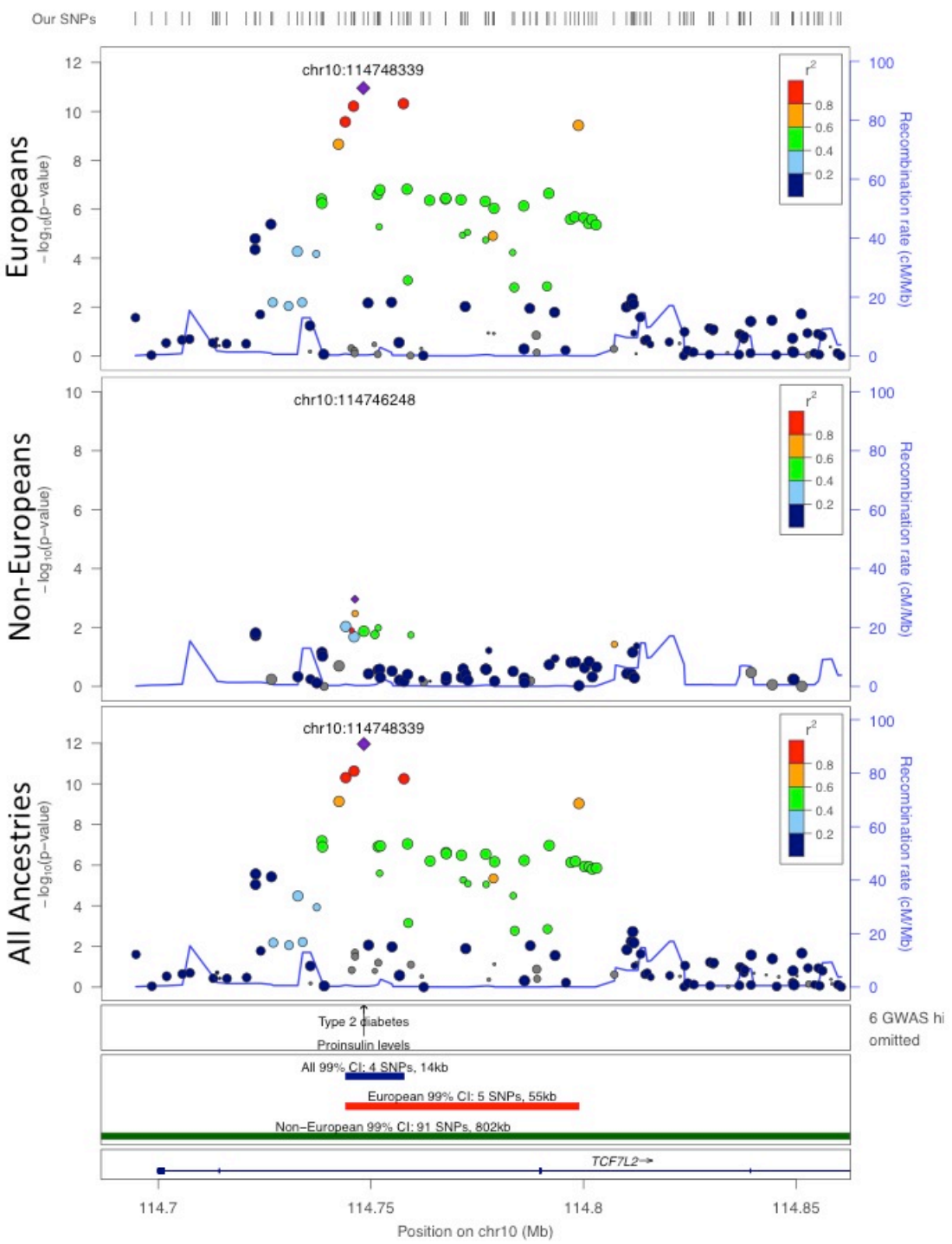
Supplementary Figure 9 | Regional association plots for all ancestries sex-combined meta-analysis. A. Regional plots for novel loci. B. Regional plots for previously identified loci.

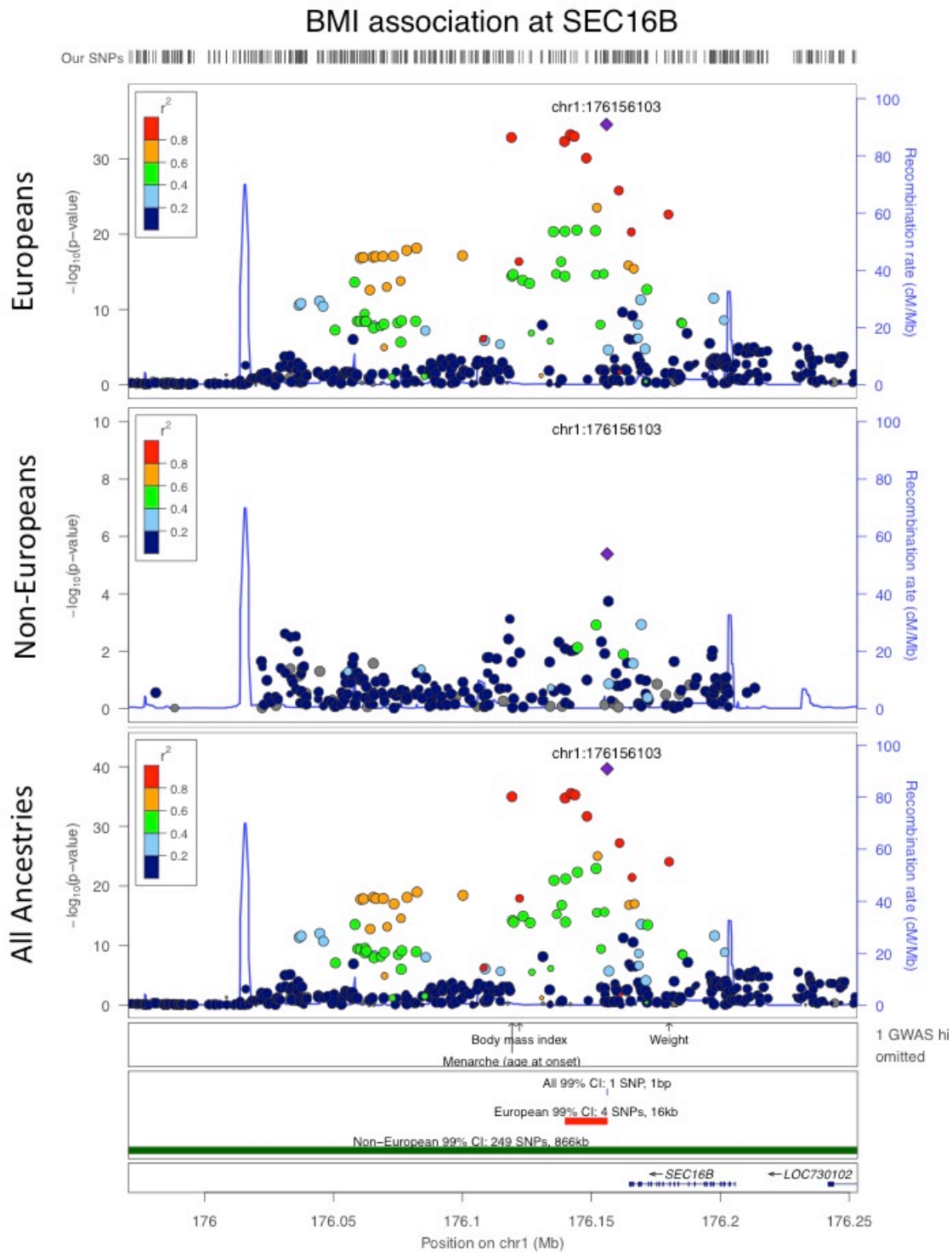



rs2080454 – CBLN1 (All Ancestries)
rs9914578 – SMG6 (All Ancestries)
rs2836754 – ETS2 (All Ancestries)
b
rs7715256 – GALNT10 (All Ancestries)
rs2080454
rs9914578
rs2836754
rs7715256
Position on chr16 (Mb)
Position on chr17 (Mb)
Position on chr21 (Mb)
Position on chr5 (Mb)
Recombination rate (cM/Mb)
Coronary heart disease
Coronary heart disease
Aortic root size
Ankylosing spondylitis
C−reactive protein
Ulcerative colitis
5 GWAS hits omitted
CBLN1
SMG6
ETS2
LINC00114
GALNT10
FAM114A2
MFAP3
FLJ38109

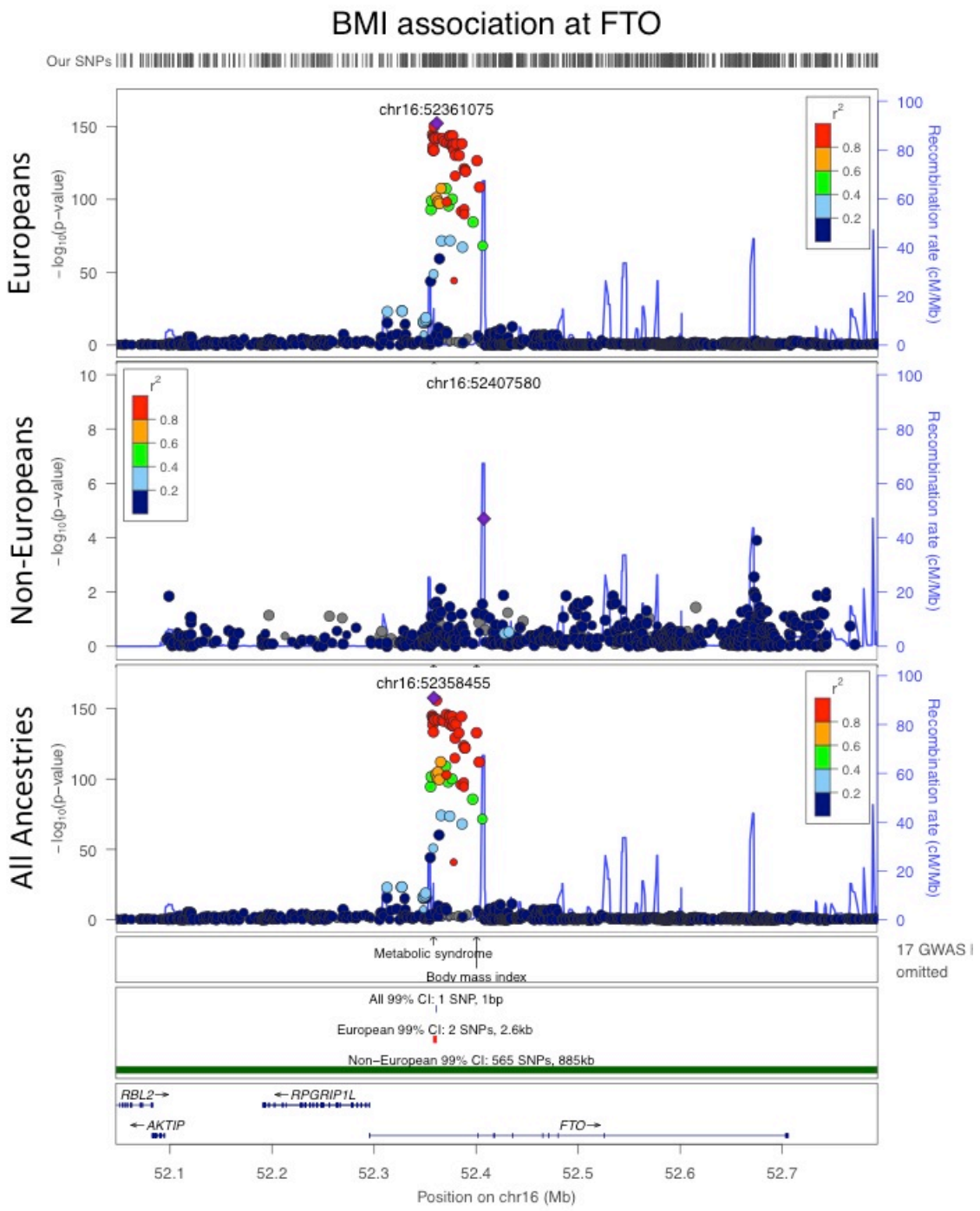
Supplementary Figure 10 | Regional plots showing fine mapping at three loci. Each plot shows the regional association plot for European sex-combined meta-analysis, non-European sex-combined meta-analysis, and all ancestries meta-analysis. The credible intervals for each analysis are plotted at the bottom (non-European in green, European in red, and all ancestries in blue), along with the length and number of SNPs in the credible set. LD for European and All Ancestries plots was calculated using 1000 Genomes CEU individiduals, while YRI samples were used to calculate LD in the non-European plots. A. Plots for *TCF7L2* region. B. Plots for *SEC16B* region. C. Plots for *FTO* region.

a


BMI association at TCF7L2
Our SNPs
Europeans
Non-Europeans
All Ancestries
chr10:114748339
chr10:114746248
chr10:114748339
Recombination rate (cM/Mb)
Type 2 diabetes
Proinsulin levels
All 99% CI: 4 SNPs, 14kb
European 99% CI: 5 SNPs, 55kb
Non−European 99% CI: 91 SNPs, 802kb
TCF7L2
114.7
114.75
114.8
114.85
Position on chr10 (Mb)
6 GWAS hi
omitted


BMI association at SEC16B
Our SNPs
Europeans
Non-Europeans
All Ancestries
chr1:176156103
r²
0.8
0.6
0.4
0.2
−log10(p−value)
Recombination rate (cM/Mb)
Body mass index
Weight
Menarche (age at onset)
1 GWAS hi
omitted
All 99% CI: 1 SNP, 1bp
European 99% CI: 4 SNPs, 16kb
Non−European 99% CI: 249 SNPs, 866kb
SEC16B
LOC730102
176
176.05
176.1
176.15
176.2
176.25
Position on chr1 (Mb)

c


BMI association at FTO
Our SNPs
Europeans
Non-Europeans
All Ancestries
chr16:52361075
chr16:52407580
chr16:52358455
r²
0.8
0.6
0.4
0.2
− log10(p−value)
Recombination rate (cM/Mb)
Metabolic syndrome
Body mass index
17 GWAS I
omitted
All 99% CI: 1 SNP, 1bp
European 99% CI: 2 SNPs, 2.6kb
Non−European 99% CI: 565 SNPs, 885kb
RBL2→
←RPGRIP1L
←AKTIP
FTO→
52.1
52.2
52.3
52.4
52.5
52.6
52.7
Position on chr16 (Mb)

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