## 1. Supplementary Figures

**Supplementary Figure 1.** European sex-combined meta-analysis summary  
A. Quantile-quantile plot  
B. Manhattan plot  

**Supplementary Figure 2.** Regional association plots from European sex-combined meta-analysis  
A. Novel loci  
B. Previously identified loci  

**Supplementary Figure 3.** European sex-stratified meta-analysis summaries  
A. Quantile-quantile plot from European women-only meta-analysis  
B. Quantile-quantile plot from European men-only meta-analysis  
C. Chicago plot  

**Supplementary Figure 4.** Regional association plots from European men meta-analysis  
A. Novel loci  
B. Previously identified loci  

**Supplementary Figure 5.** Regional association plots from European women meta-analysis  
A. Novel loci  
B. Previously identified loci  

**Supplementary Figure 6.** European population-based meta-analysis summary  
A. Quantile-quantile plot  
B. Manhattan plot  

**Supplementary Figure 7.** Regional association plots from European population-based meta-analysis  
A. Novel loci  
B. Previously identified loci  

**Supplementary Figure 8.** All ancestries meta-analysis summary  
A. Quantile-quantile plot  
B. Manhattan plot  

**Supplementary Figure 9.** Regional association plots from all ancestries meta-analysis  
A. Novel loci  
B. Previously identified loci  

**Supplementary Figure 10.** Regional association plots showing cross-ancestry fine mapping at three loci.  
A. TCF7L2 locus  
B. SEC16B locus  
C. FTO locus
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.
Supplementary Figure 3 | Summary plots of European Sex-specific meta-analyses. A. Quantile-quantile plot of SNP associations for female-specific meta-analysis. 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 (-log₁₀ (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)

**b**

rs16907751 – ZBTB10 (European Men)

rs2176040 – LOC646736 (European Men)
Supplementary Figure 5 | Regional association plots for European female-specific meta-analysis. A. Regional plots for previously identified loci. B. Regional plots for novel loci.
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.
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 individuals, 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.
BMI association at TCF7L2

European 

- log10(p-value)

Non-European

- log10(p-value)

All Ancestries

- log10(p-value)

chr10:114748339

chr10:114748248

chr10:114748339

Type 2 diabetes
Protein levels

At 95% CI 6 SNPs, 144b
European 95% CI 5 SNPs, 864a
Non-European 95% CI 31 SNPs, 692b

Position on chr10 (Mb)
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