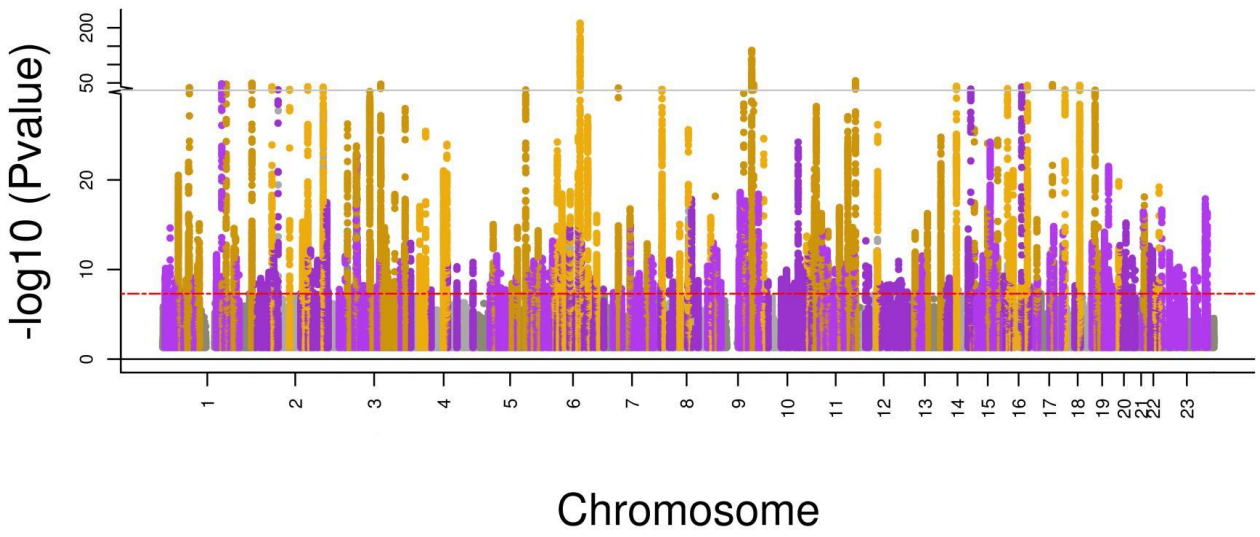
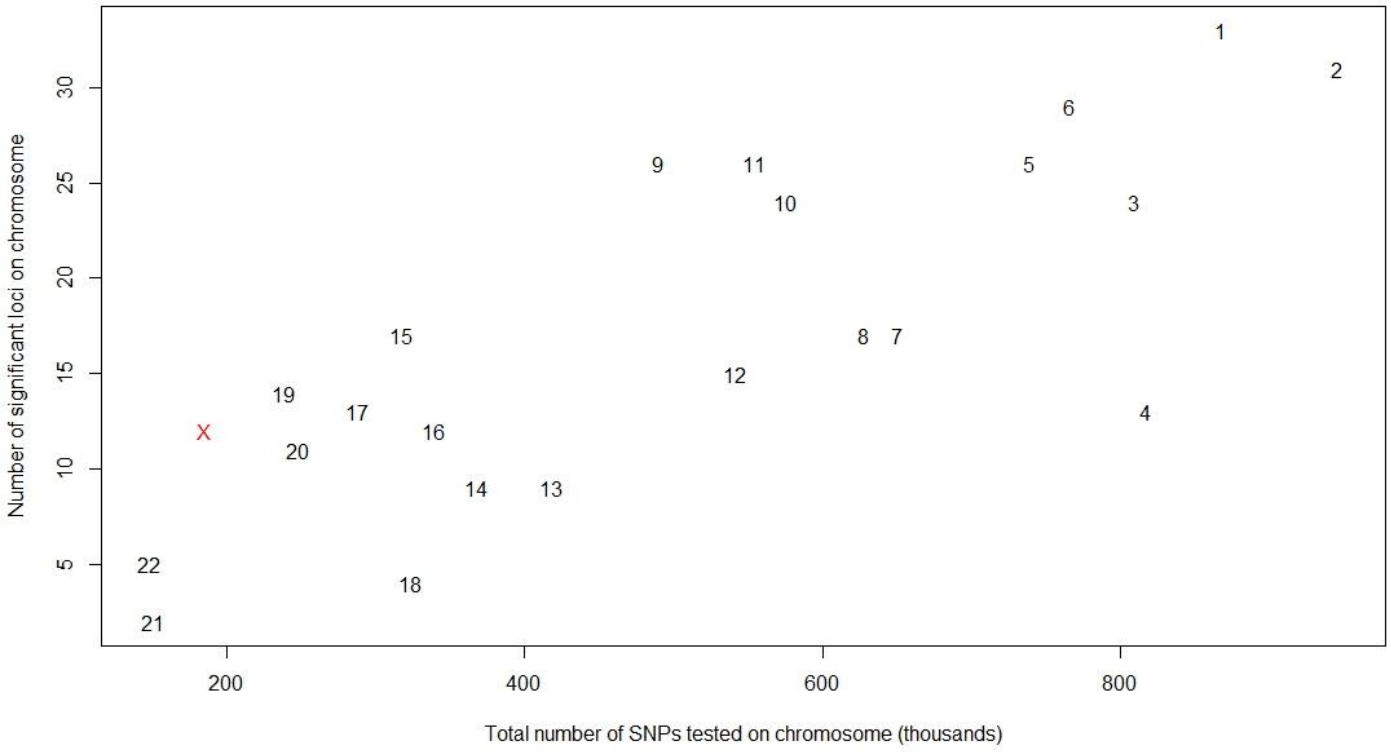


Supplementary Figure 1

Manhattan plot displaying the genomic locations of the 389 genome-wide significant loci.

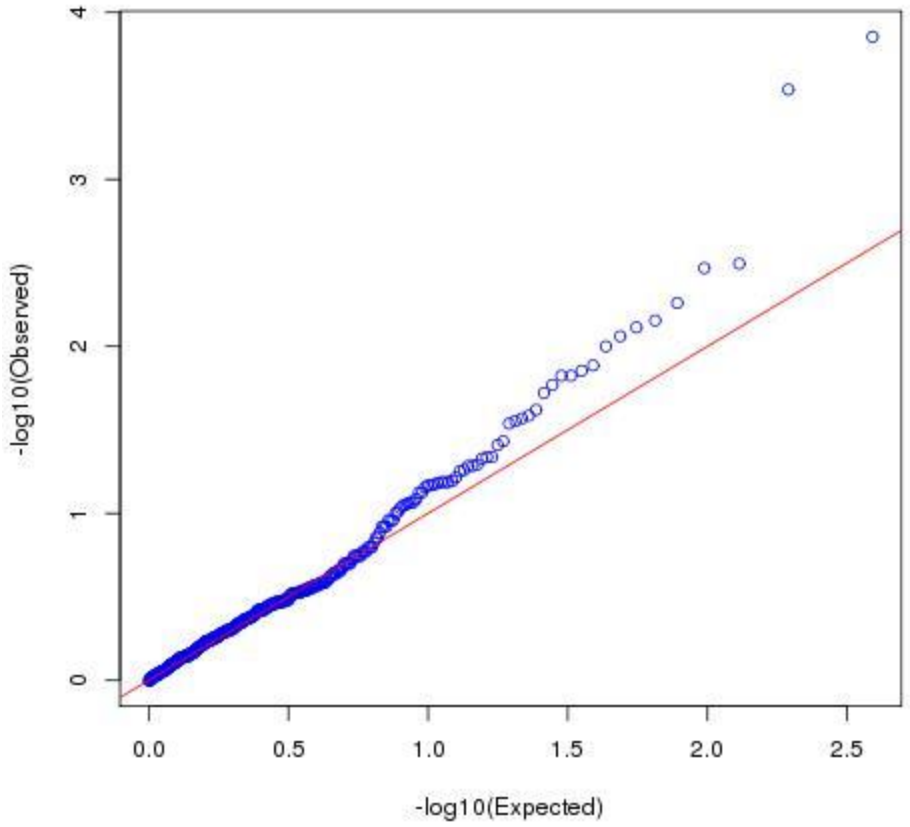
Previously identified genome-wide significant loci are shown in gold, and new loci are shown in purple. SNPs within 300 kb of the lead SNP at each locus are highlighted. The y axis has been truncated above 30.



Supplementary Figure 2

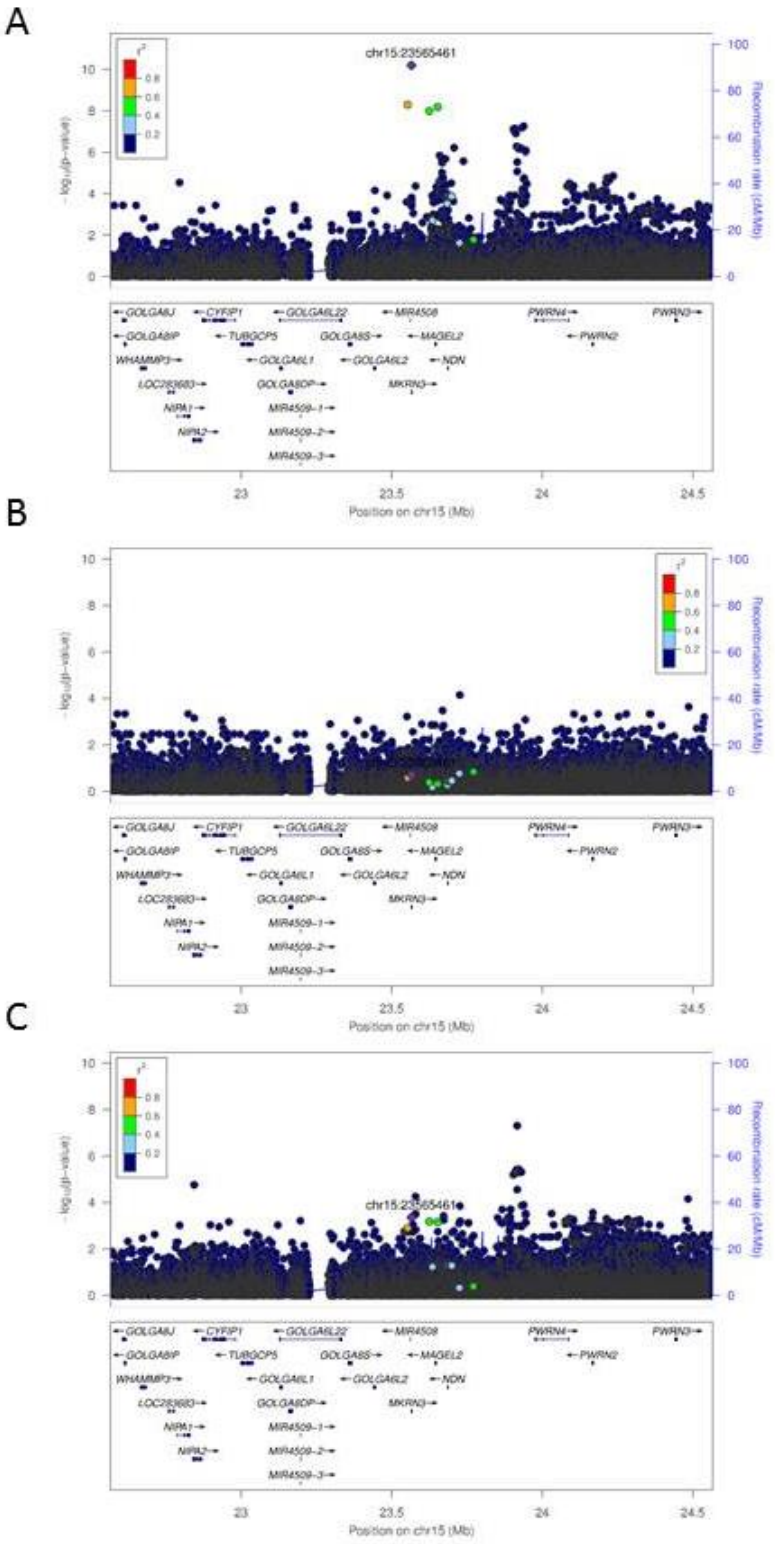
Number of genome-wide significant menarche loci per chromosome by chromosome size.

The X chromosome is highlighted in red.



Supplementary Figure 3

Quantile–quantile plot of heterogeneity *P* values between maternal and paternal parent-of-origin association testing for all 389 index variants.

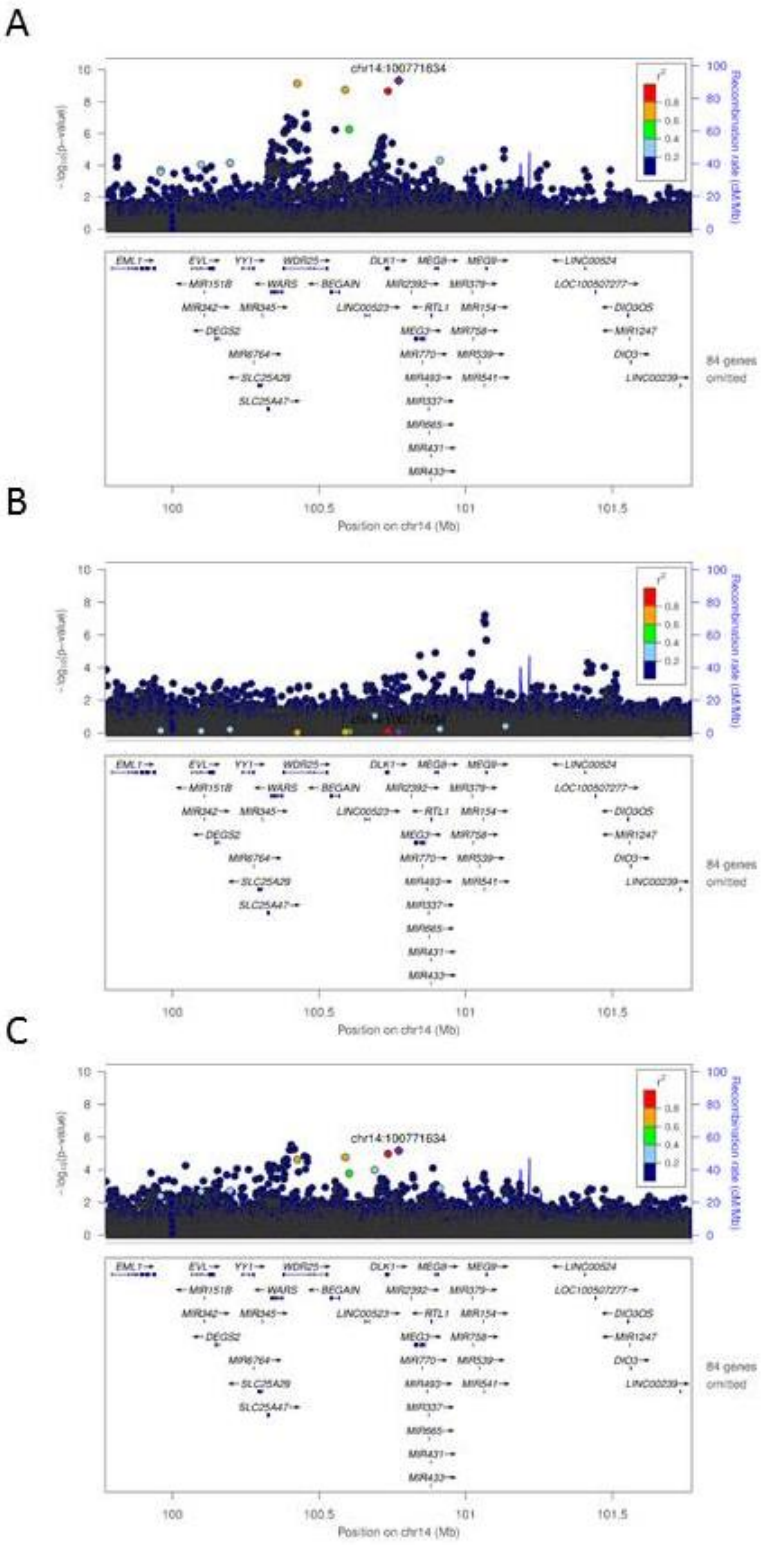


Supplementary Figure 4

LocusZoom plots of menarche-associated variants at the *MKRN3* locus (hg38) in the deCODE study, Iceland.

The 5′ UTR variant rs530324840 at position chr15:23565461 is labeled as a diamond and shown in purple; other variants are colored

according to correlation (r^2) with rs530324840 (see legends). $-\log_{10}$ *P* values are shown along the left *y* axis, and the right *y* axis corresponds to recombination rate, plotted as a solid gray line. (**a**) Associations under the paternal model, where the signal near 24 Mb corresponds to the common reported variant rs12148769. (**b**) Associations under the maternal model. (**c**) Associations under the additive model.

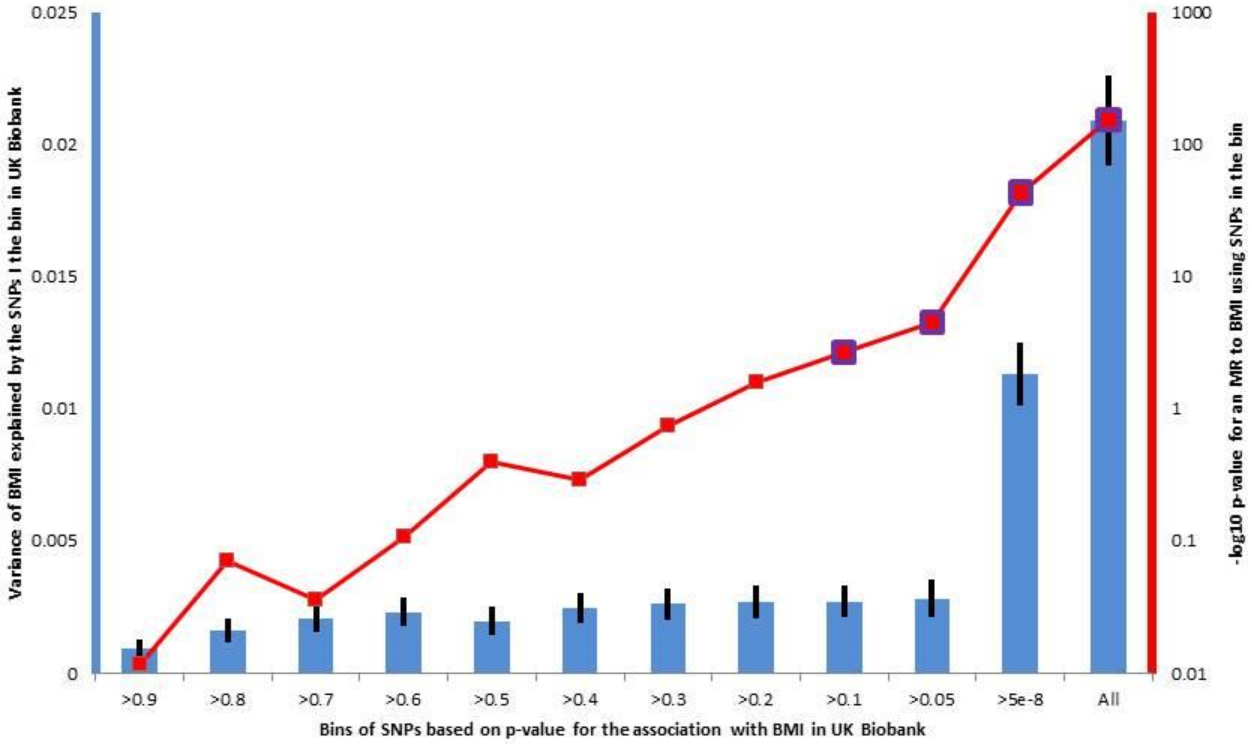


Supplementary Figure 5

LocusZoom plots of menarche-associated variants at the *DLK1* locus (hg38) in the deCODE study, Iceland.

The variant rs138827001 at position chr14:100771634 is labeled as a diamond and shown in purple; other variants are colored

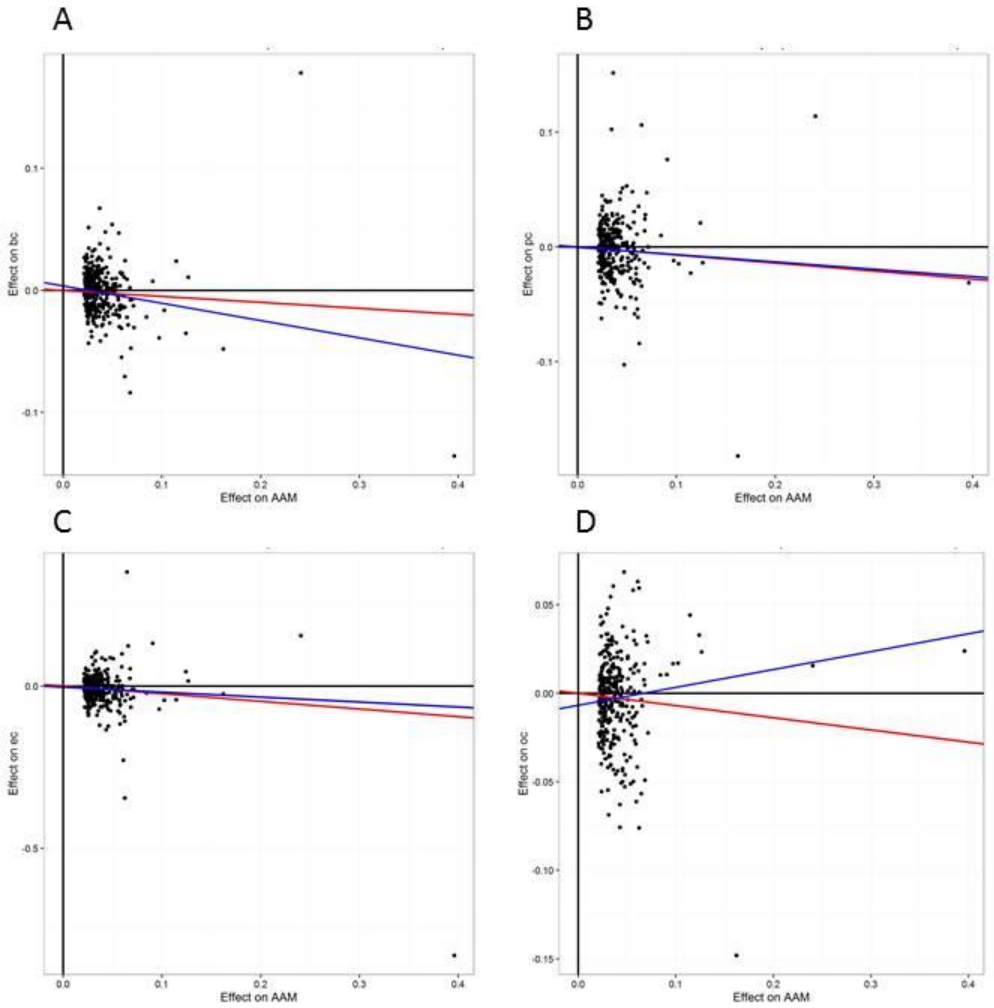
according to correlation (r^2) with rs138827001 (see legends). $-\log_{10}$ *P* values are shown along the left *y* axis, and the right *y* axis corresponds to recombination rate, plotted as a solid gray line. (**a**) Associations under the paternal model. (**b**) Associations under the maternal model. (**c**) Associations under the additive model.



Supplementary Figure 6

Association of menarche-associated variants with adult body mass index.

The blue bars (and left *y* axis) indicate the collective variance explained in adult BMI (with bootstrap-generated 95% CIs) by index menarche-associated SNPs grouped by their individual associations with BMI (in UK Biobank using an additive model controlling for chip and principal components). The red line (and right *y* axis) indicates the $-\log_{10} P$ value for the collective association with BMI of each group of SNPs. Purple squares correspond to collective associations with BMI at $P < 0.05$.



Supplementary Figure 7

Dose-response plots for Mendelian randomization analyses.

(**a**–**d**) The individual effects on AAM of the 314 'BMI-unrelated' autosomal AAM variants are plotted against risks for breast (**a**), prostate (**b**), endometrial (**c**) and ovarian (**d**) cancer. Red line, IVW regression; blue line, MR-Egger regression. MR-Egger supports the protective effect of later age at puberty on breast, prostate and endometrial cancers, but indicates pleiotropy in the association with ovarian cancer.

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ALSPAC	“We are extremely grateful to all the families who took part in this study, the midwives for their help in	The UK Medical Research Council and the Wellcome Trust (Grant ref:

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