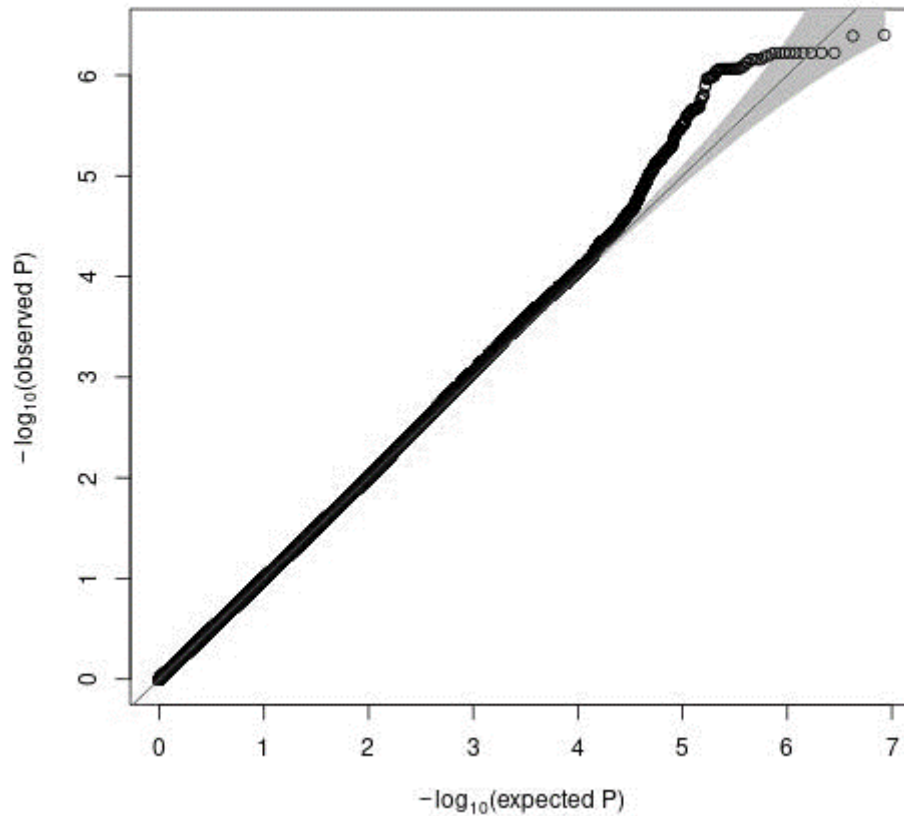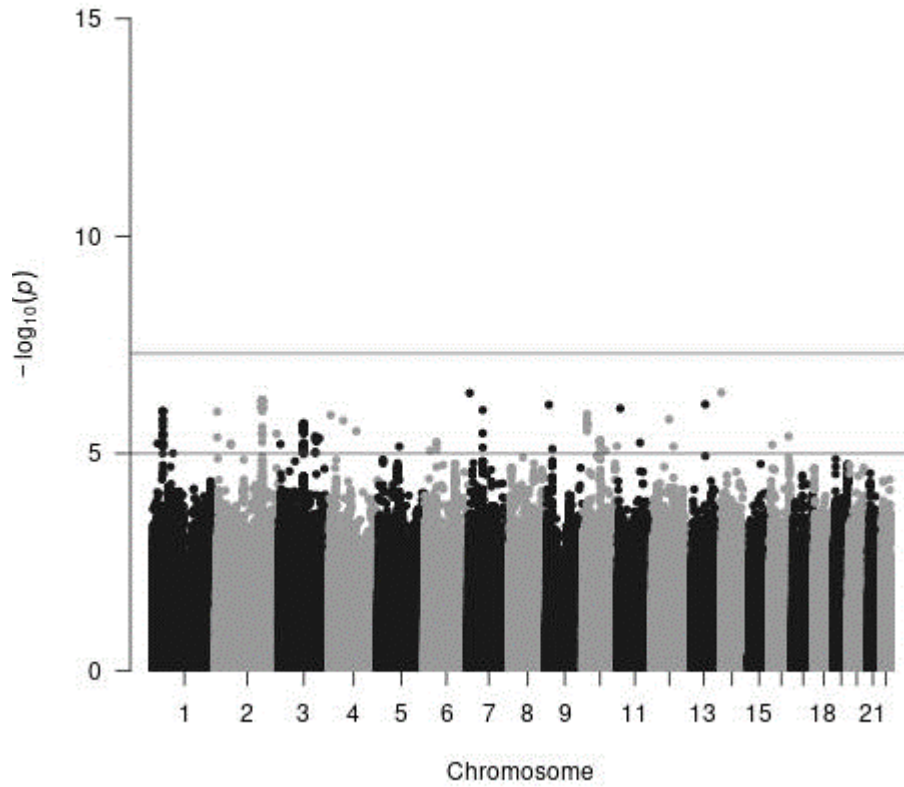**Supplementary Figures**

Figure S1

A quantile-quantile plot (black) for the sex-stratified GWAS of meat intake (g/1000 kcal/d) in men. The x-axis shows the expected -log10 P-values under the null hypothesis. The y-axis expresses the observed -log10 P-values obtained by a linear regression model using PLINK [27, 28]. The line represents y = x, which corresponds to the null hypothesis. The gray shaded area expresses the 95% confidence interval of the null hypothesis. The inflation factor (λ) is the median of the observed test statistics divided by the median of the expected test statistics. An R package for creating the Q-Q plot, GWASTools was used [37]. Chromosomal position (GRCh37/hg19)
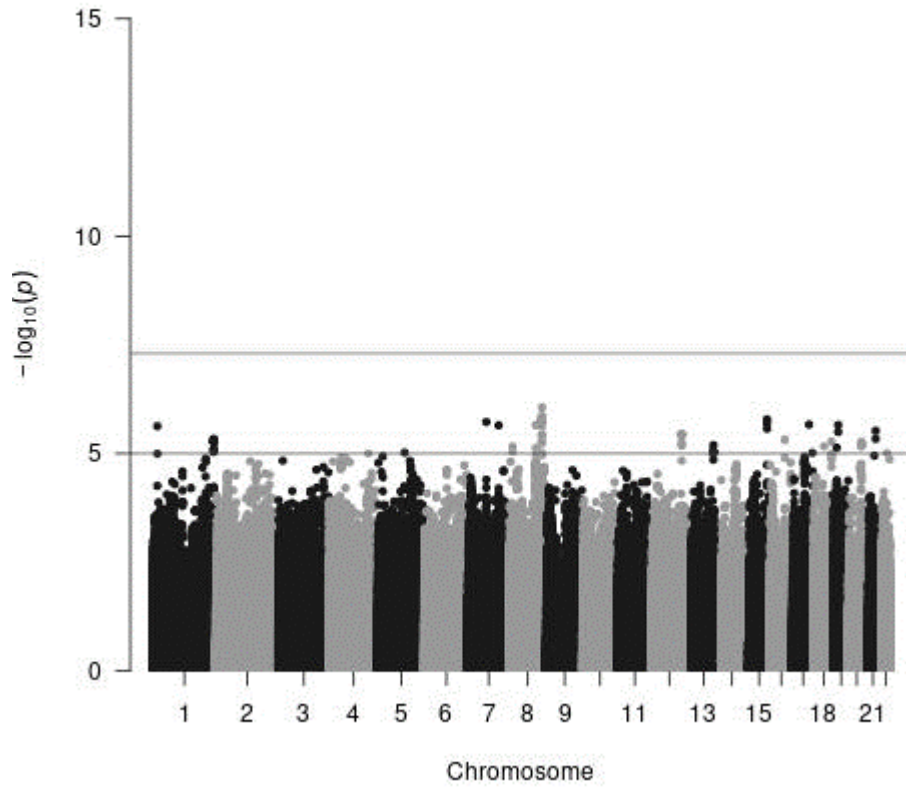
Figure S2

A Manhattan plot of the results from the sex-stratified GWAS of meat intake (g/1000 kcal/d) in men. The x-axis indicates chromosomal positions and the y-axis represents –log10 P-values obtained by linear model association analysis. The software qqman was used [38].

Chromosomal position (GRCh37/hg19).

Figure S3
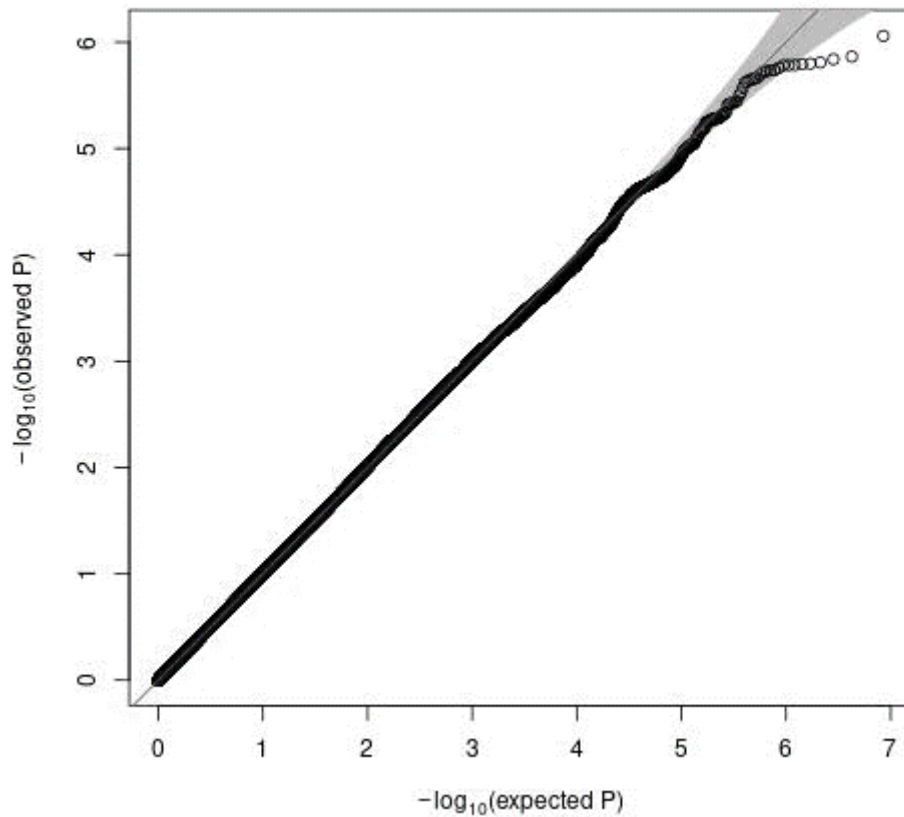
A quantile-quantile plot (black) for the GWAS by a logistic analysis of meat intake (high vs low). The x-axis shows the expected -log10 P-values under the null hypothesis. The y-axis expresses the observed -log10 P-values obtained by a linear regression model using PLINK [27, 28]. The line represents $y = x$, which corresponds to the null hypothesis. The gray shaded area expresses the 95% confidence interval of the null hypothesis. The inflation factor (λ) is the median of the observed test statistics divided by the median of the expected test statistics. An R package for creating the Q-Q plot, GWASTools was used [37]. Chromosomal position (GRCh37/hg19)
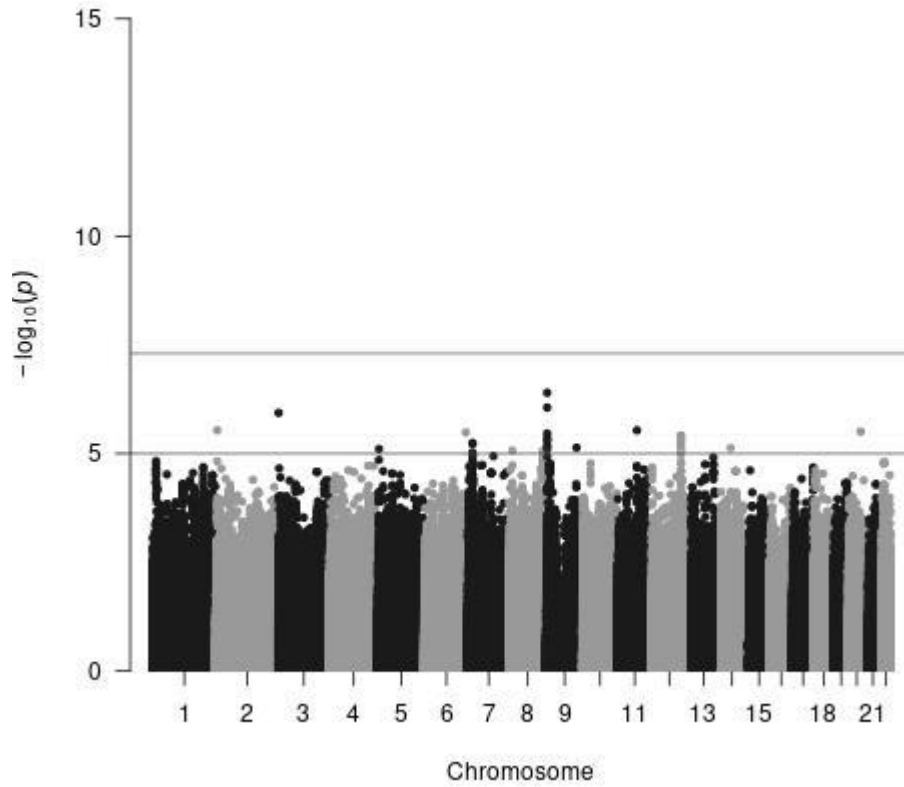
Figure S4

A Manhattan plot of the results from the GWAS by a logistic analysis of meat intake (high vs low). The x-axis indicates chromosomal positions and the y-axis represents –log10 P-values obtained by linear model association analysis. The software qqman was used [38].
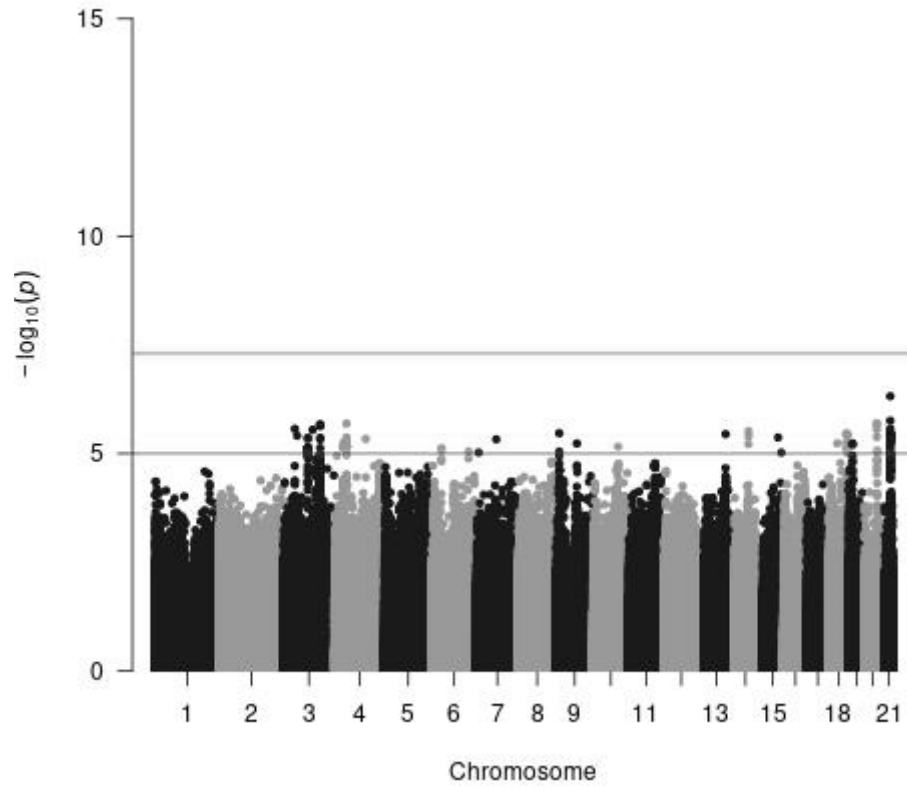
Chromosomal position (GRCh37/hg19).

Figure S5

A Manhattan plot of the results from the GWAS by sex-stratified logistic analysis of meat intake (high vs low) in men. The x-axis indicates chromosomal positions and the y-axis represents –log10 P-values obtained by linear model association analysis. The software qqman was used [38]. Chromosomal position (GRCh37/hg19).

Figure S6

A Manhattan plot of the results from the GWAS by sex-stratified logistic analysis of meat intake (high vs low) in women. The x-axis indicates chromosomal positions and the y-axis represents –log10 P-values obtained by linear model association analysis. The software qqman was used [38]. Chromosomal position (GRCh37/hg19).