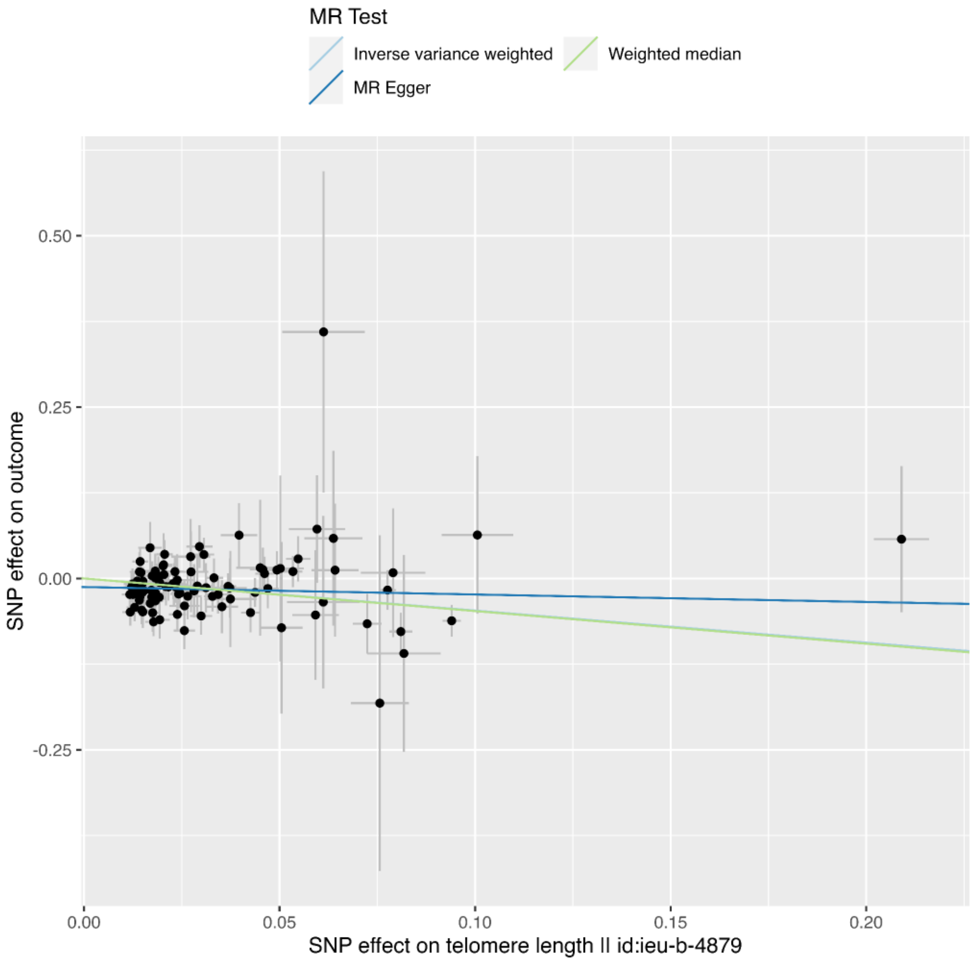
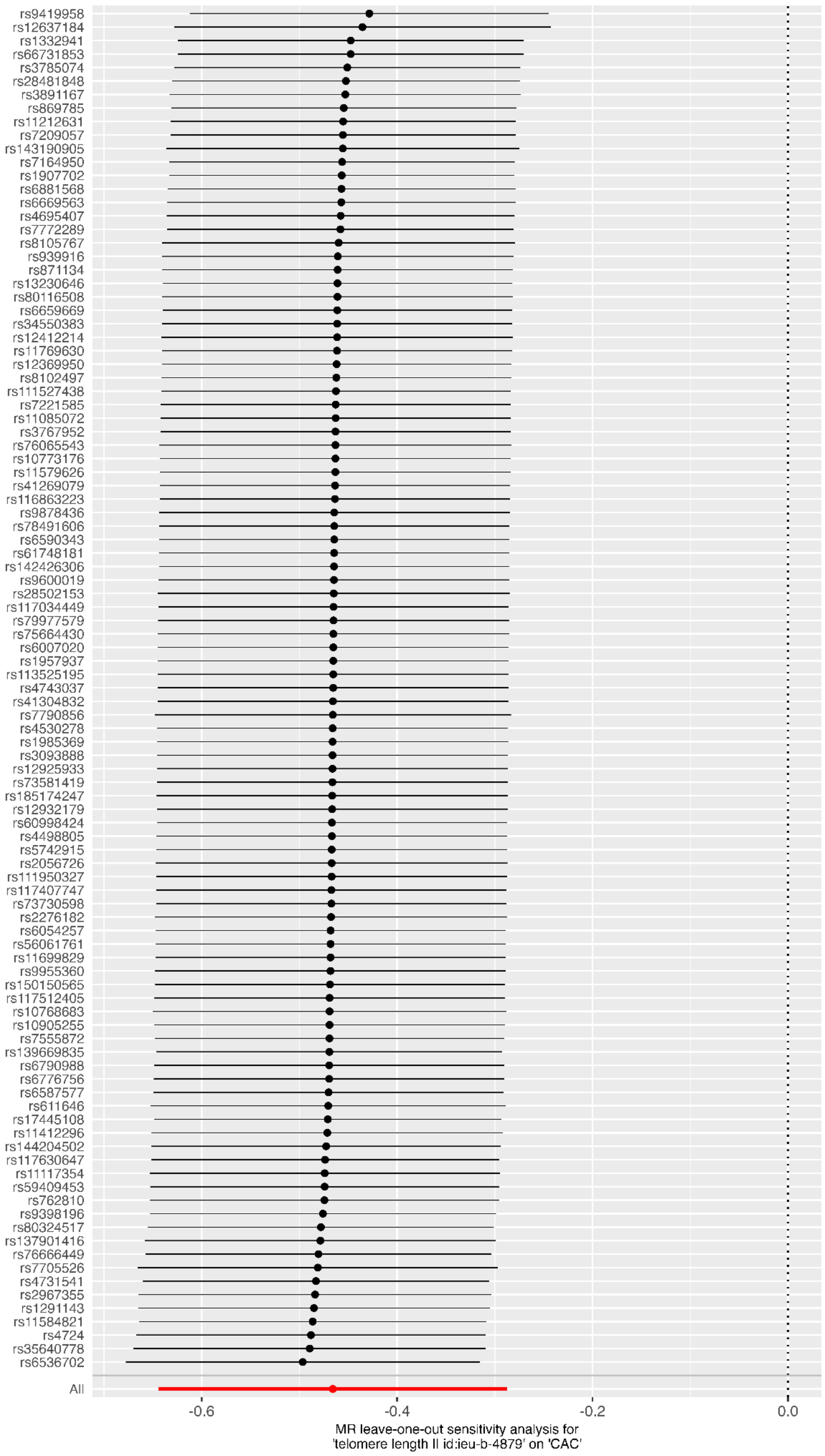


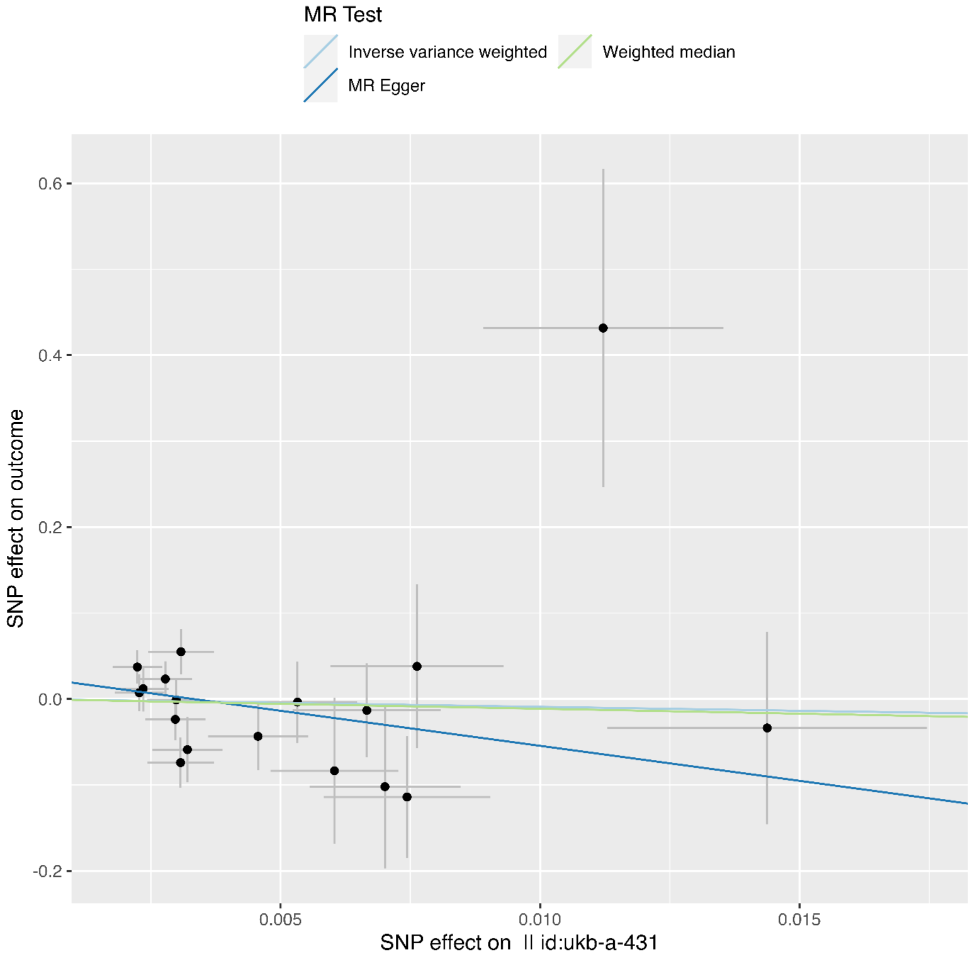
Supplementary Figure S1. Associations between SNPs correlated to TL and CAC (initial analysis)

Each genetic variant included in the analysis is represented as a point + 95% CI. Location on the horizontal axis represents the correlation between the variant and exposure; location on the vertical axis represents the correlation between the variant and the outcome. Lines represent estimates of different MR methods.
Abbreviation: MR, Mendelian Randomization; SNP, Single Nucleotide Polymorphism



Supplementary Figure S2. Leave-one-out analysis for TL and CAC (initial analysis)

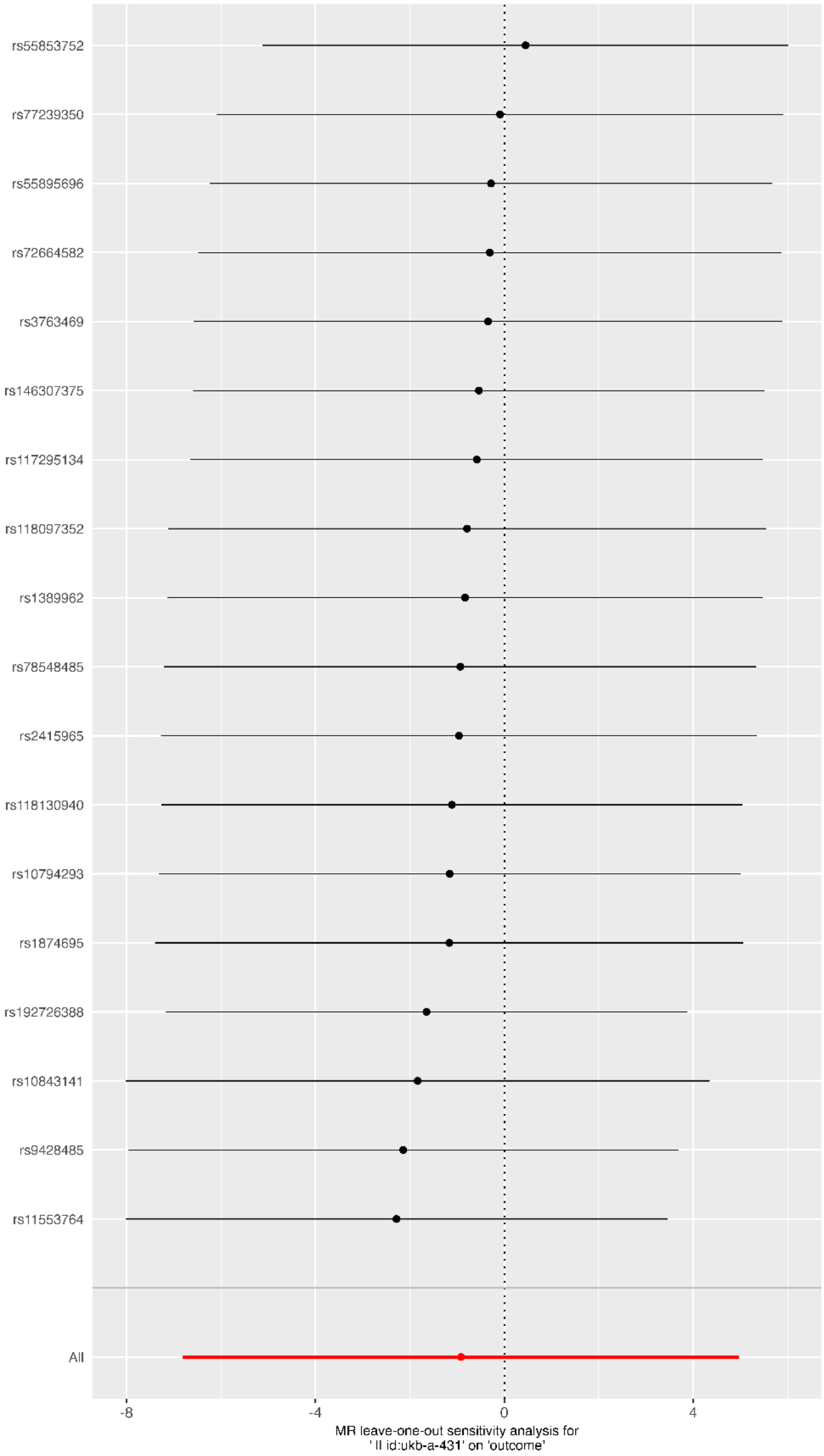
Horizontal axis—inverse-variance weighted-mean estimate with 95% confidence intervals of genetic associations between exposure and outcome. Each dot and confidence interval represents an inverse-variance weighted mean obtained when a variant listed on the left side is removed from the analysis.



Supplementary Figure S3. Associations between SNPs correlated to loose teeth and CAC

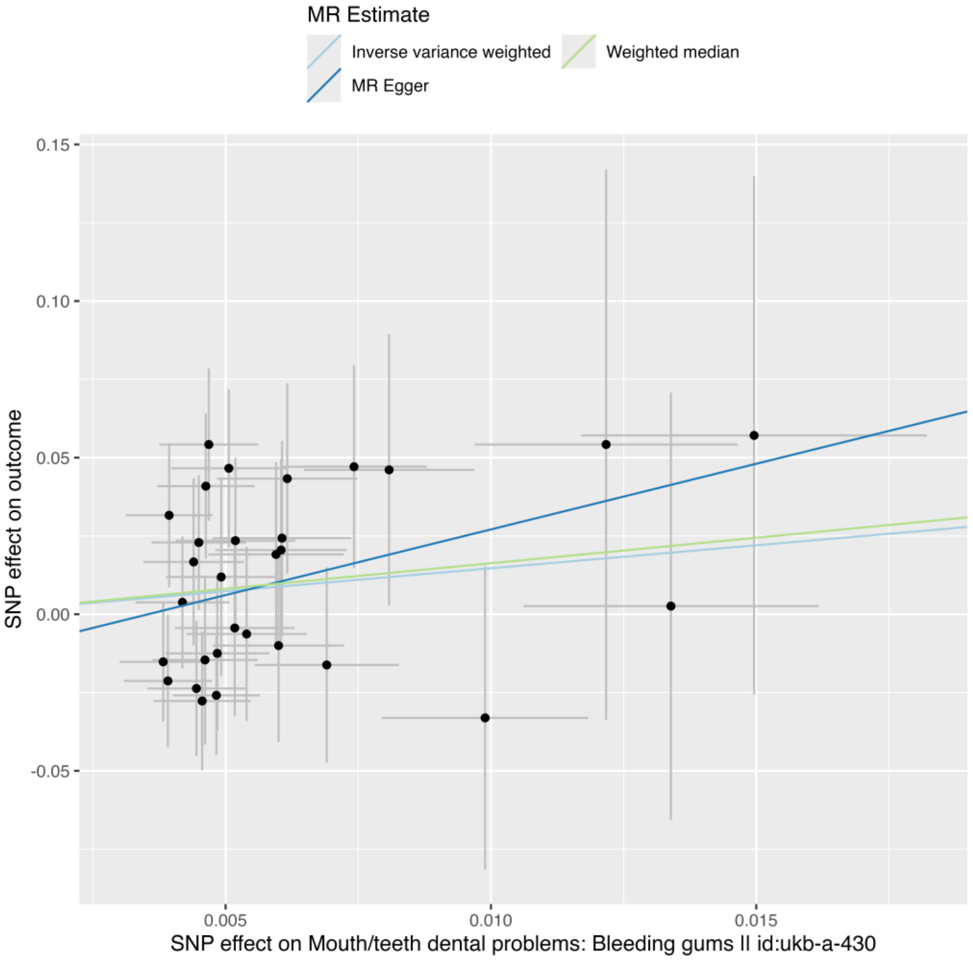
Each genetic variant included in the analysis is represented as a point + 95% CI. Location on the horizontal axis represents the correlation between the variant and exposure; location on the vertical axis represents the correlation between the variant and the outcome. Lines represent estimates of different MR methods.

Abbreviation: MR, Mendelian Randomization; SNP, Single Nucleotide Polymorphism



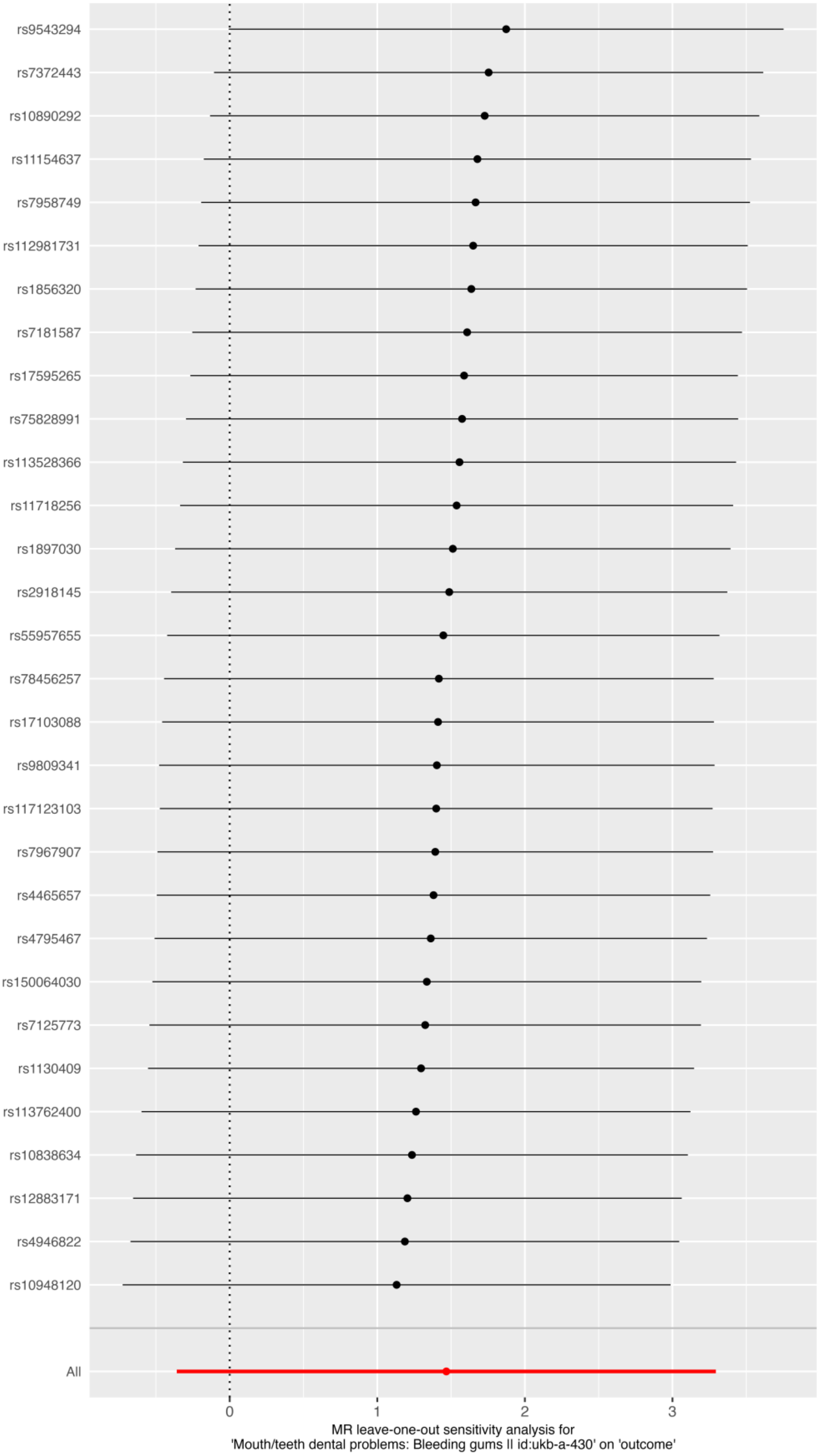
Supplementary Figure S4. Leave-one-out analysis for loose teeth and CAC

Horizontal axis—inverse-variance weighted-mean estimate with 95% confidence intervals of genetic associations between exposure and outcome. Each dot and confidence interval represents an inverse-variance weighted mean obtained when a variant listed on the left side is removed from the analysis.



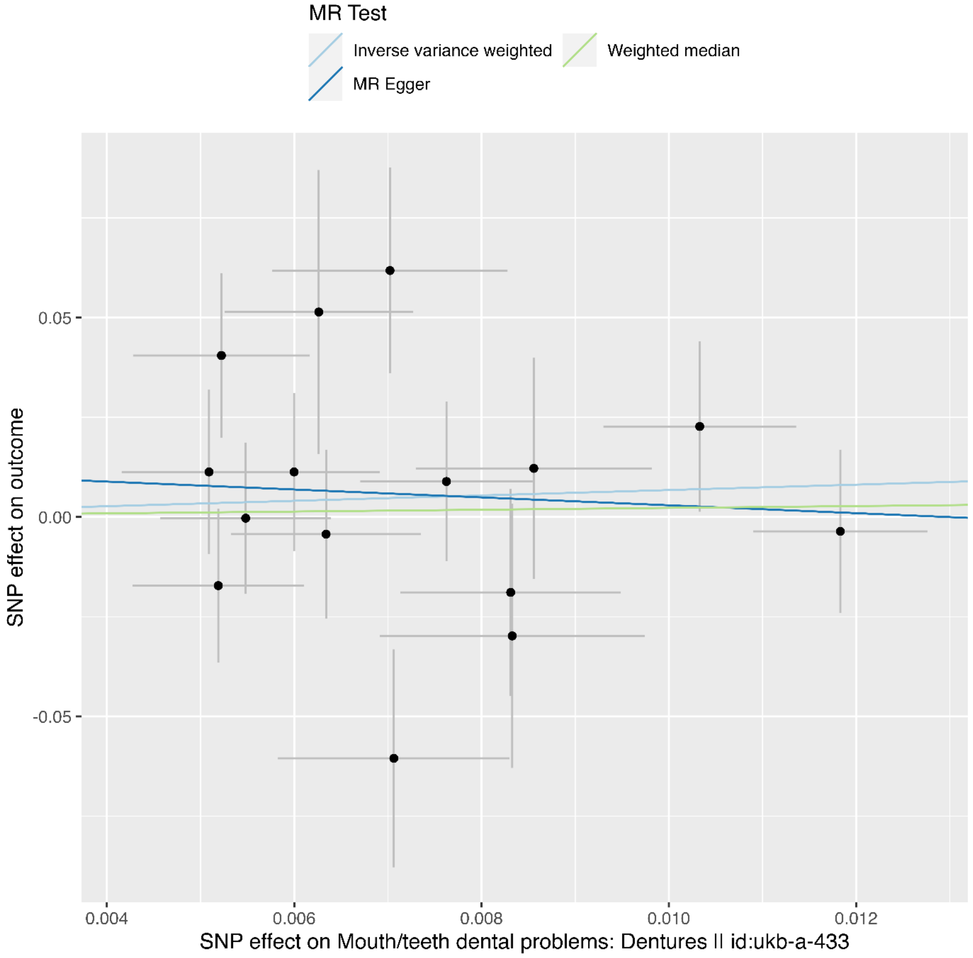
Supplementary Figure S5. Associations between SNPs correlated to bleeding gums and CAC

Each genetic variant included in the analysis is represented as a point + 95% CI. Location on the horizontal axis represents the correlation between the variant and exposure; location on the vertical axis represents the correlation between the variant and the outcome. Lines represent estimates of different MR methods.
Abbreviation: MR, Mendelian Randomization; SNP, Single Nucleotide Polymorphism



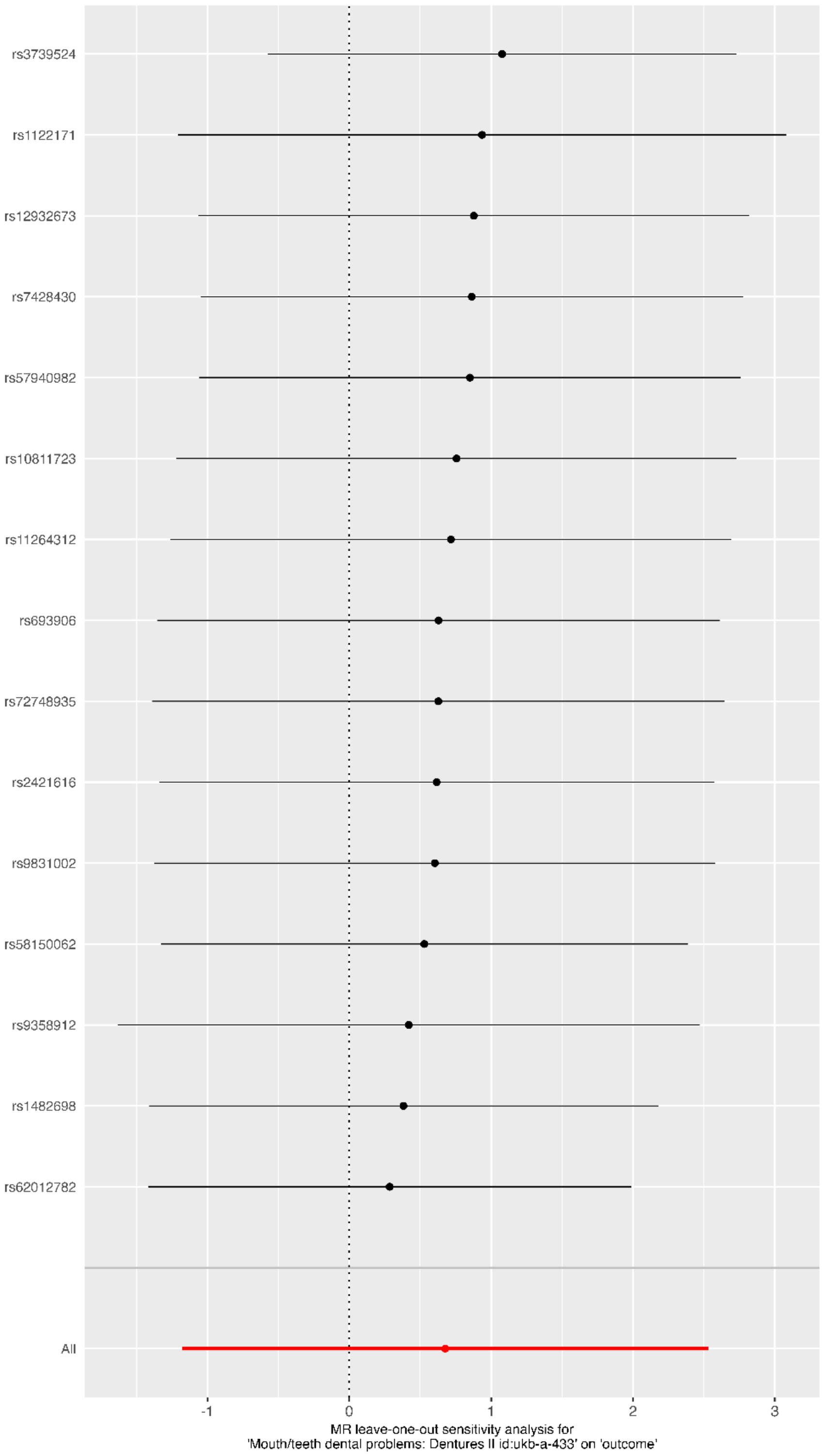
Supplementary Figure S6. Leave-one-out analysis for bleeding gums and CAC

Horizontal axis—inverse-variance weighted-mean estimate with 95% confidence intervals of genetic associations between exposure and outcome. Each dot and confidence interval represents an inverse-variance weighted mean obtained when a variant listed on the left side is removed from the analysis.



Supplementary Figure S7. Associations between SNPs correlated to denture use and CAC

Each genetic variant included in the analysis is represented as a point + 95% CI. Location on the horizontal axis represents the correlation between the variant and exposure; location on the vertical axis represents the correlation between the variant and the outcome. Lines represent estimates of different MR methods.
Abbreviation: MR, Mendelian Randomization; SNP, Single Nucleotide Polymorphism



Supplementary Figure S8. Leave-one-out analysis for denture use and CAC

Horizontal axis—inverse-variance weighted-mean estimate with 95% confidence intervals of genetic associations between exposure and outcome. Each dot and confidence interval represents an inverse-variance weighted mean obtained when a variant listed on the left side is removed from the analysis.