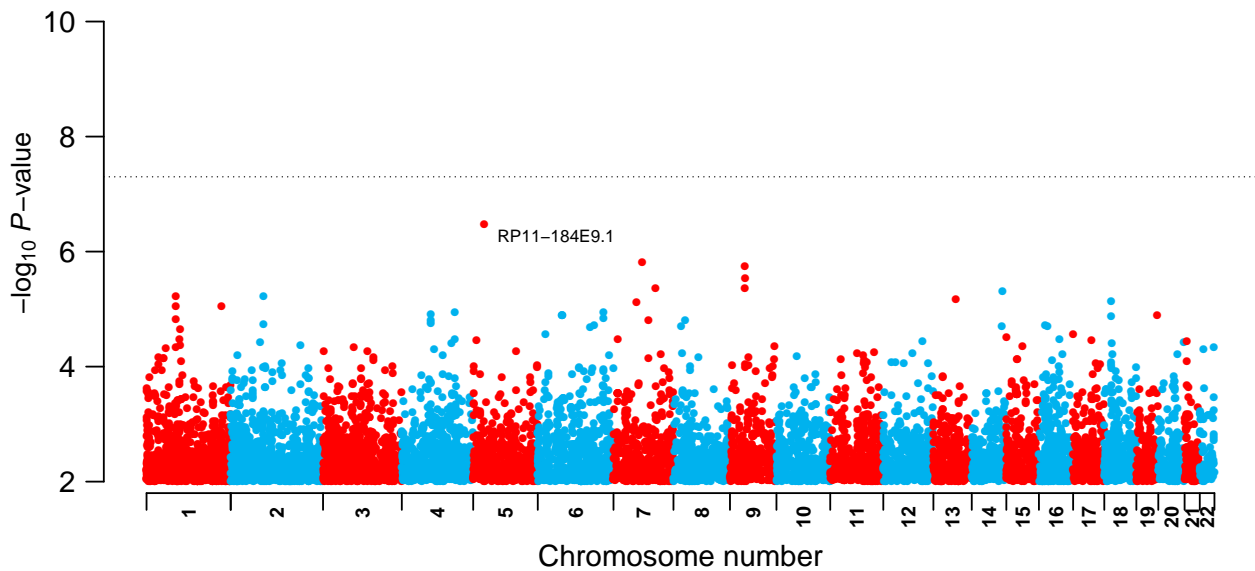


SUPPLEMENTARY FILES

<https://www.overleaf.com/project>

Supplementary Figures



Supplementary Figure 1. Manhattan plot for APV in boys. Genome-wide association P -values, expressed as $-\log_{10}(P\text{-value})$. Highlighted are genes linked to variants with $P\text{-value} < 10^{-6}$. Variants with $-\log_{10}(P\text{-value})$ between 0 and 2 are not shown.

Supplementary Tables

SNP ID-Allele	Conseq	Biotype	Gene	β_{GT}	P_{GT}	$\beta_{GT \times Sex}$	$P_{GT \times Sex}$	$\beta_{GT \times LA}$	$P_{GT \times LA}$
<i>rs148840332-C</i>	intron/NCT	lincRNA	<i>RP11-184E9.1</i>	1.96	3.4E-07	-1.66	4.8E-04	-1.13	2.7E-02

Supplementary Table 1. Strongest association for APV in boys. Shown is the SNP rs ID with the associated allele, consequence type, biotype, gene, effect size of the genotype (β_{GT}), association P -value of the genotype (P_{GT}), effect size of the interaction between genotype and sex ($\beta_{GT \times Sex}$) with the corresponding association P -value ($P_{GT \times Sex}$), effect size of the interaction between genotype and Native American local ancestry ($\beta_{GT \times LA}$) with the corresponding association P -value ($P_{GT \times LA}$). The effect of the SNP allele in males corresponds to the β_{GT} column, and the effect of the SNP allele in females is the sum of the effects in the β_{GT} and $\beta_{GT \times Sex}$ columns. Local ancestry is coded as 0, 1 or 2 depending on the number of alleles at each SNP that originate from Native America.