$$\boldsymbol{y} = 1\mu + \boldsymbol{x}b + \boldsymbol{u} + \boldsymbol{e}$$

where **y** represents pre-adjusted phenotypes of the trait; μ is the overall mean; b is the additive fixed effect of the variant tested; $\boldsymbol{x}$ is the vector of imputed genotypes coded in 0, 1, 2 (copy number of the alternative allele); $\boldsymbol{u}$ is the vector of random additive polygenic effects, $\boldsymbol{u} \sim N(\mathbf{0}, \boldsymbol{G}\sigma^2)$ with **G** the genomic relationship matrix; $\boldsymbol{e}$ is the vector of random residual effects normally distributed. The genomic relationship **G** matrix was calculated on 50k genotypes using PLINK [25].

The four traits were subjected to within-breed association analysis (Table 1). Variants with a within-breed MAF lower than 1% were excluded, leaving 11,933,965 and 12,449,740 variants in Alpine and Saanen goats, respectively, when sequences were imputed within-breed, and 14,695,413 and 15,404,361 variants in Alpine and Saanen goats, respectively, when imputation was performed using the French multi-breed panel. A Bonferroni correction was applied to the significance thresholds to account for multiple testing. The average chromosomal significance level was calculated as follows: $-log_{10}(0.05/(number\ of\ variants/29))$.

The results of the sequence data association analysis were then compared with 50k-genotypes results, by performing a GWAS on the 40,491 SNPs found both in the filtered sequence data and the cleaned GoatSNP50 BeadChip SNPs.

Annotations were extracted from VCF files for variants with a -$\log_{10}$(p-value) above the chromosomal threshold. The RumimiR database (http://rumimir.sigenae.org/) [27] was also checked for miRNAs located close to a significant variant.