Table S2. Two best associated SNPs of the genome-wide association study (GWAS).

The corresponding allele frequencies and genotype distribution in goats with (W/. genotype) and without wattles (w/w genotype) is shown (0: reference allele; 1: variant allele).

SNP	**CHIR 10 position**	**Allel frequencies (%)**				***P*-value**	**Genotype distribution (n)**							
		w/w		**W/.**			**w/w**				**W/.**			
		0	**1**	**0**	**1**		**0/0**	**0/1**	**1/1**	**total**	**0/0**	**0/1**	**1/1**	**total**
SNP31048-SCAFFOLD343-1829065	g.26,397,973T>C	0.49	0.51	0.73	0.27	8.90×10^{-09}	37	91	39	167	91	72	11	174
SNP31044-SCAFFOLD343-1700935	g.26,526,103T>C	0.98	0.02	0.88	0.12	5.22×10^{-07}	160	6	0	166	135	34	3	172