

TABLE

p-values of *DEFB1* polymorphisms association with human papillomavirus according to different correction methods

<i>DEFB1</i> SNPs	UNADJ	BONF	HOLM	SIDAK_SS	SIDAK_SD	FDR_BH	FDR_BY
Alleles							
g-52G>A rs1799946	0.405	1	1	0.925	0.874	0.800	1
g-44C>G rs1800972	1	1	1	1	1	1	1
g-20G>A rs11362	0.480	1	1	0.962	0.874	0.800	1
c.*5G>A rs1047031	0.003 ^a	0.013 ^a	0.013 ^a	0.013 ^a	0.013 ^a	0.013 ^a	0.030 ^a
c.*87A>G rs1800971	1	1	1	1	1	1	1
Genotypes - dominant model							
g-52G>A rs1799946	0.389	1	1	0.915	0.860	0.781	1
g-44C>G rs1800972	0.942	1	1	1	0.993	0.943	1
g-20G>A rs11362	0.468	1	1	0.958	0.860	0.781	1
c.*5G>A rs1047031	0.002 ^a	0.013 ^a	0.012 ^a	0.012 ^a	0.012 ^a	0.013 ^a	0.029 ^a
c.*87A>G rs1800971	0.916	1	1	1	0.993	0.943	1

a: statistically significant p-values (< 0.05); BONF: Bonferroni single-step adjusted p-values; FDR_BH: adjusted p-values for Benjamini and Hochberg step-up false discovery rate controlling procedure; FDR_BY: adjusted p-values for Benjamini and Yekutieli step-up false discovery rate controlling procedure; HOLM: Holm step-down adjusted p-values; SIDAK_SD: Sidak step-down adjusted p-values; SIDAK_SS: Sidak single-step adjusted p-values; SNPs: single-nucleotide polymorphisms; UNADJ: unadjusted p-value.