Table 2. Association between *HSD17B13 rs72613567* genotypes and abnormal albuminuria in patients with biopsy-proven NAFLD.

	***HSD17B13* rs72613567 genotype**	**N**	**B coeff.**	**Wald**	**Odds ratio**	**95% CI**	***p***
Unadjusted model	-/-	93	*Ref.*	*Ref.*	*Ref.*	*Ref.*	
	A/-	96	-1.28	6.65	0.28	0.11-0.74	**0.010**
	A/- + A/A	122	-1.54	9.65	0.22	0.08-0.57	**0.002**
Adjusted model 1	-/-	93	*Ref.*	*Ref.*	*Ref.*	*Ref.*	
	A/-	96	-1.56	7.96	0.21	0.07-0.62	**0.005**
	A/- + A/A	122	-1.81	10.75	0.17	0.06-0.48	**0.001**
Adjusted model 2	-/-	93	*Ref.*	*Ref.*	*Ref.*	*Ref.*	
	A/-	96	-1.47	6.48	0.23	0.08-0.71	**0.011**
	A/- + A/A	122	-1.83	10.26	0.16	0.05-0.49	**0.001**

Sample size, $n = 215$. Data are expressed as odds ratio and 95% confidence intervals as tested by univariable and multivariable logistic regression analyses. The depenedent variable was abnormal albuminuria defined as defined as u-ACR ≥30 mg/g creatinine. *Ref.* = reference category.
Model 1 adjusted for age, sex, BMI, HOMA-IR, hypertension, diabetes and hyperuricemia.
Model 2 adjusted for the same covariates of Model 1 *plus* e-GFR levels, presence of NASH (defined as NAFLD Activity Score ≥4), and histological stages of liver fibrosis.