Table 4: Distribution of NOD2 SNP[α] results in patients with a family history of inflammatory bowel disease as compared to control patients.

NOD2 variant	Test Patients (n=10)	Control Patients (n=12)	P value
P268S	4 (40.0)*	6 (50.0)	0.6914
R702W	1 (10.0)	1 (8.3)	1.0000
G908R	1 (10.0)	0	0.4545
1007fs	0	0	1.0000
At least 1 main risk allele#	2 (20.0)	1 (8.3)	0.5710

[α]Single Nucleotide Polymorphism
*Number of individuals (percentage); for P268S in the family history inflammatory bowel disease group group, one individual was homozygous for the variant allele; for all other data, carriers were heterozygous for the variant allele
R702W, G908R or 1000fs; there were no individuals who carried the main risk alleles as compound heterozygotes