**Supplemental Table 3.** Distribution of genotypic frequencies of *ATG16L1*, *IL23R* and *NOD2* variants among CD and UC patients

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene / SNP (alleles)** | **Genotype** | **CD (%)** | **UC (%)** | **p-value** |
| ***ATG16L1* /****rs2241880 (A/G)** | AA Wild type | 3 (25) | 1 (14.2) | 0.69 |
| AG Heterozygote | 3 (25) | 3 (42.9) |
| GG Mutation | 6 (50) | 3 (42.9) |
| ***IL23R* /****rs11209026 (G/A)** | GG Wild type | 10 (83.3) | 7 (100) | - |
| GA Heterozygote | 2 (16.7) | 0 |
| AA Mutation | 0 | 0 |
| ***NOD2* /****rs2066844 (C/T)** | CC Wild type | 12 (100) | 7 (100) | - |
| CT Heterozygote | 0 | 0 |
| TT Mutation | 0 | 0 |
| ***NOD2* /****rs2066845 (G/C)** | GG Wild type | 12 (100) | 7 (100) | - |
| GC Heterozygote | 0 | 0 |
| CC Mutation | 0 | 0 |
| ***NOD2* /****rs2066847 ()** | Wild type | 12 (100) | 7 (100) | - |
| Heterozygote | 0 | 0 |
| Mutation | 0 | 0 |