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| **Variant HGVS nomenclature: DNA (protein)** | **dbSNP ID** | **American College of Medical Genetics and Genomics and the Association for Molecular Pathology category** | **Revel and Gavin scores** | **Number of subjects in our study population** | **MAF in our cohort - affected individuals (n=1216) (%)** | **MAF in GnomAD exomes and genomes (%)** |
| c.47G>A (p.R16H) | rs145047094 | benign | 0.777 / benign | 4 (all affected) | 0.3289 | 0.2082 |
| c.100-18C>T (p?) | rs202156895 | likely benign | \*n/a / benign | 7 (all affected) | 0.5757 | 0.3147 |
| c.132C>T (p.D44=) | rs11822907 | benign | \*n/a / benign | 3 (all affected) | 0.2467 | 0.7984 |
| c.144C>T (p.T48=) | rs772658134 | benign | \*n/a / benign | 1 (affected) | 0.0822 | 0.0064 |
| c.468+9C>T (p?) | rs373159347 | likely benign | \*n/a / benign | 1 (affected) | 0.0822 | 0.0066 |
| c.469-13C>T (p?) | n/a | VUS | \*n/a / benign | 1 (affected) | 0.0822 | n/a |
| c.516C>T (p.D172=) | rs2276020 | benign | \*n/a / benign | 22 (nineteen affected, three unaffected [one homozygous]) | 1.56 | 3.4314 |
| c.579G>T (p.G193=) | rs1194122725 | likely benign | \*n/a / benign | 1 (unaffected) | 0 | n/a |
| c.682A>C (p.K228Q) † | rs641081 | likely benign | 0.117 / benign | 18 (all affected) | 1.4803 | 5.0202 |
| c.787+9C>T (p?) | rs749392143 | VUS | \*n/a / benign | 1 (affected) | 0.0822 | 0.0047 |
| c.807C>T (p.F269=) | rs139407567 | VUS | \*n/a / benign | 11 (five affected) | 0.4112 | 0.0550 |
| c.831C>T (p.A277=) | rs531331351 | VUS | \*n/a / pathogenic | 1 (affected) | 0.0822 | 0.0016 |
| c.891C>A (p.A297=) | rs35665586 | benign | \*n/a / benign | 2 (affected) | 0.1645 | 0.1813 |
| c.896C>T (p.A299V) | rs148986773 | likely benign | 0.292 / pathogenic | 5 (one affected)# | 0.0822 | 0.0544 |
| c.906G>A (p.V302=) | rs142912418 | benign | \*n/a / benign | 2 (one affected) | 0.0822 | 0.0086 |
| c.911G>A (p.R304Q) | rs104894190 | VUS | 0.31 / benign | 32 (sixteen affected) | 1.32 | 0.1568 |

**Supplemental Table 3: List of non-pathogenic *AIP* variants identified in the study population.** n/a, not available; VUS, variant of uncertain significance. \*n/a, Revel score not available as this scoring system only consider missense variants. †There is a Q at this position in the AIP reference sequence, but we consider K as the wild-type amino acid, due to its higher prevalence in the population screened so far (GnomAD, 1000Genomes); we considered A at this position as the reference allele when analyzing GnomAD data. #Two of the unaffected subjects carry the R304\* and the A299V variants on 2 different alleles, strongly suggesting that the A299V variant is benign (Williams *et al.* JCEM, 2014). Variant nomenclature was based on transcript NM\_003977.4. Categorization of variants was based on the combination of multiple *in silico* prediction tools, clinical and experimental data, as specified in the Methods section.