**S1 Table. Predicted ITPase activity according to genotype of *ITPA*-1 and *ITPA*-2**

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| --- | --- | --- | --- | --- |
| ***ITPA*-1 genotype a** | ***ITPA*-2 genotype a** | **Predicted ITPase activity (%) a** | **ITPase deficient a** | **Distribution within cohort n (%)** |
| Wild type (CC) | Wild type (AA) | 100 | No | 152 (67%) |
| Wild type (CC) | Heterozygote (AC) | 60 | Yes | 40 (18%) |
| Wild type (CC) | Homozygote (CC) | 30 | Yes | 5 (2.2%) |
| Heterozygote (CA) | Wild type (AA) | 25 | Yes | 12 (5.3%) |
| Heterozygote (CA) | Heterozygote (AC) | 10 | Yes | 4 (1.8%) |
| Homozygote (AA) | Wild type (AA) | <5 | Yes | 0 (0%) |

1. Abbreviations: ITPase, inosine triphosphate pyrophosphatase; ITPA, inosine triphosphatase