**Table S1**. Quality of the sequencing and read depth regarding the variants of interest

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **ID** | **Gene** | **QUAL** | **AD** | **Change in DNA** | **Change in protein** |
| 1 | MEFV | 1073,77 | 105 | c.2080A>G | p.(M694V) |
| MEFV | 1168,77 | 86 | c.2177T>C | p.(V726A) |
| PSTPIP1 | 1524,77 | 135 | c.831G>T | p.(E277D) |
| 2 | NCSTN | 1147,6 | 61 | c.1140\_1141del | p.(D381Sfs\*7) |
| 3 | NCSTN | 132,6 | 79 | c.482delA | p.(I162Yfs\*57) |
| 4 | NLRC4 | 1038,6 | 79 | c.2668T>C | p.(C890R) |
| 5 | WDR1 | 1062,6 | 83 | c.323A>G | p.(H108R) |
| 6 | NLRC4 | 2617,6 | 124 | c.541C>T | p.(R181X) |
| 7 | NOD2 | 891,77 | 89 | c.2104C>T | p.(R702W) |
| OTULIN | 423,77 | 34 | c.209T>C | p.(I70T) |
| 8 | NOD2 | 1134,73 | 79 | c.3017dupC | p.(L1007Pfs\*2) |
| 9 | GJB2 | 1497,6 | 103 | c.35delG | p.(G12Vfs\*2) |
| OTULIN | 2178,6 | 170 | c.345G>T | (p.Q115H) |
| 10 | NOD2 | 2031,6 | 182 | c.2722G>C | p.(G908R) |