**S1 Table**. **Truncating *TTN* mutations identified in 1000 Genomes Project Cohort (P1V1).**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Location | Transcript | Nucleotide Change | Amino Acid Change | GMAF (N=2184) |
| 2:179395288 | ENST00000589042 | c.106054delT | p.Ser35352Leufs\*53 | 0.0032 (7) |
| 2:179407647-179407648 | ENST00000589042 | c.96933dupG | p.Pro32312Alafs\*35 | 0.024 (53)† |
| 2:179428912-179428913 | ENST00000589042 | c.81946dupC | p.Leu27316Profs\*2 | 0.0005 (1) |
| 2:179430946-179430947 | ENST00000589042 | c.79912dupC | p.Gln26638Profs\*3 | 0.08 (176)† |
| 2:179431336-179431337 | ENST00000589042 | c.79522\_79523insC | p.Trp26508Serfs\*3 | 0.02 (44)† |
| 2:179435016-179435017 | ENST00000589042 | c.75842dupC | p.Val25282Serfs\*8 | 0.02 (50)† |
| 2:179439949 | ENST00000589042 | c.70910delG | p.Gly23637Alafs\*29 | 0.0005 (1) |
| 2:179455726 | ENST00000589042 | c.60726T>A | p.Tyr20242\* | 0.00019 (1) |
| 2:179458827-179458828 | ENST00000589042 | c.58292\_58293insG | p.Asp19431Glufs\*38 | 0.10 (209)† |
| 2:179487490-179487491 | ENST00000589042 | c.44819dupC | p.His14941Serfs\*14 | 0.04 (83)† |
| 2:179494977 | ENST00000589042 | c.44272C>T | p.Arg14758\* | 0.00019 (1) |
| 2:179495075-179495076 | ENST00000589042 | c.44173\_44174delGA | p.Glu14725Argfs\*27 | 0.0014 (3) |
| 2:179505311-179505312 | ENST00000589042 | c.40679dupC | p.Thr13561Tyrfs\*11 | 0.0005 (1) |
| 2:179517381-179517382 | ENST00000589042 | c.39041\_39042delAA | p.Lys13014Serfs\*11 | 0.0005 (1) |
| 2:179532190 | ENST00000589042 | c.35692A>T | p.Arg11898\* | 0.0009 (2) |
| 2:179548796 | ENST00000589042 | c.32736delG | p.Lys10913Argfs\*10 | 0.0005 (1) |
| 2:179549673-179549674 | ENST00000589042 | c.32513dupC | p.Ala10839Cysfs\*5 | 0.0018 (4) |
| 2:179554281 | ENST00000589042 | c.31888delA | p.Thr10630Profs\*3 | 0.0005 (1) |
| 2:179632509 | ENST00000589042 | c.9448C>T | p.Arg3150\* | 0.0005 (1) |
| 2:179640461-179640462 | ENST00000589042 | c.6129dupA | p.Glu2044Argfs\*4 | 0.0009 (2) |
| 2:179658211-179658212 | ENST00000589042 | c.1455dupA | p.Ala486Serfs\*26 | 0.0027 (6) |
| 2:179666885-179666886 | ENST00000589042 | c.274dupA | p.Thr92Asnfs\*3 | 0.0037 (8) |

Marked (†) are the false positives that were filtered out in the subsequent version. Abbreviations: P1V1 – phase 1 version 1; GMAF – Global minor allele frequency.