**Table S3** Primer sequences used for validation of the mutation detected by whole genome and Sanger sequencing.

| Gene | Polymorphism | Forward primer (5’-3’) | Reverse primer (5’-3’) | AS (bp) | AT (°C) | Restriction enzyme | IT  (°C) |
| --- | --- | --- | --- | --- | --- | --- | --- |
| *EDA* | c.458delT | ATAGAGGGGTCAGGAAAGGAG | TTTCAACAATAACTGGCCGTG | 608 | 61.3 | *Alu*I | 37 |
| *EDA* | c.458delT | GCCTCAGAGAGTGGGTGTCT (Waluk et al. 2016) | CCTGGAGTCACTGGGGAATA (Waluk et al. 2016) | 1346 |  |  |  |
| *EDA* | c.458delT | CTAGAGTTGCGCTCCGAGTT (Waluk et al. 2016) |  | - |  |  |  |

The variant *EDA*:c.458delT was validated by the use of restriction fragment length polymorphism (RFLP). Primer pairs, amplicon size (AS) in base pairs (bp), annealing temperature (AT), restriction enzyme and incubation temperature (IT) are given. Also depicted are the three primers used for cDNA Sanger sequencing.