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Fig. S1. c.892-2A> T mutation of *TMC6* was found in the EV patient and it was suggested that this mutation induced an amino acid mutation of p.Gly298*. (a) Genomic DNA sequences of the healthy control (WT) and the patient (PT) are shown. The c.892-2A>T mutation of TMC6 was detected on intron 8 in the patient. The sequences shown were reverse-complemented. (b) cDNA sequences reverse-transcribed from mRNA are shown. In TMC6 exon 9 of the patient, 41 base pairs of c.892_932 were missing and a stop codon appeared at the beginning of exon 9. Thus, c.892-2A>T was estimated to induce an amino acid mutation of p.Gly298*. (c) Differences in splice sites between a healthy control (WT) and the patient (PT) are shown. In the patient, a mutation occurred in the splice acceptor site of intro 8 of TMC6, and c.930_931AG was estimated to function as a novel splice site. EV, epidermodysplasia verruciformis.

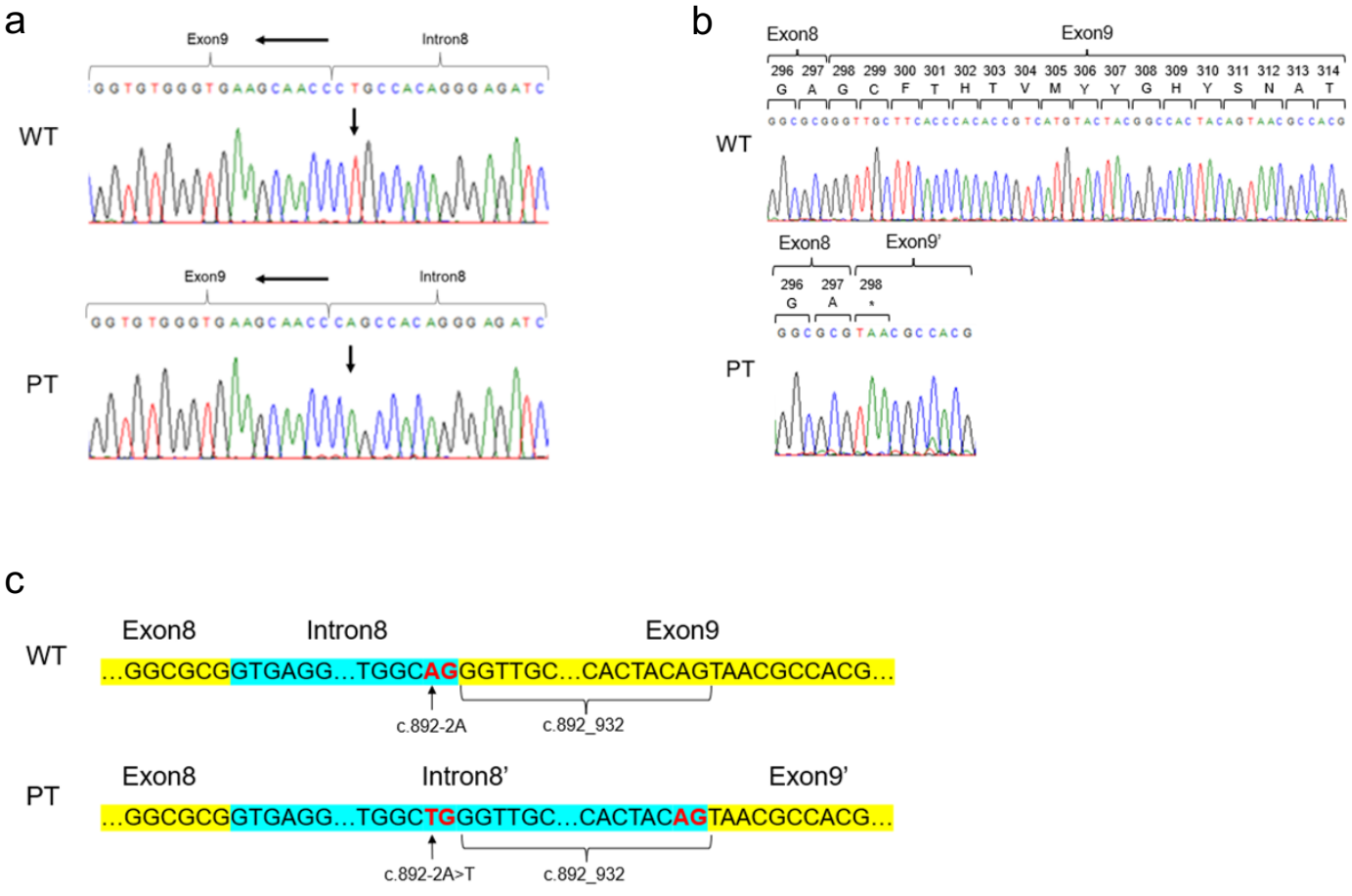

Fig. S2. HPV-5 was detected in the SCC on the back. (a) Gel-electrophoresed PCR products were shown. A band of nested amplicon (235bp) was detected. Nuclease free water (Water) and genomic DNA extracted from whole blood of a healthy donor (DNA_Healthy) were used as negative controls. (b) The sequence 'TACTGTTTTCTGTATCTTTTACTTTATTGAAA' found in the nested amplicon (reverse-complemented) was identical with that of L1 region of HPV-5 in the BLAST web site of NCBI.