Corrigendum: Natural history of human papillomavirus infection of sun-exposed healthy skin of immunocompetent individuals over three climatic seasons and identification of HPV209, a novel betapapillomavirus

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The published article included an incorrect version of Fig. 2. The correct Fig. 2 is displayed below.
Fig. 2. Phylogeny of HPV types/putative types identified in this study with respect to all officially recognized HPVs. Phylogenetic analysis of partial L1 gene sequences (~370 bp for CUT and ~235 bp for FAP primer pairs) of HPV types/putative types identified in this study and 187 reference HPVs from α-, β-, γ-, μ- and ν-PV genera. Bayesian posterior probability values (BPP) >0.50 are shown. HPV types/putative types identified with FAP (solid dot) and CUT (empty dot) primers are shown. Novel putative HPV types identified in this work are indicated with empty squares.