**Supporting Information.**

**Supplementary Text 3. Additional comments on the molecular dating of HPV58 sequences and potential limitations.**

**Study Limitations and Perspectives:** In this study, our results showed that HPV16 and HPV58 have followed different evolutionary patterns in association with human populations. Nevertheless, our results should be interpreted cautiously, due to the small region of DNA sequence analyzed, low sample size and the large confidence intervals with our estimates. Moreover, different substitution rates have been proposed for papillomavirus genes, ranging from 10-7 s/s/yfor non-coding regions to 10-8 s/s/yfor L1 (the one used in this study) (Halpern, 2000). Hence, by considering an alternative theoretical value of 10-7 s/s/y, Marin et al, (2015) estimate that the root of HPV58 E6 gene can be placed at 100.000ybp with all sub-lineages evolving nearly 55,951 ybp (Marín et al., 2015). Which places HPV58 evolution in a different scenario than the one described here, close to the date of coalescence of mtDNA from African (100,000 – 150,000 ybp) and Asian populations (60,000 – 65,000 ybp) (Torroni et al., 2006).Under this hypothesis, a fastest substitution rate of 10-7 s/s/y will provide a plausible time-frame for the phylogeographical model proposed by Li et al, (2009) in which HPV58 emergence is pointed out in Africa and the diversification to Asia, being this continent a second “rely center” from which the infection was spreaded worldwide (Li et al., 2009).

Interestingly, several authors have reported diversifying selection among some regions of the HPV16 genome (Chen et al., 2005; DeFilippis et al., 2002), but little is known about what kind of selective processes operate on HPV58 genomes (Chen et al., 2005). The deployment of a vaccine that raises an effective immune response will probably place the virus under pressures that are different from those that have apparently shaped the diversity of papillomavirus to date (Halpern, 2000). Understanding HPV evolution will be fundamental in the vaccine era.

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