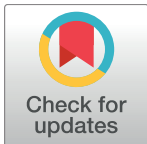


CORRECTION

Correction: The high prevalence of HPV and HPV16 European variants in cervical and anal samples of HIV-seropositive women with normal Pap test results

The *PLOS ONE* Staff

The image for [Fig 2](#) is incomplete. Please see the complete, correct [Fig 2](#) here. The publisher apologizes for the error.



OPEN ACCESS

Citation: The *PLOS ONE* Staff (2017) Correction: The high prevalence of HPV and HPV16 European variants in cervical and anal samples of HIV-seropositive women with normal Pap test results. *PLoS ONE* 12(5): e0178357. <https://doi.org/10.1371/journal.pone.0178357>

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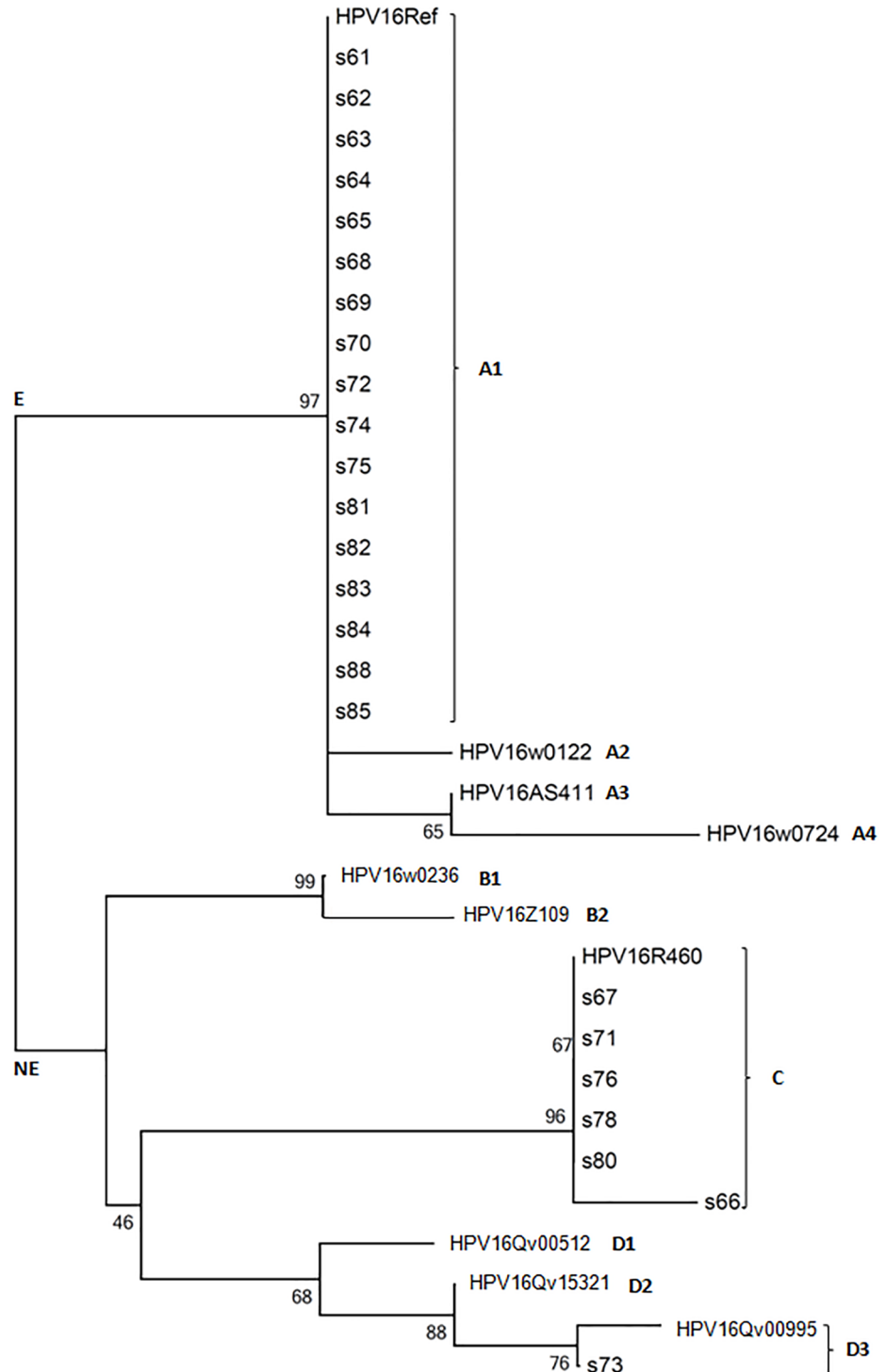


Fig 2. Tree topology. The phylogenetic tree created using the neighbour-joining method from the global alignment of full and partial sequences of the HPV16 genome. E-European variants (sublineages A1-A4); NE-non-European variants (sublineages B1-D3). The reference sequences of each HPV16 lineage was obtained from GenBank (ID/lineage/accesion number: 16Ref/A1/K02718; w0122/A2/AF536179; AS411/A3/HQ644236; w0724/A4/AF534061; w0236/B1/AF536180; Z109/B2/HQ644298; R460/C/AF472509; Qv00512/D1/HQ644257; Qv15321/D2/AY686579; Qv00995/D3/AF402678).

<https://doi.org/10.1371/journal.pone.0178357.g001>

Reference

1. Volpini LPB, Boldrini NAT, de Freitas LB, Miranda AE, Spano LC (2017) The high prevalence of HPV and HPV16 European variants in cervical and anal samples of HIV-seropositive women with normal Pap test results. PLoS ONE 12(4): e0176422. doi:[10.1371/journal.pone.0176422](https://doi.org/10.1371/journal.pone.0176422) PMID: [28426837](https://pubmed.ncbi.nlm.nih.gov/28426837/)