



Correction

Correction: Yu et al. HPV16 and HPV18 Genome Structure, Expression, and Post-Transcriptional Regulation. *Int. J. Mol. Sci.* 2022, 23, 4943

Lulu Yu , Vladimir Majerciak and Zhi-Ming Zheng *

Tumor Virus RNA Biology Section, HIV Dynamics and Replication Program, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Frederick, MD 21702, USA; lulu.yu@nih.gov (L.Y.); majerciv@mail.nih.gov (V.M.)

* Correspondence: zhengt@exchange.nih.gov; Tel.: +1-301-846-7634

In the published review [1], the HPV16 late promoter P_L in Figure 1a was wrongly labeled in the E6 open reading frame. The corrected Figure 1a below shows the HPV16 P_L promoter in the E7 open reading frame.

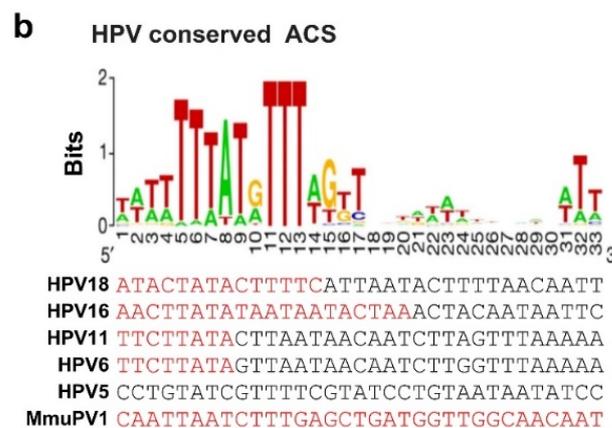
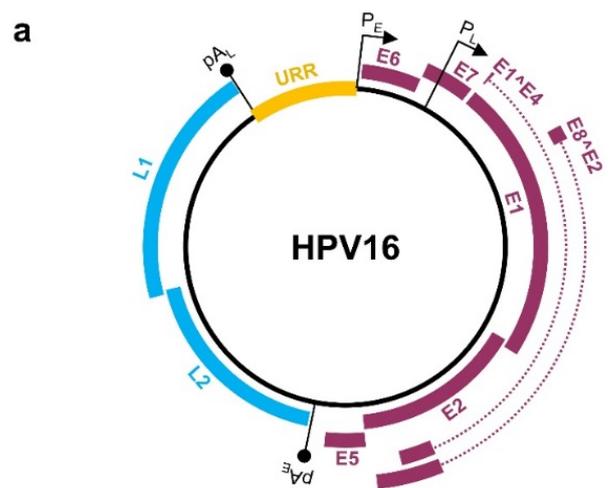


Figure 1. Papillomavirus genome structure, annotated ORFs, and conserved ACS in the origin of replication (Ori). (a) HPV16 genome and annotated ORFs. The non-structural proteins from the early region of the genome, including E1, E2, E1-E4, E5, E6, E7, and E8-E2, are shown in purple. The viral



Citation: Yu, L.; Majerciak, V.; Zheng, Z.-M. Correction: Yu et al. HPV16 and HPV18 Genome Structure, Expression, and Post-Transcriptional Regulation. *Int. J. Mol. Sci.* 2022, 23, 4943. *Int. J. Mol. Sci.* 2022, 23, 7903. <https://doi.org/10.3390/ijms23147903>

Received: 24 June 2022

Accepted: 27 June 2022

Published: 18 July 2022

Publisher's Note: MDPI stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.



Copyright: © 2022 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

capsid proteins, L1 and L2, from the late region of the genome are shown in blue. URR (yellow), upstream regulatory region. P_E and P_L mark the early and late promoters, and pA_E and pA_L stand for the early and late polyadenylation sites. **(b)** Conservation of the mammalian ARS consensus sequence (ACS) [16] in the Ori of selected papillomavirus genomes. Shown in this panel are conserved bases with position weight matrix (sequence logo bits) of the 167 predicted ACS elements [16] in comparison with the viral Ori sequences from the selected viral URR tail (red)-head (black) regions. Adapted with permission from Ref. [16]. Copyright 2018 Springer Nature. ARS—autonomously replicating sequence.

The authors apologize for any inconvenience caused and state that the scientific conclusions are unaffected. This correction was approved by the Academic Editor. The original publication has also been updated.

Reference

1. Yu, L.; Majerciak, V.; Zheng, Z.-M. HPV16 and HPV18 Genome Structure, Expression, and Post-Transcriptional Regulation. *Int. J. Mol. Sci.* **2022**, *23*, 4943. [[CrossRef](#)] [[PubMed](#)]