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CORRECTION **OPEN**

Correction: Tumour budding-based grading as independent prognostic biomarker in HPV-positive and HPV-negative head and neck cancer

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The original version of this article contained a mistake. In the Methods section, under the heading TCGA cohort, the sentence originally read as follows:

"HPV status was determined based on the number of RNA sequencing reads aligning to the viral genes E6 and E7 as previously described [27, 28]."

The corrected version is:

"HPV status was determined by investigating the tumour DNA with a PCR based assay interrogating 16 HPV types (16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, 68, 73, and 90) as previously described [27]. Tumours were classified as HPV+ when the test result was positive, as HPV- when the test result was negative and excluded from the analysis when the test result was indeterminate."

The complete, corrected section can be found below. The correction does not have any effect on the results or conclusions of the paper.

TCGA cohort

The TCGA-HNSC cohort included a total of 528 patients who were treated for HNSCC [27, 28]. Digitised H&E-stained diagnostic slides of 471 cases were available from the GDC Data Portal (https://portal.gdc.cancer.gov). A total of 331 tumours consisting of conventional, basaloid, verrucous, and papillary HNSCC were included into the study after exclusion of 140 cases. Cases were excluded due to the following reasons: small biopsy specimen precluding the analysis of 10 HPF, a different tumour entity, sarcomatoid histomorphology, not enough tumour on slide, inferior scan quality, exposed carcinoma without relation to surrounding stroma precluding the analysis of TB, duplicates and a history of neoadjuvant treatment. HPV status was determined by investigating the tumour DNA with a PCR based assay interrogating 16 HPV types (16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, 59, 66, 68, 73, and 90) as previously described [27]. Tumours were classified as HPV+ when the test result was positive, as HPV- when the test result was negative and excluded from the analysis when the test result was indeterminate. The clinicopathological characteristics of the study cohort are shown in Supplementary Table S1.

The original article has been corrected.