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Universitat Oberta de Catalunya

1	THE ISOTHERMAL AMPLIFICATION AMPFIRE ASSAY FOR HPV DETECTION AND GENOTYPING				
2	IN FORMALIN-FIXED PARAFFIN-EMBEDDED OROPHARYNGEAL CANCER SAMPLES				
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#### **ABSTRACT**

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HPV-related oropharyngeal squamous cell carcinomas (OPSCC) represent a distinct clinical entity compared to HPV-negative tumours with particular regard to treatment-response and survival outcome. The aim of this study was to assess the AmpFire Multiplex HR-HPV tests, for the detection and genotyping of 15 HR-HPV types in formalin-fixed paraffin-embedded (FFPE) samples and identify HPV-driven OPSCC. DNA from 160 OPSCC FFPE specimens, plus 23 samples from other head and neck primary sites were tested. Results were compared with those obtained using Linear Array HPV-DNA Genotyping Test. LA and AmpFire Multiplex HR-HPV tests showed, for all samples and specifically for OPSCCs, an overall concordance agreement of 98.9% and 99.4% and a Cohen's Kappa coefficient of 0.972 and 0.984, respectively. A concordance of 100% for HPV16 and HPV18 was observed. The overall agreement between p16<sup>INK4a</sup> overexpression and HPV detection by the Ampfire Multiplex HR-HPV assay in 145 OPSCC samples was 93.8% with a Cohen's Kappa coefficient of 0.848. The AmpFire HPV Tests are simple assays for detection and genotyping of HPV-DNA in OPSCC FFPE samples and can be easily implemented in the clinical practice setting for HPV-DNA detection.

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### 76 **1. INTRODUCTION**

About a decade ago the International Agency for Research on Cancer (IARC) established highrisk Human papillomavirus as the main cause of HPV-driven OPSCC <sup>1</sup>. Since then, it has been estimated that approximately 42,000 new HPV-related OPSCC cases occur every year, corresponding to 30% of the worldwide number of the overall incident OPSCC cases <sup>2</sup>, with a clear geographical variation in HPV-attributable fractions of OPSCC ranging from <20% to more than 60%, depending on the world region (reviewed in <sup>3</sup>).

The detection of the attributable fraction of OPSCC associated with HPV is a powerful prognostic marker in OPSCC and despite is not used for treatment selection is described in the clinical guidelines as a useful diagnostic tool to anticipate the clinical outcome. The E6/E7 HPV mRNA detection on fresh frozen samples is the reference standard for the identification of the HPV-driven cases <sup>4–6</sup>. However, its application on the clinical settings is still challenging and, consequently, the lack of a gold standard testing method hampers the judgment of the real HPV-driven cases.

90 Currently, p16<sup>INK4a</sup>-IHC evaluation is the most recommended technique for OPSCC 91 HPV diagnostic (NCCN Guidelines for Head and Neck Cancers, Version 3.2021 available at 92 https://www.nccn.org/guidelines/guidelines-detail?category=1&id=1437, last accessed date july 10, 2021). p16<sup>INK4a</sup> is considered positive when more than 70% of the tumour tissue shows 93 94 moderate to strong diffuse nuclear and cytoplasmic immunoreactivity <sup>7</sup>. However, previous 95 studies have demonstrated a proportion (up to 20%) of patients who have tumours that are p16<sup>INK4a</sup> positive, but negative on testing for HPV-DNA <sup>8,9</sup>. Importantly, the outcome of these 96 97 patients seems to be significantly worse than the outcomes of patients who are double positive for HPV and p16<sup>INK4a</sup> positive <sup>10,11</sup>. 98

99 In view of these considerations, the College of American Pathologists and the American Joint 100 Committee on Cancer produced an evidence-based guideline on testing, application, 101 interpretation, and reporting of human papillomavirus (HPV) and surrogate marker tests in 102 head and neck carcinomas <sup>7</sup>. For OPSCC tissue specimens, pathologists should perform HR-HPV testing by surrogate marker p16<sup>INK4a</sup> immunohistochemistry (IHC). Additional HPV-specific 103 testing may be done at the discretion of the pathologist and/or treating clinician, or in the 104 105 context of a clinical trial <sup>7,12,13</sup>. However, double positivity for HPV-DNA/p16<sup>INK4a</sup> is the 106 diagnostic strategy showing the best prognostic value for HPV-driven OPSCC patients as also 107 reported in a recent work <sup>11</sup>.

108 Nevertheless, the assays for HPV-DNA detection in OPSCC have not yet been entirely defined
 109 (reviewed in <sup>14</sup>). The HPV tests currently used for OPSCC diagnosis are those intended for use

in cervical carcinoma. Additionally, HPV-DNA automatic platforms developed for cervical
cancer screening, which frequently work with liquid-based cytology, are usually expensive,
require well trained staff and have been designed for a high-throughput workflow, hampering
its implementation for OPSCC diagnosis and raising the need for cheaper molecular methods.
Different PCR assays will vary in their performance based on the choice of primer sets, PCR
protocols and the type of tissue analysed.

Identifying molecular diagnostic tests that are able to discriminate those cancers etiologically associated with HPV is a priority for researchers and clinicians. Our objective was to evaluate the suitability and performance of the Ampfire HPV tests (Atila Biosystems) for the detection and genotyping of HPV in OPSCC. The tests were compared to Linear Array assay, one of the most extensively used assays for the detection and genotyping of FFPE samples (reviewed in <sup>15</sup>).

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#### 123 2. MATERIALS AND METHODS

#### 124 **2.1 Study samples**

125 A retrospective series of 183 FFPE cases, diagnosed between 2014 and 2019, were retrieved 126 from the archives of the Hospital Universitari de Bellvitge, Spain. Among the 183 samples of 127 head and neck origin (HNSCC), 160 were of oropharyngeal origin (OPSCC) and 23 from other 128 head and neck sites (non-OPSCC) (11 Oral Cavity, 6 Nasopharynx, 3 Larynx and 3 129 Hypopharynx). All the samples had previously been genotyped for the presence of HPV-DNA by 130 Linear Array assay and 165 samples were evaluated for the expression of p16<sup>INK4a</sup> by IHC. 131 Pathological classification was based on the World Health Organization pathological criteria for head and neck cancer <sup>16</sup>. 132

The study was approved by the Ethics Committee of Hospital Universitari de Bellvitge (Protocolcode: PR342/20).

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#### 136 2.2 FFPE blocks processing

Four paraffin sections were obtained for each block. First and last sections of 3 μm were used for histopathological evaluation after hematoxylin and eosin (HE) staining to perform tumour confirmation, and the second and third in-between sections of 5 μm were used for HPV testing and genotyping (sandwich method) <sup>11</sup>. FFPE blocks were processed under strict pre/post polymerase chain reaction (PCR) physical separation, and blank paraffin blocks were systematically tested in parallel to serve as sentinels for contamination as previously published.

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#### 145 **2.3 DNA extraction**

Total nucleic acids were extracted from one FFPE section using the Maxwell 16 FFPE Plus LEV DNA Purification kit (Promega Corp., Madison, WI, USA). The DNA was eluted with 100 µl of nuclease free water and the isolated DNA was diluted 10 times. A given volume of the 1/10 dilution of the extracted DNA, stated in each assay section, was used as a template for the amplification reaction. Extracted DNA and their corresponding 1/10 dilutions were stored at -80°C immediately after isolation. Mean storage time was 786 days (standard deviation = 511 days).

153

## 154 **2.4 Linear Array genotyping**

155 For all the samples collected, the Roche Linear Array HPV Genotyping test (Roche Molecular 156 Systems Inc., Alameda, CA, USA) was used to detect the 37 HPV-types. This assay involves a 157 PCR amplification of target DNA followed by nucleic acid hybridization on a nylon strip and 158 detection of up to 37 high- and low-risk HPV genotypes (6, 11, 16, 18, 26, 31, 33, 35, 39, 40, 42, 159 45, 51, 52, 53, 54, 55, 56, 58, 59, 61, 62, 64, 66, 67, 68, 69, 70, 71, 72, 73, 81, 82, 83, 84, IS39 160 and CP6108). PCR was performed in a 50  $\mu$ l reaction volume composed of 25  $\mu$ l Linear Array 161 master mix and 25  $\mu$ l of the 10-fold diluted DNA mentioned above. Amplification was 162 performed in a GeneAmp PCR System 9700 (Applied Biosystems, Foster City, CA, USA) using 163 the recommended cycle parameters: 2 min at 50 °C and 9 min at 95 °C, followed by 40 cycles 164 of 30 s at 95 °C, 1 min at 55 °C, and 1 min at 72 °C, followed by a final extension at 72 °C for 5 165 min. 50  $\mu$ l of PCR amplicons were denatured with 50  $\mu$ l of denaturing solution and detected by 166 nucleic acid hybridization and colorimetric detection. All washes and hybridization steps were 167 undertaken in a 48-well tray and the robot Auto-LiPA48 (Innogenetics N.V. (now Fujirebio Europe N.V.), Ghent, Belgium) was used for this purpose. The denatured amplicons were 168 169 hybridized on to the strip containing specific probes for 37 HPV genotypes and  $\beta$ -globin 170 reference lines before undergoing stringent washes. Colorimetric determination was 171 performed with the Linear Array Detection Kit. The colour change reaction was from 172 Streptavidin-horseradish peroxidase mediated precipitation of working substrate. Positive 173 reactions appeared as blue lines on the strip. The strips were interpreted using the HPV 174 reference guide provided to visually match the vertical locations of the horizontal bars in the 175 LA strip to specific types of HPV. The interpretation of the results was done by two evaluators 176 that determined the positivity and the intensity of the band as strong or weak.

The genotyping strip contains probes that specifically hybridize with HPV6, 11, 16, 18, 26, 31,
33, 35, 39, 40, 42, 45, 51, 53, 54, 55, 56, 58, 59, 61, 62, 64, 66, 67, 68, 69, 70, 71, 72, 73, 81, 82,

- 179 83, 84, IS39 and CP6108. Also, the strip includes a cross reactive probe that detects HPV33, 35,
- 52 and 58 as a pool; therefore the probe cannot exclude an HPV52 co-infection. Those samples
  with a positive result for this probe were re-tested using a specific HPV52 PCR system <sup>17</sup>.
- 182

# 183 2.5 Ampfire Assays (Multiplex HR-HPV Real Time Fluorescent Detection with HPV16/18 184 Genotyping test and Genotyping HR-HPV Real Time Fluorescent Detection test)

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186 The Multiplex HR-HPV Real Time Fluorescent Detection with HPV16/18 Genotyping (developed 187 by Atila Biosystems, Inc, Mountain View, CA, USA) (from now on referred to as Ampfire 188 Multiplex HR-HPV) performs isothermal nucleic acid amplification of around 100 bp targets of 189 E1 and/or L1 and uses real-time fluorescence detection for the qualitative detection of high-190 risk HPV (HR-HPV) types. The detection assay allows pooled real time fluorescent detection of 191 15 HR-HPV types (16, 18, 31, 33, 35, 39, 45, 51, 52, 53, 56, 58, 59, 66 and 68) and individual 192 genotyping of HPV16 and 18 in a single assay tube. The assay uses specific probes labelled with 193 CY5, ROX, FAM, HEX to detect HV16, HPV18, HR-HPV non-HPV16/18 and also an internal 194 control, respectively. The presence and integrity of DNA in all samples is verified by  $\beta$ -globin 195 gene amplification tested in HEX channel (internal control, IC). The lack of an exponential 196 amplification curve in that channel is interpreted as an invalid result. According to the 197 manufacturer, the threshold per reaction is 80 copies of the 13 non-HPV16/18 types, and 20 198 copies of HPV16 or HPV18. However, other studies have shown a limit of detection ranging from 2 to 20 copies/reaction for the 15 HPV genotypes <sup>18</sup>. 199

A second kit, Genotyping HR-HPV Real Time Fluorescent Detection test (from now on referred to as Ampfire Genotyping HR-HPV), to individually genotype 15 high-risk HPV types was used. In this case, the specific genotyping of the 15 high-risk HPV types is performed in 4 wells. The AmpFire Genotyping HR-HPV kit includes a reaction mix and primer sets 1, 2, 3, and 4, which cover the 31/51/39/16, 35/68/18/59, 33/66/IC/45, and 58/56/53/52 HPV genotypes, respectively. Probes for the 16/59/45/52, 39/18/66/53, 31/35/33/58, and 51/68/IC/56 HPV genotypes are labelled with CY5, ROX, FAM, and HEX, respectively.

Both kits also provide positive (containing synthetic plasmids) and negative controls to ensurethe results are trustworthy.

First of all, 9.5  $\mu$ l of the 10-fold diluted DNA sample was mixed with 0.5  $\mu$ l of 20x lysis buffer included in the kit and incubated at 95 °C for 15 min in a microcentrifuge tube. Next, the sample was briefly spun and 2  $\mu$ l of the sample was added to a reaction mix and used for the isothermal amplification following manufacturer's instructions.

Viral DNA was amplified and detected in a CFX96 real time qPCR instrument (Bio-Rad, Hercules, CA, USA) using a 60°C isothermal reaction for 74 min with fluorescence being recorded once every minute (74 cycles) from the according channels. The results of the cycle thereshold (Ct) values for each amplification curve in all fluorescence channels are automatically reported by the CFX Manager Software IVD Edition 1.6 (Bio-Rad). A value of 55 Ct was chosen as a cutoff value.

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#### 220 2.6 HPV52 genotyping

221 In order to retest positive samples detected by Linear Array using the probe that combines 222 HPV33, HPV35, HPV52 and HPV58 detection, a HPV52 Real-Time PCR single assaywas performed <sup>17</sup>. FastStart Essential DNA Green Master (Roche Diagnostics, Mannheim, Germany) 223 224 was used for this purpose and according to manufacturer instructions, in combination with 5  $\mu$ l 225 of 1/10 diluted DNA. The primers used were (5'-3') E6-52F (GAACACAGTGTAGCTAACGCACG) 226 and E6-52R (GCATGACGTTACACTTGGGTCA). HPV52 DNA was amplified and detected in a 227 LightCycler 96 real time qPCR instrument (Roche Diagnostics, Mannheim, Germany), using the following cycle parameters: 10 min at 95 °C, followed by 45 cycles of 10 s at 95 °C, 10 s at 55 228 229 °C, and 10 s at 72 °C, followed by a melting cycle of 10 s at 95 °C, 1 min at 65 °C and 1 s at 97 230 °C. The results of the Ct values for each amplification curve and the melting curve were 231 automatically reported by the LightCycler 96 v1.1 software (Roche Diagnostics GmbH, 232 Mannheim, Germany). Samples with a negative result were retested using 5  $\mu$ l of DNA sample 233 directly extracted from the FFPE specimens.

234

## 235 **2.7 p16**<sup>INK4a</sup> immunohistochemistry

When needed additional slides were processed to assess expression of cellular proteins by immunohistochemistry (IHC). The expression of p16<sup>INK4a</sup> was analysed through IHC under the manufacturer's standards. Commercially available p16<sup>INK4a</sup>-specific monoclonal antibody clone (Roche MTM Laboratories AG, Heidelberg, Germany), were used. For p16<sup>INK4a</sup>, the intensity of nuclear and cytoplasmic staining within the tumours was scored and those with a strong staining of > 70% were considered p16<sup>INK4a</sup> positive <sup>7</sup>.

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#### 243 2.8 Statistical Analysis

The raw agreement proportions and Cohen's Kappa coefficient were calculated to measure the inter-rater agreement between the AmpFire and Linear Array HPV test techniques (HPV negative vs. positive irrespective of the specific genotype/s identified).

A Kappa value of 0 indicates no agreement and a value of 1 indicates perfect agreement. Values from 0.00–0.20 indicate poor agreement, 0.21–0.40 fair, 0.41–0.60 moderate, 0.61– 0.80 good, and 0.81–0.99 very good agreement. The raw agreement proportions and Cohen's Kappa were also used to assess the concordance between the HPV test results and p16<sup>INK4a</sup> outcomes. Statistical significance for all analyses was set at the 2-sided 0.05 level. Data analyses were performed with STATA software v.16 (Stata Corp., College Station, TX, USA).

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#### 254 **2.9 Informed Consent**

Samples were received in encrypted form (with a local identifier) and once received, the DNA was extracted and a new identifier was assigned to ensure its traceability. The remaining sample DNA, initially obtained and used for diagnostic purposes, was analysed retrospectively. Given the characteristics of the study, patient consent was waived because of the vital status of the patients and the retrospective nature of this study which represented an unreasonable effort (disproportionate time, work and expenses).

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#### 262 2.10 Institutional Review Board Statement

The study was conducted in accordance with the Declaration of Helsinki, and the protocol was approved by the Ethics Committee of Hospital Universitari de Bellvitge (Protocol code: PR342/20).

266

#### 267 **3. RESULTS**

#### 268 **3.1 Ampfire Multiplex HR-HPV test versus Linear Array**

269 DNAs obtained from 183 Head and Neck (160 OPSCC and 23 non-OPSCC) carcinomas were 270 analysed using the Ampfire Multiplex HR-HPV test and the Linear Array assay. Amongst the 271 183 FFPE samples, three samples were found invalid, as the  $\beta$ -GLobin gene was not detected. 272 One was invalid for both techniques and two of them only for the Ampfire Multiplex HR-HPV 273 test, which means an invalid rate of 1.63% (3/183). According to the Ampfire Multiplex HR-274 HPV test, HPV-DNA was found in 47 samples (26.1%) (Table 1). Comparing the positive and 275 negative agreement with Linear Array HPV test, a 95.9% (47/49) and a 100% (133/133) was 276 observed, respectively (Table 1). This represents an overall agreement between the Ampfire 277 Multiplex HR-HPV test and the Linear Array test of 98.9% (178/180; CI: 97.3%-100.0%) and a 278 very good agreement according to Cohen's Kappa coefficient index (0.972; p-value<0.001; 95% 279 CI: 0.932-1.000).

Comparing samples from different head and neck primary sites, the concordance of both techniques did not show statistically differences (p-value = 0.361). That is, either on OPSCC and non-OPSCC samples (Table 1), the performance of both tests showed a very good agreement (OPSCC samples, 99.4% concordance; Cohen's Kappa = 0.984; p-value<0.001; 95% CI: 0.953-1.000 and non-OPSCC samples, 95.7% concordance; Cohen's Kappa = 0.832; 95% CI: 0.489-1.000).

A concordance of 100% (40/40) for the presence of types HPV16 (39/39) and 18 (1/1) between Ampfire Multiplex HR-HPV assay and Linear Array was observed. In terms of "Other HR-HPV non-HPV16/18" concordance, the agreement between both assays was 70% (7/10) (Table 2). Two of the discordant samples were positive for HPV45 type, according to Linear Array, however the Ampfire Multiplex HR-HPV assay yielded a negative result. Similarly, Linear Array detected HPV16 and HPV52 in a sample where the Ampfire test was only able to genotype HPV16.

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#### 294 **3.2 Concordance between Linear Array and Ampfire Genotyping HR-HPV test**

295 Samples positive for high-risk types other than HPV16 or HPV18 were tested with the Ampfire 296 Genotyping HR-HPV test to elucidate the HR-HPV types present. Agreements and discrepancies 297 between both techniques and types are shown in Table 3. HPV33 type was detected by the 298 Ampfire Genotyping HR-HPV assay in 5 out of the 6 samples identified by Linear Array. HPV35 299 type was present in only one sample and it was equally detected by both techniques. In 300 addition, those samples discordant between Linear Array and the Ampfire Multiplex HR-HPV 301 test were also tested with the Ampfire Genotyping HR-HPV to assess whether the 302 discrepancies were dragged to this assay. This is the case of HPV45 that was identified in two 303 samples by Linear Array, but not by the Ampfire Multiplex HR-HPV assay. When the Ampfire 304 Genotyping HR-HPV assay was used, HPV45 was only amplified in one of the two samples.

305 In all the samples tested, HPV52 detected by Linear Array, was always in combination with 306 genotypes HPV33 or HPV35, with the exception of one sample where HPV52 was found with 307 HPV16. The Ampfire Genotyping HR-HPV test did not detect HPV52 in any of the 6 samples. 308 To rule out the genuine presence of HPV52 in the genotype-discordant samples, real-time PCR 309 was performed using specific primers to detect HPV52. Indeed, the results confirmed that 310 HPV52 was not present in those samples. Thus, a 100% agreement between the Ampfire 311 assays and the specific HPV52 testing was observed. Also, in agreement with the PCR result, in 312 the particular case of that sample were HPV16 co-exists with a low HPV52 load, the Ampfire 313 Multiplex HR-HPV and Genotyping HR-HPV tests classified this sample as positive for a single 314 infection with HPV16.

315

#### 316 **3.3 Ampfire HPV detection test versus p16**<sup>INK4a</sup> IHC in OPSCC cases

Out of the 157 HPV-valid oropharyngeal samples, 145 had the p16<sup>INK4A</sup> immunostaining completed. As shown in Table 4, almost all the cases that tested positive for Linear Array were also p16<sup>INK4A</sup>-positive (38/42). Similarly, 37 out of 41 of the AmpFire Multiplex HR-HPV-positive cases displayed a p16<sup>INK4A</sup> positive staining (Table 4). The concordance between positives and negatives for HPV and p16<sup>INK4A</sup> was not statistically significant if we compare the performance of both dual tests as the p-value comparing both Cohen's Kappa index was 0.791.

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## 324 **4. DISCUSION**

325 Several studies from different cohorts of OPSCC have shown that double positivity for HPV-DNA and p16<sup>INK4A</sup>-IHC provide strongest diagnostic accuracy and prognostic value for HPV-326 327 driven OPSCC than any of both techniques alone, thus allowing a more accurate patient 328 classification <sup>11,19</sup>. Importantly, these tests can both be straightforwardly implemented and 329 used in the clinical setting <sup>11</sup>. Considerable HPV-DNA testing options are currently available on the market <sup>20</sup> and a few have been clinically validated for the detection and genotyping of HPV 330 331 in liquid-based cytology samples for detecting cervical lesions <sup>21</sup>. All commercial HPV tests have been developed mainly to achieve optimal performance for cervical cancer screening although 332 333 have not been validated using formalin-fixed, paraffin-embedded biopsies. Conversely, 334 formalin-fixed, paraffin-embedded (FFPE) biopsies, which require specific processing before 335 PCR amplification, are one of the most widely practiced methods for clinical sample 336 preservation and are frequently the only existing samples for molecular testing. Currently 337 there is no agreement on the finest detection method that should be used to classify HPV 338 positive OPSCC and serve as a standard test for routine diagnostic use.

339 The present study compares two commercial HPV tests in a routine diagnostic setting. We 340 have analysed the performance of the AmpFire Multiplex HR-HPV assay on 183 DNA samples 341 extracted from primary tumour FFPE samples from patients with HNSCC, and compared the 342 results with those obtained with the HPV Linear Array assay, one of the most widely used 343 methods for testing and genotyping of FFPE samples (reviewed in  $^{15}$ ). Moreover, the results of 344 HPV obtained by the Ampfire test in OPSCC samples were compared with the immunohistochemical expression of p16<sup>INK4A</sup>, the last being available for 145 cases. To our 345 346 knowledge, this is the largest study that tests the AmpFire assay for a set of OPSCC FFPE 347 samples. Although most of the samples analysed were small diagnostic biopsies and some 348 authors claim that unremoved paraffin can lead to PCR inhibition and thus to invalid results <sup>22</sup>,

349 this was not a main issue in this study. Indeed, the rate of invalid test results was low (3/183, 350 1.63%) compared to other previously published studies showing invalid rates around 7-9% <sup>23,24</sup>. 351 Although in the present study, extracted DNA was used and showed a good performance; the 352 Ampfire test, contrarily to Linear Array, has the capacity to be used with or without DNA 353 extraction. As an example, a recent work that detected HPV from FFPE specimens but did not perform DNA extraction <sup>18</sup> have shown a 0.5% rate of invalid samples. This is an important 354 355 point because DNA extraction step is time-consuming, increase the costs of HPV-DNA testing, could increase the rate of invalid samples <sup>25</sup> and inevitably introduces a source of variability. 356

357 When comparing both tests -Linear Array and Ampfire Multiplex HR-HPV assays- an excellent 358 agreement was achieved (Cohen's Kappa = 0.972, 95% CI: 0.932-1.000). Prominently, this large 359 agreement between assays was not only observed for the HPV status (positive or negative) but 360 also for the genotyping results. The AmpFire Multiplex HR-HPV assay allows pooled real time 361 fluorescent detection of 15 HR-HPV types in addition to individual genotyping of HPV16 and 362 HPV18 in a single assay tube. This represents an advantage of the test since HPV16 is by far the 363 most common of the types found amongst HPV-driven OPSCCs (prevalence over the 80%)<sup>26</sup>. 364 The Ampfire test identified HPV16 (39/39) and HPV18 (1/1) in all the samples that tested 365 HPV16/18-positive with Linear Array. A 70% agreement between both assays was also 366 observed for the detection of other HR-HPV non-HPV16/18 genotypes in 10 samples including 367 HPV33 and HPV35 being beyond the HPV16, the most prevalent types in oropharyngeal tumours <sup>26,27</sup>. 368

369 The full set of samples that tested positive for other HR-HPV non-HPV16/18, were specifically 370 genotyped with the Ampfire Genotyping HR-HPV test (Linear array-blinded). Despite the high 371 overall agreement rate between both techniques, discordant results for HPV52 in 6 specimens 372 were detected. Five out of six samples that showed a HPV52-negative result by the Ampfire 373 Genotyping HR-HPV test but positive by Linear Array showed a coinfection for HPV33 and 374 HPV35. It is worth to mention a reported limitation of Linear Array is that additional testing is 375 necessary to detect the high-risk HPV52 genotype when HPV33, HPV35 and/or HPV58 are 376 present in the same sample <sup>28</sup>. Real-Time PCR using specific HPV52 probes confirmed the 377 negativity of HPV52 in the 5 samples co-infected with HPV33 or HPV35 and suggested a 378 probable false-positive result of the Linear Array test.

Additionally, the Ampfire Genotyping HR-HPV Real Time Fluorescent Detection test identified five out of the six HPV33 genotypes detected by Linear Array and also, a single HPV35 was identified by both techniques.

All the experiments were carried out using the same DNA sample. However, it is worth to mention that both assays were not performed contemporaneously, and thus, the invalidity or

negativization of some samples could be explained for this reason. Discordant results could also be associated with the DNA quantity recommended by the manufacturer used by each test, as the amount of DNA added to the Ampfire tests was much lower than the amount added to Linear Array.

388 To the best of our knowledge, only 2 studies have previously evaluated the Ampfire tests on 389 Head and Neck specimens, however, both assays included a small number of OPSCC samples. 390 Jang and colleagues analysed 81 samples directly from saliva by Ampfire Multiplex HR-HPV test 391 and compared the results to a well-validated technique, Cobas4800. The percentage of overall 392 agreement between both assays was 65.4% (Cohen's Kappa=0.34) due to a poor positivity 393 agreement between both techniques. Similarly, when comparing the results of the 71 samples with a p16<sup>INK4A</sup> immunostaining test done, a low 40.3% sensitivity and a 93.3% specificity was 394 395 found. Authors claim that the low sensitivity was probably due to the type of sample used or to the large dilution of samples before freeze storage <sup>29</sup>. During the same year, another 396 397 manuscript evaluated the performance of AmpFire assays for the detection and genotyping of 398 HPV on 214 DNA samples extracted from FFPE from several localisations (including 17 samples 399 of oropharynx). The test was evaluated in comparison with the Cobas4800 system and Linear 400 Array assay. The invalid rate was 0.5% and the detection agreement was 100% for both, 401 detection and identification <sup>18</sup>.

As mentioned above, the double positivity for HPV-DNA and p16<sup>INK4A</sup> can provide better 402 403 diagnostic accuracy and prognostic value than one test alone and can also allow a more 404 accurate patient classification <sup>11,30</sup>. In our study, 145 OPSCC samples with a valid HPV result had previously been analysed for p16<sup>INK4A</sup> status by IHC. Nine samples tested by the Ampfire 405 Multiplex HR-HPV assay delivered discordant results with respect to p16<sup>INK4A</sup> expression (93.8% 406 407 concordance). Similarly, 8 samples were discordant when the HPV test used was Linear Array 408 (94.5% concordance). Within the oropharynx, HPV-DNA/p16<sup>INK4A</sup> discordance rates have been 409 reported to range from 4% to 20% <sup>11,31–34</sup>. In the present study, a 6.2% HPV-DNA/p16<sup>INK4A</sup> 410 discordance was observed, which falls in the above mentioned range.

411 Earlier studies that used HR-HPV detection methods to test OPSCC specimens showed a similar 412 or slightly lower performance compared to the Ampfire Multiplex HR-HPV test. A very recent study using a large set of OPSCC samples compared Anyplex II HPV28 with p16<sup>INK4A</sup>-IHC 413 414 expression <sup>35</sup>. The results released by Anyplex II HPV28 showed a Cohen's Kappa index of 0.76 415 versus the 0.85 assessed in our study. Another study that used Cepheid Xpert HPV assay in the detection of HPV in 159 FFPE samples of OPSCC origin and compared it to p16<sup>INK4A</sup> IHC, 416 417 exposed a 0.87 Cohen's Kappa coefficient similar to the Ampfire Multiplex HR-HPV test 418 (Cohen's Kappa=0.85, 95% CI 0.751-0.945). Guerendiain and colleagues also tested Cepheid

Xpert HPV assay on 50 OPSCC samples finding a 90% agreement with p16<sup>INK4A</sup> immunostaining
 <sup>24</sup>, a concordance slightly lower than the 93.8% displayed by the Ampfire test in the present
 study.

The Roche Linear Array HPV Genotyping test is a robust method for determining HPV genotype in the routine analysis of OPSCC in FFPE <sup>36,37</sup>. Moreover, this technique is effective in detecting 37 HPV genotypes (including all high-risk types) with high precision <sup>36</sup> in both, preserved cytology and FFPE samples. Unfortunately, the assay is costly and low throughput, and requires a long time of technical handling. Additionally, the amplicons detected by the Ampfire assay are smaller (100 bp E1 and/or L1) than the ones detected by Linear Array (450 bp) which would normally represent an increase of sensitivity due to a better amplification efficiency <sup>38</sup>.

429 From a biological point of view the detection of HPV E6/E7 mRNA constitutes the current gold 430 standard to identify transcriptionally-active HR-HPV and thus an etiological role of HPV in 431 OPSCC. It has shown superior patient survival stratification, slightly better than p16<sup>INK4A</sup> 432 immunohistochemistry alone and better than DNA in situ hybridization and DNA PCR <sup>39</sup>. Nevertheless, expression of p16<sup>INK4A</sup> as detected by IHC is a widely available surrogate 433 biomarker that has very good agreement with HPV status as determined by HPV E6/E7 mRNA 434 435 expression (National Comprehensive Cancer Network Guidelines for Head and Neck Cancers, 436 Version 3.2021, https://www.nccn.org/guidelines/guidelines-detail?category=1&id=1437, last 437 accessed date July 10, 2021). Both high sensitivity and specificity have been demonstrated when p16<sup>INK4A</sup> IHC is combined with HPV DNA detection by PCR <sup>30</sup>. Moreover, HPV E6/E7 mRNA 438 439 detection from FFPE samples is still difficult to implement in certain settings.

Ampfire assays, instead, rely on real-time isothermal PCR, which is an easier and faster procedure as compared with the Linear Array technique which appears more tedious and involves specific material for hybridisation of the strip following PCR amplification. Using the Ampfire assay as the initial screen could significantly decrease the turnaround time, labor and costs associated with our current testing strategy.

The data shown in this manuscript demonstrate that the commercially available Ampfire Multiplex HR-HPV and Genotyping HR-HPV tests show a similar performance to Linear Array on the detection and genotyping of HPV on FFPE OPSCC samples. In conclusion, the Ampfire tests appear to be a trustable HPV detection method that could be used in clinical laboratories with good performance in routine OPSCC FFPE samples, thus meeting the latest recommendations for direct HPV testing in OPSCC.

451

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### 458 AUTHOR CONTRIBUTIONS

- SP and MAP contributed to the investigation and writing of the manuscript. MAP, FXB and LAcontributed to the conceptualization of the work. BQ contributed to the statistical analysis.
- 461 MT was involved in patient recruitment and clinical data collection. MM contributed to 462 epidemiological analysis and MG in histopathological examination and p16<sup>INK4A</sup> IHC.
- 463 MAP and SP are the guarantors of this work and, as such, have full access to all the data in the
- study and take responsibility for the integrity of the data and the accuracy of the data analysis.
- 465

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- 467 Atila did not play any role in the study design, conduction, data analysis; in the writing of the 468 report; and in the decision of submitting the article for publication.
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## Table 1. HPV-DNA positivity percentage agreement between Linear Array and AmpfireMultiplex HR-HPV tests in total HNSCC, OPSCC and non-OPSCC

	HNSCC		Ampfire Mu	Ampfire Multiplex HR-HPV Test		-
			Positive	Negative	Total	98.9 % concordance
	Linear Array	Positive	47 (26.1%)	2 (1.1%)	49 (27.2%)	Cohen's Kappa 0.972
		Negative	0 (0.0%)	131 (72.8%)	131 (72.8%)	(95% CI Kappa 0.932-1.000)
		Total	47 (26.1%)	133 (73.9%)	180 (100%)	p-value <0.001
	OPSCC		Ampfire Mu	ltiplex HR-HPV Test		_
			Positive	Negative	Total	99.4% concordance
	Linear Array	Positive	44 (28.0%)	1 (0.6%)	45 (28.7%)	Cohen's Kappa 0.984
		Negative	0 (0.0%)	112 (71.3%)	112 (71.3%)	(95% CI Kappa 0.953-1.000)
		Total	44 (28.0%)	113 (72.0%)	157 (100%)	p-value <0.001
	Non-OPSCC		Ampfire Mu	ltiplex HR-HPV Test		_
			Positive	Negative	Total	95.7 % concordance
	Linear Array	Positive	3 (13.0%)	1 (4.3%)	4 (17.4%)	Cohen's Kappa 0.832
		Negative	0 (0.0%)	19 (82.6%)	19 (82.6%)	(95% CI Kappa 0.489-1.000)
		Total	3 (13.0%)	20 (87.0%)	23 (100%)	p-value <0.001
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667Table 2. HPV genotyping and detection agreement, in single and multiple infections,668between Linear Array and Ampfire Genotyping HR-HPV Real Time Fluorescent Detection

**tests** 

	HPV-Positive samples, n				
HPV-type	Linear Array	Ampfire Multiplex HR-HPV Assay			
	(HR-HPV)	(HPV16, HPV18 & Other HR-HPV)			
HPV16	39	39			
HPV18	1	1			
Other HR-HPV non-HPV16/18	10	7			

# Table 3. HPV-types agreement and discrepancies, between Linear Array and Ampfire Genotyping HR-HPV Real Time Fluorescent Detection Assay

	HPV Genotypes in HPV-Positive Cases, n					
HPV-type	Linear Array	Ampfire Genotyping HR-HPV				
	(HR-HPV)	Assay (HR-HPV non-HPV16/18)				
HPV16	1	1				
HPV45	2	1				
HPV33	6	5				
HPV35	1	1				
HPV52	6	0				
infections (16 and .	52, 33 and 52 and 35 and 52	2)				

# 721 Table 4. Concordance between Linear Array versus p16<sup>INK4A</sup>-IHC and Ampfire Multiplex HR-

# 722 HPV DNA versus p16<sup>INK4A</sup>-IHC in OPSCC

P16-IHC					
		Positive	Negative	Total	94.5%concordance
Linear Array	Positive	38 (26 2%)	4 (2.8%)	12 (29.0%)	Cohen's Kappa 0.866*
Linear Array	rositive	38 (20.270)	4 (2.070)	42 (25.070)	(95% CI Kappa 0.775-0.957)
	Negative	4 (2.8%)	99 (68.3%)	103 (71.0%)	n.voluo <0 001
	Total	42 (29.0%)	103 (71.0%)	145 (100%)	p-value <0.001
		Positive	Negative	Total	- 93.8 % concordance
Ampfire HR-HPV	Positive	37 (25.5%)	4 (2.8%)	41 (28.3%)	Cohen's Kappa 0.848*
Multiplex Test	Negative	5 (3.4%)	99 (68.3%)	104 (71.7%)	(95% CI Kappa 0.751-0.945)
	Total	42 (29.0%)	103 (71.0%)	145 (100%)	p-value <0.001

723 \* The p-value between Cohen's Kappa coefficient of the dual testing Linear Array/p16<sup>INK4A</sup>-IHC versus Ampfire HR-HPV Multiplex/

724 p16<sup>INK4A</sup>-IHC is 0.791 (not significant)