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Multicenter Evaluation of a Novel ROS1 Immunohistochemistry Assay (SP384) for Detection of ROS1 Rearrangements in a Large Cohort of Lung Adenocarcinoma Patients

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► **To cite this version:**

Véronique Hofman, Isabelle Rouquette, Elodie Long-Mira, Nicolas Piton, Emmanuel Chamorey, et al.. Multicenter Evaluation of a Novel ROS1 Immunohistochemistry Assay (SP384) for Detection of ROS1 Rearrangements in a Large Cohort of Lung Adenocarcinoma Patients. *Journal of Thoracic Oncology*, 2019, 14 (7), pp.1204-1212. 10.1016/j.jtho.2019.03.024 . hal-02421514

HAL Id: hal-02421514

<https://hal.umontpellier.fr/hal-02421514v1>

Submitted on 25 Oct 2021

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1 **Multicenter evaluation of a novel ROS1 immunohistochemistry**
2 **assay (SP384) for detection of *ROS1* rearrangements in a large**
3 **cohort of lung adenocarcinoma patients**

4
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33

34 **Abstract**

35 **INTRODUCTION:** The detection of a *ROS1* rearrangement in advanced and
36 metastatic lung adenocarcinoma (LUAD) lead to a targeted treatment with tyrosine
37 kinase inhibitors, with favorable progression-free survival and overall survival of the
38 patients. Thus, it is mandatory to screen for the *ROS1* rearrangement in all these
39 patients. *ROS1* rearrangements can be detected using break-apart fluorescence *in*
40 *situ* hybridization (FISH), which is the “gold standard”; however, ROS1
41 immunohistochemistry (IHC) can be used as a screening test since it is widely
42 available, easy and rapid to perform, and cost-effective.

43 **METHODS:** We evaluated the diagnostic accuracy and inter-pathologist agreement
44 of two anti-ROS1 IHC clones, SP384 (Ventana, Tucson, AZ) and D4D6 (Cell
45 Signaling, Danvers, MA), in a training cohort of 51 positive *ROS1* FISH LUAD cases,
46 and then in a large validation cohort of 714 consecutive cases of LUAD from six
47 routine molecular pathology platforms.

48 **RESULTS:** In the two cohorts, the SP384 and D4D6 clones demonstrate variable
49 sensitivity and specificity rates on the basis of two cutoff points $\geq 1+$ (all % tumor cells
50 and $\geq 2+$ ($>30\%$ stained tumor cells). In the validation cohort, the D4D6 yielded the
51 best accuracy for the presence of a *ROS1* rearrangement by FISH. Inter-pathologist
52 agreement was moderate to good (ICC, 0.722–0.874) for the D4D6 clone and good
53 to excellent (ICC, 0.830–0.956) for the SP384 clone.

54 **CONCLUSIONS:** ROS1 IHC is an effective screening tool for the presence of ROS1
55 rearrangements. However, users must be acutely aware of the variable diagnostic
56 performance of different anti-ROS1 antibodies prior to implementation into routine
57 clinical practice.

58

59 **Keywords:** ROS1; SP384; D4D6; immunohistochemistry; FISH; lung
60 adenocarcinoma.

61

INTRODUCTION

Patients with advanced and metastatic lung adenocarcinoma (LUAD) harboring a *ROS1* rearrangement respond effectively to crizotinib, as well as to the other tyrosine kinase inhibitors that are currently used in clinical trials.¹⁻⁵ *ROS1* screening is thus recommended in most guidelines. *ROS1* rearrangement detection using fluorescence *in situ* hybridization (FISH) is the typical approach that is consistently performed to identify patients with LUAD who would be eligible for these treatments. Based on its high sensitivity and specificity, this method is considered to be the “gold standard” for determining *ROS1* positivity.^{6, 7} However, given the low incidence of *ROS1* rearrangements in lung adenocarcinoma (1% to 2%),⁶ detection of *ROS1* protein expression by immunohistochemistry (IHC) can be used as a surrogate, cost-effective screening test that is preferable to FISH analysis for screening the *ROS1* status.⁸ Furthermore, the expression of the *ROS1* protein, as detected by IHC, may indicate a functional gene product, which is necessary for effective drug targeting.⁹ Moreover, FISH testing requires high-level expertise for technical and diagnostic issues, which is not widely available in all laboratories. Finally, the turnaround time for getting the final result can sometimes delay an urgent treatment decision.¹⁰

Considering these latter constraints, *ROS1* IHC was recommended as a frontline screening test prior to confirmatory FISH analysis in *ROS1*-positive cases and to avoid unnecessary FISH analysis in *ROS1*-negative cases.⁸ To date, a single commercially available antibody (D4D6 clone, Cell Signaling Technology, Danvers, MA, USA) has been used in several studies and is currently used worldwide in routine clinical practice.¹¹⁻¹³ Given the high sensitivity of IHC relative to FISH or other molecular approaches, such as next generation sequencing (NGS) technologies, 97-98% of tumors that clearly lack *ROS1* staining can be safely interpreted as negative for *ROS1* rearrangement.^{6, 11-13}

Conversely, the interpretation of a positive *ROS1* D4D6 IHC test may be challenging and can lead to false-positive results (related to a patchy pattern and weak intensity of the staining) that do not harbor an underlying *ROS1* rearrangement as detected by FISH.¹⁴⁻¹⁶ Therefore, the variability of specificity reported for the *ROS1* D4D6 IHC assay requires caution and subsequent confirmation of the *ROS1* status by a validated method, irrespective of the staining intensity and the percentage

95 of positive tumor cells.^{15, 17} Only the confirmation of a *ROS1* rearrangement by a
96 molecular or cytogenetic method (e.g., FISH, NGS) can be used prior to considering
97 a patient with LUAD for *ROS1*-targeted therapy.^{8, 18}

98 In this context, the development of a new anti-*ROS1* antibody (SP384 clone,
99 Ventana, Tucson, AZ, USA) prompted the evaluation of its diagnostic performance to
100 predict the presence of a *ROS1* rearrangement in a routine clinical setting.

101 This study aimed to investigate the correlation between two *ROS1* IHC assays
102 and paired *ROS1* FISH analysis as well as inter-pathologist agreement for IHC
103 interpretation in two large-scale multicenter cohorts of LUAD cases.

104

105 **PATIENTS AND METHODS**

106 **Case selection**

107 The training cohort was comprised of retrospective archival formalin-fixed
108 paraffin-embedded (FFPE) tumor samples from 51 patients with stage IIIB/IV LUAD
109 and *ROS1* FISH positive. None of the *ROS1* positive cases harbored concurrent *ALK*
110 rearrangements nor *EGFR* or *BRAF* activating mutations. In *ROS1* positive patients,
111 tumor response was evaluated per RECIST 1.1 on target lesions, 3 months after the
112 initiation of crizotinib and was compared with baseline results.

113 In the validation cohort, 714 cases of consecutive LUAD diagnosed in the
114 Laboratory of Clinical and Experimental Pathology (Pasteur Hospital, Université Côte
115 d'Azur, Nice, France) between 2006 and 2017 were integrated in tissue microarray
116 (TMA) FFPE blocks. Three tissue cores of 600 µm in diameter were taken from
117 different tumor areas within the same FFPE block for each case.

118 A signed informed consent was obtained from all patients. The study was
119 approved by the local ethics committee (Human Research Ethics Committee, Nice
120 University Hospital Center/hospital-related Biobank BB-0033-00025) and was
121 performed in accordance with the guidelines of the Declaration of Helsinki. *ROS1*
122 FISH positive tissue samples were provided by 6 pathology laboratory centers in
123 France (University Hospitals of Bordeaux, Caen, Nancy, Nice, Rouen and Toulouse)
124 and centralized for IHC and FISH analysis in the Laboratory of Clinical and
125 Experimental Pathology (Nice, France), which is accredited by COFRAC (French
126 National Authority for Accreditation delivery, n°8-3034; www.cofrac.fr) for FISH and
127 IHC testing according to the ISO 15189 norm.

128 **ROS1 FISH analysis**

129 Tumor samples were fixed in formaldehyde 10% and paraffin, embedded at
130 each participating center before centralization. Tissue sections (4 µm thick) were
131 stained with hematoxylin eosin and the percentage of tumor cells was assessed
132 independently by three senior thoracic pathologists (VH, MI, PH). Briefly, FISH
133 analysis was conducted using the Abbott Molecular FISH probe (Abbott Molecular
134 Inc., Des Plaines, IL, USA), LSI ROS1 (Tel) SpectrumOrange Probe and LS1 ROS1
135 (Cen) SpectrumGreen Probe. Additionally, some tumors were assessed for *ROS1*
136 rearrangement using the ZytoLight SPEC ROS1 Dual Colour Break Apart Probe
137 (ZytoVision, Bremerhaven, Germany). FISH was performed according to the
138 manufacturer's recommendations. Interphase signals were manually counted in at
139 least 100 tumor nuclei per case using an epi-fluorescence microscope (Eclipse 80i,
140 Nikon, Champigny-sur-Marne, France) supported in parallel by the PathScan®
141 Viewer software (Excilone, Elancourt, France).

142 A positive case was defined if more than 15% of tumor cells in more than 100
143 tumor cells demonstrated a split signal at least 2 signal distances apart or an isolated
144 centromeric 3' (green signal) pattern.

145 **ROS1 IHC analysis**

146 ROS1 IHC analysis was performed using the D4D6 clone (Cell Signaling
147 Technology, Danvers, MA, USA; CC1 buffer for 64 min, 1:50 dilution for 32 min,
148 ultraView Universal DAB Detection Kit, Ventana, Tucson, AZ, USA) and the SP384
149 clone (Ventana, Tucson, AZ, USA; CC1 buffer for 64 min, 1:50 dilution for 16 min,
150 OptiView DAB IHC Detection Kit, Ventana) and processed on the Ultra Benchmark
151 autostainer (Ventana) according to the manufacturer's recommendations.
152 Immunostainings were interpreted independently by three senior lung pathologists
153 (VH, MI, PH), blinded to FISH results, for the following criteria: signal intensity (0; no
154 staining, 1+; weak, 2+; moderate; and 3+; strong) and percentage of stained cells,
155 topography and characteristics of the signal (cytoplasmic – diffuse or focal and/or
156 granular; cytoplasmic and membranous; membranous). Results were quantified by
157 multiplying the percentage of ROS1 positive tumor cells by the intensity (H-score,
158 range, 0–300). For each case included on the TMA FFPE blocks, the mean H-score
159 of the three cores was recorded. Non-specific staining of macrophages and type II

160 pneumocytes was disregarded. ROS1 negative and positive controls were put on
161 each IHC slide (HCL0024, HistoCyte Laboratories Ltd, Newcastle University, UK).

162 **Statistical analysis**

163 Statistical analyses assessing agreement between the D4D6 and SP384
164 antibodies with the ROS1 FISH analysis (gold standard) were performed on
165 dichotomized variables using two positivity cutoff points: IHC ROS1 positive (intensity
166 $\geq 1+$, any percentage of tumor cells) and IHC ROS1 strongly positive (intensity $\geq 2+$,
167 $>30\%$ tumor cells), as recently described.^{17, 19} Sensitivity, specificity, positive
168 predictive value (PPV), negative predictive value (NPV), and accuracy were
169 calculated for the comparison between the dichotomized results using each of the
170 two antibodies relative to the FISH results. The Spearman's rank correlation test (*rho*)
171 was used for a correlation analysis between the H-scores as continuous variables of
172 each clone. Intra-class correlation coefficients were calculated for the comparison of
173 H-scores as continuous variables from each of the ROS1 clones, and κ scores were
174 calculated for dichotomized results based on two positivity cutoff points, as described
175 above, to assess the inter-pathologist agreement for each of the clone. The paired
176 Student's t-test was used to assess the correlation between the ROS1 IHC status
177 and RECIST 1.1. All statistical analyses were carried out using R software (version
178 3.2.2, R Core Team, Vienna, Austria). Any *P*-value <0.05 was assumed to indicate a
179 statistically significant difference.

180

181 **RESULTS**

182 **Training cohort**

183 In a clinically selected cohort enriched for tumors with FISH-identified ROS1
184 rearrangements, the frequency of split or isolated centromeric signals averaged 64%
185 and ranged from 15% to 100%. IHC SP384 showed strong 3+ expression in 40/51
186 (78%), 2+ moderate in 10/51 (20%) and 1+ weak in 1/51 (2%) of cases (**Table 1,**
187 **Figure 1**). IHC D4D6 showed a wider range of intensity in 15/51 (30%) with 3+
188 staining, 16/51 (31%) with 2+ staining and 20/51 (39%) with 1+ staining (**Table 1,**
189 **Figure 1**). Inter-pathologist agreement was high in interpreting both ROS1 IHC
190 clones (**Supplementary Table S1**).

191 On the basis of the $\geq 1+$ expression cutoff, both ROS1 IHC clones are 100%
192 sensitive, whereas if $\geq 2+$ tumors are considered positive, the SP384 clone is 98%

193 sensitive and D4D6 is only 61% sensitive for the detection of a ROS1 rearrangement
194 by FISH (**Table 1**).

195 H-scores ranged from 5 to 300 and from 50 to 300 when using the D4D6 and
196 SP384 clones, respectively. However, the Spearman's rank correlation was not linear
197 ($\rho=0.508$; 95% CI, 0.19–0.72) between the two clones (**Figure 1, Supplementary**
198 **Figure S1**).

199 Neither the intensity nor the percentage of ROS1 protein expression detected
200 with both SP384 and D4D6 antibodies correlated with the percentage of ROS1 split
201 signals by FISH (**Supplementary Figure S2**).

202 In most of the cases analyzed with the SP384 clone, a diffuse cytoplasmic
203 staining was observed with or without membranous staining (**Figure 2**). Less
204 frequently, a granular cytoplasmic or a membranous staining alone was noted
205 (**Figure 2**). Corresponding D4D6 IHC staining was weaker and in some cases the
206 percentage of positive tumor cells was lower than those noted in the corresponding
207 tumors stained with the SP384 clone (**Figure 1, Supplementary Figure S1**). ROS1
208 protein expression was also seen with both D4D6 and SP384 antibodies in non-
209 neoplastic alveolar epithelium at the tumor periphery, in sub-pleural pneumocytes or
210 in areas of type II pneumocyte hyperplasia and bronchiolar metaplasia. However, the
211 expression in this epithelium was weak in intensity in most cases.

212 In this retrospective study, at the time of clinical care, the vast majority of
213 ROS1 positive patients, as confirmed by FISH, were treated with crizotinib in the
214 second and third line settings. After 3 months, 18% of patients had a complete
215 response, 19% demonstrated a partial response, 19% had stable disease, and 44%
216 had progressive disease (**Supplementary Figure S3**). In total, 56% of patients had
217 disease control after 3 months on crizotinib. However, no significant difference
218 existed between the two IHC clones (**Supplementary Figure S3**) nor between the %
219 of rearranged tumor cells by FISH and the response by RECIST (t-test, P -
220 value=0.306). In order to identify putative resistance mechanisms²⁰, an NGS analysis
221 (Ion AmpliSeq Cancer Hotspot Panel, ThermoFisher Scientific, San Francisco, CA,
222 USA) was performed in two patients with progressive disease and available tumor
223 material. In one patient, we found a mutation in the gene encoding for β -catenin
224 (CTNNB1 p.S45F, VAF 43%). The NGS analysis detected no copy-number

225 variations. Moreover, these cases had no *ROS1* copy-number gain, as determined by
226 FISH.²⁰

227 **Validation cohort**

228 A total of 714 cases of LUAD with an unknown *ROS1* rearrangement status
229 were screened on TMA blocks using paired a ROS1 IHC and FISH assay. *ROS1*
230 rearrangements were detected in this screening cohort by FISH at a rate of 9 of 714
231 cases (1.3%).

232 On the basis of the $\geq 1+$ expression cutoff, both ROS1 IHC clones are 100%
233 sensitive for the presence of a ROS1 translocation detected by FISH, while the D4D6
234 clone was deemed more specific and accurate (**Table 1, Figure 3**). Conversely, on
235 the basis of the $\geq 2+$ expression cutoff, the SP384 clone was more sensitive than the
236 D4D6 clone, while the D4D6 was more specific and accurate than SP384 (**Table 1,**
237 **Figure 3**).

238 Inter-pathologist agreement ranged from moderate to good (ICC, 0.722–0.874)
239 in interpreting the D4D6 IHC assay and from good to excellent (ICC, 0.830–0.956) for
240 the SP384 IHC assay (**Supplementary Table S1**).

241

242

243 DISCUSSION

244 This is the first study to assess the diagnostic performance of a newly
245 developed anti-ROS1 antibody (SP384 clone) by comparison to two diagnostic ROS1
246 assays that are validated for a clinical setting (e.g., D4D6 IHC and ROS1 break-apart
247 FISH assays) in two large-scale multicenter cohorts of LUAD cases.

248 We considered two cutoffs for positivity and showed that none of the ROS1
249 IHC assays demonstrated 100% accuracy in detection of *ROS1* rearrangements as
250 identified by FISH. In the validation cohort of ROS1-positive LUAD cases, while these
251 two clones demonstrate similar sensitivity around the $\geq 1+$ cutoff, the sensitivity rate
252 dropped at 61% for the D4D6 clone when the $\geq 2+$ cutoff was applied. In addition, the
253 intensity and the percentage of stained tumor cells were higher when using the
254 SP384 clone than with the D4D6 clone. Inter-reader agreement varied from moderate
255 to good when interpreting the D4D6 assay, while it was deemed good to excellent for
256 the SP384 clone, as recently reported.¹⁹ Most of the cases analyzed with the SP384
257 clone showed diffuse cytoplasmic staining, with or without membranous labeling.

258 It is noteworthy that the percentage and the intensity of SP384 and D4D6 IHC
259 did not correlate with the percentage of *ROS1* FISH split signals, as had previously
260 been reported.¹² No significant difference was noted between the different ROS1 IHC
261 assays and the RECIST 1.1 subgroups in patients treated with crizotinib.

262 In our screening cohort, which was drawn from a clinical molecular diagnostics
263 practice, ROS1 rearrangement was detected in 1.3% of tumors, compared to 1–2%
264 of unselected LUAD cases, as previously reported.⁶ Around the $\geq 1+$ cutoff, sensitivity
265 was similar for both IHC assays; however, the specificity of the D4D6 clone (97.87%)
266 was higher than that of the SP384 clone (87.38%). We also explored the recently
267 described $\geq 2+$ cutoff in $>30\%$ tumor cells.^{17, 19} Whereas the sensitivity of the D4D6
268 clone declined to 66.67% under these criteria, and was 88.89% for the SP384
269 antibody, the specificity was still higher for the D4D6 assay (99.57%) than the SP384
270 clone (91.06%).

271 The average H-score of the SP384 clone was higher than the D4D6 antibody,
272 which led to easier interpretation. However, if an algorithm for *ROS1* testing that is
273 similar to that established for *ALK* status testing were used and if the $\geq 1+$ cutoff were
274 to be used for both IHC clones, this could lead to an increase of nearly 10% in
275 unnecessary FISH testing based on screening with the SP384 clone. Moreover, in

276 our study, the $\geq 2+$ cutoff in $>30\%$ tumor cells did not improve the sensitivity and
277 specificity rates of either IHC assay.

278 When newly developed diagnostic assays for the detection of rare events such
279 as *ROS1* rearrangements are considered for implementation in a routine clinical
280 setting, our findings highlight the importance of their evaluation in large-scale cohorts,
281 and the necessity of both positive and negative cases. As accurate detection of
282 *ROS1* rearrangements in clinical tumor samples is mandatory for optimal targeted
283 treatment, investigation of new testing modalities should not be limited to positive
284 samples only.¹⁸

285 Previous studies reported *ROS1* D4D6 IHC as being highly sensitive, but less
286 specific compared with FISH for the detection of *ROS1* rearrangements. *ROS1*
287 D4D6-positive tumors, especially when the tumor is stained with moderate to strong
288 intensity or a diffuse pattern, are recommended to undergo FISH to confirm the
289 presence of *ROS1* rearrangement.¹²⁻¹⁴ Besides the assessment of the *ROS1*
290 rearrangement status, it is mandatory to systematically detect other genomic
291 alterations in advanced and metastatic lung adenocarcinoma. This can be performed
292 by molecular biology (e.g., *EGFR* mutation) and by molecular and/or IHC approaches
293 (e.g., *BRAFV600* mutation, *ALK* rearrangement). Moreover, PD-L1 IHC is now
294 required in this population. Additionally, the evaluation of other genomic alterations
295 (e.g., *RET* rearrangement, *MET* mutations, *HER2* mutations, *NTRK* rearrangement)
296 can be required if the tumors are *EGFR*, *ALK*, *ROS1* and *BRAF* wild-type and with
297 less than 50% of PD-L1 positive tumor cells. Moreover, recent clinical trials for
298 immunotherapy associated with the assessment of the tumor mutation burden (TMB)
299 have indicated some promising results for the systemic use of this predictive
300 biomarker in the near future.^{21, 22} In this context, one challenge is to be able to
301 perform these analyses on smaller tissue biopsies and/or samples with low
302 proportions of tumor cells (less than 20%). Considering that a minimum number of
303 tissue sections are required for the diagnosis of NSCLC, it is critical to conserve
304 tissue as much as possible for ancillary analyses (different predictive IHC, targeted
305 sequencing analyses or NGS panels – potentially including TMB assessment). In this
306 context, it is of interest to economize and only use tissue sections for *ROS1* FISH
307 analysis in IHC positive cases. More importantly, the feasibility of using *ROS1* IHC for
308 *ROS1* status assessment has many advantages in comparison with the *ROS1* FISH.

309 IHC is available in all pathology laboratories and can easily be conducted. The
310 turnaround time to get the results is much shorter than the FISH approach. IHC is a
311 cost-effective technology. Finally, shipment and archiving of stained slides can be
312 done at room temperature.

313 Different testing approaches, such as DNA-based hybrid capture library
314 preparation followed by NGS, RNA-based anchored multiplex polymerase chain
315 reaction library preparation followed by NGS or nCounter technologies could allow
316 the simultaneous detection of gene rearrangements such *ALK*, *ROS1*, *RET*, or
317 *NTRK*.^{18, 23, 24} Thus, it might be questionable whether the development of IHC assays
318 for the detection of these alterations should continue, in particular for *ROS1*
319 rearrangement. However, some difficulties can be encountered for the NGS
320 approach in comparison with the IHC method in a clinical setting.²⁵ Depending on the
321 quantity and quality of nucleic acids present in the FFPE tissue biopsy, NGS can give
322 false negative results, in particular in small specimens and/or when a low percentage
323 of tumor cells are present. Moreover, the technology is not available in all
324 laboratories and requires specific and high-level expertise. The time lag for results is
325 also much longer than for IHC testing. Finally, the accreditation is certainly easier to
326 obtain for an IHC test than for a test developed on an NGS platform.

327 Assuming that the implementation of the SP384 IHC assay in the testing
328 algorithm of advanced and metastatic LUAD patients can be considered, following
329 the results showed in the present work and probably other forthcoming studies,
330 independent validation studies need to be performed. In addition, it will be of interest
331 to further assess the performance of the SP384 clone on cytology samples such as
332 cellblocks.^{26, 27} Finally, as a perspective, the ROS1 IHC assay could be a good
333 candidate to be associated with other “predictive” antibodies such as the anti-ALK,
334 anti-BRAFV600E and anti-PD-L1 in a chromogenic multiplex IHC assay for small
335 tissue biopsies.²⁸

336 In conclusion, ROS1 IHC testing is an effective screening tool for the presence
337 of *ROS1* rearrangements. However, users must be aware of the variable diagnostic
338 performance of different commercialized anti-ROS1 antibodies before incorporation
339 into the diagnostic molecular pathology workup of LUAD cases.

340
341

342 **Funding**

343 This work was supported by a grant from the Canceropôle PACA and the “Conseil
344 Départemental des Alpes-Maritimes”. SH is a research fellow of the Labex Program
345 Signalife (Université Côte d’Azur).

346

347 **Conflict of interests:**

348 I.R. has received honoraria from AstraZeneca, MSD, Bristol-Myers Squibb,
349 Boehringer-Ingelheim, Roche and Takeda.

350 J.M has received research grant and honoraria from Roche, AstraZeneca and Bristol-
351 Myers Squibb, and honoraria from Boehringer-Ingelheim, MSD, PharmaMar, Pfizer,
352 Takeda.

353 F.B. has received honoraria from Bristol-Myers Squibb, MSD, Amgen, Merck & Co.,
354 Sanofi, Haliodx and AstraZeneca, and grants and travel expenses from Bristol-Myers
355 Squibb and MSD.

356 J-C.S. has received honoraria from Amgen, Roche, Pfizer, MSD, Bristol-Myers
357 Squibb, Merck & Co., AstraZeneca and Boehringer-Ingelheim.

358 M.I. has received honoraria and travel grants from AstraZeneca, Bristol-Myers
359 Squibb, Roche, Boehringer-Ingelheim and Merck & Co.

360 P.H. has received honoraria and travel grants from AstraZeneca, Roche, Bristol-
361 Myers Squibb, Novartis, MSD, Qiagen, Thermofisher, Biocartis, and Merck & Co.

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363 The remaining authors have declared no conflict of interests.

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376 **Legend to Figures**

377

378 **Figure 1. Representative images of ROS1 IHC using the D4D6 and the SP384**
379 **antibodies in the training cohort. (A)** Strong diffuse staining with the SP384
380 antibody, and **(B)** weak to moderate diffuse staining with the D4D6 antibody in the
381 same case as in (A). **(C)** Weak to moderate diffuse staining with the SP384 antibody,
382 and **(D)** weak focal staining with the D4D6 antibody in the same case as in (C). A
383 *ROS1* rearrangement was identified in both cases (A-B, and C-D) by FISH. (Scale
384 bars are shown on the figures).

385

386 **Figure 2. Representative immunostaining localization in tumor cells using the**
387 **SP384 antibody. (A)** Diffuse cytoplasmic. **(B)** Membranous and cytoplasmic. **(C)**
388 Membranous. **(D)** Cytoplasmic granular. Scale bars are shown on the figures.

389

390 **Figure 3. Representative comparative images between the ROS1 IHC using the**
391 **D4D6 and the SP384 antibodies and the ROS1 FISH analysis in the validation**
392 **cohort.**

393 **(A)** Strong diffuse (3+) staining with the D4D6 and SP384 antibodies in a LUAD case
394 positive by ROS1 FISH.

395 **(B)** Weak diffuse staining (1+) with the D4D6 antibody but strong staining (3+) with
396 the SP384 clone in a LUAD case positive by ROS1 FISH.

397 **(C)** Weak diffuse staining (1+) with the D4D6 antibody and moderate staining (2+)
398 with the SP384 clone in a LUAD case positive by ROS1 FISH.

399 **(D)** Lack of staining with both D4D6 and SP384 clones in a LUAD negative by ROS1
400 FISH.

401 **(E)** No staining with the D4D6 clone in a LUAD case moderately stained (2+) with
402 SP384 clone and positive by ROS1 FISH.

403 **(F)** No staining with the D4D6 clone in a LUAD case strongly stained (3+) with the
404 SP384 clone but revealed negative by ROS1 FISH.

405 Red circles; positive tumor cells by FISH; green circles, negative tumors cells by
406 ROS1 FISH.

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410 **Legend to Supplementary Figures**

411

412 **Supplementary Figure S1.** Distribution plot of H-scores for each anti-ROS1
413 antibody.

414

415 **Supplementary Figure S2.** Correlation analysis between the H-scores of **(A)** D4D6
416 or **(B)** SP384 clones and the percentage of tumor cells harboring *ROS1*
417 rearrangement by FISH. *Note: the X-axis in (A) is manually set to have a maximum of*
418 *300 to match with SP384.*

419

420 **Supplementary Figure S3.** Correlation analysis between response assessments by
421 RECIST 1.1 after 3 months under crizotinib and the IHC status by D4D6 (paired
422 Student's t-test; P=0.002) and SP384 (paired Student's t-test; P=0.006) clones.
423 Abbreviations: Progressive Disease (PD), Stable Disease (SD), Partial Response
424 (PR), Complete Response (CR).

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Table 1. Comparative performance analyses between *ROS1* FISH and SP384 and D4D6 IHC clones.

Training cohort	SP384 IHC				D4D6 IHC			
FISH ROS1	Strong 3+	Moderate 2+	Weak 1+	Negative 0	Strong 3+	Moderate 2+	Weak 1+	Negative 0
Positive n = 51	40 (78%)	10 (20%)	1 (2%)	0 (0%)	15 (30%)	16 (31%)	20 (39%)	0 (0%)
Sensitivity Cutoff ≥1+ Cutoff ≥2+	100% (95% CI, 93.02%–100%) 98.04% (95% CI, 89.55%–99.95%)				100% (95% CI, 93.02%–100%) 60.78% (95% CI, 46.11%–74.16%)			
Validation cohort	SP384 IHC				D4D6 IHC			
FISH ROS1								
Positive n = 9 (1.3%)	6 (67%)	2 (22%)	1 (11%)	0 (0%)	3 (33%)	3 (33%)	3 (33%)	0 (0%)
Negative n = 705 (98.7%)	0 (0%)	63 (9%)	26 (4%)	616 (87%)	0 (0%)	3 (1%)	12 (2%)	690 (97%)
Cutoff ≥1+								
Sensitivity	100% (95% CI, 66.37%–100%)				100% (95% CI, 66.37%–100.00%)			
Specificity	87.38% (95% CI, 84.70%–89.74%)				97.87% (95% CI, 96.51–98.80%)			
PPV	9.18% (95% CI, 7.69%–10.94%)				37.50% (95% CI, 26.67%–49.75%)			
NPV	100%				100%			
Accuracy	87.54% (95% CI, 84.89%–89.87%)				97.90% (95% CI, 96.56%–98.82%)			
Cutoff ≥2+								
Sensitivity	88.89% (95% CI, 51.75%–99.72%)				66.67% (95% CI, 29.93%–92.51%)			
Specificity	91.06% (95% CI, 88.71%–93.06%)				99.57% (95% CI, 98.76%–99.91%)			
PPV	11.27% (95% CI, 8.37%–15.01%)				66.67% (95% CI, 37.12%–87.14%)			
NPV	99.84% (95% CI, 99.02%–99.98%)				99.57% (95% CI, 98.93%–99.83%)			
Accuracy	91.04% (95% CI, 88.70%–93.03%)				99.16% (95% CI, 98.18%–99.69%)			

Abbreviations: FISH, Fluorescence in situ hybridization; NPV, Negative Predictive Value; PPV, Positive Predictive Value.

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Figure 1

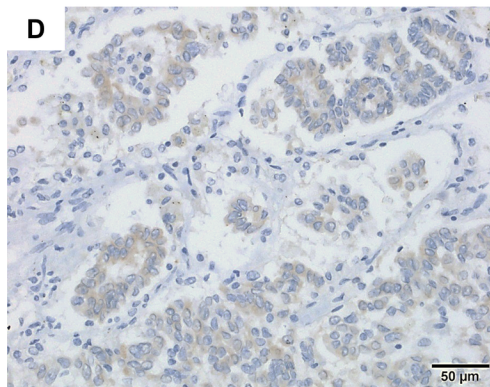
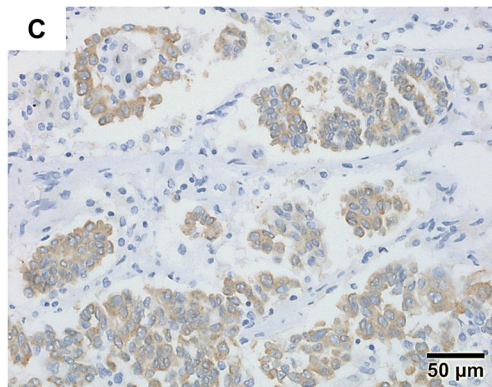
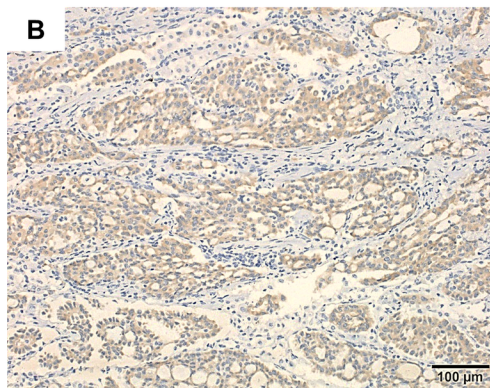
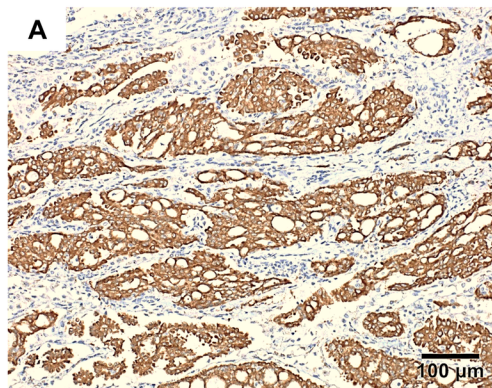


Figure 2

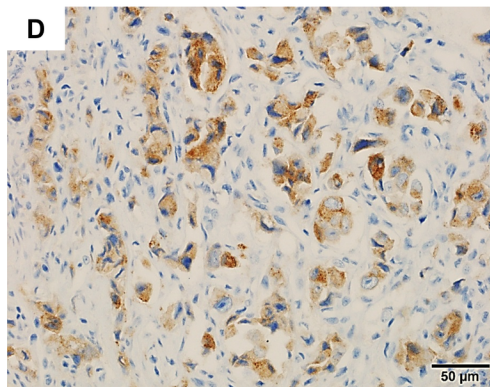
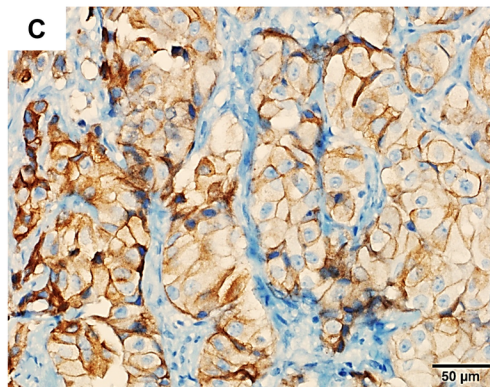
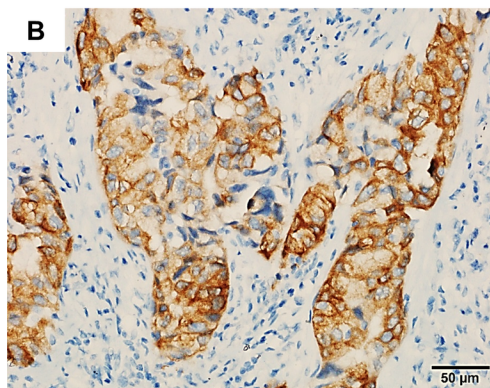
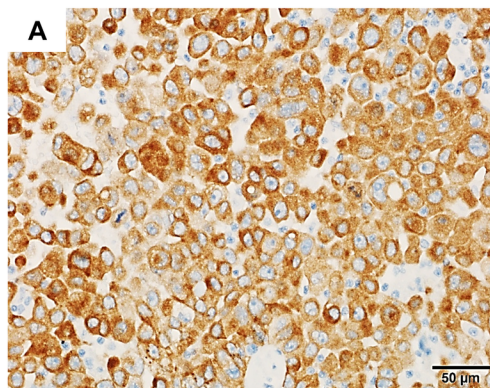
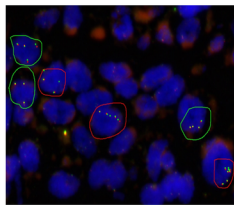
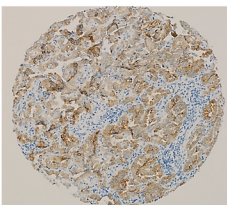
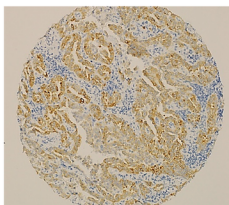
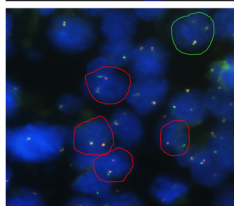
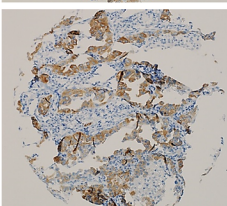
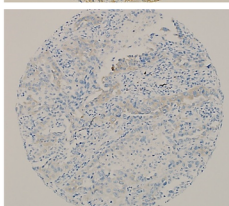
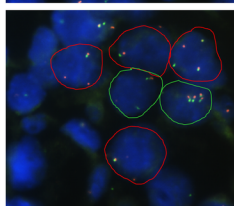
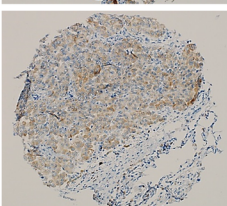
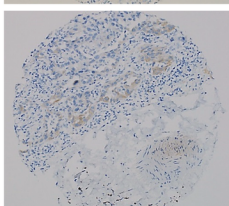
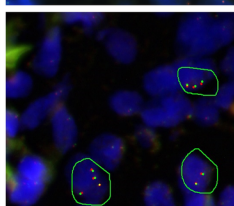
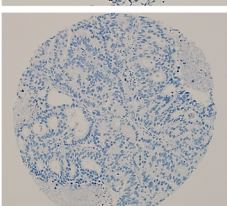
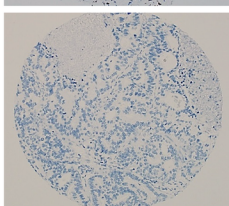
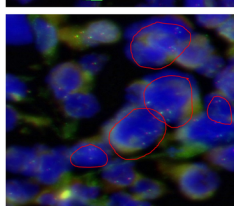
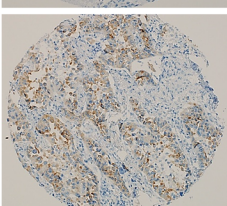
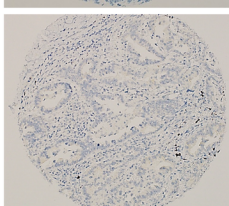


Figure 3**D4D6****SP384****FISH****A****B****C****D****E****F**