Comparison of PD-L1 tumor cell expression with 22C3, 28-8, and SP142 IHC assays across multiple tumor types

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ABSTRACT
Background Multiple PD-L1 immunohistochemistry (IHC) assays, including DAKO 22C3, DAKO 28-8, and Ventana SP142 PD-L1 IHC assays, have been approved by the Food and Drug Administration as a companion diagnostic (CDx) for various antiprogrammed death-1 and antiprogrammed death ligand 1 (PD-L1) based cancer immunotherapies. Here we present 22C3, 28-8, and SP142 analysis of 418 tumor specimens encountered in routine clinical practice.

Methods All specimens were tested with 22C3, 28-8, and SP142 assays following the manufacturer’s established staining protocols.

Results The same PD-L1 status (defined as tumor cell expression (TC) scores with all three assays ≥1% or all <1%) was observed in 60.0% (251/418) tumor specimens (45.9% (192/418) were triple negative and 14.1% (59/418) were triple positive). A total of 54.1% (226/418) tumor cases were positive with at least one IHC assay (94.2% (213/226), 77.0% (174/226), and 28.8% (65/226) of these were positive for 22C3, 28-8, and SP142, respectively). Among the 40.0% (167/418) tumor cases that showed a different status among the three IHC assays, 62.3% (104/167) were 22C3+/28-8+/SP142−, and 28.7% (48/167) were 22C3+/28-8−/SP142+. The same PD-L1 status with all three antibody clones was observed in 48.7% (97/199) of NSCLC cases, and among these, 54.6% (53/97) were triple negative, 32.2% (n=47/146) were positive for 22C3, 28-8, and SP142, respectively. Among the 40.0% (167/418) tumor cases that showed a different PD-L1 status, 62.3% (104/167) were 22C3+/28-8+/SP142−, and 28.7% (48/167) were 22C3+/28-8−/SP142+. The same PD-L1 status with all three antibody clones was observed in 48.7% (97/199) of NSCLC cases, and among these, 54.6% (53/97) were triple negative, 32.2% (n=47/146) were positive for 22C3, 28-8, and SP142, respectively. Among the 51.3% (102/199) NSCLC cases that showed a different status among the three IHC assays, 67.6% (65/96) were 22C3+/28-8+/SP142−, and 23.5% (24/102) were 22C3+/28-8−/SP142+. A total of 81.1% (43/53) lung squamous cell carcinoma, 72.1% (88/122) of lung adenocarcinoma, 89.6% (16/23) of non-small cell lung cancer (NSCLC) not otherwise specified (NOS), and 50.0% (4/8) of small cell lung carcinoma cases were positive with at least one IHC assay.

Conclusions Our data suggest that 22C3 is the most sensitive PD-L1 IHC assay for tumor cell expression, followed by 28-8 and in turn by SP-142. These findings represent an additional factor for clinical teams to consider when deciding which PD-L1 IHC assay (and in turn which CDX-associated PD-L1 based immunotherapy) is most appropriate for each individual patient.

WHAT IS ALREADY KNOWN ON THIS TOPIC
⇒ Prior studies have shown high concordance between 22C3 and 28-8 programmed death ligand 1 (PD-L1) immunohistochemistry (IHC) assays, with lower tumor cell (TC) expression with the SP142 assay in various controlled and clinical settings, which focused on either a limited number (<100) of tumor specimens, or a larger number (>100) of tumor specimens but of a single tumor type, or were unable to assess all three (22C3, 28-8, and SP142 assays) on each tumor specimen.

WHAT THIS STUDY ADDS
⇒ We present the PD-L1 TC expression scores of 22C3, 28-8, and SP142 IHC assays performed on 418 specimens of multiple tumor types encountered in routine clinical practice. We demonstrate that 22C3 is the most sensitive PD-L1 IHC assay, followed in turn by 28-8 and SP-142.

HOW THIS STUDY MIGHT AFFECT RESEARCH, PRACTICE OR POLICY
⇒ The findings represent an additional factor for clinicians to consider when selecting which PD-L1 IHC assay is most appropriate for each individual patient.

INTRODUCTION
Immunotherapy has revolutionized cancer care over the past decade, and new treatment strategies continue to evolve. Programmed death-1/programmed death ligand 1 (PD-1/PD-L1) inhibitors have been approved in the USA and around the world to treat and improve outcomes for patients with a range of tumor types, including non-small cell lung cancer (NSCLC),1 melanoma,2 triple-negative breast cancer,3,4 and small cell lung cancer.5,6

PD-L1 is a transmembrane protein that binds to receptors, PD-1 or B7.1, to downregulate the immune response. PD-1 is an inhibitory receptor predominantly expressed on T cells following T cell activation in response to chronic inflammation, as may occur during infection or within the tumor...
Binding of PD-L1 to PD-1 inhibits T cell proliferation, cytokine production, and cytolytic activity, leading to functional inactivation of T cells. PD-L1 expression can occur on the surface of both tumor cells (TCs) and tumor-associated immune cells (ICs). Upregulated PD-L1 expression on TCs can therefore enable the tumor to evade the immune response. Blockade of PD-L1/PD-1 ligation has become a strategy to restore tumor-specific T cell immunity, and positive expression of PD-L1 on the surface of TCs or ICs has been correlated with clinical benefit and successful treatment with PD-L1/PD-1 inhibitors across a range of cancer types.

The PD-1/PD-L1 treatment landscape is continually adapting to new clinical trial and outcomes data and new Food and Drug Administration (FDA) approvals. Alongside the generation of new PD-1/PD-L1 inhibitors, various immunohistochemistry (IHC) assays have been developed to measure PD-L1 expression and have received approval from the FDA as either companion or complementary diagnostic assays. A companion diagnostic assay (CDx) is defined by the FDA as a diagnostic test that provides required information that is ‘essential for the safe and effective use of a corresponding drug or biological product’. In the European Union, a CDx is defined as ‘a device which is essential for the safe and effective use of a corresponding medicinal product to (a) identify, before and/or during treatment, patients who are most likely to benefit from the corresponding medicinal product; or (b) identify, before and/or during treatment, patients likely to be at increased risk of serious adverse reactions as a result of treatment with the corresponding medicinal product’. To date, the FDA has approved four CDx PD-L1 IHC assays: Dako 22C3 (hereon referred to as 22C3; as a CDx for treatment with pembrolizumab in patients with a range of solid tumors, see table 1); Ventana SP142 (hereon referred to as SP142; as a CDx for treatment with atezolizumab in patients with urothelial carcinoma or NSCLC); Dako 28-8 (hereon referred to as 28-8; as a CDx for treatment with combination of ipilimumab and nivolumab in patients with NSCLC); and Ventana SP263 (hereon referred to as SP263; as a CDx for treatment with atezolizumab in patients with NSCLC). It should be noted, however, that pembrolizumab is also FDA approved for the treatment of all solid tumors regardless of PD-L1 status if microsatellite instability - high (MSI-H) or tumor mutational burden ≥10 mutations/megabase.

| US –FDA diagnostic name | Manufacturer | Tumor type | IHC scoring system | Cut-off score | Treatment | Diagnostic type | Year of FDA approval |
|-------------------------|--------------|------------|--------------------|---------------|------------|-----------------|---------------------|
| **PD-L1 IHC 22C3 pharmDx** | Dako North America, Inc. | Non-small cell lung cancer (NSCLC) | TPS | ≥1 (≥50=high expression) | Pembrolizumab, cemiplimab-rwlc | Companion | 2015 |
| | | Cervical cancer | CPS | ≥1 | Pembrolizumab | Companion | 2018 |
| | | TNBC | CPS | ≥10 | Pembrolizumab | Companion | 2020 |
| | | Head and neck squamous cell carcinoma (HNSCC) | CPS | ≥1 | Pembrolizumab | Companion | 2019 |
| | | Esophageal squamous cell carcinoma | CPS | ≥10 | Pembrolizumab | Companion | 2019 |
| **Ventana PD-L1 (SP142) Assay** | Ventana Medical Systems, Inc. | Urothelial carcinoma | IC | ≥5 | Atezolizumab | Companion | 2018 |
| | | NSCLC | TC and IC | TC ≥50 or IC ≥10 | Atezolizumab | Companion | 2016 |
| **PD-L1 IHC 28-8 pharmDx** | Dako North America, Inc. | NSCLC | TC | ≥1 | Nivolumab in combination with ipilimumab | Companion | 2016 |
| | | Non-squamous NSCLC | TC | ≥1, ≥5, or ≥50 | Nivolumab | Complementary | 2015 |
| | | HNSCC | TC | ≥1 | Nivolumab | Complementary | 2018 |
| | | Urothelial carcinoma | TC | ≥1 | Nivolumab | Complementary | 2018 |
| | | Melanoma | TC | ≥1 | Nivolumab in combination with ipilimumab | Complementary | 2016 |
| **Ventana PD-L1 (SP263) Assay** | Ventana Medical Systems, Inc. | NSCLC | TC | ≥1 | Atezolizumab | Companion | 2021 |
| | | UC | TC and IC | TC ≥25; or ICP ≥1 and IC+ ≥25; or ICP=1 and IC+=100% | Durvalumab | Complementary | 2017 |

Please check FDA website for most current indications. ICP = per cent of tumor area occupied by any tumor-associated immune cells. ICP is used to calculate IC+, which is the per cent area of ICP exhibiting PD-L1 positive immune cell staining. CPS, combined positive score; FDA, Food and Drug Administration; IC, immune cell; IHC, immunohistochemistry; NSCLC, non-small cell lung cancer; PD-L1, programmed death ligand 1; TC, tumor cell; TNBC, triple negative breast cancer; UC, urothelial carcinoma.
A complementary diagnostic test is broadly defined as ‘a test that identifies a biomarker-defined subset of patients that respond particularly well to a drug and aid risk/benefit assessments for individual patients, but that are not prerequisites for receiving the drug’. In the USA, the currently approved complementary diagnostic PD-L1 assays include the 28-8 assay for identifying patients with non-squamous NSCLC, head and neck squamous cell carcinoma (HNSCC) and urothelial carcinoma for treatment with nivolumab and the SP263 assay for identifying patients with urothelial carcinoma for treatment with durvalumab. Treatment with PD-1/PD-L1 inhibitors is indicated when the FDA-approved companion or complementary diagnostic assay demonstrates PD-L1 expression in the patient’s tumor above a specified cut-off. Table 1 lists the cut-offs and various other features of the four main PD-L1 assays available in the USA.

Prior studies have investigated the concordance between two or more PD-L1 IHC assays in controlled and clinical settings. The consensus of these reports is that there is high concordance in TC expression scores between 22C3 and 28-8 IHC assays and much lower TC expression with the SP142 assay. However, several of these studies focused on a limited number (<100) of tumor specimens, while others that evaluated a larger number (>100) of specimens were unable to assess all three IHC assays (22C3, 28-8, and SP142) or analyze more than a single tumor type. In the current study, we analyzed 418 specimens from multiple tumor types (including 199 NSCLC specimens) with three PD-L1 IHC assays (22C3, 28-8, and SP142) during routine clinical practice. These specimens included a range of resection, core needle biopsy, and cytology patient samples. We present the PD-L1 TC expression scores for each specimen, as well as the histology and IHC staining patterns for select clinical cases to showcase important implications for patient treatment and clinical decision making.

**MATERIALS AND METHODS**

**Patient cohort**

The Foundation Medicine database (Morrisville, North Carolina, USA) was searched to collect advanced solid tumor specimens that were tested with all three PD-L1 IHC assays (DAKO 22C3, DAKO 28-8, and Ventana SP142) during the year starting in December 2020 and ending in December 2021. A total of 418 patient specimens (including 199 patient NSCLC specimens) were identified that fulfilled these criteria. Of these 418 specimens, 55.3% (231/418) were biopsies, 41.6% (174/418) were resection specimens, and 3.1% (13/418) were cytology specimens.

**DAKO PD-L1 IHC 22C3 pharmDx assay**

The DAKO PD-L1 IHC 22C3 pharmDx assay was performed per manufacturer’s instructions in a Clinical Laboratory Improvement Amendments (CLIA)-certified and College of American Pathologists (CAP)-accredited reference laboratory (Foundation Medicine). The DAKO PD-L1 22C3 pharmDx assay is an immunohistochemical assay using mouse monoclonal anti-PD-L1 (22C3 clone) for use in the detection of PD-L1 protein in formalin-fixed, paraffin-embedded (FFPE) tissue using the EnVision FLEX visualization system on Autostainer Link 48 and associated staining protocol provided by the package insert and interpreted with the guidelines of the DAKO interpretation guide. All cases had accompanying controls, H&E-stained patient slide, negative reagent control stained patient slide, and a DAKO PD-L1 22C3-stained patient slide. PD-L1 stained slides were evaluated using a tumor proportion score (TPS) method, where TPS=(number of PD-L1-stained tumor cells/total number of viable tumor cells) × 100. A cut-off of TPS ≥1 was used to determine positivity for the 22C3 assay. It should be noted here that the terms TPS and TC expression (see below for 28-8) are often used interchangeably and refer to essentially the same scoring system. Of note, positivity in NSCLC was determined using a cut-off of TPS ≥1 per CDx for pembrolizumab.

**DAKO PD-L1 28-8 pharmDx assays**

The DAKO PD-L1 28-8 pharmDx assay was performed per manufacturer’s instructions in a CLIA-certified and CAP-accredited reference laboratory (Foundation Medicine). In brief, the DAKO PD-L1 28-8 pharmDx assay is an immunohistochemical assay using rabbit monoclonal anti-PD-L1, for use in the detection of PD-L1 protein in FFPE tissue with the EnVision FLEX visualization system on Autostainer Link 48, and associated staining protocol provided by the package insert and interpreted with the guidelines of the DAKO interpretation guide. All cases had accompanying controls, H&E-stained patient slide, negative reagent control-stained patient slide, and a DAKO PD-L1 28-8-stained patient slide. PD-L1 stained slides were evaluated using a tumor cell expression (TC) scoring method, where TC=(number of PD-L1-stained tumor cells/total number of viable tumor cells) × 100. A cut-off of TC ≥1% was used to determine positivity for the DAKO PD-L1 28-8 pharmDx assay. Of note, positivity in NSCLC was determined using a cut-off per CDx for nivolumab in combination with ipilimumab using a TC cut-off score of 1.

**Ventana PD-L1 SP142 CDx assay**

PD-L1 SP142 testing was performed using the Ventana SP142 CDx assay per manufacturer’s instructions in a CLIA-certified and CAP-accredited reference laboratory (Foundation Medicine). In brief, the Ventana SP142 CDx assay consists of the rabbit monoclonal anti-PD-L1 SP142 clone, the Opti-View DAB IHC detection kit, and the Opti-View Amplification Kit stained on the Ventana BenchMark ULTRA instrument using the staining protocol provided by the package insert and interpreted with the guidelines of the Ventana interpretation guide. All cases had an accompanying H&E-stained patient
slide, negative regent control stained patient slide with an on-slide tonsil control and a Ventana PD-L1 SP142 stained patient slide with an on-slide tonsil control. TC levels were determined similarly to the TPS method. A cut-off level of ≥1% staining TCs was used to determine tumor cell expression. (As part of routine clinical practice, the tumor infiltrating ICs scoring method was also used to generate an IC score, which is defined as proportion of tumor area that is occupied by PD-L1 staining IC of any intensity and is not reported in this study).

Data analysis
Comparison of all continuous variables were performed using Kruskal-Wallis test using the R software V.4.0.3.

RESULTS
Patient cohort demographics
A detailed summary of patient cohort demographics is provided in Table 2. The mean and median ages of the entire patient cohort were 67.3 and 68.5 years old, respectively. A total of 48.1% (201/418 cases) of the patients were female. A total of 39.0% (163/418) specimens were from a primary tumor site, 32.8% (137/418) specimens from a metastatic site, and in the remaining 28.2% (118/418) of specimens the tumor site was ambiguous or unknown.

The mean and median ages of the NSCLC patient cohort were 69.7 and 69.0 years old, respectively. A total of 41.7% (83/199 cases) of the patients were female. A total of 52.8% (105/199) NSCLC specimens were from the primary tumor site (lungs), 30.7% (61/199) specimens from a metastatic site, and 16.6% (33/199) from a specimen site that was either ambiguous or unknown.

In addition, NSCLC specimens were received from patients with unknown stage of disease (9.0%, 18/199). The disease diagnoses for NSCLC specimens included lung adenocarcinoma (61.3%, 122/199 cases), lung squamous cell carcinoma (26.6%, 53/199 cases), NSCLC (not otherwise specified) (11.6%, 23/199 cases), and adenosquamous carcinoma (0.5%, 1/199 cases). In addition, the total tumor cohort included eight small cell lung cancer (SCLC) specimens (8/418 total tumor cases, or 1.9% of all tumor cases).

| Tumor type                      | Number of cases (n) | Mean age (years) | Median age (years) | Female patients (%) | Specimen site (% samples in each tumor type) |
|---------------------------------|---------------------|------------------|-------------------|---------------------|-----------------------------------------------|
| NSCLC                           | 199                 | 69.7             | 69.0              | 41.7 (n=83)         | Primary site: 52.8 (n=105) Metastatic: 30.7 (n=61) Ambiguous or unknown: 16.6 (n=33) |
| Gastrointestinal                | 70                  | 65.7             | 65.5              | 55.7 (n=39)         | Primary site: 28.6 (n=20) Metastatic: 54.3 (n=38) Ambiguous or unknown: 17.1 (n=12) |
| Gynecological                   | 37                  | 64.1             | 67.0              | 100 (n=37)          | Primary site: 27.0 (n=11) Metastatic: 32.4 (n=12) Ambiguous or unknown: 37.8 (n=14) |
| Genitourinary                   | 19                  | 72.3             | 72.0              | 0 (n=0)             | Primary site: 52.7 (n=10) Metastatic: 26.3 (n=5) Ambiguous or unknown: 21.1 (n=4) |
| Neuroendocrine tumor            | 17                  | 68.7             | 70.0              | 41.2 (n=7)          | Primary site: 17.6 (n=3) Metastatic: 58.8 (n=12) Ambiguous or unknown: 11.8 (n=2) |
| Head and neck tumor             | 7                   | 57.6             | 62.0              | 71.4 (n=5)          | Primary site: 0 (n=0) Metastatic: 57.1 (n=4) Ambiguous or unknown: 42.9 (n=3) |
| Melanoma                        | 16                  | 70.6             | 73.0              | 31.3 (n=5)          | Primary site: 50 (n=8) Metastatic: 37.5 (n=6) Ambiguous or unknown: 12.5 (n=2) |
| Soft tissue                     | 15                  | 59.4             | 63.0              | 46.7 (n=7)          | Primary site: 60.0 (n=9) Metastatic: 13.3 (n=2) Ambiguous or unknown: 26.7 (n=4) |
| Central nervous system          | 10                  | 51.3             | 53.5              | 50.0 (n=5)          | Primary site: 90.0 (n=9) Metastatic: 0 (n=0) Ambiguous or unknown: 10.0 (n=1) |
| Unknown primary malignant neoplasm | 28              | 63.2             | 69.0              | 46.4 (n=13)         | N/A Metastatic: N/A Ambiguous or unknown: N/A |
| Total                           | 418                 | 67.3             | 68.5              | 48.1 (n=201)        | Primary site: 39.0 (n=163) Metastatic: 32.8 (n=137) Ambiguous or unknown: 28.2 (n=118) |

NSCLC, non-small cell lung cancer.
Overall PD-L1 tumor cell expression patterns

Table 3 shows the PD-L1 status with all three antibody clones in resection, biopsy and cytology specimens. No appreciable difference in tumor cell expression was observed between specimens types. A higher percentage of triple negative (22C3-/28-8-/SP142−) cases are observed in cytology specimens, but this corresponds to only 7 out of 13 total cytology specimens. The proportion of resection, biopsy and cytology specimens with an IC score of ≥1 were 62.6% (65/174), 46.3% (107/231), and 30.8% (4/13), respectively, and the proportion of resection, biopsy and cytology specimens with an IC score <1 were 37.4% (65/174), 53.2% (123/231), and 69.2% (9/13), respectively.

Tumor cell PD-L1 expression as detected with 22C3, 28-8, and SP142 IHC assays across all tumor types are shown in figure 1. Higher positive tumor cell staining was observed with 22C3 compared with 28-8 and SP142 in NSCLC, neuroendocrine tumor, melanoma, soft tissue, and overall tumor specimens. There were no clear differences in positive tumor cell staining between the three different antibody clones for GYN, genitourinary, GI, or CNS tumor specimens. IHC, immunohistochemistry; NSCLC, non-small cell lung cancer; PD-L1, programmed death ligand 1.

**Figure 1** Tumor cell PD-L1 expression detected with 22C3, 28-8, and SP142 IHC assays across all tumor types. Higher positive tumor cell staining was observed with 22C3 compared with 28-8 and SP142 in NSCLC, neuroendocrine tumor, melanoma, soft tissue, and overall tumor specimens. There were no clear differences in positive tumor cell staining between the three different antibody clones for GYN, genitourinary, GI, or CNS tumor specimens. IHC, immunohistochemistry; NSCLC, non-small cell lung cancer; PD-L1, programmed death ligand 1.

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was observed with the three antibody clones in 40.0% (167/418) of all tumor specimens; and among these cases, 62.3% (104/167) were 22C3+/28-8+/SP142−, and 28.7% (48/167) were 22C3+/28−/SP142−. A total of 54.1% (226/418) of all tumor cases were positive with at least 1 IHC assay (22C3, 28−8, or SP142) and among these cases, 94.2% (213/226) were positive for 22C3, 77.0% (174/226) were positive for 28−8, and 28.8% (65/226) were positive for SP142.

**Figure 3B** shows the positive and negative PD-L1 status with all three antibody clones for NSCLC specimens (n=199). The same PD-L1 status with all three antibody clones (either all assays demonstrating TC ≥1% or all demonstrating TC<1%) was observed in 48.7% (97/199) of all NSCLC specimens. Of these NSCLC specimens showing the same PD-L1 status with all three antibody clones, 54.6% (53/97) were triple negative, and 45.4% (44/97) were triple positive. A different PD-L1 status was observed among all three antibody clones in 51.3% (102/199) of all NSCLC specimens. Among these NSCLC cases showing a different status, 67.6% (69/102) of cases were 22C3+/28-8+/SP142−, and 23.5% (24/102) were 22C3+/28−/SP142−. A total of 73.4% (146/199) of all NSCLC cases were positive with at least one IHC assay (22C3, 28−8, or SP142), compared with 54.1% (226/418) of tumor specimens overall. Among these cases that were positive with at least one IHC assay, 22C3 was positive in 95.2% (139/146) of cases, 82.2% (120/146) were positive for 28−8, and 32.2% (47/146) were positive for SP142.

**Table 4** shows the positive and negative PD-L1 status with all three antibody clones for different types of lung cancer specimens. The PD-L1 status was the same (≥1% TC expression with all three clones, or <1% TC expression with all three clones) with all three antibody clones in 50.8% (62/122) of all lung adenocarcinoma specimens, 32.1% (17/53) of all lung squamous cell carcinoma specimens, 69.6% (16/23) of all NSCLC (NOS) specimens, and 62.5% (5/8) of all small cell lung carcinoma specimens. A total of 72.1% (88/122) of adenocarcinoma cases were positive with at least one antibody clone, compared with 81.1% (43/53) of all squamous cell carcinoma specimens, 69.6% (16/23) of all NSCLC (NOS) specimens, and 75.0% (5/8) of all small cell lung carcinoma specimens.
Figure 3   (A) Analytical concordance in status of PD-L1 result with 22C3, 28-8, and SP142 IHC assays, in all tumor specimens (n=418). Most cases (60.0% of all tumor specimens, n=251) showed the same PDL-1 status, and the remainder (40.0% of all tumor specimens, n=167) showed different status between the three antibody clones. Among cases that showed the same status, most were negative for all antibody clones (45.0%, n=192), and the remainder were all positive (14.1%, n=59). Among cases that showed a different status, most were either 22C3+/28-8+/SP142− (24.9%, n=104) or 22C3+/28-8−/SP142− (11.5%, n=48).

(B) Analytical concordance in status of PD-L1 result with 22C3, 28-8, and SP142 IHC assays, in NSCLC tumor specimens. A percentage of 51.3 (102/199) of all NSCLC specimens showed a different PDL1 status between the three antibody clones, while 48.7% (97/199) showed the same status. Among NSCLC cases that showed a different status, most were either 22C3+/28-8+/SP142− (34.7%, n=69) or 22C3+/28-8−/SP142− (12.1%, n=24). IHC, immunohistochemistry; NSCLC, non-small cell lung cancer; PD-L1, programmed death ligand 1.
and 50.0% (4/8) of all small cell lung carcinoma specimens. Among lung adenocarcinoma specimens that were positive with at least one antibody clone: 95.5% (84/88) were positive for 22C3, 83.0% (73/88) were positive for 28-8, and 23.8% (29/122) were positive for SP142. Among squamous cell carcinoma specimens that were positive with at least one antibody clone: 93.0% (40/43) were positive for 22C3, 79.1% (34/43) were positive for 28-8, and 16.3% (7/43) were positive for SP142. Among NSCLC (NOS) specimens that were positive with at least one antibody clone: 100.0% (4/4) were positive for 22C3, 75.0% (3/4) were positive for 28-8, and 25.0% (1/4) were positive for SP142. Among NSCLC (NOS) specimens that were positive with at least one antibody clone: 100.0% (16/16) were positive for 22C3, 75.0% (12/16) were positive for 28-8, and 62.5% (10/16) were positive for SP142. Finally, among small cell lung carcinoma specimens that were positive with at least one antibody clone: 100.0% (4/4) were positive for 22C3, 75.0% (3/4) were positive for 28-8, and 25.0% (1/4) were positive for SP142.

Table 5 shows the positive and negative PD-L1 status with all three antibody clones for primary versus metastatic NSCLC specimens. The PD-L1 status was the same (either ≥1% TC expression with all three clones, or <1% TC expression with all three clones) with all three antibody clones in 42.5% (45/106) of all primary NSCLC specimens, 50.7% (35/69) of all metastatic NSCLC specimens, and 50.0% (12/24) of all NSCLC specimens with undetermined specimen location. It was observed that 78.3% (83/106) primary NSCLC specimens were positive with at least one antibody clone, compared with 65.2% (45/69) of metastatic NSCLC specimens, and 83.3% (20/24) of all NSCLC specimens with undetermined specimen location. Among primary NSCLC specimens that were positive with at least one antibody clone: 97.6% (81/83) were positive for 22C3, 78.3% (65/83) were positive for 28-8, and 27.7% (23/83) were positive for SP142. Among metastatic NSCLC specimens that were positive with at least one antibody clone: 93.3% (42/45) were positive for 22C3, 80.0% (36/45) were positive for 28-8, and 31.1% (14/45) were positive for SP142. Among NSCLC cases with undetermined specimen location that were positive with at least one antibody clone: 91.7% (22/24) were positive for 22C3, 100.0% (24/24) were positive for 28-8, and 50.0% (12/24) were positive for SP142.

Clinical implication with clinical vignettes
The histology and PD-L1 tumor cell expression pattern for each of the three antibody clones (22C3, 28-8 and SP142) for three separate NSCLC patient specimens are shown in figure 4. These cases are representative of most tumor specimens observed with a positive PD-L1 status, in that TC score is greatest with 22C3, followed by SP142 having the lowest TC score. A score of TC ≥1 was reported with 22C3 for all three specimens, qualifying all three patients for treatment with pembrolizumab or nivolumab. Furthermore, a score of TC ≥1 with 28-8 was reported for all three specimens, qualifying all three patients for treatment with nivolumab or nivolumab in combination with ipilimumab. While specimens from patient 1 and patient 3 both exhibited SP142 scores of TC ≥1 (and are therefore considered having a positive PD-L1 status for purposes of this study), the scores of TC 5 for each of these specimens did not reach the NSCLC SP142 CDx threshold of TC ≥50 to qualify for treatment with atezolizumab. However, in should be noted that patient 3 also had an IC ≥10 (not reported here), which reached the NSCLC SP142 CDx threshold of IC ≥10 for treatment with atezolizumab.
CDx assays, each specifically linked to a different cancer treatment. For example, there are four PD-L1 IHC CDx assays for NSCLC, including 22C3 (linked to pembrolizumab or cemiplimab-rwlc treatment), 28-8 (linked to nivolumab in combination with ipilimumab), SP142 and SP263 (both linked to atezolizumab treatment). Several factors might be considered when selecting a PD-L1 IHC assay for each individual patient, including which IHC assay has a CDx indication for the patient’s specific tumor type, which CDx-associated cancer treatment is preferred by the clinician, which immunotherapy has the least side effects, as well as the current clinical status of the patient. The findings presented here, including the sensitivity of various PD-L1 IHC assays across a range of tumor types, represent an additional factor to consider when selecting which PD-L1 IHC assay is most appropriate for each individual patient. It should also be noted that, while PD-L1 assays can help to establish the eligibility of patients for immune checkpoint inhibitors, additional biomarkers such as tumor mutational burden (TMB) can be useful to anticipate the efficacy and durability of benefit of these drugs, in an additive and independent manner across many tumor types.33–35

Selecting the most appropriate PD-L1 assay to run for a particular patient, especially in cases of tissue specimen scarcity, is important. For example, an NSCLC case with a positive 22C3 result (tumor cell expression, or TC ≥1) and negative 28-8 result (TC <1), would lead to an FDA-approved indication for treatment with pembrolizumab or cemiplimab-rwlc, but not with nivolumab in combination with ipilimumab (the CDx-associated treatment for 28-8). In this scenario, if the clinician had ordered a 28-8 assay only, without 22C3 (eg, due to limited tissue), a single negative 28-8 PD-L1 score would likely be reported, and the patient would not be eligible for any specific PD-L1 immunotherapy. In this study of 418 tumor specimens tested with 22C3, 28-8 and SP142 assays, the same PD-L1 status (either all three assays scored with TC ≥1, or all scored with TC <1) was observed in 60.0% (251/418) of all tumor specimens, and 48.7% (97/199) of all NSCLC specimens. In these cases that received the same PD-L1 status with all three IHC assays, if one IHC assay was ordered instead of all three, the final PD-L1 score would likely be reported, and the patient would not have been altered (although the patient would only be eligible for the CDx indicated treatment associated with the single IHC assay that was ordered). However, in a significant proportion of cases (ie, 40.0% (167/418) of all tumor specimens, and 51.3% (102/199) of all NSCLC specimens), the PD-L1 status was different among the three assays. In these cases that received a different PD-L1 status, if one IHC assay was ordered instead of all three, the final PD-L1 status reported for that patient may have been altered if only one IHC assay was ordered instead of all three assays. This raises the question, which PD-L1 IHC assay should the patient’s clinical team choose, especially if they have no CDx treatment preference, or if the sample size is not sufficient for multiple PD-L1 IHC assays?

Figure 4 PD-L1 IHC (22C3, 28-8 and SP142) in NSCLC patient specimens. The H&E histology and PD-L1 IHC (22C3, 28-8 and SP142) is shown for three separate NSCLC specimens (patients 1–3). All three specimens received a score of PD-L1 tumor expression score (TC) of TC >1 with 22C3 and 28-8, qualifying each patient for treatment with pembrolizumab (or cemiplimab-rwlc) and nivolumab (or nivolumab in combination with ipilimumab), respectively. The SP142 score of TC 5 for specimens from patients 1 and 3 was a positive PD-L1 status for purposes of this study, but was <50 and therefore did not qualify for treatment with atezolizumab based on TC alone. It should be noted that patient 3 also received an SP142 immune cell (IC) score of 10 (not shown), qualifying them for CDx-associated treatment atezolizumab. IHC, immunohistochemistry; NSCLC, non-small cell lung cancer; PD-L1, PD-L1; TC, tumor cell.

DISCUSSION

This report represents one of the largest studies to date of tumor specimens analyzed with multiple PD-L1 IHC assays in routine clinical practice. The result of each FDA-approved PD-L1 IHC CDx assay is an indication for a specific cancer treatment (table 1). Some tumor types, such as NSCLC, have multiple associated PD-L1 IHC

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In this study, our data suggest that 22C3 is the most sensitive IHC CDx assay for tumor cell PD-L1 expression and identifies a positive PD-L1 status more frequently than 28-8, which in turn is positive more often than SP142. These findings are consistent with previous reports, such as Blueprint phase 1 and phase 2 studies, as well as analyses of PD-L1 IHC assays in cell lines and lung cancer specimens, all of which reported greater sensitivity with 22C3 and 28-8 assays and consistently lower TC staining with the Ventana SP142 assay. In this study, the 22C3, 28-8 and SP142 assays were positive (TC ≥1) in 94.2% (213/226), 77.0% (174/226), and 28.8% (65/226), respectively, of all tumor cases that were positive with at least one IHC assay (ie, 54.1% (226/418) of all tumor cases that were positive with at least one IHC assay). Similarly, among the 73.4% (146/199) NSCLC specimens that were positive with at least one IHC assay, 22C3 was positive in 95.2% (139/146), 28-8 was positive in 82.2% (120/146), and SP142 was positive in 32.2% (47/146) of cases. While the Blueprint phase 2 study (which evaluated 39 NSCLC tumor specimens that were positive with at least one IHC assay (ie, 54.1% (226/418) of all tumor cases that were positive with at least one IHC assay), 22C3 was positive in 95.2% (139/146), 28-8 positive in 82.2% (120/146), and SP142 was positive in 32.2% (47/146) of cases. Therefore, it is also important to point out that other factors could contribute to the different sensitivities and staining characteristics among the three assays. Some studies indicate that variation in TC PD-L1 staining between 22C3, 28-8 and SP142 (see figure 2A,B) could be a factor. However, it is also important to point out that other factors could contribute to the different sensitivities and staining characteristics among the three assays. Some studies indicate that variation in TC PD-L1 staining between 22C3, 28-8 and SP142 (see figure 2A,B) could be a factor.

Our data show that 81.1% (43/53) of lung squamous cell carcinoma cases were positive with at least one IHC assay, compared with 72.1% (88/122) cases of lung adenocarcinoma. This finding is consistent with several recent studies that have shown greater tumor cell PD-L1 expression in squamous cell carcinoma compared with lung adenocarcinoma. While it is a limited number of samples, our data also show that an even lower proportion (50.0%, 24/48) of NSCLC cases demonstrate positive PD-L1 status with at least one IHC assay, a finding consistent with previous reports of lower, although variable, PD-L1 tumor cell expression in NSCLC ranging from 0–5% to 71%. Finally, we show that a greater proportion (34.8%, 24/69 cases) of metastatic NSCLC specimens were triple negative, compared with only 21.7% (23/106) of primary NSCLC cases. While some reports have demonstrated similarly lower PD-L1 tumor cell expression in metastatic versus primary sites, others have reported higher PD-L1 tumor cell expression in metastatic specimens. This variation in reported TC expression in metastatic versus primary sites might be due to differences in the various PD-L1 IHC assays available today. Some reports suggest that differences in the number, size, and accessibility of specific epitopes recognized by the various PD-L1 antibodies (22C3, 28-8 and SP142) could be a factor. PD-L1 is a 290-amino acid transmembrane glycoprotein, with two extracellular immunoglobulin (Ig) domains and a 31-amino acid cytoplasmic domain. The greater sensitivity of 22C3 and 28-8 IHC assays (compared with SP142) might be explained by the findings that DAKO 22C3 and DAKO 28-8 antibodies each bind multiple epitopes in the extracellular domain of PD-L1 (although at different sites), while the Ventana SP142 antibody binds to a single 7-amino acid stretch (DTHLEET290) epitope in the cytoplasmic domain and that therefore the 22C3 and 28-8 antibodies have more binding ‘targets’ per PD-L1 molecule with which to bind. Furthermore, the 22C3 and 28-8 antibodies recognize larger epitopes that are possibly more accessible to antibodies during the IHC assay. The epitope recognized by 22C3 spans 31 amino acids and lies predominantly in extracellular residues 166–190, while the main epitopes recognized by 28-8 lie within extracellular residues 86–93, 125–145, and 205–223. However, it is also important to point out that other factors could contribute to the different sensitivities and staining characteristics among the three assays. Some studies indicate that variation in TC PD-L1 staining between 22C3, 28-8 and SP142 (see figure 2A,B) could be a factor.
specific tumor type studied, differences in the local tumor microenvironment such as the local cytokine milieu, or the specific metastatic site in question. For example, in metastatic triple negative breast cancer, TC expression of the specific metastatic site in question. For example, in
and lymph nodes.55
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Data availability statement All data relevant to the study are included in the article or uploaded as supplementary information.

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Conclusion In conclusion, we show that 22C3 is the most sensitive PD-L1 IHC assay for tumor cell expression and returns a positive PD-L1 status more frequently than 28-8, which in turn is positive more often than SP-142. Multiple factors should be considered in the selection of a PD-L1 IHC assay for a particular patient, including which IHC assay is a CDx for the patient’s specific tumor type, which CDx-associated therapy is most clinically appropriate, the side effect profile of that therapy, as well as the current clinical status of the patient. The findings presented here represent an additional resource to help guide clinicians select which PD-L1 IHC CDx assay is most suitable for their patient.
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