# Performance of four automated SARS-CoV-2 serology assay platforms in a large cohort including susceptible COVID-19 negative and COVID-19 positive patients

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**Running Title:** SARS-CoV-2 serology assay discordance
**Key words:** serology, automated platforms, COVID-19, SARS-CoV-2

**Abbreviations:** US Food and Drug Administration, FDA; Severe acute respiratory syndrome coronavirus 2, SARS-CoV-2; Real-time reverse transcriptase polymerase chain reaction, RT-PCR; Corona virus disease 2019, COVID-19; Nucleic acid amplification testing, NAAT; Enzyme-linked immunosorbant assay, ELISA; Immunoglobulin G, IgG; Immunoglobulin M, IgM; Immunoglobulin A, IgA; Spike, S; Nucleocapsid, N; Emergency Use Authorization, EUA.

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**ABSTRACT**

***Background.*** *Anti*-SARS-CoV-2 serological responses may have a vital role in controlling the spread of the disease. However, the comparative performance of automated serological assays has not been determined in susceptible patients with significant co-morbidities.

***Methods****.* In this study, we used a large number of COVID-19 negative patient samples (n=2030) as well as COVID-19 positive patient samples (n=112) to compare the performance of four serological assay platforms; Siemens Healthineers Atellica IM Analyzer, Siemens Healthineers Dimension EXL Systems, Abbott ARCHITECT, and Roche cobas.

***Results.*** All four serology assay platforms exhibited comparable negative percent agreement with negative COVID-19 status ranging from 99.2-99.7%, and positive percent agreement from 84.8-87.5% with positive real-time reverse transcriptase polymerase chain reaction (RT-PCR) results. Of the 2142 total samples, only 38 samples (1.8%) yielded discordant results on one or more platforms. However, only 1.1% (23/2030) of COVID-19 negative cohort results was discordant whereas discordance was 10-fold higher for the COVID-19 positive cohort at 11.3% (15/112). Of the total 38 discordant results, 34 were discordant on only one platform.

***Conclusion*****.** Serology assay performance was comparable across the four platforms assessed in a large population of COVID-19 negative patients with relevant comorbidities. The pattern of discordance shows that samples were discordant on a single

assay platform, and discordance rate was 10-fold higher in the COVID-19 positive population.

***Impact statement.*** High negative percent agreement reinforces the reliability of serology testing especially in a cohort of at-risk patients. Serology platform discordance highlights the importance of a two-test strategy for properly identifying seroconverted patients.

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## INTRODUCTION

The COVID-19 pandemic has challenged the capacity and capabilities of national medical systems and has highlighted the importance of laboratory and diagnostic testing to control the spread of the disease through timely diagnosis and robust contact tracing. Nucleic acid amplification testing (NAAT) detecting the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is central to identifying individuals with active infection and a COVID-19 diagnosis (1). To enhance surveillance efforts and control the virus spread, serological testing has emerged as an opportunity to identify patients who may have been exposed to the virus, who have recently recovered from an infection whether or not they were symptomatic, or to assess or identify the durability of immune responses (2).

The rapid emergence of serological assays has also challenged, and often out-paced, regulatory agencies as well as our understanding of COVID-19 serological responses. The quality and performance of these assays was initially unknown, leading the US Food and Drug Administration (FDA) to generate a “removed” test list, for all assays considered for an emergency use authorization (EUA), but demonstrating poor clinical

performance (3). The overall utility of the assay, regardless of the manufacturer, has also been challenged, due to lack of supporting data for the proposed applications and the value of the test (4). These questions surrounding test utility and assay performance remain unresolved.

Many serological tests have entered the healthcare market, most employing an immunoassay sandwich method using a SAR-CoV-2 envelope protein as an antigen 'bait' to detect immunoglobulins. The bait for these assays is often either recombinant-derived ectodomain of the spike (S) protein or the nucleocapsid (N), which is used as antigen to bind IgG, IgA, and/or IgM in a patient sample. Previous studies using commercially-available ELISA kits, have shown that both S and N proteins have near equivalent performance characteristics in detecting serological responses (5).

The present study was designed to compare head-to-head the performance characteristics of four automated analyzers, using a large and diverse population of patients. The study population was carefully selected to include a large number of COVID-19 positive patients (n=93; total samples, n=112) confirmed by reverse-transcriptase real-time polymerase chain reaction (RT-PCR), as well as a large group of COVID-19 negative patient samples (n=2030), collected in the United States (USA) prior to October 2019 and diagnosed with a respiratory or cardiovascular disorder that would otherwise increase risk for COVID-19 mortality (6).

## METHODS

***Study design and patient cohort.*** Study samples belonged to two general groups, a COVID-19 negative group (Table 1) collected in the USA prior to October 2019 (March 2009 to September 2019), the onset of the global pandemic in the USA, or a COVID-19

positive group (Table 2), diagnosed based on recent RT-PCR test. Both cohorts included remnant samples from patient plasma collected in lithium heparin collection containers. To compare assay agreement using a COVID-19 negative cohort, 1 mL frozen aliquots were withdrawn from a sample bank maintained by the study sponsor (Siemens). Samples were identified based on an associated diagnosis or condition causing dyspnea. To compare assay agreement using a COVID-19-positive cohort, remnant samples were collected from patients treated at the University of Maryland Medical Center with a diagnosis of COVID-19 and deidentified under IRB protocol HP-00092112. Samples were designated as positive based on a recent positive SARS-CoV-2 RT-PCR test. Due to logistical constraints including limited supply of reagents, several RT-PCR testing platforms and assays were used in the care and management of the COVID-19 positive patients (Supplemental Table 1). These platforms were validated, and shown to provide comparable results.

***Analysis using four serology assay systems.*** Four testing platforms were used to compare serology assay performance including the Siemens Healthineers Atellica IM (SARS-CoV-2 Total (COV2T) Assay; Siemens Healthcare Diagnostics Inc., Tarrytown, NY, USA) (referred to as Siemens Atellica), Siemens Healthineers Dimension EXL (SARS-CoV-2 Total Antibody (CV2T) assay; Siemens Healthcare Diagnostics Inc., Tarrytown, NY, USA) (referred to as Siemens EXL), Abbott ARCHITECT (SARS-CoV-2 IgG assay; Abbott Laboratories, Abbott Park, IL, USA), and Roche cobas (Elecsys Anti-SARS-CoV2 assay; Roche Diagnostics GmbH, Mannheim, Germany) ((7–10) summarized in Table 3). All instruments were operated and maintained according to each respective manufacturer's operations manual. Quality control and calibration materials

were prepared using the Instruction for Use document, and control results were within acceptable ranges prior to acceptance of study samples.

***Sample handling.*** Specimens used in this study were frozen prior to use. Frozen specimens were thawed, mixed thoroughly, then centrifuged to remove particulates prior to testing. All specimens were assayed on the same freeze thaw cycle and assayed in parallel on each of the four platforms in singlicate.

***Serology results interpretation.*** Serology results were reported as dichotomous outcomes, either 'positive' or 'negative' based on manufacturer determined threshold values. Results were reported as 'positive' if specimen values exceeded 1.0 index value (Siemens Atellica), 1000 qual units (Siemens EXL), 1.4 index value (ARCHITECT), and 1.0 index value (Cobas).

***Statistical analysis.*** Assay performance was compared head-to-head using a paired Chi-squared analysis (McNemar's test). Other statistical analysis, descriptive statistics and confidence intervals were generated using GraphPad Prism statistical software (San Diego, California USA).

***Ethics statement.*** Sample collection and study design were approved by the University of Maryland Medical Center Institutional Review Board.

## RESULTS

***Sample collection and patient population.*** The COVID-19-negative group included 2,030 unique patient samples (850 female, 1147 male, 33 not indicated; median age 69 years), including a range of pulmonary and cardiac diseases identified as conditions of breathlessness (Table 1). The COVID-19-positive group included 112 samples from 93

unique patients (41 female, 53 male; median age 55) (Table 2). Repeat samples from 18 patients were used in the COVID-19 positive group, however, these samples were drawn on different days following their first SARS-CoV-2 RT-PCR positive result.

***Head-to-head comparison of serological assay performance.*** Each specimen was analyzed on each platform in parallel and their results were aggregated to include combined COVID-19 positive and COVID-19 negative groups (Table 4). The only statistically significant difference in assay performance by paired chi-squared analysis were the Abbott ARCHITECT and the Roche cobas platforms with a total of 22 discordant results; 5 negative serology results and 17 positive results on the Abbott ARCHITECT platform showed opposing results on the Roche cobas system. Although not statistically significant, the highest overall number of discordant results was observed when comparing the Abbott ARCHITECT and the Siemens EXL systems with a total of 31 discordant results out of 2142 samples, and the lowest discordance was observed when comparing the Siemens Atellica with the Roche cobas system with only 11 discordant results out of 2142 samples. Discordance was apparent between all platforms, including 22 samples for Abbott ARCHITECT vs Roche cobas, 25 samples for Abbott ARCHITECT vs Siemens Atellica, as compared to 13 samples for Siemens EXL vs Roche cobas, and 12 samples for Siemens EXL vs Siemens Atellica.

***Negative and positive agreement and discordance of serology results.*** When compared to patient SARS-CoV-2 status, all platforms exhibited comparable agreement, with negative percent agreement from 99.2-99.7%, and positive percent agreement from 84.8-87.5% (Table 5). In the COVID-19 negative group, the Siemens Atellica and Roche cobas platforms had the highest percent negative agreement, and in the COVID-19

positive group, the Siemens Atellica had the highest percent positive agreement with SARS-CoV-2 positive RT-PCR test result.

The apparent pattern of discordance between the four platforms was perceptibly unique to each instrument (Table 6). Of the 38 discordant samples, 34 samples reported discordant results by only one platform with the other three platforms in agreement, without regard for SARS-CoV-2 status, either positive or negative for COVID-19. The four discordant samples reporting two positive results from the Siemens Atellica and EXL platforms and two negative results from the Roche cobas/Abbott ARCHITECT platforms were all from the COVID-19 positive group (see samples 1075, 1080, 1025-2, 1039). Notably, three discordant results (3/42; 7.1%) were near their respective cut-off values for the instruments; however, the accompanying concordant results were well above or below the imprecision of the instruments at the cut-off values.

It is important to note samples 1025-1 and 1025-2 were from the same patient, both reported discordant serology results, however the samples drawn 0-6 days post first positive RT-PCR test was only serology positive in the Siemens EXL, and a second positive serology result was only apparent in the Siemens Atellica from a sample drawn 7-14 days post-first positive RT-PCR test. The Abbott ARCHITECT and Roche cobas platforms were both negative at both time points.

**DISCUSSION**

In this study, we reported serology testing of the largest cohort of COVID-19 negative, high risk patients with significant co-morbidities causing dyspnea which has not been previously shown. This large study population demonstrated a high degree of negative agreement in serological responses across the four commercial platforms tested. Central

to this portion of the study was the inclusion of plasma samples collected prior to October 2019, intentionally including a population of COVID-19 negative patients with conditions of breathlessness, a group of co-morbidities that would otherwise have a higher mortality risk during the on-going pandemic (6). We have also shown a high degree of positive agreement across these serology platforms as compared to a recent COVID-19 diagnosis. Seroconversion and antibody responses to infection are of vital interest in vaccination efforts and understanding effectiveness and persistence of immunity. This work joins several studies in describing the performance characteristics of rapidly emerging SARS-CoV-2 serological assays (11,12,21,13–20).

***Comparison with other studies.***

By comparison, most similar studies have used a considerably smaller COVID-19 negative cohort from a collection of historic patient samples simply termed pre-COVID-19 or pre-pandemic samples without regard for co-morbidities (12,15–17,21), or from healthy individuals (19). The benefit of using pre-pandemic samples allows for definitive identification of any apparent false positives, since the virus was not known to exist prior to the year 2019. Other studies have collected contemporaneous patient samples during the pandemic with an associated negative RT-PCR test (18,20). We believe the use of COVID-19 negative patient samples with specific high-risk co-morbidities is most representative of patients likely to receive a COVID-19 associated test, including SARS-CoV-2 RT-PCR or SARS-CoV-2 serological test, during the pandemic. Without regard for cohort selection criteria, the majority of the platforms compared in these studies demonstrate sensitivities (positive percent agreement) and specificities (negative percent

agreement) greater than 90%, using their select populations of COVID positive and COVID negative study participants.

Another important consideration in selection of COVID-19 negative samples is cross-reactivity from similar viral respiratory infections or other coronaviruses. Several studies have previously shown minimal or no cross-reactivity with these other infectious diseases (15,17,19,21). That said, these issues will be studied systematically when the manufacturers seek FDA clearance or approval for their assays.

***Considerations and limitations.*** We avoided comments on specificity and sensitivity of the assay performance since a "gold standard" for SARS-CoV-2 serology has not been established. Therefore, discordant results were not considered false positive or false negatives for the purposes of this study, even though the FDA has applied a standard in which positive percent agreement is used as a surrogate for sensitivity and negative percent agreement for specificity (22). It is important to note that RT-PCR positive COVID-19 patients with an undetectable serological response may always result as a 'false negative' using this scheme(12). For this reason, the Center for Disease Control (CDC) does not recommend using serology testing to diagnose previous SARS-CoV-2 infection (23).

The cause of disagreement between serological testing and RT-PCR is summarized in CDC guidance for the use and interpretation of serological testing (23). A negative serology test may not preclude a previous infection, as some infected patients may never develop antibodies. And, a positive serology test may not indicate a previous or current infection, because these antibodies may reflect an infection with a different virus from the same family of viruses.

Similar studies have analyzed how serological sensitivity changes over time using serial blood draws from the same patients (11–13). One study has shown higher positive agreement between assays >14 days post first-positive RT-PCR test (13). One head-to-head comparison study employed two assays both targeting the SARS-CoV-2 nucleocapsid (N) antibodies, displaying similar degrees of assay platform discordance with serial samples from the same patients (12). Future studies investigating the complete serological response using multiple platforms and serial blood draws will identify if there is, or is not, a time point of convergence for positive agreement in these assays.

***Implications.*** These results suggest that a two-test strategy to serology testing using two systems will improve overall agreement with RT-PCR results, as suggested previously (20). Using this two-test strategy, a single positive result would indicate a positive result, increasing positive percent agreement with a modest decrement in negative percent agreement.

In this study, the detected immunoglobulin sub-type (IgG, IgM, IgA) and the antigen employed as bait, spike (S) or nucleocapsid (N), do not seem to be important factors based on the pattern of discordance observed in this study. Elucidating the explicit cause of discordance among the serology assays is complicated and was not part of this study's design. Because the virus was unknown to exist prior to 2019, the false positive results are thought to be the result of non-specific or cross-reactivity in antibody binding, perhaps with other related viruses. However, it is also possible that other unspecified interferences to each assay's individual reagents, measurement strategy and principles may have contributed to the observed discordance. It is noteworthy that all of the assays included here were available by EUA, and have not yet undergone the full rigor of FDA

clearance or approval that, in part, includes thorough investigation of cross-reactivity and interferences."

***Conclusion.*** We have completed the largest serology platform comparison to-date including 93 unique COVID-19 positive patients and 2030 COVID-19 negative patients, with samples run in parallel on four different platforms. We have shown a unique pattern of discordance across these platforms, which have implications in assay selection and suggests a two-testing strategy will improve overall agreement and reduce apparent false negative results.

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**Table 1. Patient demographics and characteristics; COVID-19 negative group.**

| | n (%) |
|---|---|
| **All patients** | **2030** |
| **Sex, n (%)** | |
| Women | 850 (41.8%) |
| Men | 1147 (56.4%) |
| Not indicated | 33 (1.6%) |
| **Age, n (%)** | |
| 0-10 | 6 (0.3%) |
| 11-20 | 45 (2.2%) |
| 21-30 | 158 (7.8%) |
| 31-40 | 142 (7.0%) |
| 41-50 | 157 (7.7%) |
| 51-60 | 214 (10.5%) |
| 61-70 | 344 (16.9%) |
| 71-80 | 400 (19.7%) |
| 81-90 | 409 (20.1%) |
| 91-100 | 103 (5.1%) |
| Not indicated | 52 (2.6%) |
| **Associated diagnosis** | |
| ***Conditions of breathlessness*** | |
| Unspecified, elevated BNP | 1266 (62.2%) |
| COPD | 212 (10.4%) |
| CHF | 89 (4.4%) |
| Pneumonia | 60 (3.0%) |
| SOB | 58 (2.9%) |
| Bronchitis | 30 (1.5%) |
| Cystic Fibrosis | 19 (0.9%) |
| Respiratory failure | 19 (0.9%) |
| Dilated cardiomyopathy | 16 (0.8%) |
| Asthma | 4 (0.2%) |
| Lung cancer | 2 (0.1%) |
| Pulmonary edema | 2 (0.1%) |
| Cough congestion | 1 (0.05%) |
| Lung injury | 1 (0.05%) |
| MI | 1 (0.05%) |
| Pulmonary Congestion | 1 (0.05%) |
| Respiratory distress | 1 (0.05%) |
| Multiple diagnoses; Pneumonia, MI, CHF, and/or COPD | 12 (0.6%) |
| ***Other Conditions*** | |
| Normal | 199 (9.8%) |
| Colorectal cancer | 37 (1.9%) |

Abbreviations: BNP, B-type natriuretic peptide; COPD, Chronic obstructive pulmonary disease; CHF, Congestive heart failure; SOB, Shortness of breath; MI, myocardial infarction

**Table 2. Patient, sample characteristics; COVID-19 positive group.**

| | n (%) |
|---|---|
| **Number of unique samples, total** | **112** |
| ***Days since positive SARS-CoV-2 PCR assay*** | |
| 0-6 days | 62 (55.3%) |
| 7-14 days | 16 (14.2%) |
| 15-62 days | 34 (30.4%) |
| **Number of unique patients** | **93** |
| Patients with 2 serial blood draws | 17 |
| Patients with 3 serial blood draws | 1 |
| **Sex,** | |
| Female | 41 (43.6%) |
| Male | 53 (56.4%) |
| **Age, years** | |
| 0-10 | 0 |
| 11-20 | 3 (3.2%) |
| 21-30 | 8 (8.6%) |
| 31-40 | 16 (17.2%) |
| 41-50 | 13 (14.0%) |
| 51-60 | 22 (23.7%) |
| 61-70 | 17 (18.3%) |
| 71-80 | 10 (10.8%) |
| 81-90 | 4 (4.3%) |
| 91-100 | 0 |

**Table 3. Serology platforms and assays used in comparison study.**

| Manufacturer | Platform | Assay | Principle of test | Antigen | Ig |
|---|---|---|---|---|---|
| Siemens | Atellica | SARS-CoV-2 Total (COV2T) | sandwich chemiluminescent immunoassay (acridinium ester) | Spike (S); S1 receptor binding domain (RBD) | Total Ig (IgG and IgM) |
| Siemens | EXL | SARS-CoV-2 Total Antibody (CV2T) | sandwich chemiluminescent immunoassay (fluorescein-isothiocyanate; LOCI-reagents) | Spike (S); S1 receptor binding domain (RBD) | Total Ig (IgG and IgM) |
| Abbott | ARCHITECT | SARS-CoV-2 IgG assay | chemiluminescent microparticle immunoassay (CMIA; acridinium ester) | Nucleocapsid (N) | IgG |
| Roche | cobas | Elecsys Anti-SARS-CoV2 | sandwich chemiluminescent immunoassay (ruthenium complex) | Nucleocapsid (N) | Total Ig (IgG, IgA, IgM) |

**Table 4. Head-to-head comparison of serological assay performance.**

| | | | Method | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | Siemens Atellica | | Siemens EXL | | Abbott ARCHITECT | | Roche Cobas Elecsys | |
| | | | + | - | + | - | + | - | + | - |
| **Method** | Siemens Atellica | + | 104 | | | | | | | |
| | | - | | 2038 | | | | | | |
| | | | | | | | | | | |
| | Siemens EXL | + | 99 | 7 | 106 | | | | | |
| | | - | 5 | 2031 | | 2036 | | | | |
| | | | *p = 0.77283* | | | | | | | |
| | Abbott ARCHITECT | + | 96 | 17 | 94 | 19 | 113 | | | |
| | | - | 8 | 2021 | 12 | 2017 | | 2029 | | |
| | | | *p = 0.1096* | | *p = 0.2812* | | | | | |
| | Roche Cobas Elecsys | + | 97 | 4 | 95 | 6 | 96 | 5 | 99 | |
| | | - | 7 | 2034 | 11 | 2030 | 17 | 2024 | | 2043 |
| | | | *p = 0.54649* | | *p = 0.33198* | | * *p = 0.01902* | | | |

**Table 5. Negative and positive percent agreement (NPA/PPA) relative to positive/negative SARS-CoV-2 status.**

| | **NPA (CI)** | **PPA** (CI) |
|---|---|---|
| Siemens Atellica | 99.7% (99.4-99.9%)<br>n = 2024 / 2030 | 87.5% (80.1-92.4%)<br>n = 98 / 112 |
| Siemens EXL | 99.6% (99.2-99.8%)<br>n = 2021 / 2030 | 86.6% (79.1-91.7%)<br>n = 97 / 112 |
| Abbott ARCHITECT | 99.2% (98.7-99.5%)<br>n = 2014 / 2030 | 86.6% (79.1-91.7%)<br>n = 97 / 112 |
| Roche cobas | 99.7% (99.4-99.9%)<br>n = 2024 / 2030 | 84.8% (77.0-90.3%)<br>n = 95 / 112 |
| Combined agreement for all platforms and SARS-CoV-2 status | 98.7% (98.1-99.1%)<br>n = 2004 / 2030 | 79.5% (79.4-92.4%)<br>n = 89 / 112 |

Abbreviations: CI, 95% Confidence Interval; NPA, negative percent agreement; PPA, positive percent agreement

Note: NPA = (Neg serology / Neg SARS-CoV-2); PPA = (Pos serology / Pos SARS-CoV-2)

**Table 6. Discordant SARS-CoV-2 serology specimens.**

| Discordant samples in COVID-19 negative group | | | | | | | |
|---|---|---|---|---|---|---|---|
| **Patient ID** | **Sex** | **Age** | **Medical diagnosis / condition of breathlessness** | **Siemens Atellica** | **Siemens EXL** | **Abbott ARCHITECT** | **Roche cobas Elecsys** |
| PM412180 | F | 21-30 | COPD | Pos | Pos | Neg | Pos |
| 12227238 | M | 81-90 | Unspecified, elevated BNP | Pos | Neg | Neg | Neg |
| 12236951 | M | 31-40 | Unspecified, elevated BNP | Pos | Neg | Neg | Neg |
| 20918128 | F | 31-40 | Normal | Neg | Pos | Neg | Neg |
| 3911P302 | M | 81-90 | Unspecified, elevated BNP | Neg | Pos | Neg | Neg |
| 3911P361 | M | 51-60 | Unspecified, elevated BNP | Neg | Pos | Neg | Neg |
| 12301252 | M | 71-80 | Unspecified, elevated BNP | Neg | Pos | Neg | Neg |
| PM412119 | F | 31-40 | COPD | Neg | Pos | Neg | Neg |
| PM412226 | M | 41-50 | COPD | Neg | Neg | Pos | Neg |
| 5530262987 | M | 51-60 | Normal | Neg | Neg | Pos | Neg |
| 5530263144 | F | 21-30 | Normal | Neg | Neg | Pos | Neg |
| DLS0087086 | M | 71-80 | Unspecified, elevated BNP | Neg | Neg | Pos | Neg |
| CPTR01-00113 | M | 51-60 | MI & CHF | Neg | Neg | Pos | Neg |
| 895100342 | M | 81-90 | Pneumonia | Neg | Neg | Pos | Neg |
| 38P9059 | M | 81-90 | Unspecified, elevated BNP | Neg | Neg | Pos | Neg |
| 38P9064 | M | 81-90 | Unspecified, elevated BNP | Neg | Neg | Pos | Neg |
| 12229935 | F | 81-90 | Unspecified, elevated BNP | Neg | Neg | Pos | Neg |
| 12233081 | M | 51-60 | Unspecified, elevated BNP | Neg | Neg | Pos | Neg |
| 12237007 | M | 61-70 | Unspecified, elevated BNP | Neg | Neg | Pos | Neg |
| 12330737 | M | 71-80 | Unspecified, elevated BNP | Neg | Neg | Pos | Neg |
| PM412246 | M | 51-60 | COPD | Neg | Neg | Pos | Neg |
| 12330387 | F | 81-90 | Unspecified, elevated BNP | Neg | Neg | Neg | Pos |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| PM412190 | F | 71-80 | COPD | Neg | Neg | Neg | Pos |

| Discordant samples in COVID-19 positive group | | | | | | | |
|---|---|---|---|---|---|---|---|
| **Patient ID** | **Sex** | **Age** | **Days since 1st PCR, diagnosis** | **Siemens Atellica** | **Siemens EXL** | **Abbott ARCHITECT** | **Roche cobas Elecsys** |
| 1070 | F | 41-50 | 0-6 days, COVID-19 positive | Neg | Neg | Neg | Pos |
| 1063 | F | 61-70 | 0-6 days, COVID-19 positive | Neg | Neg | Pos | Neg |
| 1099 | M | 51-50 | 0-6 days, COVID-19 positive | Neg | Neg | Pos | Neg |
| 1093 | F | 51-60 | 0-6 days, COVID-19 positive | Neg | Neg | Pos | Neg |
| 1025-1 | M | 51-60 | 0-6 days, COVID-19 positive | Neg | Pos | Neg | Neg |
| 1089 | F | 61-70 | 7-14 days, COVID-19 positive | Neg | Pos | Pos | Pos |
| 1069 | M | 51-60 | 0-6 days, COVID-19 positive | Pos | Neg | Pos | Pos |
| 1096 | M | 31-40 | 0-6 days, COVID-19 positive | Pos | Neg | Pos | Pos |
| 1074 | F | 51-60 | 0-6 days, COVID-19 positive | Pos | Neg | Pos | Pos |
| 1075 | F | 31-40 | 7-14 days, COVID-19 positive | Pos | Pos | Neg | Neg |
| 1080 | F | 11-20 | 0-6 days, COVID-19 positive | Pos | Pos | Neg | Neg |
| 1025-2 | M | 51-60 | 7-14 days, COVID-19 positive | Pos | Pos | Neg | Neg |
| 1039 | F | 31-40 | 0-6 days, COVID-19 positive | Pos | Pos | Neg | Neg |
| 1036 | M | 21-30 | >14 days, COVID-19 positive | Pos | Pos | Neg | Pos |
| 1020 | F | 31-40 | 0-6 days, COVID-19 positive | Pos | Pos | Pos | Neg |

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