

Serologic Response to mRNA COVID-19 Vaccination in Lymphoma Patients

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Abstract

Currently available COVID-19 mRNA vaccines have demonstrated high efficacy in clinical trials.¹⁻³ However, cancer patients, including those with hematological malignancies, were largely excluded from these trials. In this prospective, observational study we measured anti-S protein IgG titers as well as avidity in lymphoma patients (n=67) vaccinated with a COVID-19 mRNA vaccine. Serological response rates in lymphoma patients who were treatment naïve (100% in CLL, 88.9% in other, non-CLL non-Hodgkin lymphoma patients), or who were last treated more than 24 months prior to vaccination (100% in CLL, 90% in other-NHL), were similar to healthy controls (100%). Patients on active therapy, however, had a diminished response rate (40% in CLL, 21.0% in other-NHL). No patient who received anti-CD20 monoclonal antibodies (mAb) within six months of vaccination responded. Thus, the utility of testing anti-S titers should be explored in patients on active therapy or with recent anti-CD20 mAb exposure, to assess their response to vaccination. We also propose studying passive protection with S-protein mAbs as an alternative prophylactic strategy for patients who respond poorly to vaccination.

Introduction:

The ongoing COVID-19 pandemic has affected over 172 million people globally with over 3.7 million deaths.⁴ Three vaccines have received Emergency Use Authorizations (EUA) from the Food and Drug Administration (FDA) for use in the USA. Two mRNA-based vaccines encoding the SARS-CoV-2 spike protein (S), BNT162b2 (BioNtech/Pfizer) and mRNA-1273 (Moderna), have 95% and 94.1% efficacy against COVID-19, respectively.¹⁻³ Over 90% of study participants seroconvert by one week after the second dose of these vaccines, and remain antibody-positive for at least six months.^{1-3,5,6} Both vaccines consistently elicit anti-S binding and neutralizing antibodies and T cell responses.^{2,7}

The efficacy of SARS-CoV-2 vaccines in cancer patients may be more variable, particularly for individuals with hematologic malignancies or receiving immunosuppressive therapies. These patients may be at high risk for developing severe COVID-19 with poor outcomes.⁸⁻¹¹ To guide their care, it is important to understand how the approved COVID-19 vaccines perform in this patient population and identify subgroups that may not respond. Individuals receiving anti-CD20 monoclonal antibody (mAb) therapy, including lymphoma patients, are known to have relatively weak antibody responses to influenza vaccines.¹²⁻¹⁵ A similar problem arises with influenza vaccination in CLL patients receiving the BTK inhibitor (BTKi), ibrutinib.^{16,17} Similarly, only 3.8% of CLL patients taking a BTKi seroconverted to a hepatitis B vaccine, far lower than the 28% rate seen in the treatment-naïve patient group.¹⁸ In turn, the latter seroconversion rate was much less than the >90% frequencies typically seen when hepatitis B vaccines are tested in healthy individuals.¹⁹⁻²¹ Overall, there is now substantial evidence that B-cell targeted therapies, including anti-CD20 mAbs and BTKis, impede how vaccines perform.^{16,17,22-24}

Very few cancer patients were included in the COVID-19 mRNA vaccine trials and any individuals receiving chemotherapy or immunotherapy within six months were excluded.^{1,3} Consequently, we have an inadequate knowledge of how well these vaccines work in the

cancer patient population. However, by extrapolation from other vaccines, we hypothesized that patients with hematologic malignancies, especially those on immunosuppressive therapy, would produce poor serological responses to a COVID-19 vaccine.²⁵ We therefore measured anti-S protein ELISA titers induced by mRNA vaccines in lymphoma patients receiving various therapeutic interventions, especially B-cell targeted therapies. The avidity of antibody binding to the S-protein receptor binding domain (RBD) was also measured to determine if lymphoma or lymphoma therapies adversely affected the maturation of the antibody response. Finally, we determined whether any patients had serum antibodies to the SARS-CoV-2 nucleocapsid (N) protein, a marker for prior infection.²⁶ A past history of infection has been associated with a robust serological response to vaccination.²⁷⁻³⁰

Methods:

Study Design and Participants

In this single-center, observational cohort study we assessed antibody responses in lymphoma patients receiving a COVID-19 mRNA vaccine (BNT162b2 by BioNtech/Pfizer or mRNA-1273 by Moderna). All patients had provided written informed consent to participate in observational research, and this study was approved by the Weill Cornell Medicine IRB (IRB 21-02023288). Lymphoma patients, regardless of treatment status, underwent serum collection before and after vaccination. Whole blood samples used in this study were collected as part of standard of care laboratory testing protocols. Pre-vaccination samples were obtained at any time prior to the first vaccine dose, while post-vaccine samples were from at least 11 days after the second dose. When the mRNA vaccines became generally available, the study participants were strongly encouraged to receive a vaccine at the earliest opportunity and many did so. Thus, 22 patients had already received their first dose prior to sample collection. Pre- and post-vaccination samples were available from 22 of the 67 study participants, but only post-vaccination samples from the other 45.

We also include data from a healthy control group of 35 healthcare workers (HCWs) enrolled in the NYP-WELCOME (WEiLL CORnell Medicine Employees) observational trial (IRB 20-04021831). The use of this cohort in an mRNA vaccine study has been previously described.³¹

Anti-S protein IgG ELISA

The assay to quantify IgG antibodies to the SARS-CoV-2 S-protein has been described previously.³¹ Briefly, purified S-proteins (200 ng in 100 μ l) were coated overnight onto 96-well plates at 4°C. After 3 washes with PBS/0.05% Tween-20 (PBST), the wells were blocked for 1 h with 4% (w/vol) powdered milk/PBS (150 μ l/well). Serum was initially diluted 1/100 in PBS containing 4% milk and 20% sheep serum, serially diluted as needed, and added to wells for 1 h. Bound antibodies were detected using goat anti-human IgG horse radish peroxidase (HRP)-conjugated antibodies from Jackson ImmunoResearch (109-035-008), diluted 1/5000 in 4% milk/PBS. After washing, 50 μ l of HRP substrate (Thermo Scientific 34029) was added to each well for 3 min. Color development was terminated with 0.3 N sulfuric acid, and plates were read at 450 nm using an Enspire instrument (Perkin Elmer).

ELISA-derived net OD₄₅₀ values were determined by subtracting background values from control wells containing no S-protein. Net OD₄₅₀ values were plotted vs. log₁₀ serum dilution before 3-parameter sigmoidal dose-response curves, constrained to zero, were fit (GraphPad Prism 9 software). The endpoint dilution cut-off was set to 0.100 net OD₄₅₀ (i.e., 6 times the standard deviation of values from control wells with no S-protein). For inter-group comparison purposes, an endpoint titer value of 1:10,000 is marked on Figure 1A.

The Roche Elecsys Anti-SARS-CoV-2 N antigen assays

The Elecsys® Anti-SARS-CoV-2 electrochemiluminescence immunoassay was used to detect antibodies to the nucleocapsid (N) antigen in serum samples processed using the Roche Cobas e411 system (Roche Diagnostics, Indianapolis, IN). This assay has received EUA approval from the FDA and was used here to identify or confirm SARS-CoV-2 infection.

SARS-CoV-2 antibody avidity assay

The avidity assay measures the rate of antibody dissociation from the S-protein RBD, which is inversely correlated with antibody avidity. The assay is performed using the Pylon P3D analyzer (ET Healthcare, Palo Alto, CA) and has been described previously.³² A probe coated with RBD proteins is sequentially exposed to diluted serum samples, a biotinylated-RBD protein and a Streptavidin-Cy5 conjugate to form a specific immunocomplex. *Signal_0* is the fluorescent signal before dissociation is measured. The probe and its immobilized immunocomplex then enters multiple repetitive dissociation cycles. *Signal_t* is the fluorescent signal measured at the end of each cycle, and directly correlates with the amount of antibody that remains probe-bound at the time of measurement. The *Signal_t* / *Signal_0* ratio at each time point is a measure of how much of the originally bound antibody has dissociated (i.e., [bound Ab] / [total Ab]). The dissociation profile is constructed by plotting the fluorescence signal ratio as a function of time. The relative dissociation rate (dR) is calculated by fitting the first order rate equation to the dissociation profile: $\text{Ln}(\text{Signal}_t / \text{Signal}_0) = \text{Ln}([\text{bound}]/[\text{total}]) = -dR t$.

Statistics

Data analysis and figures were produced in Prism 9 (GraphPad Software, La Jolla, Ca). Where indicated, p values to determine significance were calculated using unpaired, two-tailed t tests.

Results

The anti-S protein response to mRNA vaccination was assessed by ELISA using sera from 67 patients with lymphoma and 35 healthy HCW controls. The demographics and clinical characteristics of the lymphoma patients are listed in Table 1. The majority of patients in this study were white (74.6%). All patients were vaccinated with an mRNA vaccine (31 BNT162b2, 36 mRNA-1273). The patients were categorized as having Hodgkin lymphoma (n=4), chronic lymphocytic leukemia (n=21), or other non-Hodgkin lymphomas (n=42). No SARS-CoV-2 infections were identified during this study (February to April 2021).

Serum samples were obtained before (when possible) and after vaccination. Post-vaccination samples were collected within 11-70 days of the second dose (median 24.5 days). In the HCW control group, the post-vaccination samples were obtained within 10-68 days of dose-2 (median 40 days) (Figure S1).

Of the 22 lymphoma patients with samples available both pre- and post-vaccination, all but one were negative for S-protein antibodies prior to vaccination (Figure S2). That single S-protein antibody-positive patient was also positive for antibodies against the SARS-CoV-2 N-protein. This serology pattern implies that this patient had recovered from an undocumented, asymptomatic SARS-CoV-2 infection.

In total, 8 lymphoma patients were anti-N positive (including the individual referred to above); they are highlighted in blue in Figures 2-4. Notably, all members of the HCW control group were anti-N negative. As of now, no lymphoma patients have had a positive SARS-CoV-2 PCR test since the start of this study (i.e., when pre-vaccination sample collection commenced). For 4 of the 8 anti-N positive lymphoma patients, there was evidence of COVID-19 prior to the start of this study (Table S1). Thus, 3 patients had prior documented positive SARS-CoV-2 PCR tests, while the fourth was not PCR-tested but later had a positive commercial antibody test. Seven of these 8 anti-N positive patients responded to vaccination. Taken together, anti-N positive lymphoma patients had significantly higher mean anti-S protein titers than their anti-N negative counterparts ($p < 0.0001$), and than the HCW group ($p = 0.02$) (Figure S3). However, when anti-N positive lymphoma patients were separated by treatment status (i.e. naïve, active therapy) the sample sizes were too small for comparisons to the anti-N negative group.

The single anti-N positive patient who did not respond to vaccination is receiving active therapy with venetoclax and also receives a monthly IVIG infusion. IVIG is a possible alternative source of antibodies that react with the S- and N-proteins.³³⁻³⁶ Hence it is possible that the positive N-protein serology seen in this patient arose from an IVIG infusion that was last given 3-weeks

before the date of post-vaccination sample collection. An alternative explanation is a previously undetected SARS-CoV-2 infection.

The vaccine-induced IgG antibody responses to the SARS-CoV-2 S-protein are shown in Figure 1A. The median and mean endpoint titers in the HCW control group were higher than in the lymphoma patients, although the difference was not significant. There were also no significant differences in mean titers when patients with different lymphomas were compared. However, while all 35 healthy control group members responded to the vaccine, a substantial proportion of the lymphoma patients did not. Thus, the anti-S endpoint titers in 9 of the 21 CLL patients and 17 of the 42 other NHL patients were <10,000 (a cut-off level marked on Figure 1A), and were often undetectable. In contrast, the 4 Hodgkin lymphoma patients all responded to the vaccines (Table S2). When the data were grouped according to whether the participants received the BNT162b2 or mRNA-1273 vaccine, no differences were apparent (Figure 1B).

We studied the CLL and other NHL patients in more detail to understand the implications of their treatment (Figure 2A). Every treatment-naïve and remote-therapy (no treatment in over 24 months) CLL patient responded to vaccination whereas only 40% (6/15) of those currently being treated had anti-S protein titers above the designated cut-off value (Figure 2A). Response rates in CLL patients receiving different therapy regimens are shown in Table S3.

A similar pattern was seen for the other NHL patients, although one individual in each of the treatment-naïve and remote-therapy groups failed to respond to the vaccine (Figure 2B). Active therapy in this sub-group was again associated with a poor vaccine response, with only 21.4% (3/14) developing anti-S protein titers above the cut-off (Figure 2B). Response rates in other NHL patients, grouped by therapy regimen, are listed in Table S4. The off-therapy sub-group, who had received treatment within 2 years but not at the time of vaccination, also had a lower vaccine response rate of 55.5% (5/9). The four non-responders in this group had all received an anti-CD20 mAb within the previous two years; two within 6 months, one within one year, and

one within 18 months (Table S5). None of the patients currently on anti-CD20 mAb therapy (1 CLL, 7 other NHL) seroconverted after vaccination (Fig. 2).

We next studied the relationship between when anti-CD20 mAb therapy ceased and the vaccine response (Figure 3). None of the 11 CLL and other NHL patients receiving this treatment within 6 months of vaccination had anti-S protein titers above the cut-off, but longer intervals were associated with higher titers. Thus, CLL and other NHL patients who were last treated >24 months before vaccination had response rates of 66.7% (6/9) and 71.4% (10/14), respectively. Of note is that 3/3 CLL and 3/4 other NHL non-responders in this sub-group were receiving a different type of active therapy at the time of vaccination (Table S6). We suggest that even when anti-CD20 mAb therapy ceased >24 months before vaccination, other forms of ongoing active therapy can compromise the vaccine response.

Finally, we studied the avidity of IgG antibodies to the RBD in the lymphoma and healthy control patients (Figure 4). The avidity was significantly higher ($p < 0.0001$) for individuals in both the lymphoma and control groups who had anti-N antibodies (Figure 4A). That finding is expected, as COVID-19 convalescent patients (i.e., anti-N positive) have had longer to affinity mature their anti-S antibodies, which are boosted by the mRNA vaccines.³⁷⁻⁴¹ We noted that patients currently receiving venetoclax or a BTKi had lower avidity S-protein antibodies than the other groups, although the group sizes were too small for statistical significance (Figure 4B). If this preliminary observation is confirmed, an explanation might be reduced T-cell help for antibody maturation.

Discussion

We found that most lymphoma patients respond to vaccination with an mRNA-based COVID-19 vaccine, but a substantial fraction (>40%) do not and therefore may remain at risk of infection and disease. It is not yet known what constitutes a protective titer of S-protein antibodies after vaccination. Here, our primary endpoint was an ELISA that quantifies binding antibodies against

the S-protein, a subset of which will be capable of virus-neutralization. We consider an endpoint titer >1:10,000 in this assay to be a suitable indicator of a good response to vaccination.

Eight lymphoma patients were anti-N positive, which likely indicates prior SARS-CoV-2 infection (although one patient may have received N-protein antibodies via IVIG infusions). These patients had significantly higher anti-S IgG titers compared to anti-N negative lymphoma patients ($p < 0.0001$) and HCW (all of whom were anti-N negative) ($p = 0.02$). This result is consistent with reports that mRNA vaccines induce higher anti-S IgG titers in convalescent than naïve individuals.²⁷⁻³⁰

There were no significant differences in the S-protein IgG antibody response rates or titers between the different lymphoma histologic subtypes. Treatment status was, however, a relevant variable. Treatment-naïve lymphoma patients responded to vaccination similarly to the HCW group, as did patients who had not received therapy for at least two years.

There are reports of diminished mRNA vaccine responses in immunocompromised patients, including those receiving various lymphoma therapies.^{12-18,25} For example, patients with chronic inflammatory diseases responded poorly compared to healthy controls, particularly those receiving glucocorticoids and B-cell depleting therapies.⁴² In another study, nearly 20% of solid organ transplant patients were non-responsive to mRNA vaccination.^{43,44} When 151 cancer patients received one dose of the BNT162b2 vaccine, only 38% of the solid cancer patients and 18% of those with hematologic malignancies ($n = 56$) seroconverted, compared to 95% of the healthy controls.⁴⁵ Among 67 patients with hematologic malignancies, including 34 lymphoma patients, nearly half did not respond to an mRNA vaccine.⁴⁶ Finally, when 44 CLL patients received an mRNA vaccine, only 23% of those on active therapy were positive for antibodies to the S-protein using a commercial assay.⁴⁷ These various reports are generally consistent with what we found. Specifically, commonly used lymphoma therapies can adversely influence the performance of COVID-19 vaccines, with anti-CD20 mAbs having the greatest impact.

To our knowledge, our study involves the largest cohort of non-CLL, non-Hodgkin lymphoma patients. In addition to assessing anti-S titers, our use of an avidity assay indicated that lymphoma patients who responded to the vaccines produced antibodies of comparable avidity to those found in the HCW group. Access to this healthy control group strengthens our conclusions about the lymphoma patients, as the vaccine response rate in the HCWs was similar to those seen in mRNA vaccine clinical trials.^{1,3} Our study also offers a more detailed assessment of the temporal relationship between lymphoma treatment and vaccine response than has been the case to date, especially for anti-CD20 mAb therapy.

Among the cancer therapies monitored here, only the recent use of anti-CD20 antibodies was clearly associated with a poor response to the mRNA vaccines. In various studies, anti-CD20 mAb therapy causes B-cell depletion that is sustained for at least 6-12 months.^{12,48-50} Given this knowledge, it is not surprising that 0% (0/11) of the patients who had received anti-CD20 mAb therapy within the prior 6 months had high-titer antibodies after vaccination. Better responses were seen as the time since anti-CD20 mAb infusion increased; after two years off therapy, 15 of 22 patients developed high-titer S-protein IgG antibodies (Figure 3). These observations have significant implications for patient care; the benefits of anti-CD20 therapy for CLL and other lymphomas should be balanced against the likely ablation of vaccine-mediated protection against COVID-19.

Recent studies suggest that using BTKi's in CLL patients also compromises SARS-CoV-2 vaccines.^{16-18,22,24} Here, we found that 60% (6/10) of patients on BTKi monotherapy (4/6 in CLL, 2/4 in other NHL) did develop high-titer IgG antibodies after mRNA vaccination. There were some indications that antibody affinity was reduced compared to treatment naïve patients, perhaps reflecting reduced T-cell help, but our sample size was too small for us to draw strong conclusions. A larger cohort would be needed to further study the impact of this inhibitor class on vaccine-mediated protection.

The major weakness of this study is the sample size, which limited the statistical significance of observations made on subgroups of patients receiving specific therapies. Furthermore, many of our patients were on combination regimens (Tables S3-S4), which complicates analyses of the individual components. Also, we did not analyze T-cell responses to vaccination. Larger studies with longer follow-up, perhaps on a multi-center basis, would be required to address these lacunae. However, this controlled study presents compelling evidence that patients on active therapy for lymphoma may not respond to vaccination. Our results are particularly concerning for patients on anti-CD20 mAb therapy given that no patients who had received treatment within six months responded well to mRNA vaccination.

While we are not suggesting that COVID-19 vaccines are unsuitable for lymphoma patients, indeed any cancer patients, it would be prudent to assess whether they induce potentially protective S-protein antibodies, particularly when there are good grounds to believe the patient may be a non-responder. Another option may be to alter the timing of vaccination (i.e., before treatment begins) when possible. An attractive strategy may be an alternative way to protect against COVID-19: passive immunization with mAbs against the S-protein.⁵¹ For example, REGEN-COV, a two-mAb combination (casirivimab and indevimab), has clinical efficacy as both a prophylactic and therapeutic agent. Preliminary Phase 3 trial results indicate that passive vaccination with REGEN-COV reduced the risk of symptomatic disease by 81% for household contacts of COVID-19 patients.⁵² In another study, the same mAb combination also prevented symptomatic infection by 100% and PCR-detected infection by 50%, compared to placebo, with the infected participants in the mAb group having lower viral loads.⁵³ Similar results were reported for bamlanivimab, another anti-S mAb, in a non-peer reviewed press release.⁵⁴ In a Phase 3 clinical trial involving nursing home employees and residents, bamlanivimab reduced the risk of symptomatic infection by 80% compared to placebo.^{54,55} When used as therapies, both REGEN-COV and bamlanivimab reduce viral loads in COVID-19 patients.⁵⁶⁻⁵⁸

Passive immunization with anti-S mAbs for patients who do not respond to vaccination also has important public health implications. Several case reports have documented intra-host viral evolution within immunocompromised patients who have persistent SARS-CoV-2 infection, including ones with hematological malignancies.⁵⁹⁻⁶³ Accordingly, there are concerns that new SARS-CoV-2 variants could arise under such circumstances.⁶⁴ Preventing infections with anti-S mAbs when active immunization is ineffective may reduce this risk to the community.

For various reasons, it is therefore appropriate to consider passive mAb protection for lymphoma patients who have recently (within 6-12 months) received anti-CD20 mAb therapy. Since anti-CD20 mAbs are commonly used in many other human diseases, the same COVID-19 protection strategy should also be considered more widely. While our study was not sufficiently powered to reach definitive conclusions about whether BTKi's and venetoclax reduce mRNA vaccine responses, there were indications of potential concerns that could be further evaluated in larger studies. A goal would, again, be to assess whether patients receiving these therapies may also benefit from passive mAb protection against COVID-19.

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FIGURES AND TABLES

FIGURES AND TABLES

Characteristics		
Sex		
Male	36	
Female	31	
Mean Age	68.8	
Median Age	71 (24-90)	
Ethnicity		
Hispanic or Latino	0	
White	50	
Black	1	
Asian	1	
American Indian or Alaska Native	0	
Native Hawaiian or Other Pacific Islander	1	
Multiracial	4	
Not reported or unknown	10	
Vaccine		
BNT162b2 (BioNTech/Pfizer)	31	
mRNA-1273 (Moderna)	36	
Comorbidities		
Hypertension	25	
Chronic lung disease	1	
Liver Disease	0	
Heart Disease	17	
Kidney Disease	5	
Autoimmune Disease	8	
Diabetes	4	
HIV	0	
Other Cancer	21	
Hyperlipidemia	34	
Mean BMI	26.59 (\pm 4.49)	
Malignancy		
HL	4	
CLL	21	
other NHL	42	
	FL	7
	MZL	10
	MCL	8
	DLBCL	8
	WM	7
	Other	2

Table 1: Baseline characteristics of lymphoma patients (n=67).

(HL = Hodgkin Lymphoma, CLL = chronic lymphocytic leukemia, NHL = non-Hodgkin

lymphoma, FL = follicular lymphoma, MZL = marginal zone lymphoma, MCL = mantle cell lymphoma, DLBCL = diffuse large B-cell lymphoma, WM = Waldenstrom's macroglobulinemia)

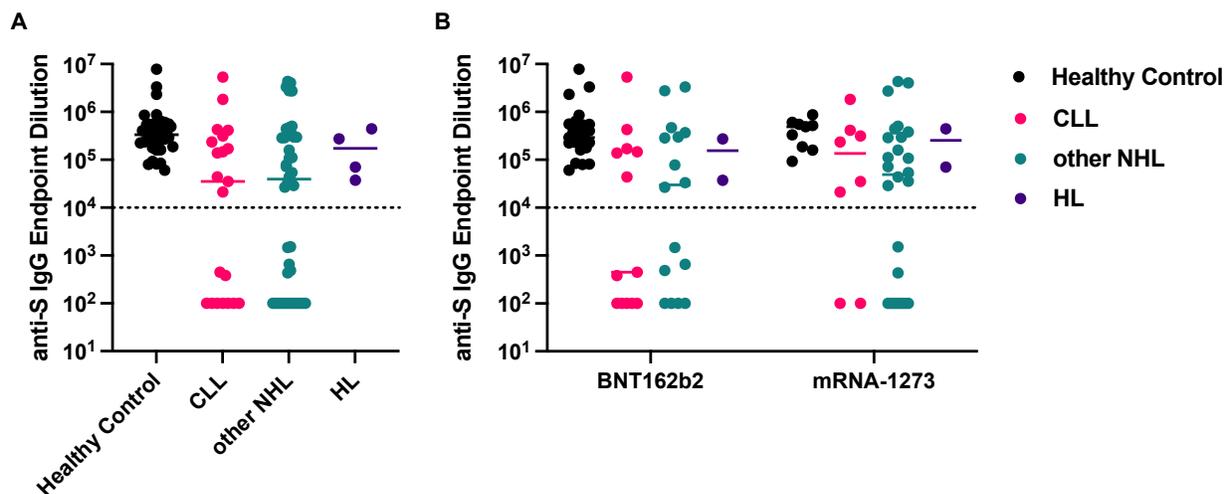


Figure 1: Anti-S IgG titers for healthy control and lymphoma patients (A) SARS-CoV-2 S-protein antibody (anti-S IgG) endpoint ELISA titers for healthy control (n=35), chronic lymphocytic leukemia (n=21), and other non-Hodgkin lymphoma (n=42) patients. Blood samples were collected at least 11 days following inoculation with the second dose of an mRNA vaccine. The dotted line represents an endpoint anti-S protein titer (1:10,000) that we judge to be an indicator of a strong response to vaccination. The small solid lines indicated the median titers for each group. There were no significant differences between the groups (unpaired, two-tailed t-tests). (B) Anti-S IgG titers for the indicated study groups, categorized by the mRNA vaccine used: BNT162b2 (Pfizer) or mRNA-1273 (Moderna).

Figure 2

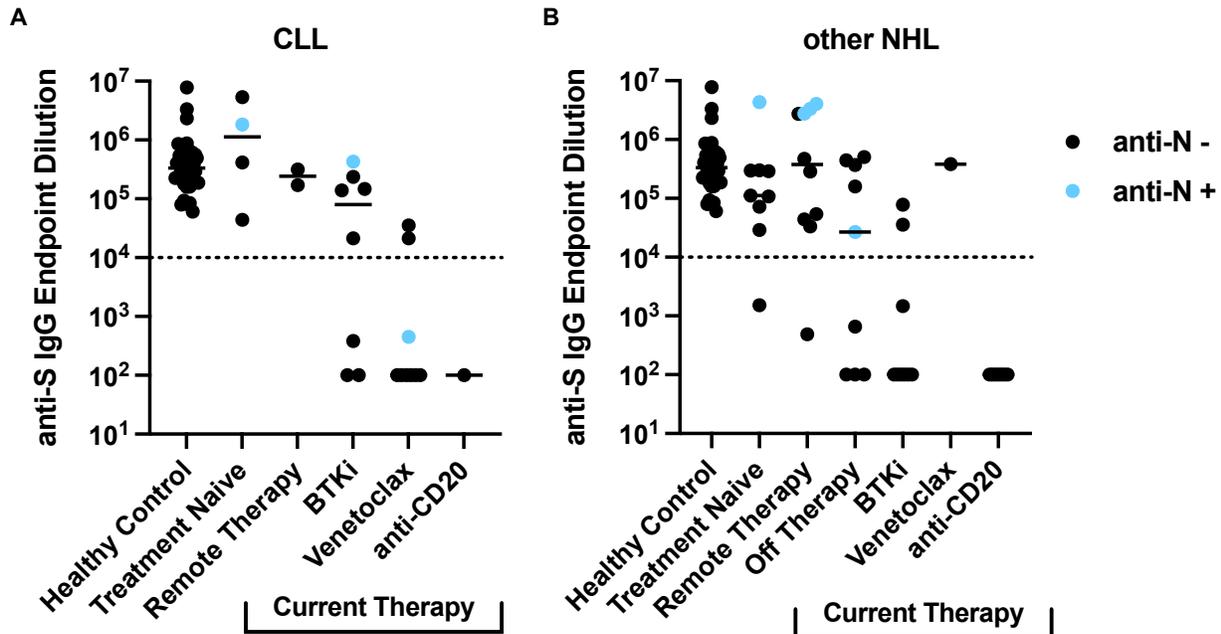


Figure 2: Anti-S IgG titers by therapy (A) Anti-S IgG for CLL patients separated by treatment status and for the healthy control group. The treatment-naïve patients (n=4) received no therapy at any time. The remote-therapy patients (n=2) received no treatment within the 24 months prior to vaccination. The off-therapy patients received treatment within 24 months of vaccination but not during or after (this sub-group does not overlap with either the remote- or current-therapy groups, and applies only to the other NHL patients). Patients currently receiving therapy were treated as indicated: Bruton's tyrosine kinase inhibitor (BTKi; n=7), venetoclax (n=9), anti-CD20 therapy (n=1). The blue symbols indicate patients (n=3) who were positive for anti-N antibodies, which most likely arise from prior SARS-CoV-2 infection (see main text). (B) As for panel-A, but for Other NHL patients. Treatment-naïve (n=9); remote-therapy (n=10); off-therapy (n=9); current therapies including BTKi (n=6), venetoclax (n=1), anti-CD20 (n=6). Anti-N positive patients (n=5) are again in blue.

Figure 3

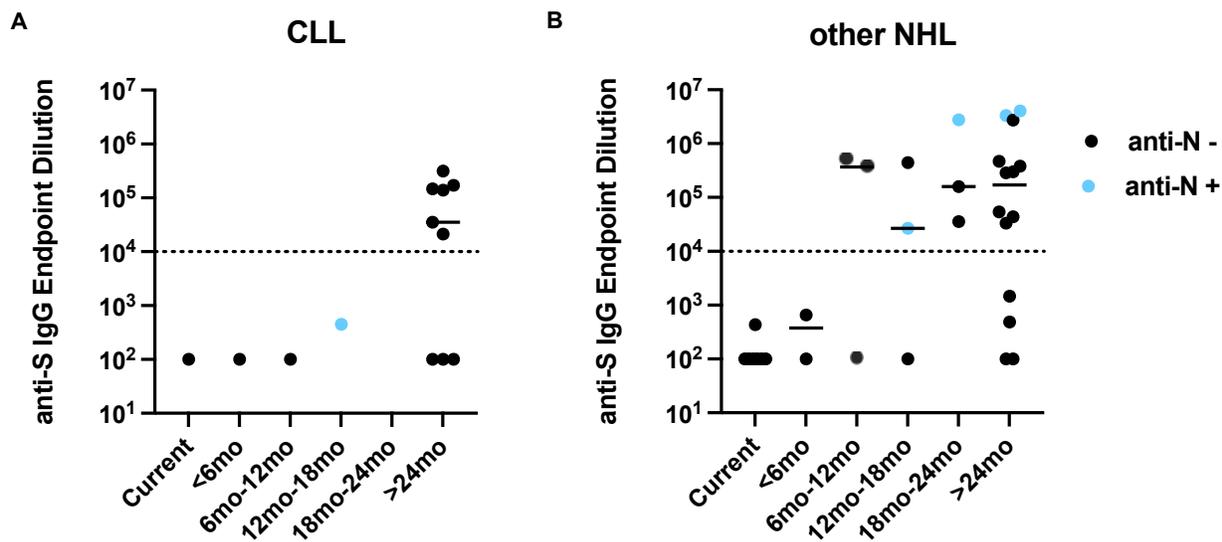


Figure 3: Anti-S IgG titers according to last anti-CD20 therapy (A) Anti-S IgG titers for CLL patients grouped by the time interval since anti-CD20 therapy ended. The Current group was receiving anti-CD20 at the time of vaccination (n=1). The other groups are designated according to how long therapy ceased before vaccination: <6mo (n=1); 12-18 months (n=1); 18-24 months (n=1); > 24 months (n=8). Anti-N positive patients are highlighted in blue. (B) As for panel-A but for other NHL patients: Current (n=7); <6 months (n=2); 6-12 months (n=3); 12-18 months (n=3); 18-24 months (n=3), >24 months (n=17).

Figure 4

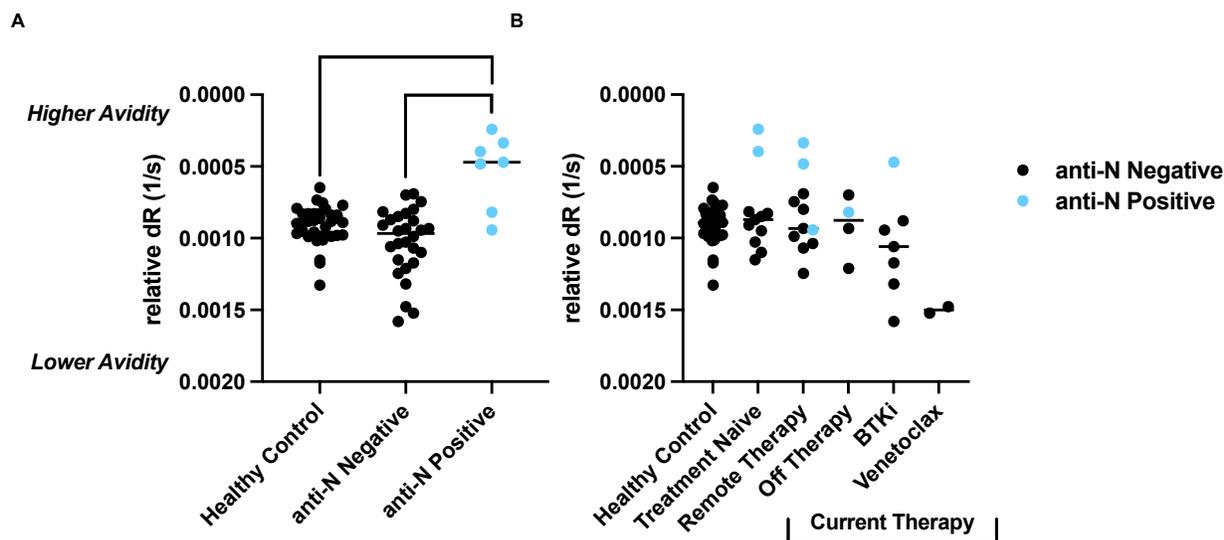


Figure 4: anti-S total antibody avidity (A) Avidity of healthy control (n=35), anti-N negative lymphoma patients (n=28) and anti-N positive lymphoma patients (n=7). A low relative dissociation rate (relative dR, y-axis) corresponds to high avidity and as such the y-axis is inverted. There were significant differences between the indicated (****) groups ($p < 0.0001$), as determined using an unpaired, two tailed t-test. (B) As for panel-A but with CLL and other NHL patients grouped by therapy type: treatment-naïve (n=11); remote-therapy (n=11); off-therapy (n=4); BTKi (n=7); venetoclax (n=2). Avidity in patients on venetoclax was significantly decreased compared to treatment naïve ($p=0.0073$), remote therapy ($p=0.0063$), and off therapy ($p=0.0238$) groups. There were no significant differences between other treatment groups.

SUPPLEMENTARY TABLES AND FIGURES

Patient	Lymphoma	Pre anti-S IgG	Post anti-S IgG	Positive SARS-CoV-2 PCR	Commercial Serology	Clinical History	IVIg
24	WM	N/A	4349034	No	Positive (4/2020)	Yes (03/2020)	No
27	DLBCL	N/A	3338448	No	No	No	No
64	MCL	N/A	4070709	No	No	No	No
23	CLL	N/A	426856	Yes (04/2020)	Positive (07/2020)	Yes (hospitalized 04/2020)	No
44	FL	1657	26870	No	No	No	No
32	CLL	N/A	1835830	Yes (03/2020)	No	Yes (03/2020)	No
29	DLBCL	N/A	2759055	Yes (06/2020)	No	Yes (06/2020)	No
7	CLL	N/A	451	No	Negative (02/09/2021)	No	Monthly

Table S1: Anti-N positive patients listed according to lymphoma subtype and history of SARS-CoV-2 infection. Note that the commercial serology test for these patients detects antibodies to the SARS-CoV-2 N protein. Clinical history refers to documented symptoms consistent with COVID-19. Patient 7 last received IVIG, 21 days prior to their post-vaccination sample collection.

(DLBCL = diffuse large B-cell lymphoma, MCL = mantle cell lymphoma, FL = follicular lymphoma)

	Response	Mean anti-S IgG
Healthy Control	35/35 (100%)	707491
CLL	12/21 (57.14%)	434858
other NHL	25/42 (59.52%)	508316
HL	4/4 (100%)	206207

Table S2: Response rate and mean anti-S IgG tiers for healthy controls and lymphoma patients

	Response	anti-S IgG
Treatment Naïve	4/4 (100%)	1910213
Remote Therapy	2/2 (100%)	241468
Off Therapy	N/A	N/A
Active Therapy	6/15 (40%)	67216
BTKi	4/6 (66.67%)	166062
Venetoclax	1/4 (25%)	9018
BTKi+Venetoclax	1/2 (50%)	10716
PI3Ki + Venetoclax	0/2 (0%)	100
PI3Ki + Venetoclax + anti-CD20 mAb	0/1 (0%)	100
Total	12/21 (57.14%)	

Table S3: Vaccine response in CLL patients according to therapy. Note that no CLL patients were considered “off therapy.”

(BTKi = Bruton’s tyrosine kinase inhibitor, PI3Ki = PI3 kinase inhibitor)

	Response	anti-S IgG
Treatment Naïve	8/9 (88.89%)	1112801
Remote Therapy	9/10 (90%)	819119
Off Therapy	5/9 (55.55%)	117310
Active Therapy	3/14 (21.43%)	35767
BTKi	2/4 (50%)	28880
Venetoclax	1/1 (100%)	383979
anti-CD20 mAb	0/1 (0%)	100
PI3Ki + BTKi	0/1 (0%)	100
Bendamustine + BTKi	0/1 (0%)	100
Bendamustine + anti-CD20 mAb	0/1 (0%)	100
Lenalidomide + anti-CD20 mAb	0/1 (0%)	100
BTKi + Lenalidomide + anti-CD20 mAb	0/3 (0%)	211
Total	25/42 (59.52%)	

Table S4: Vaccine response in non-NHL patients according to therapy

(BTKi = Bruton's tyrosine kinase inhibitor, PI3Ki = PI3 kinase inhibitor)

Patient	Lymphoma	Pre IgG	Post IgG	Last Therapy	Last anti-CD20 mAb (days)
66	MZL	N/A	100	Rituximab	156
47	DLBCL	N/A	100	R-CHOP	469
53	DLBCL	N/A	100	R-CHOP	270
61	DLBCL	100	655	R-CHOP	165

Table S5: Off-therapy other-NHL patients who did not respond to vaccination. All of these patients were last treated with an anti-CD20 mAb as part of their most recent therapy. Each patient is listed with lymphoma subtype and most recent therapy (R-CHOP = rituximab + cyclophosphamide, doxorubicin, vincristine, and prednisolone). Also shown is the time (in days) between date of last anti-CD20 mAb therapy and the date of second vaccine dose. (DLBCL = diffuse large B-cell lymphoma, MZL = marginal zone lymphoma)

Patient	Lymphoma	Pre anti-S IgG	Post anti-S IgG	Current Therapy
13	CLL	N/A	100	Ibrutinib+venetoclax+IVIG
17	CLL	100	101	Venetoclax
41	CLL	N/A	100	Venetoclax+IVIG
22	MZL	N/A	100	Bendamustine+Ibrutinib
25	MCL	N/A	100	Zanubrutinib
34	MZL	N/A	1476	Zanubrutinib+Plasmapheresis
56	MZL	100	487	None

Table S6: Patients treated with anti-CD20 mAb over 24 months prior to vaccination

Ibrutinib and zanubrutinib are BTKi's. (MZL = marginal zone lymphoma, MCL = mantle cell lymphoma)

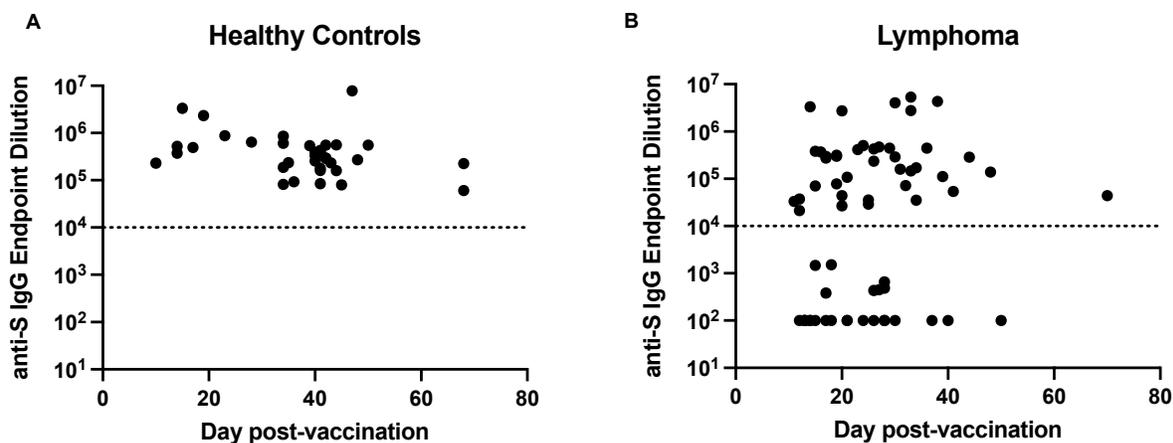


Figure S1: Anti-S IgG Titers by sample collection day post-vaccination (A) Anti-S IgG in healthy control patients plotted against the time of sampling post-vaccination. (B) As for panel-A but for lymphoma patients.

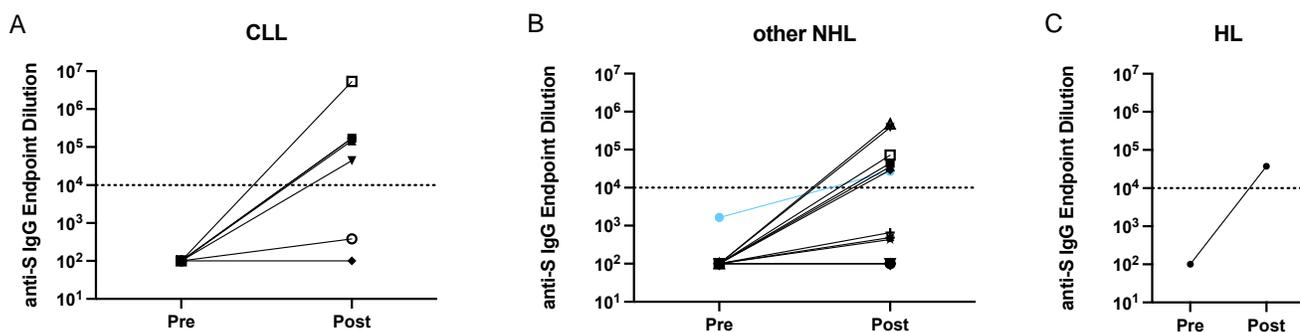


Figure S2: Pre and post vaccination titers by lymphoma subtype (A) Anti-S IgG titers for CLL patients (n=7). Each symbol represents a single patient, with the line connecting the pre- and post-vaccination titers. (B) As for panel-A but for other NHL patients (n=14). Note that the one patient with a quantifiable (although low) anti-S titer pre-vaccination titer was also anti-N positive, suggestive of a prior SARS-CoV-2 infection. (C) As for panel-A but for a HL patient (n=1)

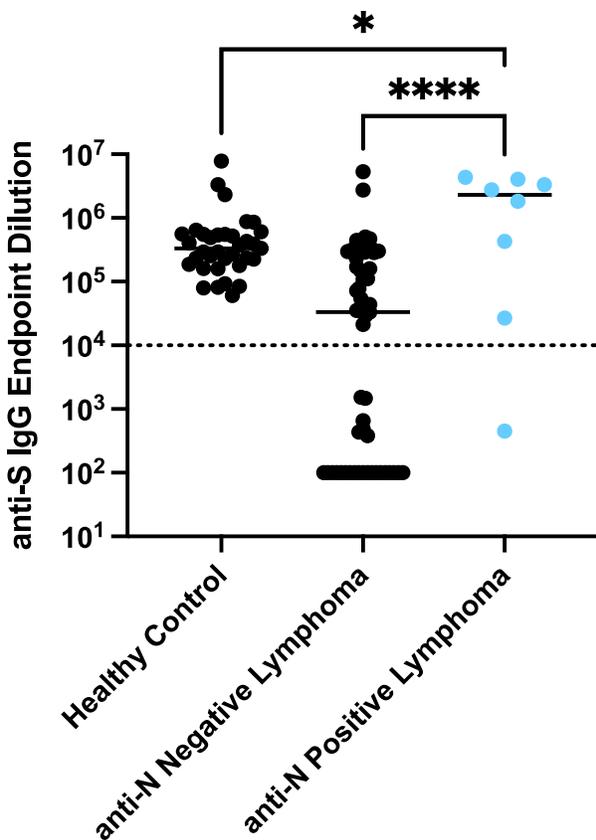


Figure S3: anti-S IgG titers by prior infection. Anti-N positive lymphoma patients had significantly higher anti-S IgG titers compared to anti-N negative lymphoma patients (****, $p < 0.0001$) and anti-N negative HCW (*, $p = 0.02$) as determined by unpaired, two-sided t tests. The difference between anti-N negative lymphoma patients and anti-N negative HCW was not significant ($p = 0.05$). Note that the one patient in the anti-N positive group who fell below the titer threshold for a meaningful response (1:10000) was receiving IVIG.