

Fig. S1. Neutralizing titers and abundance of IgG1 Fc afucosylation in COVID-19 outpatients over time. (A) Half-maximal SARS-CoV-2 pseudovirus neutralizing titers (pNT50) are shown for each study time point. Left panel: graphed to match format of Figure 1A. Right panel: plotted to clearly show the median pNT50 at each study time point. Horizontal bars indicate median. (B) The kinetics of neutralizing antibody response are shown over time in progressors in Cohort 1. (C) Multivariate regression analysis was used to test the contribution of age, sex, weight, or duration since COVID-19 onset on abundance of afucosylated anti-RBD IgG1 in two cohorts (D) Abundance of SARS-CoV-2 specific afucosylated IgG1 (afucFc) is shown for Cohort 1 COVID-19 outpatients over time (n=18). RU, relative units. P values in (A) and (D) were calculated using Kruskal Wallis test with Dunn's correction for multiple comparisons. **P < 0.01; ****P < 0.0001; ns, not significant.

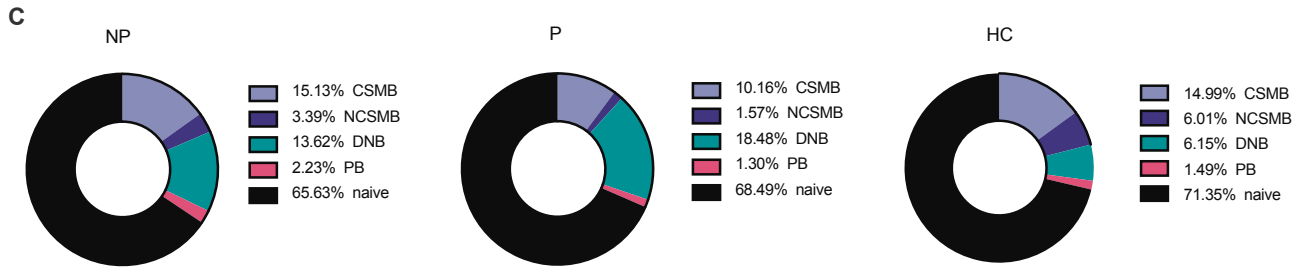
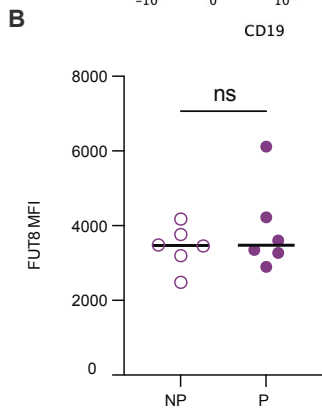
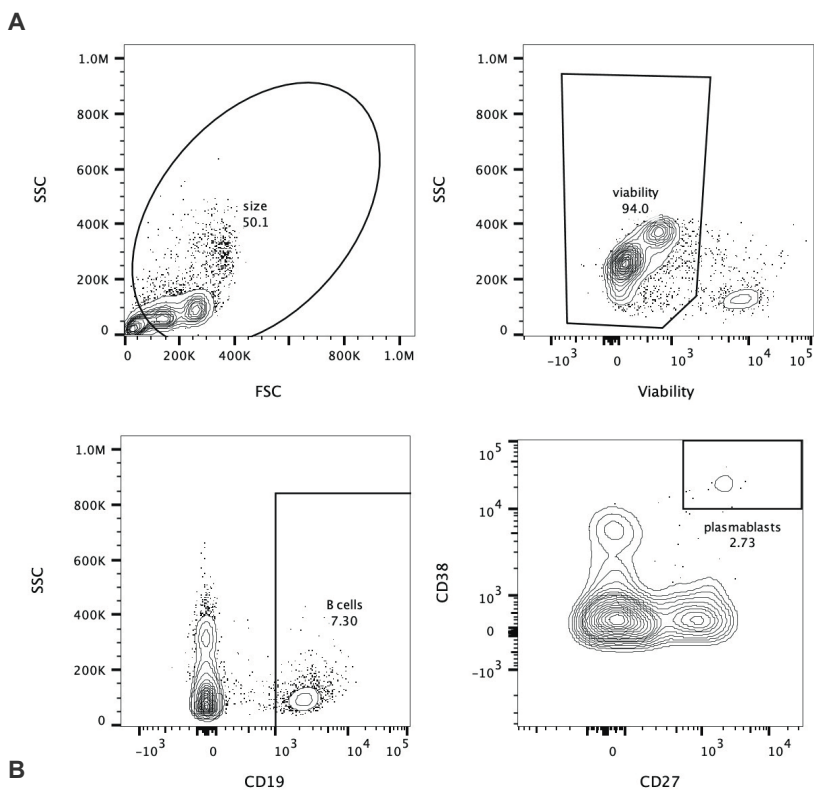


Fig. S2. Characterization of B cell subsets in COVID-19 outpatients. (A) The gating strategy for B cell subsets is shown. Total CD19⁺ B cells were assessed from within viable peripheral blood mononuclear cells (PBMCs). Plasmablasts were further defined as CD19⁺ CD27⁺ CD38⁺. Memory B cells were defined as CD19⁺ CD27⁺ IgD⁻, double negative (DN) B cells were CD19⁺ CD27⁻ IgD⁻, and naïve B cells were CD19⁺ CD27⁻ IgD⁺. FSC, forward scatter; SSC, side scatter. (B) FUT8 expression is shown within total viable PBMCs in progressors (P; n = 6) and sex-matched non-progressors (NP; n = 6). MFI, median fluorescence intensity. Horizontal bars indicate median. (C) Distribution of B cell subsets (class switched memory B cells (CSMB), non-class switched memory B cells (NCSMB), CD27⁻ IgD⁻ double negative B cells (DNB), plasmablasts (PB), and naïve B cells in progressors (P; n = 6), non-progressors (NP, n = 6), and healthy controls (HC, n = 4) are shown. P values in (B) was calculated using unpaired Student's t test; ns, not significant.

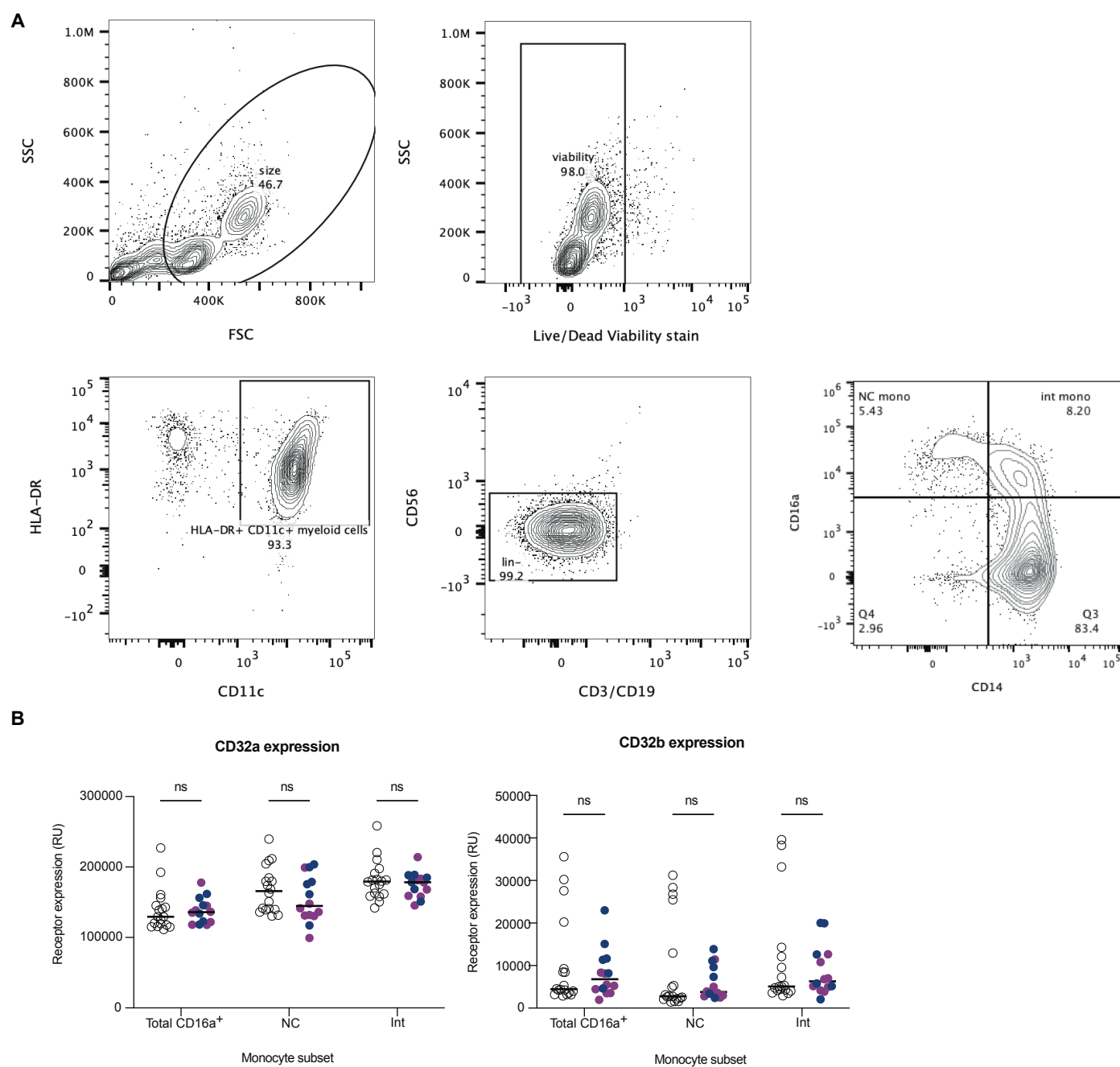


Fig. S3. Characterization of monocyte subsets in COVID-19 outpatients. (A) The gating strategy for day 0 monocyte subsets and Fc γ R expression is shown. Bulk myeloid cells were defined as viable CD3⁻ CD19⁻ CD56⁻ CD11c⁺ HLA-DR⁺ cells, while CD16a⁺ monocytes within this population were additionally positive for CD16a. Within CD16a⁺ monocytes, non-classical (NC) monocytes were CD16a⁺ CD14⁻ while intermediate (Int) monocytes were CD16a⁺ CD14⁺. **(B)** Fc γ R (CD32a and CD32b) expression on myeloid cell subsets is shown. Horizontal bars indicate median. P values were determined by unpaired Student's test. ns, not significant.

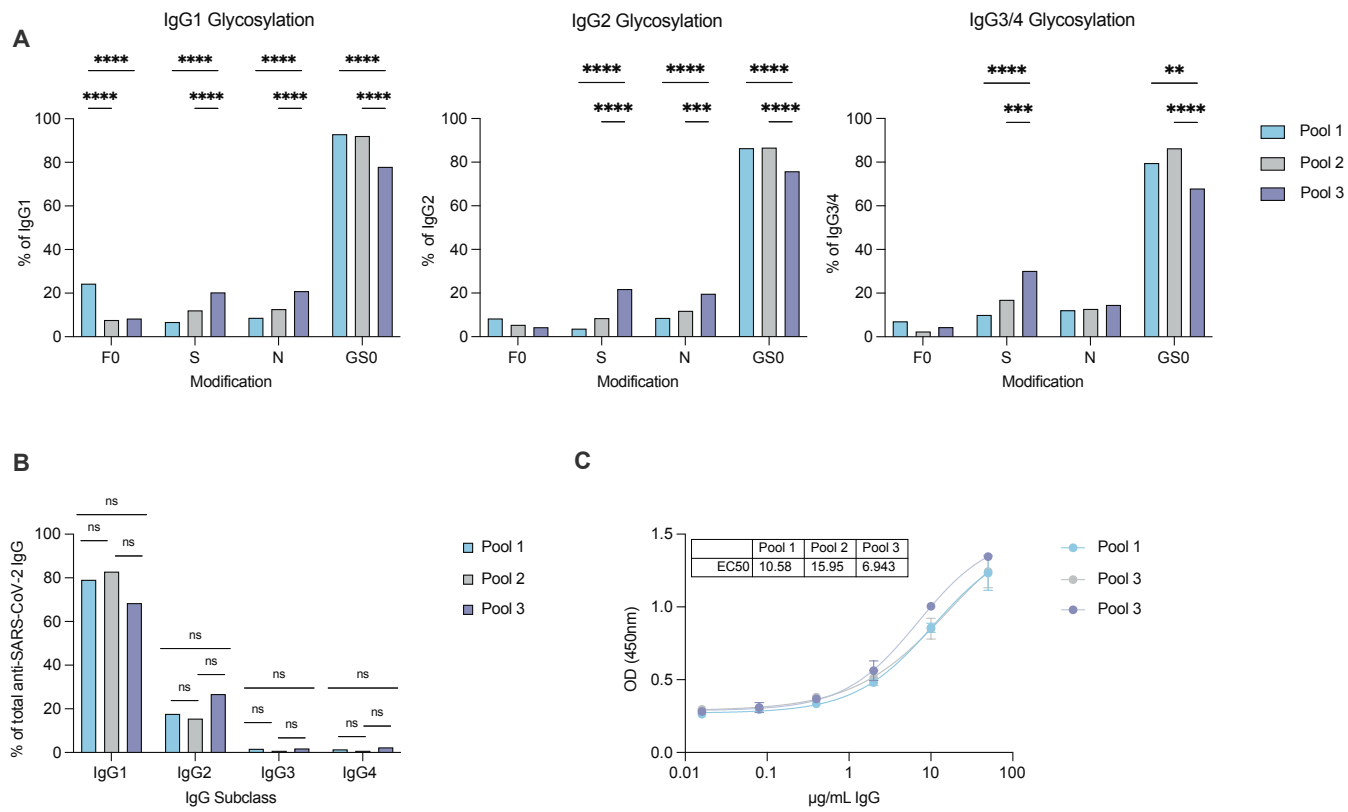


Fig. S4. Characterization of polyclonal IgG pools. (A) Glycan composition (F0-afucosylation, GS0-Galactosylation, S-Sialylation and N-Bisection) of IgG1, IgG2 and IgG3/4 was measured for individually purified patient IgG comprising polyclonal pool 1 (F0, F0>20%), pool 2 (F, F0<10%), and pool 3 (Vax). **(B)** IgG subclass distribution is shown for the individually purified patient IgG comprising polyclonal pool 1, pool 2, and pool 3. **(C)** SARS-CoV-2 full length spike binding to polyclonal pool 1, pool 2, and pool 3 is shown; OD, optical density. Data in (C) are presented as mean \pm SD; EC50, half maximal binding concentration. P values in (A and B) were calculated using two-way ANOVA with Sidak's correction. **P < 0.01; ***P < 0.001; ****P < 0.0001; ns, not significant.

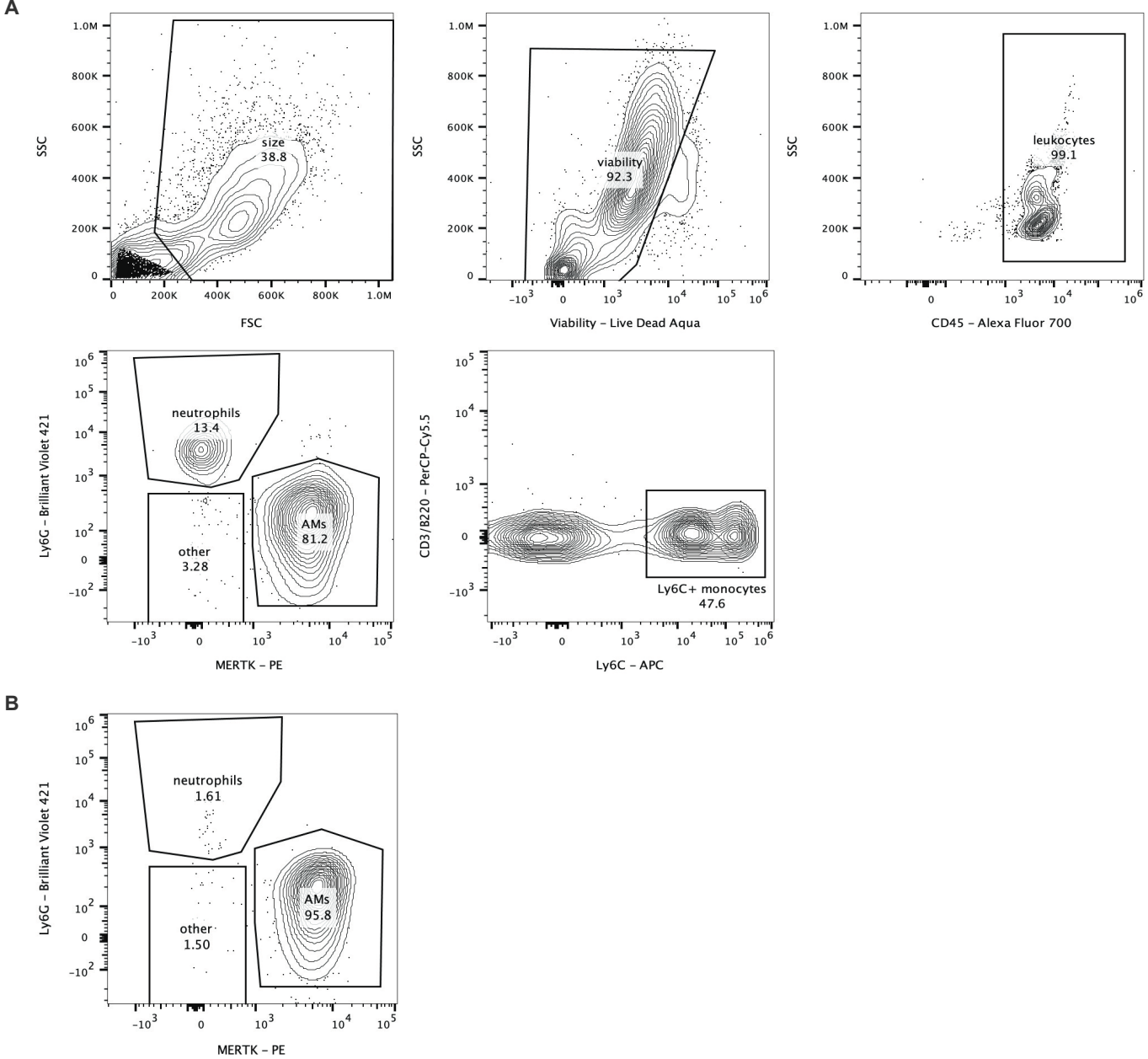


Fig. S5. Gating strategy for immune cell infiltrates in mouse BAL. (A) Neutrophils were defined as viable Ly6G⁺ CD11b⁺ CD3⁻ B220⁻ leukocytes. Monocytes were defined as viable CD11b⁺ Ly6G⁻ MERTK⁻ MHC IA/IE⁻ CD3⁻ B220⁻ or Ly6C⁺ CD11b⁺ Ly6G⁻ MERTK⁻ MHC IA/IE⁻ CD3⁻ B220⁻ leukocytes. **(B)** Alveolar macrophages were magnetically sorted based on positive expression of MERTK. This sorting method consistently resulted in >90% purity, as determined by flow cytometry. PE, phycoerythrin; APC, allophycocyanin.

Tables

Table S1. Demographics of the COVID-19 infection cohorts

Stanford Lambda cohort (Cohort 1)	Non-progressor (n=102)	Missing values	Progressor (n=8)	Missing values	p value
Age, years (median, 95%CI)	36 (32.8-38.2)	0	45 (34.4-55.7)	0	ns
Sex Female	45 (44.1%)	0	3 (38%)	0	ns
Race/Ethnicity		0		0	
Latinx	65 (63.7%)		5 (62.5%)		
White	29 (28.4%)		2 (25%)		
Asian	7 (6.9%)		0 (0%)		
Others	1(1%)		1 (12.5%)		
Weight (lbs) (median, 95% CI)	175 (168.1-181.9)	1	198.5 (148.8-248.2)	0	ns
Body mass index (BMI) (median, 95% CI)	27.2 (26.5-28.9)	3	28.8 (23.9-33.7)	0	ns
<25	25 (25.3%)		2 (25%)		
25-30	38 (38.4%)		3 (37.5%)		
>30	36 (36.4%)		3 (37.5%)		
Median days from symptoms onset to study enrollment	4	17	3.5	0	ns
Mean days from symptoms onset to study enrollment	5	17	3.6	0	ns
Median days from randomization to disease resolution	9	0	16	4	ns
Stanford Favipiravir Cohort (Cohort 2)	Non-progressor (n=67)	Missing values	Progressor (n=7)	Missing values	p value
Age, years (median, 95%CI)	40 (36.9-43.1)	0	52 (45.9-58)	0	**
Sex Female	35 (52.2%)	0	3 (42.9%)	0	ns
Race/Ethnicity		4		0	
Latinx	26 (38.8%)		5 (71.4%)		
White	27 (40.2%)		1 (14.3%)		
Asian	7 (10.4%)		0 (0%)		
Others	3(4.5%)		1 (14.3%)		
Weight (lbs) (median, 95% CI)	180 (170.4-189.6)	0	190 (146.5-233.4)	0	ns
Body mass index (BMI) (median, 95% CI)	28.3 (26.8-29.7)	0	30.8 (24.7-37)	0	ns
<25	20 (29.9%)		2 (28.6%)		
25-30	21 (31.3%)		1 (14.3%)		
>30	26(38.8%)		4 (57.1%)		
Median days from symptoms onset to study enrollment	5	3	5	0	ns
Mean days from symptoms onset to study enrollment	5.7	3	6.4	0	ns
Median days from randomization to disease resolution	11	0	16	0	ns
Mount Sinai Cohort	Hospitalized (n=52)				
Age, years (median, 95%CI)	65(60.6-69.4)				
Sex Female	21(40.4%)				
Race/Ethnicity					
Latinx	13 (25%)				
White	7 (13.5%)				
Asian	3 (5.8%)				
Others	29 (55.8%)				
Weight (lbs) (median, 95% CI)	N/A				
Body mass index (BMI) (median, 95% CI)	26.79(24.6-29.01)				
<25	15(28.8%)				
25-30	21(40.4%)				
>30	16(30.8%)				
Median days of sample time point post hospitalization (95% CI)	4(2.87-5.13)				

P values were calculated by comparing features between the progressors and non-progressors using unpaired t-tests with Welch's correction for categorical variables or Fisher's t-test for continuous variables. CI, confidence intervals; lbs, pounds; N/A not available; ns, not significant

Table S2. Description of progressors from Cohort 1

Age	Sex	Days of symptoms prior to enrollment	Days to Hospitalization/ED visit post assessment of mild COVID-19
25	Female	3	0; progressive symptoms leading to hospitalization within 24-hours.
58	Male	4	5; progressively worsening respiratory symptoms. Referred to ED by study-associated physician on study day 5.
44	Female	3	1; progressively worsening respiratory symptoms.
34	Male	2	13; worsening symptoms.
47	Male	5	3; two ED visits within first 3 days for worsening respiratory symptoms.
59	Female	7	0; progressive symptoms leading to hospitalization within 24-hours.
28	Male	4	0; progressive symptoms leading to hospitalization within 24-hours.
46	Male	1	2; progressive symptoms leading to hospitalization.

Table S3. Description of progressors from Cohort 2

Age	Sex	Days of symptoms prior to enrollment	Days to Hospitalization/ED visit post assessment of mild COVID-19
44	Female	8	8; worsening respiratory symptoms
54	Male	2	1; sent by study team to ED for worsening respiratory symptoms and leg swelling, resulted in hospitalization
57	Male	4	2; sent by study team to ED for worsening respiratory symptoms; hospitalized
46	Male	5	3; worsening symptoms and new rash
63	Female	10	5; sent by study team to ED for worsening symptoms
52	Male	4	10; sent by study team to ED for worsening respiratory symptoms; hospitalized
50	Female	8	3; sent by study team to ED for worsening respiratory symptoms; hospitalized

Table S4: Demographics of the Stanford Adult Vaccination Cohort

Characteristics	
Age, years (median, 95%CI)	36(28.3-43.7)
Sex Female	11(64.7%)
Race/Ethnicity	
Latinx	0(0.0%)
White	7(41.2%)
Asian	8(47.1%)
Others	2(11.8%)
