Supplemental Tables

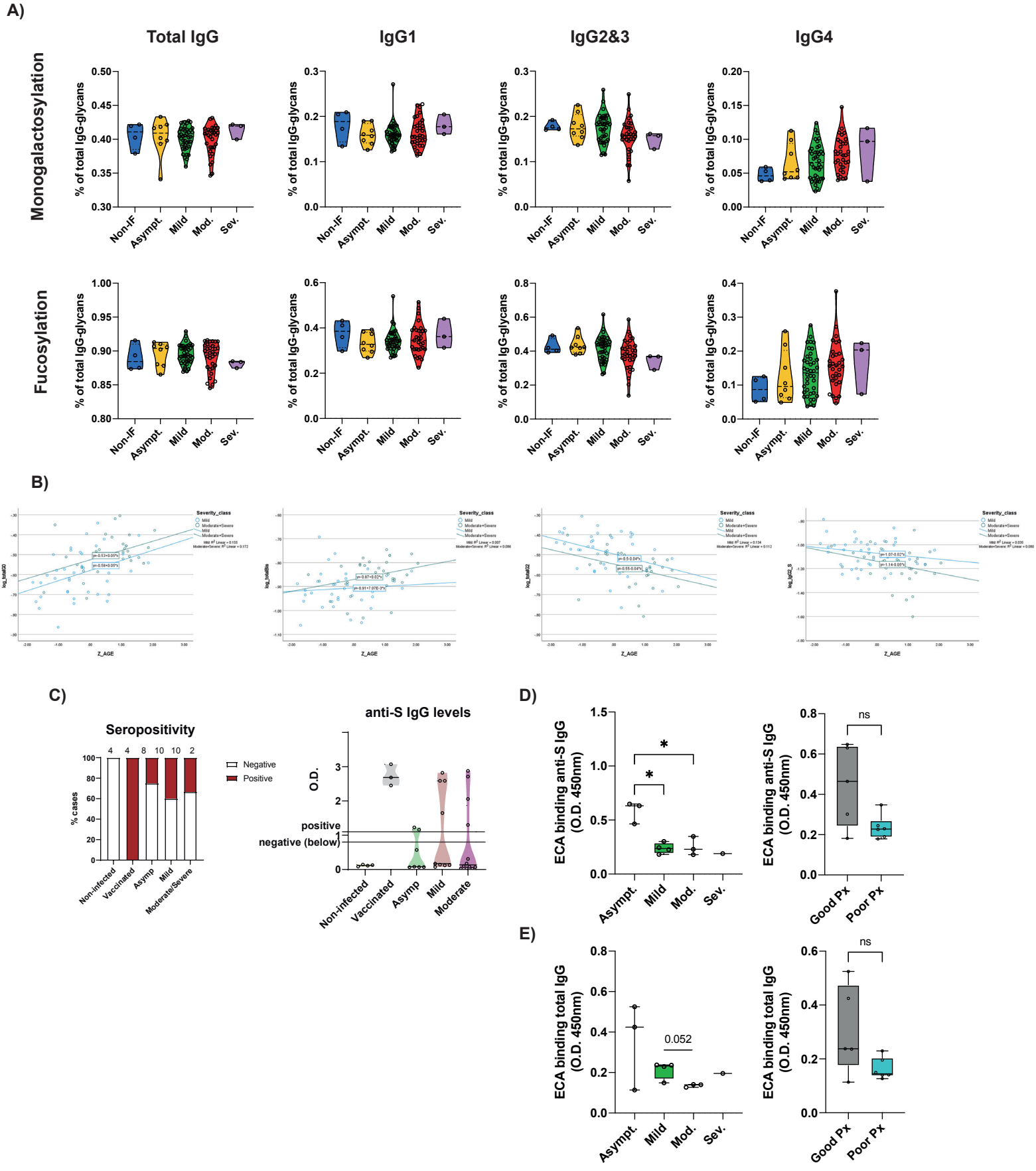
Supplemental Table 1 - Demographics of COVID-19 patients at time of sample collection. The following comorbidities were considered: heart disease (HD), obesity (Ob) or pulmonary disease (PD); other diseases (other) includes: diabetes, cancer and arterial hypertension.

	Asymptomatic n=8 (%)		**Mild** n=40 (%)		**Moderate/Severe** n=33 (%)	
Age						
21-30	1	(12.5)	5	(12.5)	1	(3.03)
31-40	1	(12.5)	5	(12.5)	1	(3.03)
41-50	1	(12.5)	10	(25.0)	2	(6.06)
51-60	2	(25.0)	6	(15.0)	4	(12.1)
61-70	2	(25.0)	8	(20.0)	8	(24.2)
71-80	1	(12.5)	3	(7.50)	7	(21.2)
81-100	0	(0)	3	(7.50)	10	(30.3)
Gender						
F	6	(75,0)	21	(52,5)	10	(30,3)
M	2	(25,0)	19	(47,5)	23	(69,7)
Comorbidities						
HD, Ob or PD	0	(0,0)	4	(10,0)	8	(24,2)
other	5	(62,5)	9	(22,5)	22	(66,7)
No	3	(37,5)	27	(67,5)	3	(9,1)

Supplemental Table 2 - Demographics of COVID-19 patients for the longitudinal analysis. The following comorbidities were considered: heart disease (HD), obesity (Ob) or pulmonary disease (PD); other diseases (other) includes: diabetes, cancer and arterial hypertension.

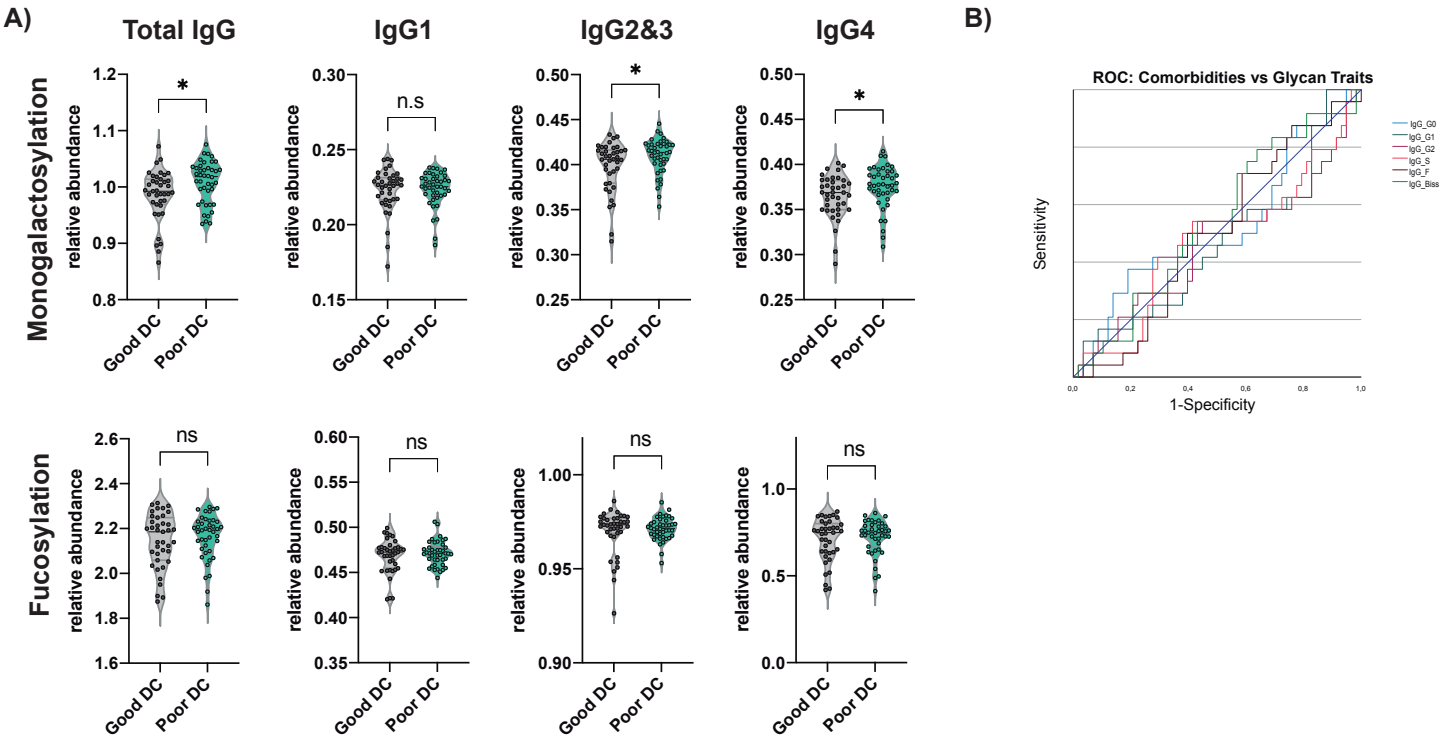
	Good Prognosis n=26 (%)	**Poor Prognosis** n=51 (%)
Age		
21-30	4 (15.4)	2 (3.92)
31-40	0 (0)	6 (11.8)
41-50	5 (19.2)	7 (13.7)
51-60	4 (15.4)	8 (15.7)
61-70	8 (30.8)	10 (19.6)
71-80	1 (3.85)	9 (17.6)
81-100	4 (15.4)	9 (17.6)
Gender		
F	14 (53,8)	21 (41,2)
M	12 (46,2)	30 (58,8)

Supplemental Figure 1



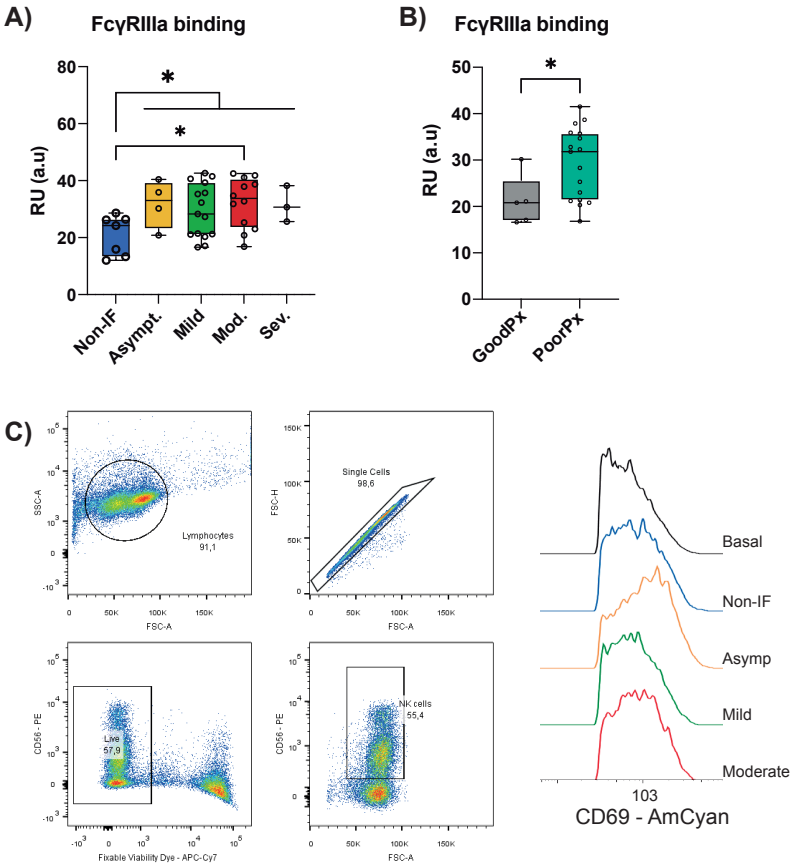
Supplemental Figure 1 - A) Relative abundance of total and isotypes IgG Fc monogalactosylation and fucosylation in different COVID-19 severities (asymptomatic n=8, mild n=40, moderate n=31, severe n=3) and non-IF individuals (n=4). B) Linear regression analysis for age and IgG glycan traits. C) ELISA relative quantification of anti-Spike IgG in serum from COVID-19 patients. D) Levels of terminal galactosylation of anti-Spike IgG, according to severity and prognosis of COVID-19 disease. E) Levels of terminal galactosylation of total IgG, according to severity and prognosis of COVID-19 disease. Each data point represents the data from a single patient/subject isolated IgG's in a single LC-MS analysis (one replicate).

Supplemental Figure 2



Supplemental Figure 2 – A) Relative abundance of total and isotypes IgG Fc monogalactosylation and fucosylation in good versus poor prognosis (good prognosis n=51; poor prognosis n=26) and non-IF individuals (n=4). B) Receiver Operating Characteristic (ROC) curve plotter for the IgG Fc N-glycan traits' levels of COVID-19 patients with comorbidities (heart disease, obesity and/or lung disease). Each data point represents the data from a single patient/subject isolated IgG's in a single LC-MS analysis (one replicate).

Supplemental Figure 3



Supplemental Figure 3 – A) SPR response unit (R.U) quantification of human recombinant FcγRIIIa binding to the IgGs from patients with COVID-19 disease severities (n=31) and (B) prognosis (n=22). C) Gating strategy for the identification of NK cells through the expression of marker CD56, and representative histograms showing the differences in the median intensity fluorescence (MFI) of activation marker CD69. Results shown from at least two independent experiments. Each point represent data from a single patient/subject.