1	Title: Diverging maternal and infant cord antibody functions from SARS-CoV-2 infection and
2	vaccination in pregnancy
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19	The authors have declared that no conflict of interest exists.

21 Abstract

22	Immunization in pregnancy is a critical tool that can be leveraged to protect the infant with an
23	immature immune system but how vaccine-induced antibodies transfer to the placenta and protect the
24	maternal-fetal dyad remains unclear. Here, we compare matched maternal-infant cord blood from
25	individuals who in pregnancy received mRNA COVID-19 vaccine, were infected by SARS-CoV-2, or
26	had the combination of these two immune exposures. We find that some but not all antibody neutralizing
27	activities and Fc effector functions are enriched with vaccination compared to infection. Preferential
28	transport to the fetus of Fc functions and not neutralization is observed. Immunization compared to
29	infection enriches IgG1-mediated antibody functions with changes in antibody post-translational
30	sialylation and fucosylation that impact fetal more than maternal antibody functional potency. Thus,
31	vaccine enhanced antibody functional magnitude, potency and breadth in the fetus are driven more by
32	antibody glycosylation and Fc effector functions compared to maternal responses, highlighting prenatal
33	opportunities to safeguard newborns as SARS-CoV-2 becomes endemic.
34	
35	One Sentence Summary: SARS-CoV-2 vaccination in pregnancy induces diverging maternal and infant

36 cord antibody functions

38 INTRODUCTION

39	With over 140 million women giving birth every year, the newborn immature immune system
40	and maternal immune adaptation to pregnancy represent widespread challenges to surviving COVID-19.
41	Infants > 6 months old have higher rates of hospitalization compared to those older for SARS-CoV-2
42	infection (1, 2). Similarly, pregnant individuals are more likely to need intensive care unit and ventilatory
43	support compared to the general population (3, 4), and have increased risk of obstetrical and fetal
44	complications (5, 6). Beyond the short-term consequences, a growing number of long-term multi-system
45	sequelae for adults are being recognized (7). Moreover, emerging data suggest that even without vertical
46	transmission there may be infant neurodevelopmental impacts from prenatal exposure to SARS-CoV-2
47	yet to be fully understood (8-10). Thus, immunizations could be critical to safeguarding maternal, fetal
48	and newborn health as SARS-CoV-2 becomes endemic and public health precautions wane but how they
49	can be harnessed to provide optimal protection are less clear.
50	Before vaccine availability, COVID-19 contributed to ~25% of maternal deaths (11, 12) and was
51	the number one cause of infection-related deaths in children (13). Recent studies show that as in the
52	general population, monovalent mRNA immunization in pregnancy decreases the risk of maternal and
53	infant SARS-CoV-2 infection, disease, and mortality (14-19). Unraveling the maternal responses to the
54	different immune exposures of infection and vaccination during pregnancy and what transfers into the
55	placenta can guide vaccine design and implementation strategies to enhance protection of the maternal-
56	fetal dyad.
57	Multiple human and animal studies show that leveraging a breadth of immune responses to
58	differentially target several steps in viral infection and pathogenesis is likely necessary to provide durable
59	protection (20-25). After mRNA vaccination, the primary form of immunity transferred to the fetus is
60	antibodies, specifically IgG. If we understand the spectrum of IgG-mediated functions in the fetus then
61	we can design ways to leverage maternal immunity to protect the infant.
62	SARS-CoV-2 mRNA vaccines and infection generate IgG with neutralizing and antibody Fc

63 effector functions in the non-pregnant (26-29) and pregnant populations (30-35). With Fc-Fc receptor

64 engagement on innate and adaptive immune cells (36, 37), induced effector functions can prevent disease 65 even after infection has occurred by eliminating infected cells and blocking spread (25, 38-44). Diversity 66 of the Fc domain through differential subclass and post-translational glycosylation modulates binding to 67 Fc receptors and the spectrum of effector functions (45-52). Moreover, antibody functional potency, 68 breadth and coordination between neutralizing and Fc effector responses likely contribute to protection 69 (26, 53-57). Some data demonstrate that maternal immune adaptation to pregnancy alters antibody 70 subclass and glycosylation (30, 58-65), but the implications for antibody functions and what exists for the 71 fetus are only just beginning to be appreciated (66-70). 72 To understand how SARS-CoV-2 mRNA vaccination in pregnancy impacts the newborn, we 73 collected paired maternal-infant cord blood samples at delivery. We evaluated neutralization against live 74 SARS-CoV-2 and the Fc effector functions of natural killer cell activation that leads to antibody-75 dependent cellular cytotoxicity, antibody-dependent monocyte phagocytosis, antibody-dependent 76 complement deposition, and Fcy receptor binding specific for the Spike glycoprotein receptor binding 77 domain (RBD). We determined relative levels of RBD-specific antibody subclass, isotype and post-78 translational glycosylation to assess how these different features contribute to function. The data show 79 that compared to SARS-CoV-2 infection, vaccination in pregnancy enhances some but not all neutralizing 80 and Fc effector functions, with preferential transport of Fc functions and not neutralization. All functions 81 are primarily driven by IgG1 which is enhanced by vaccination. However, vaccination in pregnancy 82 changes glycosylation of cord and not maternal RBD IgG and the impact of glycosylation on antibody 83 functional potency is observed more in cord compared to maternal responses. Thus, while vaccination 84 compared to infection in pregnancy boosts antibody functions, the maternal and fetal paths begin to 85 diverge.

86 **RESULTS**

87 Study subjects

88 We collected paired maternal-umbilical cord blood at deliveries from individuals who during 89 pregnancy received mRNA vaccination targeting WA1 RBD (n=19 vaccine only) and or infected with 90 SARS-CoV-2 (n=22 infection only and n=28 both vaccine and infection) at Parkland Health, the Dallas 91 County's public hospital in Texas (Table and Supplemental Table 1). Clinical groups were defined by 92 clinical history, documented vaccination in pregnancy, SARS-CoV-2 nasal swab PCR and SARS-CoV-2 93 nucleocapsid IgG (Supplemental Figure 1). Of the 47 vaccinated, four received mRNA-1273 and 43 94 BNT162b2 with no significant difference between the two (Supplemental Table 2). The mean age of 95 individuals with only infection was lower compared to those who received vaccination in pregnancy 96 (p=0.005). Body mass index (BMI), gestational age at delivery (75% full term), infant sex and an 97 additional 21 clinical outcomes were not significantly different (Table and Supplemental Table 1). Of the 98 infected, 20% were asymptomatic, 40% mild, 10% moderate, 14% severe and 16% critical. Of the 99 vaccinated, the majority received two doses (68%) before delivery with their last dose in the third 100 trimester (Supplemental Figure 1). With 94% of participants Hispanic, this study population represents a 101 subset of the 11,170 deliveries at Parkland Health in 2021 and a patient population from social-economic 102 communities disproportionately impacted by SARS-CoV-2 (Supplemental Table 3) (71-73). 103 Infant-cord SARS-CoV-2 neutralizing and Fc effector functions 104 Infants of individuals with monovalent COVID-19 mRNA vaccination in pregnancy have 105 decreased risk of SARS-CoV-2 infection, hospitalization, and mortality up to 6 months after birth (15, 106 19). This is irrespective of whether SARS-CoV-2 infection occurred. To begin to investigate the antibody 107 functions induced by vaccination, we measured neutralizing activity that prevents viral entry and infection 108 (74-77). Through focus reduction neutralization tests (FRNT) using live SARS-CoV-2 (WA1/2020) and 109 variants Delta (B.1.617.2) and Omicron (BA.2) (Supplemental Figure 2), we observed higher cord 110 neutralizing activities against WA1 in those with mRNA vaccination compared to SARS-CoV-2 infection 111 and non-significant changes against Delta and Omicron (Figure 1A, F). Subanalyses showed that while

neutralizing activity from the combination of vaccine and infection compared to vaccine alone trended higher, this was not statistically significant (Figure 1F). Thus, vaccination compared to infection alone in pregnancy induces higher cord neutralizing activity for protection against subsequent challenges by the same viral strain.

116 Decay studies show that antibody Fc effector functions are more durable than neutralization (23, 117 29, 78) and data from animal models show that Fc-Fc receptor engagement impacts viral load and disease 118 (25, 38-42, 44, 57). We examined RBD-specific Fc effector functions induced by vaccination and SARS-119 CoV-2 infection (26-28, 30, 32, 43, 46): antibody-dependent natural killer cell activation (ADNKA) 120 which leads to antibody-dependent cellular cytotoxicity (ADCC) (Figure 1B), antibody-dependent 121 complement deposition (ADCD) (Figure 1C) and antibody-dependent cellular phagocytosis (ADCP) 122 (Figure 1D). We found that vaccination in pregnancy compared to infection alone is linked to higher RBD 123 ADNKA including CD107a degranulation and intracellular IFNy and TNFa production (Figure 1B) and 124 ADCD (Figure 1C), not ADCP (Figure 1D). Antibody Fc domain engagement of low affinity Fc receptors 125 is the first step in the signaling and initiation of effector functions while the high affinity FcRN is 126 responsible for transport across the placenta and recycling (37, 79-81). We found that binding to the low 127 affinity activating FcyRIIIa/CD16a and FcyRIIa/CD32a, the inhibitory FcyRIIb/CD32b and high affinity 128 FcRN were elevated after vaccination compared to infection in pregnancy (Figure 1E). Again, the 129 combination of vaccine and infection compared to vaccine alone was not statistically different (Figure 130 1F). Thus, the magnitude of some but not all cord RBD Fc effector functions and Fc receptor binding are 131 enhanced with vaccination.

Sex (82, 83), infant prematurity (69), trimester of vaccination (31, 33), mRNA vaccine platform
(27, 33) and disease severity (45, 46, 84) impact antibody responses. Though limited by power, no
significant differences were observed in these data. Consistent with findings in the general population
(85), there were no significant differences with respect to the order of vaccination and infection in the
combination group (Supplemental Figure 1).

137 In addition to magnitude, greater polyfunctional antibody breadth is associated with increased

138 protection (26). For each cord sample, we categorized the proportion of detectable SARS-CoV-2

neutralizing and Fc effector responses as high (>90%), medium (80-90%) or low (<80%) responder

140 (Supplemental Figure 3). We observed more high responders with greater functional breadth in the

141 vaccinated compared to infected (Figure 1G).

142 Maternal SARS-CoV-2 neutralizing and Fc effector functions

143 To understand how infant cord antibody responses are shaped, we next measured neutralizing

144 activities and Fc effector functions in paired maternal samples obtained at delivery. Like cord samples,

145 maternal blood from those vaccinated compared to infected enhanced the magnitude of neutralization

146 against SARS-CoV-2 WA1 and not Delta or Omicron (Figure 2A). RBD ADNKA (Figure 2B), ADCD

147 (Figure 2C), and not ADCP (Figure 2D) were increased. Relative binding of RBD IgG to

148 FcyRIIIa/CD16a, FcyRIIa/CD32a, FcyRIIb/CD32b and FcRN were higher (Figure 2E). There was a non-

149 statistically significant trend towards increased antibody functions with combination vaccine and

150 infection compared to vaccine alone (Figure 2F) and greater polyfunctional breadth with vaccination

151 (Figure 2G). Thus, vaccination in pregnancy enhances the magnitude and breadth of neutralizing and Fc

152 effector functions across the maternal-fetal dyad.

153 Maternal-fetal transfer of antibody functions

154 The maternal response to an immune exposure and transfer of that response across the placenta 155 determine fetal antibody functions. In examining transfer, we found that neutralizing activities did not 156 differ between paired maternal and cord samples irrespective of immune exposure (Figure 3A). However, 157 levels of RBD Fc effector functions of ADNKA were lower in maternal compared to cord blood (Figure 158 3B). This was not observed for RBD ADCD (Figure 3C) but was for ADCP (Figure 3D). Consistent with 159 the low affinity activating and inhibitory FcyRs modulating ADNKA and ADCP, relative binding for 160 FcyRIIIa/CD16a, FcyRIIa/CD32a and FcyRIIb/CD32b were all lower in maternal compared to cord blood 161 (Figure 3E). In contrast, no difference was observed for the high affinity FcRN that mediates IgG

162 transport across the placenta (Figure 3E). These data show preferential transfer of a subset of Fcγ effector 163 functions compared to viral neutralization and C1q mediated C3 complement deposition that leads to 164 ADCD. In the case of Fcγ receptor binding the transfer ratio was inversely related to the magnitude of the 165 maternal response (Figure 3F). Highest transfer was observed after infection with the lowest maternal 166 response and lowest transfer after vaccination and infection inducing the highest maternal response 167 (Figure 3F). Overall transport of antibody functions across the placenta was based on the nature of the 168 antibody function and maternal levels.

169 **RBD-specific isotype and subclass**

170 Differential isotypes and subclass drive diversity in antibody functions (36, 86). To determine 171 which are induced by vaccination we measured RBD IgG, IgA and IgM and IgG1, IgG2, IgG3 and IgG4. 172 In cord samples, we observed that the magnitude of RBD IgG, specifically IgG1 and not IgG2-4, was 173 enhanced (Figure 4A), with no differences in control influenza-specific IgG (Supplemental Figure 4). 174 RBD IgM and IgA were minimally detected (Figure 4A and Supplemental Figure 4 and 5A). Similarly, in 175 maternal samples vaccination linked to enhanced RBD IgG, specifically IgG1 (Figure 4B). While RBD 176 IgA and IgM were detectable and trended higher with vaccination, no differences were significant 177 (Supplemental Figure 5B). Thus, vaccination in pregnancy enhances the magnitude of RBD IgG, 178 specifically IgG1, in both maternal and fetal responses. 179 IgG subclasses and antibody functions

With the increased magnitude of RBD IgG1 after vaccination, we expected this subclass to drive
antibody functions targeting SARS-CoV-2. Using linear regression to assess the dependency of each
neutralizing and Fc effector function on RBD-specific subclasses we found that this was the general case
for maternal and cord responses across immune exposures (Figure 4C, D). A greater breadth of subclasses
(RBD IgG1, IgG2, IgG3 and IgG4) was linked to antibody functions in maternal blood, which focused on
IgG1 with vaccination (Figure 4D). **RBD-specific IgG glycosylation**

187	Differential post-translational IgG glycosylation modulates Fc effector functions in SARS-CoV-2		
188	infection and vaccination (26, 45-48, 50) and potentially placental transfer (31, 66, 67, 87). A core bi-		
189	antennary structure of mannose and N-acetylglucosamine on a conserved N297 of the Fc domain is		
190	modified with the addition and subtraction of galactose (G), sialic acid (S), fucose (F) and a bisecting N-		
191	acetylglucosamine GlcNAc (B) (Figure 5, Supplemental Figure 6) (52) into diverse forms. We quantitated		
192	the relative abundance of the individual glycoforms (Figure 5 and Supplemental Figure 6) and found		
193	differences between RBD and non-antigen specific IgG in both maternal and cord blood (Figure 5A, B).		
194	However, vaccination increased fucosylated (F) and decreased di-sialylated (S) structures on cord RBD		
195	IgG (Figure 5C and Supplemental Figure 7A). These differences were not observed on non-antigen		
196	specific (Supplemental Figure 7B) or on maternal IgG (Figure 5D and Supplemental Figure 7C-D). Thus,		
197	RBD-specific IgG glycosylation highlights differences in maternal-cord blood with vaccination compared		
198	to infection in pregnancy.		
199	IgG glycosylation and antibody functional potency		
200	Antibody glycosylation impacts functional potency, the level of function relative amount of		
201	antibodies (88, 89). Of all antibody functions measured, potency of viral neutralization against WA1 and		
202	ADCD were significantly enhanced in the vaccinated compared to only infected (Figure 6A, B). No		
203	differences were observed for ADNKA and ADCP (Figure 6A, B). Thus, vaccination in pregnancy		
204	enhances the potency of a subset of maternal and fetal antibody functions.		
205	To examine how differential RBD IgG glycans influence antibody functional potency, we used		
206	linear regression. Antibody functional potency in cord compared to maternal samples was generally more		
207	dependent on glycans (Figure 6A, B). The most prominent difference was observed in the combination		
208	vaccine and infection group, highlighting the negative effect of fucose and positive of di-sialic acid, the		

209 only RBD IgG glycans that changed significantly with vaccination compared to infection (Supplemental

210 Figure 7A).

211 Vaccine mediated polyfunctional antibody coordination

212	Polyclonal responses offer protection against subsequent viral challenge through a integration of
213	multiple antibody functions (42, 55). We found partial overlap in the coordination between neutralizing
214	and Fc effector functions in maternal and cord responses (Figure 7A). Correlations between viral
215	neutralization and RBD ADNKA and Fcy receptor binding were relatively preserved across the maternal-
216	fetal dyad irrespective of immune exposure. Links to RBD ADCP were observed more in maternal
217	samples after vaccination. In contrast, links to RBD ADCD were observed in both maternal and cord
218	samples after infection. Finally, more differences between maternal and cord samples were apparent after
219	vaccination as compared to natural infection, suggesting diverging responses in the context of specific
220	immune exposures.
221	To globally assess responses by maternal-fetal origin and immune exposure, we performed
222	principal component analysis using all 38 measured antibody features with the capacity to modify SARS-
223	CoV-2 in subsequent challenge. We found partial overlap between vaccine and infection groups and
224	within the maternal-fetal dyad (Figure 7B, C). Explaining the most amount of variance in the data through
225	PC1 were the top antibody features that distinguished the vaccine from infection group- RBD $Fc\gamma$
226	receptor binding and IgG levels- affirming our univariate analyses (Figure 1, 2, 4). Explaining the second
227	most amount of variance through PC2 was RBD-specific antibody glycosylation, driving differences
228	between maternal and cord samples. Thus, vaccination in pregnancy enriches multiple antibody
229	neutralizing and Fc functions with glycosylation differentiating fetal from maternal responses.

231 DISCUSSION

232 Neutralizing and antibody Fc effector functions transfer to the fetus

233 Observational studies show that two doses of monovalent mRNA vaccines in pregnancy protect 234 infants up to 6 months after birth from complications and morbidity associated with COVID-19 but what 235 mediates protection is less clear (15, 19). The data here shows that in cord blood vaccination compared to 236 infection enhances overall magnitude, polyfunctional breadth (Figure 1 and 2) and antibody potency 237 (Figure 6) against SARS-CoV-2 through RBD IgG (Figure 4 and Supplemental Figure 5), specifically 238 IgG1 (Figure 4) and differential antibody glycosylation (Figure 5-7) that drives coordinated (Figure 7A). 239 These include neutralization of SARS-CoV-2 WA1 (Figure 1A, F) and binding of RBD-specific 240 antibodies to Fcy receptors (Figure 1E, F) involved in the induction of natural killer cell activation and 241 concomitant cellular cytotoxicity (Figure 1B, F). Complementary to Fc receptor binding, C1q engagement 242 of the antibody Fc domain to induce C3 mediated complement activation is enhanced, offering protection 243 via a separate mechanism from neutralizing and other Fcy effector functions (Figure 1C, 7A). Not all 244 functions are enriched in vaccination compared to infection as in the case of cord antibody-dependent 245 cellular phagocytosis (Figure 1D, 7). However, Fcy receptor mediated functions compared to neutralizing 246 and complement activities are preferentially transported to the fetus regardless of whether the immune 247 exposure is infection or vaccination (Figure 3). Thus, a subset of vaccine-induced maternal antibody 248 neutralizing and Fc effector functions is transferred to the fetus. 249 Accumulating data suggest that immune responses beyond direct neutralization likely shape 250 protection in subsequent viral challenge (20-25, 55). In animal models testing monoclonal antibodies and 251 vaccination, the absence of Fc domain-Fcy receptor engagement leads to increased viral load and 252 pathology (25, 38-42). As such, preserved Fc effector functions (25, 26, 43) likely do not prevent

253 acquisition of infection but rather limit disease in the absence of high neutralization as is observed with

the monovalent WA1-based mRNA vaccines against Delta and Omicron (90, 91).

255 Fc effector functions may be particularly relevant for the fetus. Similar to HIV, CMV and malaria 256 and some vaccines (67-69, 92), the data from this study show that Fcy receptor mediated functions are 257 transferred along with IgG across the placenta (Figure 1, 3). Higher natural killer cell activation and 258 cellular phagocytosis in cord compared to paired maternal samples (Figure 3B, D) irrespective of immune 259 exposure suggest preferential transport of Fcy functions that contrast equivalent levels of neutralizing 260 (Figure 3A) and complement (Figure 3C) activities. Longitudinal studies show that Fc functions persist 261 longer than neutralizing activities (23, 29, 78). Thus, Fc functions have the localization and durability to 262 offer protection across the gestational and neonatal periods when the immune system is immature. 263 Vaccine-induced maternal antibody functions transfer to the fetus 264 The data from this study show that vaccination as compared to a spectrum of SARS-CoV-2 265 infection from asymptomatic to severe COVID-19 (Supplemental Figure 1) in pregnancy enhances 266 maternal antibody neutralizing and Fc effector functions. Mirroring paired cord responses, neutralization 267 against WA1, Fcy receptor binding mediated natural killer cell activation and C1q-C3 driven complement 268 activation are elevated in maternal responses to vaccination compared to infection alone (Figure 2, Figure 269 3A-C). This occurs even in the context of co-morbidities including pre-gestational diabetes and chronic 270 hypertension (Supplemental Table 1). Thus, like the fetus, maternal vaccination likely also benefits the 271 pregnant individual through enhanced neutralizing and Fc effector functions. 272 Antibodies and their associated functions traffic across the placenta. The primary transporter of 273 IgG from the pregnant individual to the fetus is the neonatal FcRN (80, 81), though FcyRIIIa/CD16a, 274 FcyRIIa/CD32a, FcyRIIb/CD32b and other Fcy receptors expressed in the placenta could be additional 275 factors (31, 67). Consistent with its high affinity nature, relative binding to FcRN is equivalent in cord 276 and maternal responses irrespective of immune exposure (Figure 3E). Yet with antibodies binding to the 277 low affinity Fcy receptors there is preferential fetal localization when the maternal magnitude is low

278 (Figure 3E, F). Upon vaccination, the difference in FcyRIIIa/CD16a but neither FcyRIIa/CD32a nor

279 FcyRIIb/CD32b disappears (Figure 3E), suggesting that when maternal antibodies are elevated,

280 FcyRIIIa/CD16a binding is saturated. This effect is more apparent when maternal antibodies are highest 281 after the combination of infection and vaccination (Figure 3F). Altered placental IgG transfer has been 282 described in chronic infections such as HIV (67) and SARS-CoV-2 infection in pregnancy (31). Thus it is 283 plausible that vaccination could similarly impact FcR levels and the transfer of distinctly glycosylated 284 IgG. However, the data here shows that the large enhancement of the initial maternal response with 285 vaccination compared to infection overshadows the smaller effects of differential transfer. 286 Differential glycosylation contributes to antibody functional potency in the fetus 287 While vaccine-induced RBD IgG1 drives functions across the maternal-fetal dyad (Figure 4C, 288 D), post-translational antibody glycosylation appears to contribute more to potency in the fetus than the 289 pregnant individual (Figure 5, 6, 7B, 7C, Supplemental Figure 7 and 8). All polyclonal IgG have N-linked 290 glycans on the Fc domain that drive Fcy receptors binding and effector functions (38, 39, 54, 88) and 20% 291 of the population have additional modifications on the Fab domain (93, 94) that have the potential to 292 impact stability, half-life and avidity to antigens (59, 61, 95). Subtle differences between maternal and 293 cord IgG glycosylation have been reported (87, 96). In COVID-19 disease and upon mRNA vaccination, 294 changes in fucose and sialic acid alter antibody-dependent natural killer cell activity that leads to cellular 295 cytotoxicity and are associated with different clinical outcomes (45-48, 97, 98). Our data show that these 296 same glycans are altered on cord and not maternal RBD IgG with vaccination (Figure 5 and Supplemental 297 Figure 7), impacting RBD ADNKA potency in the newborn (Figure 6). Recent data in a mouse model of 298 Listeria infection show that vaccination during as compared to before pregnancy induces Fab domain 299 sialylation that enhances protection for pups (61). Whether pregnancy-specific changes in antibody 300 glycosylation could similarly improve infant protection against COVID-19 is not known. Beyond 301 COVID-19, different vaccine adjuvants and platforms can modulate antibody glycosylation as well as 302 subclass that could impact Fc effector functions (99, 100). Thus, what is learned in COVID-19 has 303 implications for the design of vaccines across infections that disproportionately impact the maternal-fetal

304 dyad (62, 68, 101, 102).

305	The mechanism by which IgG is differentially glycosylated between the maternal and fetal sides
306	of the placenta are not known. One explanation could be differential transfer (31, 66, 103, 104). Another
307	is that B cell extrinsic glycosidases and glycosyltransferases could modify antibodies as they traffic from
308	the pregnant individual to the fetus (105, 106). Because immunity directly passed to the fetus is primarily
309	IgG, this single isotype is the main source of protection and differential glycosylation a significant
310	determinant of diversity. Pregnant individuals have a greater breadth of responses to subsequent viral
311	challenge with isotypes and cellular immunity (22, 107, 108) that could leave IgG post-translational
312	modifications less critical.
313	Maternal vaccination enriches antibody functions with and without SARS-CoV-2 infection
314	In the general population, the combination of vaccine and infection boosts antibody responses
315	compared to either immune exposure alone (56, 85, 109, 110). This similarly occurs in pregnancy where
316	levels of antibody functions, Fc receptor binding and subclasses with the combination is statistically
317	significantly higher compared to infection alone and non-significantly higher compared to vaccine alone
318	(Figure 1, 2). Thus, maternal immunization likely benefits the pregnant individual and the fetus regardless
319	of the presence of infection-derived immunity.
320	The preponderance of data show that immunity from vaccination compared to SARS-CoV-2
321	infection provides more effective protection against disease across different populations including the
322	immunocompromised and the elderly. COVID-19 vaccines may be an annual recommendation for the
323	general population but how these tools can be best leveraged with respect to trimester of immunization
324	(33), vaccine platforms (27), and adjuvants (100) that alter antibody glycosylation and potentially
325	functions remains to be seen. Moreover, maternal comorbid conditions that affect the immune substrate
	functions femalits to be seen. Moreover, maternal co-morbid conditions that affect the minimum substrate
326	such as gestational diabetes could impact how antibody functions are transferred to the fetus (111).
326 327	such as gestational diabetes could impact how antibody functions are transferred to the fetus (111). Finally, newborn immunity can be further supported by maternal IgA, IgG and IgM in the colostrum
326 327 328	such as gestational diabetes could impact how antibody functions are transferred to the fetus (111). Finally, newborn immunity can be further supported by maternal IgA, IgG and IgM in the colostrum (112). Studies powered to address how these factors influences antibody functions will illuminate ways to

330	With no evidence of serious mRNA vaccine related adverse effects in pregnancy (114-116) and
331	the potential benefits of maternal antibodies in preventing disease for the maternal-fetal dyad, pregnancy
332	is argued to be a condition that should be eligible for additional doses (117). That infants under 6 months
333	of age are the only ones with no available COVID-19 vaccines further supports this argument. However,
334	the transfer of maternal antibodies to the fetus has many potential consequences yet to be unraveled.
335	Some data suggest that maternal antibodies blunt infant responses to vaccines given after birth via
336	mechanisms still debated (118-121) while others show a priming effect on infant cellular and humoral
337	responses (122). Beyond the infant, data from animal models suggest that maternal antibodies can shape
338	the B cell repertoire of the offspring long after the maternal antibodies themselves become undetectable
339	(123), suggestive of a "vaccinal" effect (124). Thus, diverging maternal and cord antibody functions from
340	SARS-CoV-2 infection and vaccination in pregnancy could have implications for the development of
341	immune responses to subsequent coronavirus challenges reaching beyond infancy and into adulthood.

343 MATERIALS AND METHODS

344 Study design and participant recruitment

345	We approached individuals at Parkland Health, the Dallas County public hospital in Texas.	
346	Eligible participants were pregnant, ≥18 years, able to provide informed consent, and received at least one	
347	dose of mRNA vaccine and or were infected with SARS-CoV-2 in pregnancy. Individuals with infection	
348	or vaccination outside of pregnancy were excluded. Clinical COVID-19, pregnancy and obstetric data	
349	were determined through electronic health record review. Disease severity was classified per NIH	
350	COVID-19 guidelines (125).	
351	Study Approval	
352	This study was conducted in accordance with the UTSW and Parkland Health IRBs (STU2020-	
353	0375, STU2020-0214) and approved by the Oregon Health & Science University IRB	
354	(PROTO202000015). Written informed consent was received from all study individuals prior to	
355	participation.	
356	Sample collection	
357	Paired maternal and infant cord blood were collected in deliveries (February 17, 2021 - May 27,	
358	2022) by venipuncture or from umbilical vein in ACD and SST tubes. Plasma and serum were isolated by	
359	centrifugation at 1400RPM and 3400RPM respectively for 10minutes at RT, aliquoted into cryogenic	
360	vials, stored at -80°C, and heat-inactivated at 55°C for 10minutes prior to use in assays.	
361	Cell lines	
362	Vero E6 cells (ATCC VERO C1008) were grown at 37°C, 5% CO2 in Dulbecco's Modified	
363	Eagle Medium supplemented with 10% fetal bovine serum, 1% penicillin/streptomycin, 1% non-essential	
364	amino acids. THP-1 cells (ATCC TIB-202) were grown at 37°C, 5% CO2 in RPMI-1640 supplemented	
365	with 10% fetal bovine serum, 2mM L-glutamine, 10mM HEPES, and 0.05mM β -mercaptoethanol.	
366	CD16.NK-92 (ATCC PTA-6967) were grown at 37°C, 5% CO2 in MEM-α supplemented with 12.5%	

FBS, 12.5% horse serum, 1.5g/L sodium bicarbonate, 0.02mM folic acid, 0.2mM inositol, 0.1mM 2-βmercaptoethanol, 100U/mL IL-2.

369 Viruses

370 SARS-CoV-2 clinical isolates were passaged once before use: USA-WA1/2020 [original strain]
371 (BEI Resources NR-52281); hCoV-19/USA/PHC658/2021 [B.1.617.2] (BEI Resources NR-55611), and
372 hCoV-19/USA/CO-CDPHE-2102544747/2021 [B.1.1.529 - BA.2] (BEI Resources NR-56520). Isolates
373 were propagated in Vero E6 cells for 24-72hours until cultures displayed at least 20% cytopathic effect
374 (CPE) (97).

375 Focus Reduction Neutralization Test (FRNT)

376 Focus forming assays were performed as described (26, 126). Sub-confluent Vero E6 cells were 377 incubated for 1hour with 30µL of diluted sera (5x4-fold starting at 1:20) which was pre-incubated for 378 1hour with 100 infectious viral particles per well. Samples were tested in duplicate. Wells were covered 379 with 150uL of overlay media containing 1% methylcellulose and incubated for 24hours. Plates were fixed 380 by soaking in 4% formaldehyde in PBS for 1hour at RT. After permeabilization with 0.1% BSA, 0.1% 381 saponin in PBS, plates were incubated overnight at 4°C with primary antibody (1:5,000 anti-SARS-CoV-382 2 alpaca serum) (Capralogics Inc) (126). Plates were then washed and incubated for 2hours at RT with 383 secondary antibody (1:20,000 anti-alpaca-HRP) (NB7242 Novus) and developed with TrueBlue 384 (SeraCare) for 30minutes. Foci were imaged with a CTL Immunospot Analyzer, enumerated using the 385 viridot package (127) and %neutralization calculated relative to the average of virus-only wells for each 386 plate. FRNT50 values were determined by fitting %neutralization to a 3-parameter logistic model as 387 described previously (126). The limit of detection (LOD) was defined by the lowest dilution tested, values 388 below the LOD were set to LOD - 1. Duplicate FRNT50 values were first calculated separately to 389 confirm values were within 4-fold. When true, a final FRNT50 was calculated by fitting to combined 390 replicates.

391 Antigen-specific antibody isotype and subclass

392	Quantification of antigen-specific IgG and subclasses, IgM, and IgA1 was performed as described
393	(26, 128). Carboxylated microspheres (Luminex) were coupled with recombinant SARS-CoV-2 RBD
394	(129) (BEI Resources NR-52309) by covalent NHS-ester linkages via EDC (1-Ethyl-3-[3-
395	dimethylaminopropyl] carbodiimide hydrochloride) and Sulfo-NHS (N-hydroxysulfosuccinimide)
396	(ThermoScientific) per manufacturer instructions. A mixture of influenza antigens from strain H1N1
397	(NR-20083 and NR-51702, BEI Resources), H5N1 (NR-12148, BEI Resources), H3N2, B Yamagata
398	lineage, and B Victoria lineage (NR-51702, BEI Resources) was used as a control. Antigen-coupled
399	microspheres (1000/well) were incubated with serially diluted samples (IgG at 1:100, 1:1000, 1:10,000;
400	IgM at 1:100, 1:300, 1:900; IgA1 at 1:30, 1:90, 1:270) in replicates in Bioplex plates (Bio-Rad) at 4°C for
401	16hours. After washing away the unbound antibodies, bead bound antigen-specific antibodies were
402	detected by using PE-coupled detection antibody (anti-IgG, IgA1, IgM, IgG1, IgG2, IgG3 and IgG4 from
403	Southern Biotech) (1 μ g/mL). After 2hours of incubation at RT, the beads were washed with PBS 0.05%
404	Tween20 and PE signal measured on a MAGPIX (Luminex). The background signal (PBS) was
405	subtracted. Experiments were conducted two independent times. Representative data from one dilution
406	was chosen by the highest signal-to-noise ratio.
407	Antigen-specific antibody Fc receptor binding
408	Relative Fc receptor binding was assessed as described (26, 130). Luminex carboxylated
409	microspheres were coupled with antigens as described for antigen subclass and isotype above. Antigen-

410 coupled microspheres (1000/well) were incubated with serially diluted samples (1:100, 1:1000, 1:10,000)

411 in replicates in Bioplex plates (Bio-Rad) at 4°C for 16hours. Recombinant Fc receptors (FcyRIIIa/CD16a,

412 FcγRIIa/CD32a H167, FcγRIIb/CD32b, Neonatal Fc receptor/FcRN) (R&D Systems) were labeled with

- 413 PE (Abcam) per manufacturer's instructions, added (1µg/mL) to bead bound antigen-specific immune
- 414 complexes. After 2hours of incubation at RT, the beads were washed and antigen-specific antibody bound
- 415 Fc receptors were measured on MAGPIX (Luminex). The background signal (PBS) was subtracted.

416 Experiments were conducted two independent times. Representative data from one dilution was chosen

- 417 by the highest signal-to-noise ratio.
- 418 Antigen-specific antibody-dependent cellular phagocytosis (ADCP)

419 The THP-1 (TIB-202, ATCC) ADCP with antigen-coated beads was conducted as described (26).

- 420 SARS-CoV-2 RBD (BEI Resources NR-52309) was biotinylated with Sulfo-NHS-LC Biotin (Thermo
- 421 Fisher), then incubated with 1µm fluorescent neutravidin beads (Invitrogen) at 4°C for 16hours. Excess
- 422 antigen was washed away and RBD-coupled neutravidin beads were resuspended in PBS-0.1% bovine
- 423 serum albumin (BSA). RBD-coupled beads were incubated with serially diluted samples (1:100, 1:500,
- 424 1:2500) in duplicate for 2hours at 37°C. THP1 cells (1×10^5 per well) were then added. Serum opsonized
- 425 RBD-coupled beads and THP1 cells were incubated at 37°C for 16hours, washed and fixed with 4% PFA.
- 426 Bead uptake was measured on a BD LSRFortessa and analyzed by FlowJo10. Phagocytic scores were
- 427 calculated as the integrated median fluorescence intensity (MFI) (%bead-positive frequency×MFI/10,000)
- 428 (131). The background signal (PBS) was subtracted. Experiments were conducted two independent times.
- 429 Representative data from one dilution was chosen by the highest signal-to-noise ratio.
- 430 Antibody-dependent complement deposition (ADCD)
- 431 The ADCD assay was performed as described (26, 132). Luminex carboxylated microspheres
- 432 were coupled with antigens as described for antigen subclass and isotype above. Antigen-coated
- 433 microspheres (2500/well) were incubated with serially diluted heat inactivated samples (1:10, 1:50,
- 434 1:250) at 37°C for 2hours. Guinea pig complement (Cedarlane) freshly diluted 1:60 in PBS was added for
- 435 20minutes at 37°C. After washing off excess with PBS 15mM EDTA, anti-C3 PE-conjugated goat
- 436 polyclonal IgG (MP Biomedicals) (1µg/mL) was added. The beads were then washed and C3 deposition
- 437 quantified on a MAGPIX (Luminex). The background signal (PBS) was subtracted. Experiments were
- 438 conducted two independent times. Representative data from one dilution was chosen by the highest
- 439 signal-to-noise ratio.
- 440
- 441

442 Antibody-dependent NK cell activation (ADNKA)

443 ADNKA was performed as described (26, 133). ELISA plates were coated with recombinant 444 RBD (300 ng/well) (BEI Resources NR-52309). Wells were washed, blocked, and incubated with serially 445 diluted samples (1:10, 1:100, 1:1000) in duplicate for 2hours at 37°C prior to adding CD16a.NK-92 cells 446 (PTA-6967, ATCC) (5 \times 10⁴ cells/well) for 5hours with brefeldin A (Biolegend), Golgi Stop 447 (BDBiosciences) and anti-CD107a (clone H4A3, BDBiosciences). Cells were stained with anti-CD56 448 (clone 5.1H11, BDBiosciences) and anti-CD16 (clone 3G8, BDBiosciences) and fixed with 4%PFA. 449 Intracellular cytokine staining to detect IFN γ (clone B27, BDBiosciences) and TNF α (clone Mab11, 450 BDBiosciences) was performed in permeabilization buffer (Biolegend). Markers were measured using a 451 BD LSRFortessa and analyzed by FlowJo10. CD16 expression was confirmed. NK cell degranulation and 452 activation were calculated as %CD56+CD107a+, IFN γ + or TNF α +. Representative data from one dilution 453 was chosen by the highest signal-to-noise ratio. Experiments were conducted two independent times. 454 Non-antigen and RBD-specific IgG glycosylation 455 Non-antigen and RBD-specific IgG glycans were purified and relative levels were quantified as 456 described with modifications (26, 94, 134). RBD (BEI Resources NR-52309) was biotinylated with 457 sulfosuccinimidyl-6-[biotinamido]-6-hexanamido hexanoate (sulfo-NHS-LC-LC biotin; 458 ThermoScientific) and coupled to streptavidin beads (New England Biolabs). Patient samples were 459 incubated with RBD-coupled beads and excess sera washed off with PBS (Sigma). RBD-specific 460 antibodies were eluted from beads using 100mM citric acid (pH 3.0) and neutralized with 0.5M potassium 461 phosphate (pH 9.0). Non-antigen specific IgG and RBD-specific IgG were isolated from serum and eluted 462 RBD-specific antibodies respectively by protein G beads (Millipore). Purified IgG was denatured and 463 treated with PNGase enzyme (New England Biolabs) for 12hours at 37°C to release glycans. 464 To isolate bulk IgG glycans, proteins were removed by precipitation using ice cold 100% ethanol 465 at -20°C for 10minutes. To isolated RBD-specific IgG glycans, Agencourt CleanSEQ beads (Beckman 466 Coulter) were used to bind glycans in 87.5% acetonitrile (Fisher Scientific). The supernatant was

467	
107	removed, glycans were eluted from beads with HPLC grade water (FisherScientific) and dried by
468	centrifugal force and vacuum (CentriVap). Glycans were fluorescently labeled with a 1.5:1 ratio of 50mM
469	APTS (8-aminoinopyrene-1,3,6-trisulfonic acid, ThermoFisher) in 1.2M citric acid and 1M sodium
470	cyanoborohydride in tetrahydrofuran (FisherScientific) at 55°C for 3hours. Labeled glycans were
471	dissolved in HPLC grade water (FisherScientific) and excess unbound APTS removed using Agencourt
472	CleanSEQ beads (non-antigen specific glycans) and Bio-Gel P-2 (Bio-rad) size exclusion resin (RBD-
473	specific glycans). Glycan samples were run with a LIZ 600 DNA ladder in Hi-Di formamide
474	(ThermoFisher) on an ABI 3500xL DNA sequencer and analyzed with GlycanAssure Data Acquisition
475	Software v.1.0. Each glycoform was identified by standard libraries (GKSP-520, Agilent). The relative
476	abundance of each glycan was determined as the proportion of each individual peak with respect to all
477	captured.
478	Statistical analyses
479	Statistical analyses were performed using R4.1.2, Stata17 and GraphPad 9.0. Data are
480	
100	summarized using median (Q1-Q3), mean \pm standard deviation, percent (%). Data were evaluated for
481	summarized using median (Q1-Q3), mean \pm standard deviation, percent (%). Data were evaluated for normality and independence of the residuals, heteroscedasticity and linear relationships between
481 482	summarized using median (Q1-Q3), mean ± standard deviation, percent (%). Data were evaluated for normality and independence of the residuals, heteroscedasticity and linear relationships between dependent and independent variables and log transformed as needed to meet these assumptions. Linear
480 481 482 483	summarized using median (Q1-Q3), mean ± standard deviation, percent (%). Data were evaluated for normality and independence of the residuals, heteroscedasticity and linear relationships between dependent and independent variables and log transformed as needed to meet these assumptions. Linear regression models were used to adjust for the effect of maternal age and BMI (Figure 1-2, 4,
481 482 483 484	summarized using median (Q1-Q3), mean ± standard deviation, percent (%). Data were evaluated for normality and independence of the residuals, heteroscedasticity and linear relationships between dependent and independent variables and log transformed as needed to meet these assumptions. Linear regression models were used to adjust for the effect of maternal age and BMI (Figure 1-2, 4, Supplemental Figure 4-5, 7) and determine the effects of fetal sex and disease severity. Wilcoxon-
481 482 483 484 485	summarized using median (Q1-Q3), mean ± standard deviation, percent (%). Data were evaluated for normality and independence of the residuals, heteroscedasticity and linear relationships between dependent and independent variables and log transformed as needed to meet these assumptions. Linear regression models were used to adjust for the effect of maternal age and BMI (Figure 1-2, 4, Supplemental Figure 4-5, 7) and determine the effects of fetal sex and disease severity. Wilcoxon- matched pair signed rank tests were used to compare between maternal-cord pairs (Figure 3). For
481 482 483 484 485 486	summarized using median (Q1-Q3), mean ± standard deviation, percent (%). Data were evaluated for normality and independence of the residuals, heteroscedasticity and linear relationships between dependent and independent variables and log transformed as needed to meet these assumptions. Linear regression models were used to adjust for the effect of maternal age and BMI (Figure 1-2, 4, Supplemental Figure 4-5, 7) and determine the effects of fetal sex and disease severity. Wilcoxon- matched pair signed rank tests were used to compare between maternal-cord pairs (Figure 3). For antibody function radar plots (Figure 1F, 2F, 4), Z-scored data for each feature were calculated and the
 481 482 483 484 485 486 487 	summarized using median (Q1-Q3), mean ± standard deviation, percent (%). Data were evaluated for normality and independence of the residuals, heteroscedasticity and linear relationships between dependent and independent variables and log transformed as needed to meet these assumptions. Linear regression models were used to adjust for the effect of maternal age and BMI (Figure 1-2, 4, Supplemental Figure 4-5, 7) and determine the effects of fetal sex and disease severity. Wilcoxon- matched pair signed rank tests were used to compare between maternal-cord pairs (Figure 3). For antibody function radar plots (Figure 1F, 2F, 4), Z-scored data for each feature were calculated and the median values for each group plotted. For the antibody glycan radar plots (Figure 5, C and D), Z scores of
 481 482 483 484 485 486 487 488 	summarized using median (Q1-Q3), mean ± standard deviation, percent (%). Data were evaluated for normality and independence of the residuals, heteroscedasticity and linear relationships between dependent and independent variables and log transformed as needed to meet these assumptions. Linear regression models were used to adjust for the effect of maternal age and BMI (Figure 1-2, 4, Supplemental Figure 4-5, 7) and determine the effects of fetal sex and disease severity. Wilcoxon- matched pair signed rank tests were used to compare between maternal-cord pairs (Figure 3). For antibody function radar plots (Figure 1F, 2F, 4), Z-scored data for each feature were calculated and the median values for each group plotted. For the antibody glycan radar plots (Figure 5, C and D), Z scores of individual RBD-specific relative to non-antigen specific IgG glycoforms were calculated and the medians
 481 482 483 484 485 486 487 488 489 	summarized using median (Q1-Q3), mean ± standard deviation, percent (%). Data were evaluated for normality and independence of the residuals, heteroscedasticity and linear relationships between dependent and independent variables and log transformed as needed to meet these assumptions. Linear regression models were used to adjust for the effect of maternal age and BMI (Figure 1-2, 4, Supplemental Figure 4-5, 7) and determine the effects of fetal sex and disease severity. Wilcoxon- matched pair signed rank tests were used to compare between maternal-cord pairs (Figure 3). For antibody function radar plots (Figure 1F, 2F, 4), Z-scored data for each feature were calculated and the median values for each group plotted. For the antibody glycan radar plots (Figure 5, C and D), Z scores of individual RBD-specific relative to non-antigen specific IgG glycoforms were calculated and the medians for each group plotted. Simple linear regression was used to examine the relationships between IgG

- 491 IgG glycoforms as the independent and antibody functional potencies as the dependent variables (Figure
- 492 6). Spearman rank correlations were used to examine bivariate associations between antibody functions

493 (Figure 7A). Principal component analysis (135) was used to reduce variable dimensions (Figure 7B-C,

494 Supplemental Figure 8). For clinical data in Tables, analysis of variance was used for age as it was

495 normally distributed, Kruskal-Wallis test was used for all other continuous variables and Chi-square and

- 496 Fisher's exact tests for categorical variables. All p-values are two-sided, and <0.05 considered significant.
- 497 In Figures, asterisks denote statistical significance (* $p \le 0.05$; ** $p \le 0.01$; *** $p \le 0.001$; *** $p \le 0.0001$).
- 498 Author contributions

499 EA obtained patient samples, collected clinical data, and prepared the manuscript. PL designed

500 and conducted experiments, analyzed data, and prepared the manuscript. YJK assisted in conducting

501 experiments, analyzing data, and preparing the manuscript. AM and JP analyzed the data. TAB, MGT,

502 and SKM conducted the neutralization assays and analyzed data. FGT supervised neutralization assays,

503 analyzed data, and provided critical revisions to the manuscript. LLL conceived, designed, coordinated,

and supervised the work, analyzed the data, and wrote the manuscript.

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Figure 1: A subset of infant cord SARS-CoV-2 neutralizing and RBD Fc effector antibody functions is enhanced with vaccination compared to infection in pregnancy. The medians (bars) for cord sample (**A**) neutralization (FRNT50) against SARS-CoV-2 WA1 (infection n=14, vaccine n=13, vaccine+infection n=19), Delta and Omicron viruses (infection n=12, vaccine n=8, vaccine+infection n=14), (**B**) RBD antibody-dependent natural killer cell activation (ADNKA) by CD107a, IFN γ , and TNF α , (**C**) RBD antibody-dependent complement deposition (ADCD), (**D**) RBD antibody-dependent cellular phagocytosis (ADCP), and (**E**) relative binding of RBD-specific antibodies to Fc γ RIIa/CD16a, Fc γ RIIa/CD32a, Fc γ RIIb/CD32b and FcRN are shown. For B-E, sample sizes are infection n=20, vaccine n=18, vaccine+infection n=27. P-values for A-E are adjusted for maternal age and body mass index using linear regression. (**F**) The magnitude of cord functions are summarized in the radar plot. Each line represents the median Z-scored data for each clinical group. (**G**) The proportion of detectable functions was used to categorize individuals as a high, medium or low responder. The percentages of each type of responder within each clinical group depict the polyfunctional antibody breadth.



Figure 2: A subset of maternal SARS-CoV-2 neutralizing and RBD Fc effector antibody functions is enhanced with vaccination compared to infection in pregnancy. The medians (bars) of the maternal pair of the cord samples in Figure 1 in (**A**) neutralization (FRNT50) against SARS-CoV-2 WA1 (infection n=14, vaccine n=13, vaccine+infection n=19), Delta and Omicron viruses (infection n=12, vaccine n=8, vaccine+infection n=14), (**B**) RBD antibody-dependent natural killer cell activation (ADNKA) as measured by CD107a, IFN γ , and TNF α , (**C**) RBD antibody-dependent complement deposition (ADCD), (**D**) RBD antibody-dependent cellular phagocytosis (ADCP), and (**E**) relative binding of RBD-specific antibodies to Fc γ RIIIa/CD16a, Fc γ RIIa/CD32a, Fc γ RIIb/CD32b and FcRN. For B-E, sample sizes are infection n=22, vaccine n=19, vaccine+infection n=28. P-values for A-E are adjusted for maternal age and body mass index using linear regression. (**F**) The magnitude of maternal functions are summarized in the radar plot. Each line represents the median Z-scored data for each clinical group. (**G**) The proportion of detectable functions was used to categorize individuals as a high, medium or low responder. The percentages of each type of responder within each clinical group depict the polyfunctional antibody breadth.



Figure 3: SARS-CoV-2 neutralizing and RBD Fc effector functions are differentially transferred across the placenta. (**A**) Neutralization against live SARS-CoV-2 WA1, variant Delta and Omicron, (**B**) RBD ADNKA, (**C**) RBD ADCD, (**D**) RBD ADCP, and (**E**) relative binding of RBD-specific IgG to $Fc\gamma$ RIIIa/CD16a, $Fc\gamma$ RIIa/CD32a, $Fc\gamma$ RIIb/CD32b and FcRN are compared with the values of the medians for maternal (grey) and matched cord (blue) samples listed below. Statistical significance was calculated by Wilcoxon-matched pairs test. (**F**) Antibody function transfer ratios (the proportion of cord to maternal levels) are shown with medians (bars), interquartile ranges (boxes), and ranges (whiskers).



Figure 4: Vaccination in pregnancy enhances RBD IgG1. The magnitude of RBD-specific total IgG and subclasses in (**A**) cord and (**B**) maternal responses are shown. P-values are adjusted for maternal age and body mass index using linear regression. Radar plots summarize the magnitude of RBD-specific isotype and subclass. Each line represents the median Z-scored data for each clinical group (infection n=20, vaccine n=18, vaccine+infection n=27). Heatmaps of the regression coefficients (r²) summarize the dependency of RBD-specific antibody functions on subclasses in cord (**C**) and maternal (**D**) samples by simple linear regression. * p<0.05; ** p<0.01; *** p<0.001; **** p<0.001.



Figure 5: Vaccination in pregnancy changes glycosylation of infant cord and not maternal RBD-specific IgG. The relative abundance of (**A**) RBD and (**B**) non-antigen specific IgG individual glycoforms are depicted by the medians in each clinical group. Radar plots summarize (**C**) cord and (**D**) maternal glycoforms on RBD relative to non-antigen specific IgG for each sample with lines showing the medians for each clinical group.



Figure 6: Differential RBD IgG glycosylation impacts antibody functional potency more in infant cord compared to maternal responses. For every patient sample, potency was calculated for each antibody function. The medians (bars), interquartile ranges (boxes), and ranges (whiskers) of the Z-scored data for (**A**, left) cord and (**B**, left) maternal samples in each clinical group are shown. Heatmap of the regression coefficients (r²) summarizes the dependency of RBD-specific antibody functions on RBD-specific IgG glycans in (**A**, right) cord and (**B**, right) maternal samples by simple linear regression. Fucosylated (F), monogalactosylated (G1), digalactosylated (G2), monosialylated (S1), disialylated (S2) and bisecting n-acetyl-glucosamine (B) glycoforms are shown. * p≤0.05; ** p≤0.001; **** p≤0.0001.



Figure 7: Antibody functions highlight the effect of differential immune exposure in pregnancy while glycosylation marks diverging maternal and infant cord responses. Bubble plots (**A**) show the correlation between neutralizing activities against SARS-CoV-2 WA1, Delta and Omicron and RBD-specific Fc effector functions of antibody-dependent natural killer cell activation (CD107a, IFN γ , TNF α), antibody-dependent complement deposition (ADCD), antibody-dependent cellular phagocytosis (ADCP) and relative binding to Fc γ R (Fc γ RIIIa/CD16a, Fc γ RIIa/CD32a, Fc γ RIIb/CD32b, FcRN). The Spearman's rank correlation coefficient is shown by color and significance (-log p) by size with those p<0.05 depicted. Principle-component analysis (PCA) using 38 SARS-CoV-2 antibody functions and features show separations between infection and vaccine clinical groups and maternal and cord responses. Each symbol in the (**B**) score plot represents a single maternal or cord sample. Each antibody feature is represented in the (**C**) loadings plot, where its location reflects the distribution of the individual samples in the (**B**) score plot.

Table. Clinical characteristics of study patients

	Infection	Vaccine	Vaccine and infection	P value
Characteristic	n = 22	n = 19	n = 28	
Age, years	28.3 ± 6.5	32.4 ± 5.8	34.4 ± 6.7	0.005
Race/ethnicity				0.151
Hispanic	20 (91)	17 (90)	28 (100)	
Black, non-Hispanic	2 (9)	1 (5)	0 (0)	
White, non-Hispanic	0 (0)	1 (5)	0 (0)	
Other				
Maternal BMI at first visit, kg/m ²	32 (26-36)	30 (27-33)	34 (30-39)	0.147
Male infant sex	12 (55)	12 (63)	15 (54)	0.789
EGA at delivery, weeks	38 (36-38)	38 (38-39)	37 (37-38)	0.300

Data shown as n (%), mean ± standard deviation (SD), or median (Q1-Q3) as appropriate. BMI= body mass index, EGA= estimated gestational age

			Vaccine and	
	Infection	Vaccine	infection	P value
Characteristic	n = 22	n = 19	n = 28	
Nulliparous	9 (41)	5 (26)	3 (11)	0.0481
Pregestational diabetes	3 (14)	2 (11)	8 (29)	0.266
Chronic hypertension	3 (14)	5 (26)	4 (14)	0.562
Preeclampsia with severe features	3 (14)	2 (11)	7 (25)	0.444
Chorioamnionitis	2 (9)	0 (0)	1 (4)	0.481
Prelabor rupture of membranes	2 (9)	0 (0)	5 (18)	0.139
Induction of labor	13 (59)	8 (42)	12 (43)	0.439
Cesarean delivery	7 (32)	11 (58)	13 (46)	0.241
EGA <37 weeks at delivery	7 (32)	4 (21)	6 (21)	0.684
Infant birth weight <10 th percentile	2 (9)	3 (16)	5 (18)	0.690
Neonatal intensive care unit			= (()	
admission	4 (18)	0 (0)	5 (18)	0.130

Supplemental Table 1. Additional clinical characteristics of study patients

Data shown as n (%), mean ± standard deviation (SD), or median (Q1-Q3) as appropriate. BMI= body mass index, EGA= estimated gestational age, NICU= neonatal intensive care unit

Supplemental Table 2: Comparison of clinical characteristics of individuals receiving mRNA-1273 and BNT1262b2

	mRNA-1273	BNT1262b2
Characteristic	n = 4	n = 43
Age, years	36.8 (4.7)	33.3 (6.4)
Race/ethnicity		
Hispanic	4 (100)	41 (95)
Black, non-Hispanic	0 (0)	1 (2)
White, non-Hispanic	0 (0)	1 (2)
Other	0 (0)	0 (0)
Nulliparous	0 (0)	8 (19)
BMI at first visit, kg/m ²	37.5 (34.5-39.6)	32.1 (28.5-36.4)
SARS-CoV-2 in pregnancy	3 (75)	25 (58)
mRNA Vaccination in pregnancy booster	2 (50)	7 (16)
Pregestational diabetes	2 (50)	8 (19)
Chronic hypertension	1 (25)	8 (19)
Preeclampsia with severe features	2 (50)	7 (16)
Chorioamnionitis	0 (0)	1 (2)
Induction of labor	1 (25)	19 (44)
Cesarean	3 (75)	21 (49)
EGA at delivery, weeks	29.9 (27.5-33.2)	25.4 (16.8-29.8)
EGA<37 weeks delivery	2 (50)	8 (19)
Infant birth weight <10 th percentile	2 (50)	6 (14)
NICU admission	1 (25)	4 (9)
Male infant sex	1 (25)	26 (60)

Data shown as n (%), mean ± standard deviation (SD), or median (Q1-Q3) as appropriate. BMI= body mass index, EGA= estimated gestational age, NICU= neonatal intensive care unit

Supplemental Table 3. Characteristics of study cohort compared with deliveries at Parkland Health, 2021

	Study patients	Deliveries 2021
Characteristic	n = 69	n = 11,170
Age, years	31.9 ± 6.8	27.5 ± 6.4
Race/ethnicity		
Hispanic	65 (94)	8643 (77)
Black, non-Hispanic	3 (4)	1799 (16)
White, non-Hispanic	1 (1)	448 (4)
Other		280 (3)
Nulliparous	17 (25)	3431 (31)
BMI at first visit, kg/m ²	32 (28-37)	29 (25-33)
Documented SARS-CoV-2 in pregnancy	50 (72)	2681 (24)
Any mRNA vaccination in pregnancy	47 (68)	2772 (25)
Pregestational diabetes	13 (19)	210 (2)
Chronic hypertension	12 (17)	847 (8)
Preeclampsia with severe features	12 (17)	1158 (10)
Chorioamnionitis	3 (4)	911 (8)
Prelabor rupture of membranes	7 (10)	2444 (22)
Induction of labor	33 (48)	3047 (27)
Cesarean delivery	31 (45)	3248 (29)
EGA at delivery, weeks	38 (37-38)	39 (38-40)
EGA <37 weeks at delivery	17 (25)	1057 (9)
Infant birth weight <10 th percentile	10 (14)	1173 (11)
NICU admission	9 (13)	572 (5)
Male infant sex	39 (57)	5774 (52)

Data shown as n (%), mean ± standard deviation (SD), or median (Q1-Q3) as appropriate. BMI= body mass index, EGA= estimated gestational age, NICU= neonatal intensive care unit