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Seroconversion and seroprevalence of TORCH infections in a pregnant women cohort 1 2 study, Mombasa, Kenya, 2017-2019

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19 Summary

20 Women infected during pregnancy with TORCH (Toxoplasmosis, Other, Rubella, Cytomegalovirus, and Herpes simplex viruses) pathogens have a higher risk of adverse birth outcomes including stillbirth and 21 22 miscarriage because of mother-to-child transmission. To investigate these risks in pregnant women in 23 Kenya, we analyzed serum specimens from a pregnancy cohort study at three healthcare facilities. A 24 sample of 481 participants were selected for TORCH pathogen antibody testing to determine seroprevalence. A random selection of 285 from the 481 participants were selected to measure 25 seroconversion. These sera were tested using an IgG enzyme linked immunosorbent assay against 10 26 TORCH pathogens. We found that the seroprevalence of antibodies against all but three of the 10 27 28 TORCH pathogens at enrollment was >30%, except for Bordetella pertussis (3.8%), Treponema pallidum (11.4%) and varicella zoster virus (0.5%). Conversely, very few participants seroconverted 29 during their pregnancy and of those were herpes simplex virus type 2 (n=24, 11.2%), parvovirus B19 30 (n=14, 6.2%), and rubella (n=12, 5.1%). For birth outcomes, 88% of the participant had live births and 31 12% had stillbirths or miscarriage. Cytomegalovirus positivity at enrollment had a statistically significant 32 33 positive association with a live birth outcome (p=0.0394). Of the 10 TORCH pathogens tested, none had an association with adverse pregnancy outcome. 34

35 Word count: 204

Key Words: TORCH, pregnancy cohort, cytomegalovirus, herpes virus type 1 and 2, varicella zoster
 virus, Kenya, rubella, *Treponema pallidum, Bordetella pertussis, Toxoplasmosis gondii,* parvovirus B19,
 and *Chlamydia trachomatis*

40 Introduction

41 Pathogens that cause congenital infections worldwide are referred to as TORCH pathogens. Initially, TORCH pathogens have primarily included Toxoplasmosis gondii, Other (syphilis, varicella zoster virus, 42 parvovirus B19) rubella, cytomegalovirus (CMV), and herpes simplex virus type 1 and 2 (HSV-1 and 43 44 HSV-2) when detected during the early stages of pregnancy. Over the years, this list of pathogens has grown significantly to include, most recently, Zika virus (ZIKV), Chlamydia trachomatis, and human 45 immunodeficiency virus (HIV). Depending on when the expecting mother is exposed to any of these 46 pathogens, a myriad of different adverse outcomes may arise. Some of the notable adverse outcomes 47 upon exposure during the first trimester of pregnancy include congenital malformations, intrauterine 48 49 growth restriction or fetal death, whereas exposure during late pregnancy (i.e., third trimester) may result in adverse outcomes that present later after delivery. 50

In this study, we aimed to detect pre-existing antibodies against TORCH pathogens in pregnant 51 women to understand previous exposure to these pathogens, susceptibility, and risk factors associated 52 with infection of any of these pathogens during pregnancy. This information could tailor control and 53 54 prevention programs by public health authorities towards these specific high-risk pathogens in Kenya. 55 However, some of these TORCH pathogens can reinfect the host or reactivate in regions where they lie dormant within the host, such as several of the Herpesviridae family of viruses (i.e., HSV-1, HSV-2, 56 CMV, and VZV). In sub-Sahara African countries such as Kenya, there is limited information on the 57 burden and epidemiology of these pathogens in pregnant women. A recent study in the Kenya coastal 58 59 region identified a 1.9% microcephaly birth outcome rate that was not associated with the ZIKV in newborns (Barsosio et al. 2019). For these microcephaly cases, the causative etiology was not 60 61 determined; however, the authors state that most of these microcephaly cases were also in infants determined to be small for gestational age (SGA). Of the limited information available from many 62 African countries, epidemiological studies have shown that the burden of disease is greatest, where 63 TORCH infections significantly contribute to prenatal and infant morbidity and mortality. 64

65 We conducted a study on ZIKV amongst pregnant women in Mombasa, Kenya. This ZIKV pregnancy cohort study was designed to detect active transmission of ZIKV and determine if infection 66 during pregnancy with the African strain of ZIKV caused adverse birth outcomes (Osoro et al. 2022). 67 68 Using this pregnancy cohort study, we conducted a secondary analysis to determine the presence of 69 other TORCH pathogens (excluding ZIKV) and their association with adverse birth outcomes. Thus, we 70 determined the seroprevalence of 10 different TORCH pathogens within this pregnancy cohort and their association with adverse birth outcomes. In addition, we measured the seroconversion rate for these 71 pathogens during the participant's pregnancy and matched this information to observed adverse birth 72 73 outcomes. A secondary objective was to examine the seroprevalence by maternal age and HIV status 74 as predictors of infection with TORCH pathogens.

75

76 METHODS

77 Pregnancy cohort

From October 2017 - March 2019, we consented and enrolled pregnant women at <28 weeks 78 estimated gestational age visit and \geq 15 years of age that presented at antenatal clinics in 3 hospitals: 79 Bomu, Coast General, and Port Ritz hospital (1 private and 2 public, respectively) in Mombasa, Kenya. 80 Each enrolled participant was administered a questionnaire, was evaluated clinically, an obstetric 81 ultrasound was conducted, and was asked to provide a blood sample of 5mL at enrollment and then 82 83 monthly throughout their pregnancy until delivery. During the first antenatal care (ANC) visit, we 84 collected a urine specimen as well as clinical, obstetric history, demographic, socioeconomic status and exposure to mosquito bites from a total of 2312 participants. Monthly follow-up visits were performed 85 where the participants completed a questionnaire on risk factors and submitted a 5ml blood specimen. 86 During these follow-up visits, participants were asked of any symptoms of fever or rash within the last 7 87 days as part of the ZIKV monitoring. After delivery, we collected birth outcome data, including stillbirth 88 89 and miscarriage, and postnatal parameters (such as head circumference, length, and birth weight) within 24 hours of birth. We did not measure neurological outcomes such as hearing loss often 90

- associated with CMV infections. We randomly selected 481 women from the pregnancy cohort study
- 92 who were ZIKV negative with an enrollment specimen (Figure 1). A subset of women of the initial
- random selection (n=285), were selected based on the availability of both enrollment and delivery
- 94 specimens. From this subset, whose enrollment specimen for each TORCH pathogen was
- seronegative, were selected to assess for seroconversion of TORCH pathogens.
- 96

97 Laboratory diagnostic testing

- 98 Commercial enzyme linked immunoassays (ELISAs) were used to detect IgG antibodies against 10
- 99 different TORCH pathogens (Euroimmun, Germany). The 10 TORCH pathogens included:
- 100 Toxoplasmosis gondii (T. gondii), cytomegalovirus (CMV), Bordetella pertussis (B. pertussis),
- 101 parvovirus B19, herpes simplex viruses 1 and 2 (HSV-1, 2), rubella, *Treponema pallidum*, varicella
- 102 zoster virus (VZV) and Chlamydia trachomatis. Both enrollment and delivery blood specimens from the
- 103 participants were tested for the presence of IgG for all 10 TORCH pathogens. Sera collected from 5 mL
- 104 of venous blood were separated by centrifugation, and 5ul of serum from each participant was tested
- 105 by ELISA in duplicates according to the manufacturer's recommendations. See appendix for
- 106 manufacturer's validation studies for each TORCH test.
- 107

108 Statistical analysis

The study cohort enrolled 2312 participants, among whom 1967 (85.1%) formed the sampling frame for the current study because they had complete outcome data (birth weight, miscarriage, stillbirth, live birth). Previous studies have reported TORCH seroprevalence estimates ranging from 2-98% in Kenya (Nisbet et al. 2018; Otieno-Nyunya et al. 2011). Using this information, we assumed a seroprevalence of at least 6% for the TORCH pathogens tested, an absolute precision level of 2%, and applied finite population correction for a minimum sample size of 425.

115 We determined seroprevalence, defined as the proportion of participants who tested positive for 116 any of the TORCH pathogens at enrollment. Furthermore, seroconversion was defined as a participant who tested negative for any of the 10 TORCH pathogens at enrollment, followed by a positive test atdelivery.

We described the study variables (demographic variables and pathogen status) using frequencies and 119 percentages (95% confidence interval (CI)), and graphically using bar charts. Seroprevalence and 120 121 seroconversion were calculated by maternal age category, HIV status, and SGA status. SGA was defined as a birth weight z-score of ≤ 1.28 at birth (equivalent to the 10th percentile) and extreme SGA 122 as a birth weight z-score of ≤ 1.88 (equivalent to the 3rd percentile) based on INTERGROWTH-21st 123 standards, and the corresponding p-values were estimated using either Pearson Chi-Square or Fisher's 124 125 Exact test (Villar et al. 2014). For participants who had birth outcome data, we investigated the association of each pathogen with adverse birth outcomes (stillbirth or miscarriage) using logistic 126 regression and quantified the association with the odds ratio (OR). We calculated the 95% CI for the 127 OR estimate. A multivariable regression analysis was not performed on this data set because no 128 independent variables reached a p<0.1 cut-off value. The analyses were conducted using SAS 129 software version 9.4 (SAS Institute Inc, Cary, NC). The level of significance was defined as $\alpha \leq 0.05$. 130

131

132 **RESULTS**

133 The study

A total of 481 participants who were ZIKV negative and had an enrollment specimen were selected 134 using simple random selection from the pregnancy cohort and tested for 10 TORCH pathogens. A 135 second subset of 285 participants who had both an enrollment specimen and a delivery specimen 136 available were tested for the 10 TORCH pathogens to determine seroconversion rates. ZIKV positive 137 specimens were excluded from this study analysis and previously published (Osoro et al. 2022). A total 138 of 62 (13.4%) of the women were ≤20 years old, 333 (71.9%) were between the ages of 21-35 years 139 old, and 68 (14.7%) were >35 years old. There were 130 (27%) enrolled during their first trimester, 296 140 141 (61.5%) that were enrolled within the second trimester [14-26 weeks], and 55 (11.4%) enrolled during their third trimester (Table 1). 142

143

144 Participants' demographics at enrollment

Fewer than half the women enrolled in this study had a secondary-school level of education, and 145 almost equal numbers of women had either a primary or below (27.5%) or tertiary education (29.3%) 146 147 (Table 1). Similar proportion of pregnant women were employed (42.6%), unemployed (41.5%), and 15.9% were self-employed. There was also a similar distribution of participants from the three study 148 sites in Mombasa (Bomu 34%, Coast General 29.,9% and Port Reitz 36.1%). The majority were HIV 149 negative (79.3%), between 21-35 years old (71.9%,) and enrolled within the 2nd trimester of their 150 SÜ 151 pregnancy (61.5%).

152

Seroprevalence: Past exposure to 10 TORCH pathogens 153

154 Of the 481 pregnant women tested at enrollment, all had detectable IgG to at least one of the 10 155 TORCH pathogens tested (HSV-1 (97.3%), CMV (94%), rubella (86.5%), parvovirus B19 (55.4%), HSV-2 (48.9%), Chlamydia trachomatis (39.9%), B. pertussis (3.8%), T. pallidum (11.4%) and VZV 156 (0.5%)) (Figure 2). All participants were simultaneously seropositive to at least two TORCH pathogens 157 during either enrollment or delivery, driven primarily by HSV-1 and CMV (Table 2). Also, 78% of 158 159 enrollment samples and 75% of delivery samples were positive for 4 to 6 TORCH pathogens. When categorizing the cohort by age, women ≤ 20 years old, representing the age group for 160 adverse birth outcomes (Cavazos-Rehg et al. 2015), had lower seroprevalence to CMV (88.1% vs. 161 94%), Chlamvdia trachomatis (35.9% vs. 39.9%) T. gondii (28.6% vs. 33.1%), VZV (0% vs. 0.5%), 162 163 HSV-2 (39.3% vs. 48.9%) and rubella (83.9% vs. 86.5%) compared to the overall rates for all age 164 groups. The seroprevalence of those within the age group (21-35 years old) had similar or higher seroprevalence compared to the overall rates of the entire cohort for most of the 10 TORCH pathogens 165 166 except for parvovirus B19 (52.9% vs. 55.4%), and T. gondii (31.8% vs. 33.1%). The age category (>35 years old) had higher seroprevalence than the overall rate of the entire cohort for parvovirus B19 167 (71.2% vs. 55.4%), T. gondii (46.9% vs. 33.1%), VZV (1.7% vs. 0.5%), HSV-2 (63.3% vs. 48.9%) and 168 169 rubella (92.9% vs. 86.5%).

170

171 Seroconversion to TORCH pathogens during pregnancy

- Of the 285 women that were tested at enrollment and delivery, we observed seroconversion to TORCH pathogens for HSV-2 (11.2%), parvovirus B19 (6.2%), rubella (5.1%), *T. pallidum* (3.2%), *Chlamydia trachomatis* (2.1%), CMV (1.6%), HSV-1(1.6%), and VZV (0.4%) (Figure 3). When we analyzed seroconversion results by age groups, we observed that none of the low-risk age groups of \leq 20 years had seroconversion to any of the 10 TORCH pathogens. The medium-risk group (21-35 years old) had
- similar seroconversion results as the overall cohort, and the high-risk age group >35 years old had
- higher seroconversion for 7 of the 10 TORCH pathogens than the overall cohort: CMV (5.3% vs. 1.6%),
- 179 Chlamydia trachomatis (7.1% vs. 2.1%), parvovirus B19 (12.1% vs. 6.2%), T. gondii (5.6% vs. 2.7%), T.
- 180 *pallidum* (9.1% vs. 3.2%), HSV-1 (2.5% vs. 1.6%), and HSV-2 (16.7% vs. 11.2%).
- 181

182 Birth outcomes related to seroprevalence of 10 TORCH pathogens

Of the 481 study participants selected for TORCH testing at enrollment, 362 (75.2%) had live births, 52 (10.8%) had miscarriages, 21 (4.4%) had stillbirths, and 46 (9.5%) did not have an outcome recorded (Table 3). CMV positivity at enrollment was the only serostatus group that had statistically significant decreased odds of non-live birth (OR=0.378 (0.145; 0.985) and p-value=0.0394).

When analyzing the seroprevalence of TORCH pathogens in women with the birth outcome of SGA, we found that, among live births, 225 (62.1%) deliveries had normal birth weight, 18 (5.0%) had low birth weight (<25,00g) and 119 (32.8%) did not have birth weight recorded (Table 4). For pathogen seroprevalence by SGA, none of the TORCH pathogens were associated with a significant difference in the birth outcome of SGA.

192

193 The association of HIV status and seroconversion and seroprevalence of 10 TORCH pathogens

194 We also determined the seroprevalence by HIV status and found that none of the *B. pertussis* and VZV

- 195 positive cases were HIV-positive (Table 5). However, *T. gondii* (45.7% p=0.046) and HSV-2 (73.2%
- 196 p<.001) were significantly higher in HIV-positive women, whereas *B. pertussis* (0%, p=0.046) was

significantly higher in HIV-negative women. When comparing HIV status and seroconversion, only *T. gondii* was significantly higher among HIV-positive women (p=0.03) (Table 6). Seroconversion for all
 other pathogens did not differ by HIV status.

200

201 **DISCUSSION**

Our objective was to study the seroprevalence of TORCH pathogens using specimens collected from a 202 203 cohort of pregnant women enrolled in a ZIKV study in Mombasa, Kenya. Our study showed detectable IgG antibodies in all women for at least one of the 10 TORCH pathogens. We found that there was 204 relatively low seroconversion in this cohort for most of the TORCH pathogens suggesting that few 205 206 acquired an infection during their pregnancy, thus, risk factors associated with acute infections could 207 not be calculated. Among those that had detectable seroconversion, the majority were women that fell within the two ages categories (21-25 and >35 years old) compared to the ≤20 years old. Overall, B. 208 pertussis had very low seroprevalence (3.8%) and no seroconversion, whereas HSV-1 (97.3%), CMV 209 210 (94%), and rubella (86.5%) had the highest scroprevalence, and HSV-2 (11.2%), parvovirus B19 211 (6.2%) and rubella (5.1%) had the highest seroconversion within this cohort. Neither CMV and rubella seroprevalence were associated with SGA or HIV status; however, CMV was significantly associated 212 with live birth outcome, suggesting that prior exposure was protective. 213

There were two viruses, of the four tested in this study, belonging to the *Herpesviridae* family 214 (HSV-1 and CMV) had the highest percentage of seropositives within this cohort. This family of viruses 215 are well adapted to their human host and thus highly infectious even within the general population. 216 217 HSV-1 antibodies were detected in 97.3% of all the women selected for testing and had the highest seroprevalence of all the pathogens tested. Although HSV-1 had the highest seroprevalence within this 218 219 cohort, it had a very low seroconversion rate of 1.6%, perhaps suggesting that few of the study participants acquired HSV-1 during their pregnancy, and almost all had prior immunity upon entering 220 221 the study. When comparing miscarriage or stillbirth with live birth outcomes for HSV-1, the majority of 222 live births were seropositive for HSV-1 (96.6%) and within the category of stillbirths and miscarriages

most were also seropositive for HSV-1 (98.6%) which may have falsely suggest that this adverse birth
outcomes could have been associated with HSV-1. However, when we compared the live birth to nonlive birth overall odds ratio, there was no significant difference between that observed with HSV-1.
Interestingly HSV-2, another virus belonging to the *Herpesviridae* family, had a much lower
seroprevalence (48.6%) compared to HSV-1 but had the highest seroconversion rate (11.2%) of all the
TORCH pathogens tested and the majority of the detectable seroconversion were within the 21–35year-old group (75%).

CMV from the Herpesviridae virus family had the second highest seroprevalence (94%) 230 231 compared to the other TORCH pathogens tested in our cohort. CMV is a very common infection with an overall seroprevalence among adults in the United States of America of 50% (Boeckh and Geballe 232 2011) and has been found to be even higher in LMIC (Shet 2011). The greatest risk to the fetus is 233 234 found with exposure to CMV within the first trimester of pregnancy compared to the second or third 235 trimesters (Gandhi and Khanna 2004). Primary CMV infection can cause a range of clinical symptoms, including permanent hearing and vision loss, neurological impairments, and even death by miscarriage 236 (Cannon and Davis 2005). CMV is the leading cause of long-term disabilities in children and the leading 237 cause of hearing loss worldwide. In pregnant women, the most common source of transmission of CMV 238 239 is either sexual transmission or contact with urine or saliva from young children (Pass et al. 1986). Previous studies in Africa indicated that there is an overall high prevalence of CMV in pregnant women, 240 demonstrated in multiple African countries, including Kenya (Hamdan et al. 2011; Kamel et al. 2014; 241 Maingi and Nyamache 2014; Yeshwondm et al. 2016). A study in Thika, Kenya, showed 77% 242 243 prevalence with 8% IgM positivity suggesting recent infection (Maingi and Nyamache 2014). Although 244 the prevalence of CMV in our study was much higher (94%) than previously shown in Kenya, we only had 4 women (1.6%) who seroconverted in this cohort, suggesting that few of the expecting mothers 245 246 were either infected early in their pregnancy prior to our sampling or perhaps had prior immunity to CMV. We suspect the latter since high seroprevalence was associated with lower odds of non-live birth 247 248 (stillbirth or miscarriage) that was found to be significant (OR= 0.378 p-value 0.0394) compared to the overall birth outcomes within this cohort. Unfortunately, we were unable to measure infant outcomes 249

such as hearing loss or other neurological impairments following delivery. The high seroprevalence of
CMV may be associated with household size related to transmission within this setting (Hoehl et al.
2020).

Rubella had the third highest seroprevalence (86.5%) and the third highest seroconversion rate
(5.1%) in our cohort. Rubella vaccination was incorporated into Kenya's national childhood
immunization schedule in 2016 [1]. Therefore, Rubella exposure or seroconversion among study
participants was likely due to infection rather than vaccination.

Women who have no immunity to rubella are at very high risk for congenital rubella infection and 257 potentially adverse outcomes (congenital rubella syndrome (CRS)). CRS can only be detected many 258 259 months after the baby is born; we were unable to determine if any of the infants in our cohort had CRS since we did not follow the women and infants after delivery. Although the exact number of CRS cases 260 is unknown due to the lack of CRS surveillance, prior studies indicated that 6% of measles/rubella 261 cases were women of reproductive age in Kenya (Nieru et al. 2015). Most participants were enrolled 262 during the second trimester when the risk of CRS following rubella infection is low. The rubella vaccine 263 264 program for Kenya has had various interruptions since 2002. In 2016, Kenya introduced the combined measles and rubella (MR) vaccine in an attempt to improve vaccine coverage, but the coverage in 265 266 pregnant women is not well documented, including in our study cohort participants 267 (Manakongtreecheep and Davis 2017). Since our study was conducted between 2017-2019, the participants were not eligible to receive the rubella vaccine through the Kenya routine vaccination 268 269 (https://www.afro.who.int/news/kenya-rolls-out-massive-measles-rubella-and-tetanus-campaign). The results from this study may provide sufficient information to estimate the seroprevalence of rubella and 270 271 support policy for strengthening vaccination efforts in Kenya.

In our study, *T. pallidum* had a relatively high seroprevalence of 11.4% compared to that observed in North America (0.67%) (Neu et al. 2015). A recent study by Warnecke et al. in 2020, demonstrated that the average seroprevalence of *T. pallidum* was between 1-3% in 6 different countries (Mexico, China, Poland, Germany, Brazil, and Turkey), demonstrating that this cohort in

276 Kenya had between 3-10-fold higher levels in comparison to all 6 countries (Warnecke et al. 2020). 277 Overall countries in Africa tend to have much higher prevalence of syphilis than the global average ranging from an average of 4.6% in Eastern African countries to 6.5% in Southern African countries 278 (Joseph Davey et al. 2016). Although our results are ~2-fold higher than the average reported 279 280 prevalence for the East African region, the ELISA used in our study was validated by the manufacturer with 139 clinical specimens using the gold standard TPHA test and the performance of their test 281 indicated 100% sensitivity and specificity. One of the most surprising findings from this study was the 282 very low seroprevalence (0.5%) and seroconversion (0.4%) of VZV amongst pregnant women in 283 284 Kenya. Again, in Warnecke et al., the authors reported that all 6 countries tested had very high VZV seroprevalence with a mean of 95.9% and a range of 92.3-99.4% (Warnecke et al. 2020). There are 285 very few studies of prevalence of VZV in Kenya however a study by Hussey et al., 2017 showed a VZV 286 prevalence of 23% which is also significantly lower than detected globally (Hussey et al. 2017; 287 288 Korenromp et al. 2019). Our findings are significantly lower than even the Hussey et al., study and this could be due to the ELISA test parameters used to measure anti-VZV IgG antibodies. The 289 manufacturer may have used a higher titer antibody cut-off to detect acute cases. Although the test 290 application is to confirm a VZV suspected infection and/or reactivation, the manufacturer also claims 291 that the test can determine immune status in early pregnancy. Nevertheless, our results are much lower 292 293 than expected and must be taken with caution and requires further verification of this finding which we were unable to perform. 294

295 There were study limitations that should be considered. First, most of the cases were enrolled in 296 the second trimester, thus missing the window of identifying potential seroconversions that may have happened earlier in the pregnancy. Also, we relied on seroconversion as a surrogate marker for acute 297 infection leading to vertical transmission to the fetus. Second, most of the cohort fell into a single age 298 299 category of 21-35 years old (71.9%), where age-related adverse outcomes are not commonly observed. Third, the vaccine status for some of the vaccine-preventable diseases was not known. 300 301 Fourth, a full description of poor infant outcomes, such as hearing, or vision loss was outside of the scope of our study, thus limiting our analysis. Our analysis of co-infection used seroprevalence results 302

due to the limited seroconversions observed; however, co-infections with any of these TORCH
pathogens often culminate into a higher risk of adverse birth outcomes especially spontaneous
abortions (Rasti et al. 2016). The causes of stillbirth and miscarriage could not be further determined
and only 66 stillbirths were examined at delivery with no gross anomalies noted. Finally, the results
may need to be interpreted with caution since multivariable models could not be used due to because
no independent variables reached a p<0.1 cut-off value.

In summary, this is the first study to measure 10 TORCH pathogens in a large pregnancy cohort in Kenya. The seroprevalence of many of the TORCH pathogens in this cohort resembled those findings in Brazil except for *T. pallidum* and VZV. We found that only CMV antibodies at enrollment was negatively associated with adverse birth outcomes; however, prior exposure to other TORCH pathogens was not associated with adverse pregnancy outcomes. These findings support the inclusion of routine screening for those TORCH pathogens in national guidelines, especially those with high seroprevalence, where there are vaccines or prophylactic treatments available.

316 Ethical Approval and consent to participants:

This study was approved by the University of Nairobi/ Kenyatta National Hospital ethics and research committee (P71/02/2017). Concurrence from the Kenya Medical Research Institute's Scientific Ethics and Research Unit (SERU), Washington State University Institutional Review Board (IRB). It was also reviewed by CDC and was conducted consistent with applicable federal law and CDC policy[§]. ^{§See 45 C.F.R.} part 46; ^{21 C.F.R. part 56}. All participants enrolled in this study consented to participate. Ethical approval was obtained through SERU and CDC ethical committee.

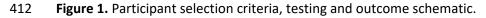
Availability of data and materials: The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

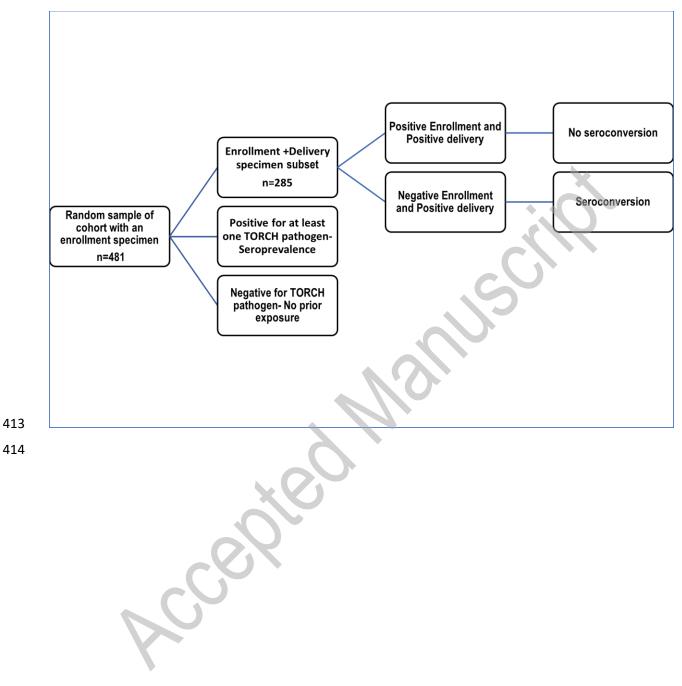
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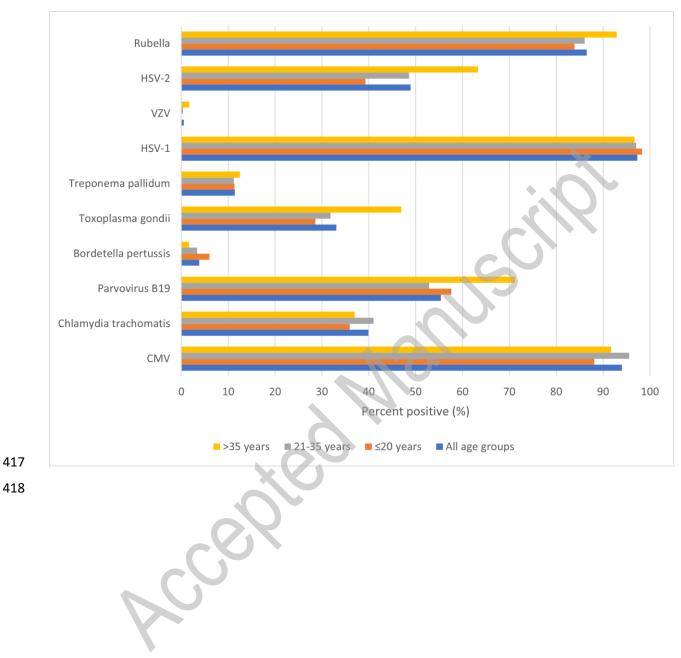
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415 **Figure 2.** Seroprevalence of TORCH pathogens by age group. CMV=cytomegalovirus; HSV-1=herpes simplex

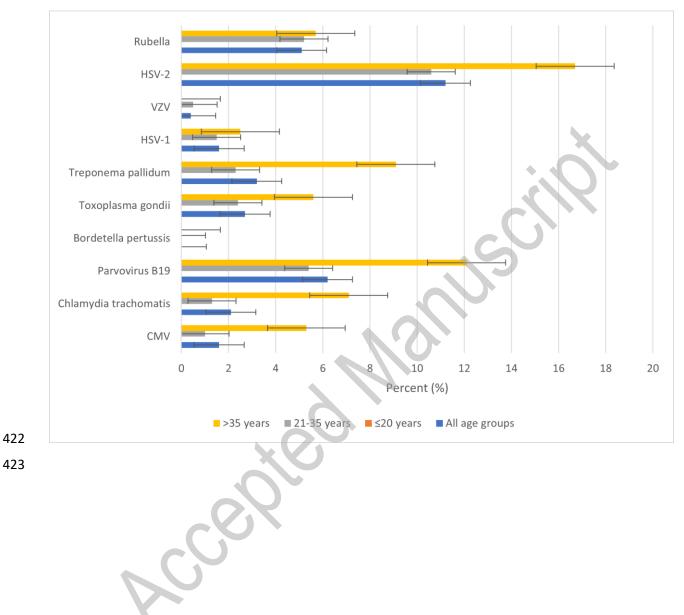
416 virus type 1; HSV-2=herpes simplex virus type 2; VZV=varicella zoster virus.



419 **Figure 3.** Seroconversion of TORCH pathogens by age group. Note that there were no seroconversions observed

420 in age group <20 years old. CMV=cytomegalovirus; HSV-1=herpes simplex virus type 1; HSV-2=herpes simplex

421 virus type 2; VZV=varicella zoster virus.



424 **Table 1.** Participants demographic characteristics from single specimen taken at enrollment (N=481) and

425 participants with two-specimens obtained at enrollment and delivery (N=285)

	Enrolm	Enrolment (N= 481)		With enrolment and delivery (N=285)	
		Percent (95% CI)	n	Percent (95%	
Demographic characteristics	n			CI	
Education					
 Primary and below 	119	27.5 (23.3; 31.7)	79	28.3 (23.1; 34.0	
· Secondary	187	43.2 (38.5; 48.0)	118	42.3 (36.4; 48.3	
· Tertiary	127	29.3 (25.1; 33.9)	82	29.4 (24.1; 35.1	
Occupation					
• Employed	188	42.6 (38.0; 47.4)	118	41.4 (35.6; 47.4	
· Self employed	70	15.9 (12.6; 19.6)	52	18.3 (13.9; 23.2	
· Unemployed	183	41.5 (36.9; 46.3)	115	40.4 (34.6; 46.3	
Site					
· Bomu	150	34.0 (29.6; 38.6)	97	34.0 (28.6; 39.9	
· Coast General	132	29.9 (25.7; 34.4)	90	31.6 (26.2; 37.3	
· Port Reitz	159	36.1 (31.6; 40.7)	98	34.4 (28.9; 40.2	
HIV status					
· Yes	85	20.7 (16.9; 25.0)	62	23.2 (18.3; 28.8	
· No	325	79.3 (75.0; 83.1)	205	76.8 (71.2; 81.7	
Maternal age (years)					
· ≤20	62	12.9 (10.0; 16.2)	10	3.5 (1.7; 6.4	
21-35	351	73.0 (68.8; 76.9)	229	80.4 (75.3; 84.8	
· > 35	68	14.1 (11.2; 17.6)	46	16.1(12.1; 20.9	
Gestational age at enrollment (weeks)					
· 0-13 (1st trimester)	130	27.0 (23.1; 31.2)	60	21.1 (16.5; 26.3	
· 14-26 (2nd trimester)	296	61.5 (57.0; 65.9)	192	67.4 (61.6; 72.8	
· 27 + (3rd trimester)	55	11.4 (8.7; 14.6)	33	11.6 (8.1; 15.9	

- 427 **Table 2.** Seroprevalence of TORCH pathogens and the number of pathogens exposures from enrollment and
- 428 delivery. CMV=cytomegalovirus; HSV-1=herpes simplex virus type 1; HSV-2=herpes simplex virus type 2;
- 429 VZV=varicella zoster virus.

TORCH target	Enrollment, N = 159 ¹	Delivery N = 159 ¹			
B. pertussis	6 (3.8%)	4 (2.5%)			
HSV-1	153 (96%)	157 (99%)			
chlamydia	61 (38%)	55 (35%)			
CMV	155 (97%)	154 (97%)			
HSV-2	78 (49%)	76 (48%)			
rubella	124 (78%)	130 (82%)			
VZV	0 (0%)	0 (0%)			
T. gondii	52 (33%)	50 (31%)			
Parvo B19	80 (50%)	79 (50%)			
Treponema pallidum	19 (12%)	14 (8.8%)			
No. of TORCH pathogens that were seropositive					
2	8 (5.0%)	9 (5.7%)			
3	18 (11%)	23 (14%)			
4	50 (31%)	48 (30%)			
5	49 (31%)	43 (27%)			
6	26 (16%)	28 (18%)			
7	7 (4.4%)	7 (4.4%)			
8	1 (0.6%)	1 (0.6%)			

¹n (%)

- 431 **Table 3.** Distribution of pathogen status at enrollment by newborn outcomes non-live birth outcome status, the
- 432 odds ratio quantifies the association of presence of an antibody to a pathogen at enrollment with the odds of a
- 433 non-live birth outcome. CMV=cytomegalovirus; HSV-1=herpes simplex virus type 1; HSV-2=herpes simplex virus
- 434 type 2; VZV=varicella zoster virus.

PATHOGEN AT ENROLLMENT	OUTCOMES			ODDS OF NON- LIVEBIRTH	
	Status	Non-livebirth	Live	OR (95% CI)	P-value
		(miscarriage/	birth		
		stillbirth)			
OVERALL*		73	362		
CMV	Pos	62	305	0.378 (0.145; 0.985)	0.0394
	Neg	7	13		
CHLAMYDIA TRACHOMATIS	Pos	26	119	0.954 (0.554; 1.642)	0.8648
	Neg	41	179		
PARVOVIRUS B19	Pos	42	171	1.514 (0.876; 2.619)	0.1357
	Neg	24	148		
BORTEDELLA PERTUSSIS	Pos	2	11	0.872 (0.189; 4.030)	0.8608
	Neg	64	307		
TOXOPLASMA GONDII	Pos	12	66	0.857 (0.410; 1.793)	0.6821
	Neg	28	132		
TREPONEMA PALLIDUM	Pos	8	34	1.128 (0.496; 2.562)	0.7738
	Neg	58	278		
HSV-1	Pos	70	316	2.436 (0.309; 19.179)	0.3824
	Neg	1	11		
VZV	Pos	0	2	^a	0.5240
	Neg	64	315		
HSV-2	Pos	37	145	1.373 (0.803; 2.346)	0.2458
	Neg	29	156		
RUBELLA	Pos	58	270	1.350 (0.579; 3.147)	0.4855
	Neg	7	44		

435

^a-OR could not be calculated due to 0 positive cases

438 **Table 4.** Pathogen seroprevalence for birth outcome of small for gestational age (SGA) among live births (n=362)

PATHOGEN	SG	P- VALUE ^A	
	No	Yes	
CMV	182/189 (96.3)	22/22 (100)	1.000
CHLAMYDIA TRACHOMATIS	70/173 (40.5)	8/24 (33.3)	0.503
PARVOVIRUS B19	99/188 (52.7)	12/23 (52.2)	0.965
BORDETELLA PERTUSSIS	5/195 (2.6)	1/23 (4.4)	0.492
TOXOPLASMA GONDII	35/112 (31.3)	4/11 (36.4)	0.742
TREPONEMA PALLIDUM	21/186 (11.3)	4/21 (19.1)	0.294
HSV-1	191/195 (98.0)	24/24 (100)	1.000
VZV	0/188 (0.0)	0/25 (0.0)	1.000
HSV-2	88/180 (48.9)	7/21 (33.3)	0.177
RUBELLA	155/186 (83.3)	21/24 (87.5)	0.773

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^A P-value calculated using either Pearson Chi-Square or Fisher's Exact Test

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441 **Table 5.** Pathogen seroprevalence by human immunodeficiency virus (HIV) status

Yes	No	
	INU	
73/75 (97.3)	273/290 (94.1)	0.386
23/72 (31.9)	109/269 (40.5)	0.185
40/73 (54.8)	164/290 (56.6)	0.787
0/80 (0.0)	14/284 (4.9)	0.046
21/46 (45.7)	52/180 (28.9)	0.030
9/75 (12.0)	32/281 (11.4)	0.883
73/75 (97.3)	293/300 (97.7)	1.000
0/74 (0.0)	2/285 (0.7)	1.000
52/71 (73.2)	122/276 (44.2)	< 0.001
66/74 (89.2)	239/282 (84.8)	0.332
	73/75 (97.3) 23/72 (31.9) 40/73 (54.8) 0/80 (0.0) 21/46 (45.7) 9/75 (12.0) 73/75 (97.3) 0/74 (0.0) 52/71 (73.2) 66/74 (89.2)	73/75 (97.3) 273/290 (94.1) 23/72 (31.9) 109/269 (40.5) 40/73 (54.8) 164/290 (56.6) 0/80 (0.0) 14/284 (4.9) 21/46 (45.7) 52/180 (28.9) 9/75 (12.0) 32/281 (11.4) 73/75 (97.3) 293/300 (97.7) 0/74 (0.0) 2/285 (0.7) 52/71 (73.2) 122/276 (44.2)

442 ^A P-value calculated using either Pearson Chi-Square or Fisher's Exact Test

443

Table 6. Pathogen seroconversion by human immunodeficiency virus (HIV) status.

PATHOGEN	HIV	STATUS	P-VALUE ^A
	Yes	No	
CMV	0/52 (0.0)	3 /176 (1.7)	1.000
CHLAMYDIA TRACHOMATIS	1/41 (2.4)	3/137 (2.2)	1.000
PARVOVIRUS B19	5/44 (11.4)	8/165 (4.9)	0.153
BORDETELLA PERTUSSIS	0/53 (0.0)	0/163 (0.0)	b
TOXOPLASMA GONDII	3/30 (10.0)	1/111 (0.9)	0.030
TREPONEMA PALLIDUM	0/50 (0.0)	6/153 (3.9)	0.340
HSV-1	1/51 (2.0)	2/180 (1.1)	0.529
VZV	0/48 (0.0)	1/167 (0.6)	1.000
HSV-2	6/43 (14.0)	18/160 (11.3)	0.601
RUBELLA	5/52 (9.6)	7/169 (4.1)	0.159

⁴⁴⁵ ^A P-value calculated using either Pearson Chi-Square or Fisher's Exact Test; ^b P-value cannot be calculated due to

- 446 zero counts