

Out-of-home child care as a risk factor for pre-pandemic endemic human coronavirus infections in a birth cohort of children 0-2 years

Ardythe L. Morrow^{1,2}, S.C. Conrey^{1,2}, L. Niu¹, A.R. Burrell^{1,2}, C.P. Mattison³, Z. Teoh^{1,2}, M. McMorrow³, M. McNeal², D.C. Payne³, M.A. Staat^{1,2}

¹University of Cincinnati College of Medicine, ²Cincinnati Children's Hospital Medical Center, ³The Centers for Disease Control and Prevention

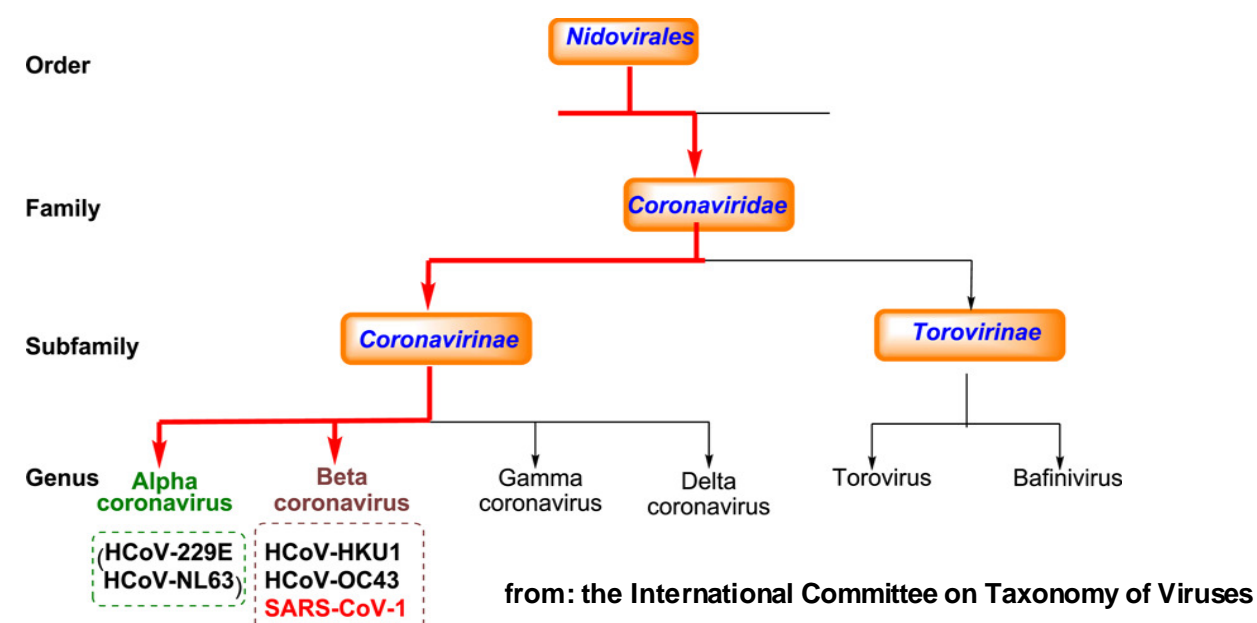
Email: morrowa@ucmail.uc.edu



Background

- Four endemic human coronaviruses (HCoV) - HKU1, OC43, 229E, NL63 - belong to Coronaviridae, the viral subfamily of SARS-CoV-2. These occur seasonally, routinely circulate worldwide, and typically cause only mild illness
- The COVID-19 pandemic has increased interest in understanding these HCoV for comparison to pandemic coronaviruses
- Group or out of home child care has been a concern during the pandemic as a potential reservoir of infection in the community
- Here we examine the strength of association in out-of-home child care and other potential risk factors for HCoV infection among children enrolled in PREVAIL, a CDC-funded birth cohort study of healthy, term singleton infants followed in Cincinnati, OH

Figure 1: Taxonomy of Coronaviridae



Methods

Data Collection (April 2017 - October 2020)

- Prenatal (3rd trimester) enrollment visit
- Weekly postnatal nasal swabs from study children collected, tested by Luminex Respiratory Pathogen Panel
- Risk factor data collected during quarterly study surveys
- Analysis restricted to 91 of 245 children who were the most adherent ($\geq 75\%$ of weekly swab collection)

Definitions

- HCoV infectious episode** – any positive swabs within 30-day window of previous positive
- Out of home child care** – any care arrangement that does not occur in the child's own home.
 - Child care home** – providers care for small groups of children in a residence that is not the child's
 - Child care center** – group child care in a non-residential setting (licensed child care center)

Statistical Analysis

- Anderson-Gill model: risk of any HCoV infection
- Covariates: prior infection, childcare, child sex, race, insurance type, maternal education, maternal age, number of persons in the household, breastfeeding status
- All analysis performed using the R Environment for Statistical Computing²

Figure 2: Demographics of 91 PREVAIL highly adherent children studied

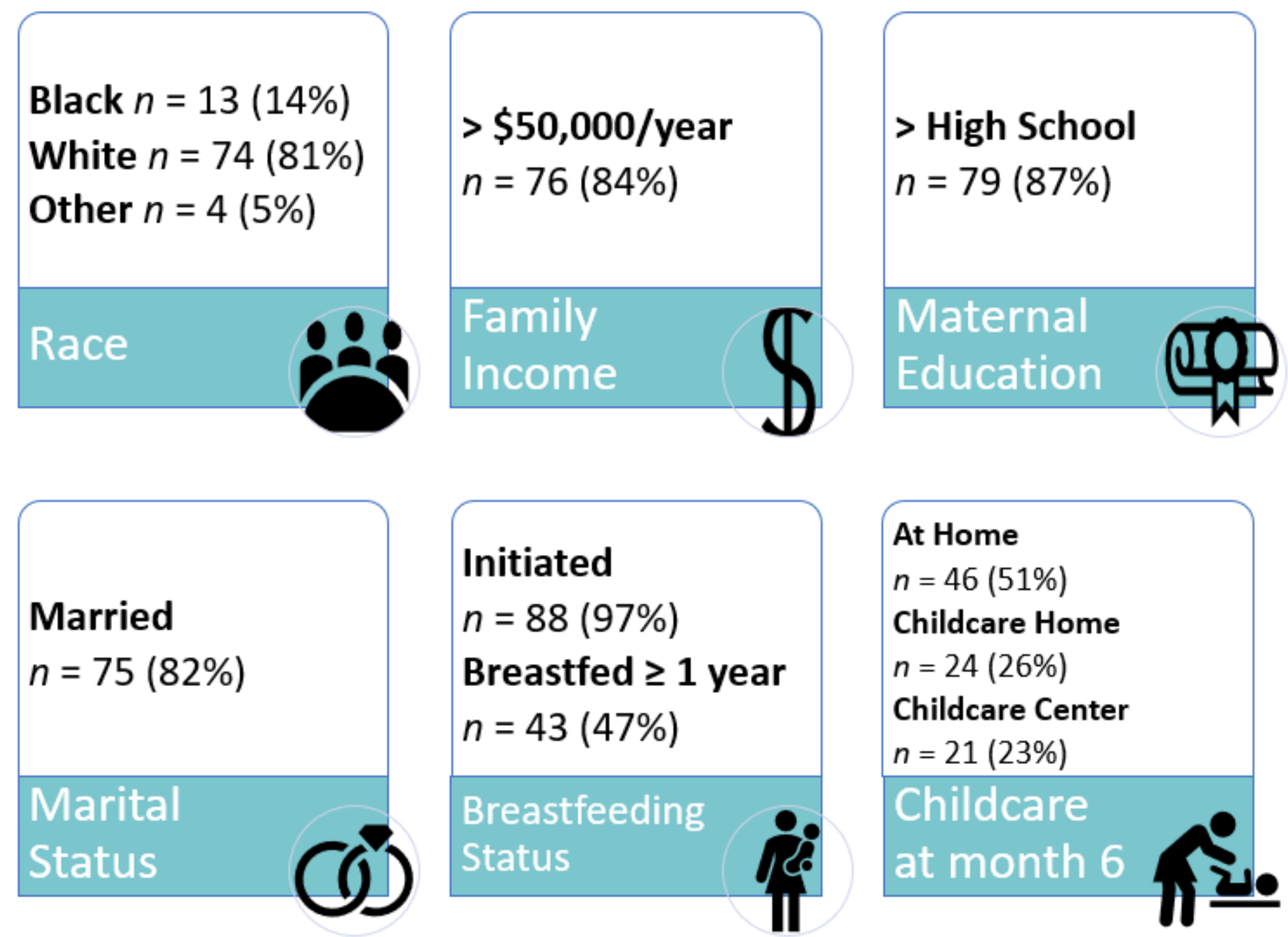


Figure 3: Out-of-home childcare use by child age/study visit

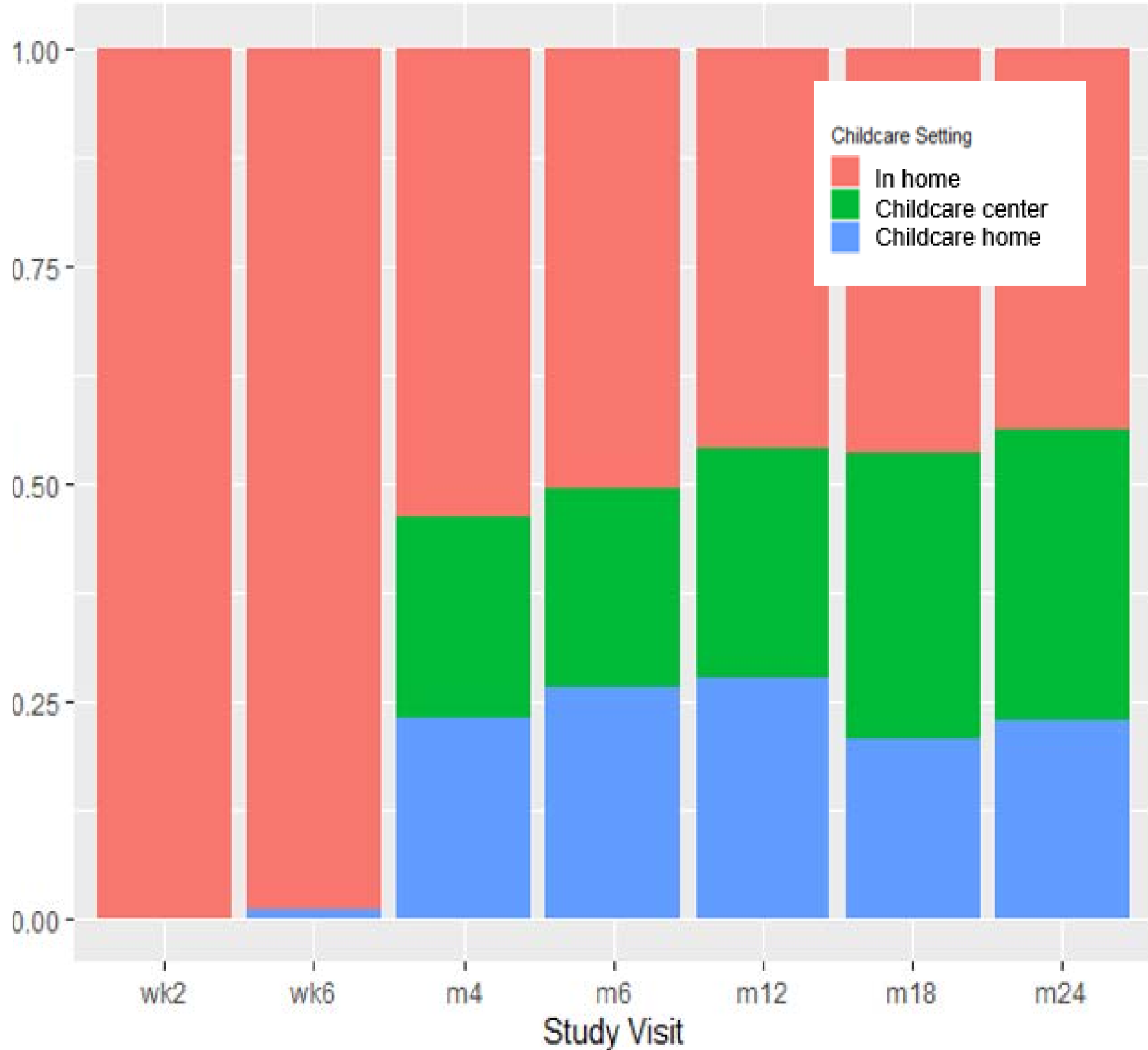


Figure 4: Prevalence map of HCoV infection in PREVAIL

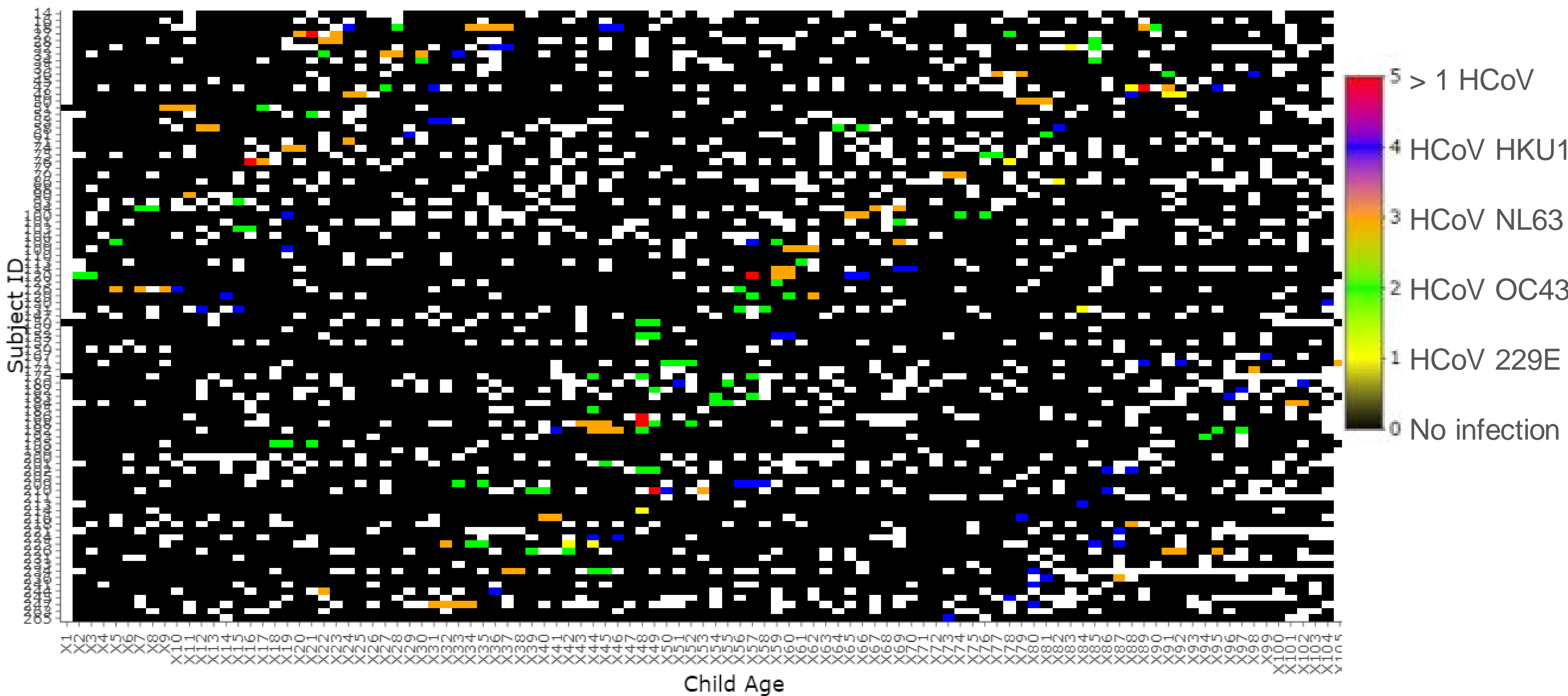
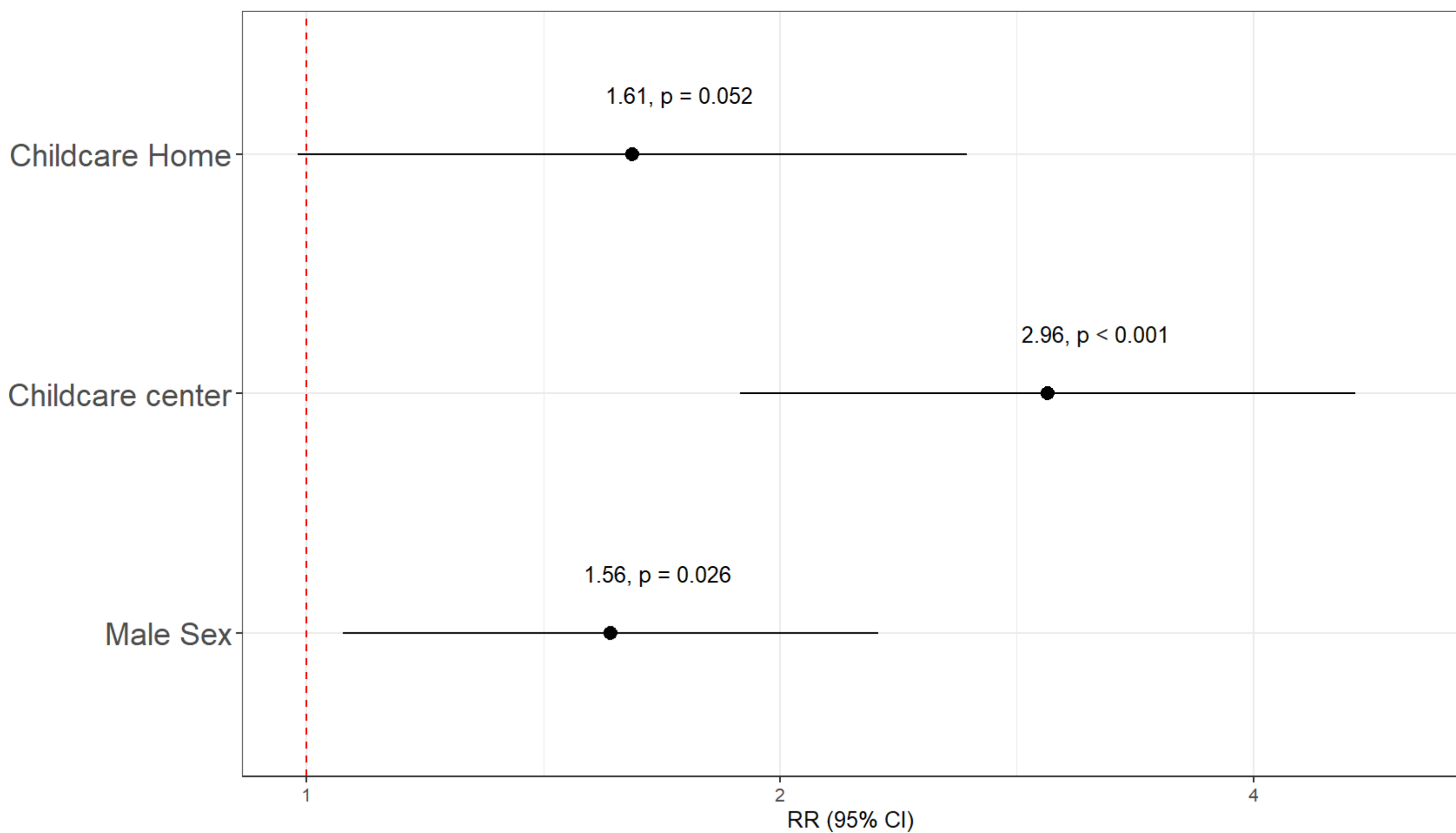


Figure 5: Anderson Gill model: Risk estimates for HCoV infection



Results

- Demographics in line with Greater Cincinnati region in terms of race, income; higher than region maternal education, married status³, and breastfeeding initiation
- By 6 months, $\frac{1}{2}$ of children were in out-of-home childcare
 - Use of childcare homes & childcare centers evenly split
 - Peer group size was $>$ in childcare centers than child care homes (med. = 9 vs 4/group; $p<0.001$)
- HCoV prevalence in first two years of life
 - 131 HCoV infectious episodes detected
 - 70 (77%) children had ≥ 1 HCoV infection
 - 40 (44%) had ≥ 2 HCoV infections
- Anderson Gill survival model:
 - Use of childcare centers (RR 3.0, 95%CI 1.9, 4.6) and male sex (1.6, 95%CI 1.1, 2.3) increased risk for HCoV infection
 - Use of childcare homes borderline significant (RR 1.6, 95%CI 1.0, 2.6)
 - Not significant: race, insurance type, maternal education, maternal age, number of persons in the household, breastfeeding status

Conclusions

- HCoV infections were highly prevalent for all children
- The majority of children used out-of-home childcare after 6 months of age
 - Relative risk of HCoV was higher in both child care homes and centers.
 - While confidence bands overlap between these two child care settings and home care, the trend suggested $<$ risk for child care homes (RR=1.6) compared to child care centers (RR=3.0), consistent with differences in peer group size
- Our findings are limited to endemic HCoV, but may be relevant to pandemic HCoV as well

Strengths

- Ability to assess time-varying and stable risk factors
- High sample adherence = ability to detect infections

Limitations

- Small sample size, lack of SARS-CoV2 for comparison
- Compliance restricted diversity, higher SES than region

Future Directions

- Add serologic-identified infections
- Compare symptoms, severity

References

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