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Assessment of the accuracy of hepatitis B vaccination records among Cuban refugees and parolees

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By

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Bachelor of Arts
Georgia State University
2010

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An abstract of
A thesis submitted to the Faculty of the
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ABSTRACT

Assessment of the accuracy of hepatitis B vaccination records among Cuban refugees and parolees

By Anna Catherine Fulton

The United States (US) accepts large numbers of Cuban refugees and parolees, yet there are no published reports assessing the quality of the overseas vaccination records of this population. The objective of this analysis was to evaluate the quality of Cuban refugees' and parolees' overseas vaccination records by comparing reported history of hepatitis B virus (HBV) immunization to demonstrated serologic immunity during the first domestic medical screening.

The study population consisted of all Cuban refugees and parolees who arrived in Texas between January 2010 through December 2013 and whose domestic records could be matched with overseas records. Multivariate logistic regression was used to obtain prevalence ratios (PR) determining the prevalence of immunity to HBV in Cuban refugees and parolees with a complete vaccination series compared to those with no vaccination history and comparing those with an incomplete vaccination series to those with no vaccination history.

The study included 1,416 Cuban refugees and parolees. Prevalence of immunity was 42.9% among those reporting a complete series of hepatitis B vaccination, 44.7% among those reporting an incomplete series of hepatitis B vaccinations, and 29.0% among those reporting no history of hepatitis B vaccination. Individuals with records indicating a complete hepatitis B vaccination series were only 1.48 (95% confidence interval: 1.27, 1.73) times more likely to demonstrate immunity to HBV compared to those with no history of hepatitis B vaccination.

The results suggest that overseas records of hepatitis B vaccination for Cuban refugees and parolees are poor predictors of immunity to HBV, both overall and among all subgroups. Medical providers conducting the initial domestic medical screening for Cuban refugees and parolees arriving in the US should screen all arrivals for antibodies to HBV and vaccinate those who do not demonstrate immunity, rather than relying on overseas vaccination records.

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INTRODUCTION

Background

The United States (US) is the most common resettlement country for refugees seeking resettlement through the United Nations High Commissioner for Refugees (UNHCR), providing admission to 257,903 refugees between Fiscal Year (FY) 2010 and FY 2013 (1-4). During that same time period, Cuban refugees were the fifth largest group to resettle in the US, with 13,883 (5.4%) of admitted refugees originating in Cuba (1-4). In addition, through the US Department of Homeland Security's Cuban/Haitian Entrant Program, up to 20,000 additional Cuban immigrants are allowed to enter the US annually under parole status, and these individuals are referred to as "Havana Parolees" (5). Havana Parolees that resettle in states with a Cuban/Haitian Entrant Program are eligible for refugee benefits and services administered by the Office of Refugee Resettlement (ORR) (5).

The most recent available data reported 16,378 Havana Parolees admitted to the US during FY 2010 (1, 5). Most Havana Parolees arrived in Florida (14,845 or 83.6%), but the second most common destination was Texas, which accepted 954 (5.4%) in FY 2012 (6). From FY 2010 through FY 2013, the state of Florida resettled the largest number of Cuban refugees in the US (8,174 or 58.9%), with the state of Texas resettling the second largest number of Cuban refugees (879 or 6.3%) (4).

Overseas Regulations

Cuba is one of the few countries where the US processes individuals as refugees while these individuals are still in their country of origin (3). Cuban citizens may apply to come to the US as a refugee for any of the following reasons: religious or political

persecution, forced-labor, deprivation of professional credentials, or any other discriminatory treatment based on actual or perceived political, religious, social, or familial beliefs, activities, or relations (3). In addition, Cuban citizens may apply for US Refugee Admissions Program (USRAP) access if any of their immediate family members have been admitted to the US as a refugee or asylee (3).

All US-bound refugees and parolees are required by the US Department of State (DOS) to undergo an overseas medical examination performed by a panel physician (7, 8). Panel physicians are selected by DOS consular officials and must abide by technical instructions and guidance provided by the US Centers for Disease Control and Prevention's (CDC) Division of Global Migration and Quarantine (DGMQ) (7, 8). The Technical Instructions for the overseas Medical Examination of Aliens requires obtaining a medical history and conducting a physical examination; performing a screening for tuberculosis (TB) and providing treatment if necessary; testing for syphilis and other sexually transmitted diseases; evaluating for Hansen's Disease; evaluating for physical or mental disorders resulting in harmful behaviors and substance-related disorders, as well as other physical or mental abnormalities, diseases, or disabilities; evaluating for communicable diseases of public concern; and administering routine vaccinations following recommendations by the Advisory Committee on Immunization Practices for the US domestic population (9, 10). However, immigrants coming to the US as refugees or parolees are not required by law to receive any vaccinations prior to arrival (11).

Domestic Regulations

Upon arrival to the US, refugees and parolees are recommended to undergo the required domestic health screening within 30 days of arrival (12). Based on CDC

domestic medical screening guidelines, each screening should include a review of the overseas medical documents; a complete medical history; a physical examination that screens for particular health conditions, such as viral hepatitis, intestinal parasites, human immunodeficiency virus (HIV), and TB, among others; and the provision of preventative health interventions such as immunizations (13). As a result of the aforementioned provision that refugees and parolees are not required to receive routine vaccinations prior to arrival in the US, clinicians performing the required domestic medical examination must review overseas records for indication of immunizations received overseas (11). Clinicians may choose to perform serologic testing for immunity to certain vaccine-preventable diseases, such as hepatitis B, prior to administering vaccinations, but clinicians sometimes prefer to immunize prior to receiving test results due to potential logistical and financial difficulties the individual may face in returning for a follow-up visit and in order to protect susceptible individuals as soon as possible (11, 14).

Purpose of Study

Despite the large numbers of Cuban refugee and parolee arrivals in recent years, limited information is available on the current health conditions of this population immediately after their arrival to the US, and there are no published reports assessing the quality of the overseas vaccination records of this population. In order to better understand the appropriateness of the CDC Domestic Medical Screening Guidelines for newly arriving refugees and parolees from Cuba, this assessment will evaluate the quality of this population's overseas vaccination records by comparing overseas records of hepatitis B immunization to demonstrated serologic immunity during the first domestic medical screening.

REVIEW OF THE LITERATURE

Overview of Hepatitis B Virus

Hepatitis B virus (HBV) affects humans on a global scale and is known to cause both acute and chronic hepatitis and cirrhosis (15). Estimates from the year 2000 reported the number of annual deaths worldwide from HBV-associated acute and chronic liver disease to be approximately 600,000 worldwide (16). HBV is commonly transmitted through parenteral or mucosal exposure to persons with acute or chronic HBV infection, either through sexual intercourse; use of contaminated needles during injection-drug use, tattooing, bodily piercing, acupuncture, or needlesticks or other injuries sustained by medical professionals; or through perinatal transmission from a mother with HBV infection to her infant at birth (15).

The recombinant hepatitis B vaccine was introduced in 1986 and has been incorporated into the infant vaccination schedules of 179 countries, as of 2011 (17). The recommended dosing schedule, according to the CDC, is to administer the first dose as soon as possible after birth, followed by two additional doses with a minimal spacing interval of four weeks between the first and second dose, and at least eight weeks between the second and third dose, leaving at least 16 weeks between the first and third doses (15).

HBV has several antigenic components, including hepatitis B surface antigen (HBsAg), hepatitis B core antigen (HBcAg), and hepatitis B e antigen (HBeAg) (15). HBsAg, which is used for estimating prevalence of HBV, can be detected in serum between 30 and 60 days post-exposure and may persist for a longer period of time depending on host response (15). HBcAg can be detected in live tissue of persons with acute or chronic HBV infection, while HBeAg can be detected in serum samples and

indicates a high level of infectivity (15). Antibody to HBsAg (anti-HBs) develops after an acute HBV infection is resolved or after uptake of the hepatitis B vaccine (15).

Burden of Disease

The most recent estimate reports that 240 million people worldwide are chronically infected with HBV (18). While the prevalence of chronic HBV infection has decreased in most regions since the widespread introduction of the hepatitis B immunization programs, the absolute number of HBsAg positive persons increased between 1990 and 2005 (18-22). Studies have repeatedly shown that HBV is moderately to highly endemic in many parts of Asia, the Pacific Islands, Eastern and Central Europe, the Eastern Mediterranean, and sub-Saharan Africa (22-26). Overall prevalence of HBV in Western Europe and the Americas is low (less than 2%), but there is a high variability in the distribution of HBV prevalence in Central and South America (18, 21, 23-26).

There are many factors that affect the patterns of distribution of HBV infection, especially in Latin America, where HBV prevalence less than 2.0% in some countries, such as Argentina and Chile, and as high as 5.2% in other countries, such as Peru and Brazil (23). Within these countries of high endemicity, it is estimated that prevalence among certain subpopulations is even higher than the national average, such as among people living in the Amazon basin (21, 24). Geographical, socio-economic, and cultural factors can affect the distribution of the burden of HBV, both within and between countries and continents, including factors such as migration to urban areas in search of economic opportunities, unsafe sexual and medical practices due to lack of resources or knowledge, and serological differences in susceptibility from variations in genealogical heritages due to colonization (21, 25). In areas of low endemicity, HBV infection is

likely to be acquired during adult life by way of intravenous (23) drug use or unprotected sexual activities (19, 24, 27)

In the US, where prevalence of HBV is low among the general population, there still exists a disparity in HBV prevalence of infection between various subpopulations, such as IV drug users and immigrant populations (20, 21, 24, 27, 28). Studies have found significantly higher seroprevalence of HBV infection among foreign-born populations compared to the US-born population (27-30). The foreign-born populations in the US with the highest prevalence of HBV infection are those populations originating in Asia and Africa, with estimated HBV prevalence ranging from 7.4% to 13.2% (27-30). The burden of HBV infection in immigrant and refugee populations in the US is estimated to be even higher than in other high-risk groups such as IV drug users (27).

When comparing refugee and asylee populations in the US to immigrants, the overall seroprevalence of HBV among refugees and asylum seekers was found to be significantly higher than in immigrants, in populations from all geographic regions of the world except Eastern Europe and Central Asia (27). Prevalence of HBV infection in refugee populations in the US has been reported to range from 2.8% to 23%, depending on location and geographic region of origin of the study population (27, 30-33). On average, these prevalence estimates are much higher than the overall estimated US prevalence of 0.2% - 0.5%, demonstrating that the burden of HBV infection in the US weighs more heavily on refugee populations (23). Studies have estimated a low overall seroprevalence of HBV among foreign-born populations from Latin America and the Caribbean (1.7%), but the estimated prevalence among refugee populations from this region was estimated to be higher, at 3.1% (27). However, there are limitations on these

estimates, as many of the studies include a very small sample size of immigrants or refugees from this region, or people from this region are excluded from the study altogether (19, 30, 32-35).

Emigration of people from areas of high HBV endemicity to regions of low endemicity, such as the US and Western Europe, may lead to an increase in overall seroprevalence of HBV infection in the destination regions (21, 36). There are an estimated 3.5 million immigrants and refugees currently residing in a country not their own who are estimated to be chronically infected with HBV, and the largest estimated number of these people are in the US (1.6 million, or 6.7% of the worldwide immigrant population) (27). History has shown a marked decrease of the burden of HBV due to infant hepatitis B immunization programs, and as these programs continue to increase, improve, and spread to new countries, the incidence of HBV infection is expected to continue to decline, as it has over the past two decades (18-22, 24).

Hepatitis B Immunology

Immunity to HBV is detected by presence of anti-HBs (or anti-HBs greater than or equal to 10 mlU/mL) and can be attributed to vaccination if antibody to HBcAg (anti-HBc) is negative; otherwise, if anti-HBc is positive, immunity is a result of natural exposure (15). The CDC reports that 16% to 40% of infants who have received one dose of hepatitis B vaccine demonstrate protective levels of anti-HBs, and this percentage increases to 80- 95% after two doses, and 98-100% after three doses (15). Clinical trials of the hepatitis B vaccine have demonstrated similar responses in study participants, with seroprotection consistently being at least 90% and up to 100% after a completed vaccine

series of three doses (37-40). However, immune response may be lower in adults aged 40 years or older (15).

Immune response to the hepatitis B vaccine is affected by a variety of factors, with age being one of the most important; adults who receive the vaccine consistently demonstrate poorer immune response than children and infants receiving the same vaccine (38, 39). Other factors, including the vaccine brand, procedure used, genetics, body mass index (BMI), psychological stress, nutrition, and infectious disease may also impact the immune response to the hepatitis B vaccine (37, 39). Anti-HBs levels have been shown to decrease over time, but adequate infant vaccination has been estimated to produce effective immunity for more than 20 years following immunization (15, 22, 37, 38, 41).

Studies aiming to assess immunity to HBV in immigrant and refugee populations in the US have shown that immunity is highest among populations coming from regions with high prevalence of infection but that over half of all migrants are susceptible to HBV and would benefit from immunization (27, 30). It is typically more likely that demonstrated immunity among refugee populations is due to exposure to HBV rather than vaccination (31). One systematic review reported that refugees demonstrated a higher seroprevalence of immunity than immigrants (41.5% compared to 33.7%, respectively), which is likely due to the higher prevalence of HBV infection among refugee populations as compared to immigrants (27). Other studies have reported prevalence of immunity ranging from 24.2% to 39% in refugee populations (31, 32).

A review of over 12,000 medical records in Minnesota revealed a seroprevalence of immunity to HBV of 31.1% in refugees, but one limitation to this study was that it

excluded 111 individuals whose medical records indicated at least one dose of hepatitis B vaccine prior to arrival in the US (30). This exclusion criteria does not take into account the possibility of inaccuracy of overseas medical records, improper vaccine procedures used overseas, or misreporting of doses (30). Several studies of HBV screening for internationally adopted children have shown lack of immunity to HBV in 31-32% of children with documentation indicating at least three doses of hepatitis B vaccine (42, 43). Reasons for the lack of antibodies could include vaccine nonresponse, waning immunity, or inaccuracy of overseas reporting (42, 43). Oftentimes, vaccination history will be missing, due in part to the fact that it is not required for refugees receive any vaccinations prior to entry into the US (11). This was found to be the case in a review of screening forms of refugees arriving in Minnesota, where the researchers found only 4.1% of non-immune study participants had documentation of at least one dose of hepatitis B vaccine, and 0.5% of non-immune participants had documentation of three doses (34).

There is limited information available on the seroprevalence of immunity among immigrants and refugees from Latin America, with one study reporting a low seroprevalence (33%) of anti-HBs in this population from a study which included only two participants from Latin America (27). Other studies reporting immunity in refugee and immigrant populations either did not report on people from this region due to similarly small sample sizes, or because of study exclusion criteria which excluded individuals listing Spanish as a first language (30, 44). However, it is estimated that overall hepatitis B vaccine coverage in Cuba is 99%, due to the success of the infant immunization program introduced in 1990 (45).

Refugee Health

Challenging living conditions in refugee camps, such as overcrowding, poverty, lack of sanitation and healthcare access, and poor public health infrastructure, can contribute to high morbidity and mortality from infectious disease and malnutrition, which are the two largest contributors to death in complex humanitarian emergencies (46, 47). Some of the most common infectious diseases in refugee camp settings are diarrheal disease, acute respiratory infections, measles, malaria, meningitis, TB, intestinal parasites, and HIV/AIDS, among others (46-48). Outbreaks of certain vaccine-preventable diseases have contributed to the disruption of resettlement among refugee populations in Kenya, Tanzania, Thailand, Ethiopia, and the Ivory Coast several times since 2004 (48).

However, in well-established refugee camps, it is possible to observe better health outcomes among the refugees compared to the host population, due to targeted health interventions such as vaccine campaigns or nutritional supplement programs provided by relief organizations in the camps (47). Unfortunately, not all refugees reside in established camps, which often leads to the exclusion of urban refugees from both national health programs and those programs provided by relief organizations (47).

Domestically, some of the most common health problems and conditions observed in refugees include mental health issues, pain, such as in the abdomen or back, and undiagnosed chronic conditions, such as anemia, asthma, diabetes mellitus, or hypertension (49). Screening programs for refugees also often report infectious diseases such as the ones previously mentioned as common issues in the camps, as well as sexually transmitted infections (STIs), Helicobacter pylori bacteria, and HBV infection

(49, 50). Women's health can also present challenges among the refugee population, as one study reported that 25% of their sample were pregnant, half of whom did not know they were pregnant, and none of whom were receiving prenatal care at the time of the exam (50). In this same study, only 14% of the women aged 40 or older reported having had at least one mammogram, and only 24% of the women had received a Pap smear in the previous three years (50).

One limitation to the available data for refugee health assessed through domestic medical screening results is that providers may not always adhere to national guidelines for refugee medical exams, according to one recent study of the primary clinics of Boston Medical Center (44). According to this study, only 36% of refugees were screened for HBV infection, 36% were tested for HIV, and 5% were tested for ova and parasites (44). While this study may not be generalizable to other clinics or states, it does demonstrate potential opportunities for improvement in regards to clinic adherence to recommended guidelines for refugee screenings.

Cuban Refugee Health

Several reports on the health status of Cuban refugees were published immediately after the Mariel boatlift of 1980, but there is limited information available on the current health status of newly-arriving Cuban refugees and parolees in the US (51-53). One study of Cuban refugee children arriving in Miami-Dade County, Florida, between 1999 and 2000 reported a low prevalence of HBV infection (0.4%), positive PPD skin test (0.4%), and anemia (4.3%), and a high prevalence of infection with some type of organism (31.1%) and elevated blood lead levels (22.9%) (54). The previously-mentioned study on refugee women's health and low rates of prenatal care,

mammograms, and Pap smears was based on a study population that included 31.1% Cubans (50).

Just as there is limited information on the current health status of newly-arriving Cuban refugees and parolees, there is also very little information on the prevalence of HBV infection or immunity among this population. One study conducted in Cuba among HIV-positive individuals reported that 30.4% of study participants had immunity to HBV due to prior exposure (positive for both anti-HBs and anti-HBc), with 54.5% of those who were immune showing low immunity (55). In one study which reviewed records from refugees entering the US between 2006 and 2008, the prevalence of HBV infection among refugees from Cuba was found to be 1.0%, which shows no change from the estimate provided in a study from 1992 (56). However, no studies were found which provided an estimate for immunity to HBV among Cuban refugees or parolees in the US.

METHODS

Overview

This study used overseas medical examination data from the Electronic Disease Notification (EDN) system to assess Cuban refugees and parolees who arrived in Texas from January 2010 through December 2013 (Appendix A). The EDN system collects data from the required overseas medical examinations for newly arriving immigrants and refugees in the US. Domestic medical screening data from the first domestic medical exam of Cuban refugees and parolees who arrived in Texas during this same time period were also assessed (Appendix B). This set of data was provided by the Texas Department of State Health Services.

Variables

The exposure of interest was an indication from overseas medical records of hepatitis B vaccination, and the outcome of interest was demonstrated immunity to HBV during the first domestic medical examination. Potential confounders that were considered for inclusion in the model were sex, immigration status, age at arrival to the US, anemia, and presence of infectious disease. BMI was considered as a potential confounder for adults only. Data indicating presence of a psychological disorder, current or previous tobacco use, and diabetes mellitus were available but were not considered for the final model because the data for these variables were too few to include in an analysis.

Data Sources and Measurement

The main exposure variable—history of hepatitis B vaccination—was provided by overseas records through the EDN system. The number of doses and dosage spacing

in weeks of hepatitis B vaccine were determined by recorded dates of hepatitis B vaccination doses. This exposure variable was divided into three categories: complete vaccination series, which was defined as three or more doses of hepatitis B vaccine; incomplete vaccination series, defined as one or two doses of hepatitis B vaccine; and no history of hepatitis B vaccine, which was defined as no indication of any doses of hepatitis B vaccine from overseas records (15). The only other variable considered for inclusion in the model that also came from the EDN system was immigration status, of which the categories were refugee, parolee, and asylee. Due to the small number of asylees in the study population, asylees were grouped with refugees for purposes of analysis.

The outcome variable—demonstrated immunity to HBV—was determined from the laboratory results of domestic serologic testing using enzyme immunoassay (EIA). Immunity to HBV was assumed if domestic laboratory results were positive for anti-HBs, with negative results assumed to indicate non-immunity to HBV.

Data for sex and age at arrival to the US were provided by the domestic medical screening records. Age at arrival to the US was split into two categories: less than 18 years of age and 18 years of age or older. Age was categorized in this way in order to have separate groups for children and adults, by legal definition in the US.

The domestic records provided data on HIV status, syphilis, TB, hepatitis C virus, and parasitic infections, all of which were used for the creation of a variable indicating presence of any infectious disease. These variables were grouped together into one indicator variable because of the small numbers of positive test results for each of these conditions. Testing results for HIV were based on an antigen and antibody combination

EIA followed by a Western blot for confirmation. Testing results for syphilis were based on presence or absence of rapid plasma reagin (RPR) for initial screening and treponema pallidum particle agglutination (TP-PA) for confirmation. Testing results for hepatitis C virus were determined using EIA to detect antibody to hepatitis C virus. Presence of parasitic infection was calculated using an indicator variable which indicated whether or not the individual tested positive for any of the following parasites or parasitic diseases: *Ascaris lumbricoides*, *Clonorchis*, *Dientamoeba fragilis*, amebiasis, *Giardia*, hookworm, schistosomiasis, *Strongyloides*, or *Trichuris trichiura*.

The domestic medical screening results also provided capillary hemoglobin measures which were used to determine presence of anemia. Maximum capillary hemoglobin concentrations for anemia were defined by age- and sex-specific cutoff values, with a separate category for pregnant women, all of which were based on the 5th percentile from the third National Health and Nutrition Examination Survey (NHANES III) (57). These cutoff values were as follows: <11.0 g/dL for children aged 6 months to < 2 years; <11.1 g/dL for children aged 2 years to <5 years; <11.5 g/dL for children aged 5 years to <8years; <11.9 g/dL for children aged 8 years to <12 years; <12.5 g/dL for males aged 12 years to <15 years; <13.3 g/dL for males aged 15 years to <18 years; <13.5 g/dL for males aged ≥18 years; <11.8 g/dL for non-pregnant females aged 12 years to <15 years; <12.0 g/dL for non-pregnant females aged ≥15 years; and <11.0 g/dL for pregnant females (57).

For the variable measuring BMI, which was considered as a potential confounder in a sub-analysis of adults only, BMI was calculated based on height and weight measurements provided by domestic data, and a categorical variable was created using

four categories: underweight, normal, overweight, and obese. Underweight included those with a BMI of less than 18.5 kg/m^2, normal included those with a BMI between 18.5 kg/m^2 and 24.99 kg/m^2, overweight included those with a BMI between 25 kg/m^2 and 29.99 kg/m^2, and obese included those with a BMI of at least 30 kg/m^2, according to cutoff values specified by the World Health Organization (WHO) (58).

Sources of Bias

One potential source of selection bias is that, although domestic medical examination data from Texas were available for 4,935 Cuban refugees and parolees arriving during the specified time period, only 1,548 records were matched with overseas data in the EDN system (prior to applying exclusion criterion). The remaining 3,387 records were unable to be matched to overseas data due to the fact that the CDC is not able to collect medical information for all arriving refugees and parolees due to complexities in the immigration process. In addition, 20 individuals were missing information on their HBV immunity status, which led to their exclusion from the analysis. If these individuals were systemically different from those who did have this information available, this could bias the effect estimate.

Misclassification of the main exposure variable—history of hepatitis B vaccination—was of primary concern for the purpose of this analysis. However, it is also possible that the outcome—demonstrated immunity to HBV—could have been misclassified in some cases. If the serologic test failed to detect anti-HBs when anti-HBs were present, the individual would be errantly classified as non-immune. Conversely, if the serologic test detected anti-HBs when none were actually present, the individual would be misclassified as immune. Either of these scenarios could influence the effect

estimate, biasing the estimate either toward or away from the null depending on whether the misclassification was differential or non-differential. However, the diagnostic methods for detecting the presence of anti-HBs are known to be high, with sensitivity ranging from 93.5% to 100% and specificity ranging from 96.8% to 100%, depending on the brand of test used (59).

There was also the possibility of misclassification as it relates to exclusion criteria, including presence of HBsAg and anti-HBc. If either of these serologic tests led to a false positive or a false negative, this would have affected the final study population, either causing ineligible people to be included in the study or eligible people to be excluded from the study. Either of these scenarios could result in a biased effect estimate in the same way as previously described as it relates to the detection of anti-HBs. However, the diagnostic methods for detecting HBsAg and anti-HBc are high, with sensitivity for the detection of HBsAg ranging from 94.5% to 100% and specificity ranging from 96.4% to 100%, depending on the brand of test used (60). For detection of anti-HBc, sensitivity ranges from 96.4% to 99.3%, and specificity ranges from 99.9% to 100%, depending on the brand of test used (61).

Study Population

The initial population considered for inclusion in the study consisted of all Cuban refugees and parolees who arrived in Texas between January 2010 through December 2013 and whose domestic records could be matched with overseas records in the EDN system. Matching was performed using the alien number as the identifying variable, prior to the de-identification of the data. Individuals were eligible for inclusion in the final study population if they were negative for HBsAg; were negative for anti-HBc if

domestic results were positive for anti-HBs; were born in Cuba; had available results for anti-HBs; and did not have a discrepancy between sex or date of birth between domestic and overseas records.

Statistical Methods

Data were de-identified by a CDC epidemiologist, and analyses were performed on a secure CDC computer using SAS software, Version 9.3 of the SAS System for Windows, copyright © 2002-2010 by SAS Institute Inc., Cary, NC, USA. Microsoft Excel and Word were used for the creation of tables and figures.

All two-way interactions for effect modification between potential confounders and the exposure variable were assessed for significance independently from other potential effect modifiers and confounders. For each potential effect modifier, a test statistic was obtained for the interaction term in a model containing the predictor, the potential modifying confounder, and the interaction term between the potential confounder and the predictor. Using the p-value produced by Type 3 Analysis of Effects, if the interaction term was significant at an alpha level of 0.05, the interaction term was included in the final interaction model; otherwise, the interaction term was dropped.

After assessing effect modification, potential confounders were assessed for significance. First, the full model was run, which contained all potential confounders and significant interaction terms, in order to obtain a test statistic and p-value for each variable in the model. If any previously-significant interaction terms were no longer significant (p-value greater than 0.05) in a model containing the potential confounders, the interaction term was dropped. For potential confounding variables, the p-value for the test statistic was assessed for significance at an alpha of 0.05, and all significance

variables were kept in the final model and considered to be statistically-independent predictors of demonstrated immunity to HBV.

For all potential confounding variables with a p-value greater than 0.05, each variable was dropped from the model individually and in all possible grouped combinations with other non-significant variables, in order to compare the effect estimate and the 95% confidence interval obtained from the reduced model to that produced by the full model. If the effect estimate from a reduced model was within 10% of the effect estimate produced by the full model, then the confidence intervals were compared to see if the full model had a substantially greater precision than the reduced model. The final model was determined by choosing the model with an effect estimate within 10% of the estimate produced by the full model and the highest, substantial gain in precision.

If a variable modified the effect of the main exposure and was thus included in the model as an interaction term, the lower order of that variable was kept in the model in order to maintain a hierarchically well-formulated model regardless of its p-value. The final interaction model was assessed for collinearity using a conditional index cutoff value of 30. However, no collinearity issues were found. Additionally, a no-interaction model was constructed using the same methods of confounding and collinearity assessment but without the interaction terms, in order to describe the primary effect estimate with more simplicity of interpretation.

For the main analysis, logistic regression was conducted in order to obtain prevalence ratio (PR) estimates. The prevalence ratio (PR) estimates were used to determine the prevalence of immunity to HBV in Cuban refugees and parolees with a complete vaccination series compared to Cuban refugees and parolees with no

vaccination history. The PR estimates were also used to determine the prevalence of immunity to HBV in Cuban refugees and parolees with an incomplete vaccination series compared to those with no vaccination history. All PR estimates for the main analysis were calculated controlling for sex, age at arrival to the US, anemia, and immigration status. The interaction model controlled for sex, age at arrival to the US, anemia, presence of infectious disease, immigration status, an interaction between age at arrival to the US and vaccination history, and an interaction term between presence of infectious disease and vaccination history.

One sub-analysis was conducted using only adults in order to assess BMI as a potential confounder. For this sub-analysis, the model was built using the same methods as described for the main analysis, and logistic regression was conducted in order to obtain the same PR estimates as those obtained in the main analysis. All PR estimates for the sub-analysis were calculated controlling for immigration status and BMI.

RESULTS

Participants

The selection of study participants is displayed in Figure 1. Of the 1,548 domestic records matched with overseas records in the EDN system, 7 individuals reported a place of birth other than Cuba and were excluded from the final study sample. In addition, 15 individuals had domestic laboratory results indicating current or previous HBV infection, 18 individuals had domestic laboratory results indicating immunity to HBV based on natural exposure to the virus, and 20 individuals were missing information on immunity to HBV. There were 41 records demonstrating a discrepancy between sex reported from overseas and domestic data, and 37 records had the same type of discrepancy with the reported age at arrival to the US. These individuals were excluded due to the likelihood of an error with the identifying number used to match overseas and domestic records. There were six individuals who met at least two exclusion criteria, resulting in the total exclusion of 132 persons and a final sample size of 1,416 individuals.

Descriptive Data

The distribution of characteristics among the study population is shown in Table 1. The study population consisted of 752 (53.1%) refugees and 664 (46.9%) parolees. Males comprised 48.0% of the study population. Children under 18 years of age at arrival to the US represented 27.1% of the study population, and ages ranged from less than one year of age to older than 89 years of age. There were 541 (38.2%) persons in the study population with overseas vaccination records indicating no history of hepatitis B vaccine, while 94 (6.6%) had records indicating an incomplete series of hepatitis B vaccine, and 781 (55.2%) had records indicating a complete series of hepatitis B vaccine.

History of hepatitis B vaccination history is shown in Table 2. Hepatitis B vaccination history did not differ by sex, but there were differences by age group. Only 65 (17.0%) children younger than 18 years of age had records indicating no history of hepatitis B vaccination, while 476 (46.1%) adults 18 years of age or older had no history of hepatitis B vaccine. Additionally, 263 (68.7%) children younger than 18 years of age had records indicating a complete hepatitis B vaccination series, while 518 (50.2%) adults 18 years of age or older had records indicating a complete hepatitis B vaccination series. The highest prevalence of records indicating an incomplete hepatitis B vaccination series was among children younger than five years of age (30, or 42.3%).

According to domestically-reported hemoglobin results, 213 (15.1%) persons were anemic at the time of their domestic medical examination, with the highest prevalence of anemia occurring in children between six months and two years of age (13, or 72.2%). Only 43 (4.6%) adults were underweight according to measures of BMI, but 283 (30.4%) had a BMI indicating overweight, and 156 (16.8%) were obese at the time of the domestic medical examination.

Outcome Data

The prevalence of demonstrated immunity to HBV across selected characteristics is shown in Table 1. There were 534 (37.7%) persons with demonstrated serologic immunity to HBV (positive anti-HBs). Immunity to HBV differed by recorded overseas vaccination history, with 157 (29.0%) of those with no history of hepatitis B vaccination demonstrating immunity to HBV; 42 (44.7%) of those with an incomplete series of hepatitis B vaccine demonstrating immunity to HBV; and 335 (42.9%) of those with a complete series of hepatitis B vaccine demonstrating immunity to HBV.

The prevalence of immunity to HBV among males and females was 35.3% and 39.9%, respectively. Prevalence of immunity was highest among children (57.0%), while adults demonstrated an immunity prevalence of 30.6%. Comparing HBV immunity across smaller age categories demonstrated a general decreasing trend in immunity as age increased.

Prevalence of HBV immunity was highest among those who entered the US as parolees compared to refugees (43.8% and 32.3%, respectively). Among those who were anemic, 53.1% demonstrated immunity to HBV, while those who were not anemic demonstrated a prevalence of immunity of 34.8%. Those with at least one infectious disease had a prevalence of immunity to HBV of 34.7%, while those without any infectious disease had a prevalence of 38.1%. Among adults, immunity to HBV was highest among those with a normal or underweight BMI (37.1% and 37.2%, respectively), while those categorized as overweight had a prevalence of immunity of 24.7%, and those categorized as obese had a prevalence of 20.5%.

Main Results

Results of the analysis are shown in Table 1. An adjusted analysis of the effect of hepatitis B vaccine history on demonstrated immunity to HBV produced a PR of 1.54 (95% confidence interval [CI]: 1.19, 2.00) when comparing an incomplete vaccination history to no history of vaccination and a PR of 1.48 (95% CI: 1.27, 1.73) when comparing a complete vaccination history to no history of vaccination.

The initial variables considered as potential confounders were sex, immigration status, age at arrival to the US, anemia, and presence of infectious disease. The final logistic regression model for the main analysis contained the following variables:

hepatitis B vaccine history, immigration status, sex, age at arrival to the US, and anemia. Hepatitis B vaccine history was the main exposure variable, and immigration status, sex, age at arrival to the US, and anemia were all statistically significant independent predictors of the outcome ($P < 0.05$). The variable indicating presence of infectious disease did not produce a 10% change in the PR estimates when dropped from the model containing all potential confounders and predictors and did not lead to a gain in precision when included in the full model. As a result, it was not included in the final model.

The adjusted analysis, controlling for the variables listed above, produced a PR of 1.15 (95% CI: 0.88, 1.50) when comparing an incomplete vaccination history to no history of vaccination and a PR of 1.23 (95% CI: 1.05, 1.45) when comparing a complete vaccination history to no history of vaccination. This adjusted analysis used 1,410 of the 1,416 individuals in the study population, due to missing values for anemia for six of the individuals.

Other Analyses

Results of additional analyses and sub-analyses are shown in Table 1. The main analysis found that prevalence of immunity to HBV was 1.23 (95% CI: 1.08, 1.40) times higher among parolees than among refugees. A similar PR was found when comparing immunity to HBV among females versus males, with females demonstrating 1.22 (95% CI: 1.06, 1.40) higher immunity to HBV than males. Individuals positive for anemia were 1.34 (95% CI: 1.14, 1.58) times more likely to demonstrate immunity to HBV than those without anemia. Of particular interest was the comparison between adults and children, which results in a PR of 0.63 (95% CI: 0.55, 0.73), indicating that adults were 37% less likely to demonstrate immunity to HBV compared to children.

An additional model was analyzed for the main analysis to assess interaction between the main exposure and confounders or independent predictors. This model assessed interaction between hepatitis B vaccine history and the following variables: immigration status, sex, age at arrival to the US, anemia, presence of infectious disease, psychological disorder, current or previous tobacco use, and diabetes mellitus. The variables indicating a psychological disorder, current or previous tobacco use, and diabetes mellitus had data too sparse to produce a p-value for both levels of hepatitis B vaccine history and were subsequently excluded from remaining analyses.

The interaction terms determined to be significant ($P < 0.05$) include an interaction term between age at arrival to the US and hepatitis B vaccine history, and an interaction term between infectious disease and hepatitis B vaccine history. Thus, the final interaction model contained the following variables: immigration status, sex, age at arrival to the US, anemia, presence of infectious disease, an interaction term between age at arrival to the US and hepatitis B vaccine history, and an interaction term between infectious disease and hepatitis B vaccine history. This adjusted analysis using this interaction model used 1,410 of the 1,416 individuals in the study population, due to missing values for anemia for six of the individuals.

The results for the interaction model are displayed in Appendix D. The logistic regression using the interaction model found that, among children, hepatitis B vaccine history did not have a statistically significant ($P < 0.05$) association with demonstrated immunity to HBV. Among adults, an incomplete hepatitis B vaccine history was not significantly associated with HBV immunity, but those with a vaccine history reporting a

complete series of hepatitis B vaccine were 1.50 (95% CI: 1.24, 1.83) times more likely to be immune to HBV than those with no reported hepatitis B vaccine history.

Additionally, the interaction model found that the association between hepatitis B vaccine history and immunity to HBV differed by infectious disease status. Among those negative for an infectious disease, there were no statistically significant association between hepatitis B vaccine history and immunity to HBV. However, among those positive for an infectious disease, the only statistically significant association found was that those with a complete series of hepatitis B vaccine were 49% less likely to have immunity to HBV compared to those with no history of hepatitis B vaccination (PR 0.51; 95% CI: 0.30, 0.85).

A sub-analysis was conducted using only adults in order to assess the effects of BMI on HBV immunity, resulting in a sample size of 1,033. The adjusted results from this sub-analysis produced a PR of 0.93 (95% CI: 0.52, 1.70), comparing incomplete hepatitis B vaccine history to no vaccine history, and a PR of 1.49 (95% CI: 1.23, 1.81) comparing complete hepatitis B vaccine history to no vaccine history.

The initial variables considered as potential confounders in this sub-analysis were sex, immigration status, anemia, presence of infectious disease, and BMI. Hepatitis B vaccine history was the main exposure variable, and BMI was a statistically significant independent predictor of the outcome ($P < 0.05$). The variables for sex, anemia, and presence of infectious disease did not produce a 10% change in the PR estimates when dropped independently and in all combinations of groupings from the model containing all potential confounders and predictors, and there was no substantial gain in precision from the inclusion of any of these variables in the full model. As a result, none of these

three variables were included in the final model for the sub-analysis. The sub-set of data was also assessed for interaction between the main exposure variable and all potential predictors and confounders, but none were found.

The final logistic regression model for this sub-analysis contained the following variables: hepatitis B vaccine history, immigration status, and BMI. The adjusted sub-analysis used 930 of the 1,033 adults, due to missing values for BMI. Controlling for the variables listed above, the adjusted sub-analysis did not find a statistically significant association between an incomplete vaccination history and immunity to HBV compared to no history of vaccination, but it did produce a PR of 1.51 (95% CI: 1.23, 1.86) when comparing a complete vaccination history to no history of vaccination.

Additionally, the sub-analysis found that those who were overweight were 33% times less likely to demonstrate immunity to HBV compared to those with a normal BMI (PR 0.67, 95% CI: 0.53, 0.84), and those who were obese were 45% less likely to demonstrate immunity to HBV compared to those with a normal BMI (PR 0.55, 95% CI: 0.40, 0.76). There was no statistically significant association between being underweight and demonstrating immunity to HBV.

DISCUSSION

Key Results

The main objective of this analysis was to assess how well the overseas hepatitis B vaccination records predicted demonstrated immunity to HBV after arrival to the US. The results showed that, in both the main analysis and the sub-analysis on adults only, records indicating a complete series of hepatitis B vaccine provided only a moderate prediction of demonstrated immunity to HBV, adjusting for other significant predictors of HBV immunity. That is to say, overall, those with records reporting a complete series were only 1.23 times more likely to demonstrate immunity to HBV compared to those with no record of hepatitis B vaccination, and among adults, those with a complete series were only 1.51 times more likely to demonstrate immunity to HBV.

The poor predictive quality of the overseas hepatitis B vaccine records is more apparent in the comparison of anti-HBs prevalence across the three categories of hepatitis B vaccine history. According to overseas records, prevalence of anti-HBs was 29.0% among those with no history of hepatitis B vaccine. The expected prevalence of anti-HBs among this subgroup is 0%, since all those who were immune due to natural exposure (anti-HBc positive) were excluded from the analysis.

Additionally, among those whose overseas records indicated a complete series of hepatitis B vaccine, the prevalence of anti-HBs was only 42.9%. The expected prevalence of anti-HBs immunity among this subgroup is much higher, with the CDC reporting anti-HBs in 98% to 100% of infants and in 90% to 95% of teens and adults after three doses of hepatitis B vaccine (15). Even though a portion of this difference in demonstrated immunity between observed and expected could be accounted for by

waning immunity, one would still expect a higher prevalence of anti-HBs than what was observed, especially considering 41.2% of the study population was below the age of 26, and the hepatitis B vaccine is estimated to provided adequate protection for at least 20 years (15).

Although the main analysis assessed the interactions between hepatitis B vaccine history and age at arrival to the US, as well as the interaction between hepatitis B vaccine history and infectious disease status, the only important conclusion that can be drawn from these results are that overseas vaccine records provide a moderately better prediction of vaccine immunity among adults (PR 1.50, 95% CI: 1.24, 1.83) than among children (PR 0.95, 95% CI: 0.77, 1.17). As overseas records of hepatitis B vaccination are a poor predictor of immunity to HBV overall, they remain poor predictors of immunity to HBV among subgroups of the study population.

Strengths and Limitations

One of the strengths of this analysis was the ability to use data from the state receiving the second largest number of Cuban refugee and parolee arrivals, with data from over three years of arrivals available for analysis. In addition, there was enough data available to control for most of the major confounders and predictors of immunity to HBV according to published literature.

However, even though this analysis controlled for many significant independent predictors, confounders, and effect modifiers between the main exposure and the outcome, there may be additional significant variables that were not included in the analysis. For instance, vaccine-induced immunity to HBV is known to wane over time, so the number of years that have passed since a person completed the hepatitis B

vaccination series would likely effect the probability of that person demonstrating immunity to HBV (22, 37, 38, 41). However, it was not possible to control for this factor in this analysis which may have led to a bias towards the null.

Another factor that may affect an individual's production of immune response to HBV is the dose spacing and timing of the hepatitis B vaccine (62). The CDC recommends at least four weeks between the first and second dose, and at least eight weeks between the second and third dose, leaving at least 16 weeks between the first and third dose (15). Factors that could contribute to an individual's ability to produce an immune response include inappropriate spacing of the hepatitis B vaccine doses and the individual's age at time of vaccination. Due to the complexities presented by this issue, vaccination spacing and age at receipt of vaccination were not controlled for in the analysis.

However, the distribution of dose spacing was examined in order to assess the frequency of improper dose spacing, and these results are described in Appendix C. This descriptive analysis found that 6.4% of study participants had improper spacing between their first and second doses of hepatitis B vaccine (median 4.6 weeks; range 0.1 to 2,066.1 weeks); 4.1% of participants had improper spacing between their first and third doses (median 27.1 weeks; range 7.9 to 2,073.1 weeks); and 84.1% of participants had improper spacing between their second and third doses (median 22.1 weeks; range 1.4 to 593.3 weeks), using CDC recommendations as a guideline. It should be noted that dates of vaccination on overseas records may have been entered incorrectly, thus contributing to an inflated estimate of improper dosage spacing.

Interpretation

The results of this analysis suggest that overseas hepatitis B vaccination records are not useful predictors of immune response to HBV. However, it is important to consider the potential biases incurred by residual confounding due to unmeasured variables, such as time since receipt of the hepatitis B vaccine, timing and spacing of hepatitis B vaccine doses, and other factors known to affect immune response to hepatitis B vaccination, such as vaccine brand, procedure used, genetics, and psychological stress (37, 39). The effects of these limitations may have produced a bias towards the null, thus minimizing the observed predictive value of the overseas vaccination records.

However, the distribution of immune response across the three levels of reported vaccine history do demonstrate a much higher proportion of anti-HBs among those with no reported history of hepatitis B vaccine, which strongly suggests some reporting error from overseas medical records, regardless of the previously-mentioned limitations. Medical providers conducting the initial domestic medical screening for refugees and parolees from Cuba should consider screening all arrivals for anti-HBs and vaccinating those not immune. It may also be advisable to conduct a follow-up titer for anti-HBs after the first dose administered domestically, in the event that the patient arrived to the US with a history of less than two doses of hepatitis B vaccine.

Generalizability

It is reasonable to assume that the results found in this analysis can be generalized to all Cuban refugees and parolees who arrived in the US during the same time period as those comprising this study population. Although this study population included only those individuals who arrived in Texas between January 2010 and December 2013, the

specified state for resettlement of refugees and parolees does not differ depending on characteristics of the arriving persons. Therefore, a person being resettled to another state is just as likely to have been examined by the same panel physician and to demonstrate the same immune response to HBV as a person being resettled to Texas.

However, it should be noted that the prevalence of immune response to HBV in this study population cannot be generalized to any current or previous general population in Cuba. There is no evidence to suggest that persons emigrating from Cuba to the US as refugees or parolees are representative of those who remain in Cuba.

Additionally, the validity of overseas hepatitis B vaccination records outlined by this study is only applicable to refugees and parolees from Cuba and cannot be expanded to describe the any overseas records from panel physicians in other countries from which refugees to the US originate. However, the quality of hepatitis B vaccination records determined by this analysis may be generalizable to other portions of the overseas medical records among refugees and parolees from Cuba. That is to say, if reporting of history of hepatitis B vaccination is of poor quality, then reported history of other vaccines, conditions, and treatments may also contain inaccuracies and should thus be interpreted with caution.

Future Directions

It would be of use to conduct similar analyses on other populations of refugees arriving in the US, particularly among refugees originating in countries where hepatitis B vaccination is routine or is an established component of the refugee resettlement process. These additional analyses could provide insight as to whether hepatitis B vaccination history among refugees is a useful predictor of immunity in any refugee population.

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TABLES

Table 1. Selected characteristics, prevalence, and prevalence ratios of demonstrated immunity to hepatitis B virus among Cuban refugees and parolees undergoing part or all of the standard refugee medical assessment – Texas, January 2010 - December 2013[a]

	Arrivals		Anti-HBs Positive		Prevalence Ratios					
				Prevalence	All[c]			Adults only[d]		
Characteristic	**N**	**(%)[b]**	**n**	**(%)[b]**	**PR**	**95% CI**	**P-value**	**PR**	**95% CI**	**P-value**
HBV vaccine history[e]										
No history	541	(38.2)	157	(29.0)	1.00			1.00		
Incomplete series	94	(6.6)	42	(44.7)	1.15	(0.88, 1.50)	0.3130	0.90	(0.50, 1.63)	0.7380
Complete series	781	(55.2)	335	(42.9)	1.23	(1.05, 1.45)	0.0101	1.51	(1.23, 1.86)	<0.0001
Immigration status[f]										
Refugee	750	(53.0)	242	(32.3)	1.00			1.00		
Parolee	664	(46.9)	291	(43.8)	1.23	(1.08, 1.40)	0.0015	1.47	(1.23, 1.78)	<0.0001
Asylee	2	(0.1)	1	(50.0)	-	-	-	-	-	-
Sex										
Male	679	(48.0)	240	(35.3)	1.00			-	-	-
Female	737	(52.1)	294	(39.9)	1.22	(1.06, 1.40)	0.0068	-	-	-
Age group (yrs)										
<5	71	(5.0)	54	(76.1)	-	-	-	-	-	-
5-17	312	(22.0)	164	(52.6)	-	-	-	-	-	-
18-25	201	(14.2)	113	(56.2)	-	-	-	-	-	-
26-45	555	(39.2)	161	(29.0)	-	-	-	-	-	-
46-65	240	(17.0)	34	(14.2)	-	-	-	-	-	-
>65	37	(2.6)	8	(21.6)	-	-	-	-	-	-

Table continues

Table 1. continued

	Arrivals		Anti-HBs Positive		Prevalence Ratios					
				Prevalence	All[c]			Adults only[d]		
Characteristic	**N**	**(%)[b]**	**n**	**(%)[b]**	**PR**	**95% CI**	**P-value**	**PR**	**95% CI**	**P-value**
Age group (yrs) - dichotomized										
<18	383	(27.1)	218	(56.9)	1.00			-	-	-
≥18	1,033	(73.0)	316	(30.6)	0.63	(0.55, 0.73)	<0.0001	-	-	-
Anemia[g]										
Negative	1,197	(84.9)	417	(34.8)	1.00			-	-	-
Positive	213	(15.1)	113	(53.1)	1.34	(1.14, 1.58)	0.0005	-	-	-
BMI category[h]										
Underweight	43	(4.6)	16	(37.2)	-	-	-	0.94	(0.63, 1.39)	0.7489
Normal	448	(48.2)	166	(37.1)	-	-	-	1.00		
Overweight	283	(30.4)	70	(24.7)	-	-	-	0.67	(0.53, 0.84)	0.0006
Obese	156	(16.8)	32	(20.5)	-	-	-	0.55	(0.40, 0.76)	0.0003
Overall	1,416	(100.0)	534	(37.7)	-	-	-	-	-	-

Abbreviations: anti-HBs: antibody to hepatitis B surface antigen; BMI: body mass index; CI: confidence interval; HBV: hepatitis B virus; PR: prevalence ratio; yrs: years

[a] "-" indicates the variable was not a significant predictor or confounder and was not included in the final model. Signficance was assessed at an alpha level of 0.05.

[b] Percentages may not total to 100% because of rounding

[c] N=1,416

[d] N=1,033

[e] No history: 0 reported doses; incomplete: 1-2 reported doses; complete: ≥3 reported doses

[f] 2 individuals arriving under asylum status were included in the refugee category for the analyses

[g] Missing=6

[h] Only calculated and analyzed for adults aged 18 years or older (n=1,033); missing=103; underweight = BMI <18.5 kg/m^2, normal = BMI 18.5–<25 kg/m^2, overweight = BMI 25–<30 kg/m^2, obese = BMI ≥30 kg/m^2

Table 2. HBV vaccine history by selected demographic characteristics among Cuban refugees and parolees undergoing part or all of the standard refugee medical assessment – Texas, January 2010 - December 2013 (N=1,416)

	HBV Vaccine History[†]							
	No history		Incomplete		Complete		Overall	
Characteristic	**n**	**(%)[‡]**	**n**	**(%)[‡]**	**n**	**(%)[‡]**	**N**	**(%)**
Sex								
Male	258	(38.0)	45	(6.6)	376	(55.4)	679	(100.0)
Female	283	(38.4)	49	(6.7)	405	(55.0)	737	(100.0)
Age group (yrs)								
<5	19	(26.8)	30	(42.3)	22	(31.0)	71	(100.0)
5-17	56	(14.7)	25	(8.0)	241	(77.2)	312	(100.0)
18-25	60	(29.9)	11	(5.5)	130	(64.7)	201	(100.0)
26-45	264	(47.6)	15	(2.7)	276	(49.7)	555	(100.0)
46-65	128	(53.3)	11	(4.6)	101	(42.1)	240	(100.0)
>65	24	(64.9)	2	(5.4)	11	(29.7)	37	(100.0)
Age group (yrs) - dichotomized								
<18	65	(17.0)	55	(14.4)	263	(68.7)	383	(100.0)
≥18	476	(46.1)	39	(3.8)	518	(50.2)	1,033	(100.0)
Overall	541	(38.2)	94	(6.6)	781	(55.2)	1,416	(100.0)

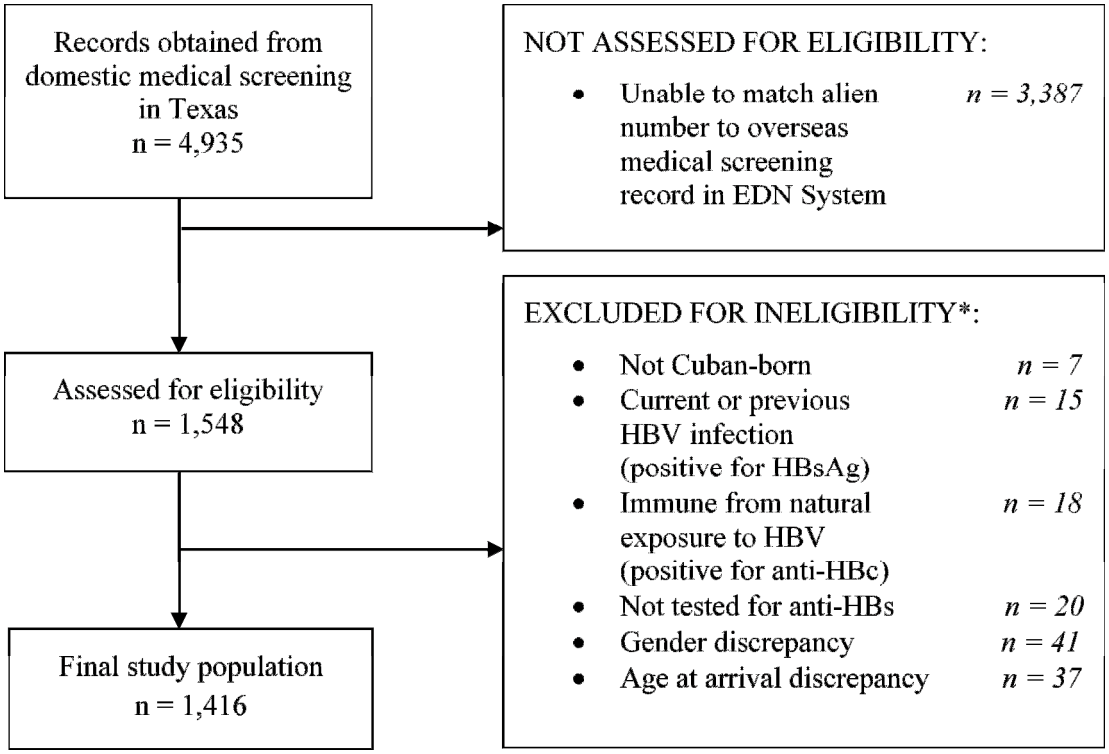
Abbreviations: anti-HBs: antibody to hepatitis B surface antigen; HBV: hepatitis B virus

[†]No history: 0 reported doses; incomplete: 1-2 reported doses; complete: ≥3 reported doses

[‡]Percentages may not total to 100% because of rounding

FIGURES

Figure 1. Selection of Cuban refugees and parolees – Texas, January 2010 – December 2013



Abbreviations: EDN: Electronic Disease Notification; HBV: hepatitis B virus; HBsAg: hepatitis B surface antigen; anti-HBc: antibody to hepatitis B core antigen; anti-HBs: antibody to HBsAg.

*Six individuals met two or more exclusion criteria

APPENDICES

Appendix A. Overseas Department of State medical examination forms received through the EDN system

The Department of State (DOS) forms for the medical examination of immigrant visa applicants (DS-2053, DS-2054, DS-3024, DS-3030, DS-3025, and DS-3026) are not available on the CDC website. Information about obtaining these forms may be requested on DOS website, at http://www.travel.state.gov/visa/visa_1750.html.

Appendix B. Texas Refugee Health Assessment Form

TEXAS Department of State Health Services

TEXAS REFUGEE HEALTH ASSESSMENT FORM

Alien #_____ **File #** _____

Last Name:_____ **First and Middle Name:**_____

Date of Birth *(mm/dd/yyyy)*:_____ **Gender:** ☐ **M** ☐ **F**

Arrival Status: ☐ **R** ☐ **A** ☐ **P** ☐ **VT** ☐ **SIV** **U.S. Arrival Date** *(mm/dd/yyyy)*: _____

Country of Origin *(or refugee group)*:_____ **City of Residence:**_____

County *(or clinic)*: _____ **Voluntary Agency:** _____

Overseas Classifications: **TB Class:** ☐ **B1** ☐ **B2** ☐ **History of Overseas Immunizations**

Overseas Medical Conditions *(from list)*:_____

☐ **I-693 Completed** ☐ **Secondary Migrant From** *(TX county or U.S. state)*:_____

First Screening Date *(mm/dd/yyyy)*: _____ **Medical Record #**_____

Vaccine-Preventable Disease / Immunization	Is there is evidence of immunity?	Domestic Immunization Date(s) (MM/DD/YYYY)				
MMR						
Varicella						
Hepatitis A						
Hepatitis B						
Diphtheria, Tetanus, Pertussis (DTap)						
Tetanus, Diphtheria, Pertussis (Tdap)						
Tetanus, Diphtheria (Td)						
Polio						
Haemophilus influenzae type b (Hib)						
Rotavirus						
Meningococcal						
Influenza						
Pneumococcal						
Human Papillomavirus (HPV)						
Zoster						

TB Screening:

1. **Tuberculin Skin Test (TST)** mm Induration: _____
   ☐ IGRA Test Only *Not Done:* ☐ Past history of positive TST ☐ Given, not read ☐ Declined test ☐ Tested elsewhere
   ☐ Previous severe reaction
2. **IGRA Test:** ☐ Positive ☐ Negative ☐ Indeterminate

Hepatitis Screening:

1. **Hepatitis B:** ☐ Not done, why not?_____
   Anti-HBs: ☐ Negative ☐ Positive **HBsAg:** ☐ Negative ☐ Positive **Anti-HBc:** ☐ Negative ☐ Positive
2. **Hepatitis C (Optional):** ☐ Negative ☐ Positive

Alien #_____ Last Name:_____

Sexually Transmitted Infections:

1. Syphilis ☐ Negative ☐ Positive ☐ Not done, why not?_____
2. Chlamydia (Females Age 15-25 Only) ☐ Negative ☐ Positive ☐ Not done, why not?_____
3. HIV ☐ Negative ☐ Positive ☐ Not done, why not ?_____
4. Other, specify: _____ ☐ Negative ☐ Positive

Intestinal Parasite Screening:

Ova & Parasite Tests:

☐ Not screened for parasites; why not? _____
☐ Screened, no parasites found
☐ Screened, non-pathogenic parasites found
☐ Screened, pathogenic parasites found (*check all that apply*):
☐ Screened, BOTH pathogenic and non-pathogenic parasites found (*check all that apply*):

☐ Ascaris	☐ Hookworm
☐ Clonorchis	☐ Schistosoma
☐ Dientamoeba	☐ Strongyloides
☐ Entamoeba hystolica	☐ Trichuris
☐ Giardia	☐ Other:

CBC with differential done? ☐Yes ☐No If not done, why not?_____
If yes, was Eosinophilia present? ☐Yes ☐No If yes, was further evaluation done? ☐Yes ☐No

Serology Tests:

Schistosoma (Sub-Saharan Africans Only) ☐ Negative ☐ Positive ☐ Not done, why not?_____
Strongyloides ☐ Negative ☐ Positive ☐ Not done, why not?_____

Currently Pregnant: ☐Yes

Malaria Screening (Sub-Saharan Africans Only):

☐ Not screened for malaria; why not? _____
☐ Screened, no malaria species found in blood smears
☐ Screened, malaria species found (*please specify*): _____

Hemoglobin (m/dL):	Hematocrit (%):	Lead Screened? ☐ Yes ☐ No (6 months - 16 yrs.) BLL (µg /dl):	Height (in):	Weight (lbs):	BP-Systolic (mm Hg):	BP- Diastolic (mm Hg):

If any of the boxes are left blank (besides lead), please check the following box and provide a reason: ☐ Not done, why not?_____

1. Cholesterol ☐ Not Elevated ☐ Elevated ☐ Not done, why not?_____
2. UA ☐ Normal ☐ Abnormal ☐ Not on protocol ☐ Not done, why not?_____
3. B/CMP ☐ Done ☐ Not done, why not ?_____

Referrals (*check all that apply*)

☐ Primary Care
☐ Mental Health
☐ WIC
☐ GI
☐ Social Work
☐ Ear, Nose & Throat (ENT)
☐ Hematology
☐ Other Referral: _____
☐ Dental
☐ Hearing
☐ Dermatology
☐ OB/GYN
☐ Endocrinology
☐ Cardiology
☐ Ortho
☐ Disability (type): _____
☐ Vision
☐ Family Planning
☐ TB Program
☐ Pediatrics
☐ Urology
☐ Neurology
☐ Pulmonology
☐ Emergency /Urgent Care (reason): _____

Interpreter needed: ☐ Yes ☐ No If Yes, language needed: _____

Date screening completed (*mm/dd/yyyy*): _____ **Date submitted to DSHS** (*mm/dd/yyyy*): _____

Outcome (*if applicable*)

☐ Moved out of state: _____
☐ Moved out of county: _____
☐ Moved to unknown destination
☐ Unable to locate
☐ Missed appointment
☐ Screened elsewhere- no results
☐ Never arrived
☐ Died before screening
☐ Refused screening
☐ Hospitalized
☐ Vaccines Only

Appendix C. Distribution of spacing between doses of HBV vaccine among Cuban refugees and parolees undergoing part or all of the standard refugee medical assessment – Texas, January 2010 - December 2013 (N=1,416)

	Weeks	Improper spacing*	
Dose interval†	**Median (Range)**	**n (%)**	**Total**
Between 1st and 2nd dose	4.6 (0.1 - 2,066.1)	49 (6.4)	768
Between 2nd and 3rd dose	22.1 (1.4 - 593.3)	617 (84.1)	734
Between 1st and 3rd dose	27.1 (7.9 - 2073.1)	30 (4.1)	734

Abbreviations: HBV: hepatitis B virus

†Records with illogical date sequences were excluded from this descriptive analysis

*CDC recommends at least 4 weeks between the 1st and 2nd dose, and at least 8 weeks between the 2nd and 3rd dose (at least 16 weeks between the 1st and 3rd dose)

Appendix D. Characteristics modifying the effect of HBV vaccine history on demonstrated immunity to HBV among Cuban refugees and parolees undergoing part or all of the standard refugee medical assessment − Texas, January 2010 - December 2013[a]

Interaction		Prevalence ratio	(95% CI)	P-value
Age group and HBV vaccine history				
Age group	**HBV vaccine history[b]**			
<18	No history	1.00		
	Incomplete series	0.93	(0.68, 1.27)	0.6491
	Complete series	0.95	(0.77, 1.17)	0.6095
≥18	No history	1.00		
	Incomplete series	0.95	(0.55, 1.65)	0.8663
	Complete series	1.50	(1.24, 1.83)	<0.0001
Infectious disease[c] and HBV vaccine history				
Infectious disease	**HBV vaccine history[b]**			
Negative	No history	1.00		
	Incomplete series	0.93	(0.68, 1.27)	0.6491
	Complete series	0.95	(0.77, 1.17)	0.6095
Positive	No history	1.00		
	Incomplete series	0.88	(0.48, 1.62)	0.6813
	Complete series	0.51	(0.30, 0.85)	0.0094

Abbreviations: CI: confidence interval; HBV: hepatitis B virus; HCV: hepatitis C virus; HIV: human immunodeficiency virus; TB: tuberculosis; PR: prevalence ratio

[a]A PR of 1.00 without a confidence interval indicates the reference group. Significance was assessed at an alpha leve of 0.05.

[b]No history: 0 reported doses; incomplete: 1-2 reported doses; complete: ≥3 reported doses

[c]Includes individuals positive for at least one of the following conditions: HIV, syphilis, HCV, TB, or any pathogenic intestinal parasite

Appendix E. SAS Output for effect modification assessment in the main analysis

For all logistic regression models presented, the variables will be represented in the following ways:

Anti-HBs = ANTIHBS

Hepatitis B vaccination history =VACCHISTORY

Sex = SEX

Age category = AGECAT

Psychological disorder = PSYCH

Anemia = ANEMIA

Diabetes mellitus = DIABETES

Current or previous tobacco use = SMOKE

Infectious disease =INFDIS

Immigration status = REFTYPE

Assessing sex variable for effect modification

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \gamma(\text{SEX}) + \delta_1(\text{VACCHISTORY}_1*\text{SEX}) + \delta_2(\text{VACCHISTORY}_2*\text{SEX})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0, and

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0.

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN
Distribution	Binomial
Link Function	Log

Model Information	
Dependent Variable	antihbs2

Number of Observations Read	1416
Number of Observations Used	1416
Number of Events	534
Number of Trials	1416

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	534
2	0	882

PROC GENMOD is modeling the probability that antihbs2='1'.

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-921.9788	
Full Log Likelihood		-921.9788	
AIC (smaller is better)		1855.9576	
AICC (smaller is better)		1856.0172	
BIC (smaller is better)		1887.4911	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates							
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**
Intercept		1	-1.3633	0.1062	-1.5714	-1.1552	164.83
vacchistory	1	1	0.5011	0.2042	0.1009	0.9012	6.02
vacchistory	2	1	0.4771	0.1228	0.2366	0.7177	15.11
gender2		1	0.2287	0.1369	-0.0395	0.4970	2.79
gender2*vacchistory	1	1	-0.1228	0.2687	-0.6495	0.4039	0.21
gender2*vacchistory	2	1	-0.1535	0.1600	-0.4671	0.1602	0.92
Scale		0	1.0000	0.0000	1.0000	1.0000	

Analysis Of Maximum Likelihood Parameter Estimates		
Parameter		**Pr > ChiSq**
Intercept		<.0001
vacchistory	1	0.0141
vacchistory	2	0.0001
gender2		0.0947
gender2*vacchistory	1	0.6476
gender2*vacchistory	2	0.3375
Scale		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	17.80	0.0001
gender2	1	2.84	0.0918
gender2*vacchistory	2	0.93	0.6288

The overall p-value for the interaction term between hepatitis B vaccination history and sex is 0.6288, so sex is not considered to be an important effect modifier.

Assessing age category variable for effect modification

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \gamma(\text{AGECAT}) + \delta_1(\text{VACCHISTORY}_1*\text{AGECAT}) + \delta_2(\text{VACCHISTORY}_2*\text{AGECAT})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0, and VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0.

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1416
Number of Observations Used	1416
Number of Events	534
Number of Trials	1416

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	534
2	0	882

PROC GENMOD is modeling the probability that antihbs2='1'.

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-888.1970	
Full Log Likelihood		-888.1970	
AIC (smaller is better)		1788.3940	
AICC (smaller is better)		1788.4536	
BIC (smaller is better)		1819.9275	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-0.4855	0.0981	-0.6777	-0.2933	24.51	<.0001
vacchistory	1	1	-0.0253	0.1474	-0.3143	0.2636	0.03	0.8637
vacchistory	2	1	-0.1099	0.1127	-0.3309	0.1110	0.95	0.3296
agecat		1	-0.9177	0.1267	-1.1661	-0.6693	52.44	<.0001
agecat*vacchistory	1	1	-0.0378	0.3371	-0.6985	0.6230	0.01	0.9108
agecat*vacchistory	2	1	0.5102	0.1500	0.2163	0.8041	11.58	0.0007
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	1.13	0.5693
agecat	1	34.21	<.0001
agecat*vacchistory	2	12.25	0.0022

The overall p-value for the interaction term between hepatitis B vaccination history and age category is 0.0022, so age category is considered to be an important effect modifier.

Assessing psychological disorder variable for effect modification

Model:

logit P(ANTIHBS) = $\alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \gamma(\text{PSYCH}) + \delta_1(\text{VACCHISTORY}_1*\text{PSYCH}) + \delta_2(\text{VACCHISTORY}_2*\text{PSYCH})$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0, and VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0.

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1416
Number of Observations Used	1339
Number of Events	502
Number of Trials	1339
Missing Values	77

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	502
2	0	837

PROC GENMOD is modeling the probability that antihbs2='1'.

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-867.7577	
Full Log Likelihood		-867.7577	
AIC (smaller is better)		1745.5154	
AICC (smaller is better)		1745.5605	
BIC (smaller is better)		1771.5138	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates							
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**
Intercept		1	-1.2937	0.0747	-1.4401	-1.1472	299.79
vacchistory	1	1	0.4987	0.1365	0.2312	0.7663	13.35
vacchistory	2	1	0.4477	0.0855	0.2801	0.6153	27.41
psych		1	-19.9874	41793.27	-81933.3	81893.31	0.00
psych*vacchistory	1	0	0.0000	0.0000	0.0000	0.0000	.
psych*vacchistory	2	1	-0.4477	51186.68	-100325	100323.6	0.00
Scale		0	1.0000	0.0000	1.0000	1.0000	

Analysis Of Maximum Likelihood Parameter Estimates		
Parameter		**Pr > ChiSq**
Intercept		<.0001
vacchistory	1	0.0003
vacchistory	2	<.0001
psych		0.9996
psych*vacchistory	1	.
psych*vacchistory	2	1.0000
Scale		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	33.20	<.0001
psych	1	0.64	0.4236
psych*vacchistory	2	3.15	0.2067

The psychological disorder variable's data were too sparse to produce a p-value for both levels of hepatitis B vaccination history, so it was not included in the final model.

Assessing anemia variable for effect modification

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \gamma(\text{ANEMIA}) + \delta_1(\text{VACCHISTORY}_1*\text{ANEMIA}) + \delta_2(\text{VACCHISTORY}_2*\text{ANEMIA})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0, and VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0.

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1416
Number of Observations Used	1410
Number of Events	530
Number of Trials	1410
Missing Values	6

Class Level Information			
Class	Value	Design Variables	
vacchistory	0	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	antihbs2	Total Frequency
1	1	530
2	0	880

PROC GENMOD is modeling the probability that antihbs2='1'.

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Log Likelihood		-907.2755	
Full Log Likelihood		-907.2755	
AIC (smaller is better)		1826.5510	
AICC (smaller is better)		1826.6109	
BIC (smaller is better)		1858.0591	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates							
Parameter		DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square
Intercept		1	-1.2805	0.0740	-1.4255	-1.1355	299.74
vacchistory	1	1	0.2127	0.1879	-0.1556	0.5809	1.28
vacchistory	2	1	0.3635	0.0881	0.1909	0.5360	17.04
anemia		1	0.2997	0.1775	-0.0482	0.6476	2.85
anemia*vacchistory	1	1	0.3263	0.2849	-0.2321	0.8848	1.31
anemia*vacchistory	2	1	0.0843	0.1990	-0.3058	0.4744	0.18
Scale		0	1.0000	0.0000	1.0000	1.0000	

Analysis Of Maximum Likelihood Parameter Estimates		
Parameter		**Pr > ChiSq**
Intercept		<.0001
vacchistory	1	0.2577
vacchistory	2	<.0001
anemia		0.0914
anemia*vacchistory	1	0.2521
anemia*vacchistory	2	0.6721
Scale		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	18.26	0.0001
anemia	1	2.48	0.1155
anemia*vacchistory	2	1.37	0.5029

The overall p-value for the interaction term between hepatitis B vaccination history and anemia is 0.5029, so anemia is not considered to be an important effect modifier.

Assessing diabetes variable for effect modification

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \gamma(\text{DIABETES}) + \delta_1(\text{VACCHISTORY}_1*\text{DIABETES}) + \delta_2(\text{VACCHISTORY}_2*\text{DIABETES})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0, and

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0.

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1416
Number of Observations Used	1338
Number of Events	502
Number of Trials	1338
Missing Values	78

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	502
2	0	836

PROC GENMOD is modeling the probability that antihbs2='1'.

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-867.6256	
Full Log Likelihood		-867.6256	
AIC (smaller is better)		1745.2513	
AICC (smaller is better)		1745.2963	
BIC (smaller is better)		1771.2459	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates							
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**
Intercept		1	-1.2922	0.0753	-1.4397	-1.1446	294.65
vacchistory	1	1	0.4972	0.1368	0.2290	0.7654	13.20
vacchistory	2	1	0.4496	0.0860	0.2811	0.6182	27.33
DiabetisMellitus		1	-0.2119	0.6281	-1.4430	1.0192	0.11
DiabetisM*vacchistor	1	0	0.0000	0.0000	0.0000	0.0000	.
DiabetisM*vacchistor	2	1	-0.7373	1.1089	-2.9107	1.4360	0.44
Scale		0	1.0000	0.0000	1.0000	1.0000	

Analysis Of Maximum Likelihood Parameter Estimates		
Parameter		**Pr > ChiSq**
Intercept		<.0001
vacchistory	1	0.0003
vacchistory	2	<.0001
DiabetisMellitus		0.7358
DiabetisM*vacchistor	1	.
DiabetisM*vacchistor	2	0.5061
Scale		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	33.10	<.0001
DiabetisMellitus	1	0.13	0.7210
DiabetisM*vacchistor	2	382.68	<.0001

The diabetes variable's data were too sparse to produce a p-value for both levels of hepatitis B vaccination history, so it was not included in the final model.

Assessing tobacco use variable for effect modification

Model:

logit P(ANTIHBS) = $\alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \gamma(\text{SMOKE}) + \delta_1(\text{VACCHISTORY}_1*\text{SMOKE}) + \delta_2(\text{VACCHISTORY}_2*\text{SMOKE})$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0, and VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0.

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1416
Number of Observations Used	84
Number of Events	24
Number of Trials	84
Missing Values	1332

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	24
2	0	60

PROC GENMOD is modeling the probability that antihbs2='1'.

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-52.3549	
Full Log Likelihood		-52.3549	
AIC (smaller is better)		114.7098	
AICC (smaller is better)		115.4790	
BIC (smaller is better)		126.8639	

WARNING: Negative of Hessian not positive definite.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.0399	0.3139	-1.6552	-0.4247	10.97	0.0009
vacchistory	1	0	0.7746	0.0000	0.7746	0.7746	.	.
vacchistory	2	1	0.5920	0.3733	-0.1396	1.3237	2.52	0.1127
smoke		1	0.2653	0.3749	-0.4695	1.0002	0.50	0.4791
smoke*vacchistory	1	0	0.0000	0.0000	0.0000	0.0000	.	.
smoke*vacchistory	2	1	-0.6606	0.4564	-1.5552	0.2339	2.09	0.1478
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

The current or previous use of tobacco variable's data were too sparse to produce a p-value for both levels of hepatitis B vaccination history, so it was not included in the final model.

Assessing infectious disease variable for effect modification

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \gamma(\text{INFDIS}) + \delta_1(\text{VACCHISTORY}_1*\text{INFDIS}) + \delta_2(\text{VACCHISTORY}_2*\text{INFDIS})$$

Where $VACCHISTORY_1$=1 if incomplete hepatitis B vaccination history; else=0, and $VACCHISTORY_2$=1 if complete hepatitis B vaccination history; else=0.

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1416
Number of Observations Used	1416
Number of Events	534
Number of Trials	1416

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	534
2	0	882

PROC GENMOD is modeling the probability that antihbs2='1'.

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-919.6975	
Full Log Likelihood		-919.6975	
AIC (smaller is better)		1851.3950	

AICC (smaller is better)		1851.4546	
BIC (smaller is better)		1882.9285	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.2642	0.0724	-1.4060	-1.1223	305.14	<.0001
vacchistory	1	1	0.4207	0.1437	0.1392	0.7023	8.58	0.0034
vacchistory	2	1	0.4566	0.0841	0.2917	0.6215	29.45	<.0001
infdis		1	0.2345	0.1933	-0.1444	0.6135	1.47	0.2251
infdis*vacchistory	1	1	0.1389	0.3575	-0.5617	0.8395	0.15	0.6976
infdis*vacchistory	2	1	-0.5640	0.2433	-1.0409	-0.0871	5.37	0.0204
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	33.53	<.0001
infdis	1	1.31	0.2521
infdis*vacchistory	2	6.87	0.0322

The overall p-value for the interaction term between hepatitis B vaccination history and infectious disease is 0.0322, so infectious disease is considered to be an important effect modifier.

Assessing immigration status variable for effect modification

Model:

$$\text{logit P(ANTIHBS)} = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \gamma(\text{REFTYPE}) + \delta_1(\text{VACCHISTORY}_1\text{*REFTYPE}) + \delta_2(\text{VACCHISTORY}_2\text{*REFTYPE})$$

Where $VACCHISTORY_1$=1 if incomplete hepatitis B vaccination history; else=0, and $VACCHISTORY_2$=1 if complete hepatitis B vaccination history; else=0.

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1416
Number of Observations Used	1416
Number of Events	534
Number of Trials	1416

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	534
2	0	882

PROC GENMOD is modeling the probability that antihbs2='1'.

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-916.0463	
Full Log Likelihood		-916.0463	
AIC (smaller is better)		1844.0925	
AICC (smaller is better)		1844.1521	

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
BIC (smaller is better)		1875.6261	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates							
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**
Intercept		1	-1.3619	0.0947	-1.5474	-1.1764	206.97
vacchistory	1	1	0.4562	0.2008	0.0627	0.8497	5.16
vacchistory	2	1	0.3679	0.1159	0.1407	0.5950	10.08
reftype		1	0.2861	0.1337	0.0241	0.5481	4.58
reftype*vacchistory	1	1	-0.0950	0.2673	-0.6188	0.4288	0.13
reftype*vacchistory	2	1	-0.0156	0.1581	-0.3255	0.2942	0.01
Scale		0	1.0000	0.0000	1.0000	1.0000	

Analysis Of Maximum Likelihood Parameter Estimates		
Parameter		**Pr > ChiSq**
Intercept		<.0001
vacchistory	1	0.0231
vacchistory	2	0.0015
reftype		0.0323
reftype*vacchistory	1	0.7222
reftype*vacchistory	2	0.9212
Scale		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	12.04	0.0024
reftype	1	4.50	0.0338
reftype*vacchistory	2	0.13	0.9377

The overall p-value for the interaction term between hepatitis B vaccination history and immigration status is 0.9377, so immigration status is not considered to be an important effect modifier.

Appendix F. SAS output for confounding assessment for the interaction model in the main analysis

For all logistic regression models presented, the variables will be represented in the following ways:

Anti-HBs = ANTIHBS

Hepatitis B vaccination history =VACCHISTORY

Sex = SEX

Age category = AGECAT

Anemia = ANEMIA

Infectious disease =INFDIS

Immigration status = REFTYPE

Full Interaction Model

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \beta_3(\text{SEX}) + \beta_4(\text{AGECAT}) + \beta_5(\text{ANEMIA}) + \beta_6(\text{REFTYPE}) + \gamma(\text{INFDIS}) + \delta_1(\text{VACCHISTORY}_1*\text{AGECAT}) + \delta_2(\text{VACCHISTORY}_2*\text{AGECAT}) + \delta_3(\text{VACCHISTORY}_1*\text{INFDIS}) + \delta_4(\text{VACCHISTORY}_2*\text{INFDIS})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0, and

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0.

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1416
Number of Observations Used	1410
Number of Events	530
Number of Trials	1410
Missing Values	6

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	530
2	0	880

PROC GENMOD is modeling the probability that antihbs2='1'.

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-868.3521	
Full Log Likelihood		-868.3521	
AIC (smaller is better)		1760.7042	
AICC (smaller is better)		1760.9275	

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
BIC (smaller is better)		1823.7203	

WARNING: The relative Hessian convergence criterion of 0.0024533617 is greater than the limit of 0.0001. The convergence is questionable.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-0.7934	0.1231	-1.0348	-0.5520	41.51	<.0001
vacchistory	1	1	-0.0718	0.1578	-0.3811	0.2375	0.21	0.6491
vacchistory	2	1	-0.0553	0.1082	-0.2674	0.1568	0.26	0.6095
gender2		1	0.1587	0.0674	0.0265	0.2909	5.54	0.0186
agecat		1	-0.7623	0.1296	-1.0163	-0.5083	34.60	<.0001
anemia		1	0.2491	0.0822	0.0879	0.4102	9.18	0.0025
infdis		1	0.3363	0.1997	-0.0552	0.7278	2.83	0.0922
reftype		1	0.2080	0.0643	0.0820	0.3341	10.47	0.0012
agecat*vacchistory	1	1	0.0246	0.3169	-0.5965	0.6458	0.01	0.9380
agecat*vacchistory	2	1	0.4633	0.1453	0.1786	0.7481	10.17	0.0014
infdis*vacchistory	1	1	-0.0561	0.3177	-0.6788	0.5665	0.03	0.8598
infdis*vacchistory	2	1	-0.6247	0.2434	-1.1017	-0.1477	6.59	0.0103
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	0.00	1.0000
gender2	1	7.37	0.0066
agecat	1	27.26	<.0001
anemia	1	9.85	0.0017
infdis	1	2.40	0.1213
reftype	1	11.18	0.0008

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
agecat*vacchistory	2	11.44	0.0033
infdis*vacchistory	2	8.25	0.0162

All variables with a p-value less than 0.05 were considered to be statistically significant independent predictors of anti-HBs and were kept in the final model. The infectious disease variable was kept in order to maintain a hierarchically well-formulated model. Thus, no variables were dropped from the full model.

Appendix G. Collinearity assessment of the interaction model for the main analysis

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1416
Number of Observations Used	1410
Number of Events	530
Number of Trials	1410
Missing Values	6

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	530
2	0	880

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information		
Parameter	**Effect**	**vacchistory**
Prm1	Intercept	
Prm2	vacchistory	1
Prm3	vacchistory	2

Parameter Information		
Parameter	**Effect**	**vacchistory**
Prm4	gender2	
Prm5	agecat	
Prm6	anemia	
Prm7	infdis	
Prm8	reftype	
Prm9	agecat*vacchistory	1
Prm10	agecat*vacchistory	2
Prm11	infdis*vacchistory	1
Prm12	infdis*vacchistory	2

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-868.3521	
Full Log Likelihood		-868.3521	
AIC (smaller is better)		1760.7042	
AICC (smaller is better)		1760.9275	
BIC (smaller is better)		1823.7203	

WARNING: The relative Hessian convergence criterion of 0.0024533617 is greater than the limit of 0.0001. The convergence is questionable.

Estimated Covariance Matrix						
	Prm1	**Prm2**	**Prm3**	**Prm4**	**Prm5**	**Prm6**
Prm1	0.01516	-0.009910	-0.009635	-0.003250	-0.01134	-0.005299
Prm2	-0.009910	0.02490	0.008883	-0.000075	0.009516	0.001908
Prm3	-0.009635	0.008883	0.01171	0.0003725	0.009238	0.001707
Prm4	-0.003250	-0.000075	0.0003725	0.004549	0.0004446	0.002148
Prm5	-0.01134	0.009516	0.009238	0.0004446	0.01679	0.003331
Prm6	-0.005299	0.001908	0.001707	0.002148	0.003331	0.006761
Prm7	-0.000328	-0.000058	-0.000123	0.0000150	-0.006565	-0.000453
Prm8	-0.002555	0.0004232	-0.000066	-0.000340	0.0007703	-0.000270
Prm9	0.009973	-0.02348	-0.008965	0.0005723	-0.01626	-0.002136

Estimated Covariance Matrix						
	Prm1	**Prm2**	**Prm3**	**Prm4**	**Prm5**	**Prm6**
Prm10	0.009629	-0.008829	-0.01151	-0.000330	-0.01566	-0.001437
Prm11	0.0008476	-0.01440	0.0005132	-0.000749	0.007075	0.001783
Prm12	0.0003281	-0.000014	-0.001175	0.0002023	0.006475	0.0003681

Estimated Covariance Matrix						
	Prm7	**Prm8**	**Prm9**	**Prm10**	**Prm11**	**Prm12**
Prm1	-0.000328	-0.002555	0.009973	0.009629	0.0008476	0.0003281
Prm2	-0.000058	0.0004232	-0.02348	-0.008829	-0.01440	-0.000014
Prm3	-0.000123	-0.000066	-0.008965	-0.01151	0.0005132	-0.001175
Prm4	0.0000150	-0.000340	0.0005723	-0.000330	-0.000749	0.0002023
Prm5	-0.006565	0.0007703	-0.01626	-0.01566	0.007075	0.006475
Prm6	-0.000453	-0.000270	-0.002136	-0.001437	0.001783	0.0003681
Prm7	0.03989	0.0008942	0.006564	0.006548	-0.04037	-0.03989
Prm8	0.0008942	0.004136	-0.000616	-0.000211	-0.002437	-0.000952
Prm9	0.006564	-0.000616	0.10044	0.01541	0.001395	-0.006451
Prm10	0.006548	-0.000211	0.01541	0.02111	-0.006770	-0.007233
Prm11	-0.04037	-0.002437	0.001395	-0.006770	0.10092	0.04029
Prm12	-0.03989	-0.000952	-0.006451	-0.007233	0.04029	0.05922

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-0.7934	0.1231	-1.0348	-0.5520	41.51	<.0001
vacchistory	1	1	-0.0718	0.1578	-0.3811	0.2375	0.21	0.6491
vacchistory	2	1	-0.0553	0.1082	-0.2674	0.1568	0.26	0.6095
gender2		1	0.1587	0.0674	0.0265	0.2909	5.54	0.0186
agecat		1	-0.7623	0.1296	-1.0163	-0.5083	34.60	<.0001
anemia		1	0.2491	0.0822	0.0879	0.4102	9.18	0.0025
infdis		1	0.3363	0.1997	-0.0552	0.7278	2.83	0.0922
reftype		1	0.2080	0.0643	0.0820	0.3341	10.47	0.0012
agecat*vacchistory	1	1	0.0246	0.3169	-0.5965	0.6458	0.01	0.9380

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
agecat*vacchistory	2	1	0.4633	0.1453	0.1786	0.7481	10.17	0.0014
infdis*vacchistory	1	1	-0.0561	0.3177	-0.6788	0.5665	0.03	0.8598
infdis*vacchistory	2	1	-0.6247	0.2434	-1.1017	-0.1477	6.59	0.0103
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

Obs	_NAME_	RowName	Prm1	Prm2	Prm3	Prm4
1	ESTIMATE		.	.	.	.
2	Intercep	Prm1	0.0151648	-0.00991	-0.009635	-0.00325
3	vacchist	Prm2	-0.00991	0.0249014	0.008883	-0.000075
4	vacchist	Prm3	-0.009635	0.008883	0.0117149	0.0003725
5	gender2	Prm4	-0.00325	-0.000075	0.0003725	0.0045493
6	agecat	Prm5	-0.011337	0.009516	0.0092383	0.0004446
7	anemia	Prm6	-0.005299	0.0019084	0.001707	0.002148
8	infdis	Prm7	-0.000328	-0.000058	-0.000123	0.000015
9	reftype	Prm8	-0.002555	0.0004232	-0.000066	-0.00034
10	agecat*v	Prm9	0.0099725	-0.023483	-0.008965	0.0005723
11	agecat*v	Prm10	0.0096291	-0.008829	-0.011515	-0.00033
12	infdis*v	Prm11	0.0008476	-0.014396	0.0005132	-0.000749
13	infdis*v	Prm12	0.0003281	-0.000014	-0.001175	0.0002023

Obs	Prm5	Prm6	Prm7	Prm8	Prm9	Prm10
1	.	.	.	.	.	.
2	-0.011337	-0.005299	-0.000328	-0.002555	0.0099725	0.0096291
3	0.009516	0.0019084	-0.000058	0.0004232	-0.023483	-0.008829
4	0.0092383	0.001707	-0.000123	-0.000066	-0.008965	-0.011515
5	0.0004446	0.002148	0.000015	-0.00034	0.0005723	-0.00033
6	0.0167946	0.0033307	-0.006565	0.0007703	-0.016256	-0.015658
7	0.0033307	0.0067605	-0.000453	-0.00027	-0.002136	-0.001437

Obs	Prm5	Prm6	Prm7	Prm8	Prm9	Prm10
8	-0.006565	-0.000453	0.0398944	0.0008942	0.0065638	0.0065482
9	0.0007703	-0.00027	0.0008942	0.0041358	-0.000616	-0.000211
10	-0.016256	-0.002136	0.0065638	-0.000616	0.1004444	0.0154091
11	-0.015658	-0.001437	0.0065482	-0.000211	0.0154091	0.0211084
12	0.007075	0.0017834	-0.040369	-0.002437	0.0013948	-0.00677
13	0.0064748	0.0003681	-0.039888	-0.000952	-0.006451	-0.007233

Obs	Prm11	Prm12	Parameter	vacchistory
1	.	.		
2	0.0008476	0.0003281	Prm1	
3	-0.014396	-0.000014	Prm2	1
4	0.0005132	-0.001175	Prm3	2
5	-0.000749	0.0002023	Prm4	
6	0.007075	0.0064748	Prm5	
7	0.0017834	0.0003681	Prm6	
8	-0.040369	-0.039888	Prm7	
9	-0.002437	-0.000952	Prm8	
10	0.0013948	-0.006451	Prm9	1
11	-0.00677	-0.007233	Prm10	2
12	0.1009199	0.0402905	Prm11	1
13	0.0402905	0.0592231	Prm12	2

Obs	_NAME_	RowName	Prm1	Prm2	Prm3	Prm4
1	ESTIMATE		.	.	.	.
2	Intercep	Prm1	0.0151648	-0.00991	-0.009635	-0.00325
3	vacchist	Prm2	-0.00991	0.0249014	0.008883	-0.000075
4	vacchist	Prm3	-0.009635	0.008883	0.0117149	0.0003725
5	gender2	Prm4	-0.00325	-0.000075	0.0003725	0.0045493
6	agecat	Prm5	-0.011337	0.009516	0.0092383	0.0004446
7	anemia	Prm6	-0.005299	0.0019084	0.001707	0.002148
8	infdis	Prm7	-0.000328	-0.000058	-0.000123	0.000015
9	reftype	Prm8	-0.002555	0.0004232	-0.000066	-0.00034

Obs	_NAME_	RowName	Prm1	Prm2	Prm3	Prm4
10	agecat*v	Prm9	0.0099725	-0.023483	-0.008965	0.0005723
11	agecat*v	Prm10	0.0096291	-0.008829	-0.011515	-0.00033
12	infdis*v	Prm11	0.0008476	-0.014396	0.0005132	-0.000749
13	infdis*v	Prm12	0.0003281	-0.000014	-0.001175	0.0002023

Obs	Prm5	Prm6	Prm7	Prm8	Prm9	Prm10
1	.	.	.	.	.	.
2	-0.011337	-0.005299	-0.000328	-0.002555	0.0099725	0.0096291
3	0.009516	0.0019084	-0.000058	0.0004232	-0.023483	-0.008829
4	0.0092383	0.001707	-0.000123	-0.000066	-0.008965	-0.011515
5	0.0004446	0.002148	0.000015	-0.00034	0.0005723	-0.00033
6	0.0167946	0.0033307	-0.006565	0.0007703	-0.016256	-0.015658
7	0.0033307	0.0067605	-0.000453	-0.00027	-0.002136	-0.001437
8	-0.006565	-0.000453	0.0398944	0.0008942	0.0065638	0.0065482
9	0.0007703	-0.00027	0.0008942	0.0041358	-0.000616	-0.000211
10	-0.016256	-0.002136	0.0065638	-0.000616	0.1004444	0.0154091
11	-0.015658	-0.001437	0.0065482	-0.000211	0.0154091	0.0211084
12	0.007075	0.0017834	-0.040369	-0.002437	0.0013948	-0.00677
13	0.0064748	0.0003681	-0.039888	-0.000952	-0.006451	-0.007233

Obs	Prm11	Prm12	Parameter	vacchistory
1	.	.		
2	0.0008476	0.0003281	Prm1	
3	-0.014396	-0.000014	Prm2	1
4	0.0005132	-0.001175	Prm3	2
5	-0.000749	0.0002023	Prm4	
6	0.007075	0.0064748	Prm5	
7	0.0017834	0.0003681	Prm6	
8	-0.040369	-0.039888	Prm7	
9	-0.002437	-0.000952	Prm8	
10	0.0013948	-0.006451	Prm9	1
11	-0.00677	-0.007233	Prm10	2

Obs	Prm11	Prm12	Parameter	vacchistory
12	0.1009199	0.0402905	Prm11	1
13	0.0402905	0.0592231	Prm12	2

VARCOV2						
	COL1	COL2	COL3	COL4	COL5	COL6
ROW1	0.0151648	-0.00991	-0.009635	-0.00325	-0.011337	-0.005299
ROW2	-0.00991	0.0249014	0.008883	-0.000075	0.009516	0.0019084
ROW3	-0.009635	0.008883	0.0117149	0.0003725	0.0092383	0.001707
ROW4	-0.00325	-0.000075	0.0003725	0.0045493	0.0004446	0.002148
ROW5	-0.011337	0.009516	0.0092383	0.0004446	0.0167946	0.0033307
ROW6	-0.005299	0.0019084	0.001707	0.002148	0.0033307	0.0067605
ROW7	-0.000328	-0.000058	-0.000123	0.000015	-0.006565	-0.000453
ROW8	-0.002555	0.0004232	-0.000066	-0.00034	0.0007703	-0.00027
ROW9	0.0099725	-0.023483	-0.008965	0.0005723	-0.016256	-0.002136
ROW10	0.0096291	-0.008829	-0.011515	-0.00033	-0.015658	-0.001437
ROW11	0.0008476	-0.014396	0.0005132	-0.000749	0.007075	0.0017834
ROW12	0.0003281	-0.000014	-0.001175	0.0002023	0.0064748	0.0003681

VARCOV2						
	COL7	COL8	COL9	COL10	COL11	COL12
ROW1	-0.000328	-0.002555	0.0099725	0.0096291	0.0008476	0.0003281
ROW2	-0.000058	0.0004232	-0.023483	-0.008829	-0.014396	-0.000014
ROW3	-0.000123	-0.000066	-0.008965	-0.011515	0.0005132	-0.001175
ROW4	0.000015	-0.00034	0.0005723	-0.00033	-0.000749	0.0002023
ROW5	-0.006565	0.0007703	-0.016256	-0.015658	0.007075	0.0064748
ROW6	-0.000453	-0.00027	-0.002136	-0.001437	0.0017834	0.0003681
ROW7	0.0398944	0.0008942	0.0065638	0.0065482	-0.040369	-0.039888
ROW8	0.0008942	0.0041358	-0.000616	-0.000211	-0.002437	-0.000952
ROW9	0.0065638	-0.000616	0.1004444	0.0154091	0.0013948	-0.006451
ROW10	0.0065482	-0.000211	0.0154091	0.0211084	-0.00677	-0.007233
ROW11	-0.040369	-0.002437	0.0013948	-0.00677	0.1009199	0.0402905
ROW12	-0.039888	-0.000952	-0.006451	-0.007233	0.0402905	0.0592231

Input DATASET covdsn, Submitted 31MAR2014
COLLINEARITY DIAGNOSTICS FOR NONLINEAR MODELS USING THE INFORMATION MATRIX: EIGENVALUES, CONDITION INDEXES, AND VARIANCE DECOMPOSITION PROPORTIONS (VDP'S)

VARIABLE	VDP1	VDP2	VDP3	VDP4	VDP5	VDP6	VDP7
EIGENVAL	0.0305	0.10551	0.17073	0.30701	0.39148	0.43047	0.57183
CONDINDX	12.2991	6.61360	5.19903	3.87713	3.43345	3.27424	2.84087
	.	.	.	.	.	.	.
Intercep	0.8517	0.06778	0.07237	0.00062	0.00264	0.00009	0.00052
vacchist	0.3267	0.01281	0.03026	0.00666	0.03183	0.49245	0.00247
vacchist	0.7278	0.00246	0.10173	0.04343	0.10961	0.00617	0.00019
gender2	0.0560	0.05599	0.32034	0.23630	0.06592	0.00128	0.22551
agecat	0.7852	0.07184	0.01179	0.01702	0.08000	0.00075	0.01264
anemia	0.1740	0.02912	0.22299	0.07920	0.08105	0.00841	0.14802
infdis	0.0148	0.75041	0.12722	0.00000	0.03353	0.00733	0.00062
reftype	0.0344	0.05984	0.07347	0.68056	0.02535	0.05334	0.03389
agecat*v	0.1316	0.01439	0.02014	0.02220	0.01243	0.26231	0.00007
agecat*v	0.6381	0.11651	0.13083	0.00002	0.02392	0.01810	0.04406
infdis*v	0.0043	0.44517	0.08312	0.01608	0.01287	0.14016	0.10787
infdis*v	0.0091	0.65640	0.14428	0.00053	0.02506	0.01973	0.01947

VARIABLE	VDP8	VDP9	VDP10	VDP11	VDP12
EIGENVAL	0.94430	1.13438	1.48217	1.81667	4.61495
CONDINDX	2.21070	2.01699	1.76455	1.59384	1.00000
	.	.	.	.	.
Intercep	0.00000	0.00084	0.00087	0.00004	0.00251
vacchist	0.00014	0.00226	0.02672	0.06598	0.00169
vacchist	0.00004	0.00075	0.00000	0.00383	0.00403
gender2	0.01997	0.00442	0.00395	0.00000	0.01027
agecat	0.00030	0.01535	0.00001	0.00199	0.00314
anemia	0.03435	0.20715	0.01113	0.00000	0.00457
infdis	0.00008	0.00032	0.04481	0.01846	0.00238

VARIABLE	VDP8	VDP9	VDP10	VDP11	VDP12
reftype	0.00175	0.01912	0.00742	0.00002	0.01086
agecat*v	0.38849	0.07335	0.04227	0.03209	0.00069
agecat*v	0.00055	0.01775	0.00091	0.00585	0.00343
infdis*v	0.11387	0.00132	0.00005	0.07419	0.00101
infdis*v	0.03467	0.00249	0.08363	0.00244	0.00218

Input DATASET covdsn, Submitted 31MAR2014
COLLINEARITY DIAGNOSTICS FOR NONLINEAR MODELS USING THE INFORMATION MATRIX: EIGENVALUES, CONDITION INDEXES, AND VARIANCE DECOMPOSITION PROPORTIONS (VDP'S)

Directory	
Libref	WORK
Engine	V9
Physical Name	F:\SAS Temporary Files_TD13656_VDS3-CTX-SAS01_
Filename	F:\SAS Temporary Files_TD13656_VDS3-CTX-SAS01_

#	Name	Member Type	File Size	Last Modified
1	ALIEN	DATA	12698624	31Mar14:10:46:17
2	COMBINED	DATA	9536512	31Mar14:10:46:17
3	COMBINED2	DATA	8471552	31Mar14:10:46:18
4	COMBINED_CLEAN	DATA	7750656	31Mar14:10:46:18
5	COMBINED_CLEAN_ADULTS	DATA	5669888	31Mar14:10:46:18
6	COVDSN	DATA	13312	31Mar14:16:50:35
7	FORMATS	CATALOG	17408	31Mar14:10:46:18
8	NEXT_1	DATA	5120	31Mar14:16:50:35
9	NEXT_1A	DATA	13312	31Mar14:16:50:35
10	NEXT_2	DATA	13312	31Mar14:16:50:35
11	NEXT_3	DATA	13312	31Mar14:16:50:36
12	NEXT_4	DATA	5120	31Mar14:16:50:36
13	NEXT_5	DATA	13312	31Mar14:16:50:36
14	PARMS	DATA	5120	31Mar14:16:50:35

#	Name	Member Type	File Size	Last Modified
15	RRMODEL	DATA	13312	31Mar14:16:50:36
16	SASMACR	CATALOG	5120	31Mar14:10:44:31
17	VACC	DATA	443392	31Mar14:10:46:17

Appendix H. SAS output of effect estimates from the interaction model in the main analysis

For the logistic regression model presented, the variables are represented in the following ways:

Anti-HBs = ANTIHBS

Hepatitis B vaccination history =VACCHISTORY

Sex = SEX

Age category = AGECAT

Anemia = ANEMIA

Infectious disease =INFDIS

Immigration status = REFTYPE

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \beta_3(\text{SEX}) + \beta_4(\text{AGECAT}) + \beta_5(\text{ANEMIA}) + \beta_6(\text{REFTYPE}) + \gamma(\text{INFDIS}) + \delta_1(\text{VACCHISTORY}_1*\text{AGECAT}) + \delta_2(\text{VACCHISTORY}_2*\text{AGECAT}) + \delta_3(\text{VACCHISTORY}_1*\text{INFDIS}) + \delta_4(\text{VACCHISTORY}_2*\text{INFDIS})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0, and VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0.

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN
Distribution	Binomial

Model Information	
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1416
Number of Observations Used	1410
Number of Events	530
Number of Trials	1410
Missing Values	6

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	530
2	0	880

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information		
Parameter	**Effect**	**vacchistory**
Prm1	Intercept	
Prm2	vacchistory	1
Prm3	vacchistory	2
Prm4	gender2	
Prm5	agecat	
Prm6	anemia	
Prm7	infdis	
Prm8	reftype	

Parameter Information		
Parameter	**Effect**	**vacchistory**
Prm9	agecat*vacchistory	1
Prm10	agecat*vacchistory	2
Prm11	infdis*vacchistory	1
Prm12	infdis*vacchistory	2

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-868.3521	
Full Log Likelihood		-868.3521	
AIC (smaller is better)		1760.7042	
AICC (smaller is better)		1760.9275	
BIC (smaller is better)		1823.7203	

WARNING: The relative Hessian convergence criterion of 0.0024533617 is greater than the limit of 0.0001. The convergence is questionable.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-0.7934	0.1231	-1.0348	-0.5520	41.51	<.0001
vacchistory	1	1	-0.0718	0.1578	-0.3811	0.2375	0.21	0.6491
vacchistory	2	1	-0.0553	0.1082	-0.2674	0.1568	0.26	0.6095
gender2		1	0.1587	0.0674	0.0265	0.2909	5.54	0.0186
agecat		1	-0.7623	0.1296	-1.0163	-0.5083	34.60	<.0001
anemia		1	0.2491	0.0822	0.0879	0.4102	9.18	0.0025
infdis		1	0.3363	0.1997	-0.0552	0.7278	2.83	0.0922
reftype		1	0.2080	0.0643	0.0820	0.3341	10.47	0.0012
agecat*vacchistory	1	1	0.0246	0.3169	-0.5965	0.6458	0.01	0.9380
agecat*vacchistory	2	1	0.4633	0.1453	0.1786	0.7481	10.17	0.0014
infdis*vacchistory	1	1	-0.0561	0.3177	-0.6788	0.5665	0.03	0.8598
infdis*vacchistory	2	1	-0.6247	0.2434	-1.1017	-0.1477	6.59	0.0103

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	0.00	1.0000
gender2	1	7.37	0.0066
agecat	1	27.26	<.0001
anemia	1	9.85	0.0017
infdis	1	2.40	0.1213
reftype	1	11.18	0.0008
agecat*vacchistory	2	11.44	0.0033
infdis*vacchistory	2	8.25	0.0162

Contrast Estimate Results								
		Mean					**L'Beta**	
Label	**Mean Estimate**	**Confidence Limits**		**L'Beta Estimate**	**Standard Error**	**Alpha**	**Confidence Limits**	
Effect of reftype=1 (parolee)	1.2313	1.0855	1.3967	0.2080	0.0643	0.05	0.0820	0.3341
Effect of gender2=1 (female)	1.1720	1.0269	1.3377	0.1587	0.0674	0.05	0.0265	0.2909
Effect of anemia=1 (pos)	1.2828	1.0919	1.5071	0.2491	0.0822	0.05	0.0879	0.4102
Effect of incomplete vacc hx among <18	0.9307	0.6831	1.2681	-0.0718	0.1578	0.05	-0.3811	0.2375
Effect of complete vacc hx among <18	0.9462	0.7653	1.1698	-0.0553	0.1082	0.05	-0.2674	0.1568
Effect of incomplete vacc hx among >17	0.9539	0.5511	1.6513	-0.0471	0.2800	0.05	-0.5959	0.5016
Effect of complete vacc hx among >17	1.5038	1.2387	1.8258	0.4080	0.0990	0.05	0.2141	0.6020

Contrast Estimate Results								
		Mean					L'Beta	
Label	Mean Estimate	Confidence Limits		L'Beta Estimate	Standard Error	Alpha	Confidence Limits	
Effect of incomplete vacc hx among ID-	0.9307	0.6831	1.2681	-0.0718	0.1578	0.05	-0.3811	0.2375
Effect of complete vacc hx among ID-	0.9462	0.7653	1.1698	-0.0553	0.1082	0.05	-0.2674	0.1568
Effect of incomplete vacc hx among ID+	0.8799	0.4779	1.6203	-0.1279	0.3115	0.05	-0.7384	0.4826
Effect of complete vacc hx among ID+	0.5066	0.3032	0.8465	-0.6800	0.2619	0.05	-1.1933	-0.1667

Contrast Estimate Results		
Label	Chi-Square	Pr > ChiSq
Effect of reftype=1 (parolee)	10.47	0.0012
Effect of gender2=1 (female)	5.54	0.0186
Effect of anemia=1 (pos)	9.18	0.0025
Effect of incomplete vacc hx among <18	0.21	0.6491
Effect of complete vacc hx among <18	0.26	0.6095
Effect of incomplete vacc hx among >17	0.03	0.8663
Effect of complete vacc hx among >17	17.00	<.0001
Effect of incomplete vacc hx among ID-	0.21	0.6491
Effect of complete vacc hx among ID-	0.26	0.6095
Effect of incomplete vacc hx among ID+	0.17	0.6813
Effect of complete vacc hx among ID+	6.74	0.0094

Appendix I. SAS output for confounding assessment for the no-interaction model in the main analysis

For all logistic regression models presented, the variables will be represented in the following ways:

Anti-HBs = ANTIHBS

Hepatitis B vaccination history =VACCHISTORY

Sex = SEX

Age category = AGECAT

Anemia = ANEMIA

Infectious disease =INFDIS

Immigration status = REFTYPE

Full, No-Interaction Model

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \beta_3(\text{SEX}) + \beta_4(\text{AGECAT}) + \beta_5(\text{ANEMIA}) + \beta_6(\text{REFTYPE}) + \gamma(\text{INFDIS})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0, and

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0.

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1416
Number of Observations Used	1410
Number of Events	530
Number of Trials	1410
Missing Values	6

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	530
2	0	880

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information		
Parameter	**Effect**	**vacchistory**
Prm1	Intercept	
Prm2	vacchistory	1
Prm3	vacchistory	2
Prm4	gender2	
Prm5	agecat	
Prm6	anemia	
Prm7	infdis	
Prm8	reftype	

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-878.0392	

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Full Log Likelihood		-878.0392	
AIC (smaller is better)		1772.0785	
AICC (smaller is better)		1772.1813	
BIC (smaller is better)		1814.0892	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.0686	0.1136	-1.2911	-0.8460	88.53	<.0001
vacchistory	1	1	0.1377	0.1354	-0.1277	0.4031	1.03	0.3092
vacchistory	2	1	0.2193	0.0822	0.0582	0.3804	7.12	0.0076
gender2		1	0.1933	0.0723	0.0516	0.3349	7.15	0.0075
agecat		1	-0.4514	0.0737	-0.5959	-0.3070	37.51	<.0001
anemia		1	0.2918	0.0845	0.1261	0.4574	11.92	0.0006
infdis		1	-0.0974	0.1053	-0.3038	0.1090	0.85	0.3552
reftype		1	0.2095	0.0660	0.0800	0.3389	10.06	0.0015
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	7.66	0.0217
gender2	1	7.18	0.0074
agecat	1	36.52	<.0001
anemia	1	10.85	0.0010
infdis	1	0.92	0.3383
reftype	1	10.36	0.0013

Contrast Estimate Results								
		Mean					L'Beta	
Label	Mean Estimate	Confidence Limits		L'Beta Estimate	Standard Error	Alpha	Confidence Limits	
VACCHISTORY=1	1.1476	0.8801	1.4964	0.1377	0.1354	0.05	-0.1277	0.4031
VACCHISTORY=2	1.2452	1.0599	1.4629	0.2193	0.0822	0.05	0.0582	0.3804

Contrast Estimate Results		
Label	Chi-Square	Pr > ChiSq
VACCHISTORY=1	1.03	0.3092
VACCHISTORY=2	7.12	0.0076

The p-values associated with each potential confounder or independent predictor demonstrated that all variables except that which measured presence of infectious disease were statistically significant independent predictors of anti-HBs ($P < 0.05$). The reduced model will drop the infectious disease variable from the model to assess whether the effect estimates for the main exposure variable, vaccine history, change by more than 10% in either direction.

The full model produced a prevalence ratio of 1.15 (95% CI: 0.88, 1.50; $P = 0.3092$) for the prevalence of anti-HBs among those with an incomplete hepatitis B vaccination series compared to those with no history of hepatitis B vaccination. When comparing those with a complete series of hepatitis B vaccination, this model produced a prevalence ratio of 1.25 (95% CI: 1.06, 1.46; $P = 0.0076$). In order for the infectious disease variable to be considered an important confounder, the reduced model would need to produce effect estimates lower than 1.035 or higher than 1.265 comparing an

incomplete history to no history, and an effect estimate lower than 1.125 or higher than 1.375 comparing a complete history to no history.

Reduced model (dropped INFDIS)

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \beta_3(\text{SEX}) + \beta_4(\text{AGECAT}) + \beta_5(\text{ANEMIA}) + \beta_6(\text{REFTYPE})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0, and VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0.

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1416
Number of Observations Used	1410
Number of Events	530
Number of Trials	1410
Missing Values	6

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	530
2	0	880

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information		
Parameter	**Effect**	**vacchistory**
Prm1	Intercept	
Prm2	vacchistory	1
Prm3	vacchistory	2
Prm4	gender2	
Prm5	agecat	
Prm6	anemia	
Prm7	reftype	

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-878.4977	
Full Log Likelihood		-878.4977	
AIC (smaller is better)		1770.9955	
AICC (smaller is better)		1771.0754	
BIC (smaller is better)		1807.7549	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.0723	0.1130	-1.2937	-0.8509	90.09	<.0001
vacchistory	1	1	0.1367	0.1355	-0.1288	0.4022	1.02	0.3130
vacchistory	2	1	0.2108	0.0819	0.0503	0.3713	6.62	0.0101

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
gender2		1	0.1948	0.0720	0.0536	0.3359	7.31	0.0068
agecat		1	-0.4563	0.0733	-0.5999	-0.3127	38.77	<.0001
anemia		1	0.2915	0.0840	0.1268	0.4562	12.03	0.0005
reftype		1	0.2096	0.0661	0.0800	0.3392	10.05	0.0015
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	7.11	0.0285
gender2	1	7.35	0.0067
agecat	1	37.87	<.0001
anemia	1	10.92	0.0009
reftype	1	10.35	0.0013

Contrast Estimate Results								
		Mean					**L'Beta**	
Label	**Mean Estimate**	**Confidence Limits**		**L'Beta Estimate**	**Standard Error**	**Alpha**	**Confidence Limits**	
VACCHISTORY=1	1.1465	0.8791	1.4951	0.1367	0.1355	0.05	-0.1288	0.4022
VACCHISTORY=2	1.2346	1.0515	1.4496	0.2108	0.0819	0.05	0.0503	0.3713

Contrast Estimate Results		
Label	**Chi-Square**	**Pr > ChiSq**
VACCHISTORY=1	1.02	0.3130
VACCHISTORY=2	6.62	0.0101

Removing the infectious disease variable from the full model did not produce effect estimates with at least a 10% difference from those produced by the full model

(1.15 compared to 1.15, and 1.23 compared to 1.25). Thus, the infectious disease variable is not an important confounder and was not included in the final, no-interaction model.

Appendix J. Collinearity assessment for the no-interaction model in the main analysis

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1416
Number of Observations Used	1410
Number of Events	530
Number of Trials	1410
Missing Values	6

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	530
2	0	880

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information		
Parameter	**Effect**	**vacchistory**
Prm1	Intercept	
Prm2	vacchistory	1
Prm3	vacchistory	2

Parameter Information		
Parameter	**Effect**	**vacchistory**
Prm4	gender2	
Prm5	agecat	
Prm6	anemia	
Prm7	reftype	

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-878.4977	
Full Log Likelihood		-878.4977	
AIC (smaller is better)		1770.9955	
AICC (smaller is better)		1771.0754	
BIC (smaller is better)		1807.7549	

Algorithm converged.

Estimated Covariance Matrix							
	Prm1	**Prm2**	**Prm3**	**Prm4**	**Prm5**	**Prm6**	**Prm7**
Prm1	0.01276	-0.006459	-0.005938	-0.003564	-0.005190	-0.004604	-0.002436
Prm2	-0.006459	0.01835	0.005465	-0.000219	0.002724	0.0004797	-0.000088
Prm3	-0.005938	0.005465	0.006706	0.0000964	0.002089	0.0003880	-0.000422
Prm4	-0.003564	-0.000219	0.0000964	0.005187	0.0002078	0.002769	-0.000321
Prm5	-0.005190	0.002724	0.002089	0.0002078	0.005370	0.001924	0.0006026
Prm6	-0.004604	0.0004797	0.0003880	0.002769	0.001924	0.007060	-0.000165
Prm7	-0.002436	-0.000088	-0.000422	-0.000321	0.0006026	-0.000165	0.004373

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.0723	0.1130	-1.2937	-0.8509	90.09	<.0001
vacchistory	1	1	0.1367	0.1355	-0.1288	0.4022	1.02	0.3130
vacchistory	2	1	0.2108	0.0819	0.0503	0.3713	6.62	0.0101

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
gender2		1	0.1948	0.0720	0.0536	0.3359	7.31	0.0068
agecat		1	-0.4563	0.0733	-0.5999	-0.3127	38.77	<.0001
anemia		1	0.2915	0.0840	0.1268	0.4562	12.03	0.0005
reftype		1	0.2096	0.0661	0.0800	0.3392	10.05	0.0015
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

Obs	_NAME_	RowName	Prm1	Prm2	Prm3	Prm4
1	ESTIMATE		.	.	.	.
2	Intercep	Prm1	0.0127623	-0.006459	-0.005938	-0.003564
3	vacchist	Prm2	-0.006459	0.018351	0.0054645	-0.000219
4	vacchist	Prm3	-0.005938	0.0054645	0.006706	0.0000964
5	gender2	Prm4	-0.003564	-0.000219	0.0000964	0.005187
6	agecat	Prm5	-0.00519	0.0027238	0.0020887	0.0002078
7	anemia	Prm6	-0.004604	0.0004797	0.000388	0.0027686
8	reftype	Prm7	-0.002436	-0.000088	-0.000422	-0.000321

Obs	Prm5	Prm6	Prm7	Parameter	vacchistory
1	.	.	.		
2	-0.00519	-0.004604	-0.002436	Prm1	
3	0.0027238	0.0004797	-0.000088	Prm2	1
4	0.0020887	0.000388	-0.000422	Prm3	2
5	0.0002078	0.0027686	-0.000321	Prm4	
6	0.0053703	0.0019236	0.0006026	Prm5	
7	0.0019236	0.0070599	-0.000165	Prm6	
8	0.0006026	-0.000165	0.0043734	Prm7	

Obs	_NAME_	RowName	Prm1	Prm2	Prm3	Prm4
1	ESTIMATE		.	.	.	.
2	Intercep	Prm1	0.0127623	-0.006459	-0.005938	-0.003564

Obs	Prm5	Prm6	Prm7	Parameter	vacchistory	
3	vacchist	Prm2	-0.006459	0.018351	0.0054645	-0.000219
4	vacchist	Prm3	-0.005938	0.0054645	0.006706	0.0000964
5	gender2	Prm4	-0.003564	-0.000219	0.0000964	0.005187
6	agecat	Prm5	-0.00519	0.0027238	0.0020887	0.0002078
7	anemia	Prm6	-0.004604	0.0004797	0.000388	0.0027686
8	reftype	Prm7	-0.002436	-0.000088	-0.000422	-0.000321

Obs	Prm5	Prm6	Prm7	Parameter	vacchistory
1	.	.	.		
2	-0.00519	-0.004604	-0.002436	Prm1	
3	0.0027238	0.0004797	-0.000088	Prm2	1
4	0.0020887	0.000388	-0.000422	Prm3	2
5	0.0002078	0.0027686	-0.000321	Prm4	
6	0.0053703	0.0019236	0.0006026	Prm5	
7	0.0019236	0.0070599	-0.000165	Prm6	
8	0.0006026	-0.000165	0.0043734	Prm7	

VARCOV2						
0.0127623	-0.006459	-0.005938	-0.003564	-0.00519	-0.004604	-0.002436
-0.006459	0.018351	0.0054645	-0.000219	0.0027238	0.0004797	-0.000088
-0.005938	0.0054645	0.006706	0.0000964	0.0020887	0.000388	-0.000422
-0.003564	-0.000219	0.0000964	0.005187	0.0002078	0.0027686	-0.000321
-0.00519	0.0027238	0.0020887	0.0002078	0.0053703	0.0019236	0.0006026
-0.004604	0.0004797	0.000388	0.0027686	0.0019236	0.0070599	-0.000165
-0.002436	-0.000088	-0.000422	-0.000321	0.0006026	-0.000165	0.0043734

Input DATASET covdsn, Submitted 31MAR2014
COLLINEARITY DIAGNOSTICS FOR NONLINEAR MODELS USING THE INFORMATION MATRIX: EIGENVALUES, CONDITION INDEXES, AND VARIANCE DECOMPOSITION PROPORTIONS (VDP'S)

VARIABLE	VDP1	VDP2	VDP3	VDP4	VDP5	VDP6	VDP7
EIGENVAL	0.05727	0.24378	0.31537	0.51861	0.99245	1.00521	3.86731
CONDINDX	8.21740	3.98295	3.50181	2.73076	1.97401	1.96145	1.00000
	.	.	.	.	.	.	.
Intercep	0.98615	0.00614	0.00213	0.00060	0.00001	0.00001	0.00496
vacchist	0.21592	0.16346	0.00129	0.00008	0.02111	0.59461	0.00353
vacchist	0.50092	0.40420	0.03271	0.02904	0.00758	0.01511	0.01045
gender2	0.17161	0.41656	0.25250	0.08271	0.06150	0.00054	0.01458
agecat	0.42377	0.00241	0.02931	0.45254	0.06819	0.01087	0.01290
anemia	0.22920	0.25902	0.08861	0.10619	0.29345	0.01380	0.00973
reftype	0.07240	0.07654	0.75437	0.07466	0.00395	0.00008	0.01800

Input DATASET covdsn, Submitted 31MAR2014
COLLINEARITY DIAGNOSTICS FOR NONLINEAR MODELS USING THE INFORMATION MATRIX: EIGENVALUES, CONDITION INDEXES, AND VARIANCE DECOMPOSITION PROPORTIONS (VDP'S)

Directory	
Libref	WORK
Engine	V9
Physical Name	F:\SAS Temporary Files_TD13656_VDS3-CTX-SAS01_
Filename	F:\SAS Temporary Files_TD13656_VDS3-CTX-SAS01_

#	Name	Member Type	File Size	Last Modified
1	ALIEN	DATA	12698624	31Mar14:10:46:17
2	COMBINED	DATA	9536512	31Mar14:10:46:17
3	COMBINED2	DATA	8471552	31Mar14:10:46:18
4	COMBINED_CLEAN	DATA	7750656	31Mar14:10:46:18
5	COMBINED_CLEAN_ADULTS	DATA	5669888	31Mar14:10:46:18

#	Name	Member Type	File Size	Last Modified
6	COVDSN	DATA	9216	31Mar14:16:54:40
7	FORMATS	CATALOG	17408	31Mar14:10:46:18
8	NEXT_1	DATA	5120	31Mar14:16:54:41
9	NEXT_1A	DATA	9216	31Mar14:16:54:41
10	NEXT_2	DATA	9216	31Mar14:16:54:41
11	NEXT_3	DATA	9216	31Mar14:16:54:41
12	NEXT_4	DATA	5120	31Mar14:16:54:41
13	NEXT_5	DATA	9216	31Mar14:16:54:41
14	PARMS	DATA	5120	31Mar14:16:54:40
15	RRMODEL	DATA	9216	31Mar14:16:54:41
16	SASMACR	CATALOG	5120	31Mar14:10:44:31
17	VACC	DATA	443392	31Mar14:10:46:17

Appendix K. SAS output for effect estimates from the no-interaction model in the main analysis

For the logistic regression model presented, the variables are represented in the following ways:

Anti-HBs = ANTIHBS

Hepatitis B vaccination history =VACCHISTORY

Sex = SEX

Age category = AGECAT

Anemia = ANEMIA

Immigration status = REFTYPE

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \beta_3(\text{SEX}) + \beta_4(\text{AGECAT}) + \beta_5(\text{ANEMIA}) + \beta_6(\text{REFTYPE})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0, and

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0.

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1416
Number of Observations Used	1410
Number of Events	530

Number of Trials	1410
Missing Values	6

Class Level Information			
Class	Value	Design Variables	
vacchistory	0	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	antihbs2	Total Frequency
1	1	530
2	0	880

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information		
Parameter	Effect	vacchistory
Prm1	Intercept	
Prm2	vacchistory	1
Prm3	vacchistory	2
Prm4	gender2	
Prm5	agecat	
Prm6	anemia	
Prm7	reftype	

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Log Likelihood		-878.4977	
Full Log Likelihood		-878.4977	
AIC (smaller is better)		1770.9955	
AICC (smaller is better)		1771.0754	
BIC (smaller is better)		1807.7549	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		DF	Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept		1	-1.0723	0.1130	-1.2937	-0.8509	90.09	<.0001
vacchistory	1	1	0.1367	0.1355	-0.1288	0.4022	1.02	0.3130
vacchistory	2	1	0.2108	0.0819	0.0503	0.3713	6.62	0.0101
gender2		1	0.1948	0.0720	0.0536	0.3359	7.31	0.0068
agecat		1	-0.4563	0.0733	-0.5999	-0.3127	38.77	<.0001
anemia		1	0.2915	0.0840	0.1268	0.4562	12.03	0.0005
reftype		1	0.2096	0.0661	0.0800	0.3392	10.05	0.0015
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	DF	Chi-Square	Pr > ChiSq
vacchistory	2	7.11	0.0285
gender2	1	7.35	0.0067
agecat	1	37.87	<.0001
anemia	1	10.92	0.0009
reftype	1	10.35	0.0013

Contrast Estimate Results								
		Mean					L'Beta	
Label	Mean Estimate	Confidence Limits		L'Beta Estimate	Standard Error	Alpha	Confidence Limits	
Effect of vacchx=1	1.1465	0.8791	1.4951	0.1367	0.1355	0.05	-0.1288	0.4022
Effect of vacchx=2	1.2346	1.0515	1.4496	0.2108	0.0819	0.05	0.0503	0.3713
Effect of reftype=1 (parolee)	1.2332	1.0833	1.4039	0.2096	0.0661	0.05	0.0800	0.3392
Effect of gender2=1 (female)	1.2150	1.0551	1.3992	0.1948	0.0720	0.05	0.0536	0.3359

Contrast Estimate Results								
		Mean					L'Beta	
Label	Mean Estimate	Confidence Limits		L'Beta Estimate	Standard Error	Alpha	Confidence Limits	
Effect of agecat=1 (>17 yrs)	0.6336	0.5489	0.7315	-0.4563	0.0733	0.05	-0.5999	-0.3127
Effect of anemia=1 (pos)	1.3384	1.1352	1.5780	0.2915	0.0840	0.05	0.1268	0.4562

Contrast Estimate Results		
Label	Chi-Square	Pr > ChiSq
Effect of vacchx=1	1.02	0.3130
Effect of vacchx=2	6.62	0.0101
Effect of reftype=1 (parolee)	10.05	0.0015
Effect of gender2=1 (female)	7.31	0.0068
Effect of agecat=1 (>17 yrs)	38.77	<.0001
Effect of anemia=1 (pos)	12.03	0.0005

Appendix L. SAS output for effect modification assessment in the sub-analysis

For all logistic regression models presented, the variables will be represented in the following ways:

Anti-HBs = ANTIHBS

Hepatitis B vaccination history =VACCHISTORY

Sex = SEX

Anemia = ANEMIA

Infectious disease =INFDIS

Immigration status = REFTYPE

BMI category = BMI

Assessing BMI variable for effect modification

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \gamma_1(\text{BMI}_1) + \gamma_2(\text{BMI}_2) + \gamma_3(\text{BMI}_3) + \delta_1(\text{VACCHISTORY}_1*\text{BMI}_1) + \delta_2(\text{VACCHISTORY}_2*\text{BMI}_1) + \delta_3(\text{VACCHISTORY}_1*\text{BMI}_2) + \delta_4(\text{VACCHISTORY}_2*\text{BMI}_2) + \delta_5(\text{VACCHISTORY}_1*\text{BMI}_3) + \delta_6(\text{VACCHISTORY}_2*\text{BMI}_3)$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0

BMI_1=1 if BMI category=0; else=0

BMI_2=1 if BMI category=2; else=0

BMI_3=1 if BMI category=3; else=0

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN_ADULTS
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1033
Number of Observations Used	930
Number of Events	284
Number of Trials	930
Missing Values	103

Class Level Information				
Class	**Value**	**Design Variables**		
vacchistory	**0**	0	0	
	1	1	0	
	2	0	1	
bmicat	**0**	1	0	0
	1	0	0	0
	2	0	1	0
	3	0	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	284
2	0	646

PROC GENMOD is modeling the probability that antihbs2='1'.

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-548.8166	
Full Log Likelihood		-548.8166	
AIC (smaller is better)		1121.6332	
AICC (smaller is better)		1121.9734	
BIC (smaller is better)		1179.6554	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter			**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**
Intercept			1	-1.2831	0.1191	-1.5164	-1.0498	116.16
vacchistory	1		1	0.0935	0.3370	-0.5669	0.7540	0.08
vacchistory	2		1	0.4804	0.1389	0.2083	0.7526	11.97
bmicat	0		1	0.0303	0.4390	-0.8301	0.8908	0.00
bmicat	2		1	-0.3263	0.2149	-0.7475	0.0948	2.31
bmicat	3		1	-0.4216	0.2870	-0.9841	0.1408	2.16
vacchistory*bmicat	1	0	1	0.0606	0.9792	-1.8585	1.9798	0.00
vacchistory*bmicat	1	2	1	-21.7651	35926.59	-70436.6	70393.05	0.00
vacchistory*bmicat	1	3	1	0.5126	0.9211	-1.2927	2.3179	0.31
vacchistory*bmicat	2	0	1	-0.0879	0.5003	-1.0685	0.8927	0.03
vacchistory*bmicat	2	2	1	-0.0616	0.2584	-0.5679	0.4448	0.06
vacchistory*bmicat	2	3	1	-0.2972	0.3586	-1.0000	0.4057	0.69
Scale			0	1.0000	0.0000	1.0000	1.0000	

Analysis Of Maximum Likelihood Parameter Estimates			
Parameter			**Pr > ChiSq**
Intercept			<.0001
vacchistory	1		0.7814
vacchistory	2		0.0005

Analysis Of Maximum Likelihood Parameter Estimates			
Parameter			**Pr > ChiSq**
bmicat	0		0.9449
bmicat	2		0.1288
bmicat	3		0.1418
vacchistory*bmicat	1	0	0.9506
vacchistory*bmicat	1	2	0.9995
vacchistory*bmicat	1	3	0.5779
vacchistory*bmicat	2	0	0.8606
vacchistory*bmicat	2	2	0.8117
vacchistory*bmicat	2	3	0.4073
Scale			

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	13.70	0.0011
bmicat	3	3.92	0.2699
vacchistory*bmicat	6	5.61	0.4679

The overall p-value for the interaction term between hepatitis B vaccination history and BMI is 0.4679, so BMI is not considered to be an important effect modifier.

Assessing sex variable for effect modification

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \gamma(\text{SEX}) + \delta_1(\text{VACCHISTORY}_1\text{*SEX}) + \delta_2(\text{VACCHISTORY}_2\text{*SEX})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN_ADULTS
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1033
Number of Observations Used	1033
Number of Events	316
Number of Trials	1033

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	316
2	0	717

PROC GENMOD is modeling the probability that antihbs2='1'.

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-624.8517	
Full Log Likelihood		-624.8517	
AIC (smaller is better)		1261.7034	
AICC (smaller is better)		1261.7852	
BIC (smaller is better)		1291.3447	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates							
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**
Intercept		1	-1.5404	0.1279	-1.7912	-1.2897	144.97
vacchistory	1	1	-0.1178	0.4677	-1.0345	0.7989	0.06
vacchistory	2	1	0.4582	0.1563	0.1519	0.7646	8.59
gender2		1	0.2451	0.1640	-0.0763	0.5665	2.23
gender2*vacchistory	1	1	0.1322	0.6113	-1.0660	1.3303	0.05
gender2*vacchistory	2	1	-0.1012	0.2015	-0.4961	0.2937	0.25
Scale		0	1.0000	0.0000	1.0000	1.0000	

Analysis Of Maximum Likelihood Parameter Estimates		
Parameter		**Pr > ChiSq**
Intercept		<.0001
vacchistory	1	0.8012
vacchistory	2	0.0034
gender2		0.1350
gender2*vacchistory	1	0.8288
gender2*vacchistory	2	0.6156
Scale		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	9.91	0.0070
gender2	1	2.28	0.1312
gender2*vacchistory	2	0.37	0.8332

The overall p-value for the interaction term between hepatitis B vaccination history and sex is 0.8332, so sex is not considered to be an important effect modifier.

Assessing anemia variable for effect modification

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \gamma(\text{ANEMIA}) + \delta_1(\text{VACCHISTORY}_1*\text{ANEMIA}) + \delta_2(\text{VACCHISTORY}_2*\text{ANEMIA})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN_ADULTS
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1033
Number of Observations Used	1032
Number of Events	316
Number of Trials	1032
Missing Values	1

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	antihbs2	Total Frequency
1	1	316
2	0	716

PROC GENMOD is modeling the probability that antihbs2='1'.

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Log Likelihood		-624.4601	
Full Log Likelihood		-624.4601	
AIC (smaller is better)		1260.9201	
AICC (smaller is better)		1261.0021	
BIC (smaller is better)		1290.5556	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates						
Parameter		DF	Estimate	Standard Error	Wald 95% Confidence Limits	Wald Chi-Square
Intercept		1	-1.3932	0.0834	-1.5567 -1.2297	278.87
vacchistory	1	1	0.0069	0.3005	-0.5820 0.5959	0.00
vacchistory	2	1	0.3644	0.1033	0.1619 0.5669	12.44
anemia		1	-0.0984	0.3051	-0.6964 0.4995	0.10
anemia*vacchistory	1	1	-20.7963	39783.97	-77995.9 77954.35	0.00
anemia*vacchistory	2	1	0.4341	0.3552	-0.2622 1.1303	1.49
Scale		0	1.0000	0.0000	1.0000 1.0000	

Analysis Of Maximum Likelihood Parameter Estimates		
Parameter		Pr > ChiSq
Intercept		<.0001
vacchistory	1	0.9816

Analysis Of Maximum Likelihood Parameter Estimates		
Parameter		**Pr > ChiSq**
vacchistory	2	0.0004
anemia		0.7469
anemia*vacchistory	1	0.9996
anemia*vacchistory	2	0.2217
Scale		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	13.49	0.0012
anemia	1	0.11	0.7414
anemia*vacchistory	2	3.59	0.1659

The overall p-value for the interaction term between hepatitis B vaccination history and sex is 0.1659, so anemia is not considered to be an important effect modifier.

Assessing infectious disease variable for effect modification

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \gamma(\text{INFDIS}) + \delta_1(\text{VACCHISTORY}_1*\text{INFDIS}) + \delta_2(\text{VACCHISTORY}_2*\text{INFDIS})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN_ADULTS
Distribution	Binomial

Model Information	
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1033
Number of Observations Used	1033
Number of Events	316
Number of Trials	1033

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	316
2	0	717

PROC GENMOD is modeling the probability that antihbs2='1'.

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-623.3037	
Full Log Likelihood		-623.3037	
AIC (smaller is better)		1258.6074	
AICC (smaller is better)		1258.6893	
BIC (smaller is better)		1288.2487	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.4124	0.0853	-1.5795	-1.2452	274.26	<.0001
vacchistory	1	1	-0.1970	0.3487	-0.8804	0.4863	0.32	0.5720
vacchistory	2	1	0.4609	0.1040	0.2570	0.6648	19.63	<.0001
infdis		1	0.0855	0.2526	-0.4095	0.5805	0.11	0.7349
infdis*vacchistory	1	1	0.8308	0.6543	-0.4516	2.1131	1.61	0.2042
infdis*vacchistory	2	1	-0.5493	0.3345	-1.2049	0.1063	2.70	0.1005
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	23.03	<.0001
infdis	1	0.11	0.7396
infdis*vacchistory	2	4.88	0.0872

The overall p-value for the interaction term between hepatitis B vaccination history and presence of infectious disease is 0.0872, so presence of infectious disease is not considered to be an important effect modifier.

Assessing immigration status variable for effect modification

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \gamma(\text{REFTYPE}) + \delta_1(\text{VACCHISTORY}_1*\text{REFTYPE}) + \delta_2(\text{VACCHISTORY}_2*\text{REFTYPE})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN_ADULTS
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1033
Number of Observations Used	1033
Number of Events	316
Number of Trials	1033

Class Level Information			
Class	**Value**	**Design Variables**	
vacchistory	**0**	0	0
	1	1	0
	2	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	316
2	0	717

PROC GENMOD is modeling the probability that antihbs2='1'.

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-617.1266	
Full Log Likelihood		-617.1266	
AIC (smaller is better)		1246.2533	
AICC (smaller is better)		1246.3351	
BIC (smaller is better)		1275.8946	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates							
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**
Intercept		1	-1.5885	0.1171	-1.8181	-1.3590	183.92
vacchistory	1	1	-0.2573	0.5426	-1.3208	0.8062	0.22
vacchistory	2	1	0.3624	0.1517	0.0651	0.6598	5.71
reftype		1	0.4086	0.1596	0.0958	0.7213	6.56
reftype*vacchistory	1	1	0.2333	0.6503	-1.0412	1.5078	0.13
reftype*vacchistory	2	1	-0.0031	0.1992	-0.3935	0.3873	0.00
Scale		0	1.0000	0.0000	1.0000	1.0000	

Analysis Of Maximum Likelihood Parameter Estimates		
Parameter		**Pr > ChiSq**
Intercept		<.0001
vacchistory	1	0.6354
vacchistory	2	0.0169
reftype		0.0105
reftype*vacchistory	1	0.7198
reftype*vacchistory	2	0.9875
Scale		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	6.67	0.0357
reftype	1	6.48	0.0109
reftype*vacchistory	2	0.14	0.9317

The overall p-value for the interaction term between hepatitis B vaccination history and immigration status is 0.9317, so immigration status is not considered to be an important effect modifier.

Appendix M. SAS output for confounding assessment in the sub-analysis

For all logistic regression models presented, the variables will be represented in the following ways:

Anti-HBs = ANTIHBS

Hepatitis B vaccination history =VACCHISTORY

Sex = SEX

Anemia = ANEMIA

Infectious disease =INFDIS

Immigration status = REFTYPE

BMI category = BMI

Full model

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \beta_1(\text{BMI}_1) + \beta_2(\text{BMI}_2) + \beta_3(\text{BMI}_3) + \beta_4(\text{REFTYPE}) + \gamma_1(\text{ANEMIA}) + \gamma_2(\text{SEX}) + \gamma_3(\text{INFDIS})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0

BMI_1=1 if BMI category=0; else=0

BMI_2=1 if BMI category=2; else=0

BMI_3=1 if BMI category=3; else=0

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN_ADULTS
Distribution	Binomial

Model Information	
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1033
Number of Observations Used	929
Number of Events	284
Number of Trials	929
Missing Values	104

Class Level Information				
Class	**Value**	**Design Variables**		
vacchistory	**0**	0	0	
	1	1	0	
	2	0	1	
bmicat	**0**	1	0	0
	1	0	0	0
	2	0	1	0
	3	0	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	284
2	0	645

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information			
Parameter	**Effect**	**vacchistory**	**bmicat**
Prm1	Intercept		
Prm2	vacchistory	1	
Prm3	vacchistory	2	
Prm4	gender2		

Parameter Information			
Parameter	**Effect**	**vacchistory**	**bmicat**
Prm5	anemia		
Prm6	infdis		
Prm7	bmicat		0
Prm8	bmicat		2
Prm9	bmicat		3
Prm10	reftype		

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-539.7391	
Full Log Likelihood		-539.7391	
AIC (smaller is better)		1099.4781	
AICC (smaller is better)		1099.7178	
BIC (smaller is better)		1147.8192	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.5142	0.1256	-1.7603	-1.2680	145.32	<.0001
vacchistory	1	1	-0.0748	0.3026	-0.6678	0.5182	0.06	0.8047
vacchistory	2	1	0.4491	0.1057	0.2420	0.6562	18.06	<.0001
gender2		1	0.1258	0.0970	-0.0643	0.3159	1.68	0.1945
anemia		1	0.2671	0.1514	-0.0296	0.5637	3.11	0.0776
infdis		1	-0.2741	0.1647	-0.5968	0.0486	2.77	0.0960
bmicat	0	1	-0.0939	0.1999	-0.4856	0.2979	0.22	0.6386
bmicat	2	1	-0.3967	0.1170	-0.6260	-0.1674	11.50	0.0007
bmicat	3	1	-0.5835	0.1656	-0.9079	-0.2590	12.42	0.0004
reftype		1	0.3824	0.0968	0.1927	0.5721	15.61	<.0001
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	21.15	<.0001
gender2	1	1.71	0.1908
anemia	1	2.55	0.1102
infdis	1	3.21	0.0732
bmicat	3	22.22	<.0001
reftype	1	15.99	<.0001

Contrast Estimate Results									
		Mean					L'Beta		
Label	**Mean Estimate**	**Confidence Limits**		**L'Beta Estimate**	**Standard Error**	**Alpha**	**Confidence Limits**		**Chi-Square**
VACC HX 1 VS. 0	0.9279	0.5128	1.6790	-0.0748	0.3026	0.05	-0.6678	0.5182	0.06
VACC HX 2 VS. 0	1.5669	1.2738	1.9275	0.4491	0.1057	0.05	0.2420	0.6562	18.06

Contrast Estimate Results	
Label	**Pr > ChiSq**
VACC HX 1 VS. 0	0.8047
VACC HX 2 VS. 0	<.0001

Reduced model (dropped SEX)

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \beta_1(\text{BMI}_1) + \beta_2(\text{BMI}_2) + \beta_3(\text{BMI}_3) + \beta_4(\text{REFTYPE}) + \gamma_1(\text{ANEMIA}) + \gamma_2(\text{INFDIS})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0

BMI_1=1 if BMI category=0; else=0

BMI_2=1 if BMI category=2; else=0

BMI_3=1 if BMI category=3; else=0

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN_ADULTS
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1033
Number of Observations Used	929
Number of Events	284
Number of Trials	929
Missing Values	104

Class Level Information				
Class	**Value**	**Design Variables**		
vacchistory	**0**	0	0	
	1	1	0	
	2	0	1	

Class Level Information				
Class	Value	Design Variables		
bmicat	0	1	0	0
	1	0	0	0
	2	0	1	0
	3	0	0	1

Response Profile		
Ordered Value	antihbs2	Total Frequency
1	1	284
2	0	645

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information			
Parameter	Effect	vacchistory	bmicat
Prm1	Intercept		
Prm2	vacchistory	1	
Prm3	vacchistory	2	
Prm4	anemia		
Prm5	infdis		
Prm6	bmicat		0
Prm7	bmicat		2
Prm8	bmicat		3
Prm9	reftype		

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Log Likelihood		-540.5947	
Full Log Likelihood		-540.5947	
AIC (smaller is better)		1099.1895	
AICC (smaller is better)		1099.3853	

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
BIC (smaller is better)		1142.6965	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.4429	0.1120	-1.6625	-1.2233	165.88	<.0001
vacchistory	1	1	-0.0962	0.3022	-0.6885	0.4962	0.10	0.7504
vacchistory	2	1	0.4444	0.1060	0.2367	0.6521	17.58	<.0001
anemia		1	0.2849	0.1530	-0.0150	0.5849	3.47	0.0626
infdis		1	-0.2799	0.1651	-0.6035	0.0438	2.87	0.0901
bmicat	0	1	-0.0712	0.1998	-0.4627	0.3204	0.13	0.7217
bmicat	2	1	-0.4037	0.1170	-0.6330	-0.1743	11.90	0.0006
bmicat	3	1	-0.5886	0.1654	-0.9128	-0.2643	12.65	0.0004
reftype		1	0.3895	0.0968	0.1998	0.5792	16.20	<.0001
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	20.85	<.0001
anemia	1	2.83	0.0926
infdis	1	3.34	0.0677
bmicat	3	22.95	<.0001
reftype	1	16.58	<.0001

Contrast Estimate Results									
		Mean					L'Beta		
Label	Mean Estimate	Confidence Limits		L'Beta Estimate	Standard Error	Alpha	Confidence Limits		Chi-Square
VACC HX 1 VS. 0	0.9083	0.5023	1.6425	-0.0962	0.3022	0.05	-0.6885	0.4962	0.10
VACC HX 2 VS. 0	1.5595	1.2670	1.9196	0.4444	0.1060	0.05	0.2367	0.6521	17.58

Contrast Estimate Results	
Label	Pr > ChiSq
VACC HX 1 VS. 0	0.7504
VACC HX 2 VS. 0	<.0001

Reduced model (dropped INFDIS)

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \beta_1(\text{BMI}_1) + \beta_2(\text{BMI}_2) + \beta_3(\text{BMI}_3) + \beta_4(\text{REFTYPE}) + \gamma_1(\text{ANEMIA}) + \gamma_2(\text{SEX})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0

BMI_1=1 if BMI category=0; else=0

BMI_2=1 if BMI category=2; else=0

BMI_3=1 if BMI category=3; else=0

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN_ADULTS
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1033
Number of Observations Used	929
Number of Events	284
Number of Trials	929
Missing Values	104

Class Level Information				
Class	**Value**	**Design Variables**		
vacchistory	**0**	0	0	
	1	1	0	
	2	0	1	
bmicat	**0**	1	0	0
	1	0	0	0
	2	0	1	0
	3	0	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	284
2	0	645

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information			
Parameter	**Effect**	**vacchistory**	**bmicat**
Prm1	Intercept		
Prm2	vacchistory	1	
Prm3	vacchistory	2	
Prm4	gender2		
Prm5	anemia		
Prm6	bmicat		0
Prm7	bmicat		2
Prm8	bmicat		3
Prm9	reftype		

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-541.3442	
Full Log Likelihood		-541.3442	
AIC (smaller is better)		1100.6884	
AICC (smaller is better)		1100.8843	
BIC (smaller is better)		1144.1954	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.5245	0.1255	-1.7706	-1.2785	147.50	<.0001
vacchistory	1	1	-0.0796	0.3028	-0.6730	0.5139	0.07	0.7927
vacchistory	2	1	0.4234	0.1054	0.2168	0.6299	16.14	<.0001
gender2		1	0.1311	0.0975	-0.0600	0.3221	1.81	0.1787
anemia		1	0.2181	0.1496	-0.0751	0.5112	2.13	0.1448
bmicat	0	1	-0.0716	0.2008	-0.4651	0.3219	0.13	0.7213
bmicat	2	1	-0.3946	0.1172	-0.6244	-0.1648	11.33	0.0008
bmicat	3	1	-0.5934	0.1663	-0.9193	-0.2676	12.74	0.0004

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
reftype		1	0.3768	0.0972	0.1863	0.5673	15.03	0.0001
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	19.12	<.0001
gender2	1	1.84	0.1751
anemia	1	1.80	0.1795
bmicat	3	22.53	<.0001
reftype	1	15.43	<.0001

Contrast Estimate Results									
Label	**Mean Estimate**	**Mean Confidence Limits**		**L'Beta Estimate**	**Standard Error**	**Alpha**	**L'Beta Confidence Limits**		**Chi-Square**
VACC HX 1 VS. 0	0.9235	0.5102	1.6718	-0.0796	0.3028	0.05	-0.6730	0.5139	0.07
VACC HX 2 VS. 0	1.5271	1.2421	1.8774	0.4234	0.1054	0.05	0.2168	0.6299	16.14

Contrast Estimate Results	
Label	**Pr > ChiSq**
VACC HX 1 VS. 0	0.7927
VACC HX 2 VS. 0	<.0001

Reduced model (dropped ANEMIA)

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \beta_1(\text{BMI}_1) + \beta_2(\text{BMI}_2) + \beta_3(\text{BMI}_3) + \beta_4(\text{REFTYPE}) + \gamma_1(\text{SEX}) + \gamma_2(\text{INFDIS})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0

BMI_1=1 if BMI category=0; else=0

BMI_2=1 if BMI category=2; else=0

BMI_3=1 if BMI category=3; else=0

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN_ADULTS
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1033
Number of Observations Used	930
Number of Events	284
Number of Trials	930
Missing Values	103

Class Level Information				
Class	**Value**	**Design Variables**		
vacchistory	**0**	0	0	
	1	1	0	
	2	0	1	
bmicat	**0**	1	0	0

Class Level Information				
Class	Value	Design Variables		
	1	0	0	0
	2	0	1	0
	3	0	0	1

Response Profile		
Ordered Value	antihbs2	Total Frequency
1	1	284
2	0	646

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information			
Parameter	Effect	vacchistory	bmicat
Prm1	Intercept		
Prm2	vacchistory	1	
Prm3	vacchistory	2	
Prm4	gender2		
Prm5	infdis		
Prm6	bmicat		0
Prm7	bmicat		2
Prm8	bmicat		3
Prm9	reftype		

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Log Likelihood		-541.2038	
Full Log Likelihood		-541.2038	
AIC (smaller is better)		1100.4075	
AICC (smaller is better)		1100.6032	
BIC (smaller is better)		1143.9242	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.4944	0.1258	-1.7410	-1.2479	141.16	<.0001
vacchistory	1	1	-0.0735	0.3023	-0.6661	0.5190	0.06	0.8078
vacchistory	2	1	0.4394	0.1058	0.2320	0.6468	17.24	<.0001
gender2		1	0.1346	0.0968	-0.0552	0.3243	1.93	0.1646
infdis		1	-0.2422	0.1652	-0.5660	0.0816	2.15	0.1426
bmicat	0	1	-0.1115	0.1993	-0.5021	0.2791	0.31	0.5758
bmicat	2	1	-0.4017	0.1172	-0.6315	-0.1720	11.75	0.0006
bmicat	3	1	-0.5864	0.1657	-0.9111	-0.2616	12.52	0.0004
reftype		1	0.3858	0.0970	0.1957	0.5759	15.83	<.0001
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	20.27	<.0001
gender2	1	1.96	0.1611
infdis	1	2.46	0.1170
bmicat	3	22.42	<.0001
reftype	1	16.20	<.0001

Contrast Estimate Results									
		Mean					**L'Beta**		
Label	**Mean Estimate**	**Confidence Limits**		**L'Beta Estimate**	**Standard Error**	**Alpha**	**Confidence Limits**		**Chi-Square**
VACC HX 1 VS. 0	0.9291	0.5137	1.6804	-0.0735	0.3023	0.05	-0.6661	0.5190	0.06

Contrast Estimate Results									
		Mean					L'Beta		
Label	Mean Estimate	Confidence Limits		L'Beta Estimate	Standard Error	Alpha	Confidence Limits		Chi-Square
VACC HX 2 VS. 0	1.5518	1.2611	1.9095	0.4394	0.1058	0.05	0.2320	0.6468	17.24

Contrast Estimate Results	
Label	Pr > ChiSq
VACC HX 1 VS. 0	0.8078
VACC HX 2 VS. 0	<.0001

Reduced model (dropped SEX and INFDIS)

logit P(ANTIHBS) = $\alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \beta_1(\text{BMI}_1) +$

$\beta_2(\text{BMI}_2) + \beta_3(\text{BMI}_3) + \beta_4(\text{REFTYPE}) + \gamma_1(\text{ANEMIA})$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0

BMI_1=1 if BMI category=0; else=0

BMI_2=1 if BMI category=2; else=0

BMI_3=1 if BMI category=3; else=0

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN_ADULTS

Model Information	
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1033
Number of Observations Used	929
Number of Events	284
Number of Trials	929
Missing Values	104

Class Level Information				
Class	**Value**	**Design Variables**		
vacchistory	**0**	0	0	
	1	1	0	
	2	0	1	
bmicat	**0**	1	0	0
	1	0	0	0
	2	0	1	0
	3	0	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	284
2	0	645

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information			
Parameter	**Effect**	**vacchistory**	**bmicat**
Prm1	Intercept		
Prm2	vacchistory	1	
Prm3	vacchistory	2	

Parameter Information			
Parameter	**Effect**	**vacchistory**	**bmicat**
Prm4	anemia		
Prm5	bmicat		0
Prm6	bmicat		2
Prm7	bmicat		3
Prm8	reftype		

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-542.2635	
Full Log Likelihood		-542.2635	
AIC (smaller is better)		1100.5270	
AICC (smaller is better)		1100.6836	
BIC (smaller is better)		1139.1999	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.4509	0.1119	-1.6703	-1.2315	167.99	<.0001
vacchistory	1	1	-0.1039	0.3022	-0.6963	0.4884	0.12	0.7310
vacchistory	2	1	0.4183	0.1057	0.2112	0.6254	15.67	<.0001
anemia		1	0.2407	0.1512	-0.0556	0.5371	2.54	0.1113
bmicat	0	1	-0.0466	0.2006	-0.4397	0.3465	0.05	0.8163
bmicat	2	1	-0.4012	0.1173	-0.6312	-0.1712	11.69	0.0006
bmicat	3	1	-0.6006	0.1660	-0.9260	-0.2753	13.09	0.0003
reftype		1	0.3836	0.0972	0.1931	0.5742	15.57	<.0001
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	18.83	<.0001
anemia	1	2.12	0.1451
bmicat	3	23.42	<.0001
reftype	1	15.98	<.0001

Contrast Estimate Results									
		Mean					L'Beta		
Label	**Mean Estimate**	**Confidence Limits**		**L'Beta Estimate**	**Standard Error**	**Alpha**	**Confidence Limits**		**Chi-Square**
VACC HX 1 VS. 0	0.9013	0.4984	1.6298	-0.1039	0.3022	0.05	-0.6963	0.4884	0.12
VACC HX 2 VS. 0	1.5194	1.2352	1.8691	0.4183	0.1057	0.05	0.2112	0.6254	15.67

Contrast Estimate Results	
Label	**Pr > ChiSq**
VACC HX 1 VS. 0	0.7310
VACC HX 2 VS. 0	<.0001

Reduced model (dropped SEX and ANEMIA)

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \beta_1(\text{BMI}_1) + \beta_2(\text{BMI}_2) + \beta_3(\text{BMI}_3) + \beta_4(\text{REFTYPE}) + \gamma_1(\text{INFDIS})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0

BMI_1=1 if BMI category=0; else=0

BMI_2=1 if BMI category=2; else=0

BMI_3=1 if BMI category=3; else=0

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN_ADULTS
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1033
Number of Observations Used	930
Number of Events	284
Number of Trials	930
Missing Values	103

Class Level Information				
Class	**Value**	**Design Variables**		
vacchistory	**0**	0	0	
	1	1	0	
	2	0	1	
bmicat	**0**	1	0	0
	1	0	0	0
	2	0	1	0
	3	0	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	284
2	0	646

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information			
Parameter	**Effect**	**vacchistory**	**bmicat**
Prm1	Intercept		
Prm2	vacchistory	1	
Prm3	vacchistory	2	
Prm4	infdis		
Prm5	bmicat		0
Prm6	bmicat		2
Prm7	bmicat		3
Prm8	reftype		

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-542.1858	
Full Log Likelihood		-542.1858	
AIC (smaller is better)		1100.3717	
AICC (smaller is better)		1100.5280	
BIC (smaller is better)		1139.0531	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.4149	0.1108	-1.6322	-1.1977	162.97	<.0001
vacchistory	1	1	-0.0969	0.3020	-0.6889	0.4951	0.10	0.7484
vacchistory	2	1	0.4320	0.1060	0.2242	0.6397	16.60	<.0001
infdis		1	-0.2503	0.1654	-0.5745	0.0739	2.29	0.1302
bmicat	0	1	-0.0870	0.1993	-0.4776	0.3036	0.19	0.6623
bmicat	2	1	-0.4074	0.1174	-0.6374	-0.1773	12.04	0.0005
bmicat	3	1	-0.5893	0.1657	-0.9142	-0.2645	12.64	0.0004
reftype		1	0.3919	0.0971	0.2017	0.5822	16.30	<.0001

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	19.80	<.0001
infdis	1	2.63	0.1050
bmicat	3	22.93	<.0001
reftype	1	16.68	<.0001

Contrast Estimate Results									
		Mean					**L'Beta**		
Label	**Mean Estimate**	**Confidence Limits**		**L'Beta Estimate**	**Standard Error**	**Alpha**	**Confidence Limits**		**Chi-Square**
VACC HX 1 VS. 0	0.9077	0.5021	1.6407	-0.0969	0.3020	0.05	-0.6889	0.4951	0.10
VACC HX 2 VS. 0	1.5403	1.2513	1.8960	0.4320	0.1060	0.05	0.2242	0.6397	16.60

Contrast Estimate Results	
Label	**Pr > ChiSq**
VACC HX 1 VS. 0	0.7484
VACC HX 2 VS. 0	<.0001

Reduced model (dropped ANEMIA and INFDIS)

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \beta_1(\text{BMI}_1) + \beta_2(\text{BMI}_2) + \beta_3(\text{BMI}_3) + \beta_4(\text{REFTYPE}) + \gamma_1(\text{SEX})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0

BMI_1=1 if BMI category=0; else=0

BMI_2=1 if BMI category=2; else=0

BMI_3=1 if BMI category=3; else=0

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN_ADULTS
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1033
Number of Observations Used	930
Number of Events	284
Number of Trials	930
Missing Values	103

Class Level Information				
Class	**Value**	**Design Variables**		
vacchistory	**0**	0	0	
	1	1	0	
	2	0	1	
bmicat	**0**	1	0	0
	1	0	0	0

Class Level Information				
Class	Value	Design Variables		
	2	0	1	0
	3	0	0	1

Response Profile		
Ordered Value	antihbs2	Total Frequency
1	1	284
2	0	646

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information			
Parameter	Effect	vacchistory	bmicat
Prm1	Intercept		
Prm2	vacchistory	1	
Prm3	vacchistory	2	
Prm4	gender2		
Prm5	bmicat		0
Prm6	bmicat		2
Prm7	bmicat		3
Prm8	reftype		

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Log Likelihood		-542.4322	
Full Log Likelihood		-542.4322	
AIC (smaller is better)		1100.8644	
AICC (smaller is better)		1101.0208	
BIC (smaller is better)		1139.5459	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.5109	0.1257	-1.7573	-1.2646	144.55	<.0001
vacchistory	1	1	-0.0751	0.3025	-0.6681	0.5178	0.06	0.8039
vacchistory	2	1	0.4210	0.1057	0.2139	0.6281	15.88	<.0001
gender2		1	0.1405	0.0970	-0.0496	0.3306	2.10	0.1474
bmicat	0	1	-0.0907	0.1999	-0.4825	0.3010	0.21	0.6499
bmicat	2	1	-0.4007	0.1174	-0.6308	-0.1707	11.66	0.0006
bmicat	3	1	-0.5959	0.1662	-0.9217	-0.2701	12.85	0.0003
reftype		1	0.3818	0.0972	0.1912	0.5723	15.42	<.0001
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	18.79	<.0001
gender2	1	2.13	0.1440
bmicat	3	22.79	<.0001
reftype	1	15.80	<.0001

Contrast Estimate Results									
Label	**Mean Estimate**	**Mean Confidence Limits**		**L'Beta Estimate**	**Standard Error**	**Alpha**	**L'Beta Confidence Limits**		**Chi-Square**
VACC HX 1 VS. 0	0.9276	0.5127	1.6784	-0.0751	0.3025	0.05	-0.6681	0.5178	0.06
VACC HX 2 VS. 0	1.5235	1.2385	1.8740	0.4210	0.1057	0.05	0.2139	0.6281	15.88

Contrast Estimate Results	
Label	**Pr > ChiSq**
VACC HX 1 VS. 0	0.8039
VACC HX 2 VS. 0	<.0001

Reduced model (dropped SEX, ANEMIA, and INFDIS)

logit P(ANTIHBS) = $\alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \beta_1(\text{BMI}_1) +$

$\beta_2(\text{BMI}_2) + \beta_3(\text{BMI}_3) + \beta_4(\text{REFTYPE})$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0

BMI_1=1 if BMI category=0; else=0

BMI_2=1 if BMI category=2; else=0

BMI_3=1 if BMI category=3; else=0

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN_ADULTS
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1033
Number of Observations Used	930
Number of Events	284
Number of Trials	930

Missing Values	103

Class Level Information				
Class	Value	Design Variables		
vacchistory	0	0	0	
	1	1	0	
	2	0	1	
bmicat	0	1	0	0
	1	0	0	0
	2	0	1	0
	3	0	0	1

Response Profile		
Ordered Value	antihbs2	Total Frequency
1	1	284
2	0	646

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information			
Parameter	Effect	vacchistory	bmicat
Prm1	Intercept		
Prm2	vacchistory	1	
Prm3	vacchistory	2	
Prm4	bmicat		0
Prm5	bmicat		2
Prm6	bmicat		3
Prm7	reftype		

Criteria For Assessing Goodness Of Fit			
Criterion	DF	Value	Value/DF
Log Likelihood		-543.4995	
Full Log Likelihood		-543.4995	

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
AIC (smaller is better)		1100.9990	
AICC (smaller is better)		1101.1205	
BIC (smaller is better)		1134.8453	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.4284	0.1108	-1.6456	-1.2112	166.16	<.0001
vacchistory	1	1	-0.1010	0.3021	-0.6931	0.4910	0.11	0.7380
vacchistory	2	1	0.4131	0.1059	0.2056	0.6206	15.22	<.0001
bmicat	0	1	-0.0640	0.1998	-0.4556	0.3277	0.10	0.7489
bmicat	2	1	-0.4061	0.1176	-0.6366	-0.1756	11.93	0.0006
bmicat	3	1	-0.6011	0.1662	-0.9268	-0.2753	13.08	0.0003
reftype		1	0.3877	0.0974	0.1968	0.5785	15.85	<.0001
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	18.30	0.0001
bmicat	3	23.44	<.0001
reftype	1	16.25	<.0001

Contrast Estimate Results									
		Mean					**L'Beta**		
Label	**Mean Estimate**	**Confidence Limits**		**L'Beta Estimate**	**Standard Error**	**Alpha**	**Confidence Limits**		**Chi-Square**
VACC HX 1 VS. 0	0.9039	0.5000	1.6340	-0.1010	0.3021	0.05	-0.6931	0.4910	0.11

Contrast Estimate Results									
		Mean					L'Beta		
Label	Mean Estimate	Confidence Limits		L'Beta Estimate	Standard Error	Alpha	Confidence Limits		Chi-Square
VACC HX 2 VS. 0	1.5115	1.2282	1.8601	0.4131	0.1059	0.05	0.2056	0.6206	15.22

Contrast Estimate Results	
Label	Pr > ChiSq
VACC HX 1 VS. 0	0.7380
VACC HX 2 VS. 0	<.0001

The p-values associated with each potential confounder or independent predictor demonstrated that BMI category and immigration status were statistically significant independent predictors of anti-HBs ($P < 0.05$). Potential confounders included anemia, presence of infectious disease, and sex. The reduced models dropped each of these variables from the model both individually and in all grouping combinations to assess whether the effect estimates for the main exposure variable, vaccine history, changed by more than 10% in either direction.

The full model produced a prevalence ratio of 0.93 (95% CI: 0.51, 1.68) for the prevalence of anti-HBs among those with an incomplete hepatitis B vaccination series compared to those with no history of hepatitis B vaccination. When comparing those with a complete series of hepatitis B vaccination, this model produced a prevalence ratio of 1.57 (95% CI: 1.27, 1.93). In order for a variable or grouping of variables to be

considered an important confounder or group of confounders, the reduced model would need to produce effect estimates lower than 0.837 or higher than 1.023 comparing an incomplete history to no history, and an effect estimate lower than 1.413 or higher than 1.727 comparing a complete history to no history. None of the reduced models produced effect estimates greater than 10% in either direction, nor did any reduced models produced a significant gain in precision. Consequently, the final model for the sub-analysis is as follows:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \beta_1(\text{BMI}_1) + \beta_2(\text{BMI}_2) + \beta_3(\text{BMI}_3) + \beta_4(\text{REFTYPE})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0

BMI_1=1 if BMI category=0; else=0

BMI_2=1 if BMI category=2; else=0

BMI_3=1 if BMI category=3; else=0.

The following table summarizes the estimates obtained in the SAS output above:

Variables in model	Vaccination history	PR	95% CI	Precision	>10% change	Precision lost
VACCHISTORY, SEX, ANEMIA, INFDIS, BMI, REFTYPE	Incomplete	0.928	(0.51, 1.68)	3.3	-	-
	Complete	1.567	(1.27, 1.93)	1.5	-	-
VACCHISTORY, ANEMIA, INFDIS, BMI, REFTYPE	Incomplete	0.908	(0.5, 1.64)	3.3	No	No
	Complete	1.560	(1.27, 1.92)	1.5	No	No
VACCHISTORY, SEX, ANEMIA, BMI, REFTYPE	Incomplete	0.924	(0.51, 1.67)	3.3	No	No
	Complete	1.527	(1.24, 1.88)	1.5	No	No
VACCHISTORY, SEX, INFDIS, BMI, REFTYPE	Incomplete	0.929	(0.51, 1.68)	3.3	No	No
	Complete	1.552	(1.26, 1.91)	1.5	No	No

Table continues

Table continued

Variables in model	Vaccination history	PR	95% CI	Precision	>10% change	Precision lost
VACCHISTORY, ANEMIA, BMI, REFTYPE	Incomplete	0.901	(0.5, 1.63)	3.3	No	No
	Complete	1.519	(1.24, 1.87)	1.5	No	No
VACCHISTORY, INFDIS, BMI, REFTYPE	Incomplete	0.908	(0.5, 1.64)	3.3	No	No
	Complete	1.540	(1.25, 1.9)	1.5	No	No
VACCHISTORY, SEX, BMI, REFTYPE	Incomplete	0.928	(0.51, 1.68)	3.3	No	No
	Complete	1.524	(1.24, 1.87)	1.5	No	No
VACCHISTORY, BMI, REFTYPE	Incomplete	0.904	(0.5, 1.63)	3.3	No	No
	Complete	1.512	(1.23, 1.86)	1.5	No	No

Appendix N. Collinearity assessment in the sub-analysis

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN_ADULTS
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1033
Number of Observations Used	930
Number of Events	284
Number of Trials	930
Missing Values	103

Class Level Information				
Class	**Value**	**Design Variables**		
vacchistory	**0**	0	0	
	1	1	0	
	2	0	1	
bmicat	**0**	1	0	0
	1	0	0	0
	2	0	1	0
	3	0	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	284
2	0	646

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information			
Parameter	**Effect**	**vacchistory**	**bmicat**
Prm1	Intercept		
Prm2	vacchistory	1	
Prm3	vacchistory	2	
Prm4	bmicat		0
Prm5	bmicat		2
Prm6	bmicat		3
Prm7	reftype		

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-543.4995	
Full Log Likelihood		-543.4995	
AIC (smaller is better)		1100.9990	
AICC (smaller is better)		1101.1205	
BIC (smaller is better)		1134.8453	

Algorithm converged.

Estimated Covariance Matrix							
	Prm1	**Prm2**	**Prm3**	**Prm4**	**Prm5**	**Prm6**	**Prm7**
Prm1	0.01228	-0.007740	-0.007512	-0.002224	-0.003668	-0.003661	-0.005445
Prm2	-0.007740	0.09125	0.008012	-0.002294	-0.000104	0.001415	-0.000358
Prm3	-0.007512	0.008012	0.01121	-0.001112	0.0001609	-0.000360	-0.000675
Prm4	-0.002224	-0.002294	-0.001112	0.03994	0.003478	0.003458	-0.000717
Prm5	-0.003668	-0.000104	0.0001609	0.003478	0.01383	0.003496	0.0000983
Prm6	-0.003661	0.001415	-0.000360	0.003458	0.003496	0.02762	0.0005947
Prm7	-0.005445	-0.000358	-0.000675	-0.000717	0.0000983	0.0005947	0.009480

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.4284	0.1108	-1.6456	-1.2112	166.16	<.0001
vacchistory	1	1	-0.1010	0.3021	-0.6931	0.4910	0.11	0.7380
vacchistory	2	1	0.4131	0.1059	0.2056	0.6206	15.22	<.0001
bmicat	0	1	-0.0640	0.1998	-0.4556	0.3277	0.10	0.7489
bmicat	2	1	-0.4061	0.1176	-0.6366	-0.1756	11.93	0.0006
bmicat	3	1	-0.6011	0.1662	-0.9268	-0.2753	13.08	0.0003
reftype		1	0.3877	0.0974	0.1968	0.5785	15.85	<.0001
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

Obs	**_NAME_**	**RowName**	**Prm1**	**Prm2**	**Prm3**	**Prm4**
1	ESTIMATE		.	.	.	.
2	Intercep	Prm1	0.0122794	-0.00774	-0.007512	-0.002224
3	vacchist	Prm2	-0.00774	0.0912507	0.0080121	-0.002294
4	vacchist	Prm3	-0.007512	0.0080121	0.0112111	-0.001112
5	bmicat	Prm4	-0.002224	-0.002294	-0.001112	0.0399382
6	bmicat	Prm5	-0.003668	-0.000104	0.0001609	0.0034779
7	bmicat	Prm6	-0.003661	0.001415	-0.00036	0.0034582
8	reftype	Prm7	-0.005445	-0.000358	-0.000675	-0.000717

Obs	**Prm5**	**Prm6**	**Prm7**	**Parameter**	**vacchistory**	**bmicat**
1	.	.	.			
2	-0.003668	-0.003661	-0.005445	Prm1		
3	-0.000104	0.001415	-0.000358	Prm2	1	
4	0.0001609	-0.00036	-0.000675	Prm3	2	
5	0.0034779	0.0034582	-0.000717	Prm4		0
6	0.0138259	0.0034961	0.0000983	Prm5		2
7	0.0034961	0.0276168	0.0005947	Prm6		3
8	0.0000983	0.0005947	0.0094798	Prm7		

Obs	_NAME_	RowName	Prm1	Prm2	Prm3	Prm4
1	ESTIMATE		.	.	.	.
2	Intercep	Prm1	0.0122794	-0.00774	-0.007512	-0.002224
3	vacchist	Prm2	-0.00774	0.0912507	0.0080121	-0.002294
4	vacchist	Prm3	-0.007512	0.0080121	0.0112111	-0.001112
5	bmicat	Prm4	-0.002224	-0.002294	-0.001112	0.0399382
6	bmicat	Prm5	-0.003668	-0.000104	0.0001609	0.0034779
7	bmicat	Prm6	-0.003661	0.001415	-0.00036	0.0034582
8	reftype	Prm7	-0.005445	-0.000358	-0.000675	-0.000717

Obs	Prm5	Prm6	Prm7	Parameter	vacchistory	bmicat
1	.	.	.			
2	-0.003668	-0.003661	-0.005445	Prm1		
3	-0.000104	0.001415	-0.000358	Prm2	1	
4	0.0001609	-0.00036	-0.000675	Prm3	2	
5	0.0034779	0.0034582	-0.000717	Prm4		0
6	0.0138259	0.0034961	0.0000983	Prm5		2
7	0.0034961	0.0276168	0.0005947	Prm6		3
8	0.0000983	0.0005947	0.0094798	Prm7		

VARCOV2						
0.0122794	-0.00774	-0.007512	-0.002224	-0.003668	-0.003661	-0.005445
-0.00774	0.0912507	0.0080121	-0.002294	-0.000104	0.001415	-0.000358
-0.007512	0.0080121	0.0112111	-0.001112	0.0001609	-0.00036	-0.000675
-0.002224	-0.002294	-0.001112	0.0399382	0.0034779	0.0034582	-0.000717
-0.003668	-0.000104	0.0001609	0.0034779	0.0138259	0.0034961	0.0000983
-0.003661	0.001415	-0.00036	0.0034582	0.0034961	0.0276168	0.0005947
-0.005445	-0.000358	-0.000675	-0.000717	0.0000983	0.0005947	0.0094798

Input DATASET covdsn, Submitted 05APR2014
COLLINEARITY DIAGNOSTICS FOR NONLINEAR MODELS USING THE INFORMATION MATRIX: EIGENVALUES, CONDITION INDEXES, AND VARIANCE DECOMPOSITION PROPORTIONS (VDP'S)

VARIABLE	VDP1	VDP2	VDP3	VDP4	VDP5	VDP6	VDP7
EIGENVAL	0.12300	0.31089	0.57691	0.95617	1.00067	1.04469	2.98767
CONDINDX	4.92858	3.10001	2.27569	1.76766	1.72791	1.69111	1.00000
	.	.	.	.	.	.	.
Intercep	0.96371	0.01177	0.00622	0.00004	0.00007	0.00001	0.01819
vacchist	0.07380	0.03989	0.00351	0.46460	0.00000	0.41526	0.00294
vacchist	0.56817	0.37125	0.02565	0.00487	0.00012	0.00519	0.02476
bmicat	0.00352	0.00428	0.25515	0.11077	0.50806	0.10764	0.01058
bmicat	0.05699	0.01118	0.58168	0.02465	0.27799	0.02219	0.02531
bmicat	0.02700	0.01702	0.27950	0.31546	0.05766	0.29085	0.01253
reftype	0.22243	0.66193	0.08392	0.00025	0.00001	0.00009	0.03137

Input DATASET covdsn, Submitted 05APR2014
COLLINEARITY DIAGNOSTICS FOR NONLINEAR MODELS USING THE INFORMATION MATRIX: EIGENVALUES, CONDITION INDEXES, AND VARIANCE DECOMPOSITION PROPORTIONS (VDP'S)

Directory	
Libref	WORK
Engine	V9
Physical Name	F:\SAS Temporary Files_TD10256_VDS3-CTX-SAS13_
Filename	F:\SAS Temporary Files_TD10256_VDS3-CTX-SAS13_

#	Name	Member Type	File Size	Last Modified
1	ALIEN	DATA	12698624	05Apr14:10:39:56
2	COMBINED	DATA	9536512	05Apr14:10:39:57
3	COMBINED2	DATA	8471552	05Apr14:10:39:57
4	COMBINED_CLEAN	DATA	7750656	05Apr14:10:39:57

#	Name	Member Type	File Size	Last Modified
5	COMBINED_CLEAN_ADULTS	DATA	5669888	05Apr14:10:39:57
6	COVDSN	DATA	9216	05Apr14:10:43:19
7	FORMATS	CATALOG	17408	05Apr14:10:39:57
8	NEXT_1	DATA	5120	05Apr14:10:43:19
9	NEXT_1A	DATA	9216	05Apr14:10:43:19
10	NEXT_2	DATA	9216	05Apr14:10:43:19
11	NEXT_3	DATA	9216	05Apr14:10:43:19
12	NEXT_4	DATA	5120	05Apr14:10:43:19
13	NEXT_5	DATA	9216	05Apr14:10:43:19
14	PARMS	DATA	5120	05Apr14:10:43:19
15	RRMODEL	DATA	9216	05Apr14:10:43:19
16	SASMACR	CATALOG	5120	05Apr14:10:39:29
17	VACC	DATA	443392	05Apr14:10:39:56

Appendix O. SAS output for effect estimates in the sub-analysis

For the logistic regression model presented, the variable will be represented in the following ways:

Anti-HBs = ANTIHBS

Hepatitis B vaccination history =VACCHISTORY

Immigration status = REFTYPE

BMI category = BMI

Model:

$$\text{logit } P(\text{ANTIHBS}) = \alpha + \beta_1(\text{VACCHISTORY}_1) + \beta_2(\text{VACCHISTORY}_2) + \beta_1(\text{BMI}_1) + \beta_2(\text{BMI}_2) + \beta_3(\text{BMI}_3) + \beta_4(\text{REFTYPE})$$

Where VACCHISTORY_1=1 if incomplete hepatitis B vaccination history; else=0

VACCHISTORY_2=1 if complete hepatitis B vaccination history; else=0

BMI_1=1 if BMI category=0; else=0

BMI_2=1 if BMI category=2; else=0

BMI_3=1 if BMI category=3; else=0

The GENMOD Procedure

Model Information	
Data Set	WORK.COMBINED_CLEAN_ADULTS
Distribution	Binomial
Link Function	Log
Dependent Variable	antihbs2

Number of Observations Read	1033
Number of Observations Used	930
Number of Events	284

Number of Trials	930
Missing Values	103

Class Level Information				
Class	**Value**	**Design Variables**		
vacchistory	**0**	0	0	
	1	1	0	
	2	0	1	
bmicat	**0**	1	0	0
	1	0	0	0
	2	0	1	0
	3	0	0	1

Response Profile		
Ordered Value	**antihbs2**	**Total Frequency**
1	1	284
2	0	646

PROC GENMOD is modeling the probability that antihbs2='1'.

Parameter Information			
Parameter	**Effect**	**vacchistory**	**bmicat**
Prm1	Intercept		
Prm2	vacchistory	1	
Prm3	vacchistory	2	
Prm4	bmicat		0
Prm5	bmicat		2
Prm6	bmicat		3
Prm7	reftype		

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Log Likelihood		-543.4995	

Criteria For Assessing Goodness Of Fit			
Criterion	**DF**	**Value**	**Value/DF**
Full Log Likelihood		-543.4995	
AIC (smaller is better)		1100.9990	
AICC (smaller is better)		1101.1205	
BIC (smaller is better)		1134.8453	

Algorithm converged.

Analysis Of Maximum Likelihood Parameter Estimates								
Parameter		**DF**	**Estimate**	**Standard Error**	**Wald 95% Confidence Limits**		**Wald Chi-Square**	**Pr > ChiSq**
Intercept		1	-1.4284	0.1108	-1.6456	-1.2112	166.16	<.0001
vacchistory	1	1	-0.1010	0.3021	-0.6931	0.4910	0.11	0.7380
vacchistory	2	1	0.4131	0.1059	0.2056	0.6206	15.22	<.0001
bmicat	0	1	-0.0640	0.1998	-0.4556	0.3277	0.10	0.7489
bmicat	2	1	-0.4061	0.1176	-0.6366	-0.1756	11.93	0.0006
bmicat	3	1	-0.6011	0.1662	-0.9268	-0.2753	13.08	0.0003
reftype		1	0.3877	0.0974	0.1968	0.5785	15.85	<.0001
Scale		0	1.0000	0.0000	1.0000	1.0000		

Note: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis			
Source	**DF**	**Chi-Square**	**Pr > ChiSq**
vacchistory	2	18.30	0.0001
bmicat	3	23.44	<.0001
reftype	1	16.25	<.0001

Contrast Estimate Results								
		Mean					**L'Beta**	
Label	**Mean Estimate**	**Confidence Limits**		**L'Beta Estimate**	**Standard Error**	**Alpha**	**Confidence Limits**	
EFFECT OF VACCHX=1	0.9039	0.5000	1.6340	-0.1010	0.3021	0.05	-0.6931	0.4910

Contrast Estimate Results								
		Mean					L'Beta	
Label	Mean Estimate	Confidence Limits		L'Beta Estimate	Standard Error	Alpha	Confidence Limits	
EFFECT OF VACCHX=2	1.5115	1.2282	1.8601	0.4131	0.1059	0.05	0.2056	0.6206
EFFECT OF BMICAT=0 (UNDERWEIGHT)	0.9380	0.6340	1.3878	-0.0640	0.1998	0.05	-0.4556	0.3277
EFFECT OF BMICAT=2 (OVERWEIGHT)	0.6662	0.5291	0.8389	-0.4061	0.1176	0.05	-0.6366	-0.1756
EFFECT OF BMICAT=3 (OBESE)	0.5482	0.3958	0.7593	-0.6011	0.1662	0.05	-0.9268	-0.2753
EFFECT OF REFTYPE=1 (PAROLEE)	1.4736	1.2176	1.7834	0.3877	0.0974	0.05	0.1968	0.5785

Contrast Estimate Results		
Label	Chi-Square	Pr > ChiSq
EFFECT OF VACCHX=1	0.11	0.7380
EFFECT OF VACCHX=2	15.22	<.0001
EFFECT OF BMICAT=0 (UNDERWEIGHT)	0.10	0.7489
EFFECT OF BMICAT=2 (OVERWEIGHT)	11.93	0.0006
EFFECT OF BMICAT=3 (OBESE)	13.08	0.0003
EFFECT OF REFTYPE=1 (PAROLEE)	15.85	<.0001

Appendix P. Institutional Review Board letter of exemption

Institutional Review Board

September 16, 2013

Anna Fulton
MPH Candidate 2014 | Epidemiology
Co-Logistician | Student Outbreak and Response Team (SORT)
Rollins School of Public Health | Emory University
Cell 678.787.0497

RE: Determination: No IRB Review Required
PI: Anna Fulton

Dear Ms. Fulton:

Thank you for requesting a determination from our office about the above-referenced project. Based on our review of the materials you provided, we have determined that it does not require IRB review because it does not meet the definition of "research" or the definition of "clinical investigation" as set forth in Emory policies and procedures and federal rules, if applicable. Specifically, in this project, you will be examining overseas medical examination data in the electronic Disease Notification system for the purpose of quality improvement. The objectives of this project are limited to identifying discrepancies between medical examination results and characterizing disease burden in U.S.-bound Cuban refugees and parolees, with the aim of informing public health programs targeting these specific refugees

This determination could be affected by substantive changes in the study design, subject populations, or identifiability of data. If the project changes in any substantive way, please contact our office for clarification.

Thank you for consulting the IRB.

Sincerely,

Steven J. Anzalone, M.S.
IRB Research Protocol Analyst
This letter has been digitally signed