

## Supplement

**Supplementary Table 1: Association between neonatal mortality (death at  $\leq 30$  days) and level of sanitation access in the community for women with and without household level access to sanitation.**

| Household Sanitation | Community-level sanitation Coverage | Unadjusted Incidence Rate Ratio (95% CI) | P-value | Adjusted Incidence Rate Ratio (95% CI) | P-value |
|----------------------|-------------------------------------|--|---------|--|---------|
|                      |                                     | <i>n</i> =832 663                        |         | <i>n</i> =823 179                      |         |
| Yes                  | 1-30%                               | Reference                                | N/A     | Reference                              | N/A     |
| Yes                  | 31-60%                              | 0.98 (0.89-1.07)                         | 0.64    | 0.98 (0.89-1.07)                       | 0.60    |
| Yes                  | 61-99%                              | 0.89 (0.82-0.97)                         | 0.01    | 0.90 (0.83-0.98)                       | 0.02    |
| Yes                  | 100%                                | 0.82 (0.75-0.89)                         | <0.001  | 0.84 (0.77-0.92)                       | <0.001  |
|                      |                                     | <i>n</i> =434 965                        |         | <i>n</i> =431 683                      |         |
| No                   | 0%                                  | 0.97 (0.92-1.02)                         | 0.27    | 0.98 (0.93-1.04)                       | 0.51    |
| No                   | 1-30%                               | Reference                                | N/A     | Reference                              | N/A     |
| No                   | 31-60%                              | 0.92 (0.86-0.98)                         | 0.01    | 0.93 (0.87-1.00)                       | 0.04    |
| No                   | 61-99%                              | 0.93 (0.87-1.01)                         | 0.07    | 0.96 (0.89-1.03)                       | 0.25    |

Poisson Regression

Unadjusted models included the dataset

Adjusted models included mother's age, mother's age squared, parity, wealth quintile, mother's education, antenatal care quality score, urban or rural, mother's stunting, child's gender, facility delivery or not, and dataset.

N/A-not applicable

**Supplementary Table 2: Association between low birth weight (<2500g at birth) and level of sanitation access in the community for women with and without household level access to sanitation.**

| Household Sanitation Access | Community-level sanitation Access | Unadjusted Odds Ratio (95% CI) | P-value | Adjusted Odds Ratio (95% CI) | P-value |
|-----------------------------|-----------------------------------|--------------------------------|---------|------------------------------|---------|
|                             |                                   | n=474 789                      |         | n=472 646                    |         |
| Yes                         | 1-30%                             | Reference                      | N/A     | Reference                    | N/A     |
| Yes                         | 31-60%                            | 0.98 (0.92-1.04)               | 0.53    | 0.98 (0.92-1.04)             | 0.56    |
| Yes                         | 61-99%                            | 0.97 (0.92-1.03)               | 0.34    | 0.98 (0.93-1.04)             | 0.49    |
| Yes                         | 100%                              | 0.89 (0.84-0.94)               | <0.001  | 0.91 (0.86-0.97)             | 0.002   |
|                             |                                   | n=151 687                      |         | n=151 321                    |         |
| No                          | 0%                                | 0.95 (0.91-1.00)               | 0.04    | 0.98 (0.94-1.03)             | 0.43    |
| No                          | 1-30%                             | Reference                      | N/A     | Reference                    | N/A     |
| No                          | 31-60%                            | 0.98 (0.93-1.04)               | 0.49    | 1.03 (0.97-1.08)             | 0.37    |
| No                          | 61-99%                            | 0.97 (0.92-1.03)               | 0.36    | 1.04 (0.97-1.10)             | 0.26    |

Logistic Regression

Unadjusted models included the dataset

Adjusted models included mother's age, mother's age squared, parity, wealth quintile, mother's education, antenatal care quality score, urban or rural, mother's stunting, child's gender, facility delivery or not, and dataset.

N/A-not applicable

**Appendix****Statistical Analysis Script**

NOTE: Files names and locations will need be changed to match where they are saved on your computer.

**Stata Script**

```

*****
***Creating dataset***
*****
use "/YEAR DHS COUNTRY household file.dta" , clear
gen notoilet = 1 if hv205 == 31
replace notoilet = 0 if hv205!=31 & hv205!=.
egen opendefecation = mean(notoilet), by (hv001)
gen surfacewater = 1 if hv201 == 43
replace surfacewater = 0 if hv201!=43 & hv201!=.
egen communitysurfacewater = mean(surfacewater), by(hv001)
egen communitywealth = mean(hv270), by (hv001)
gen preg = 0 if v213==1
replace preg = 1 if v213==2
gen child_a_twin = b0_1
replace child_a_twin = 1 if b0_1>0
drop if child_a_twin==1
rename hv001 v001
rename hv002 v002
keep v001 v002 hv025 notoilet-communitywealth
merge 1:m v001 v002 using "/YEAR DHS COUNTRY mother file.dta"
drop if _merge==1
drop _merge
gen str countryname = "COUNTRY"
gen str dataset = "COUNTRY DHS YEAR"
keep v001-communitywealth communitywealthtertile-dataset
save "/COUNTRY DHS YEAR.dta", replace

*Repeat for all datasets included in analysis*

use "/COUNTRY DHS YEAR.dta", clear
append using "/COUNTRY DHS YEAR 2.dta"
*Repeat for all datasets included in analysis*
compress
drop if notoilet==.
save "/Compiled.dta", replace
keep if preg==1
save "/Compiled pregos.dta", replace

*****
***Creating variables***
*****

*****
**Exposure variables**
*****

```

```
**Household Sanitation**
gen notoilet = 1 if hv205 == 31
replace notoilet = 0 if hv205!=31 & hv205!=.
gen toilet=0
replace toilet=1 if notoilet==0
replace toilet=. if notoilet==.

**Community Sanitation Coverage (1-30% as the Reference Group)**
egen opendefecation = mean(notoilet), by (hv001)
gen commsan=1-opendefecation
gen commsanecat=0
replace commsanecat=1 if commsan==0
replace commsanecat=2 if commsan>.30
replace commsanecat=3 if commsan>.60
replace commsanecat=4 if commsan==1

*****
***Outcome variables**
*****

*Index to birth history*
gen index_to_birth_history = midx_1

*DROPPING THE WOMEN WITHOUT A BIRTH IN LAST 2 YEARS*
drop if midx_1==.

**Neonatal Mortality**
*DHS codes this with a 3 digit number. The first digit (hundreds place) is
1=days, 2=weeks, 3=months. The second and third digit then are the number of
days, weeks or months
gen age_at_death = 999
replace age_at_death = b6_1-100 if b6_1<200
replace age_at_death = 30 if b6_1==201
gen death=0
replace death=1 if age_at_death<=30

**Death at <=28 days (neonatal death)**
gen death2=death
replace death2=0 if age_at_death>=29

**Size of Child at Birth**
*Missing = 99
gen birthsize = m18_1
gen vsmall=1
replace vsmall=0 if birthsize!=5
replace vsmall=. if birthsize>=8

**Birth Weight (kilos - 3dec)**
**800-6,000, not weighed = 9996, don't know = 9998, missing = 9999
*2: Not weighed
*99 :don't know, and missing
gen birthweight = m19_1
gen lbw=1
replace lbw=0 if birthweight>=2500
replace lbw=. if birthweight>=9996

**Anemia**
```

```
*0 no anemia or mild anemia
*1 moderate or severe anemia
gen modsevanemia = 0 if v457>2 & v457!=.
replace modsevanemia = 1 if v457<3

*****
**Matching Variables**
*****

*Household wealth in the sampling unit*
egen communitywealth = mean(hv270), by (hv001)
xtile communitywealthtertile = communitywealth, nq(3)

*Access to improved water source in sampling unit*
gen surfacewater = 1 if hv201 == 43
replace surfacewater = 0 if hv201!=43 & hv201!=.
egen communitysurfacewater = mean(surfacewater), by(hv001)
xtile communitywatertertile = communitysurfacewater, nq(3)

*Mother's education - completed primary or not*
*0 coded as incomplete primary or no education
*1 coded as completed primary
gen primaryeduc = 0 if v149!=.
replace primaryeduc = 1 if v149>1 & v149!=.

*Household above or below median household wealth*
*1 coded as below median wealth
*2 coded as above median wealth
xtile richpoor = v191, nq(2)

*****
*Regression Covariates*
*****

*Age of the mother at birth (in years) and age squared*
gen age = b2_1-v010
gen age2=age*age

*Parity*
gen parity = 2
replace parity = 1 if bord_1==1
replace parity = 3 if b11_1<25
replace parity = 4 if bord_1>2
replace parity = 5 if bord_1>2 & b11_1<25

*Wealth Quintile*
*1 : 1st quintile
*2 : 2nd quintile
*3 : 3rd quintile
*4 : 4th quintile
*5 : 5th quintile
*99 : missing
gen wealth = v190

*Mother's education*
*0 : none
*1 : some primary
```

```
*2 : completed primary
*3 : higher than primary
*99 : missing
gen educ = 0 if v149==0
replace educ = 1 if v149==1
replace educ = 2 if v149==2
replace educ = 3 if v149>2 & v149!=.

*Antenatal Care Quality*
*During pregnancy: Weighed
*no = 0
*yes = 1
*missing = 99
gen weighed_during_pregnancy = m42a_1
replace weighed_during_pregnancy = . if m42a_1>1

*During pregnancy: Height Measured
*no = 0
*yes = 1
*missing = 99
gen measured_during_pregnancy = m42b_1
replace measured_during_pregnancy = . if m42b_1>1

*During pregnancy: Urine Sample Given
*no = 0
*yes = 1
*missing = 99
gen urine_sample_during_pregnancy = m42d_1
replace urine_sample_during_pregnancy = . if m42d_1>1

*During pregnancy: Blood Pressure Measured
*no = 0
*yes = 1
*missing = 99
gen bp_taken_during_pregnancy = m42c_1
replace bp_taken_during_pregnancy = . if m42c_1>1

*During pregnancy: Blood Sample Given
*no = 0
*yes = 1
*missing = 99
gen blood_sample_during_pregnancy = m42e_1
replace blood_sample_during_pregnancy = . if m42e_1>1

*During Pregnancy: Told About Pregnancy Complications
*no = 0
*yes = 1
*don't know = 99
*missing = 99
gen told_about_pregnancy_comp = m43_1
replace told_about_pregnancy_comp = . if m43_1>1

*During Pregnancy: Took fansidar for malaria
*no = 0
*yes = 1
*don't know = 99
*missing = 99
```

```
gen fansidar_during_pregnancy = m49a_1
replace fansidar_during_pregnancy = . if m49a_1>1

*During Pregnancy: Drugs for Intestinal Parasites
*no = 0
*yes = 1
*don't know = 99
*missing = 99
gen drugs_intestinal_parasites = m60_1
replace drugs_intestinal_parasites = . if m60_1>1

*During Pregnancy: Iron Supplementation
*0 : No
*1 : Yes
gen ironsupplementation = 0 if m45_1==0
replace ironsupplementation = 1 if m45_1==1

*Running principle components analysis of binary variables
pca weighed_during_pregnancy measured_during_pregnancy
bp_taken_during_pregnancy urine_sample_during_pregnancy
blood_sample_during_pregnancy told_about_pregnancy_comp
fansidar_during_pregnancy drugs_intestinal_parasites ironsupplementation
* Predicting the score
predict ancscore
*Creating quintiles
xtile ancquality = ancscore, nq(5)

*Urban/Rural*
*0 : Rural
*1 : Urban
*99 : missing
gen urban = 0 if v025==1
replace urban = 1 if v025==2
replace urban = 99 if urban==.

*Mother's Stunting*
*0 not stunted, at least 150 cm (4.9 ft)
*1 stunted, smaller than 150 cm (4.9 ft)
gen stunted = 0 if v438<2000
replace stunted = 1 if v438<1500

*Sex of Child*
*1 = Male
*0 = Female
gen male = 0
replace male = 1 if b4_1==1

*Place of delivery*
* 0 = in a home
* 1 = in a facility
gen facilitydelivery = 0 if m15_1<20 | m15_1==96
replace facilitydelivery = 1 if m15_1>19 & m15_1!=96 & m15_1!=.

*****
***Generalized Linear Models***
*****
```

```
import delimited "/Compiled and matched.csv", clear

***REMOVING THE DATASETS WITH <5% OF HOUSEHOLDS NOT HAVING ACCESS TO
SANITATION
by dataset, sort: egen notoiletdataset=mean(notoilet)
drop if notoiletdataset<=.05
egen datasetnumeric= group(dataset)

*Drop Twins
***Child is a Twin***
*0 : No
*1 : Yes
gen child_a_twin = b0_1
replace child_a_twin = 1 if b0_1>0
drop if child_a_twin==1

xtset subclass

*****
**Neonatal Mortality**
*****

***Unadjusted regression***

xtpoisson death2 i.commsancat i.datasetnumeric if toilet==1,
exposure(exposure) irr
xtpoisson death2 i.commsancat i.datasetnumeric if toilet==0,
exposure(exposure) irr

xtpoisson death i.commsancat i.datasetnumeric if toilet==1,
exposure(exposure) irr
xtpoisson death i.commsancat i.datasetnumeric if toilet==0,
exposure(exposure) irr

***Adjusted regression***

xtpoisson death2 i.commsancat age age2 i.parity i.wealth i.educ i.ancquality
urban stunted male i.facilitydelivery i.datasetnumeric if toilet==1,
exposure(exposure) irr
xtpoisson death2 i.commsancat age age2 i.parity i.wealth i.educ i.ancquality
urban stunted male i.facilitydelivery i.datasetnumeric if toilet==0,
exposure(exposure) irr

xtpoisson death i.commsancat age age2 i.parity i.wealth i.educ i.ancquality
urban stunted male i.facilitydelivery i.datasetnumeric if toilet==1,
exposure(exposure) irr
xtpoisson death i.commsancat age age2 i.parity i.wealth i.educ i.ancquality
urban stunted male i.facilitydelivery i.datasetnumeric if toilet==0,
exposure(exposure) irr

*****
**Low Birthweight**
*****

***Unadjusted regression***

xtlogit lbw i.commsancat i.datasetnumeric if toilet==1, or
```



```
xtlogit lbw i.commsancat i.datasetnumeric if toilet==0, or
xtlogit vsmall i.commsancat i.datasetnumeric if toilet==1, or
xtlogit vsmall i.commsancat i.datasetnumeric if toilet==0, or

***Adjusted regression***

xtlogit lbw i.commsancat age age2 i.parity i.wealth i.educ i.ancquality urban
stunted male facilitydelivery i.datasetnumeric if toilet==1, or
xtlogit lbw i.commsancat age age2 i.parity i.wealth i.educ i.ancquality urban
stunted male facilitydelivery i.datasetnumeric if toilet==0, or

xtlogit vsmall i.commsancat age age2 i.parity i.wealth i.educ i.ancquality
urban stunted male facilitydelivery i.datasetnumeric if toilet==1, or
xtlogit vsmall i.commsancat age age2 i.parity i.wealth i.educ i.ancquality
urban stunted male facilitydelivery i.datasetnumeric if toilet==0, or

*****
**Anemia**
*****

***Unadjusted regression***

xtlogit modsevanemia i.commsancat i.datasetnumeric if toilet==1, or
xtlogit modsevanemia i.commsancat i.datasetnumeric if toilet==0, or

***Adjusted regression***

xtlogit modsevanemia i.commsancat age age2 i.parity i.wealth i.educ hv025
i.datasetnumeric if toilet==1, or
xtlogit modsevanemia i.commsancat age age2 i.parity i.wealth i.educ hv025
i.datasetnumeric if toilet==0, or

**Anemia in pregnant women**

import delimited "/Compiled and matched anemia pregos.csv", clear

***REMOVING THE DATASETS WITH <5% OF HOUSEHOLDS NOT HAVING ACCESS TO
SANITATION
by dataset, sort: egen notoiletdataset=mean(notoilet)
drop if notoiletdataset<=.05
egen datasetnumeric= group(dataset)

xtset subclass

***Unadjusted regression***

xtlogit modsevanemia i.commsancat i.datasetnumeric if toilet==1, or
xtlogit modsevanemia i.commsancat i.datasetnumeric if toilet==0, or

***Adjusted regression***

xtlogit modsevanemia i.commsancat age age2 i.parity i.wealth i.educ hv025
i.datasetnumeric if toilet==1, or
xtlogit modsevanemia i.commsancat age age2 i.parity i.wealth i.educ hv025
i.datasetnumeric if toilet==0, or
```

**R Script**

```
library(MatchIt)
library(foreign)

###LOADING DATASETS, setting missing values to 9999###
d = read.dta("/Compiled dataset.dta")

### RECLASSIFYING MISSING VALUES ###
d[is.na(d)] = 9999

###EXACT MATCHING###
m.out = matchit(otoilet~dataset + communitywealthtertile +
communitywatertertile + primaryeduc + richpoor, data=d, method="exact")

###CREATING DATASET WITH MATCHED VARIABLE SUBCLASS###
m.data = match.data(m.out)

###EXPORTING DATASET TO DATAFRAME###
d.matched = data.frame(m.data)

###WRITING TEXT FILES
write.table(d.matched, file="/Compiled and matched.csv", sep=",",
col.names=TRUE, row.names=FALSE)

### PREGNANT WOMEN ###

###LOADING DATASETS, setting missing values to 9999###
d.prego = subset(d, preg==1)

###EXACT MATCHING###
m.out.prego = matchit(otoilet~dataset + communitywealthtertile +
communitywatertertile + primaryeduc + richpoor, data=d.prego, method="exact")

###CREATING DATASET WITH MATCHED VARIABLE SUBCLASS###
m.data.prego = match.data(m.out.prego)

###EXPORTING DATASET TO DATAFRAME###
d.matched.prego = data.frame(m.data.prego)

###WRITING TEXT FILES
write.table(d.matched.prego, file="/Compiled and matched anemia pregos.csv",
sep=",", col.names=TRUE, row.names=FALSE)
```