**Supplementary file**

**Table 1: Sample size estimation**

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| Sample Size for males = 293  Population size (for finite correction factor or fpc) (N) = 1000000  Hypothesized % frequency of outcome factor in the population (p)= 74.4%±5  Confidence limits as % of 100 (d)=5%  Design effect (DEFF)=1  Confidence Level (%)=95% |
| Sample Size for females = 296  Population size (for finite correction factor or fpc) (N) = 1000000  Hypothesized % frequency of outcome factor in the population (p)= 74%±5  Confidence limits as % of 100 (d)=5%  Design effect (DEFF)=1  Confidence Level (%)=95% |
| Total sample N **=** 293+296= 589 |
| Taking into account 10% attrition rate, in total 684 participants were enrolled, however only 589 participants completed the study. |

The equation used to calculate the sample size for cross sectional study:

n = [DEFF\*Np(1-p)]/ [(d2/Z21-α/2\*(N-1)+p\*(1-p)]

**Table 2: Statistical codes used for calculation of probability risk of inadequacy**

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| **#Normal Intake and normal requirement#**   1. muR<-EAR ;sigR<-(RDA-EAR)/1.96 2. muIntake<-mean(Intake, na.rm=T) 3. sigIntake<-sd(Intake, na.rm=T) 4. riskN<- function(x, mu,sig) {1- pnorm(x, mu, sig)}   risk(x)<-function(x){1-pnorm(x,mean = muR, sd = sigR)}   1. y<-rnorm(n=100000, mean= muIntake,sd = sigIntake) 2. PIA<-mean(risk(y)) |
| **#Log Normal Intake and normal requirement#**   1. muR<-EAR ;sigR<-(RDA-EAR)/1.96 2. nutrientIntake<- nutrientIntake [nutrientIntake >0] 3. muIntake<-mean (log(nutrientIntake), na.rm=T) 4. sigIntake<-sd(log(nutrientIntake),na.rm=T) 5. risk(x)<-function(x){1-pnorm(x,mean = muR, sd = sigR)}   riskN<- function(x, mu,sig) {1- pnorm(x, mu, sig)}   1. y<-rlnorm(n=100000, meanlog = muIntake,sdlog = sigIntake) 2. PIA<-mean(risk(y)) |
| **#Log Normal Intake and log normal requirement#**   1. muR<-log(EAR);sigR<-(log(RDA)-log(EAR))/1.96 2. nutrientIntake <- nutrientIntake [nutrientIntake >0] 3. muIntake<-mean (log(nutrientIntake), na.rm=T) 4. sigIntake<-sd(log(nutrientIntake),na.rm=T) 5. risk(x)<-function(x){1-plnorm(x,meanlog = muR, sdlog = sigR)}   riskLN<- function(x,logmu, logsig) {1 - plnorm(x,logmu, logsig)}   1. y<-rlnorm(n=100000, meanlog = muIntake, sdlog = sigIntake) 2. PIA<-mean(risk(y)) |