**Supplementary file**

**Table 1: Sample size estimation**

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| Sample Size for males = 293Population size (for finite correction factor or fpc) (N) = 1000000Hypothesized % frequency of outcome factor in the population (p)= 74.4%±5Confidence limits as % of 100 (d)=5%Design effect (DEFF)=1Confidence Level (%)=95% |
| Sample Size for females = 296Population size (for finite correction factor or fpc) (N) = 1000000Hypothesized % frequency of outcome factor in the population (p)= 74%±5Confidence limits as % of 100 (d)=5%Design effect (DEFF)=1Confidence 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))
 |