

R CODES FOR TWO EXAMPLES

FIRST EXMAPLE

The urine concentration of monocarboxynonyl phthalate, monocarboxyoctyl phthalate, mono-2-ethyl-5-carboxypentyl phthalate, and mono-2-hydroxy-iso-butyl phthalate (all ng/mL) were used as the independent variable, respectively.

SECOND EXAMPLE

The serum concentration of PCB105, PCB114, PCB118, and PCB138 were used as the independent variable, respectively.

FIRST EXAMPLE

A. R codes to construct the analysis dataset

```
download.file("http://wwwn.cdc.gov/nchs/nhanes/2003-2004/L24PH_C.XPT", tf <- tempfile(), mode="wb")
L24PH_C <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2005-2006/PHTHTE_D.XPT", tf <- tempfile(), mode="wb")
PHTHTE_D <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2007-2008/PHTHTE_E.XPT", tf <- tempfile(), mode="wb")
PHTHTE_E <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2009-2010/PHTHTE_F.XPT", tf <- tempfile(), mode="wb")
PHTHTE_F <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2011-2012/PHTHTE_G.XPT", tf <- tempfile(), mode="wb")
PHTHTE_G <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2013-2014/PHTHTE_H.XPT", tf <- tempfile(), mode="wb")
PHTHTE_H <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2015-2016/PHTHTE_I.XPT", tf <- tempfile(), mode="wb")
PHTHTE_I <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2017-2018/PHTHTE_J.XPT", tf <- tempfile(), mode="wb")
PHTHTE_J <- foreign::read.xport(tf)
PHTHTE <- bind_rows(L24PH_C,PHTHTE_D,PHTHTE_E,PHTHTE_F,PHTHTE_G,PHTHTE_H,PHTHTE_I,PHTHTE_J)
```

```
download.file("http://wwwn.cdc.gov/nchs/nhanes/2003-2004/DEMO_C.XPT", tf <- tempfile(), mode="wb")
DEMO_C <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2005-2006/DEMO_D.XPT", tf <- tempfile(), mode="wb")
DEMO_D <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2007-2008/DEMO_E.XPT", tf <- tempfile(), mode="wb")
DEMO_E <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2009-2010/DEMO_F.XPT", tf <- tempfile(), mode="wb")
DEMO_F <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2011-2012/DEMO_G.XPT", tf <- tempfile(), mode="wb")
DEMO_G <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2013-2014/DEMO_H.XPT", tf <- tempfile(), mode="wb")
DEMO_H <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2015-2016/DEMO_I.XPT", tf <- tempfile(), mode="wb")
DEMO_I <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2017-2018/DEMO_J.XPT", tf <- tempfile(), mode="wb")
DEMO_J <- foreign::read.xport(tf)
DEMO <- bind_rows(DEMO_C,DEMO_D,DEMO_E,DEMO_F,DEMO_G,DEMO_H,DEMO_I,DEMO_J)
```

```
download.file("http://wwwn.cdc.gov/nchs/nhanes/2003-2004/BMX_C.XPT", tf <- tempfile(), mode="wb")
BMX_C <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2005-2006/BMX_D.XPT", tf <- tempfile(), mode="wb")
BMX_D <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2007-2008/BMX_E.XPT", tf <- tempfile(), mode="wb")
BMX_E <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2009-2010/BMX_F.XPT", tf <- tempfile(), mode="wb")
BMX_F <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2011-2012/BMX_G.XPT", tf <- tempfile(), mode="wb")
BMX_G <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2013-2014/BMX_H.XPT", tf <- tempfile(), mode="wb")
BMX_H <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2015-2016/BMX_I.XPT", tf <- tempfile(), mode="wb")
BMX_I <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2017-2018/BMX_J.XPT", tf <- tempfile(), mode="wb")
BMX_J <- foreign::read.xport(tf)
BMX <- bind_rows(BMX_C,BMX_D,BMX_E,BMX_F,BMX_G,BMX_H,BMX_I,BMX_J)
```

```
download.file("http://wwwn.cdc.gov/nchs/nhanes/2003-2004/MCQ_C.XPT", tf <- tempfile(), mode="wb")
MCQ_C <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2005-2006/MCQ_D.XPT", tf <- tempfile(), mode="wb")
MCQ_D <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2007-2008/MCQ_E.XPT", tf <- tempfile(), mode="wb")
MCQ_E <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2009-2010/MCQ_F.XPT", tf <- tempfile(), mode="wb")
MCQ_F <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2011-2012/MCQ_G.XPT", tf <- tempfile(), mode="wb")
MCQ_G <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2013-2014/MCQ_H.XPT", tf <- tempfile(), mode="wb")
MCQ_H <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2015-2016/MCQ_I.XPT", tf <- tempfile(), mode="wb")
MCQ_I <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2017-2018/MCQ_J.XPT", tf <- tempfile(), mode="wb")
MCQ_J <- foreign::read.xport(tf)
MCQ <- bind_rows(MCQ_C,MCQ_D,MCQ_E,MCQ_F,MCQ_G,MCQ_H,MCQ_I,MCQ_J)
```

```
download.file("http://wwwn.cdc.gov/nchs/nhanes/2003-2004/L40_C.XPT", tf <- tempfile(), mode="wb")
L40_C <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2005-2006/BIOPRO_D.XPT", tf <- tempfile(), mode="wb")
BIOPRO_D <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2007-2008/BIOPRO_E.XPT", tf <- tempfile(), mode="wb")
BIOPRO_E <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2009-2010/BIOPRO_F.XPT", tf <- tempfile(), mode="wb")
BIOPRO_F <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2011-2012/BIOPRO_G.XPT", tf <- tempfile(), mode="wb")
BIOPRO_G <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2013-2014/BIOPRO_H.XPT", tf <- tempfile(), mode="wb")
BIOPRO_H <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2015-2016/BIOPRO_I.XPT", tf <- tempfile(), mode="wb")
BIOPRO_I <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2017-2018/BIOPRO_J.XPT", tf <- tempfile(), mode="wb")
BIOPRO_J <- foreign::read.xport(tf)
BIOPRO <- bind_rows(L40_C, BIOPRO_D, BIOPRO_E, BIOPRO_F, BIOPRO_G, BIOPRO_H, BIOPRO_I, BIOPRO_J)

download.file("http://wwwn.cdc.gov/nchs/nhanes/2003-2004/L06COT_C.XPT", tf <- tempfile(), mode="wb")
```

```
L06COT_C <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2005-2006/COT_D.XPT", tf <- tempfile(), mode="wb")
COT_D <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2007-2008/COTNAL_E.XPT", tf <- tempfile(), mode="wb")
COTNAL_E <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2009-2010/COTNAL_F.XPT", tf <- tempfile(), mode="wb")
COTNAL_F <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2011-2012/COTNAL_G.XPT", tf <- tempfile(), mode="wb")
COTNAL_G <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2013-2014/COT_H.XPT", tf <- tempfile(), mode="wb")
COT_H <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2015-2016/COT_I.XPT", tf <- tempfile(), mode="wb")
COT_I <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2017-2018/COT_J.XPT", tf <- tempfile(), mode="wb")
COT_J <- foreign::read.xport(tf)
COT <- bind_rows(L06COT_C,COT_D,COTNAL_E,COTNAL_F,COTNAL_G,COT_H,COT_I,COT_J)

download.file("http://wwwn.cdc.gov/nchs/nhanes/2003-2004/RHQ_C.XPT", tf <- tempfile(), mode="wb")
```

```
RHQ_C <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2005-2006/RHQ_D.XPT", tf <- tempfile(), mode="wb")
RHQ_D <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2007-2008/RHQ_E.XPT", tf <- tempfile(), mode="wb")
RHQ_E <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2009-2010/RHQ_F.XPT", tf <- tempfile(), mode="wb")
RHQ_F <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2011-2012/RHQ_G.XPT", tf <- tempfile(), mode="wb")
RHQ_G <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2013-2014/RHQ_H.XPT", tf <- tempfile(), mode="wb")
RHQ_H <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2015-2016/RHQ_I.XPT", tf <- tempfile(), mode="wb")
RHQ_I <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2017-2018/RHQ_J.XPT", tf <- tempfile(), mode="wb")
RHQ_J <- foreign::read.xport(tf)
RHQ <- bind_rows(RHQ_C,RHQ_D,RHQ_E,RHQ_F,RHQ_G,RHQ_H,RHQ_I,RHQ_J)
```

```
PHTHTE.DEMO=left_join(PHTHTE,DEMO,by="SEQN")
PHTHTE.DEMO.BMX=left_join(PHTHTE.DEMO,BMX,by="SEQN")
```



```
PHTHTE.DEMO.BMX.MCQ=left_join(PHTHTE.DEMO.BMX,MCQ,by="SEQN")
PHTHTE.DEMO.BMX.MCQ.BIO=left_join(PHTHTE.DEMO.BMX.MCQ,BIOPRO,by="SEQN")
PHTHTE.DEMO.BMX.MCQ.BIO.COT=left_join(PHTHTE.DEMO.BMX.MCQ.BIO,COT,by="SEQN")
FINAL.DATA=left_join(PHTHTE.DEMO.BMX.MCQ.BIO.COT,RHQ,by="SEQN")
attach(FINAL.DATA)
```

```
FINAL.DATA.cr=FINAL.DATA %>% mutate(egfr=175*(LBXSCR^-1.154)*(RIDAGEYR^-
0.203)*(ifelse(RIAGENDR==2,0.742,1))*(ifelse(RIDRETH1==4,1.212,1)))
attach(FINAL.DATA.cr)
```

```
MCQ230a=MCQ230A
```

```
MCQ230b=MCQ230B
```

```
MCQ230c=MCQ230C
```

```
MCQ230d=MCQ230D
```

B. R codes for main analysis (logistic regression) with the restriction of diagnosis time within 10 years before the survey time

```
#bladder cancer
```

```
for (i in 10){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240A<=10|RIDAGEYR-MCQ240A<=10))|
```

```
    ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model7=glm(MCQ230abc~log(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
```

```
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
```

```
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
```

```
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
```

```
}
```

```
#blood cancer
```

```
for (i in 1:11){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240B<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240B<=10))|
```

```
    ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model7=glm(MCQ230abc~log(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
```

```
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
```

```
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
```

```
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
```

```
}
```

```

#bone cancer

for (i in 12){

  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)


  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240C<=10|RIDAGEYR-
MCQ240C<=10|RIDAGEYR-MCQ240C<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)


  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))

}

```

```
#brain cancer
```

```
for (i in 13){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240D<=10|RIDAGEYR-  
MCQ240D<=10|RIDAGEYR-MCQ240D<=10))|
```

```
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
```

```
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
```

```
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
```

```
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
```

```
}
```

```
#breast cancer
```

```

for (i in 14){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240E<=10|RIDAGEYR-
MCQ240E<=10|RIDAGEYR-MCQ240E<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#cervix cancer

```

```

for (i in 15){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240F<=10|RIDAGEYR-
MCQ240F<=10|RIDAGEYR-MCQ240F<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#colon cancer

```

```

for (i in 16){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240G<=10|RIDAGEYR-
MCQ240G<=10|RIDAGEYR-MCQ240G<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#esophagus cancer

```



```

for (i in 17){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240H<=10|RIDAGEYR-
MCQ240H<=10|RIDAGEYR-MCQ240H<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#gallbladder cancer

```

```

for (i in 18){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240I<=10|RIDAGEYR-MCQ240I<=10|RIDAGEYR-
MCQ240I<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#kidney cancer

```

```

for (i in 19){

  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)


  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240J<=10|RIDAGEYR-
MCQ240J<=10|RIDAGEYR-MCQ240J<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)


  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#larynx cancer

```

```

for (i in 20){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240K<=10|RIDAGEYR-
MCQ240K<=10|RIDAGEYR-MCQ240K<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

```

#leukemia cancer

for (i in 21){

  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)


  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240L<=10|RIDAGEYR-
MCQ240L<=10|RIDAGEYR-MCQ240L<=10))|

                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)


  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))

}

```

```

#liver cancer

for (i in 22){

  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)


  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240M<=10|RIDAGEYR-
MCQ240M<=10|RIDAGEYR-MCQ240M<=10))|

                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)


  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)

  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))

}

```

```

#lung cancer
for (i in 23){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240N<=10|RIDAGEYR-
MCQ240N<=10|RIDAGEYR-MCQ240N<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

```
#lymphoma/Hodgkin's disease
```

```
for (i in 24){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240O<=10|RIDAGEYR-  
MCQ240O<=10|RIDAGEYR-MCQ240O<=10))|
```

```
    ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
```

```
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
```

```
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
```

```
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
```

```
}
```



```

#melanoma

for (i in 25){

  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)


  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240P<=10|RIDAGEYR-
MCQ240P<=10|RIDAGEYR-MCQ240P<=10))|

                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)


  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)

  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))

}

```

```

#mouth/tongue/lip

for (i in 26){

  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)


  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240Q<=10|RIDAGEYR-
MCQ240Q<=10|RIDAGEYR-MCQ240Q<=10))|

                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)


  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))

}

```

```
#nervous system
```

```
for (i in 27){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240R<=10|RIDAGEYR-  
MCQ240R<=10|RIDAGEYR-MCQ240R<=10))|
```

```
    ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
```

```
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
```

```
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
```

```
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
```

```
}
```

```
#ovarian cancer
```

```
for (i in 28){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240S<=10|RIDAGEYR-  
MCQ240S<=10|RIDAGEYR-MCQ240S<=10))|
```

```
    ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
```

```
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
```

```
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
```

```
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
```

```
}
```

```
#pancreatic cancer
```

```

for (i in 29){

  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)


  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240T<=10|RIDAGEYR-
MCQ240T<=10|RIDAGEYR-MCQ240T<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)


  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#prostate cancer

```

```

for (i in 30){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240U<=10|RIDAGEYR-
MCQ240U<=10|RIDAGEYR-MCQ240U<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#rectal cancer

```

```

for (i in 31){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240V<=10|RIDAGEYR-
MCQ240V<=10|RIDAGEYR-MCQ240V<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#non-melanomatous skin cancer

```

```

for (i in 32){

  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)


  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240W<=10|RIDAGEYR-
MCQ240W<=10|RIDAGEYR-MCQ240W<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)


  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#skin cancer (unknown histologic type)

```



```

for (i in 33){

  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)


  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240X<=10|RIDAGEYR-
MCQ240X<=10|RIDAGEYR-MCQ240X<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)


  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#soft tissue (muscle or fat) cancer

```

```

for (i in 34){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240Y<=10|RIDAGEYR-
MCQ240Y<=10|RIDAGEYR-MCQ240Y<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#stomach cancer

```

```

for (i in 35){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240Z<=10|RIDAGEYR-
MCQ240Z<=10|RIDAGEYR-MCQ240Z<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#testis cancer

```

```

for (i in 36){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240AA<=10|RIDAGEYR-
MCQ240AA<=10|RIDAGEYR-MCQ240AA<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#thyroid cancer

```

```

for (i in 37){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240BB<=10|RIDAGEYR-
MCQ240BB<=10|RIDAGEYR-MCQ240BB<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#Uterus cancer

```

```

for (i in 38){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240CC<=10|RIDAGEYR-
MCQ240CC<=10|RIDAGEYR-MCQ240CC<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

C. R codes for main analysis (logistic regression) with the restriction of diagnosis time within 10 years before the survey time, adjusted for educational level and parity

```
#bladder cancer
```

```
for (i in 10){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240A<=10|RIDAGEYR-MCQ240A<=10))|
```

```
    ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
```

```
HTE.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#blood cancer
```

```
for (i in 11){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240B<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240B<=10))|
```

```
                                (((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```



```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#bone cancer
```

```
for (i in 12){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240C<=10|RIDAGEYR-MCQ240C<=10|RIDAGEYR-MCQ240C<=10))|
```

```
((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
```

```
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
```

```
}
```

```
#brain cancer
```

```
for (i in 13){
```

```
PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240D<=10|RIDAGEYR-  
MCQ240D<=10|RIDAGEYR-MCQ240D<=10))|
```

```
((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
```

```
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
```

```
}
```

```
#breast cancer
```

```
for (i in 14){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240E<=10|RIDAGEYR-  
MCQ240E<=10|RIDAGEYR-MCQ240E<=10))|
```

```
    ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```

print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}

```

#cervix cancer

```
for (i in 15){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240F<=10|RIDAGEYR-
MCQ240F<=10|RIDAGEYR-MCQ240F<=10))|
```

```
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
```

```
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECp)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))  
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))  
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))  
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))  
}
```

```
#colon cancer
```

```
for (i in 16){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240G<=10|RIDAGEYR-  
MCQ240G<=10|RIDAGEYR-MCQ240G<=10))|
```

```
((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
```

```
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))  
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))  
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))  
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))  
}
```

```
#esophagus cancer
```

```
for (i in 17){
```

```
PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240H<=10|RIDAGEYR-  
MCQ240H<=10|RIDAGEYR-MCQ240H<=10))|
```

```
((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
```

```
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
```



```
}
```

```
#gallbladder cancer
```

```
for (i in 18){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240I<=10|RIDAGEYR-MCQ240I<=10|RIDAGEYR-MCQ240I<=10))|
```

```
    ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#kidney cancer
```

```
for (i in 19){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240J<=10|RIDAGEYR-
MCQ240J<=10|RIDAGEYR-MCQ240J<=10))|
```

```
    ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#larynx cancer
```

```
for (i in 20){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240K<=10|RIDAGEYR-
```

MCQ240K<=10|RIDAGEYR-MCQ240K<=10))|

((PHTHTE.cancer\$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
```

```
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
```

```
}
```

```
#leukemia cancer
```

```
for (i in 21){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240L<=10|RIDAGEYR-  
MCQ240L<=10|RIDAGEYR-MCQ240L<=10))|
```

```
    ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```

print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}

```

#liver cancer

```
for (i in 22){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240M<=10|RIDAGEYR-
MCQ240M<=10|RIDAGEYR-MCQ240M<=10))|
```

```
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#lung cancer
```

```
for (i in 23){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240N<=10|RIDAGEYR-
MCQ240N<=10|RIDAGEYR-MCQ240N<=10))|
```

```
    ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#lymphoma/Hodgkin's disease
```

```
for (i in 24){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```



```
PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240O<=10|RIDAGEYR-  
MCQ240O<=10|RIDAGEYR-MCQ240O<=10))|  
((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))  
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))  
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))  
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))  
}
```

```
#melanoma
```

```
for (i in 25){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240P<=10|RIDAGEYR-  
MCQ240P<=10|RIDAGEYR-MCQ240P<=10))|
```

```
    ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```

print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}

```

#mouth/tongue/lip

```
for (i in 26){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240Q<=10|RIDAGEYR-
MCQ240Q<=10|RIDAGEYR-MCQ240Q<=10))|
```

```
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
```

```
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECR)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))  
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))  
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))  
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))  
}
```

```
#nervous system
```

```
for (i in 27){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240R<=10|RIDAGEYR-  
MCQ240R<=10|RIDAGEYR-MCQ240R<=10))|
```

```
((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
```

```
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))  
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))  
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))  
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))  
}
```

```
#ovarian cancer
```

```
for (i in 28){
```

```
PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240S<=10|RIDAGEYR-  
MCQ240S<=10|RIDAGEYR-MCQ240S<=10))|
```

```
((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
```

```
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
```

```
}
```

```
#pancreatic cancer
```

```
for (i in 29){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240T<=10|RIDAGEYR-  
MCQ240T<=10|RIDAGEYR-MCQ240T<=10))|
```

```
    ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```

print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}

```

#prostate cancer

```
for (i in 30){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240U<=10|RIDAGEYR-
MCQ240U<=10|RIDAGEYR-MCQ240U<=10))|
```

```
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
```



```
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))  
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))  
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))  
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))  
}
```

```
#rectal cancer
```

```
for (i in 31){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240V<=10|RIDAGEYR-  
MCQ240V<=10|RIDAGEYR-MCQ240V<=10))|
```

```
((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
```

```
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))  
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))  
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))  
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))  
}
```

```
#non-melanomatous skin cancer
```

```
for (i in 32){
```

```
PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240W<=10|RIDAGEYR-  
MCQ240W<=10|RIDAGEYR-MCQ240W<=10))|
```

```
((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
```

```
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
```

```
}
```

```
#skin cancer (unknown histologic type)
```

```
for (i in 33){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240X<=10|RIDAGEYR-  
MCQ240X<=10|RIDAGEYR-MCQ240X<=10))|
```

```
    ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#soft tissue (muscle or fat) cancer
```

```
for (i in 34){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240Y<=10|RIDAGEYR-
MCQ240Y<=10|RIDAGEYR-MCQ240Y<=10))|
```

```
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#stomach cancer
```

```
for (i in 35){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240Z<=10|RIDAGEYR-
```

MCQ240Z<=10|RIDAGEYR-MCQ240Z<=10)|

((PHTHTE.cancer\$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHTHTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
```

```
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
```

```
}
```

```
#testis cancer
```

```
for (i in 36){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240AA<=10|RIDAGEYR-  
MCQ240AA<=10|RIDAGEYR-MCQ240AA<=10))|
```

```
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT  
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```



```

print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}

```

#thyroid cancer

```
for (i in 37){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240BB<=10|RIDAGEYR-
MCQ240BB<=10|RIDAGEYR-MCQ240BB<=10))|
```

```
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#Uterus cancer
```

```
for (i in 38){
```

```
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
```

```
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240CC<=10|RIDAGEYR-
MCQ240CC<=10|RIDAGEYR-MCQ240CC<=10))|
```

```
    ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PHT
HTE.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
```

```
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
```

```
}
```

D. R codes for the main analysis (logistic regression) without any restriction on diagnosis time

```
for (i in 10:14){  
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))  
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)  
  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)  
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)  
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)  
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)  
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))  
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))  
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))  
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))  
}
```

```
for (i in 15:19){  
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))  
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)  
  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)  
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
```

```

model7=glm(MCQ230abc~log(URXEC)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

```

for (i in 20:24){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXEC)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

```

for (i in 25:29){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

```

for (i in 30:34){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)

```

```

model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

```

for (i in 35:38){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
  model5=glm(MCQ230abc~log(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model6=glm(MCQ230abc~log(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model7=glm(MCQ230abc~log(URXECF)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  model8=glm(MCQ230abc~log(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PHTHTE.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

E. R codes for linearity assumption check

```
for (i in 33){  
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))  
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)  
  logitgam1=gam(MCQ230abc~s(URXCNP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PHTHTE.cancer,family=binomial)  
  logitgam2=gam(MCQ230abc~s(URXCOP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PHTHTE.cancer,family=binomial)  
  logitgam3=gam(MCQ230abc~s(URXECP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PHTHTE.cancer,family=binomial)  
  logitgam4=gam(MCQ230abc~s(URXHIBP)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PHTHTE.cancer,family=binomial)  
  plot(logitgam1,se=T)  
  plot(logitgam2,se=T)  
  plot(logitgam3,se=T)  
  plot(logitgam4,se=T)  
}  
  
summary(logitgam1)  
summary(logitgam2)  
summary(logitgam3)  
summary(logitgam4)
```



```
logitgam21=gam(MCQ230abc~s(URXCNP,k=1)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PHTHTE.cancer,family=binomial)
logitgam22=gam(MCQ230abc~s(URXCNP,k=2)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PHTHTE.cancer,family=binomial)
logitgam23=gam(MCQ230abc~s(URXCNP,k=3)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PHTHTE.cancer,family=binomial)
logitgam24=gam(MCQ230abc~s(URXCNP,k=4)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PHTHTE.cancer,family=binomial)
logitgam25=gam(MCQ230abc~s(URXCNP,k=5)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PHTHTE.cancer,family=binomial)
logitgam26=gam(MCQ230abc~s(URXCNP,k=6)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PHTHTE.cancer,family=binomial)
logitgam27=gam(MCQ230abc~s(URXCNP,k=7)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PHTHTE.cancer,family=binomial)
logitgam28=gam(MCQ230abc~s(URXCNP,k=8)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PHTHTE.cancer,family=binomial)
logitgam29=gam(MCQ230abc~s(URXCNP,k=9)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PHTHTE.cancer,family=binomial)
logitgam30=gam(MCQ230abc~s(URXCNP,k=20)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PHTHTE.cancer,family=binomial)
```

```
plot(logitgam21,se=T)
```

```
plot(logitgam22,se=T)
```

```
plot(logitgam23,se=T)
```

```
plot(logitgam24,se=T)
```

```
plot(logitgam25,se=T)
```

```
plot(logitgam26,se=T)
```

```
plot(logitgam27,se=T)
```

```
plot(logitgam28,se=T)
```

```
plot(logitgam29,se=T)
```

```
plot(logitgam30,se=T)
```

F. R codes for descriptive analyses

```
for (i in 13){  
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))  
  
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)  
  
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240D<=10|RIDAGEYR-  
MCQ240D<=10|RIDAGEYR-MCQ240D<=10))|  
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)  
}  
  
table(PHTHTE.cancer$MCQ230abc,useNA='always')  
  
temp=PHTHTE.cancer %>% group_by(PHTHTE.cancer$MCQ230abc) %>% reframe (quantile_RIDAGEYR=quantile(RIDAGEYR,na.rm=T),  
                                quantile_URXCNP=quantile(URXCNP,na.rm=T),  
                                quantile_URXCOP=quantile(URXCOP,na.rm=T),  
                                quantile_URXECF=quantile(URXECF,na.rm=T),  
                                quantile_URXHIBP=quantile(URXHIBP,na.rm=T),  
                                quantile_egfr=quantile(egfr,na.rm=T),  
                                quantile_LBXCOT=quantile(LBXCOT,na.rm=T),  
                                quantile_BMXBMI=quantile(BMXBMI,na.rm=T),  
                                quantile_DMDEDUC2=quantile(DMDEDUC2,na.rm=T),
```

```
quantile_RHQ160=quantile(RHQ160,na.rm=T),  
mean_RIDAGEYR=mean(RIDAGEYR,na.rm=T),  
mean_URXCNP=mean(URXCNP,na.rm=T),  
mean_URXCOP=mean(URXCOP,na.rm=T),  
mean_URXECF=mean(URXECF,na.rm=T),  
mean_URXHIBP=mean(URXHIBP,na.rm=T),  
mean_egfr=mean(egfr,na.rm=T),  
mean_LBXCOT=mean(LBXCOT,na.rm=T),  
mean_BMXBMI=mean(BMXBMI,na.rm=T),  
mean_DMDEDUC2=mean(DMDEDUC2,na.rm=T),  
mean_RHQ160=mean(RHQ160,na.rm=T))
```

```
PHTHTE.cancer.0=subset(PHTHTE.cancer,PHTHTE.cancer$MCQ230abc==0); table(PHTHTE.cancer.0$RIAGENDR,useNA='always')
```

```
PHTHTE.cancer.1=subset(PHTHTE.cancer,PHTHTE.cancer$MCQ230abc==1); table(PHTHTE.cancer.1$RIAGENDR,useNA='always')
```

```
write_xlsx(temp,"C:\\Users\\pollu\\Downloads\\time considered 실험\\NGS\\descriptive_main_time.considered brain cancer.xlsx")
```

```
for (i in 17){
```

```

PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240H<=10|RIDAGEYR-
MCQ240H<=10|RIDAGEYR-MCQ240H<=10))|

((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

}

table(PHTHTE.cancer$MCQ230abc,useNA='always')

temp=PHTHTE.cancer %>% group_by(PHTHTE.cancer$MCQ230abc) %>% reframe (quantile_RIDAGEYR=quantile(RIDAGEYR,na.rm=T),

quantile_URXCNP=quantile(URXCNP,na.rm=T),

quantile_URXCOP=quantile(URXCOP,na.rm=T),

quantile_URXECF=quantile(URXECF,na.rm=T),

quantile_URXHIBP=quantile(URXHIBP,na.rm=T),

quantile_egfr=quantile(egfr,na.rm=T),

quantile_LBXCOT=quantile(LBXCOT,na.rm=T),

quantile_BMXBMI=quantile(BMXBMI,na.rm=T),

quantile_DMDEDUC2=quantile(DMDEDUC2,na.rm=T),

quantile_RHQ160=quantile(RHQ160,na.rm=T),

mean_RIDAGEYR=mean(RIDAGEYR,na.rm=T),

mean_URXCNP=mean(URXCNP,na.rm=T),

```

```

mean_URXCOP=mean(URXCOP,na.rm=T),
mean_URXECF=mean(URXECF,na.rm=T),
mean_URXHIBP=mean(URXHIBP,na.rm=T),
mean_egfr=mean(egfr,na.rm=T),
mean_LBXCOT=mean(LBXCOT,na.rm=T),
mean_BMXBMI=mean(BMXBMI,na.rm=T),
mean_DMDEDUC2=mean(DMDEDUC2,na.rm=T),
mean_RHQ160=mean(RHQ160,na.rm=T))

```

```

PHTHTE.cancer.0=subset(PHTHTE.cancer,PHTHTE.cancer$MCQ230abc==0); table(PHTHTE.cancer.0$RIAGENDR,useNA='always')

```

```

PHTHTE.cancer.1=subset(PHTHTE.cancer,PHTHTE.cancer$MCQ230abc==1); table(PHTHTE.cancer.1$RIAGENDR,useNA='always')

```

```

write_xlsx(temp,"C:\\Users\\pollu\\Downloads\\time considered 실험\\NGS\\descriptive_main_time.considered esophageal cancer.xlsx")

```

```

for (i in 23){

```

```

  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

```

```

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

```

```

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240N<=10|RIDAGEYR-
MCQ240N<=10|RIDAGEYR-MCQ240N<=10))|

```

```
((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)  
}
```

```
table(PHTHTE.cancer$MCQ230abc,useNA='always')
```

```
temp=PHTHTE.cancer %>% group_by(PHTHTE.cancer$MCQ230abc) %>%  
  reframe (quantile_RIDAGEYR=quantile(RIDAGEYR,na.rm=T),  
           quantile_URXCNP=quantile(URXCNP,na.rm=T),  
           quantile_URXCOP=quantile(URXCOP,na.rm=T),  
           quantile_URXECF=quantile(URXECF,na.rm=T),  
           quantile_URXHIBP=quantile(URXHIBP,na.rm=T),  
           quantile_egfr=quantile(egfr,na.rm=T),  
           quantile_LBXCOT=quantile(LBXCOT,na.rm=T),  
           quantile_BMXBMI=quantile(BMXBMI,na.rm=T),  
           quantile_DMDEDUC2=quantile(DMDEDUC2,na.rm=T),  
           quantile_RHQ160=quantile(RHQ160,na.rm=T),  
           mean_RIDAGEYR=mean(RIDAGEYR,na.rm=T),  
           mean_URXCNP=mean(URXCNP,na.rm=T),  
           mean_URXCOP=mean(URXCOP,na.rm=T),  
           mean_URXECF=mean(URXECF,na.rm=T),  
           mean_URXHIBP=mean(URXHIBP,na.rm=T),
```

```

mean_egfr=mean(egfr,na.rm=T),
mean_LBXCOT=mean(LBXCOT,na.rm=T),
mean_BMXBMI=mean(BMXBMI,na.rm=T),
mean_DMDEDUC2=mean(DMDEDUC2,na.rm=T),
mean_RHQ160=mean(RHQ160,na.rm=T))

```

```

PHTHTE.cancer.0=subset(PHTHTE.cancer,PHTHTE.cancer$MCQ230abc==0); table(PHTHTE.cancer.0$RIAGENDR,useNA='always')

```

```

PHTHTE.cancer.1=subset(PHTHTE.cancer,PHTHTE.cancer$MCQ230abc==1); table(PHTHTE.cancer.1$RIAGENDR,useNA='always')

```

```

write_xlsx(temp,"C:\\Users\\pollu\\Downloads\\time considered 실험\\NGS\\descriptive_main_time.considered lung cancer.xlsx")

```

```

table(PHTHTE.cancer.0$DMDEDUC2,useNA="always");table(PHTHTE.cancer.1$DMDEDUC2,useNA="always")

```

```

table(PHTHTE.cancer.0$RHQ160,useNA="always");table(PHTHTE.cancer.1$RHQ160,useNA="always")

```

```

for (i in 25){

```

```

  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

```

```

  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)

```

```

  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240P<=10|RIDAGEYR-
MCQ240P<=10|RIDAGEYR-MCQ240P<=10))|

```



```
((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)  
}
```

```
table(PHTHTE.cancer$MCQ230abc,useNA='always')
```

```
temp=PHTHTE.cancer %>% group_by(PHTHTE.cancer$MCQ230abc) %>%  
  reframe (quantile_RIDAGEYR=quantile(RIDAGEYR,na.rm=T),  
           quantile_URXCNP=quantile(URXCNP,na.rm=T),  
           quantile_URXCOP=quantile(URXCOP,na.rm=T),  
           quantile_URXECF=quantile(URXECF,na.rm=T),  
           quantile_URXHIBP=quantile(URXHIBP,na.rm=T),  
           quantile_egfr=quantile(egfr,na.rm=T),  
           quantile_LBXCOT=quantile(LBXCOT,na.rm=T),  
           quantile_BMXBMI=quantile(BMXBMI,na.rm=T),  
           quantile_DMDEDUC2=quantile(DMDEDUC2,na.rm=T),  
           quantile_RHQ160=quantile(RHQ160,na.rm=T),  
           mean_RIDAGEYR=mean(RIDAGEYR,na.rm=T),  
           mean_URXCNP=mean(URXCNP,na.rm=T),  
           mean_URXCOP=mean(URXCOP,na.rm=T),  
           mean_URXECF=mean(URXECF,na.rm=T),  
           mean_URXHIBP=mean(URXHIBP,na.rm=T),
```

```

mean_egfr=mean(egfr,na.rm=T),
mean_LBXCOT=mean(LBXCOT,na.rm=T),
mean_BMXBMI=mean(BMXBMI,na.rm=T),
mean_DMDEDUC2=mean(DMDEDUC2,na.rm=T),
mean_RHQ160=mean(RHQ160,na.rm=T))

PHTHTE.cancer.0=subset(PHTHTE.cancer,PHTHTE.cancer$MCQ230abc==0); table(PHTHTE.cancer.0$RIAGENDR,useNA='always')
PHTHTE.cancer.1=subset(PHTHTE.cancer,PHTHTE.cancer$MCQ230abc==1); table(PHTHTE.cancer.1$RIAGENDR,useNA='always')


write_xlsx(temp,"C:\\Users\\pollu\\Downloads\\time considered 실험\\NGS\\descriptive_main_time.considered melanoma.xlsx")


for (i in 30){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240U<=10|RIDAGEYR-
MCQ240U<=10|RIDAGEYR-MCQ240U<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-

```

```
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
}
```

```
table(PHTHTE.cancer$MCQ230abc,useNA='always')
```

```
temp=PHTHTE.cancer %>% group_by(PHTHTE.cancer$MCQ230abc) %>% reframe (quantile_RIDAGEYR=quantile(RIDAGEYR,na.rm=T),
```

```
quantile_URXCNP=quantile(URXCNP,na.rm=T),
```

```
quantile_URXCOP=quantile(URXCOP,na.rm=T),
```

```
quantile_URXECF=quantile(URXECF,na.rm=T),
```

```
quantile_URXHIBP=quantile(URXHIBP,na.rm=T),
```

```
quantile_egfr=quantile(egfr,na.rm=T),
```

```
quantile_LBXCOT=quantile(LBXCOT,na.rm=T),
```

```
quantile_BMXBMI=quantile(BMXBMI,na.rm=T),
```

```
quantile_DMDEDUC2=quantile(DMDEDUC2,na.rm=T),
```

```
quantile_RHQ160=quantile(RHQ160,na.rm=T),
```

```
mean_RIDAGEYR=mean(RIDAGEYR,na.rm=T),
```

```
mean_URXCNP=mean(URXCNP,na.rm=T),
```

```
mean_URXCOP=mean(URXCOP,na.rm=T),
```

```
mean_URXECF=mean(URXECF,na.rm=T),
```

```
mean_URXHIBP=mean(URXHIBP,na.rm=T),
```

```
mean_egfr=mean(egfr,na.rm=T),
```

```

mean_LBXCOT=mean(LBXCOT,na.rm=T),
mean_BMXBMI=mean(BMXBMI,na.rm=T),
mean_DMDEDUC2=mean(DMDEDUC2,na.rm=T),
mean_RHQ160=mean(RHQ160,na.rm=T))

PHTHTE.cancer.0=subset(PHTHTE.cancer,PHTHTE.cancer$MCQ230abc==0); table(PHTHTE.cancer.0$RIAGENDR,useNA='always')
PHTHTE.cancer.1=subset(PHTHTE.cancer,PHTHTE.cancer$MCQ230abc==1); table(PHTHTE.cancer.1$RIAGENDR,useNA='always')


write_xlsx(temp,"C:\\Users\\pollu\\Downloads\\time considered 실험\\NGS\\descriptive_main_time.considered prostate cancer.xlsx")


for (i in 32){
  PHTHTE.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PHTHTE.cancer$MCQ230abc=ifelse(MCQ220==2,0,PHTHTE.cancer$MCQ230abc)
  PHTHTE.cancer$MCQ230abc=ifelse((((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240W<=10|RIDAGEYR-
MCQ240W<=10|RIDAGEYR-MCQ240W<=10))|
                                ((PHTHTE.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

```

```
}
```

```
table(PHTHTE.cancer$MCQ230abc,useNA='always')
```

```
temp=PHTHTE.cancer %>% group_by(PHTHTE.cancer$MCQ230abc) %>% reframe (quantile_RIDAGEYR=quantile(RIDAGEYR,na.rm=T),
```

```
quantile_URXCNP=quantile(URXCNP,na.rm=T),
```

```
quantile_URXCOP=quantile(URXCOP,na.rm=T),
```

```
quantile_URXECF=quantile(URXECF,na.rm=T),
```

```
quantile_URXHIBP=quantile(URXHIBP,na.rm=T),
```

```
quantile_egfr=quantile(egfr,na.rm=T),
```

```
quantile_LBXCOT=quantile(LBXCOT,na.rm=T),
```

```
quantile_BMXBMI=quantile(BMXBMI,na.rm=T),
```

```
quantile_DMDEDUC2=quantile(DMDEDUC2,na.rm=T),
```

```
quantile_RHQ160=quantile(RHQ160,na.rm=T),
```

```
mean_RIDAGEYR=mean(RIDAGEYR,na.rm=T),
```

```
mean_URXCNP=mean(URXCNP,na.rm=T),
```

```
mean_URXCOP=mean(URXCOP,na.rm=T),
```

```
mean_URXECF=mean(URXECF,na.rm=T),
```

```
mean_URXHIBP=mean(URXHIBP,na.rm=T),
```

```
mean_egfr=mean(egfr,na.rm=T),
```

```
mean_LBXCOT=mean(LBXCOT,na.rm=T),
```

```
mean_BMXBMI=mean(BMXBMI,na.rm=T),  
mean_DMDEDUC2=mean(DMDEDUC2,na.rm=T),  
mean_RHQ160=mean(RHQ160,na.rm=T))
```

```
PHTHTE.cancer.0=subset(PHTHTE.cancer,PHTHTE.cancer$MCQ230abc==0); table(PHTHTE.cancer.0$RIAGENDR,useNA='always')
```

```
PHTHTE.cancer.1=subset(PHTHTE.cancer,PHTHTE.cancer$MCQ230abc==1); table(PHTHTE.cancer.1$RIAGENDR,useNA='always')
```

```
write_xlsx(temp,"C:\\Users\\pollu\\Downloads\\time considered 실험\\NGS\\descriptive_main_time.considered non-melanomatous skin cancer.xlsx")
```

SECOND EXAMPLE

A. R codes to construct the analysis dataset

```
download.file("http://wwwn.cdc.gov/nchs/nhanes/2005-2006/PCBPOL_D.XPT", tf <- tempfile(), mode="wb")
PCBPOL_D <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2007-2008/PCBPOL_E.XPT", tf <- tempfile(), mode="wb")
PCBPOL_E <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2009-2010/PCBPOL_F.XPT", tf <- tempfile(), mode="wb")
PCBPOL_F <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2011-2012/PCBPOL_G.XPT", tf <- tempfile(), mode="wb")
PCBPOL_G <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2013-2014/PCBPOL_H.XPT", tf <- tempfile(), mode="wb")
PCBPOL_H <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2015-2016/PCBPOL_I.XPT", tf <- tempfile(), mode="wb")
PCBPOL_I <- foreign::read.xport(tf)
PCBPOL <- bind_rows(PCBPOL_D,PCBPOL_E,PCBPOL_F,PCBPOL_G,PCBPOL_H,PCBPOL_I)

download.file("http://wwwn.cdc.gov/nchs/nhanes/2005-2006/DEMO_D.XPT", tf <- tempfile(), mode="wb")
```

```
DEMO_D <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2007-2008/DEMO_E.XPT", tf <- tempfile(), mode="wb")
DEMO_E <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2009-2010/DEMO_F.XPT", tf <- tempfile(), mode="wb")
DEMO_F <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2011-2012/DEMO_G.XPT", tf <- tempfile(), mode="wb")
DEMO_G <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2013-2014/DEMO_H.XPT", tf <- tempfile(), mode="wb")
DEMO_H <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2015-2016/DEMO_I.XPT", tf <- tempfile(), mode="wb")
DEMO_I <- foreign::read.xport(tf)
DEMO <- bind_rows(DEMO_D,DEMO_E,DEMO_F,DEMO_G,DEMO_H,DEMO_I)
```

```
download.file("http://wwwn.cdc.gov/nchs/nhanes/2005-2006/BMX_D.XPT", tf <- tempfile(), mode="wb")
BMX_D <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2007-2008/BMX_E.XPT", tf <- tempfile(), mode="wb")
BMX_E <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2009-2010/BMX_F.XPT", tf <- tempfile(), mode="wb")
BMX_F <- foreign::read.xport(tf)
```



```
download.file("http://wwwn.cdc.gov/nchs/nhanes/2011-2012/BMX_G.XPT", tf <- tempfile(), mode="wb")
BMX_G <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2013-2014/BMX_H.XPT", tf <- tempfile(), mode="wb")
BMX_H <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2015-2016/BMX_I.XPT", tf <- tempfile(), mode="wb")
BMX_I <- foreign::read.xport(tf)
BMX <- bind_rows(BMX_D,BMX_E,BMX_F,BMX_G,BMX_H,BMX_I)
```

```
download.file("http://wwwn.cdc.gov/nchs/nhanes/2005-2006/MCQ_D.XPT", tf <- tempfile(), mode="wb")
MCQ_D <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2007-2008/MCQ_E.XPT", tf <- tempfile(), mode="wb")
MCQ_E <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2009-2010/MCQ_F.XPT", tf <- tempfile(), mode="wb")
MCQ_F <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2011-2012/MCQ_G.XPT", tf <- tempfile(), mode="wb")
MCQ_G <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2013-2014/MCQ_H.XPT", tf <- tempfile(), mode="wb")
MCQ_H <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2015-2016/MCQ_I.XPT", tf <- tempfile(), mode="wb")
```

```
MCQ_I <- foreign::read.xport(tf)
MCQ <- bind_rows(MCQ_D,MCQ_E,MCQ_F,MCQ_G,MCQ_H,MCQ_I)
```

```
download.file("http://wwwn.cdc.gov/nchs/nhanes/2005-2006/BIOPRO_D.XPT", tf <- tempfile(), mode="wb")
BIOPRO_D <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2007-2008/BIOPRO_E.XPT", tf <- tempfile(), mode="wb")
BIOPRO_E <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2009-2010/BIOPRO_F.XPT", tf <- tempfile(), mode="wb")
BIOPRO_F <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2011-2012/BIOPRO_G.XPT", tf <- tempfile(), mode="wb")
BIOPRO_G <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2013-2014/BIOPRO_H.XPT", tf <- tempfile(), mode="wb")
BIOPRO_H <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2015-2016/BIOPRO_I.XPT", tf <- tempfile(), mode="wb")
BIOPRO_I <- foreign::read.xport(tf)
BIOPRO <- bind_rows(BIOPRO_D,BIOPRO_E,BIOPRO_F,BIOPRO_G,BIOPRO_H,BIOPRO_I)
```

```
download.file("http://wwwn.cdc.gov/nchs/nhanes/2005-2006/COT_D.XPT", tf <- tempfile(), mode="wb")
```

```
COT_D <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2007-2008/COTNAL_E.XPT", tf <- tempfile(), mode="wb")
COTNAL_E <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2009-2010/COTNAL_F.XPT", tf <- tempfile(), mode="wb")
COTNAL_F <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2011-2012/COTNAL_G.XPT", tf <- tempfile(), mode="wb")
COTNAL_G <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2013-2014/COT_H.XPT", tf <- tempfile(), mode="wb")
COT_H <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2015-2016/COT_I.XPT", tf <- tempfile(), mode="wb")
COT_I <- foreign::read.xport(tf)
COT <- bind_rows(COT_D,COTNAL_E,COTNAL_F,COTNAL_G,COT_H,COT_I)
```

```
download.file("http://wwwn.cdc.gov/nchs/nhanes/2005-2006/RHQ_D.XPT", tf <- tempfile(), mode="wb")
RHQ_D <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2007-2008/RHQ_E.XPT", tf <- tempfile(), mode="wb")
RHQ_E <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2009-2010/RHQ_F.XPT", tf <- tempfile(), mode="wb")
RHQ_F <- foreign::read.xport(tf)
```

```
download.file("http://wwwn.cdc.gov/nchs/nhanes/2011-2012/RHQ_G.XPT", tf <- tempfile(), mode="wb")
RHQ_G <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2013-2014/RHQ_H.XPT", tf <- tempfile(), mode="wb")
RHQ_H <- foreign::read.xport(tf)
download.file("http://wwwn.cdc.gov/nchs/nhanes/2015-2016/RHQ_I.XPT", tf <- tempfile(), mode="wb")
RHQ_I <- foreign::read.xport(tf)
RHQ <- bind_rows(RHQ_D,RHQ_E,RHQ_F,RHQ_G,RHQ_H,RHQ_I)
```

```
PCBPOL.DEMO=left_join(PCBPOL,DEMO,by="SEQN")
PCBPOL.DEMO.BMX=left_join(PCBPOL.DEMO,BMX,by="SEQN")
PCBPOL.DEMO.BMX.MCQ=left_join(PCBPOL.DEMO.BMX,MCQ,by="SEQN")
PCBPOL.DEMO.BMX.MCQ.BIO=left_join(PCBPOL.DEMO.BMX.MCQ,BIOPRO,by="SEQN")
PCBPOL.DEMO.BMX.MCQ.BIO.COT=left_join(PCBPOL.DEMO.BMX.MCQ.BIO,COT,by="SEQN")
FINAL.DATA=left_join(PCBPOL.DEMO.BMX.MCQ.BIO.COT,RHQ,by="SEQN")
attach(FINAL.DATA)
```

```
FINAL.DATA.cr=FINAL.DATA %>% mutate(egfr=175*(LBXSCR^-1.154)*(RIDAGEYR^-
0.203)*(ifelse(RIAGENDR==2,0.742,1))*(ifelse(RIDRETH1==4,1.212,1)))
attach(FINAL.DATA.cr)
```

MCQ230a=MCQ230A

MCQ230b=MCQ230B

MCQ230c=MCQ230C

MCQ230d=MCQ230D

B. R codes for main analysis (logistic regression) with the restriction of diagnosis time within 10 years before the survey time

```
#bladder cancer

for (i in 10){

  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240A<=10|RIDAGEYR-MCQ240A<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}
```

```
#blood cancer
```

```
for (i in 11){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240B<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240B<=10))|
```

```
    ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
```

```
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
```

```
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
```

```
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
```

```
}
```

```
#bone cancer
```

```
for (i in 12){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240C<=10|RIDAGEYR-  
MCQ240C<=10|RIDAGEYR-MCQ240C<=10))|
```

```
    ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
```

```
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
```

```
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
```

```
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
```

```
}
```



```
#brain cancer
```

```
for (i in 13){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240D<=10|RIDAGEYR-  
MCQ240D<=10|RIDAGEYR-MCQ240D<=10))|
```

```
    ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
```

```
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
```

```
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
```

```
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
```

```
}
```

```
#breast cancer
```

```

for (i in 14){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240E<=10|RIDAGEYR-
MCQ240E<=10|RIDAGEYR-MCQ240E<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#cervix cancer

```

```

for (i in 15){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240F<=10|RIDAGEYR-
MCQ240F<=10|RIDAGEYR-MCQ240F<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#colon cancer

```

```

for (i in 16){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240G<=10|RIDAGEYR-
MCQ240G<=10|RIDAGEYR-MCQ240G<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#esophagus cancer

```

```

for (i in 17){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240H<=10|RIDAGEYR-
MCQ240H<=10|RIDAGEYR-MCQ240H<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#gallbladder cancer

```

```

for (i in 18){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240I<=10|RIDAGEYR-MCQ240I<=10|RIDAGEYR-
MCQ240I<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#kidney cancer

```

```

for (i in 19){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240J<=10|RIDAGEYR-MCQ240J<=10|RIDAGEYR-
MCQ240J<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#larynx cancer

```

```

for (i in 20){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240K<=10|RIDAGEYR-
MCQ240K<=10|RIDAGEYR-MCQ240K<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```



```
#leukemia cancer
```

```
for (i in 21){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240L<=10|RIDAGEYR-  
MCQ240L<=10|RIDAGEYR-MCQ240L<=10))|
```

```
    ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
```

```
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
```

```
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
```

```
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
```

```
}
```

```

#liver cancer

for (i in 22){

  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240M<=10|RIDAGEYR-
MCQ240M<=10|RIDAGEYR-MCQ240M<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

```
#lung cancer
```

```
for (i in 23){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240N<=10|RIDAGEYR-  
MCQ240N<=10|RIDAGEYR-MCQ240N<=10))|
```

```
    ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
```

```
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
```

```
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
```

```
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
```

```
}
```

```
#lymphoma/Hodgkin's disease
```

```
for (i in 24){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240O<=10|RIDAGEYR-  
MCQ240O<=10|RIDAGEYR-MCQ240O<=10))|
```

```
    ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
```

```
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
```

```
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
```

```
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
```

```
}
```

```

#melanoma

for (i in 25){

  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)


  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240P<=10|RIDAGEYR-
MCQ240P<=10|RIDAGEYR-MCQ240P<=10))|

                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)


  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)

  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))

}

```

```
#mouth/tongue/lip
```

```
for (i in 26){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240Q<=10|RIDAGEYR-  
MCQ240Q<=10|RIDAGEYR-MCQ240Q<=10))|
```

```
    ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
```

```
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
```

```
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
```

```
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
```

```
}
```

```
#nervous system
```

```
for (i in 27){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240R<=10|RIDAGEYR-  
MCQ240R<=10|RIDAGEYR-MCQ240R<=10))|
```

```
    ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
```

```
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
```

```
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
```

```
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
```

```
}
```

```
#ovarian cancer
```

```
for (i in 28){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240S<=10|RIDAGEYR-  
MCQ240S<=10|RIDAGEYR-MCQ240S<=10))|
```

```
    ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
```

```
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
```

```
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
```

```
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
```

```
}
```

```
#pancreatic cancer
```



```

for (i in 29){

  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240T<=10|RIDAGEYR-
MCQ240T<=10|RIDAGEYR-MCQ240T<=10))|

                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#prostate cancer

```

```

for (i in 30){

  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)


  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240U<=10|RIDAGEYR-
MCQ240U<=10|RIDAGEYR-MCQ240U<=10))|

                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)


  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))

}

#rectal cancer

```

```

for (i in 31){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240V<=10|RIDAGEYR-
MCQ240V<=10|RIDAGEYR-MCQ240V<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#non-melanomatous skin cancer

```

```

for (i in 32){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240W<=10|RIDAGEYR-
MCQ240W<=10|RIDAGEYR-MCQ240W<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#skin cancer (unknown histologic type)

```

```

for (i in 33){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240X<=10|RIDAGEYR-
MCQ240X<=10|RIDAGEYR-MCQ240X<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#soft tissue (muscle or fat) cancer

```

```

for (i in 34){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240Y<=10|RIDAGEYR-
MCQ240Y<=10|RIDAGEYR-MCQ240Y<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#stomach cancer

```

```

for (i in 35){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240Z<=10|RIDAGEYR-
MCQ240Z<=10|RIDAGEYR-MCQ240Z<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

```

```

model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

```

#testis cancer

```

```

for (i in 36){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240AA<=10|RIDAGEYR-
MCQ240AA<=10|RIDAGEYR-MCQ240AA<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

#thyroid cancer

```



```

for (i in 37){

  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)


  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240BB<=10|RIDAGEYR-
MCQ240BB<=10|RIDAGEYR-MCQ240BB<=10))|

                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)


  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))

}

#Uterus cancer

```

```

for (i in 38){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240CC<=10|RIDAGEYR-
MCQ240CC<=10|RIDAGEYR-MCQ240CC<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

C. R codes for main analysis (logistic regression) with the restriction of diagnosis time within 10 years before the survey time, adjusted for educational level and parity

```
#bladder cancer
```

```
for (i in 10){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240A<=10|RIDAGEYR-MCQ240A<=10))|
```

```
    ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
```

OL.cancer)

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

#blood cancer

for (i in 11){

PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

PCBPOL.cancer\$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer\$MCQ230abc)

PCBPOL.cancer\$MCQ230abc=ifelse((((PCBPOL.cancer\$MCQ230abc==1)&(RIDAGEYR-MCQ240B<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240B<=10))|

((PCBPOL.cancer\$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
OL.cancer)

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#bone cancer
```

```
for (i in 12){
```

```
PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240C<=10|RIDAGEYR-MCQ240C<=10|RIDAGEYR-MCQ240C<=10))|
```

```
((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))  
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))  
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))  
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))  
}
```

```
#brain cancer
```

```
for (i in 13){
```

```
PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240D<=10|RIDAGEYR-  
MCQ240D<=10|RIDAGEYR-MCQ240D<=10))|
```

```
((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
```

```
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
```

```
}
```

```
#breast cancer
```

```
for (i in 14){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240E<=10|RIDAGEYR-  
MCQ240E<=10|RIDAGEYR-MCQ240E<=10))|
```

```
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```



```

print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}

```

#cervix cancer

```
for (i in 15){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240F<=10|RIDAGEYR-
MCQ240F<=10|RIDAGEYR-MCQ240F<=10))|
```

```
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
```

```
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))  
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))  
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))  
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))  
}
```

```
#colon cancer
```

```
for (i in 16){
```

```
PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240G<=10|RIDAGEYR-  
MCQ240G<=10|RIDAGEYR-MCQ240G<=10))|
```

```
((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
```

```
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))  
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))  
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))  
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))  
}
```

```
#esophagus cancer
```

```
for (i in 17){
```

```
PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240H<=10|RIDAGEYR-  
MCQ240H<=10|RIDAGEYR-MCQ240H<=10))|
```

```
((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
```

```
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
```

```
}
```

```
#gallbladder cancer
```

```
for (i in 18){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240I<=10|RIDAGEYR-MCQ240I<=10|RIDAGEYR-MCQ240I<=10))|
```

```
    ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#kidney cancer
```

```
for (i in 19){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240J<=10|RIDAGEYR-MCQ240J<=10|RIDAGEYR-MCQ240J<=10))|
```

```
    ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#larynx cancer
```

```
for (i in 20){
```

```
PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240K<=10|RIDAGEYR-
```

MCQ240K<=10|RIDAGEYR-MCQ240K<=10))|

((PCBPOL.cancer\$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)

model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)

model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)

model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)

print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))

print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))

print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))

print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))

}


```
#leukemia cancer
```

```
for (i in 21){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240L<=10|RIDAGEYR-  
MCQ240L<=10|RIDAGEYR-MCQ240L<=10))|
```

```
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```

print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}

```

#liver cancer

```
for (i in 22){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240M<=10|RIDAGEYR-
MCQ240M<=10|RIDAGEYR-MCQ240M<=10))|
```

```
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#lung cancer
```

```
for (i in 23){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240N<=10|RIDAGEYR-MCQ240N<=10|RIDAGEYR-MCQ240N<=10))|
```

```
    ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
```

```
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
```

```
}
```

```
#lymphoma/Hodgkin's disease
```

```
for (i in 24){
```

```
PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240O<=10|RIDAGEYR-  
MCQ240O<=10|RIDAGEYR-MCQ240O<=10))|  
((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
```

```
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
```

```
}
```

```
#melanoma
```

```
for (i in 25){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240P<=10|RIDAGEYR-  
MCQ240P<=10|RIDAGEYR-MCQ240P<=10))|
```

```
    ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```

print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}

```

#mouth/tongue/lip

for (i in 26){

```

PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))

```

```

PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)

```

```

PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240Q<=10|RIDAGEYR-
MCQ240Q<=10|RIDAGEYR-MCQ240Q<=10))|

```

```

((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

```

```

model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
OL.cancer)

```

```

model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP

```

```
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))  
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))  
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))  
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))  
}
```

```
#nervous system
```

```
for (i in 27){
```

```
PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240R<=10|RIDAGEYR-  
MCQ240R<=10|RIDAGEYR-MCQ240R<=10))|
```

```
((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
```



```
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))  
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))  
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))  
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))  
}
```

```
#ovarian cancer
```

```
for (i in 28){
```

```
PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240S<=10|RIDAGEYR-  
MCQ240S<=10|RIDAGEYR-MCQ240S<=10))|
```

```
((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
```

```
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
```

```
}
```

```
#pancreatic cancer
```

```
for (i in 29){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240T<=10|RIDAGEYR-  
MCQ240T<=10|RIDAGEYR-MCQ240T<=10))|
```

```
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```

print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}

```

#prostate cancer

```
for (i in 30){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240U<=10|RIDAGEYR-
MCQ240U<=10|RIDAGEYR-MCQ240U<=10))|
```

```
                                (((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
```

```
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))  
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))  
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))  
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))  
}
```

```
#rectal cancer
```

```
for (i in 31){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240V<=10|RIDAGEYR-  
MCQ240V<=10|RIDAGEYR-MCQ240V<=10))|
```

```
((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
```

```
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))  
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))  
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))  
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))  
}
```

```
#non-melanomatous skin cancer
```

```
for (i in 32){
```

```
PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240W<=10|RIDAGEYR-  
MCQ240W<=10|RIDAGEYR-MCQ240W<=10))|
```

```
((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
```

```
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
```

```
}
```

```
#skin cancer (unknown histologic type)
```

```
for (i in 33){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240X<=10|RIDAGEYR-  
MCQ240X<=10|RIDAGEYR-MCQ240X<=10))|
```

```
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```



```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#soft tissue (muscle or fat) cancer
```

```
for (i in 34){
```

```
PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240Y<=10|RIDAGEYR-
MCQ240Y<=10|RIDAGEYR-MCQ240Y<=10))|
```

```
((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBPOL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#stomach cancer
```

```
for (i in 35){
```

```
PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240Z<=10|RIDAGEYR-
```

```
MCQ240Z<=10|RIDAGEYR-MCQ240Z<=10))|
((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
OL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#testis cancer
```

```
for (i in 36){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240AA<=10|RIDAGEYR-  
MCQ240AA<=10|RIDAGEYR-MCQ240AA<=10))|
```

```
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```

print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}

```

#thyroid cancer

```
for (i in 37){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240BB<=10|RIDAGEYR-
MCQ240BB<=10|RIDAGEYR-MCQ240BB<=10))|
```

```
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP
OL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
}
```

```
#Uterus cancer
```

```
for (i in 38){
```

```
PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```

```
PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
```

```
PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240CC<=10|RIDAGEYR-
MCQ240CC<=10|RIDAGEYR-MCQ240CC<=10))|
```

```
((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT+DMDEDUC2+RHQ160,family=binomial,data=PCBP  
OL.cancer)
```

```
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[11]),2))
```

```
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[11]),2))
```

```
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[11]),2))
```

```
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[11]),2))
```

```
}
```

D. R codes for the main analysis (logistic regression) without any restriction on diagnosis time

```
for (i in 10:14){  
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))  
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)  
  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)  
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)  
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)  
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)  
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))  
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))  
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))  
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))  
}
```

```
for (i in 15:19){  
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))  
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)  
  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)  
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
```



```

model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

```

for (i in 20:24){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

```

for (i in 25:29){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

```

for (i in 30:34){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)

```

```

model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

```

for (i in 35:38){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
  model5=glm(MCQ230abc~log(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model6=glm(MCQ230abc~log(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model7=glm(MCQ230abc~log(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  model8=glm(MCQ230abc~log(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,family=binomial,data=PCBPOL.cancer)
  print(round(exp(coef(model5)[2]),2));print(round(exp(confint(model5)[2]),2));print(round(exp(confint(model5)[9]),2))
  print(round(exp(coef(model6)[2]),2));print(round(exp(confint(model6)[2]),2));print(round(exp(confint(model6)[9]),2))
  print(round(exp(coef(model7)[2]),2));print(round(exp(confint(model7)[2]),2));print(round(exp(confint(model7)[9]),2))
  print(round(exp(coef(model8)[2]),2));print(round(exp(confint(model8)[2]),2));print(round(exp(confint(model8)[9]),2))
}

```

E. R codes for linearity assumption check

```
for (i in 33){  
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))  
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)  
  logitgam1=gam(MCQ230abc~s(LBC105)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PCBPOL.cancer,family=binomial)  
  logitgam2=gam(MCQ230abc~s(LBC114)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PCBPOL.cancer,family=binomial)  
  logitgam3=gam(MCQ230abc~s(LBC118)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PCBPOL.cancer,family=binomial)  
  logitgam4=gam(MCQ230abc~s(LBC138)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PCBPOL.cancer,family=binomial)  
  plot(logitgam1,se=T)  
  plot(logitgam2,se=T)  
  plot(logitgam3,se=T)  
  plot(logitgam4,se=T)  
}  
  
summary(logitgam1)  
summary(logitgam2)  
summary(logitgam3)  
summary(logitgam4)
```

```
logitgam21=gam(MCQ230abc~s(LBC105,k=1)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PCBPOL.cancer,family=binomial)
logitgam22=gam(MCQ230abc~s(LBC105,k=2)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PCBPOL.cancer,family=binomial)
logitgam23=gam(MCQ230abc~s(LBC105,k=3)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PCBPOL.cancer,family=binomial)
logitgam24=gam(MCQ230abc~s(LBC105,k=4)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PCBPOL.cancer,family=binomial)
logitgam25=gam(MCQ230abc~s(LBC105,k=5)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PCBPOL.cancer,family=binomial)
logitgam26=gam(MCQ230abc~s(LBC105,k=6)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PCBPOL.cancer,family=binomial)
logitgam27=gam(MCQ230abc~s(LBC105,k=7)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PCBPOL.cancer,family=binomial)
logitgam28=gam(MCQ230abc~s(LBC105,k=8)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PCBPOL.cancer,family=binomial)
logitgam29=gam(MCQ230abc~s(LBC105,k=9)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PCBPOL.cancer,family=binomial)
logitgam30=gam(MCQ230abc~s(LBC105,k=20)+BMXBMI+RIDAGEYR+RIAGENDR+egfr+LBXCOT,data=PCBPOL.cancer,family=binomial)
```

```
plot(logitgam21,se=T)
```

```
plot(logitgam22,se=T)
```

```
plot(logitgam23,se=T)
```

```
plot(logitgam24,se=T)
```

```
plot(logitgam25,se=T)
```

```
plot(logitgam26,se=T)
```

```
plot(logitgam27,se=T)
```

```
plot(logitgam28,se=T)
```

```
plot(logitgam29,se=T)
```

```
plot(logitgam30,se=T)
```

F. R codes for descriptive analyses

```
for (i in 13){  
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))  
  
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)  
  
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240D<=10|RIDAGEYR-  
MCQ240D<=10|RIDAGEYR-MCQ240D<=10))|  
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-  
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)  
}  
  
table(PCBPOL.cancer$MCQ230abc,useNA='always')  
  
temp=PCBPOL.cancer %>% group_by(PCBPOL.cancer$MCQ230abc) %>% reframe (quantile_RIDAGEYR=quantile(RIDAGEYR,na.rm=T),  
                                quantile_LBC105=quantile(LBC105,na.rm=T),  
                                quantile_LBC114=quantile(LBC114,na.rm=T),  
                                quantile_LBC118=quantile(LBC118,na.rm=T),  
                                quantile_LBC138=quantile(LBC138,na.rm=T),  
                                quantile_egfr=quantile(egfr,na.rm=T),  
                                quantile_LBXCOT=quantile(LBXCOT,na.rm=T),  
                                quantile_BMXBMI=quantile(BMXBMI,na.rm=T),  
                                quantile_DMDEDUC2=quantile(DMDEDUC2,na.rm=T),  
                                quantile_RHQ160=quantile(RHQ160,na.rm=T),
```

```

mean_RIDAGEYR=mean(RIDAGEYR,na.rm=T),
mean_LBC105=mean(LBC105,na.rm=T),
mean_LBC114=mean(LBC114,na.rm=T),
mean_LBC118=mean(LBC118,na.rm=T),
mean_LBC138=mean(LBC138,na.rm=T),
mean_egfr=mean(egfr,na.rm=T),
mean_LBXCOT=mean(LBXCOT,na.rm=T),
mean_BMXBMI=mean(BMXBMI,na.rm=T),
mean_DMDEDUC2=mean(DMDEDUC2,na.rm=T),
mean_RHQ160=mean(RHQ160,na.rm=T))

```

```
PCBPOL.cancer.0=subset(PCBPOL.cancer,PCBPOL.cancer$MCQ230abc==0); table(PCBPOL.cancer.0$RIAGENDR,useNA='always')
```

```
PCBPOL.cancer.1=subset(PCBPOL.cancer,PCBPOL.cancer$MCQ230abc==1); table(PCBPOL.cancer.1$RIAGENDR,useNA='always')
```

```
write_xlsx(temp,"C:\\Users\\pollu\\Downloads\\time considered 실험\\NGS\\descriptive_main_time.considered brain cancer.xlsx")
```

```
for (i in 17){
```

```
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
```


[illegible]

```

mean_LBC118=mean(LBC118,na.rm=T),
mean_LBC138=mean(LBC138,na.rm=T),
mean_egfr=mean(egfr,na.rm=T),
mean_LBXCOT=mean(LBXCOT,na.rm=T),
mean_BMXBMI=mean(BMXBMI,na.rm=T),
mean_DMDEDUC2=mean(DMDEDUC2,na.rm=T),
mean_RHQ160=mean(RHQ160,na.rm=T))

PCBPOL.cancer.0=subset(PCBPOL.cancer,PCBPOL.cancer$MCQ230abc==0); table(PCBPOL.cancer.0$RIAGENDR,useNA='always')
PCBPOL.cancer.1=subset(PCBPOL.cancer,PCBPOL.cancer$MCQ230abc==1); table(PCBPOL.cancer.1$RIAGENDR,useNA='always')


write_xlsx(temp,"C:\\Users\\pollu\\Downloads\\time considered 실험\\NGS\\descriptive_main_time.considered esophageal cancer.xlsx")


for (i in 23){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240N<=10|RIDAGEYR-
MCQ240N<=10|RIDAGEYR-MCQ240N<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-

```

```
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
}
```

```
table(PCBPOL.cancer$MCQ230abc,useNA='always')
```

```
temp=PCBPOL.cancer %>% group_by(PCBPOL.cancer$MCQ230abc) %>% reframe (quantile_RIDAGEYR=quantile(RIDAGEYR,na.rm=T),
```

```
quantile_LBC105=quantile(LBC105,na.rm=T),
```

```
quantile_LBC114=quantile(LBC114,na.rm=T),
```

```
quantile_LBC118=quantile(LBC118,na.rm=T),
```

```
quantile_LBC138=quantile(LBC138,na.rm=T),
```

```
quantile_egfr=quantile(egfr,na.rm=T),
```

```
quantile_LBXCOT=quantile(LBXCOT,na.rm=T),
```

```
quantile_BMXBMI=quantile(BMXBMI,na.rm=T),
```

```
quantile_DMDEDUC2=quantile(DMDEDUC2,na.rm=T),
```

```
quantile_RHQ160=quantile(RHQ160,na.rm=T),
```

```
mean_RIDAGEYR=mean(RIDAGEYR,na.rm=T),
```

```
mean_LBC105=mean(LBC105,na.rm=T),
```

```
mean_LBC114=mean(LBC114,na.rm=T),
```

```
mean_LBC118=mean(LBC118,na.rm=T),
```

```
mean_LBC138=mean(LBC138,na.rm=T),
```

```
mean_egfr=mean(egfr,na.rm=T),
```

```

mean_LBXCOT=mean(LBXCOT,na.rm=T),
mean_BMXBMI=mean(BMXBMI,na.rm=T),
mean_DMDEDUC2=mean(DMDEDUC2,na.rm=T),
mean_RHQ160=mean(RHQ160,na.rm=T))

PCBPOL.cancer.0=subset(PCBPOL.cancer,PCBPOL.cancer$MCQ230abc==0); table(PCBPOL.cancer.0$RIAGENDR,useNA='always')
PCBPOL.cancer.1=subset(PCBPOL.cancer,PCBPOL.cancer$MCQ230abc==1); table(PCBPOL.cancer.1$RIAGENDR,useNA='always')


write_xlsx(temp,"C:\\Users\\pollu\\Downloads\\time considered 실험\\NGS\\descriptive_main_time.considered lung cancer.xlsx")


table(PCBPOL.cancer.0$DMDEDUC2,useNA="always");table(PCBPOL.cancer.1$DMDEDUC2,useNA="always")
table(PCBPOL.cancer.0$RHQ160,useNA="always");table(PCBPOL.cancer.1$RHQ160,useNA="always")


for (i in 25){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240P<=10|RIDAGEYR-
MCQ240P<=10|RIDAGEYR-MCQ240P<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-

```

```
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
```

```
}
```

```
table(PCBPOL.cancer$MCQ230abc,useNA='always')
```

```
temp=PCBPOL.cancer %>% group_by(PCBPOL.cancer$MCQ230abc) %>% reframe (quantile_RIDAGEYR=quantile(RIDAGEYR,na.rm=T),
```

```
quantile_LBC105=quantile(LBC105,na.rm=T),
```

```
quantile_LBC114=quantile(LBC114,na.rm=T),
```

```
quantile_LBC118=quantile(LBC118,na.rm=T),
```

```
quantile_LBC138=quantile(LBC138,na.rm=T),
```

```
quantile_egfr=quantile(egfr,na.rm=T),
```

```
quantile_LBXCOT=quantile(LBXCOT,na.rm=T),
```

```
quantile_BMXBMI=quantile(BMXBMI,na.rm=T),
```

```
quantile_DMDEDUC2=quantile(DMDEDUC2,na.rm=T),
```

```
quantile_RHQ160=quantile(RHQ160,na.rm=T),
```

```
mean_RIDAGEYR=mean(RIDAGEYR,na.rm=T),
```

```
mean_LBC105=mean(LBC105,na.rm=T),
```

```
mean_LBC114=mean(LBC114,na.rm=T),
```

```
mean_LBC118=mean(LBC118,na.rm=T),
```

```
mean_LBC138=mean(LBC138,na.rm=T),
```

```
mean_egfr=mean(egfr,na.rm=T),
```

```

mean_LBXCOT=mean(LBXCOT,na.rm=T),
mean_BMXBMI=mean(BMXBMI,na.rm=T),
mean_DMDEDUC2=mean(DMDEDUC2,na.rm=T),
mean_RHQ160=mean(RHQ160,na.rm=T))

PCBPOL.cancer.0=subset(PCBPOL.cancer,PCBPOL.cancer$MCQ230abc==0); table(PCBPOL.cancer.0$RIAGENDR,useNA='always')
PCBPOL.cancer.1=subset(PCBPOL.cancer,PCBPOL.cancer$MCQ230abc==1); table(PCBPOL.cancer.1$RIAGENDR,useNA='always')

write_xlsx(temp,"C:\\Users\\pollu\\Downloads\\time considered 실험\\NGS\\descriptive_main_time.considered melanoma.xlsx")

```

```

for (i in 30){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240U<=10|RIDAGEYR-
MCQ240U<=10|RIDAGEYR-MCQ240U<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)

```

```
}
```

```
table(PCBPOL.cancer$MCQ230abc,useNA='always')
```

```
temp=PCBPOL.cancer %>% group_by(PCBPOL.cancer$MCQ230abc) %>% reframe (quantile_RIDAGEYR=quantile(RIDAGEYR,na.rm=T),
```

```
quantile_LBC105=quantile(LBC105,na.rm=T),
```

```
quantile_LBC114=quantile(LBC114,na.rm=T),
```

```
quantile_LBC118=quantile(LBC118,na.rm=T),
```

```
quantile_LBC138=quantile(LBC138,na.rm=T),
```

```
quantile_egfr=quantile(egfr,na.rm=T),
```

```
quantile_LBXCOT=quantile(LBXCOT,na.rm=T),
```

```
quantile_BMXBMI=quantile(BMXBMI,na.rm=T),
```

```
quantile_DMDEDUC2=quantile(DMDEDUC2,na.rm=T),
```

```
quantile_RHQ160=quantile(RHQ160,na.rm=T),
```

```
mean_RIDAGEYR=mean(RIDAGEYR,na.rm=T),
```

```
mean_LBC105=mean(LBC105,na.rm=T),
```

```
mean_LBC114=mean(LBC114,na.rm=T),
```

```
mean_LBC118=mean(LBC118,na.rm=T),
```

```
mean_LBC138=mean(LBC138,na.rm=T),
```

```
mean_egfr=mean(egfr,na.rm=T),
```

```
mean_LBXCOT=mean(LBXCOT,na.rm=T),
```

```

mean_BMXBMI=mean(BMXBMI,na.rm=T),
mean_DMDEDUC2=mean(DMDEDUC2,na.rm=T),
mean_RHQ160=mean(RHQ160,na.rm=T))

PCBPOL.cancer.0=subset(PCBPOL.cancer,PCBPOL.cancer$MCQ230abc==0); table(PCBPOL.cancer.0$RIAGENDR,useNA='always')
PCBPOL.cancer.1=subset(PCBPOL.cancer,PCBPOL.cancer$MCQ230abc==1); table(PCBPOL.cancer.1$RIAGENDR,useNA='always')


write_xlsx(temp,"C:\\Users\\pollu\\Downloads\\time considered 실험\\NGS\\descriptive_main_time.considered prostate cancer.xlsx")


for (i in 32){
  PCBPOL.cancer=FINAL.DATA.cr %>% mutate(MCQ230abc=ifelse(MCQ230a==i|MCQ230b==i|MCQ230c==i,1,0))
  PCBPOL.cancer$MCQ230abc=ifelse(MCQ220==2,0,PCBPOL.cancer$MCQ230abc)
  PCBPOL.cancer$MCQ230abc=ifelse((((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240W<=10|RIDAGEYR-
MCQ240W<=10|RIDAGEYR-MCQ240W<=10))|
                                ((PCBPOL.cancer$MCQ230abc==1)&(RIDAGEYR-MCQ240A<=10|RIDAGEYR-
MCQ240B<=10|RIDAGEYR-MCQ240C<=10))),1,0)
}

```



```
table(PCBPOL.cancer$MCQ230abc,useNA='always')
```

```
temp=PCBPOL.cancer %>% group_by(PCBPOL.cancer$MCQ230abc) %>% reframe (quantile_RIDAGEYR=quantile(RIDAGEYR,na.rm=T),
```

```
quantile_LBC105=quantile(LBC105,na.rm=T),
```

```
quantile_LBC114=quantile(LBC114,na.rm=T),
```

```
quantile_LBC118=quantile(LBC118,na.rm=T),
```

```
quantile_LBC138=quantile(LBC138,na.rm=T),
```

```
quantile_egfr=quantile(egfr,na.rm=T),
```

```
quantile_LBXCOT=quantile(LBXCOT,na.rm=T),
```

```
quantile_BMXBMI=quantile(BMXBMI,na.rm=T),
```

```
quantile_DMDEDUC2=quantile(DMDEDUC2,na.rm=T),
```

```
quantile_RHQ160=quantile(RHQ160,na.rm=T),
```

```
mean_RIDAGEYR=mean(RIDAGEYR,na.rm=T),
```

```
mean_LBC105=mean(LBC105,na.rm=T),
```

```
mean_LBC114=mean(LBC114,na.rm=T),
```

```
mean_LBC118=mean(LBC118,na.rm=T),
```

```
mean_LBC138=mean(LBC138,na.rm=T),
```

```
mean_egfr=mean(egfr,na.rm=T),
```

```
mean_LBXCOT=mean(LBXCOT,na.rm=T),
```

```
mean_BMXBMI=mean(BMXBMI,na.rm=T),
```

```
mean_DMDEDUC2=mean(DMDEDUC2,na.rm=T),
mean_RHQ160=mean(RHQ160,na.rm=T))

PCBPOL.cancer.0=subset(PCBPOL.cancer,PCBPOL.cancer$MCQ230abc==0); table(PCBPOL.cancer.0$RIAGENDR,useNA='always')
PCBPOL.cancer.1=subset(PCBPOL.cancer,PCBPOL.cancer$MCQ230abc==1); table(PCBPOL.cancer.1$RIAGENDR,useNA='always')

write_xlsx(temp,"C:\\Users\\pollu\\Downloads\\time considered 실험\\NGS\\descriptive_main_time.considered non-melanomatous skin cancer.xlsx")
```