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data<-read_excel(wcfile1,sheet=wcsheet1)
data[, 'a']<-ifelse(data$Endpoint %in% c("Bacterial mutagenicity","In
vitro micronucleus",
                                "Comet assay","Micronucleus",
                                "POLY-3 lowest dose","Top dose",
                                "Inhalation risk unit","Oral
slope factor",
                                "Tumor type","Level of evidence
of carcinogenic activity") |
                                data$Endpoint=="WOE characterization" &
                                !grepl( "A (Human carcinogen)", data$Response,
fixed = TRUE) &
                                !grepl( "Carcinogenic to humans (", data$Response,
fixed = TRUE) |
                                data$Endpoint=="Cancer classification" &
                                data$Response %notin%
c("Known/likely","Classification not available") &
                                !grepl( "Not required", data$Response, fixed =
TRUE) |
                                data$Endpoint=="IARC group" & data$Response !='1' |
                                data$Endpoint=="Listing status" &
data$Response=="RAHC",1,0)
data[, 'am']<-ifelse(data$Endpoint %in% c("Bacterial mutagenicity","In
vitro micronucleus",
                                "Comet
assay","Micronucleus"),1,0)
data[, 'ac']<-ifelse(data$Endpoint %in% c("POLY-3 lowest dose","Top dose",
                                "Inhalation risk unit","Oral
slope factor",
                                "Tumor type","Level of evidence
of carcinogenic activity") |
                                data$Endpoint=="WOE characterization" &
                                !grepl( "A (Human carcinogen)", data$Response,
fixed = TRUE) &
                                !grepl( "Carcinogenic to humans (",
data$Response, fixed = TRUE) |
                                data$Endpoint=="Cancer classification" &
                                data$Response %notin%
c("Known/likely","Classification not available") &
                                !grepl( "Not required", data$Response, fixed =
TRUE) |
                                data$Endpoint=="IARC group" & data$Response !='1' |
                                data$Endpoint=="Listing status" &
data$Response=="RAHC",1,0)
data[, 'qnc']<-ifelse(data$Endpoint %in% c("Inhalation risk unit","Oral
slope factor"),1,0)
data[, 'qlc']<-ifelse(data$Endpoint %in% c("Tumor type","Level of evidence
of carcinogenic activity",
                                "WOE characterization","Cancer
classification",
                                "IARC group","Listing
status"),1,0)
data[, 'hc']<-ifelse(data$Endpoint=="WOE characterization" &

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      (grepl( "A (Human carcinogen)", data$Response,
fixed = TRUE) |
      grepl( "Carcinogenic to humans (", data$Response,
fixed = TRUE)) |
      data$Endpoint=="Cancer classification" &
data$Response=="Known/likely" |
      data$Endpoint=="IARC group" & data$Response=="1" |
      data$Endpoint=="Listing status" &
data$Response=="Known",1,0)

d1<- filter(data,data$Reference != "Not applicable")
d2<- filter(data,data$Reference=="Not applicable" &
      !grepl( "Office of Pesticide Programs", data$URL, fixed =
TRUE))
d3<- filter(data,data$Reference=="Not applicable" &
      grepl( "Office of Pesticide Programs", data$URL, fixed =
TRUE))

n1<- d1 %>% group_by(d1$CASRN,d1$Reference) %>%

summarize(a=max(a),am=max(am),ac=max(ac),qnc=max(qnc),qlc=max(qlc),hc=max
(hc))
n1a<- n1 %>% group_by(n1[,1]) %>%

summarize(a=sum(a),am=sum(am),ac=sum(ac),qnc=sum(qnc),qlc=sum(qlc),hc=sum
(hc))
colnames(n1a)<-c('CAS','a1','am1','ac1','qnc1','qlc1','hc1')

n2<- d2 %>% group_by(d2$CASRN,d2$URL) %>%

summarize(a=max(a),am=max(am),ac=max(ac),qnc=max(qnc),qlc=max(qlc),hc=max
(hc))
n2a<- n2 %>% group_by(n2[,1]) %>%

summarize(a=sum(a),am=sum(am),ac=sum(ac),qnc=sum(qnc),qlc=sum(qlc),hc=sum
(hc))
colnames(n2a)<-c('CAS','a2','am2','ac2','qnc2','qlc2','hc2')

n3a<- d3 %>% group_by(d3$CASRN) %>%

summarize(a=sum(a),am=sum(am),ac=sum(ac),qnc=sum(qnc),qlc=sum(qlc),hc=sum
(hc))
colnames(n3a)<-c('CAS','a3','am3','ac3','qnc3','qlc3','hc3')

all<-left_join(tlist, n1a, by= 'CAS')
all<-left_join(all, n2a, by= 'CAS')
all<-left_join(all, n3a, by= 'CAS')

all<-all[order(all$CID,all$CAS,na.last=FALSE),]

for (i in 1:dim(all)[1]) {
  all$animal[i]<-all$a1[i]+all$a2[i]+all$a3[i]
  all$a_muta[i]<-all$am1[i]+all$am2[i]+all$am3[i]
  all$a_carc[i]<-all$ac1[i]+all$ac2[i]+all$ac3[i]

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all$quan[i]<-all$qnc1[i]+all$qnc2[i]+all$qnc3[i]
all$qn_carc[i]<-all$qnc1[i]+all$qnc2[i]+all$qnc3[i]
all$qual[i]<-all$qlc1[i]+all$qlc2[i]+all$qlc3[i]
all$ql_carc[i]<-all$qlc1[i]+all$qlc2[i]+all$qlc3[i]
all$human[i]<-all$hc1[i]+all$hc2[i]+all$hc3[i]
all$h_carc[i]<-all$hc1[i]+all$hc2[i]+all$hc3[i]}

all[,5:ncolt][is.na(all[,5:ncolt])] <- 0

wb <- loadWorkbook(outfile)
writeData(wb, sheet = "Cancer", all[1:ncolt], colNames = F,startRow=3)
saveWorkbook(wb,outfile,overwrite = T)
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