#enter for the pathway

ps <- length(unique(sulfateKOs$Pathway.Number))

for (p in c(1)){

sulfateKO <- sulfateKOs %>%

filter(Pathway.Number == p)

# make these KOs OR steps the columns in a df and filter the results to those KOs

df <- as.data.frame(matrix(ncol=length(sulfateKO$StepKOs), nrow=0))

names(df) <- sulfateKO$StepKOs

result <- results %>% filter(KO %in% sulfateKO$KO)

#enter for the genome

for (g in 1:nrow(genomessums)){

print(g)

# we can go through the scaffolds membership file by the second column, for which we will use the genomes summary file

#genomescaffolds <- genomesscaffolds %>%

# filter(V2 == genomessums$Genome[genome])

# filter the hits in the all filtered hits file to just the one genome

result1 <- result %>% filter(genome %in% genomessums$Genome[g])

# enter for that KO

for (k in 1:length(sulfateKO$KO)){

# filter to one column at a time in the already filtered df

# add value to that row/column combination

if (sulfateKO$KO[k] %in% result1$KO){

df[g,k]<-1

} else {

df[g,k]<-0

}

}

# populate row with that genome name

row.names(df)[g] <- genomessums$Genome[g]

}

write.csv(x = df, file = paste0("june192024\_",unique(sulfateKOs$Broad.pathway.description[which(sulfateKOs$Pathway.Number == p)]), "Raw.csv"))

}