

Additional file 4. R script of the forest plots for the systematic review of Godijk et al.

#Be sure you first run the file "Script Systematic Review Godijk et al." until line 1924

```
#rm(list=ls())
```

```
library(readxl)
```

```
library(metafor)
```

```
Forest<- Eating_meat_E.coli_OR [,c(2,21,23, 34, 31, 32)]
```

```
par(xpd=FALSE)
```

```
# ODDS RATIO's
```

```
# Eating meat
```

```
forest(Eating_meat_E.coli_OR$Num_Estimate, ci.lb=Eating_meat_E.coli_OR$Num_lb,  
ci.ub=Eating_meat_E.coli_OR$Num_ub, psize=1, xlab="",
```

```
xlim=c(-10,50), slab=Eating_meat_E.coli_OR$Author, cex=0.95, ylim=c(0,20), rows=c(1:11),  
refline = 1, alim=c(0, 20))
```

```
# Sharing water
```

```
forest(Sharing_water_source_with_animals$Num_Estimate,  
ci.lb=Sharing_water_source_with_animals$Num_lb,  
ci.ub=Sharing_water_source_with_animals$Num_ub, psize=1, xlab="Odds ratio",
```

```
xlim=c(-5,26),slab=Sharing_water_source_with_animals$Author, cex=0.95, ylim=c(0,8),  
rows=c(1:5), refline = 1, alim=c(0, 20))
```

```
text(18,5.5, "Sharing water source with animals E. coli OR", pos=2,cex=1,font=2)
```

```
# Breast feeding
```

```
# E. coli
```

```
forest(BreastF_ecoli_OR$Num_Estimate, ci.lb=BreastF_ecoli_OR$Num_lb,  
ci.ub=BreastF_ecoli_OR$Num_ub, psize=1, xlab="",
```

```
xlim=c(-5,5),slab=BreastF_ecoli_OR$Author, cex=0.95, ylim=c(0,6), rows=c(1:3), refile = 1,
alim=c(0, 20))
```

```
text(18,3.5, "Breast feeding E. Coli OR", pos=2,cex=1,font=2)
```

```
# Enterobacteriae
```

```
forest(BreastF_entero_OR$Num_Estimate, ci.lb=BreastF_entero_OR$Num_lb,
ci.ub=BreastF_entero_OR$Num_ub, psize=1, xlab="",
```

```
xlim=c(-5,26),slab=BreastF_entero_OR$Author, cex=0.95, ylim=c(0,5), rows=c(1:2), refile = 1,
alim=c(0, 20))
```

```
text(17,2.5, "Breast feeding E. Coli Enterobacteriaceae", pos=2,cex=1,font=2)
```

```
# S pneumonia
```

```
forest(BreastF_spneumo_OR$Num_Estimate, ci.lb=BreastF_spneumo_OR$Num_lb,
ci.ub=BreastF_spneumo_OR$Num_ub, psize=1, xlab="",
```

```
xlim=c(-5,26),slab=BreastF_spneumo_OR$Author, cex=0.95, ylim=c(0,7), rows=c(1:3), refile = 1,
alim=c(0, 20))
```

```
text(17,4.5, "Breast feeding S. pneumoniae", pos=2,cex=1,font=2)
```

```
# Contact with infected person
```

```
# S Aureus
```

```
forest(Contact_with_infected_Saurues_OR$Num_Estimate,
ci.lb=Contact_with_infected_Saurues_OR$Num_lb,
ci.ub=Contact_with_infected_Saurues_OR$Num_ub, psize=1, xlab="",
```

```
xlim=c(-5,26),slab=Contact_with_infected_Saurues_OR$Author, cex=0.95, ylim=c(0,5),
rows=c(1:2), refile = 1, alim=c(0, 20))
```

```
text(17,2.5, "Contact with infected person S. Aureus OR", pos=2,cex=1,font=2)
```

```
# A baumannii
```

```
forest(Contact_with_infected_Abau_OR$Num_Estimate,
ci.lb=Contact_with_infected_Abau_OR$Num_lb, ci.ub=Contact_with_infected_Abau_OR$Num_ub,
psize=1, xlab="",
```

```
xlim=c(-5,26),slab=Contact_with_infected_Abau_OR$Author, cex=0.95, ylim=c(0,5), rows=c(1:2),
refline = 1, alim=c(0, 20))
```

```
text(17,2.5, "Contact with infected person A. baumannii OR", pos=2,cex=1,font=2)
```

```
# Eating meat
```

```
#Red
```

```
redmeat_or$Author<-as.character(redmeat_or$Author)
```

```
redmeat_or$Author[1:3]<-"Leistner"
```

```
forest(redmeat_or$Num_Estimate, ci.lb=redmeat_or$Num_lb, ci.ub=redmeat_or$Num_ub, psize=1,  
xlab="",
```

```
  xlim=c(-5,26), slab=redmeat_or$Author, cex=0.95, ylim=c(1,10), rows=c(1:6), refile = 1,  
  alim=c(0, 20))
```

```
text(17,7, "Eating Red meat E. coli OR", pos=2,cex=1,font=2)
```

```
# White
```

```
whitemeat_or$Author<-as.character(whitemeat_or$Author)
```

```
whitemeat_or$Author[1]<-"Leistner"
```

```
forest(whitemeat_or$Num_Estimate, ci.lb=whitemeat_or$Num_lb, ci.ub=whitemeat_or$Num_ub,  
psize=1, xlab="",
```

```
  xlim=c(-5,26), slab=whitemeat_or$Author, cex=0.95, ylim=c(1,5), rows=c(1:2), refile = 1,  
  alim=c(0, 20))
```

```
text(17,2.5, "Eating white meat E. coli OR", pos=2,cex=1,font=2)
```

```
# general
```

```
forest(generalmeat_or$Num_Estimate, ci.lb=generalmeat_or$Num_lb,  
ci.ub=generalmeat_or$Num_ub, psize=1, xlab="",
```

```
  xlim=c(-5,26), slab=generalmeat_or$Author, cex=0.95, ylim=c(0,7), rows=c(1:3), refile = 1,  
  alim=c(0, 20))
```

```
text(17,4, "Eating meat in general E. coli OR", pos=2,cex=1,font=2)
```

```
# Family member colonised
```

```
# E.coli
```

```
forest(Family_member_colonised_ecoli_OR$Num_Estimate,  
ci.lb=Family_member_colonised_ecoli_OR$Num_lb,  
ci.ub=Family_member_colonised_ecoli_OR$Num_ub, psize=1, xlab="",
```

```
  xlim=c(-5,26), slab=Family_member_colonised_ecoli_OR$Author, cex=0.95, ylim=c(0,7),  
  rows=c(1:4), refile = 1, alim=c(0, 20))
```

```
text(17,4.5, "Family member colonised E. coli OR", pos=2,cex=1,font=2)
```

```
# S aureus
```

```
Family_member_colonised_saureus_OR$Author<-
```

```
as.character(Family_member_colonised_saureus_OR$Author)
```

```
Family_member_colonised_saureus_OR$Author[1]<-"Ferreira"
```

```
forest(Family_member_colonised_saureus_OR$Num_Estimate,
```

```
ci.lb=Family_member_colonised_saureus_OR$Num_lb,
```

```
ci.ub=Family_member_colonised_saureus_OR$Num_ub, psize=1, xlab="",
```

```
xlim=c(-7,26), slab=Family_member_colonised_saureus_OR$Author, cex=0.95, ylim=c(0.8,10),
```

```
rows=c(1:6), refile = 1, alim=c(0, 20))
```

```
text(17,7, "Family member colonised S. aureus OR", pos=2,cex=1,font=2)
```

```
# Family member occupational exposure
```

```
Family_member_occupational_exposure_saureus_farming$Author<-
```

```
as.character(Family_member_occupational_exposure_saureus_farming$Author)
```

```
Family_member_occupational_exposure_saureus_farming$Author[1:3]<-"Wardyn"
```

```
forest(Family_member_occupational_exposure_saureus_farming$Num_Estimate,
```

```
ci.lb=Family_member_occupational_exposure_saureus_farming$Num_lb,
```

```
ci.ub=Family_member_occupational_exposure_saureus_farming$Num_ub, psize=1, xlab="",
```

```
xlim=c(-5,26), slab=Family_member_occupational_exposure_saureus_farming$Author,
```

```
cex=0.95, ylim=c(0.8,7), rows=c(1:4), refile = 1, alim=c(0, 20))
```

```
text(23,4.7, "Family member occupational exposure farming S. aureus OR", pos=2,cex=1,font=2)
```

```
#hospital
```

```
forest(Family_member_occupational_exposure_saureus_hospital$Num_Estimate,
```

```
ci.lb=Family_member_occupational_exposure_saureus_hospital$Num_lb,
```

```
ci.ub=Family_member_occupational_exposure_saureus_hospital$Num_ub, psize=1, xlab="",
```

```
xlim=c(-5,26), slab=Family_member_occupational_exposure_saureus_hospital$Author,
```

```
cex=0.95, ylim=c(0,5), rows=c(1:2), refile = 1, alim=c(0, 20))
```

```
text(21,2.7, "Family member occupational exposure hospital S. aureus OR", pos=2,cex=1,font=2)
```

```
#Livestock to drinking water
```

```
#Cattle
```

```
forest(Livestock_to_drinking_water_cattle$Num_Estimate,
ci.lb=Livestock_to_drinking_water_cattle$Num_lb,
ci.ub=Livestock_to_drinking_water_cattle$Num_ub, psize=1, xlab="",
      xlim=c(-5,26), slab=Livestock_to_drinking_water_cattle$Author, cex=0.95, ylim=c(0,7),
rows=c(1:4), refile = 1, alim=c(0, 20))
text(17,4.7, "Livestock (cattle) to drinking water E. coli OR", pos=2,cex=1,font=2)
```

#Poultry

```
forest(Livestock_to_drinking_water_poultry$Num_Estimate,
ci.lb=Livestock_to_drinking_water_poultry$Num_lb,
ci.ub=Livestock_to_drinking_water_poultry$Num_ub, psize=1, xlab="",
      xlim=c(-5,26), slab=Livestock_to_drinking_water_poultry$Author, cex=0.95, ylim=c(0,7),
rows=c(1:4), refile = 1, alim=c(0, 20))
text(17,4.7, "Livestock (poultry) to drinking water E. coli OR", pos=2,cex=1,font=2)
```

#Pig

```
forest(Livestock_to_drinking_water_pig$Num_Estimate,
ci.lb=Livestock_to_drinking_water_pig$Num_lb, ci.ub=Livestock_to_drinking_water_pig$Num_ub,
psize=1, xlab="",
      xlim=c(-5,26), slab=Livestock_to_drinking_water_pig$Author, cex=0.95, ylim=c(0,7), rows=c(1:4),
refline = 1, alim=c(0, 20))
text(17,4.7, "Livestock (pig) to drinking water E. coli OR", pos=2,cex=1,font=2)
```

Mother to child

```
forest(Mother_to_child_Aureus_OR$Num_Estimate, ci.lb=Mother_to_child_Aureus_OR$Num_lb,
ci.ub=Mother_to_child_Aureus_OR$Num_ub, psize=1, xlab="",
      xlim=c(-5,26), slab=Mother_to_child_Aureus_OR$Author, cex=0.95, ylim=c(0,5), rows=c(1:2),
refline = 1, alim=c(0, 20))
text(12,2.7, "Mother to child S. aureus OR", pos=2,cex=1,font=2)
```

Occupational exposure

#Cattle

```
forest(Occupational_Exposure_SAureus_OR_cattle$Num_Estimate,
ci.lb=Occupational_Exposure_SAureus_OR_cattle$Num_lb,
ci.ub=Occupational_Exposure_SAureus_OR_cattle$Num_ub, psize=1, xlab="")
```

```
xlim=c(-5,26), slab=Occupational_Exposure_SAureus_OR_cattle$Author, cex=0.95, ylim=c(0,7),  
rows=c(1:4), refline = 1, alim=c(0, 20))
```

```
text(17,4.7, "Occupational exposure to cattle S. aureus OR", pos=2,cex=1,font=2)
```

```
#Pig
```

```
forest(Occupational_Exposure_SAureus_OR_pig$Num_Estimate,  
ci.lb=Occupational_Exposure_SAureus_OR_pig$Num_lb,  
ci.ub=Occupational_Exposure_SAureus_OR_pig$Num_ub, psize=1, xlab="",
```

```
xlim=c(-45,40), slab=Occupational_Exposure_SAureus_OR_pig$Author, cex=0.95, ylim=c(1,20),  
rows=c(1:14), refline = 1, alim=c(0, 20))
```

```
text(90,16.7, "Occupational exposure to pig S. aureus OR", pos=2,cex=1,font=2)
```

```
forest(Occupational_Exposure_Enterococcus_OR_pig$Num_Estimate,  
ci.lb=Occupational_Exposure_Enterococcus_OR_pig$Num_lb,  
ci.ub=Occupational_Exposure_Enterococcus_OR_pig$Num_ub, psize=1, xlab="",
```

```
xlim=c(-5,26), slab=Occupational_Exposure_Enterococcus_OR_pig$Author, cex=0.95, ylim=c(1,5),  
rows=c(1:2), refline = 1, alim=c(0, 20))
```

```
text(23,2.7, "Occupational exposure to pig Enterobacteriaceae OR", pos=2,cex=1,font=2)
```

```
#Poultry
```

```
# E. coli
```

```
forest(Occupational_Exposure_E.coli_OR_poultry$Num_Estimate,  
ci.lb=Occupational_Exposure_E.coli_OR_poultry$Num_lb,  
ci.ub=Occupational_Exposure_E.coli_OR_poultry$Num_ub, psize=1, xlab="",
```

```
xlim=c(-5,26), slab=Occupational_Exposure_E.coli_OR_poultry$Author, cex=0.95, ylim=c(1,17.5),  
rows=c(1:14), refline = 1, alim=c(0, 20))
```

```
text(23,14.9, "Occupational exposure to poultry E. coli OR", pos=2,cex=1,font=2)
```

```
#View(Occupational_Exposure_E.coli_OR_poultry)
```

```
# Veterinarian staff
```

```
forest(Occupational_Exposure_SAureus_OR_vets$Num_Estimate,  
ci.lb=Occupational_Exposure_SAureus_OR_vets$Num_lb,  
ci.ub=Occupational_Exposure_SAureus_OR_vets$Num_ub, psize=1, xlab="",
```

```
xlim=c(-5,26), slab=Occupational_Exposure_SAureus_OR_vets$Author, cex=0.95, ylim=c(1,6),  
rows=c(1:4), refline = 1, alim=c(0, 20))
```

```
text(22,3.5, "Occupational exposure veterinarian staff S. aureus OR", pos=2,cex=1,font=2)
```

```
# Pet to human E. Coli
```

```
forest(Pet_to_human_ecoli_OR$Num_Estimate, ci.lb=Pet_to_human_ecoli_OR$Num_lb,  
ci.ub=Pet_to_human_ecoli_OR$Num_ub, psize=1, xlab="",
```

```
  xlim=c(-5,26), slab=Pet_to_human_ecoli_OR$Author, cex=0.95, ylim=c(1,5), rows=c(1:2), refile  
= 1, alim=c(0, 20))
```

```
text(11,2.5, "Pet to human E. coli OR", pos=2,cex=1,font=2)
```

```
forest(Pet_to_human_staph_OR$Num_Estimate, ci.lb=Pet_to_human_staph_OR$Num_lb,  
ci.ub=Pet_to_human_staph_OR$Num_ub, psize=1, xlab="",
```

```
  xlim=c(-10,26), slab=Pet_to_human_staph_OR$Author, cex=0.95, ylim=c(1,5), rows=c(1:2),  
refline = 1, alim=c(0, 20))
```

```
text(16,2.5, "Pet to human Staphylococci OR", pos=2,cex=1,font=2)
```

```
View(Pet_to_human_staph_OR)
```

```
# Sharing a room
```

```
Sharing_room_entero_OR$Author<-as.character(Sharing_room_entero_OR$Author)
```

```
Sharing_room_entero_OR$Author[2]<-"Schwartz-Neiderman"
```

```
forest(Sharing_room_entero_OR$Num_Estimate, ci.lb=Sharing_room_entero_OR$Num_lb,  
ci.ub=Sharing_room_entero_OR$Num_ub, psize=1, xlab="",
```

```
  xlim=c(-8,26), slab=Sharing_room_entero_OR$Author, cex=0.95, ylim=c(1,5.5), rows=c(1:3),  
refline = 1, alim=c(0, 20))
```

```
text(18,3.3, "Sharing a room Enterobacteriaceae OR", pos=2,cex=1,font=2)
```

```
# Travel
```

```
# South ASia
```

```
# S aureus
```

```
forest(Travelling_OR_saures_South_asia$Num_Estimate,  
ci.lb=Travelling_OR_saures_South_asia$Num_lb, ci.ub=Travelling_OR_saures_South_asia$Num_ub,  
psize=1, xlab="",
```

```
xlim=c(-8,26), slab=Travelling_OR_saures_South_asia$Author, cex=0.95, ylim=c(1,4.5),  
rows=c(1:2), refile = 1, alim=c(0, 20))
```

```
text(18,2.3, "Travelling to South Asia S. aureus OR", pos=2,cex=1,font=2)
```

```
# E.coli
```

```
forest(Travelling_OR_Ecoli_SA$Num_Estimate, ci.lb=Travelling_OR_Ecoli_SA$Num_lb,  
ci.ub=Travelling_OR_Ecoli_SA$Num_ub, psize=1, xlab="",
```

```
xlim=c(-8,26), slab=Travelling_OR_Ecoli_SA$Author, cex=0.95, ylim=c(1,6), rows=c(1:3), refile =  
1, alim=c(0, 20))
```

```
text(23,3.5, "Travelling to South Asia E. coli OR", pos=2,cex=1,font=2)
```

```
# Enterobacteriaceae
```

```
forest(Travelling_OR_Enterо_SA$Num_Estimate, ci.lb=Travelling_OR_Enterо_SA$Num_lb,  
ci.ub=Travelling_OR_Enterо_SA$Num_ub, psize=1, xlab="",
```

```
xlim=c(-8,26), slab=Travelling_OR_Enterо_SA$Author, cex=0.95, ylim=c(1,6), rows=c(1:3), refile  
= 1, alim=c(0, 20))
```

```
text(23,3.5, "Travelling to South Asia Enterobacteriaceae OR", pos=2,cex=1,font=2)
```

```
# South East Asia
```

```
# Enterobacteriaceae
```

```
forest(Travelling_OR_Enterо_SEA$Num_Estimate, ci.lb=Travelling_OR_Enterо_SEA$Num_lb,  
ci.ub=Travelling_OR_Enterо_SEA$Num_ub, psize=1, xlab="",
```

```
xlim=c(-10,40), slab=Travelling_OR_Enterо_SEA$Author, cex=0.95, ylim=c(1,8), rows=c(1:4),  
refline = 1, alim=c(0, 20))
```

```
text(25,5, "Travelling to South East Asia Enterobacteriaceae OR", pos=2,cex=1,font=2)
```

```
# Western Asia
```

```
# Enterobacteriaceae
```

```
forest(Travelling_OR_Enterо_WA$Num_Estimate, ci.lb=Travelling_OR_Enterо_WA$Num_lb,  
ci.ub=Travelling_OR_Enterо_WA$Num_ub, psize=1, xlab="",
```

```
xlim=c(-8,26), slab=Travelling_OR_Enterо_WA$Author, cex=0.95, ylim=c(1,6), rows=c(1:3),  
refline = 1, alim=c(0, 20))
```

```
text(18,3.5, "Travelling to Western Asia Enterobacteriaceae", pos=2,cex=1,font=2)
```

Asia (unspecified)

Enterobacteriaceae

```
forest(Travelling_OR_Enterо_Asia_unsp$Num_Estimate,  
ci.lb=Travelling_OR_Enterо_Asia_unsp$Num_lb, ci.ub=Travelling_OR_Enterо_Asia_unsp$Num_ub,  
psize=1, xlab="",  
      xlim=c(-8,26), slab=Travelling_OR_Enterо_Asia_unsp$Author, cex=0.95, ylim=c(1,6), rows=c(1:3),  
refline = 1, alim=c(0, 20))  
text(18,3.5, "Travelling to Asia Enterobacteriaceae OR", pos=2,cex=1,font=2)
```

Latin America

Enterobacteriaceae

```
forest(Travelling_OR_Enterо_LatinAmerica$Num_Estimate,  
ci.lb=Travelling_OR_Enterо_LatinAmerica$Num_lb,  
ci.ub=Travelling_OR_Enterо_LatinAmerica$Num_ub, psize=1, xlab="",  
      xlim=c(-8,26), slab=Travelling_OR_Enterо_LatinAmerica$Author, cex=0.95, ylim=c(1,4.5),  
rows=c(1:2), refile = 1, alim=c(0, 20))  
text(18,2.3, "Travelling to Laten America Enterobacteriaceae", pos=2,cex=1,font=2)
```

America

Enterobacteriaceae

```
forest(Travelling_OR_Enterо_America$Num_Estimate,  
ci.lb=Travelling_OR_Enterо_America$Num_lb, ci.ub=Travelling_OR_Enterо_America$Num_ub,  
psize=1, xlab="",  
      xlim=c(-8,26), slab=Travelling_OR_Enterо_America$Author, cex=0.95, ylim=c(1,4.5), rows=c(1:2),  
refline = 1, alim=c(0, 20))  
text(18,2.3, "Travelling to America Enterobacteriaceae", pos=2,cex=1,font=2)
```

Africa

Enterobacteriaceae

```
forest(Travelling_OR_Enterо_Africa$Num_Estimate, ci.lb=Travelling_OR_Enterо_Africa$Num_lb,  
ci.ub=Travelling_OR_Enterо_Africa$Num_ub, psize=1, xlab="",  
      xlim=c(-8,26), slab=Travelling_OR_Enterо_Africa$Author, cex=0.95, ylim=c(1,8), rows=c(1:4),  
refline = 1, alim=c(0, 20))  
text(18,5, "Travelling to Africa Enterobacteriaceae OR", pos=2,cex=1,font=2)
```

Europe

```
# Enterobacteriaceae
```

```
forest(Travelling_OR_Enterо_Europe$Num_Estimate, ci.lb=Travelling_OR_Enterо_Europe$Num_lb,  
ci.ub=Travelling_OR_Enterо_Europe$Num_ub, psize=1, xlab="",
```

```
  xlim=c(-8,26), slab=Travelling_OR_Enterо_Europe$Author, cex=0.95, ylim=c(1,6), rows=c(1:3),  
  refile = 1, alim=c(0, 20))
```

```
text(18,3.5, "Travelling to Europe Enterobacteriaceae OR", pos=2,cex=1,font=2)
```

```
# Prevalence Ratio
```

```
#Eating red meat
```

```
red_pr$Author<-as.character(red_pr$Author)
```

```
red_pr$Author[3:4]<-"Samore"
```

```
red_pr$Author[1]<-"Samore"
```

```
forest(red_pr$Num_Estimate, ci.lb=red_pr$Num_lb, ci.ub=red_pr$Num_ub, psize=1, xlab="",
```

```
  xlim=c(-5,26), slab=red_pr$Author, cex=0.95, ylim=c(0.8,7), rows=c(1:4), refile = 1, alim=c(0,  
  20))
```

```
text(15,4.5, "Eating red meat E. coli PR", pos=2,cex=1,font=2)
```

```
# Fam mem colonised
```

```
forest(Family_member_colonised_enterо_PR$Num_Estimate,  
ci.lb=Family_member_colonised_enterо_PR$Num_lb,  
ci.ub=Family_member_colonised_enterо_PR$Num_ub, psize=1, xlab="",
```

```
  xlim=c(-5,26), slab=Family_member_colonised_enterо_PR$Author, cex=0.95, ylim=c(1,5),  
  rows=c(1:2), refile = 1, alim=c(0, 20))
```

```
text(17,2.5, "Family member colonised Enterobacteriaceae PR", pos=2,cex=1,font=2)
```

```
# Occupational Exposure pig
```

```
Occupational_Exposure_SAureus_PR_Pig$Author<-  
as.character(Occupational_Exposure_SAureus_PR_Pig$Author)
```

```
Occupational_Exposure_SAureus_PR_Pig$Author[4:9]<-"Rinsky"
```

```
Occupational_Exposure_SAureus_PR_Pig$Author[1:3]<-"Wardyn"
```

```
forest(Occupational_Exposure_SAureus_PR_Pig$Num_Estimate,  
ci.lb=Occupational_Exposure_SAureus_PR_Pig$Num_lb,  
ci.ub=Occupational_Exposure_SAureus_PR_Pig$Num_ub, psize=1, xlab="",
```

```
xlim=c(-5,26), slab=Occupational_Exposure_SAureus_PR_Pig$Author, cex=0.95, ylim=c(1,20),
rows=c(1:16), reline = 1, alim=c(0, 20))
```

```
text(20,17, "Family member occupational exposure to pig S. aureus PR", pos=2,cex=1,font=2)
```

```
forest(Occupational_Exposure_Staph_pig_PR$Num_Estimate,
ci.lb=Occupational_Exposure_Staph_pig_PR$Num_lb,
ci.ub=Occupational_Exposure_Staph_pig_PR$Num_ub, psize=1, xlab="",
```

```
xlim=c(-4,26), slab=Occupational_Exposure_Staph_pig_PR$Author, cex=0.95, ylim=c(0,8),
rows=c(1:5), reline = 1, alim=c(0, 20))
```

```
text(20,5.5, "Family member occupational exposure to pig Staphylococci PR", pos=2,cex=1,font=2)
```

```
Occupational_Exposure_SAureus_PR_poultry$Author<-
as.character(Occupational_Exposure_SAureus_PR_poultry$Author)
```

```
Occupational_Exposure_SAureus_PR_poultry$Author[1:2]<-"Rinsky"
```

```
Occupational_Exposure_SAureus_PR_poultry$Author[3]<-"Wardyn"
```

```
forest(Occupational_Exposure_SAureus_PR_poultry$Num_Estimate,
ci.lb=Occupational_Exposure_SAureus_PR_poultry$Num_lb,
ci.ub=Occupational_Exposure_SAureus_PR_poultry$Num_ub, psize=1, xlab="",
```

```
xlim=c(-4,26), slab=Occupational_Exposure_SAureus_PR_poultry$Author, cex=0.95, ylim=c(0,6),
rows=c(1:3), reline = 1, alim=c(0, 20))
```

```
text(20,3.5, "Family member occupational exposure to poultry S. aureus PR", pos=2,cex=1,font=2)
```

```
#R0
```

```
#Animal to Animal
```

```
forest(animal_to_animal_Saurues_r0$Num_Estimate, ci.lb=animal_to_animal_Saurues_r0$Num_lb,
ci.ub=animal_to_animal_Saurues_r0$Num_ub, psize=1, xlab="",
```

```
xlim=c(-4,26), slab=animal_to_animal_Saurues_r0$Author, cex=0.95, ylim=c(1,5), rows=c(1:2),
reline = 0, alim=c(0, 20))
```

```
text(15,2.5, "Animal to animal S. aureus R0", pos=2,cex=1,font=2)
```

```
# Contact with infected person
```

```
Contact_with_infected_Saurues_r0$Author<-
as.character(Contact_with_infected_Saurues_r0$Author)
```

```
Contact_with_infected_Saurues_r0$Author[1]<-"Christopher"
```

```
forest(Contact_with_infected_Saurues_r0$Num_Estimate,  
ci.lb=Contact_with_infected_Saurues_r0$Num_lb,  
ci.ub=Contact_with_infected_Saurues_r0$Num_ub, psize=1, xlab="",  
xlim=c(-8,26), slab=Contact_with_infected_Saurues_r0$Author, cex=0.95, ylim=c(1,6),  
rows=c(1:11), refile = 0, alim=c(0, 20))  
text(17,3.5, "Contact with infected person S. aureus R0", pos=2,cex=1,font=2)
```

```
# Risk ratio
```

```
forest(Contact_with_infected_Saurues_RR$Num_Estimate,  
ci.lb=Contact_with_infected_Saurues_RR$Num_lb,  
ci.ub=Contact_with_infected_Saurues_RR$Num_ub, psize=1, xlab="Risk Ratio",  
xlim=c(-6,26), slab=Contact_with_infected_Saurues_RR$Author, cex=0.95, ylim=c(1,5),  
rows=c(1:2), refile = 0, alim=c(0, 20))  
text(15,2.5, "Contact with infected person S. aureus RR", pos=2,cex=1,font=2)
```

```
#Risks
```

```
# Animal to air kan niet want risk heeft geen CIs
```

```
forest(pig_to_air_Ecoli_Risk$Num_Estimate, ci.lb=pig_to_air_Ecoli_Risk$Num_lb,  
ci.ub=pig_to_air_Ecoli_Risk$Num_ub, psize=1, xlab="",  
xlim=c(-3,1), slab=pig_to_air_Ecoli_Risk$Author, cex=0.95, ylim=c(0,5), rows=c(1:2), refile = 0,  
alim=c(0, 2))
```

```
forest(Cattle_to_air_Sareus_Risk$Num_Estimate, ci.lb=Cattle_to_air_Sareus_Risk$Num_lb,  
ci.ub=Cattle_to_air_Sareus_Risk$Num_ub, psize=1, xlab="",  
xlim=c(-3,1), slab=Cattle_to_air_Sareus_Risk$Author, cex=0.95, ylim=c(0,5), rows=c(1:22), refile  
= 0, alim=c(0, 2))
```