

Diagnosis plots for all the statistical models used in “Impact of cropping system diversification on vegetative and reproductive characteristics of waterhemp (*Amaranthus tuberculatus*)” with `ggResidpanel` (Goode and Rey 2019).

Crop yield at the experiment site Crop identity in these yield models represented rotation system (2-year, 3-year or 4-year) for corn and soybean or 3-year and 4-year for oat.

Did crop identity and corn weed management affect corn yield?

```
corn.lmer <- lmer(log(Standardized_yield_MgpHa) ~ Block +
  Crop_ID*Corn_weed_management +
  (1|Year) + (1|Year:Block) +
  (1|Year:Crop_ID) + (1|Year:Corn_weed_management) +
  (1|Year:Crop_ID:Corn_weed_management) +
  (1|Block:Year:Crop_ID) ,
  data=corn) #corn was harvested on hafl-plot basis

resid_panel(corn.lmer, "all")
```

Did crop identity and corn weed management affect soybean yield?

```
soy.lmer <- lmer(log(Standardized_yield_MgpHa) ~ Block +
  Crop_ID*Corn_weed_management +
  (1|Year) + (1|Year:Block) +
  (1|Year:Crop_ID) + (1|Year:Corn_weed_management) +
  (1|Year:Crop_ID:Corn_weed_management) +
  (1|Block:Year:Crop_ID),
  data=soy) #soybean was harvested on hafl-plot basis

resid_panel(soy.lmer, "all")
```

Did crop identity affect oat yield?

crop identity represented rotation system (3-year or 4-year)

```
oat.lmer <- lmer(log(Standardized_yield_MgpHa) ~ Block + Crop_ID +
  (1|Year) + (1|Year:Block) +
  (1|Year:Crop_ID) + (1|Block:Year:Crop_ID),
  data=oat) #oat was harvested in whol-plot basis

resid_panel(oat.lmer, "all")
```

Community ecological indices Crop identities in these ecological indices models were the combinations of the crop species names’ one-letter abbreviation and the rotation to which the crop belonged.

Did crop identity and corn weed management affect weed community diversity index?

```
dens_diversity.lmer1 <- lmer(log(Diversity + 1) ~ Block +
  Crop_ID*Corn_weed_management +
  (1|Year) + (1|Year:Block) +
  (1|Year:Crop_ID) +
  (1|Year:Corn_weed_management) +
  (1|Year:Crop_ID:Corn_weed_management) +
  (1|Block:Year:Crop_ID) ,
  data = dens_ind_1720,
```

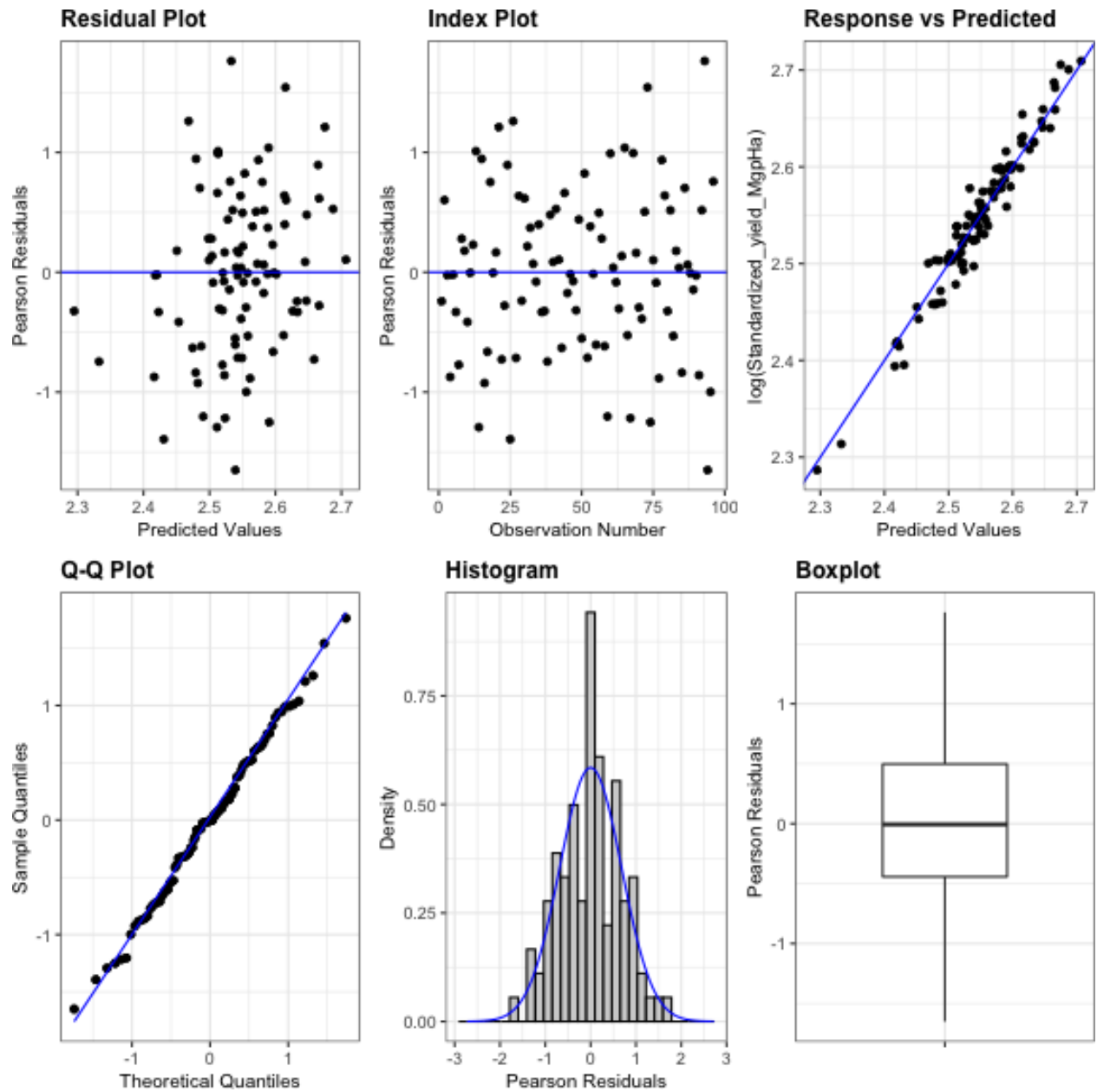


Figure 1: Diagnosis plot for the effect of crop identity and corn weed management on corn yield over four years with four blocks of replication.

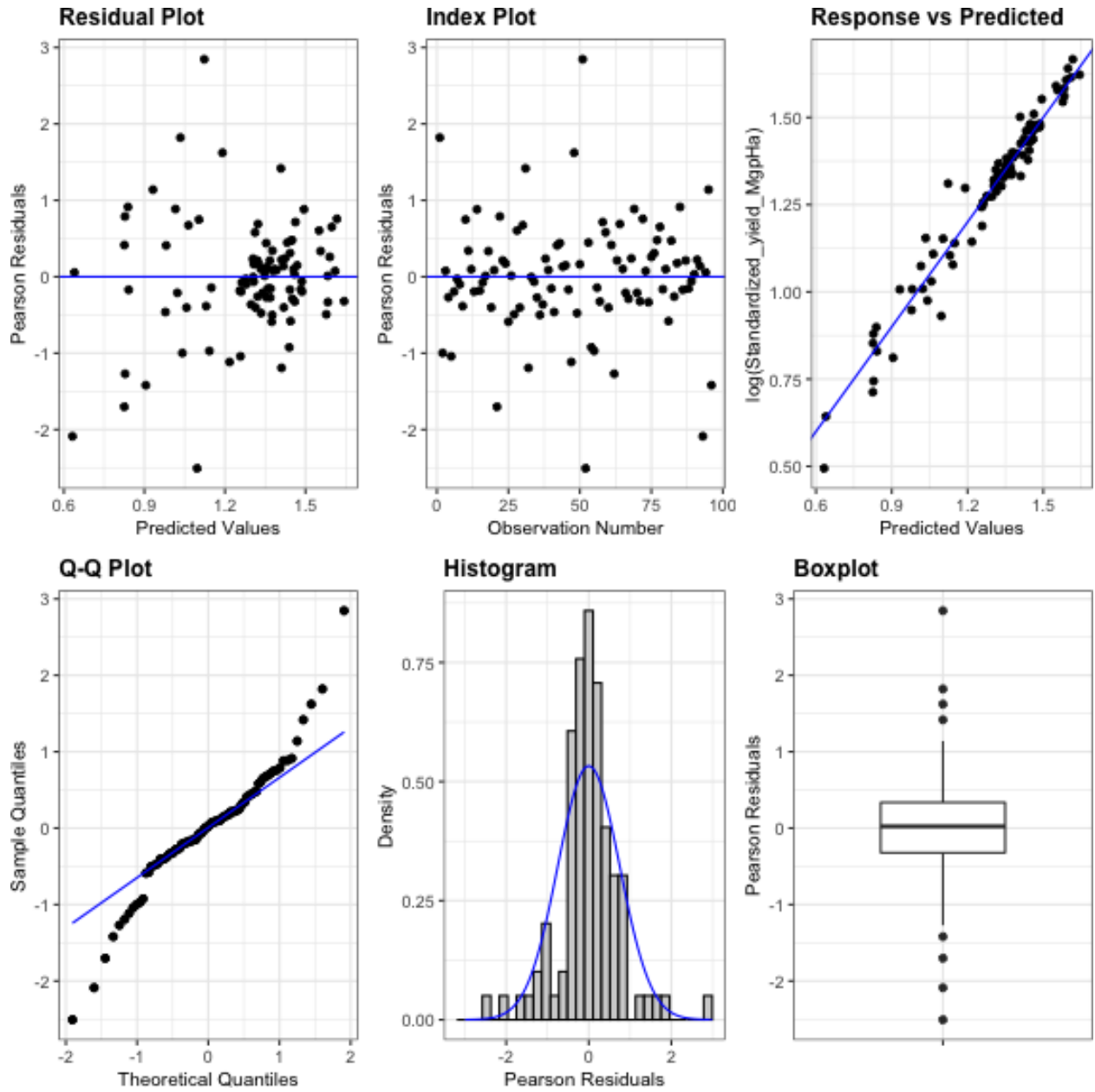


Figure 2: Diagnosis plot for the effect of crop identity and corn weed management on soybean yield over four years with four blocks of replication.

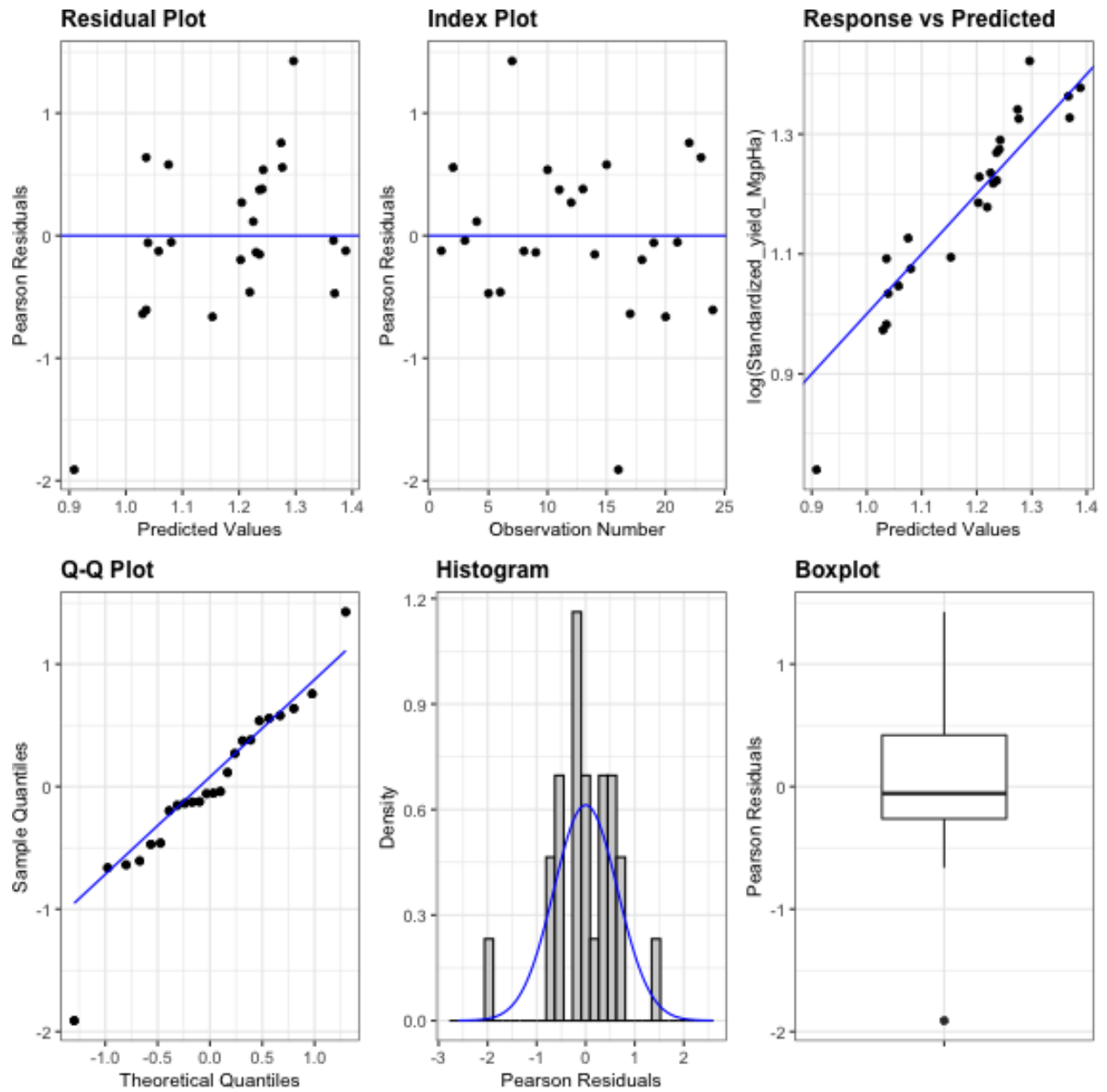


Figure 3: Diagnosis plot for the effect of crop identity on oat yield over four years with four blocks of replication.

```

control=lmerControl(check.conv.singular = .makeCC(action = "ignore", tol = 1e-4)))
# summary(dens_diversity.lmer1)$sigma #0.27
resid_panel(dens_diversity.lmer1, "all")

## Did crop identity and corn weed management affect weed community evenness index?

#min(dens_ind_1720$Evenness[dens_ind_1720$Evenness > 0]) #0.016156463
dens_even.lmer4 <- lmer(log(Evenness + 0.016156463) ~ Block +
  Crop_ID * Corn_weed_management +
  (1|Year) + (1|Year:Block) +
  (1|Year:Crop_ID) + (1|Year:Corn_weed_management) +
  (1|Year:Crop_ID:Corn_weed_management) +
  (1|Block:Year:Crop_ID) ,
  data = dens_ind_1720,
  control=lmerControl(check.conv.singular = .makeCC(action = "ignore", tol = 1e-4)))
#summary(dens_even.lmer4)$sigma # 0.68 # second best sigma, better than arcsin sqrt transform and more
resid_panel(dens_even.lmer4, "all")

## Did crop identity and corn weed management affect weed community density richness index?

dens_rich.lmer2 <- lmer(log(Richness+1) ~ Block +
  Crop_ID * Corn_weed_management +
  (1|Year) + (1|Year:Block) +
  (1|Year:Crop_ID) +
  (1|Year:Corn_weed_management) +
  (1|Year:Crop_ID:Corn_weed_management) +
  (1|Block:Year:Crop_ID) ,
  data = dens_ind_1720,
  control=lmerControl(check.conv.singular = .makeCC(action = "ignore", tol = 1e-4)))
# summary(dens_rich.lmer2)$sigma #0.288
resid_panel(dens_rich.lmer2, "all" )

## Did crop identity and corn weed management affect weed community biomass diversity index?

# min(biom_ind_1720$Diversity[biom_ind_1720$Diversity > 0])
biom_diversity.lmer1 <- lmer(log(Diversity + 1 ) ~ Block +
  Crop_ID * Corn_weed_management +
  (1|Year) + (1|Block:Year) +
  (1|Year:Crop_ID) +
  (1|Year:Corn_weed_management) +
  (1|Year:Crop_ID:Corn_weed_management) +
  (1|Block:Year:Crop_ID) ,
  data = biom_ind_1720,
  control=lmerControl(check.conv.singular = .makeCC(action = "ignore", tol = 1e-4)))
# summary(biom_diversity.lmer1)$sigma #0.25
resid_panel(biom_diversity.lmer1, "all")

## Did crop identity and corn weed management affect weed community aboveground mass evenness index?
min(biom_ind_1720$Evenness[biom_ind_1720$Evenness > 0])

## [1] 0.01510172

```

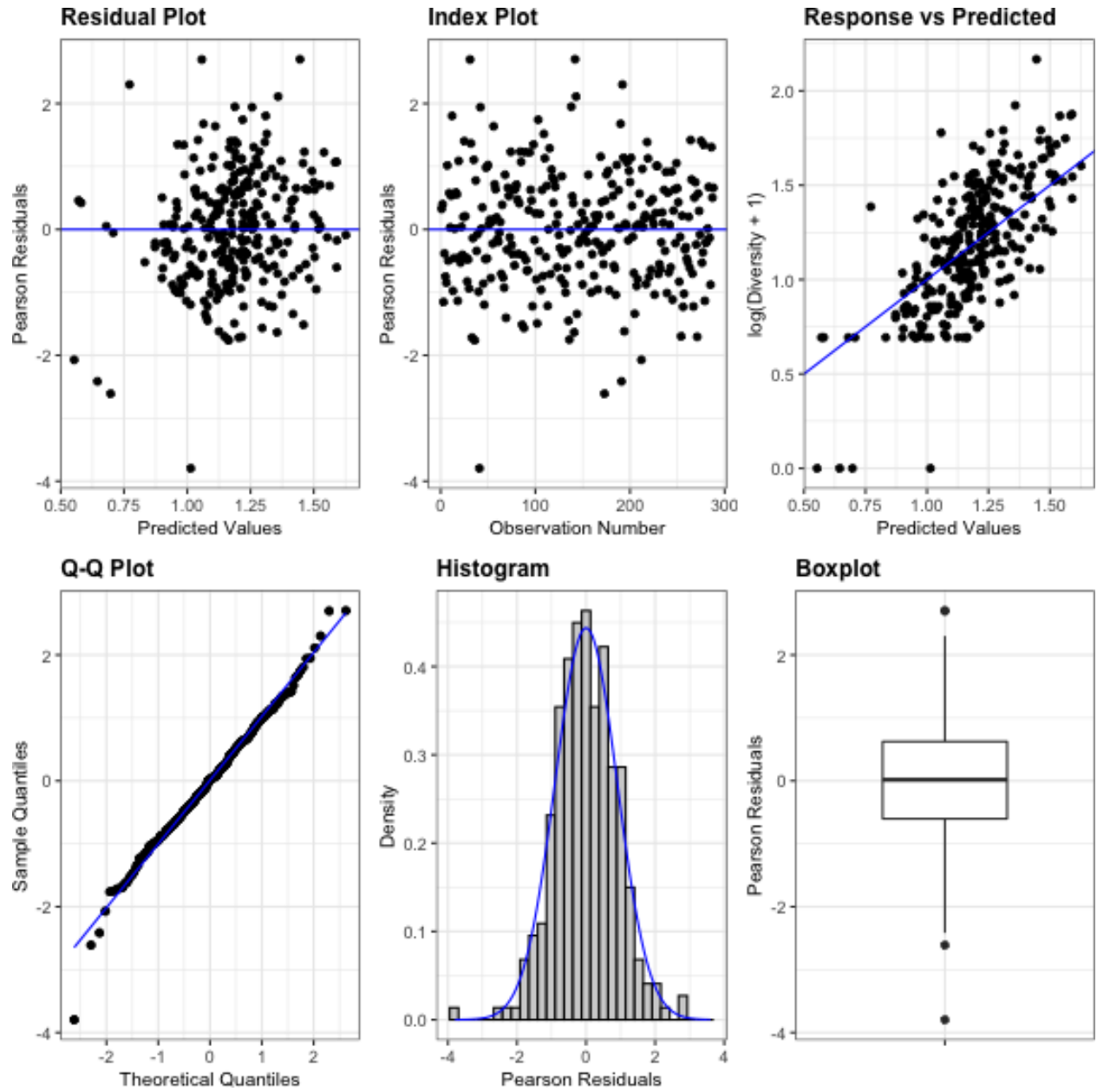


Figure 4: Diagnosis plot for the effect of crop identity and corn weed management on weed community density diversity index over four years with four blocks of replication.

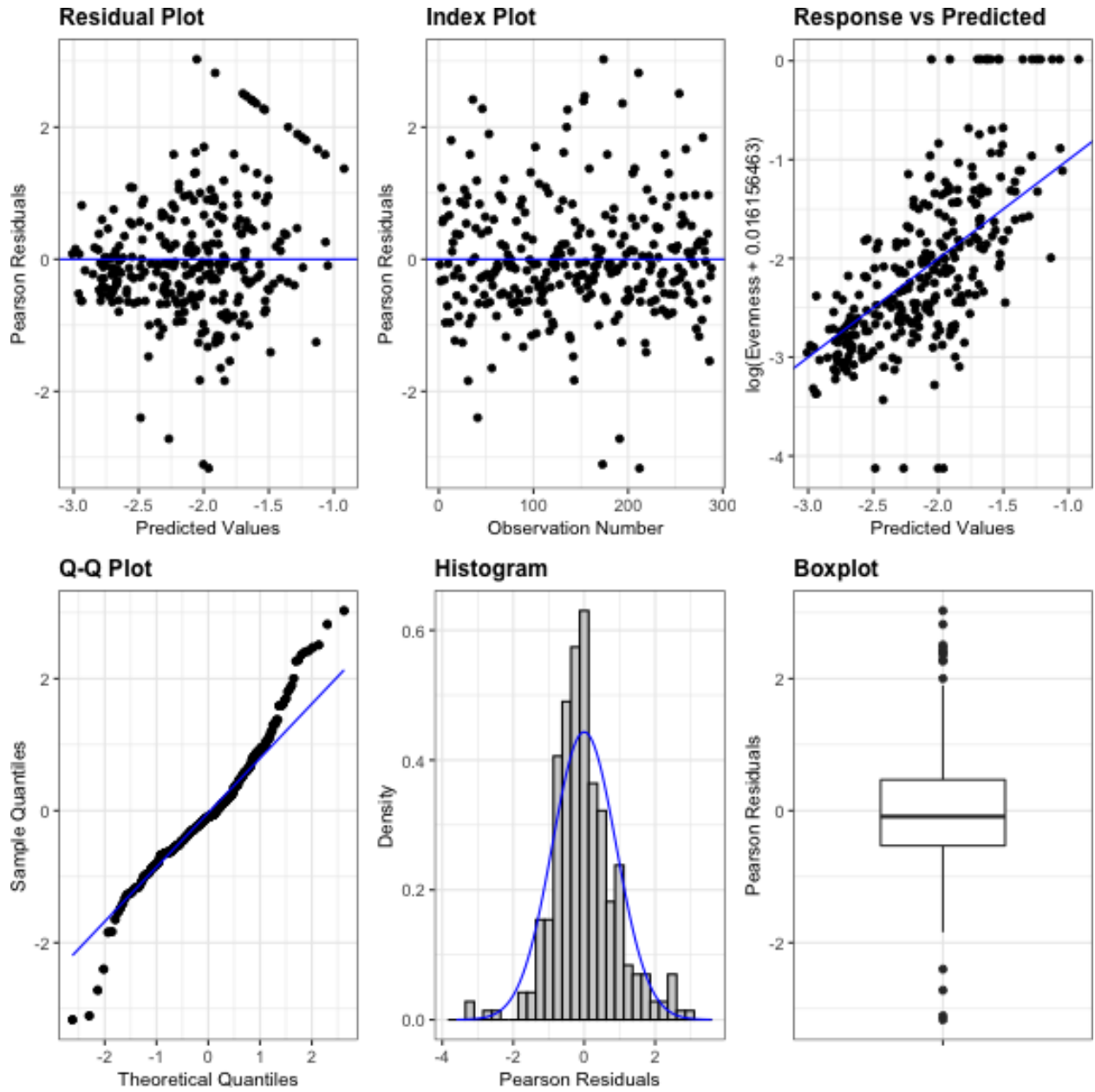


Figure 5: Diagnosis plot for the effect of crop identity and corn weed management on weed community density evenness index over four years with four blocks of replication.

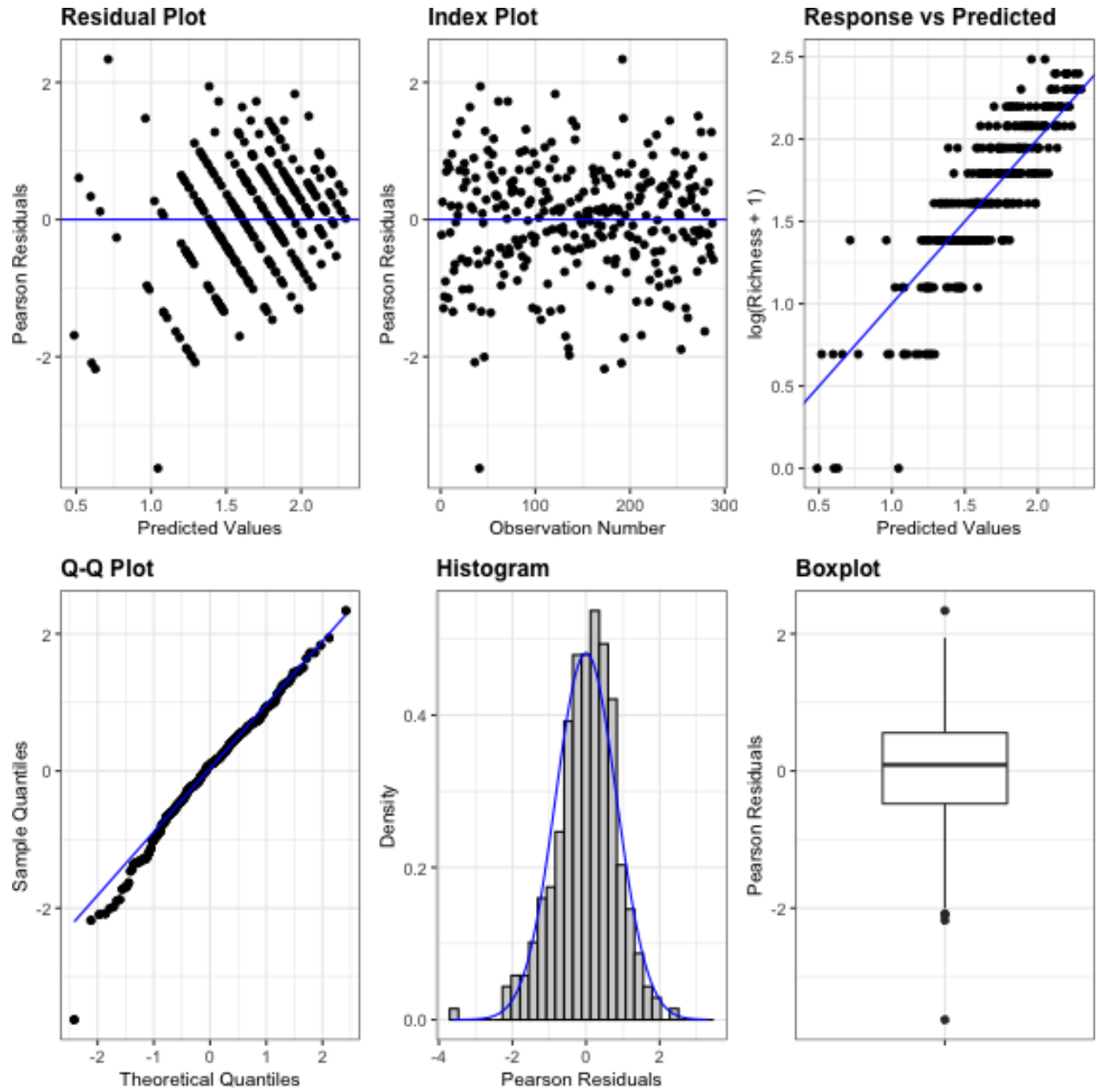


Figure 6: Diagnosis plot for the effect of crop identity and corn weed management on weed community density richness index over four years with four blocks of replication.

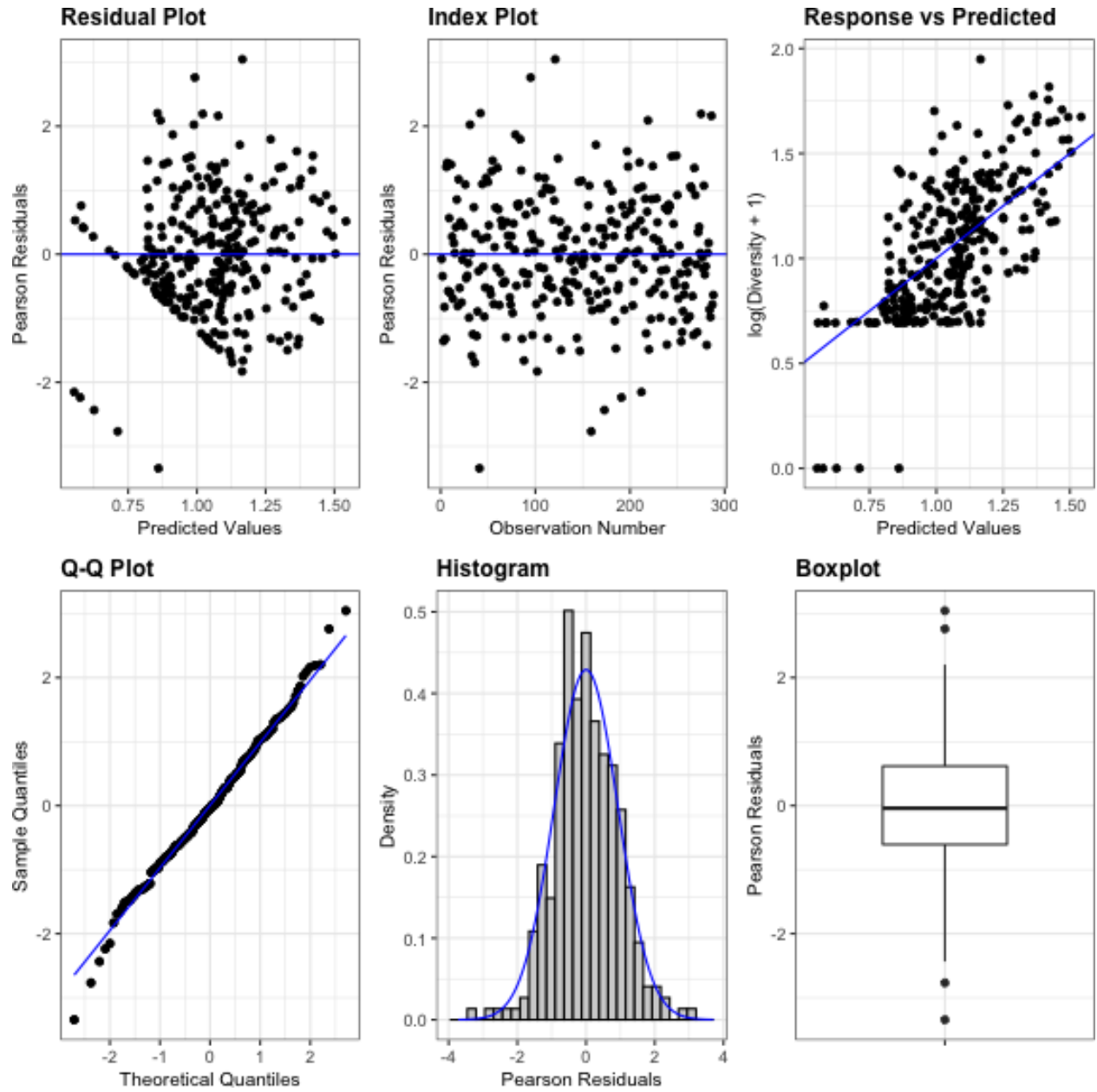


Figure 7: Diagnosis plot for the effect of crop identity and corn weed management on weed community aboveground mass diversity index over four years with four blocks of replication.

```

biom_even.lmer4 <- lmer(log(Evenness + 0.015101721 ) ~ Block +
  Crop_ID * Corn_weed_management +
  (1|Year) + (1|Year:Block) +
  (1|Year:Crop_ID) + (1|Year:Corn_weed_management) +
  (1|Year:Crop_ID:Corn_weed_management) +
  (1|Block:Year:Crop_ID) ,
  data = biom_ind_1720,
  control=lmerControl(check.conv.singular = .makeCC(action = "ignore", tol = 1e-4)))
#summary(biom_even.lmer4)$sigma # 0.72 # second best sigma, points more spread-out

resid_panel(biom_even.lmer4, "all")

## Did crop identity and corn weed management affect weed community aboveground mass richness index?

# min( biom_ind_1720$Richness[ biom_ind_1720$Richness > 0])
biom_rich.lmer2 <- lmer(log(Richness + 1) ~ Block +
  Crop_ID * Corn_weed_management +
  (1|Year) + (1|Year:Block) +
  (1|Year:Crop_ID) + (1|Year:Corn_weed_management) +
  (1|Year:Crop_ID:Corn_weed_management) +
  (1|Block:Year:Crop_ID) ,
  data = biom_ind_1720,
  control=lmerControl(check.conv.singular = .makeCC(action = "ignore", tol = 1e-4)))

#summary(biom_rich.lmer2)$sigma #0.2935

resid_panel(biom_rich.lmer2 , "all")

```

Total weed community density and aboveground mass

```

##### Fit all species at once with split-fit-combine syntax
# https://stat585-at-isu.github.io/materials-2019/04\_functional-programming/02\_purrr.html#23

# convert wide to long format

dens_1720_long <- dens_1720_clean %>%
  pivot_longer(!c(Crop:Corn_weed_management),
    names_to = "Species", values_to = "Density")

#singularity because of too many zeros in many species columns

# min(dens_1720_long$Density[dens_1720_long$Density>0]) #0.05396072

dens_result_t <- dens_1720_long %>%
  group_by(Species) %>%
  nest() %>%
  mutate(models=map(data,~lmer(log(Density + 0.05396072) ~ Block + Crop_ID +
    Corn_weed_management +
    Crop_ID:Corn_weed_management +

```

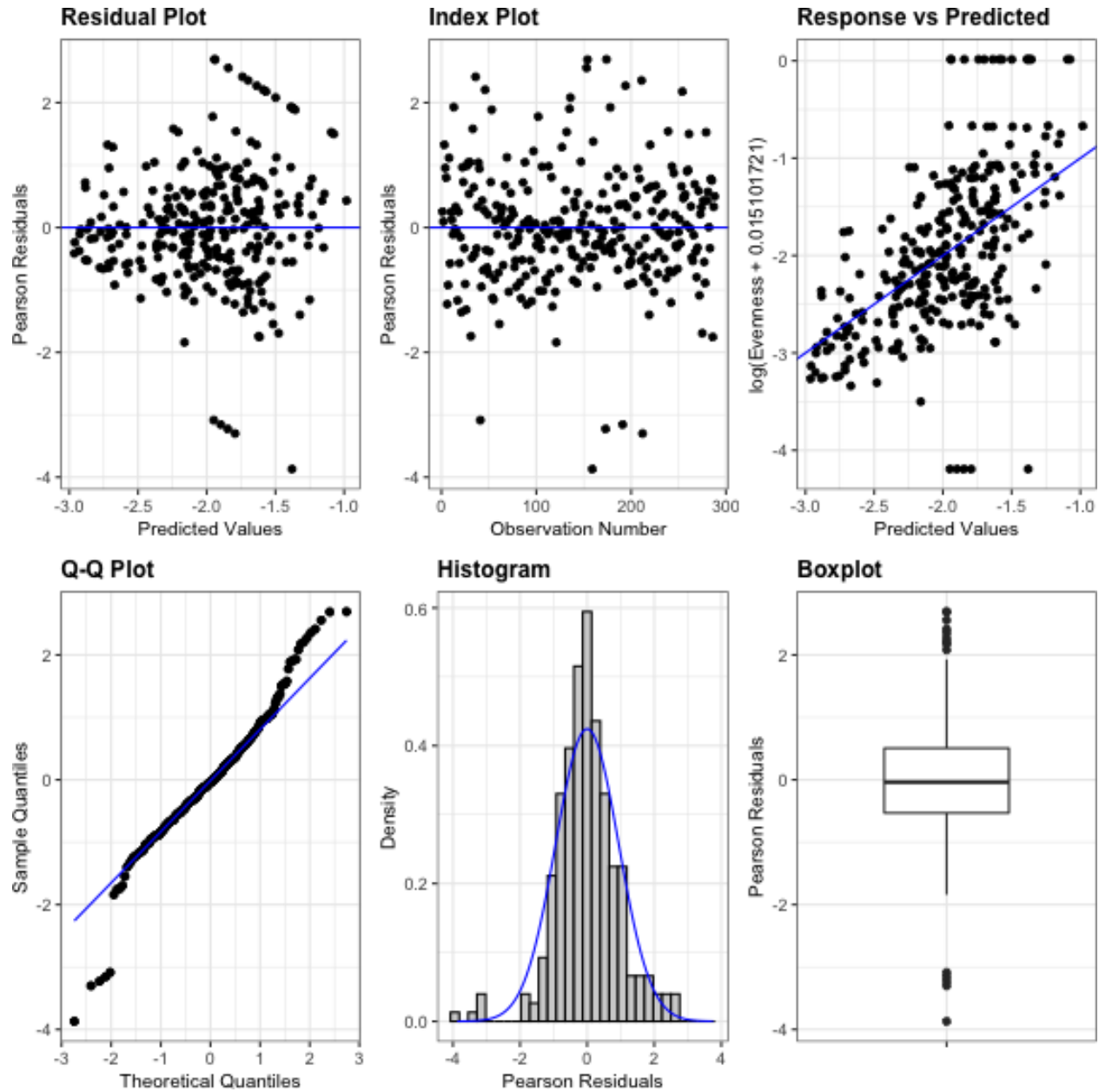


Figure 8: Diagnosis plot for the effect of crop identity and corn weed management on weed community aboveground mass evenness index over four years with four blocks of replication.

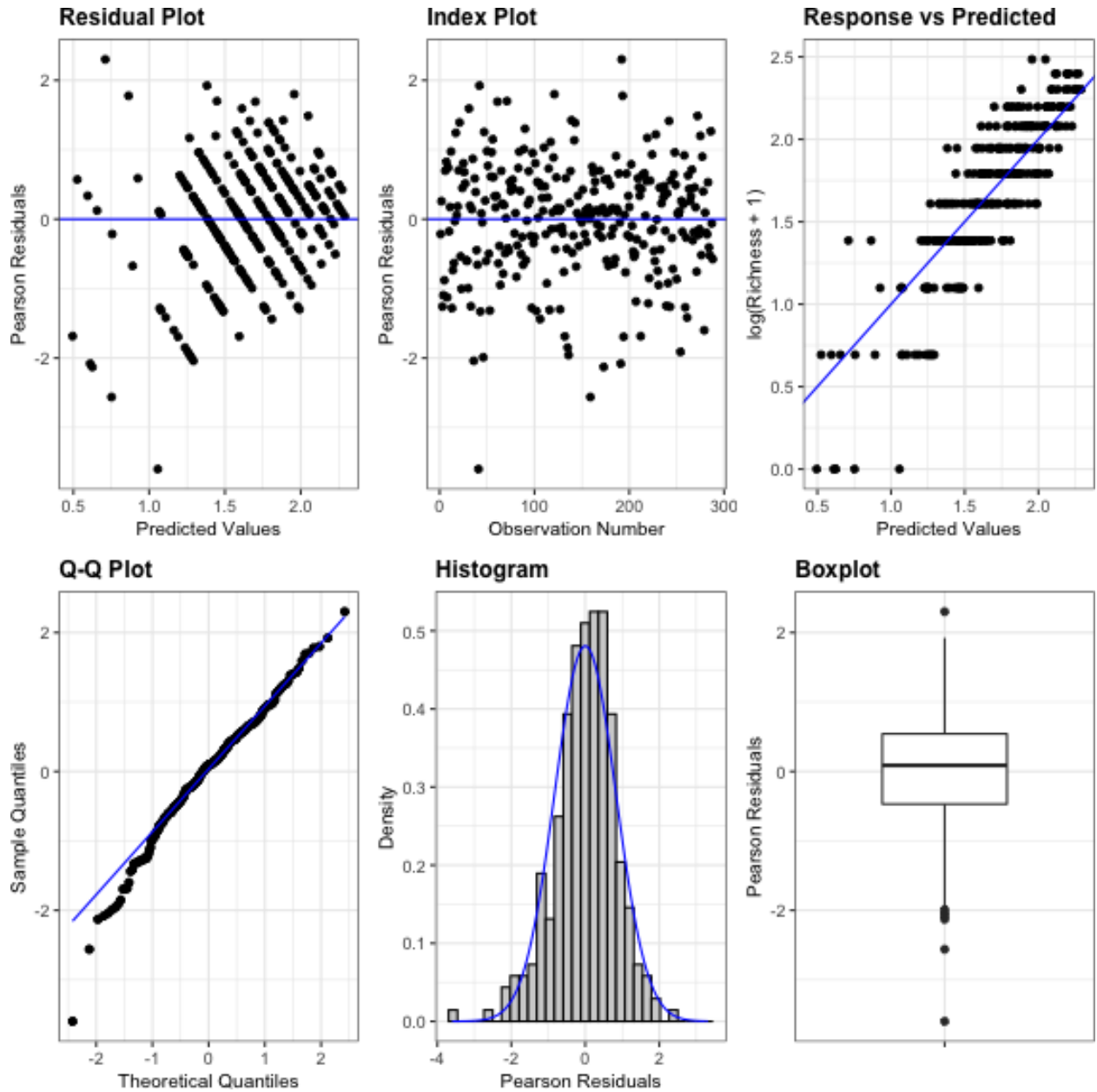


Figure 9: Diagnosis plot for the effect of crop identity and corn weed management on weed community aboveground mass richness index over four years with four blocks of replication.

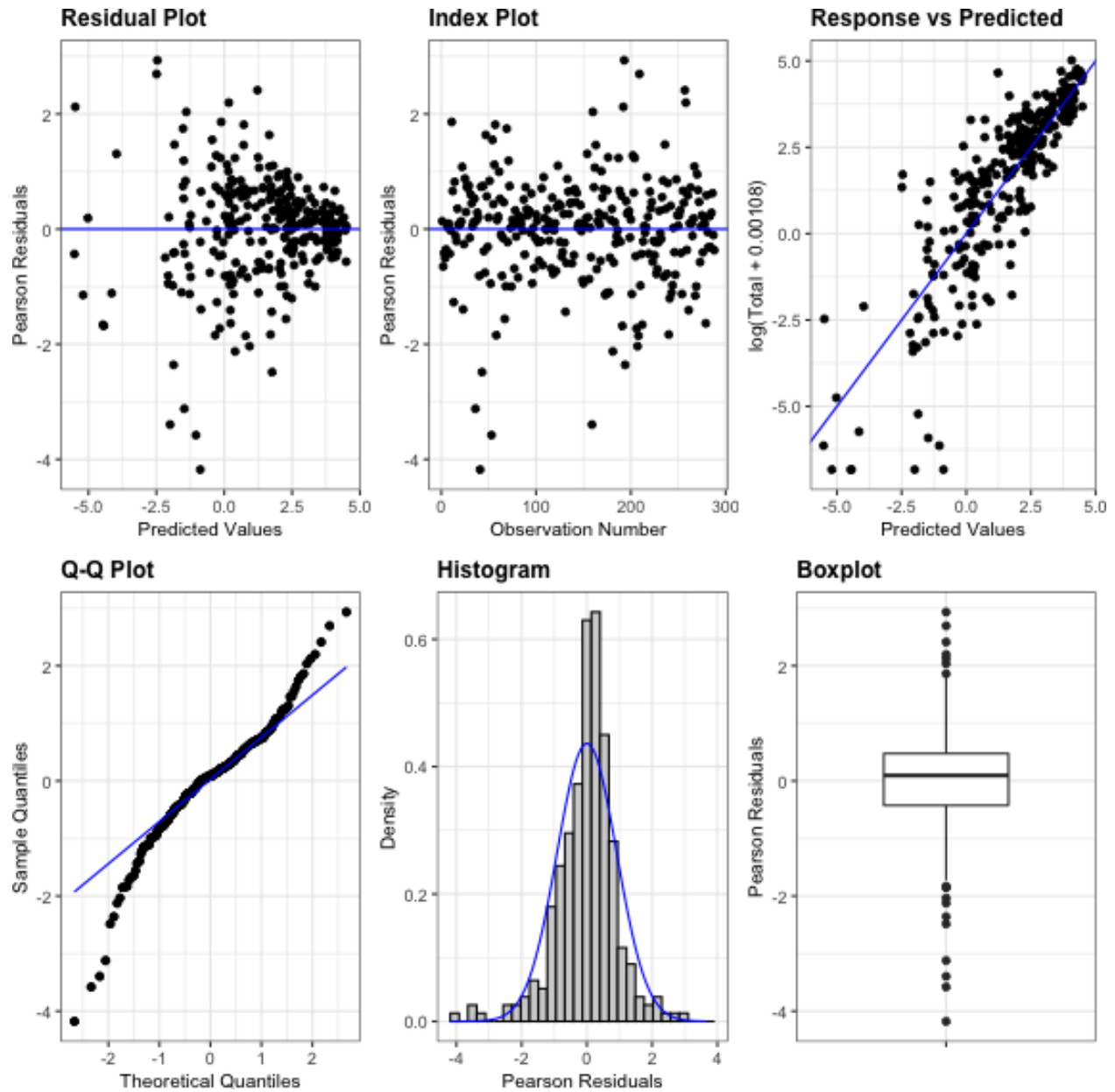


Figure 10: Diagnosis plot for the effect of crop identity and corn weed management on weed community aboveground mass over four years with four blocks of replication.

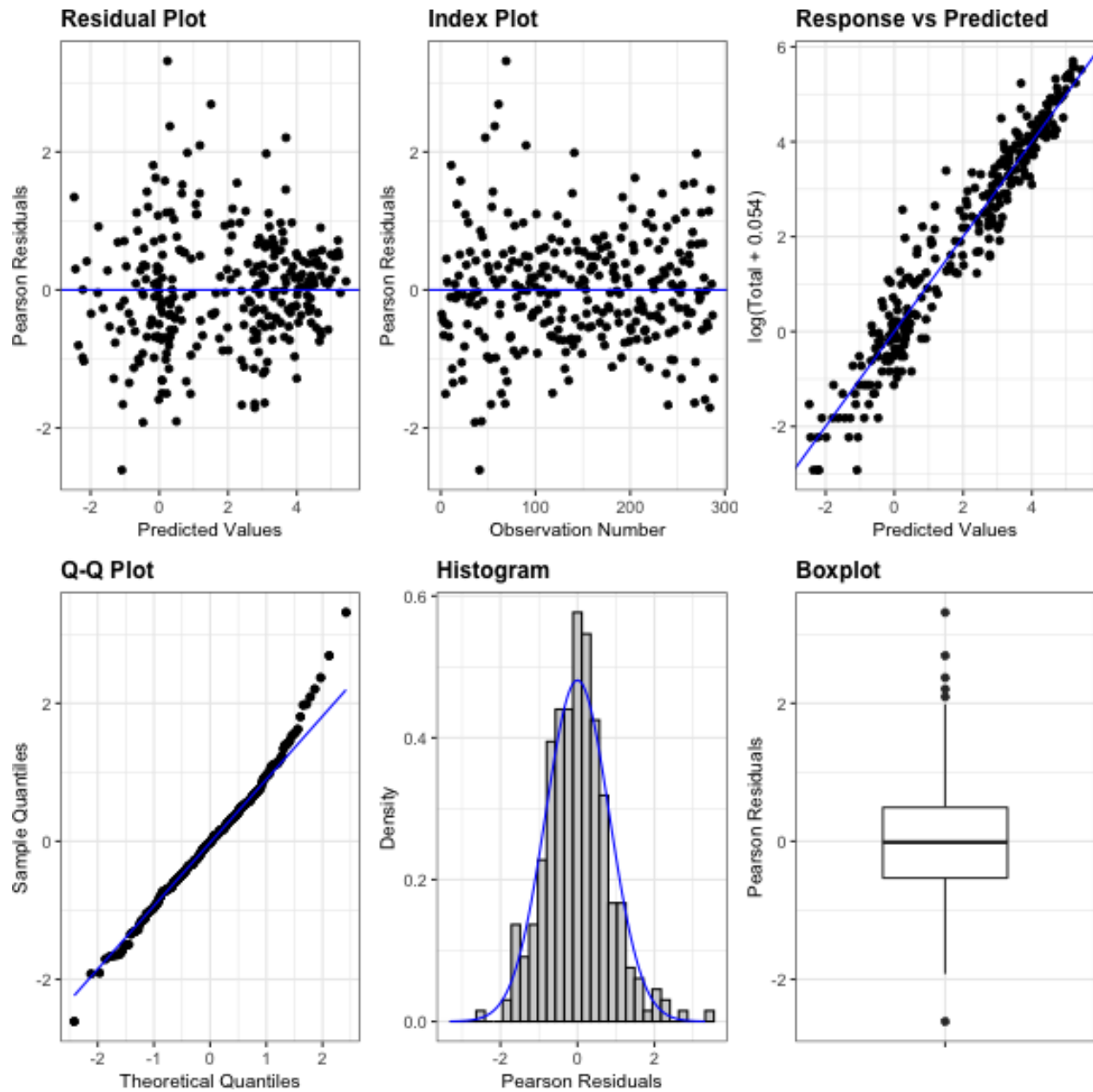


Figure 11: Diagnosis plot for the effect of crop identity and corn weed management on weed community density over four years with four blocks of replication.

```

(1|Year) + (1|Year:Block) +
(1|Year:Crop_ID) +
(1|Year:Corn_weed_management) +
(1|Year:Crop_ID:Corn_weed_management) +
(1|Block:Year:Crop_ID),data =.x))) %>%

ungroup %>%
mutate(diag_plots = map(models, resid_panel, "all"),
      jts = map(models, joint_tests),
      across(diag_plots:jts, setNames, .$Species))

```

Top seven species individual density

```

biom_1720_long <- biom_1720_clean %>%
  pivot_longer(!c(Crop:Corn_weed_management),
               names_to = "Species", values_to = "Biomass")

# min(biom_1720_long$Biomass[biom_1720_long$Biomass>0]) # 0.0005396072

biom_result_t <- biom_1720_long %>%
  group_by(Species) %>%
  nest() %>%
  mutate(models=map(data,~lmer(log(Biomass + 0.0005396072) ~ Block +
                                Crop_ID + Corn_weed_management +
                                Crop_ID:Corn_weed_management +
                                (1|Year) + (1|Year:Block) +
                                (1|Year:Crop_ID) +
                                (1|Year:Corn_weed_management) +
                                (1|Year:Crop_ID:Corn_weed_management) +
                                (1|Block:Year:Crop_ID),data =.x)))) %>%

  ungroup %>%
  mutate(jts = map(models, joint_tests),
        diag_plots = map(models, resid_panel,"all"),
  across(jts:diag_plots, setNames, .$Species))

```

Top seven species individual aboveground mass Goode, Katherine, and Kathleen Rey. 2019. "ggResidpanel: Panels and Interactive Versions of Diagnostic Plots Using 'Ggplot2'"

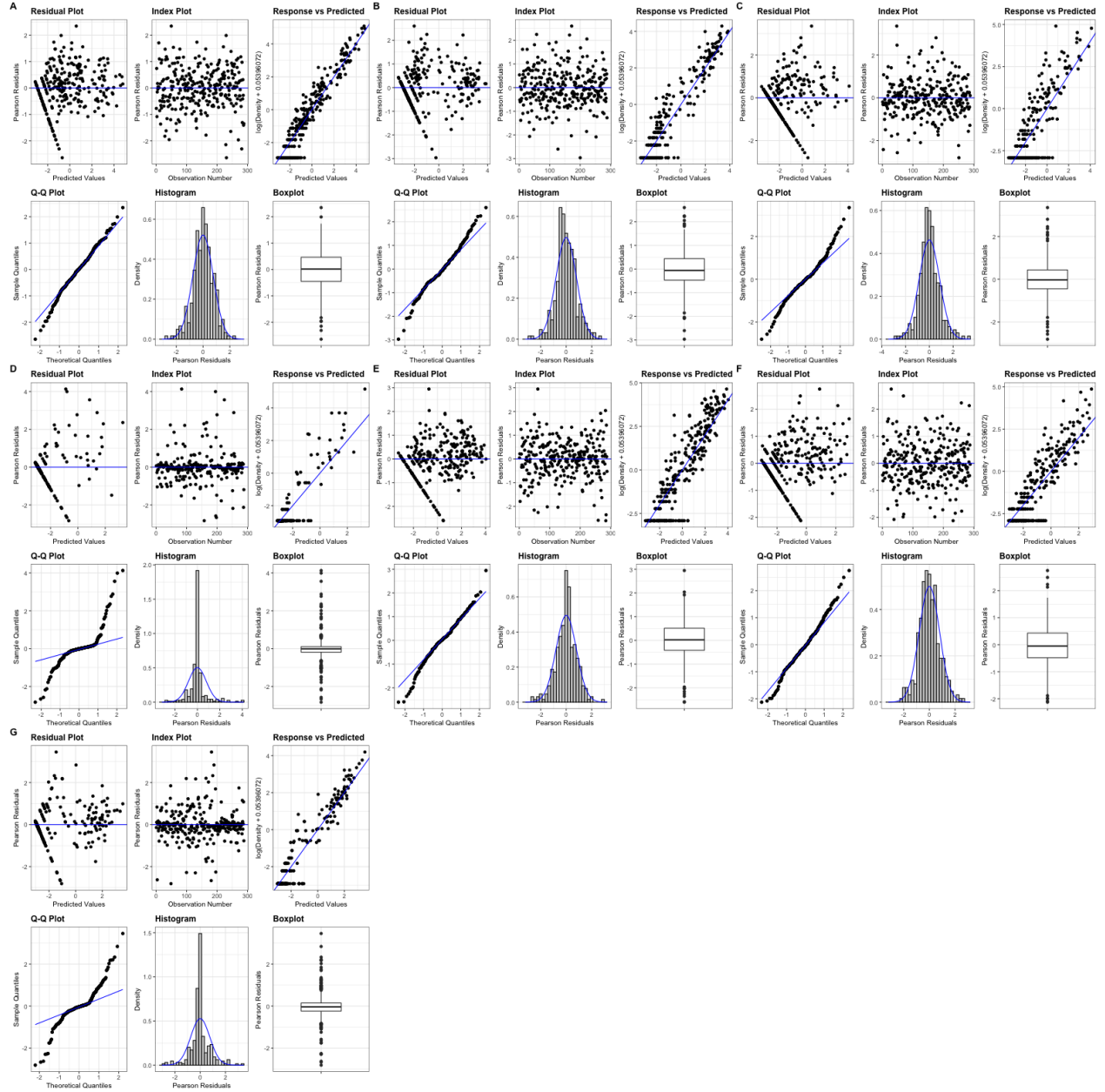


Figure 12: Diagnosis plot for the effect of crop identity and corn weed management on the aboveground mass of (A) - AMATA, (B) - CHEAL, (C) - DIGSA, (D) - ECHCG, (E) - SETFA, (F) - SETLU, and (G) - TAROF

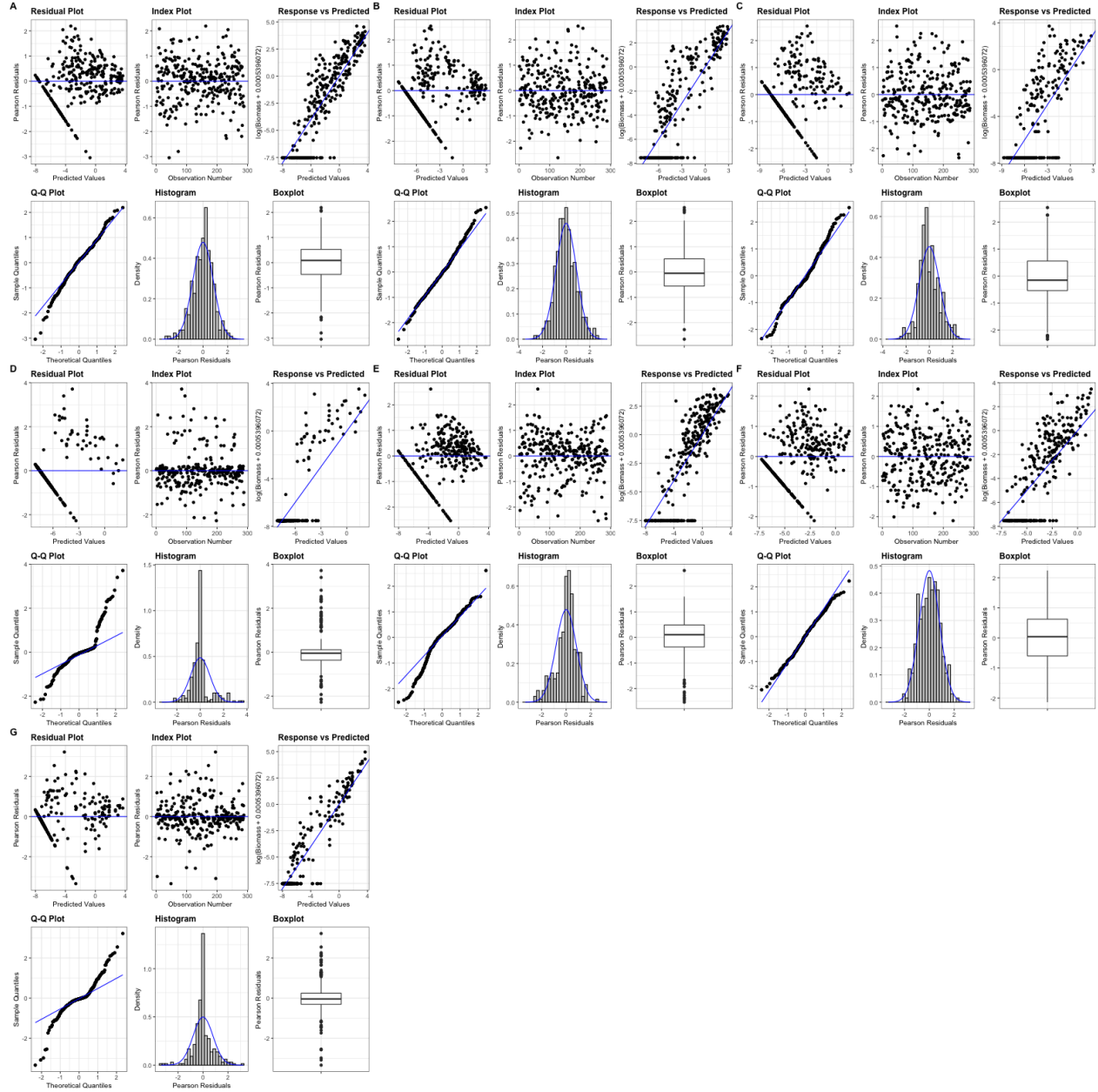


Figure 13: Diagnosis plot for the effect of crop identity and corn weed management on the density of (A) - AMATA, (B) - CHEAL, (C) - DIGSA, (D) - ECHCG, (E) - SETFA, (F) - SETLU, and (G) - TAROF