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 +
```
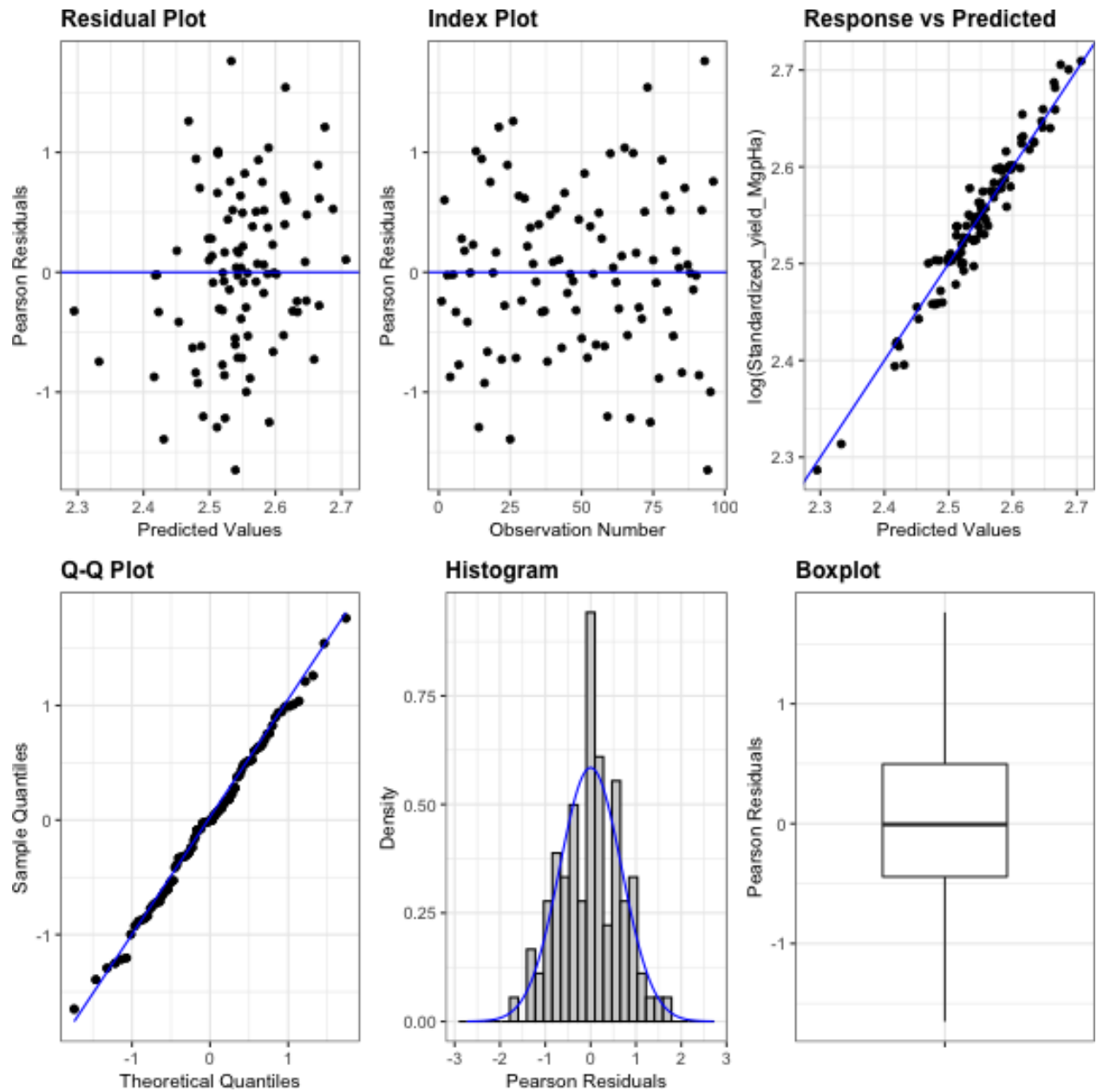
Figure 1: Diagnosis plot for the effect of crop identity and corn weed management on corn yield over four years with four blocks of replication.
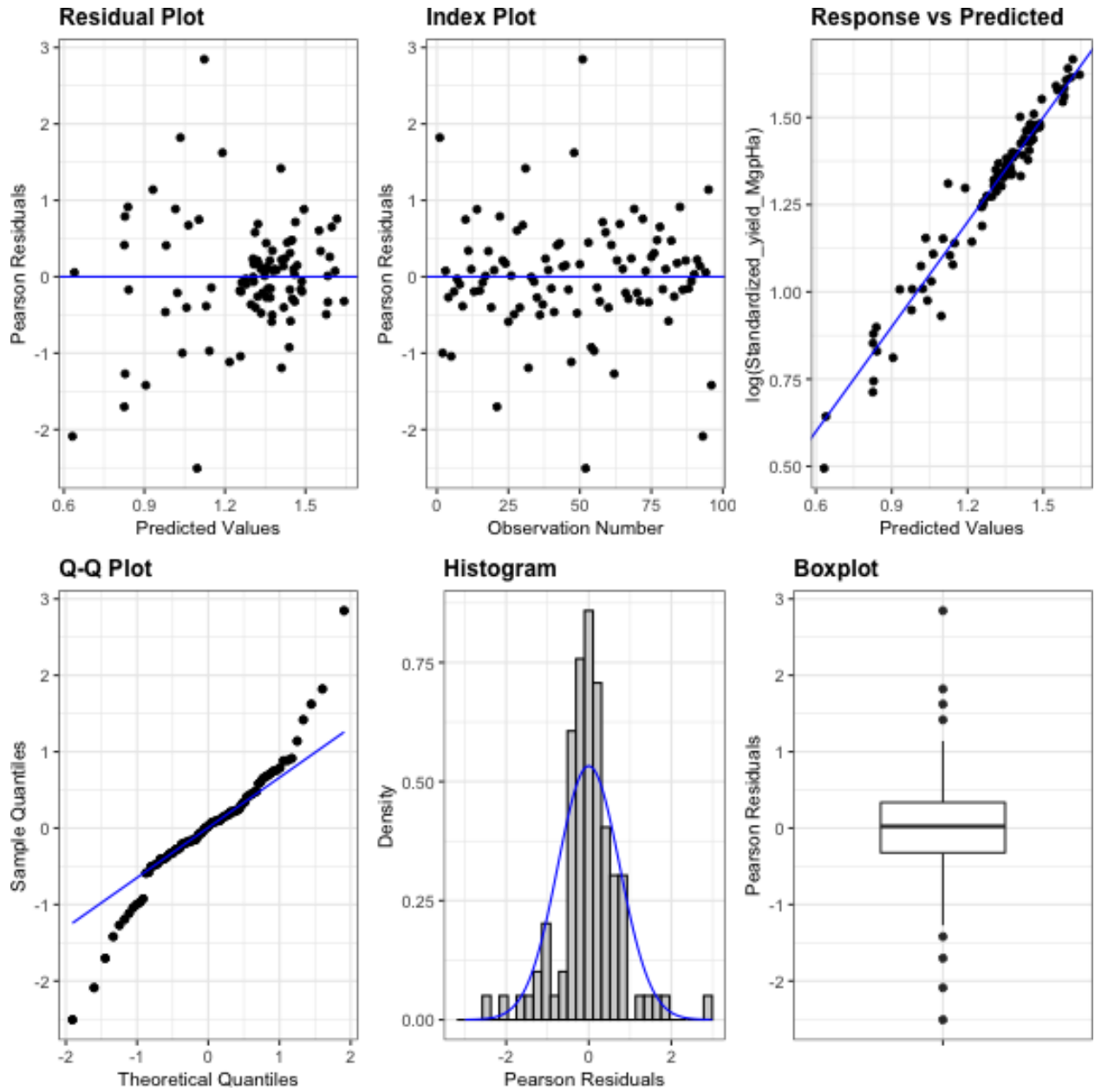
Figure 2: Diagnosis plot for the effect of crop identity and corn weed management on soybean yield over four years with four blocks of replication.
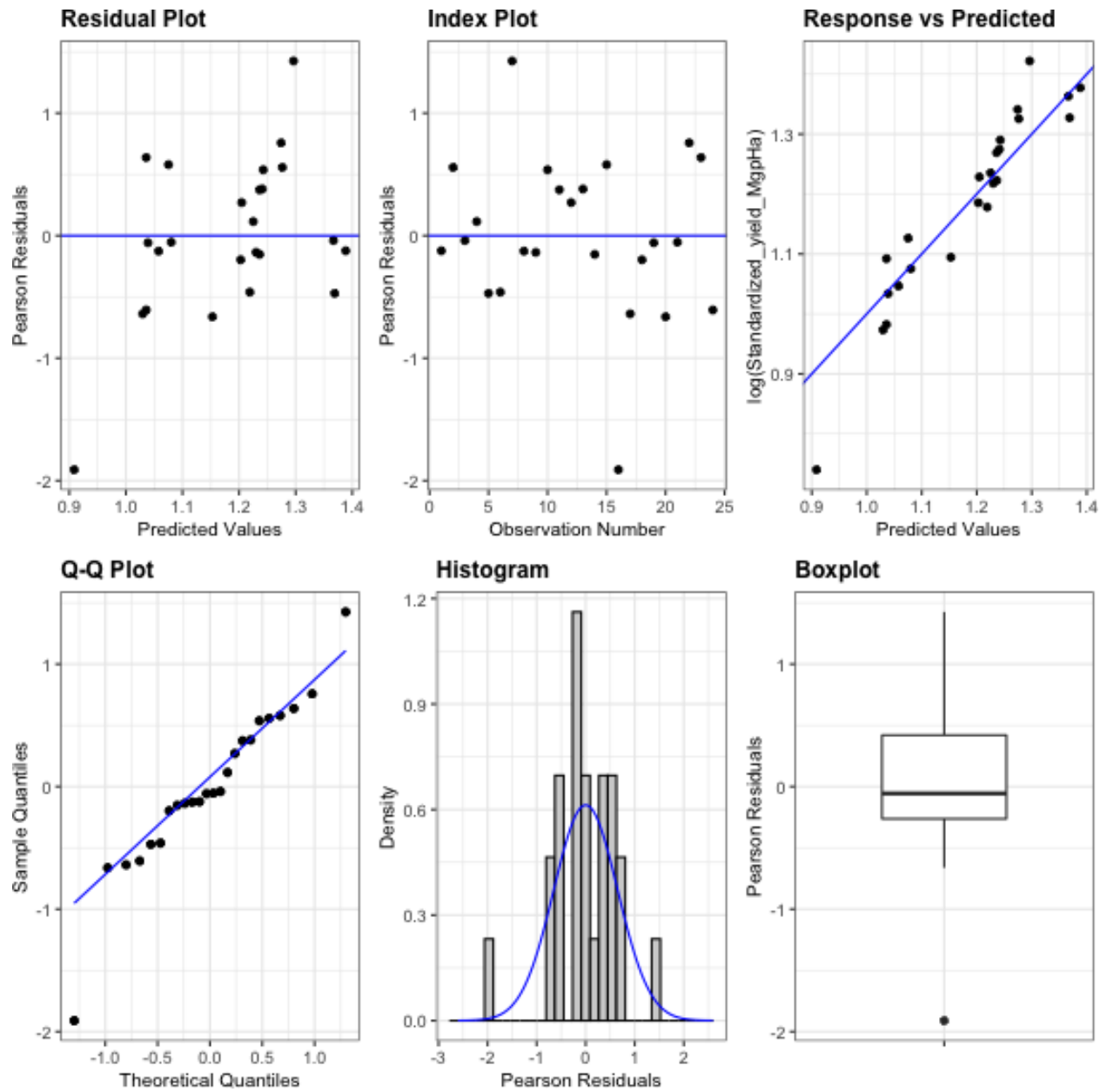
Figure 3: Diagnosis plot for the effect of crop identity on oat yield over four years with four blocks of replication.

```
                                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_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)  ,
```
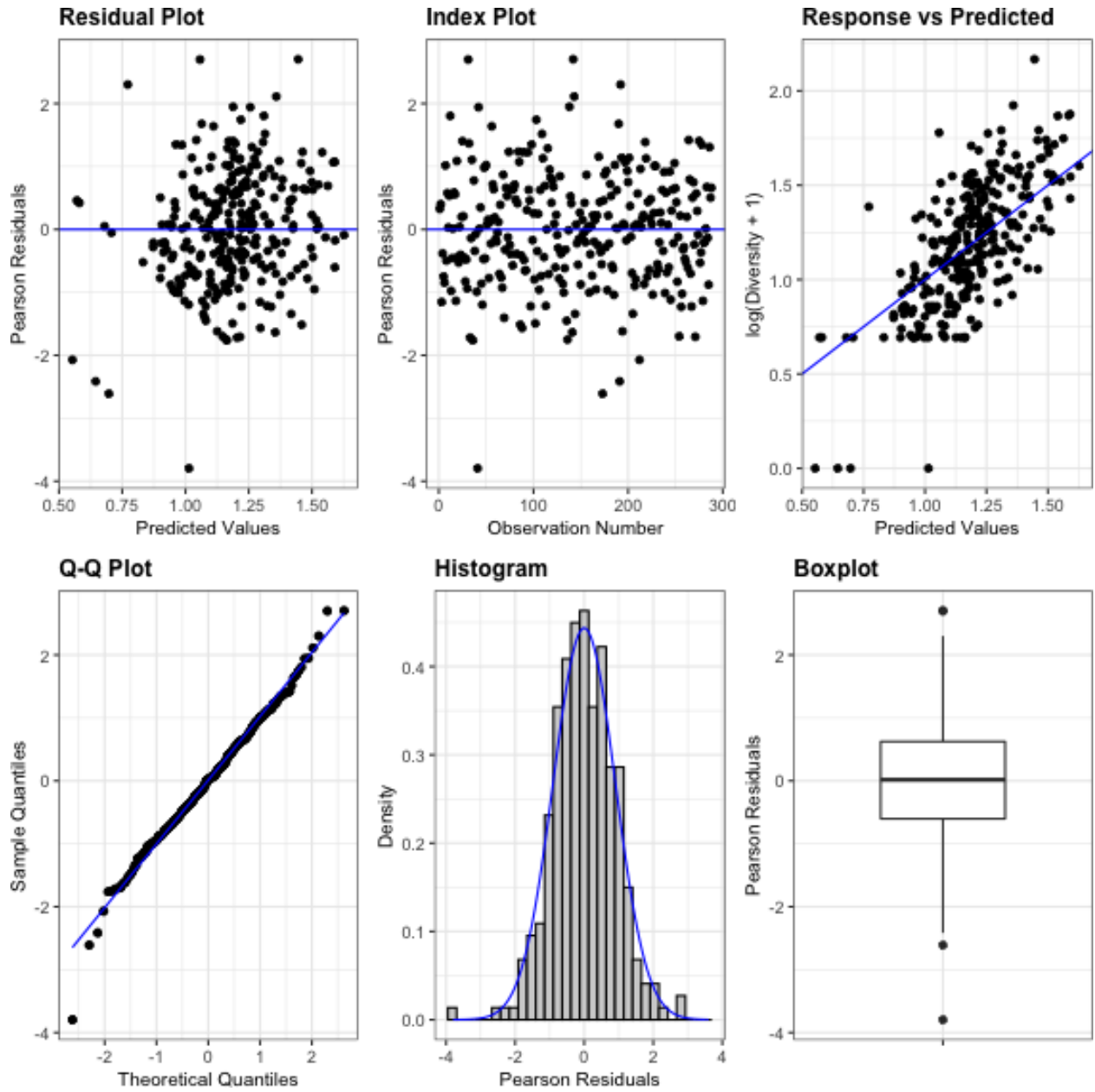
Figure 4: Diagnosis plot for the effect of crop identity and corn weed management on weed community density diversity index over four years with four blocks of replication.
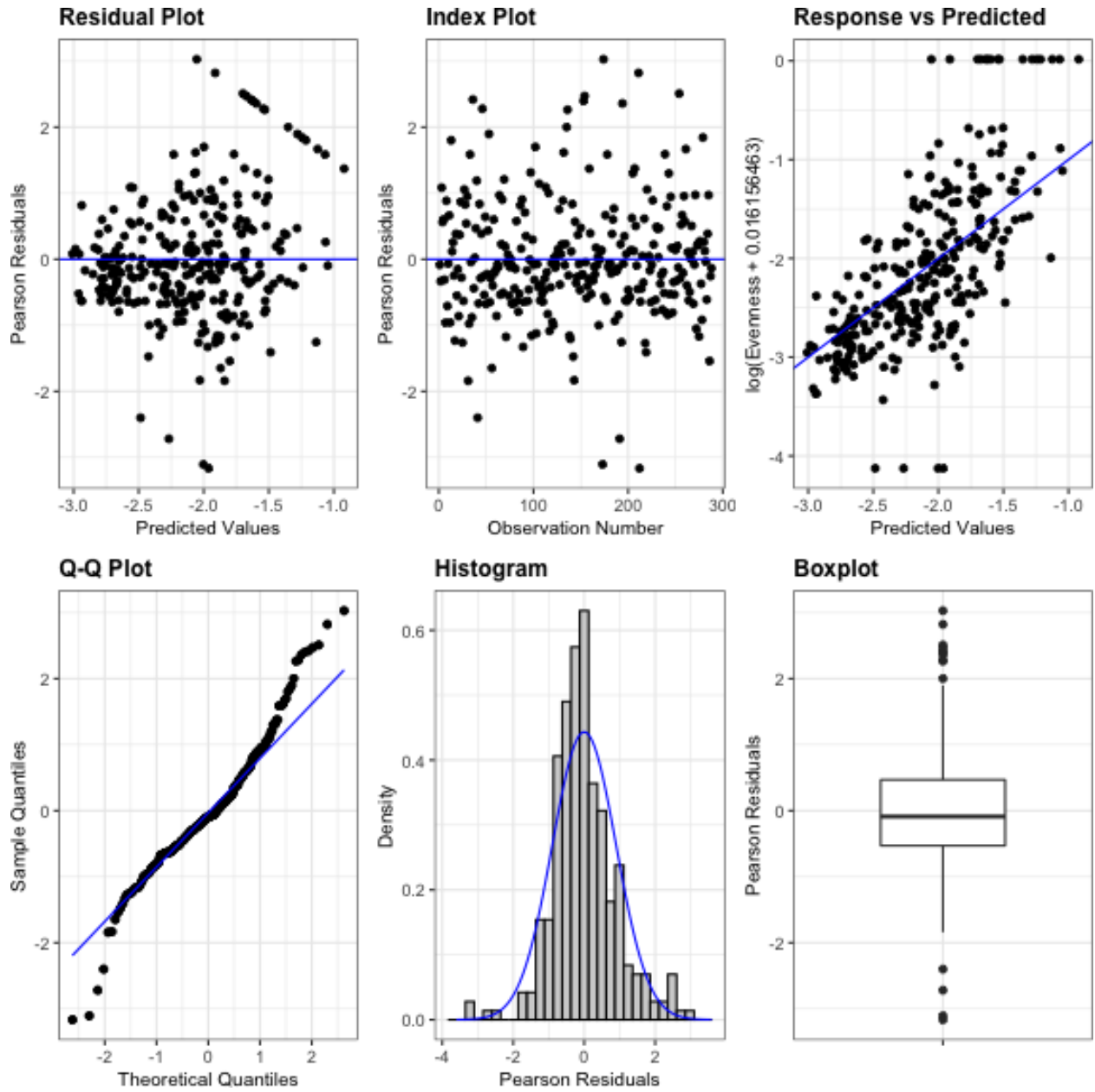
Figure 5: Diagnosis plot for the effect of crop identity and corn weed management on weed community density evenness index over four years with four blocks of replication.
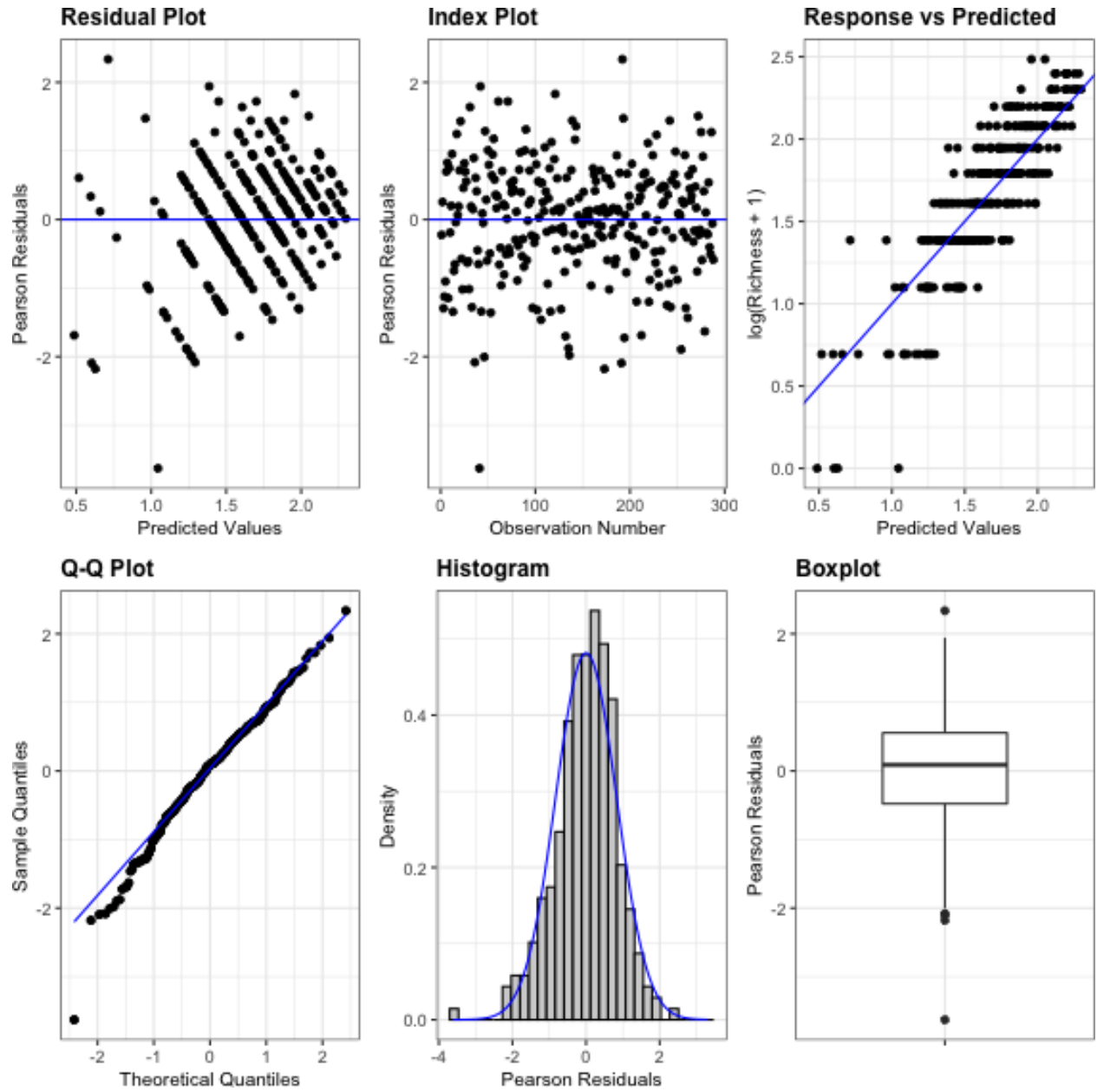
Figure 6: Diagnosis plot for the effect of crop identity and corn weed management on weed community density richness index over four years with four blocks of replication.

```
                         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
```
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")
```
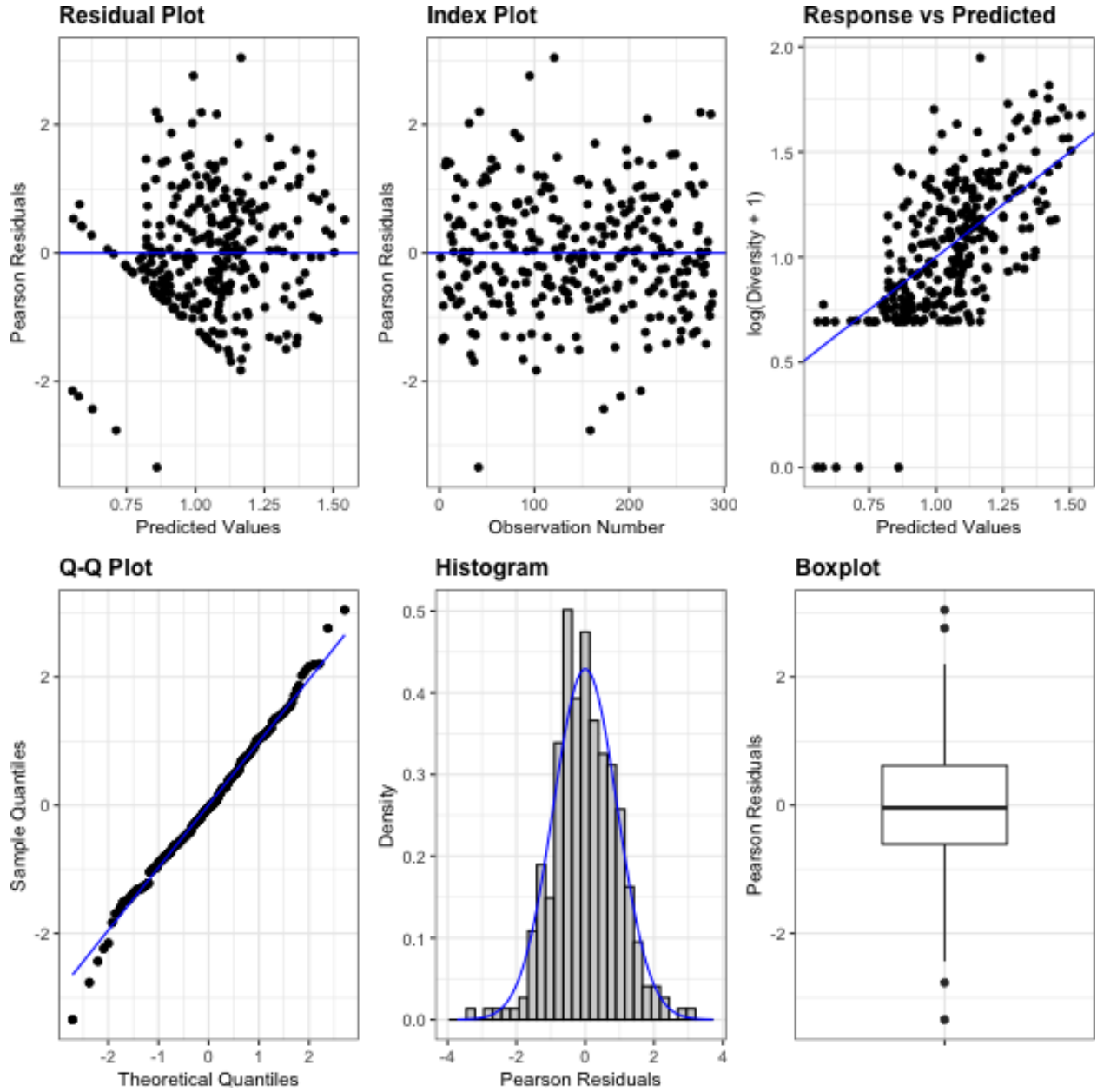
Figure 7: Diagnosis plot for the effect of crop identity and corn weed management on weed community aboveground mass diversity index over four years with four blocks of replication.
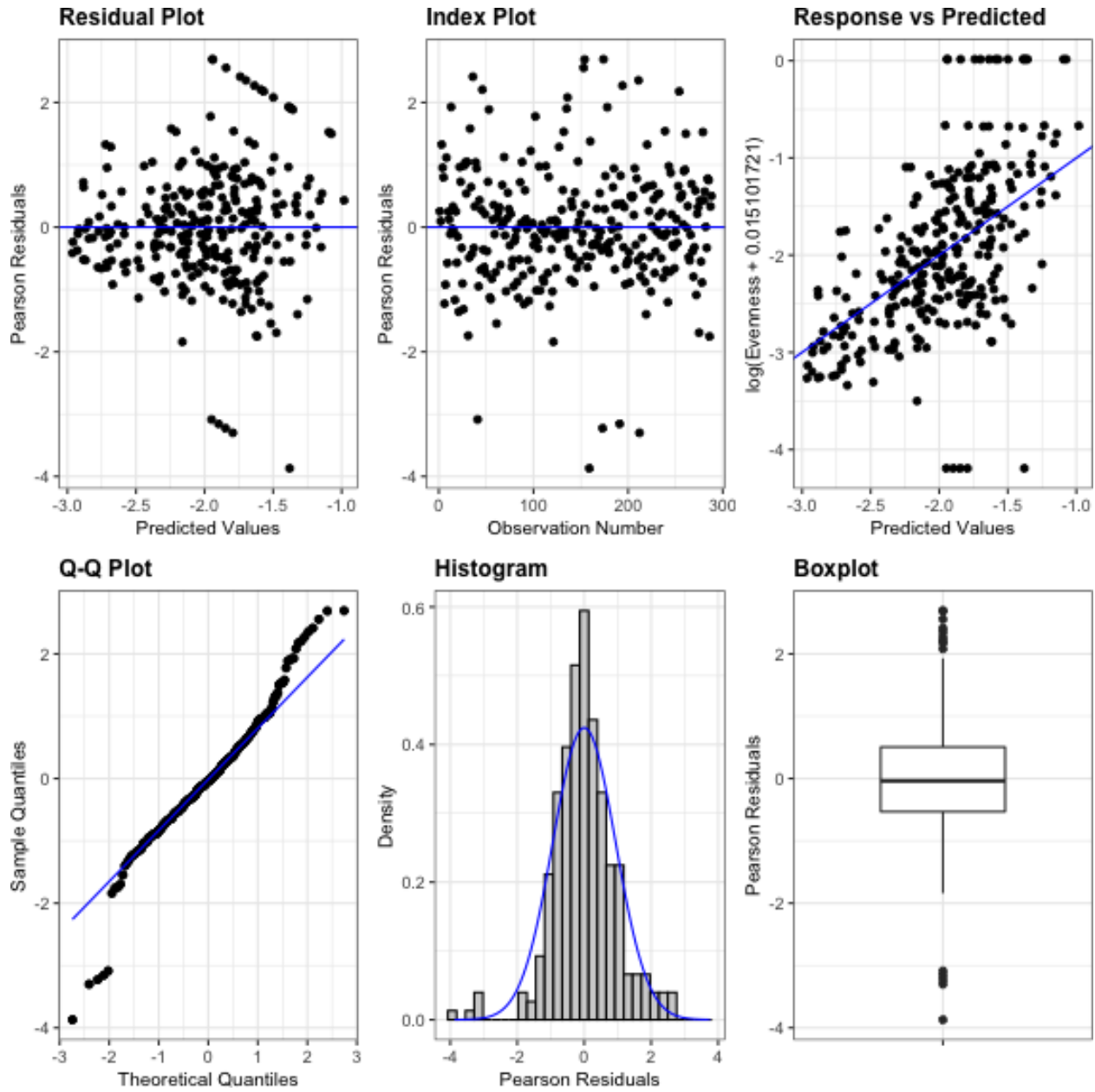
Figure 8: Diagnosis plot for the effect of crop identity and corn weed management on weed community aboveground mass evenness index over four years with four blocks of replication.
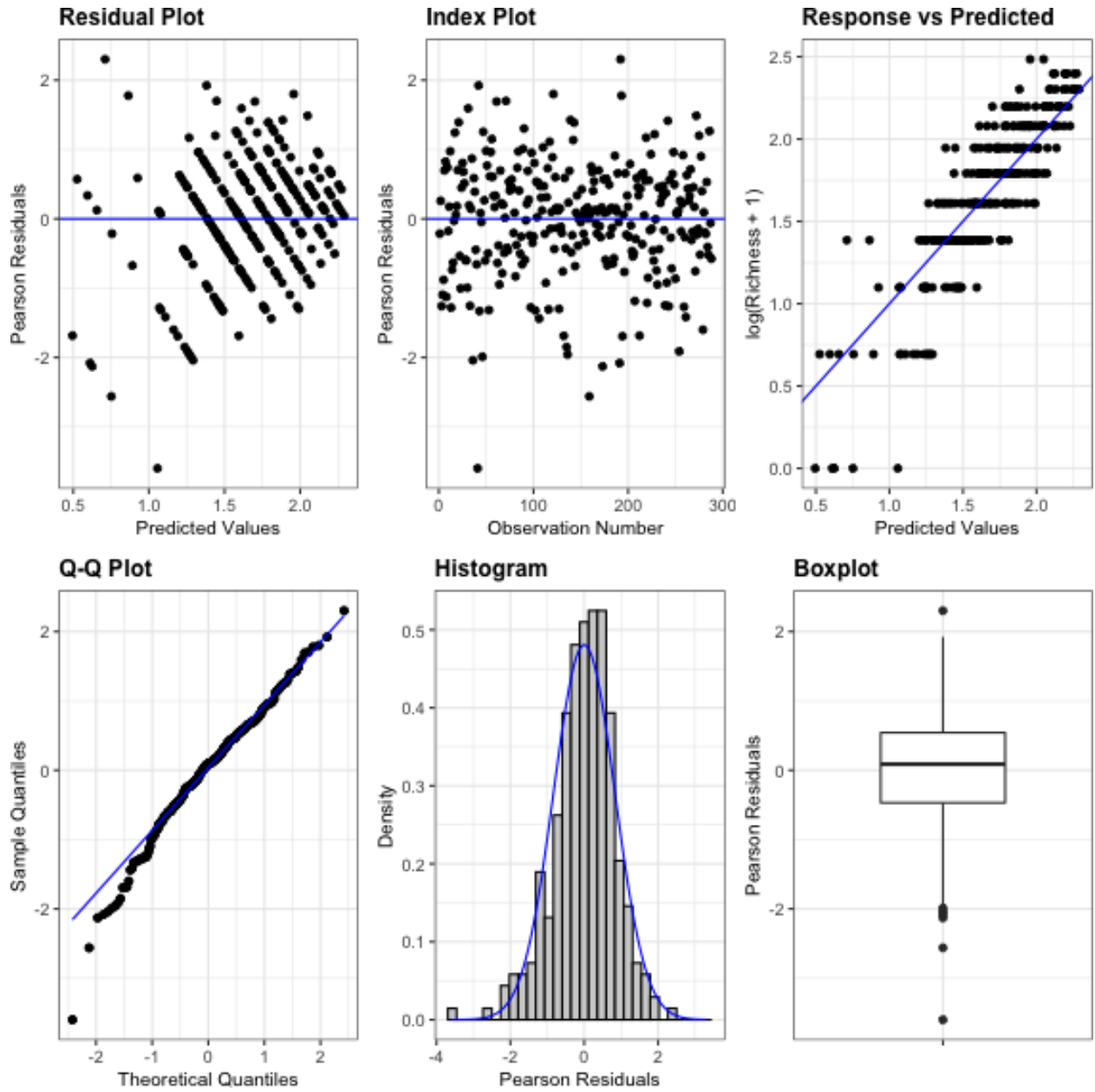
Figure 9: Diagnosis plot for the effect of crop identity and corn weed management on weed community aboveground mass richness index over four years with four blocks of replication.
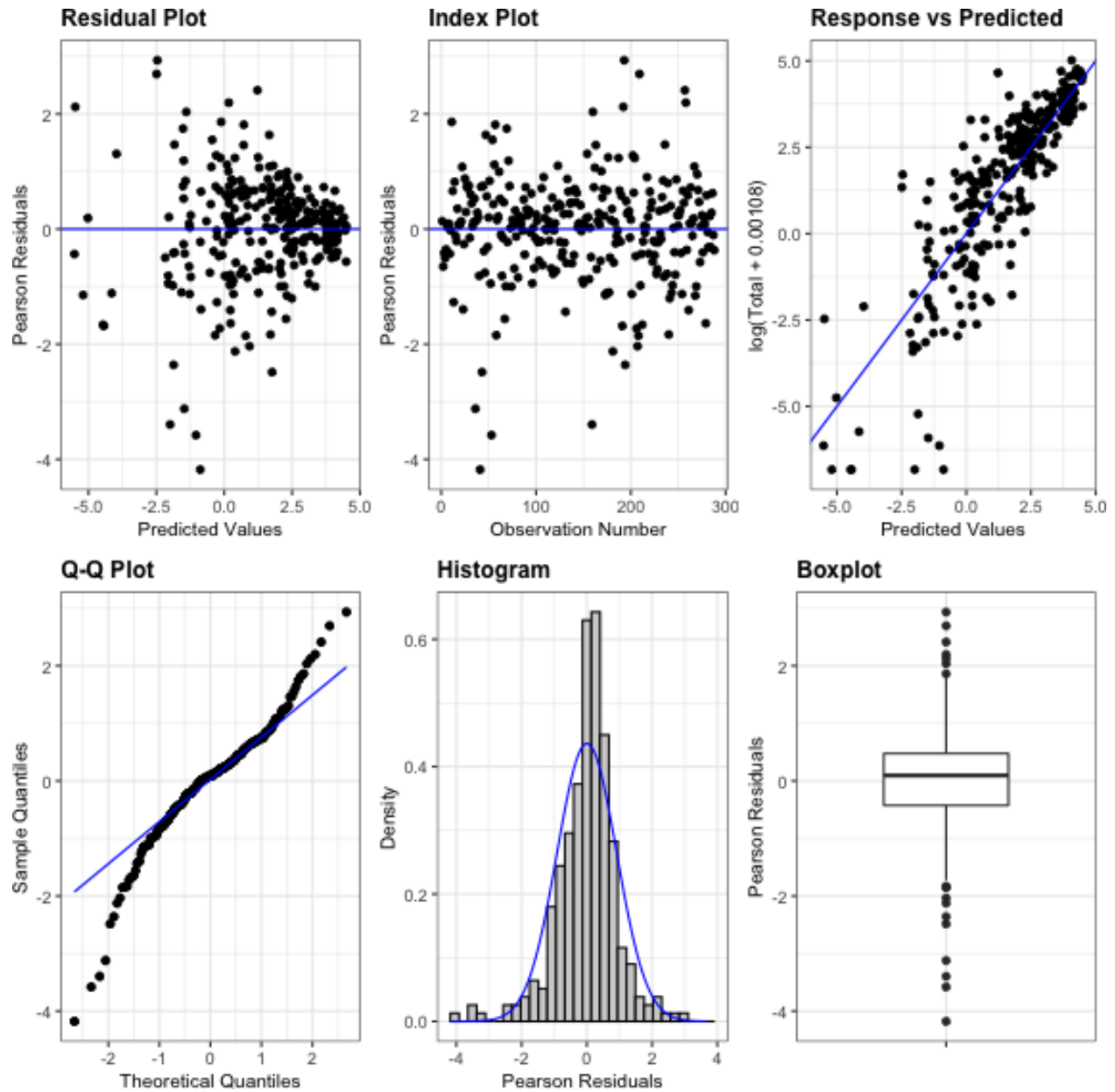
Figure 10: Diagnosis plot for the effect of crop identity and corn weed management on weed community aboveground mass over four years with four blocks of replication.
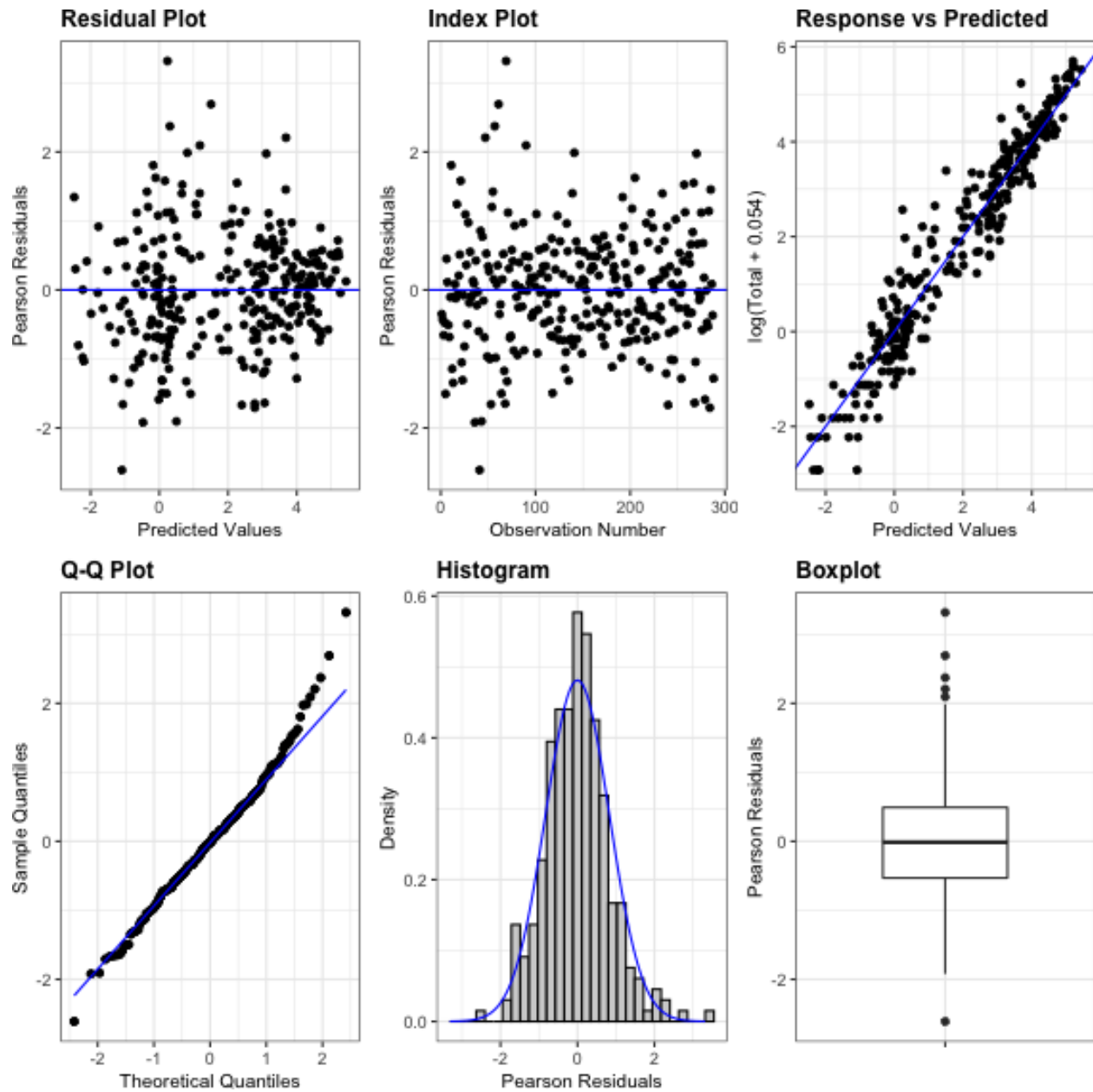
Figure 11: Diagnosis plot for the effect of crop identity and corn weed management on weed community density over four years with four blocks of replication.

```
#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 +
                               (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'."
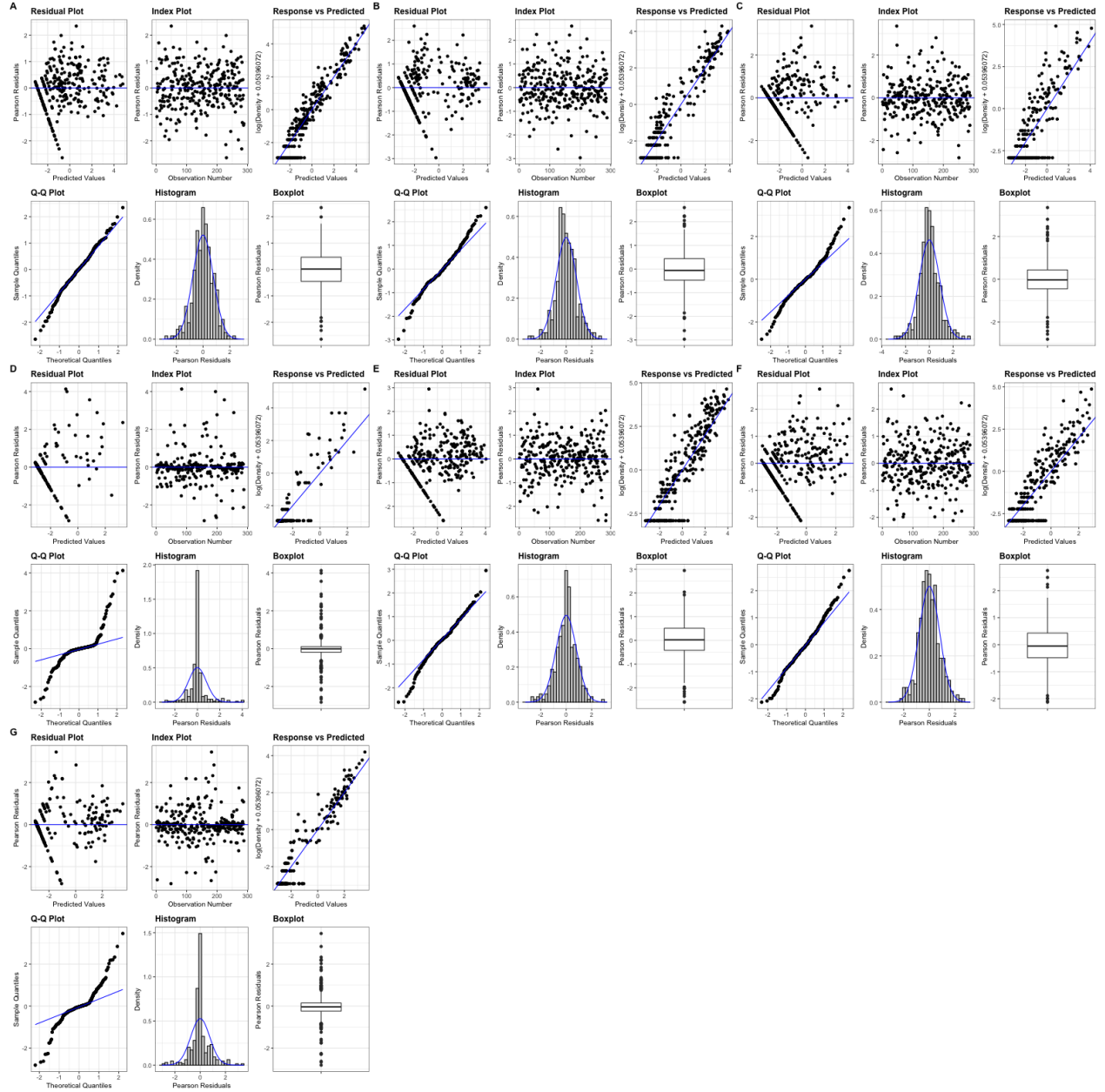
Figure 12: Diagnosis plot for the effect of crop identity and corn weed management on the aboveground mass of (A) - AMATA, (B) - CHEAL, (C) - DIGSA, (D) - ECHCG, (E) - SETFA, (F) - SETLU, and (G) - TAROF
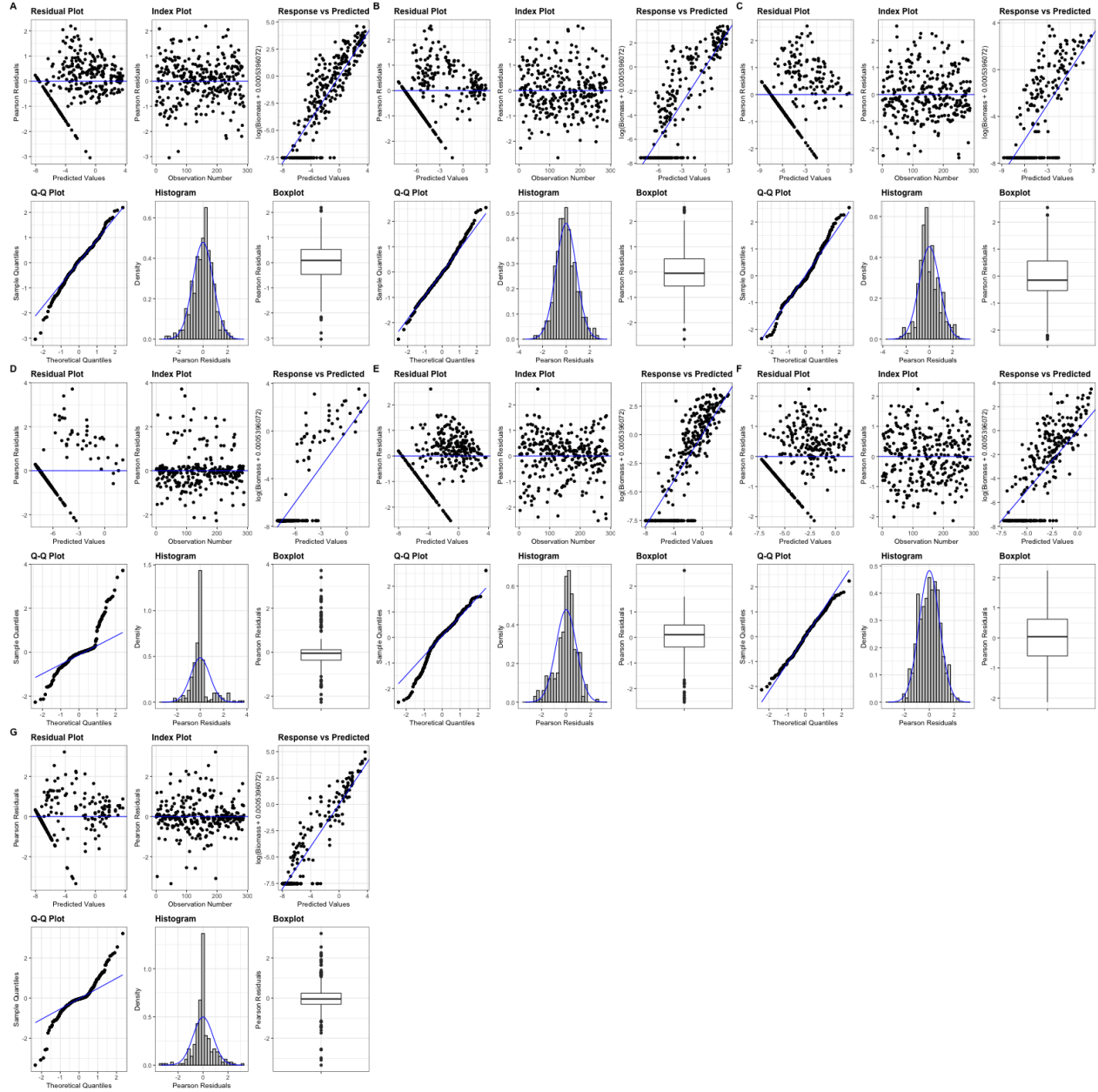
Figure 13: Diagnosis plot for the effect of crop identity and corn weed management on the density of (A) - AMATA, (B) - CHEAL, (C) - DIGSA, (D) - ECHCG, (E) - SETFA, (F) - SETLU, and (G) - TAROF