**S1 Appendix: R Code used for analyses of the litterbag**

**decomposition study.**

# R Code for analysis for pocket gopher litter bag decomposition study

# R Code below is for P at 24 months with log transformed data.

# Same code was used for: 1) N at 24 and 48 months, data not transformed;

# 2) K values, log-transformed; and 3) root in-growth in buried bags, data

# not transformed, but location (buried vs.forest floor) not included

library(car)

library(lme4)

library(lmerTest)

library (lsmeans)

library(plotrix)

library(dplyr)

setwd("~/1\_ufbiz/research/FL pocket gophers/Analysis N\_P 2018")

# Data are phosphorus values log transformed for each plot in each block for

# buried and unburied bags. Bags collected at 24 months.

data=read.csv("Final P 24 mo.csv", header = TRUE)

# Checks on data structure

# Lists variables in data

names(data)

# Lists structure of the data

str(data)

# Lists names of levels for each factor

levels(data$Litter)

levels(data$Location)

# Location is buried or forest floor

levels(data$Block)

# Assign variable to be a factor not a numeric variable

data$Sample\_Plot = as.factor(data$Sample\_Plot)

data$Months = as.factor(data$Months)

# Transform data (for k value and P content at 24 months)

data$Log\_Perc\_P = log(data$Perc\_P)

# Model run with lme4 package, includes location nested within sample\_plots

# and sample\_plots nested within blocks

lme\_P\_model <- lmer(Log\_Perc\_P ~ Litter + Location + Litter\*Location + (1|Block/Sample\_Plot/Location),data)

summary (lme\_P\_model)

anova(lme\_P\_model, type = 3)

lsm\_P<-lsmeansLT(lme\_P\_model, test.effs=NULL)

lsm\_P

difference\_lsm\_P<-difflsmeans(lme\_P\_model,test.effs=NULL)

difference\_lsm\_P

lsm\_P2<-lsmeans(lme\_P\_model, list (pairwise ~ Litter\*Location))

cld(lsm\_P2)