Supplement

Table S1. R Packages Used for Statistical Analysis and Visualization.

Package	Version	Primary Purpose / Key Functions
lme4	1.1-37	Linear Mixed-Effects Model fitting (lmer)
lmerTest	3.1-3	Calculates p-values and degrees of freedom for LMMs (Type III ANOVA with Satterthwaite df approximation)
emmeans	1.11.2-8	Calculates Estimated Marginal Means (EMMs) and performs post-hoc tests (Tukey's HSD contrasts)
vegan	2.6-8	Multivariate statistics: PERMANOVA (adonis2), PERMDISP, and NMDS ordination (metaMDS)
permute	0.9-7	Handles constrained permutation design (e.g., blocking by Location using how(blocks = Location))
dplyr	1.1.4	Data manipulation, grouping operations, and recoding
ggplot2	4.0.0	General data visualization and ordination plotting
readxl	1.4.5	Importing data from Excel spreadsheets
rstatix	0.7-2	Statistical summaries and Games-Howell post-hoc testing (also for selecting columns)
boot	1.3-31	Bootstrapping for confidence intervals (e.g., PERMANOVA R^2 confidence interval)
car	3.1-3	Homogeneity tests (Levene's test) and assumption diagnostics
Matrix	1.7-3	Linear algebra backend for mixed-effects models
ggpubr	0.6-1	Creating publication-quality figures and significance annotations
tidyr	1.3.1	Data reshaping utilities
MASS	7.3-65	Statistical utilities supporting LMM fitting
tibble	3.2.1	Modern data-frame structure
patchwork	1.1.3	Arranging multiple ggplot objects on a single page
gridExtra	2.3	Utilities for grid graphics and arranging plots

Caption: List of R packages and their versions used for data manipulation, statistical modeling (PERMANOVA, LMM), assumption checking, post-hoc testing, and figure generation. Analyses were conducted in R version 4.5.0.

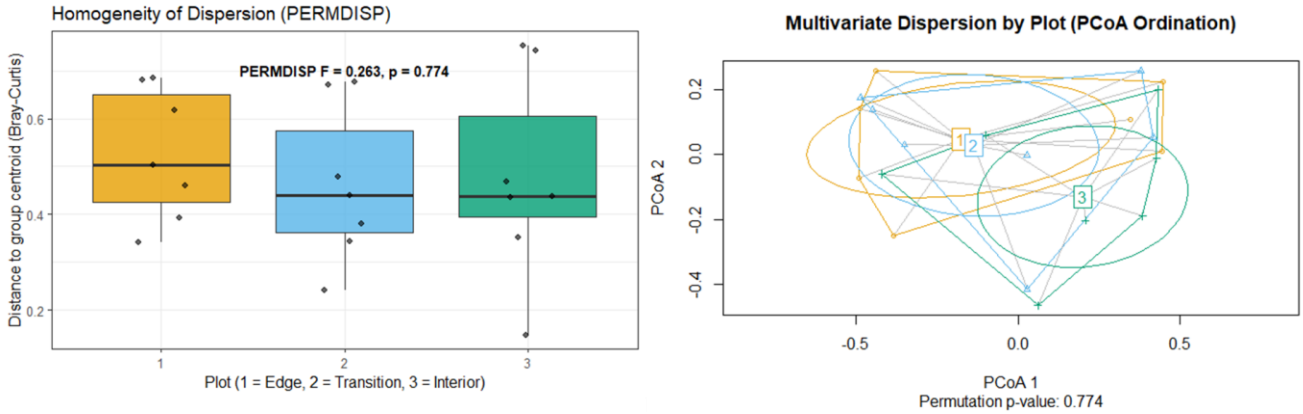

Figure S1. Analysis of Multivariate Dispersion (PERMDISP) of Tree Community Composition. (A) Boxplot showing the Bray-Curtis distance of each plot to its group (Plot Type) centroid. (B) Principal Coordinates Analysis (PCoA) ordination visualizing the dispersion of plots around their centroids. The formal test results (Table S3) indicate no significant difference in dispersion among plot types, validating a key PERMANOVA assumption

Table S2: ANOVA Table for the Test of Homogeneity of Multivariate Dispersions (PERMDISP).

Source	*df*	*Sums of Squares*	*Mean Squares*	*F value*	*p-value*
Groups (Plot)	2	0.01605	0.0080269	0.2634	0.7713
Residuals	18	0.54854	0.0304743		
Total	20	0.56459			

Caption: Results of the betadisper analysis testing the assumption of homogeneous multivariate dispersion using Bray-Curtis distances . The non-significant p-value (p = 0.771) indicates similar within-group variation across Plot Types.

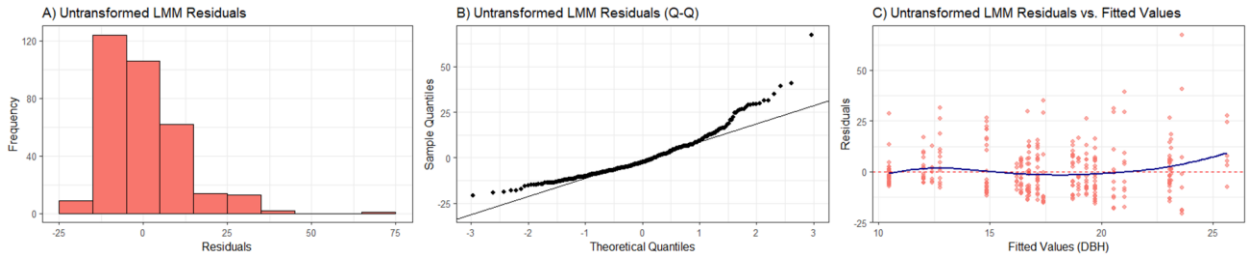

Figure S2. Diagnostic Plots for the Untransformed DBH Linear Mixed Model.

Diagnostic plots for an LMM fitted to the untransformed (raw) tree size data ('TreeSizes' ~ Plot + (1 | Location)). (A) Histogram shows right-skewed residuals. (B) Q-Q plot confirms violation of normality. (C) Residuals vs. Fitted plot shows fanning (heteroscedasticity) . These violations justified log-transformation.

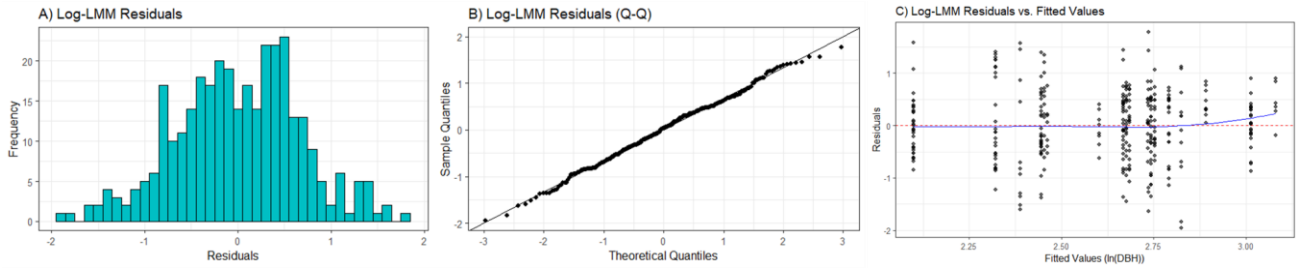

Figure S3. Diagnostic Plots for the Log-Transformed DBH Linear Mixed Model.

Diagnostic plots for the final LMM using log-transformed tree size (log('TreeSizes') ~ Plot + (1 | Location)). (A) Histogram shows approximately normal residuals. (B) Q-Q plot shows points falling closely along the line. (C) Residuals vs. Fitted plot shows random scatter, supporting homogeneity of variance. These plots confirm model assumptions were met.

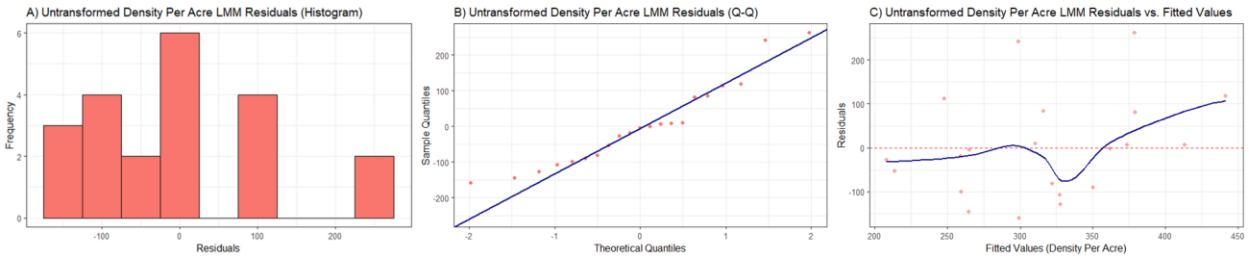

Figure S4. Diagnostic Plots for the Untransformed Density Linear Mixed Model. Diagnostic plots for an LMM fitted to the untransformed (raw) tree density data (density per ha ~ Plot + (1 | Location)). (A) Histogram shows non-normal residuals. (B) Q-Q plot confirms lack of normality. (C) Residuals vs. Fitted plot shows heteroscedasticity . These violations justified log-transformation.

Table S3. Linear Mixed Model Summary for Log-Transformed Tree Size (DBH).

Component	*Estimate (log(DBH))*	*Standard Error*	*df*	*t value*	*p-value*
Fixed Effects					
Intercept (edge)	2.471	0.109	11.27	22.635	< 0.001*
transition	0.222	0.088	324.22	2.517	0.012*
interior	0.29	0.099	327.53	2.91	0.004*
Overall F-Test	*Mean Square*	*N/A*	*NumDF/ DenDF*	*F Value*	*Pr(>F)*
Plot	2.268	N/A	2/325.34	4.968	0.007*
—	—	—	—	—	—
Random Effects	*Variance (σ^2)*	*Standard Deviation*			
Location (Intercept)	0.052	0.228			
Residual	0.457	0.676			
Model Fit	Observation: 331	Groups (Location): 7			

Note: Full summary of the LMM (log(DBH) ~ Plot + (1 | Location)). Includes fixed effects estimates, the overall F-test for Plot, and random effect variance components. Degrees of freedom calculated using Satterthwaite's method. Significance noted by (*)

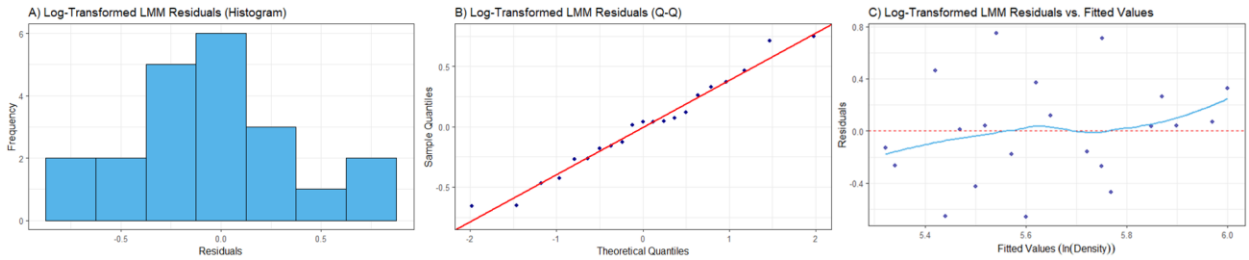

Figure S5. Diagnostic Plots for the Log-Transformed Density Linear Mixed Model. Diagnostic plots for the final LMM using log-transformed tree density (log_density ~ Plot + (1 | Location)). (A) Histogram shows approximately normal residuals. (B) Q-Q plot shows points falling reasonably along the line. (C) Residuals vs. Fitted plot shows random scatter, supporting homogeneity of variance. These plots confirm model assumptions were met.

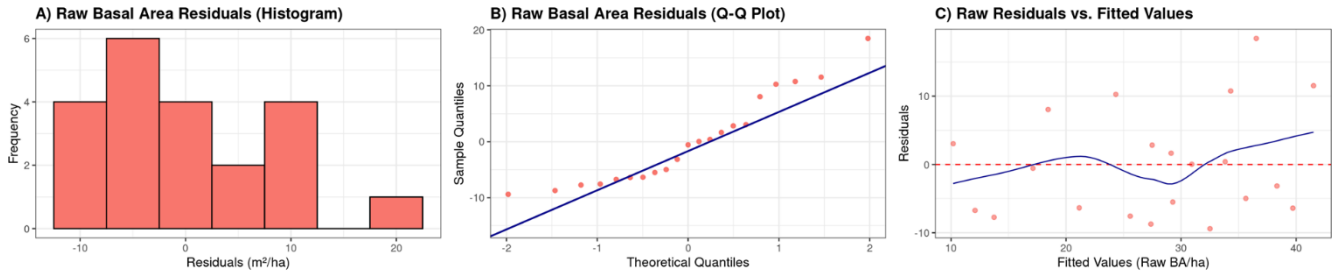

Figure S6. Diagnostic Plots for the Untransformed Basal Area Linear Mixed Model. Diagnostic plots for an LMM fitted to the untransformed (raw) stand basal area data (BA ha^{-1} ~ Plot + (1 | Location)). (A) Histogram shows right-skewed residuals indicating deviation from normality. (B) Q–Q plot confirms heavy-tailed residual distribution relative to theoretical quantiles. (C) Residuals vs. Fitted plot reveals fanning and unequal variance across fitted values. Together,

these patterns demonstrate violations of model assumptions, justifying log-transformation of basal area prior to final model fitting.

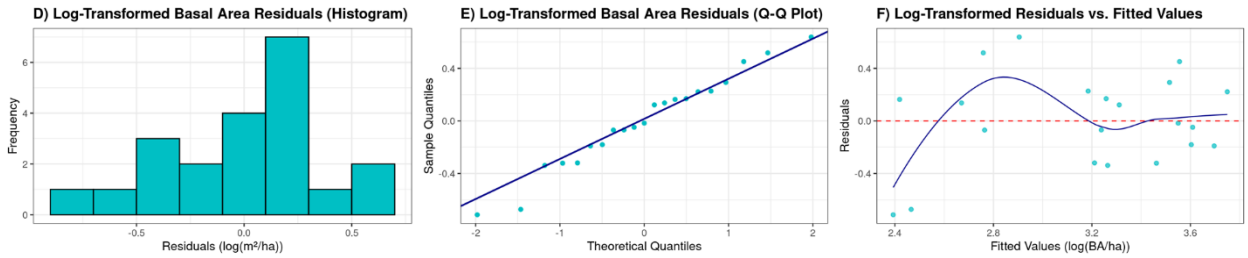

Figure S7. Diagnostic Plots for the Log-Transformed Basal Area Linear Mixed Model. Diagnostic plots for the final LMM using log-transformed stand basal area (log(BA ha^{-1}) ~ Plot + (1 | Location)). (A) Histogram of residuals shows approximate normality. (B) Q–Q plot displays residuals closely following the 1:1 line, indicating normal error structure. (C) Residuals vs. Fitted plot shows random scatter around zero, supporting homogeneity of variance. These plots confirm that the log transformation successfully satisfied LMM assumptions of normality and homoscedasticity for basal area.

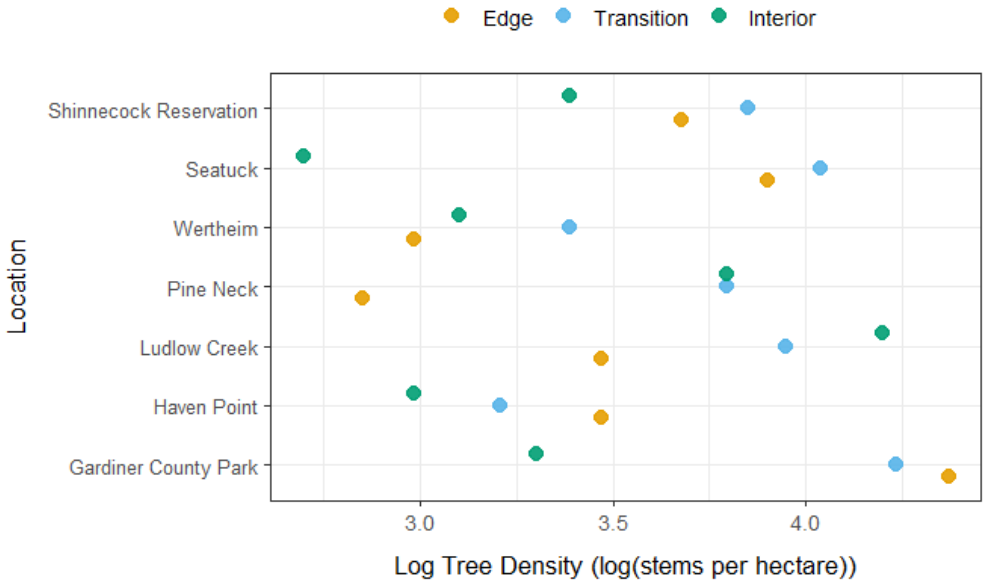

Figure S8. Raw Tree Density by Sampling Location and Plot Type. Raw tree density (trees ha^{-1}) for each plot, grouped by Sampling Location and colored by Plot Type. Illustrates variation between locations, justifying the random effect. No clear pattern across plot types is apparent.

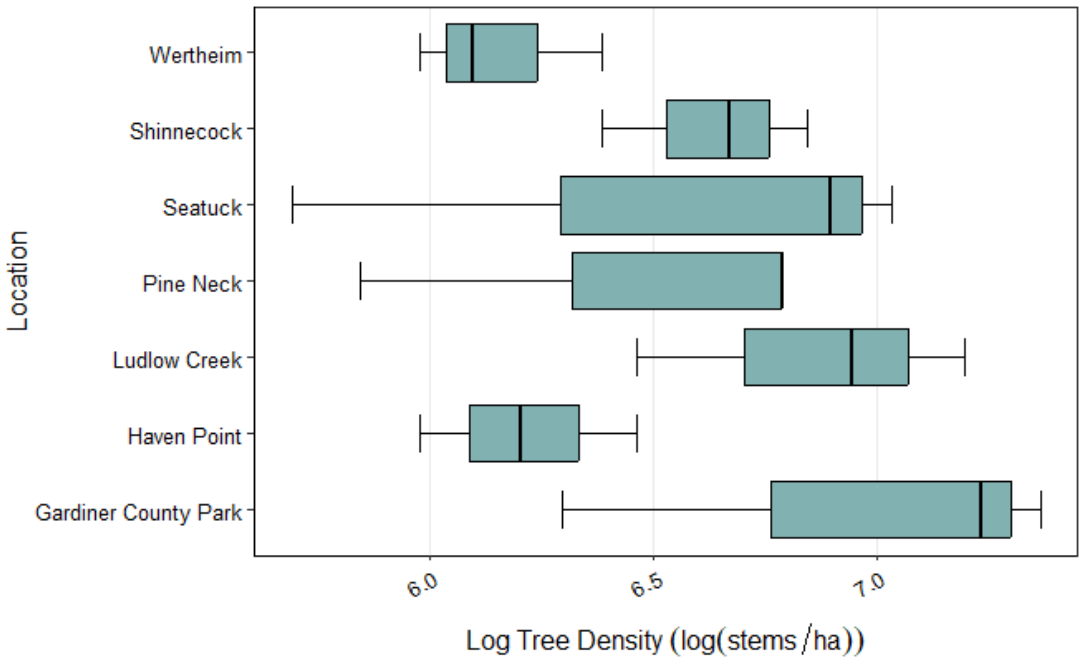

Figure S9. Distribution of Log-Transformed Tree Density by Location. Boxplot showing the distribution of log-transformed tree density (ln(trees ha^{-1})) for each sampling location. Visualizes the site-level variability accounted for by the random effect.

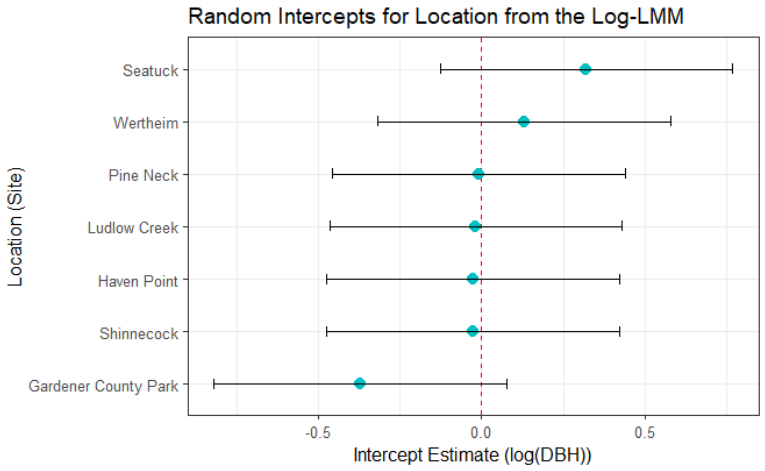

Figure S10. Random Intercepts for Location from the Log-LMM (DBH). Estimated random intercepts for the seven study sites from the DBH model . Points represent the deviation of each site's mean log(DBH) from the overall mean (red line at 0.0) . Sites whose confidence intervals do not overlap zero differ significantly from the overall average. This variation justifies including Location as a random effect.

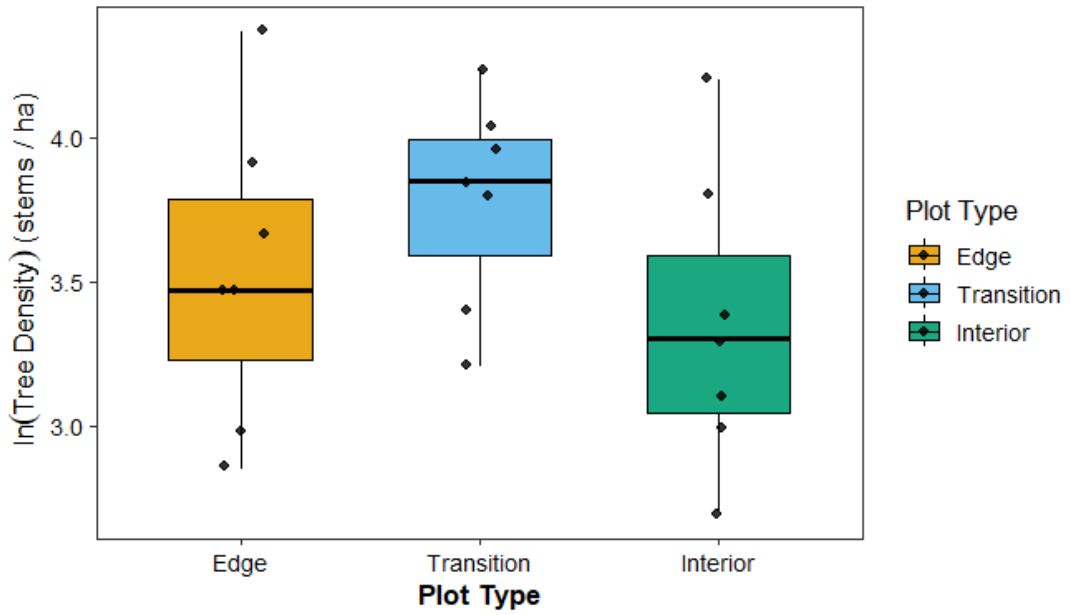

Figure S11. Distribution of log-transformed tree density by plot type. Boxplots show the distribution of log-transformed tree density (ln [stems ha^{-1}]) across plot types (edge, transition, and interior). Individual points represent observations, and the overlapping distributions indicate that plot type had no significant effect on tree density.

Table S4. Linear Mixed Model Summary for Log-Transformed Basal Area (BA_{ha}).

Component	*Estimate (log(BA_{ha}))*	*Standard Error*	*df*	*t value*	*p-value*
Fixed Effects					
Intercept (edge)	2.87	0.118	16.3	24.31	< 0.001*
transition	0.401	0.136	18	2.949	0.018*
interior	0.489	0.145	18	3.367	0.006*
Overall F-Test	*Mean Square*	*N/A*	*NumDF/ DenDF*	*F Value*	*Pr(>F)*
Plot	2.407	N/A	2/18	6.21	0.009*
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Random Effects	*Variance (σ^2)*	*Standard Deviation*
Location (Intercept)	0.063	0.252
Residual	0.389	0.624
Model Fit	Observation: 331	Groups (Location): 7

Note: Full summary for LMM ($\log(BA_{ha}) \sim Plot + (1 | Location)$). Degrees of freedom calculated using Satterthwaite's approximation. Significance indicated at $\alpha = 0.05$ level (*).

Table S5. Linear Mixed Model Summary for Log-Transformed Tree Density.

Component	*Estimate (log(Density))*	*Standard Error*	*df*	*t value*	*p-value*
Fixed Effects					
Intercept (Plot 1)	5.623	0.178	17.42	31.676	< 0.001*
Plot 2 (Transition)	0.249	0.234	12	1.064	0.308
Plot 3 (Interior)	-0.179	0.234	12	-0.763	0.46
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Overall F-Test	*Mean Square*	*N/A*	*NumDF/DenDF*	*F Value*	*Pr(>F)*
Plot	0.324	N/A	2 / 12	1.686	0.226
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Random Effects	*Variance (σ^2)*	*Std. Dev. (σ)*			
Location (Intercept)	0.0285	0.169			
Residual	0.1921	0.438			
Model Fit	Observations: 21	Groups (Location): 7			

Note: Full summary of the LMM ($\log(Density) \sim Plot + (1 | Location)$). Includes fixed effects estimates, the overall F-test for Plot, and random effect variance components. Degrees of freedom calculated using Satterthwaite's method. Significance noted by (*)