

We employed linear-mixed-effects models (lmes) to test all univariate variables for the fixed effects of ‘ice-wedge polygon type’ and ‘soil layer category’ plus their interaction. If homogeneity of variances and normality of model residuals were not given, log or sqrt transformations were applied. In case of no agreement with model assumptions after transformation, we conducted nonparametric tests, i.e. Kruskal Wallis tests were used to test the effects of polygon type and soil layer category, followed by pairwise two-sided Wilcoxon tests.

There here provided list provides details for each tested parameter:

Variable	Original distribution issues	Transformation applied	Final Test used
BD (g DW cm ⁻³)	No normality nor heteroscedasticity of model residuals	No transformation helped	Kruskal–Wallis + Wilcoxon
pH (MQ)	No heteroscedasticity of model residuals	No transformation helped	Kruskal–Wallis + Wilcoxon
SWC (g g ⁻¹ DW)	No normality nor heteroscedasticity of model residuals	log	LME + EMM
Soil d 13C (‰)	No heteroscedasticity of model residuals	No transformation helped	Kruskal–Wallis + Wilcoxon
Soil d 15N (‰)	No normality nor heteroscedasticity of model residuals	log	LME + EMM
Soil C (mg g ⁻¹ DW)	No heteroscedasticity of model residuals	log	LME + EMM
Soil N (mg g ⁻¹ DW)	No normality of model residuals	No transformation helped	Kruskal–Wallis + Wilcoxon
Soil P (mg g ⁻¹ DW)	Model assumptions met		LME + EMM
Soil C:N	No normality nor heteroscedasticity of model residuals	No transformation helped	Kruskal–Wallis + Wilcoxon
Soil C:P	No normality nor heteroscedasticity of model residuals	log	LME + EMM
Soil N:P	No normality nor heteroscedasticity of model residuals	log	LME + EMM
DOC (µg g ⁻¹ DW)	No normality nor heteroscedasticity of model residuals	No transformation helped	Kruskal–Wallis + Wilcoxon
TDN (µg g ⁻¹ DW)	No normality nor heteroscedasticity of model residuals	log	LME + EMM
DOC:TDN	No normality of model residuals	log	LME + EMM
Aromatics & Phenols (mg g ⁻¹ DW)	No normality nor heteroscedasticity of model residuals	log	LME + EMM
Carbohydrates (mg g ⁻¹ DW)	No heteroscedasticity of model residuals	log	LME + EMM
Lignins (mg g ⁻¹ DW)	No normality nor heteroscedasticity of model residuals	sqrt	LME + EMM
Lipids (mg g ⁻¹ DW)	No heteroscedasticity of model residuals	sqrt	LME + EMM
N-containing (mg g ⁻¹ DW)	No heteroscedasticity of model residuals	sqrt	LME + EMM

General & Unknown (mg g ⁻¹ DW)	No heteroscedasticity of model residuals	log	LME + EMM
Aromatics & Phenols (%)	No heteroscedasticity of model residuals	No transformation helped	Kruskal–Wallis + Wilcoxon
Carbohydrates (%)	Model assumptions met		LME + EMM
Lignins (%)	Model assumptions met		LME + EMM
Lipids (%)	No heteroscedasticity of model residuals	No transformation helped	Kruskal–Wallis + Wilcoxon
N-containing (%)	No heteroscedasticity of model residuals	No transformation helped	Kruskal–Wallis + Wilcoxon
General & Unknown (%)	Model assumptions met		LME + EMM
Bac+ Archaeal Richness (No. ASVs)	No heteroscedasticity of model residuals	log	LME + EMM
Bac+ Archaeal Diversity (Shannon)	Model assumptions met		LME + EMM
Abundance (16S rRNA Gene Copies g ⁻¹ DW)	No normality nor heteroscedasticity of model residuals	No transformation helped	Kruskal–Wallis + Wilcoxon
Abundance (16S rRNA Gene copies mg ⁻¹ soil C)	No normality nor heteroscedasticity of model residuals	sqrt	LME + EMM
Fungal Richness (No. ASVs)	Model assumptions met		LME + EMM
Fungal Diversity (Shannon)	Model assumptions met		LME + EMM
Abundance (ITS1 Gene Copies g ⁻¹ DW)	No normality nor heteroscedasticity of model residuals	No transformation helped	Kruskal–Wallis + Wilcoxon
Abundance (ITS1 Gene Copies mg ⁻¹ soil C)	No normality nor heteroscedasticity of model residuals	No transformation helped	Kruskal–Wallis + Wilcoxon
Betaglucosidase (nmol substrate g ⁻¹ soil C h ⁻¹)	No normality nor heteroscedasticity of model residuals	log	LME + EMM
Exoglucanase (nmol substrate g ⁻¹ soil C h ⁻¹)	No normality nor heteroscedasticity of model residuals	No transformation helped	Kruskal–Wallis + Wilcoxon
Exochitinase (nmol substrate g ⁻¹ soil C h ⁻¹)	No normality of model residuals	sqrt	LME + EMM
Leucine Aminopeptodase (nmol substrate g ⁻¹ soil C h ⁻¹)	No normality of model residuals	No transformation helped	Kruskal–Wallis + Wilcoxon
Acid Phosphatase (nmol substrate g ⁻¹ soil C h ⁻¹)	No normality nor heteroscedasticity of model residuals	No transformation helped	Kruskal–Wallis + Wilcoxon
Sulfatase (nmol substrate g ⁻¹ soil C h ⁻¹)	No normality nor heteroscedasticity of model residuals	log	LME + EMM
Betaglucosidase (nmol substrate g ⁻¹ DW h ⁻¹)	No normality nor heteroscedasticity of model residuals	log	LME + EMM
Exoglucanase (nmol substrate g ⁻¹ DW h ⁻¹)	No normality nor heteroscedasticity of model residuals	log	LME + EMM

Exochitinase (nmol substrate g ⁻¹ DW h ⁻¹)	No normality of model residuals	sqrt	LME + EMM
Leucine Aminopeptodase (nmol substrate g ⁻¹ DW h ⁻¹)	No normality nor heteroscedasticity of model residuals	log	LME + EMM
Acid Phosphatase (nmol substrate g ⁻¹ DW h ⁻¹)	No normality nor heteroscedasticity of model residuals	log	LME + EMM
Sulfatase (nmol substrate g ⁻¹ DW h ⁻¹)	No normality nor heteroscedasticity of model residual	log	LME + EMM