

Table S1. Ranges of variation for all unscaled reticulation traits and ecological predictors,

restricted only to non-palm angiosperms.

Type	Variable	Units	5% Quantile	50% Quantile	95% Quantile
Environment	Light environment	-	1	2	2
Environment	Mean annual precipitation	mm	1560	1980	5302
Environment	Mean annual temperature	°C	9	17.4	24.4
Trait	Amax	nmol g s ⁻¹	0.861	7.659	18.98
Trait	$\delta^{13}\text{C}$	per mil	-33.4	-30.3	-26.8
Trait	Force to punch	kN m ⁻¹	0.293	0.866	2.41
Trait	Force to tear	kN m ⁻¹	0.379	0.717	4.31
Trait	Lamina area	cm ²	9.354	58.224	632.01
Trait	Lamina thickness	mm	0.141	0.264	0.61
Trait	LDMC	-	0.24	0.425	0.69
Trait	Leaf aspect ratio	-	1.619	2.443	4
Trait	Lignin	mg g ⁻¹	9.06	23.9	39.62
Trait	LMA	g m ⁻²	64.222	106.71	189.16
Trait	Phenols	mg g ⁻¹	0.645	88.735	166.12
Trait	Tannins	100 g g ⁻¹	0	39.005	83.6
Venetion	Areole circularity ratio	-	0.634	0.755	0.86
Venetion	Areole elongation ratio	-	1.372	1.5	1.74
Venetion	Areole loop index	-	0.023	0.075	0.15
Venetion	Freely ending veinlet ratio	-	0.086	0.212	0.43
Venetion	Meshedness ratio	-	-0.018	0.051	0.11
Venetion	Minimum spanning tree ratio	-	0.604	0.681	0.85
Venetion	Vein density	mm ⁻¹	5.366	11.284	18.7
Venetion	Vein loopiness	mm ⁻²	0.899	9.319	54.5

Table S1. Axis rotations for principal components analysis of reticulation traits for the angiosperm dataset. Parentheses indicate variance fractions for each variable.

<u>Variable</u>	<u>PC1</u> <u>(0.657)</u>	<u>PC2</u> <u>(0.188)</u>	<u>PC3</u> <u>(0.1087)</u>	<u>PC4</u> <u>(0.02)</u>	<u>PC5</u> <u>(0.0141)</u>	<u>PC6</u> <u>(0.0082)</u>	<u>PC7</u> <u>(0.004)</u>	<u>PC8</u> <u>(0)</u>
Log areole elongation ratio	0.211	-0.685	0.18	-0.317	0.182	-0.163	-0.541	0
Log areole circularity ratio	-0.312	0.544	-0.159	-0.093	0.064	-0.251	-0.711	0
Log areole loop index	-0.405	0.06	0.193	-0.772	-0.026	0.125	0.236	0.355
Log minimum spanning tree ratio	0.366	0.335	0.238	-0.082	0.794	0.24	0.04	0
Log meshedness ratio	-0.321	-0.261	-0.61	0.048	0.269	0.607	-0.118	0
Log freely ending veinlet ratio	0.404	0.194	0.162	-0.134	-0.505	0.632	-0.316	0
Log vein density	-0.363	-0.107	0.531	0.516	0.056	0.197	-0.173	0.487
Log vein loopiness	-0.402	-0.038	0.41	-0.029	0.023	0.176	-0.001	0.798

Supporting Information for Blonder *et al.*, *Structural and defensive roles of angiosperm leaf venation network reticulation across an Andes-Amazon elevation gradient*

Figure S1. Dataset coverage. Each matrix entry represents an observation of a branch at a site.

Entries are colored by site if available, and colored white if missing.

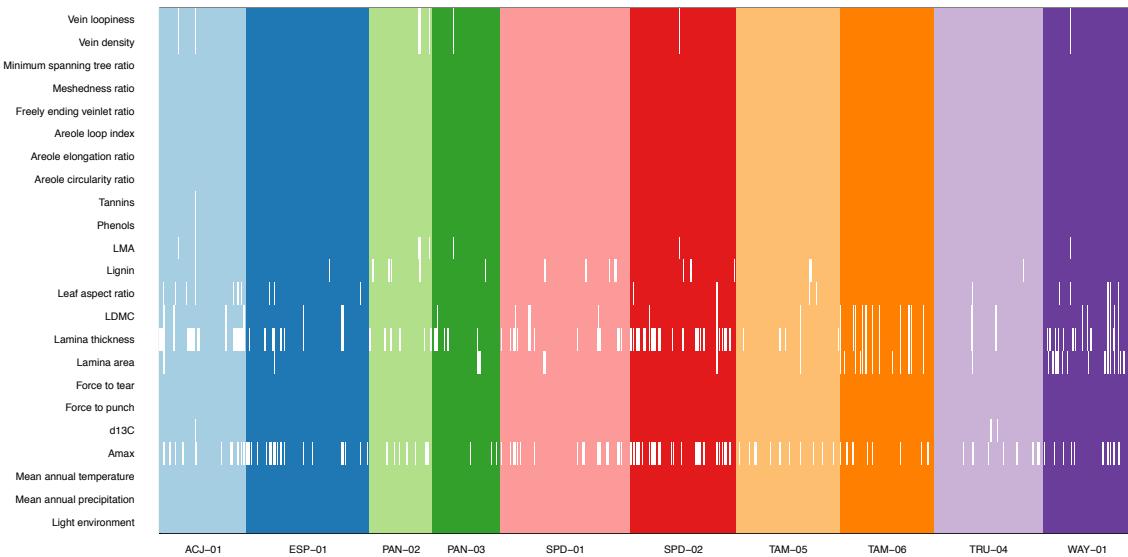


Figure S2. Minor vein reticulation trait space, as seen via principal components analysis of reticulation traits for the angiosperms excluding palms. **A, B)** Biplot of variable rotations 1 vs. 2 and 2 vs. 3. Individual leaves are shown as gray dots; axes as red arrows, with the overall trait space boundaries delineated via a purple convex hull. Labels indicate % variance explained by each axis.

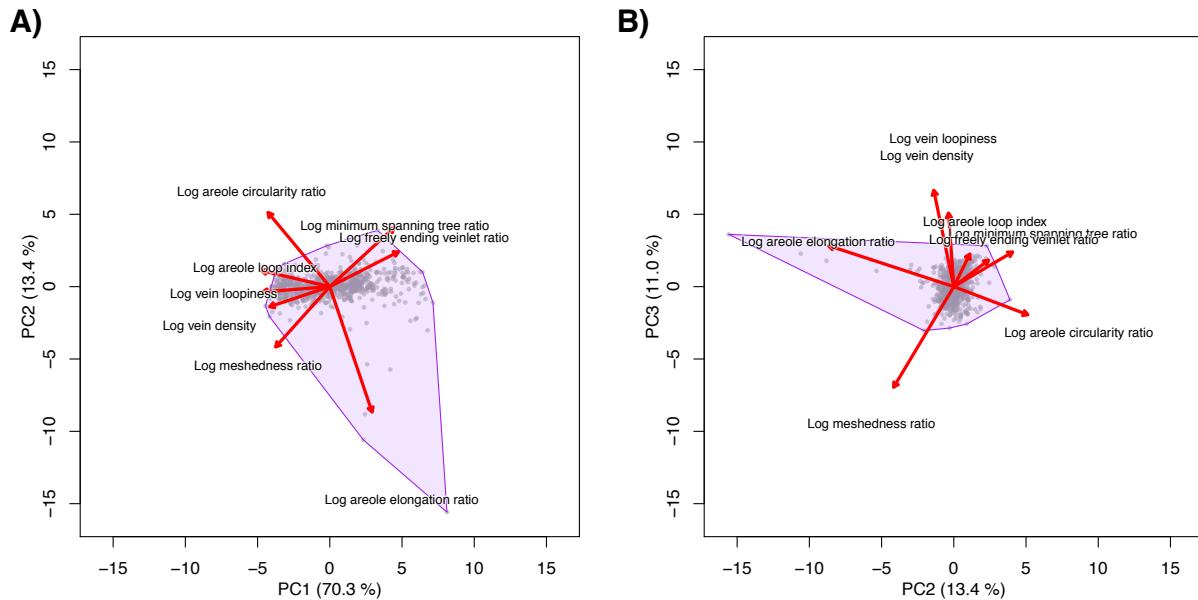


Figure S3. Hierarchical variance partitioning of reticulation traits among taxonomic scales for non-palm taxa.

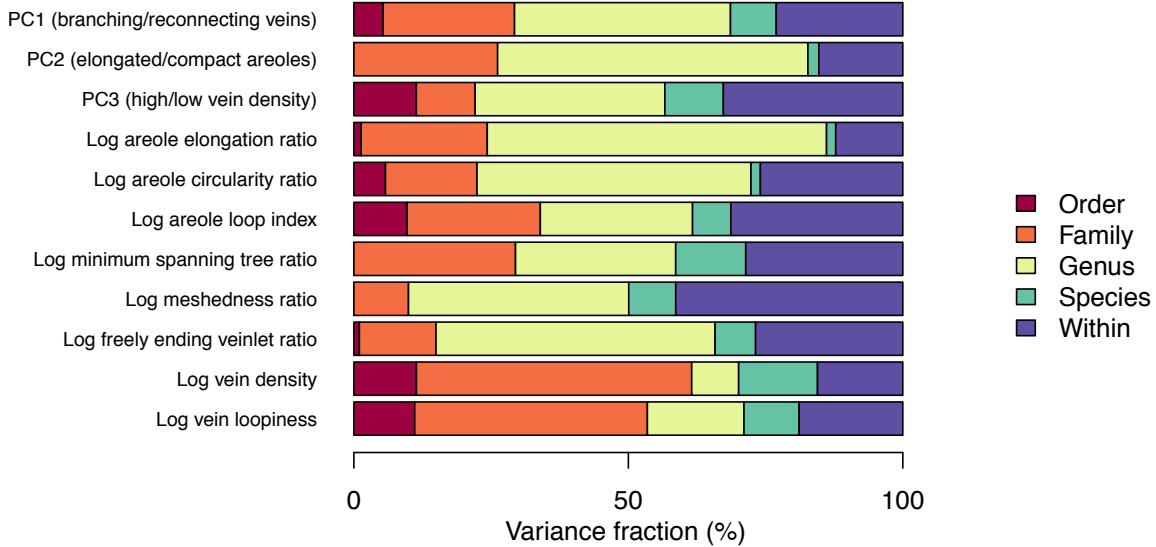


Figure S4. Evolutionary trends for reticulation principal components and individual reticulation traits for **A)** angiosperms and **B)** non-palm angiosperms. Green bars represent distributions of species within families. Regression lines (red) are drawn when statistically significant.

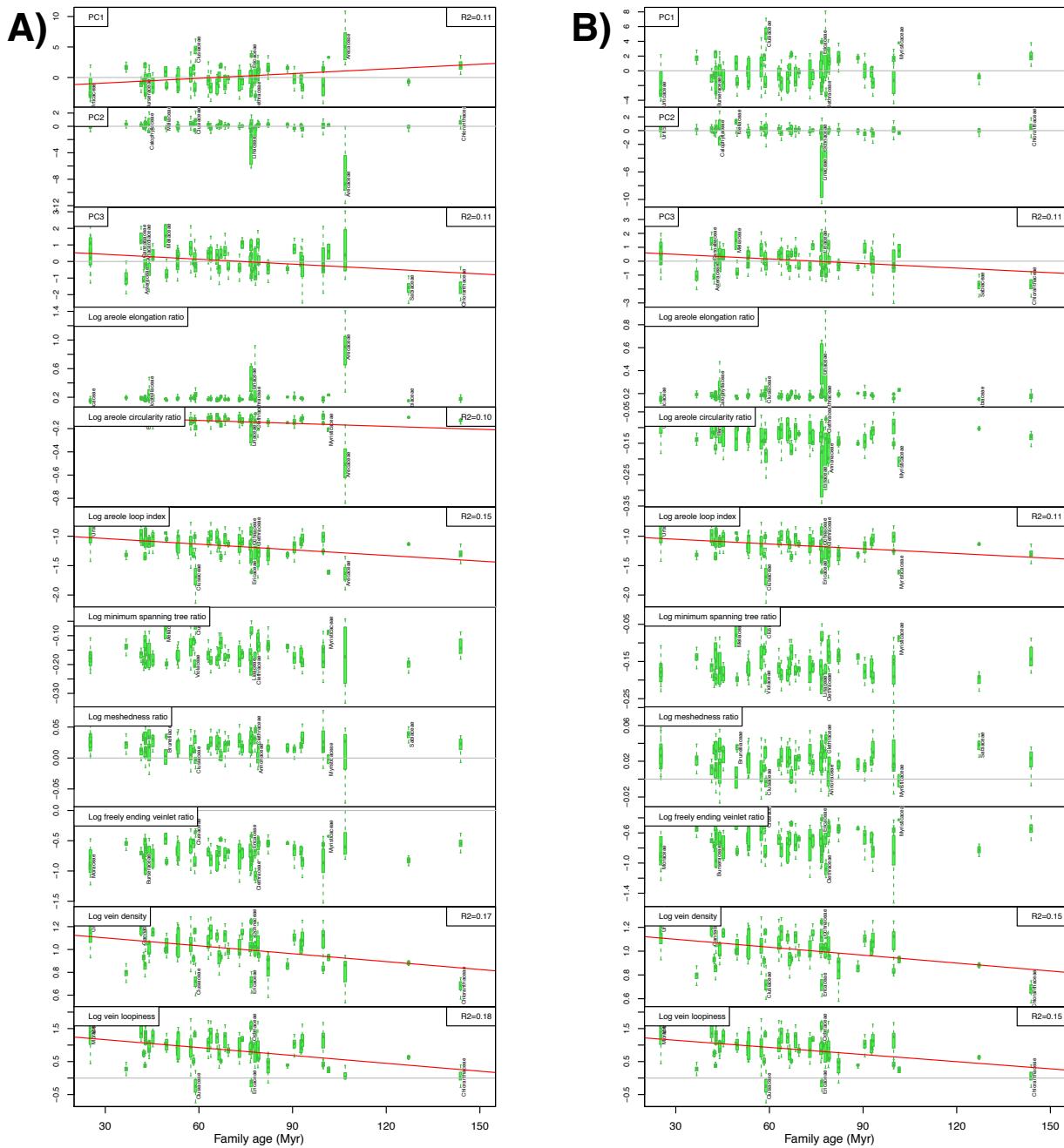


Figure S5. Effect of light availability on reticulation traits for non-palm angiosperms. Purple lines indicate the distribution of sun mean minus shade mean values within each species, across all species-sites combinations for the whole dataset. The null expectation of zero is shown as a black line. The mean of the observed distribution is shown as a solid red vertical line if significantly different from zero and dashed gray if not.

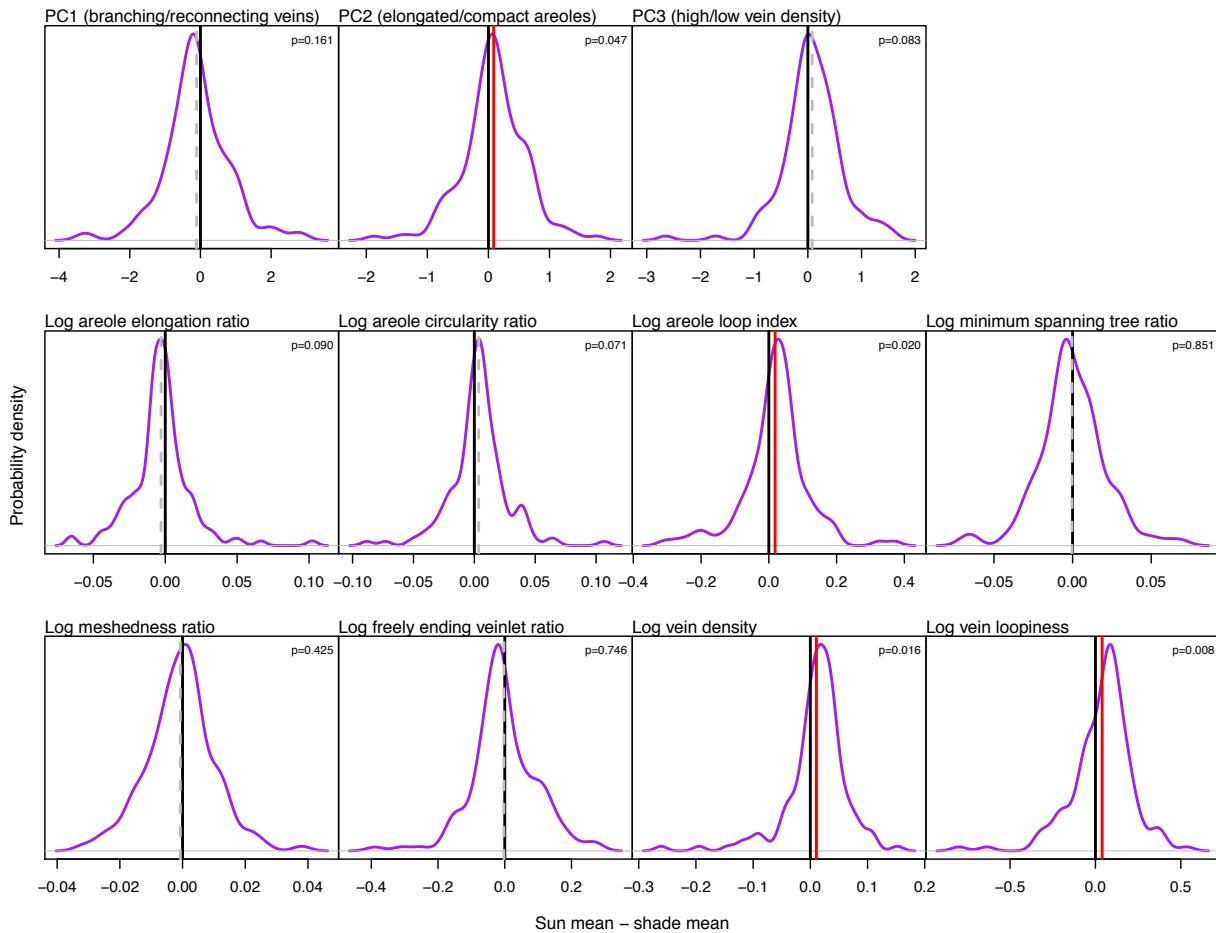


Figure S6. Elevation trends in principal component and individual reticulation traits for non-palm angiosperms. Gray points represent individual leaves; open purple circle site medians. Regression lines (red) for site-median data are drawn when statistically significant.

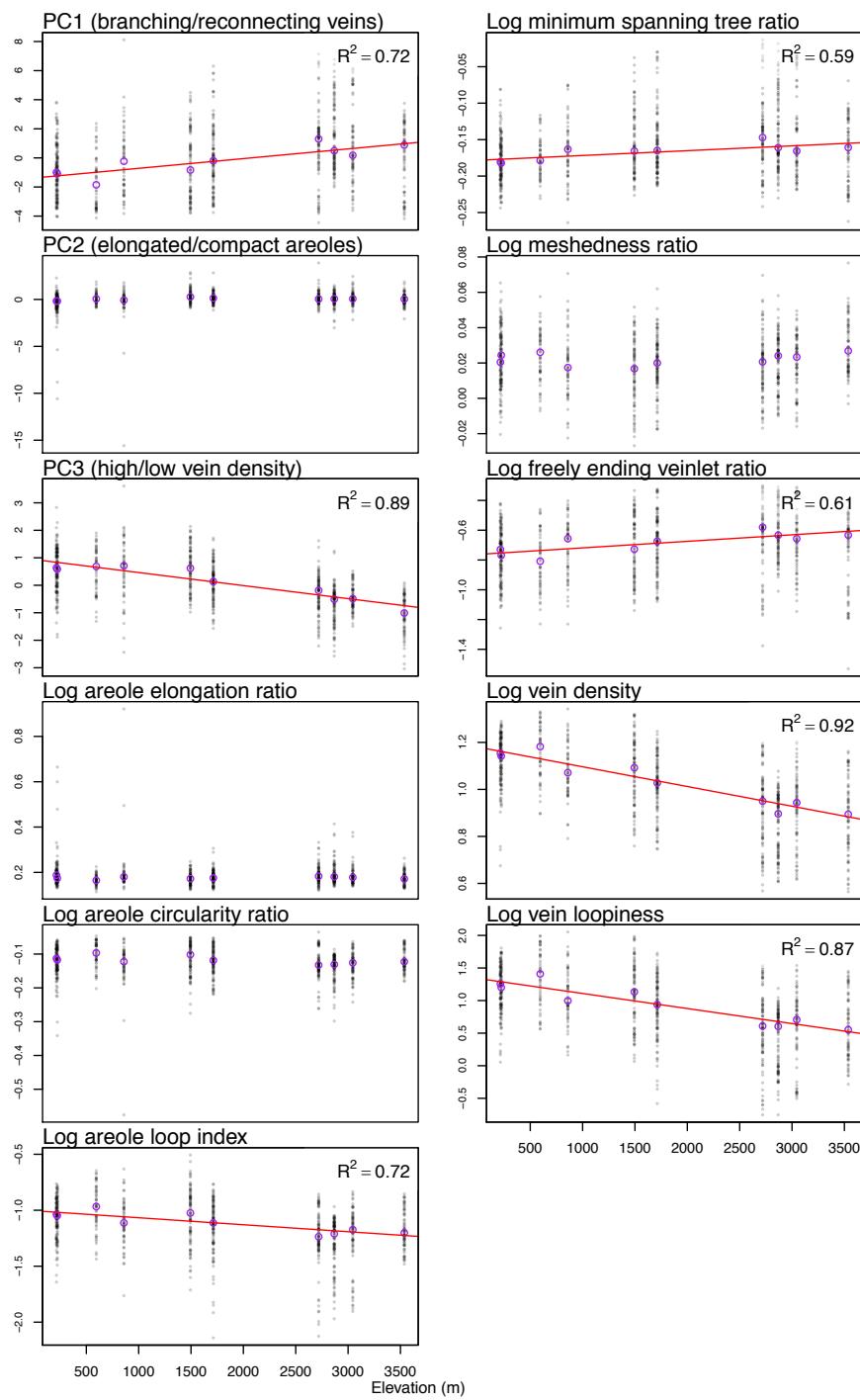


Figure S7. Posterior distribution of fixed effects for Bayesian GLMM models of reticulation principal components for the non-palm angiosperms. The analysis is scaled such that a value of +1 indicates that a 1 standard deviation change in a predictor results in a 1 standard deviation change in the reticulation principal component, after accounting for all phylogenetic effects and hierarchical structure in the data. Distributions are concatenated across ten resampled imputations of the dataset. Significant fixed effects are highlighted in dark blue and otherwise shown in light gray. Estimates are shown for **A) PC1**, **B) PC2**, and **C) PC3**.

