List of supplementary tables

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Table S1. Substitution models selected for 13 Antarctic terrestrial taxa using jModelTest.

Taxa	Model
Acutuncus	TrN+I
Alaskozetes	TrN+I+G
Bryum	HKY+I
Colobanthus	K80
Cryptopygus	GTR+G+I
Deschampsia	TIM2+I
Friesea	TIM2+G
Gomphiocephalus	GTR+G
Halozetes	GTR+G+I
Schistidium	F81
Stereotydeus	GTR+G+I
Umbilicaria	TPM1uf
Usnea	HKY K80

Table S2. Summary table of Generalised linear models of 14 environmental predictors and seven genetic diversity indices of 13 major Antarctic terrestrial taxa. Models were selected by stepwise AIC. Latitude (y) was added as a predictor to model high-level spatial autocorrelation amongst sites. Taxa and number of sequences were added as random factors.

See Tables S2-S4.xlsx

Table S3. Summary table of Generalised linear models of 14 environmental predictors and seven genetic diversity indices of 7 major Antarctic terrestrial fauna. Models were selected by stepwise AIC. Latitude (y) was added as a predictor to model high-level spatial autocorrelation amongst sites.

See Tables S2-S4.xlsx

Table S4. Summary table of Generalised linear models of 14 environmental predictors and seven genetic diversity indices of 6 major Antarctic terrestrial flora. Models were selected by stepwise AIC. Latitude (y) was added as a predictor to model high-level spatial autocorrelation amongst sites.

See Tables S2-S4.xlsx

Table S5. Summary statistics of mantel tests for 13 Antarctic terrestrial taxa. Significant values in bold. NA values were of *Gomphiocephalus* were due to having two populations. Other NA values were as a result of no difference in alleles in some populations.

	Nei R	Nei P	Hedrick R	Hedrick P	Jost R	Jost P
Acutuncus antarcticus	0.161	0.662	0.684	0.333	0.736	0.325
Alaskozetes antarcticus	0.666	**0.003**	0.289	0.170	0.293	0.165
Halozetes spp.	-0.150	0.772	0.244	0.125	0.292	0.084
Stereotydeus spp.	NA	NA	NA	NA	NA	NA
Cryptopygus spp.	0.078	0.201	0.178	**0.002**	0.177	**0.002**
Friesea griesea	-0.341	0.663	0.861	0.042	0.316	0.410
Gomphiocephalus spp.	NA	NA	NA	NA	NA	NA
Bryum argenteum	0.174	0.170	0.384	**0.021**	0.385	**0.020**
Schistidium atarctici	NA	NA	NA	NA	0.125	0.233
Deschampsia antarctica	0.347	0.294	0.978	**0.041**	0.960	**0.040**
Colobanthus quitensis	NA	NA	NA	NA	-0.119	0.763
Umbilicaria spp.	0.430	0.067	0.599	**0.013**	0.628	**0.011**
Usnea spp.	-0.098	0.635	0.024	0.431	0.048	0.400

Table S6. Global and local scores of Spatial Components Analysis (sPCA) for *Halozetes* spp.

	Observation	**Simulated p-value**	**Std.Obs**	**Expectation**	**Variance**
Global Score	0.297	0.008	1.950	0.187	0.003
Local Score	0.192	0.854	-1.061	0.286	0.008

Table S7. Observed and rarefied haplotype richness of 13 Antarctic terrestrial taxa by region.

Tables S7-S9.xlsx

Table S8. Observed and rarefied haplotype richness of 13 Antarctic terrestrial taxa by genus.

Tables S7-S9.xlsx

Table S9. Summary table of Generalised linear models of nine environmental predictors and haplotype richness of 13 major Antarctic terrestrial taxa. Models were selected by stepwise AIC. Latitude (y) was added as a predictor to model high-level spatial autocorrelation amongst sites. Response variables include observed haplotype richness, rarefied haplotype richness and its lower and upper confidence limit values.

Tables S7-S9.xlsx

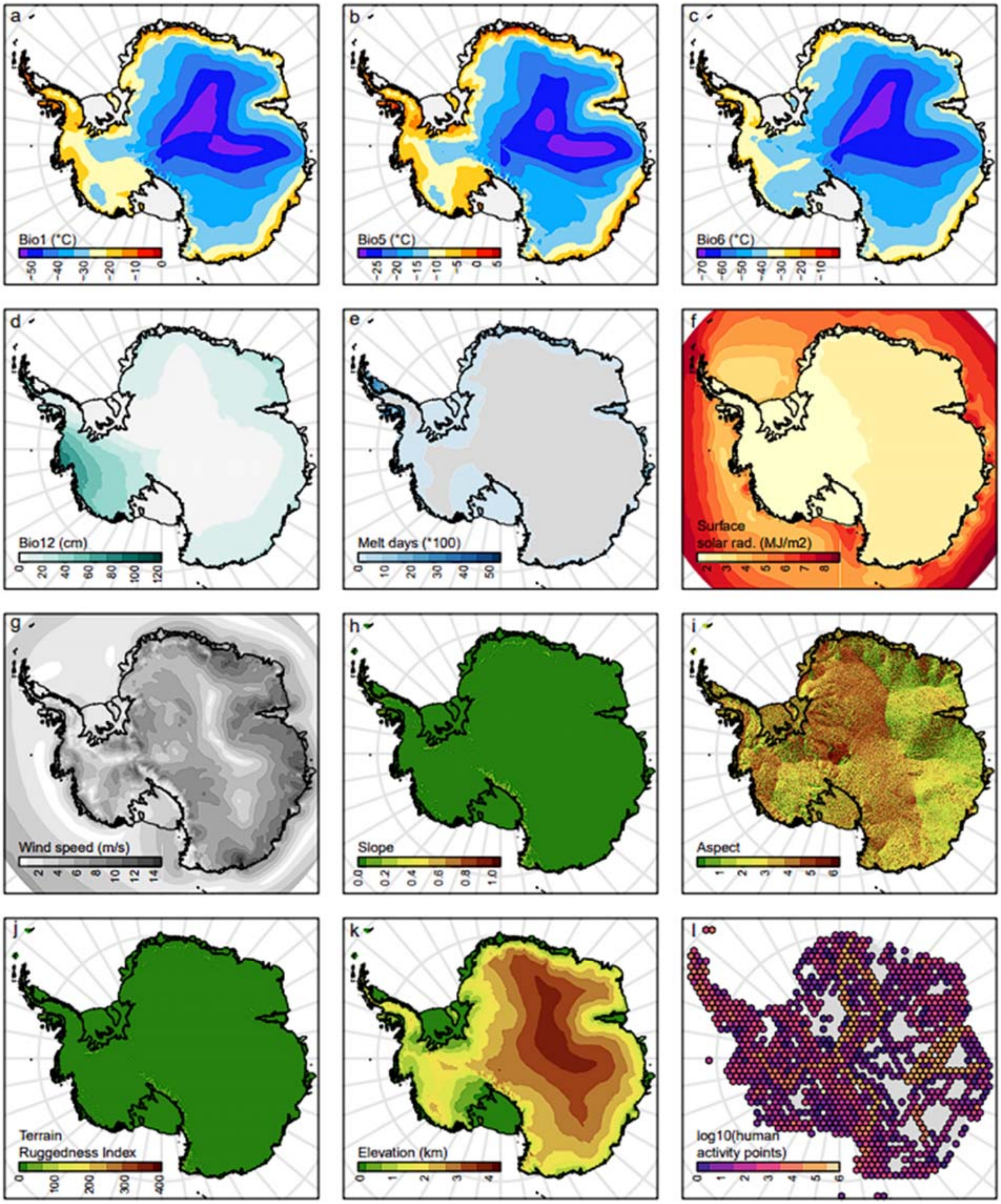


Figure S1. Maps of 12 environmental variables used in generalised linear models of terrestrial Antarctica genetic diversity.

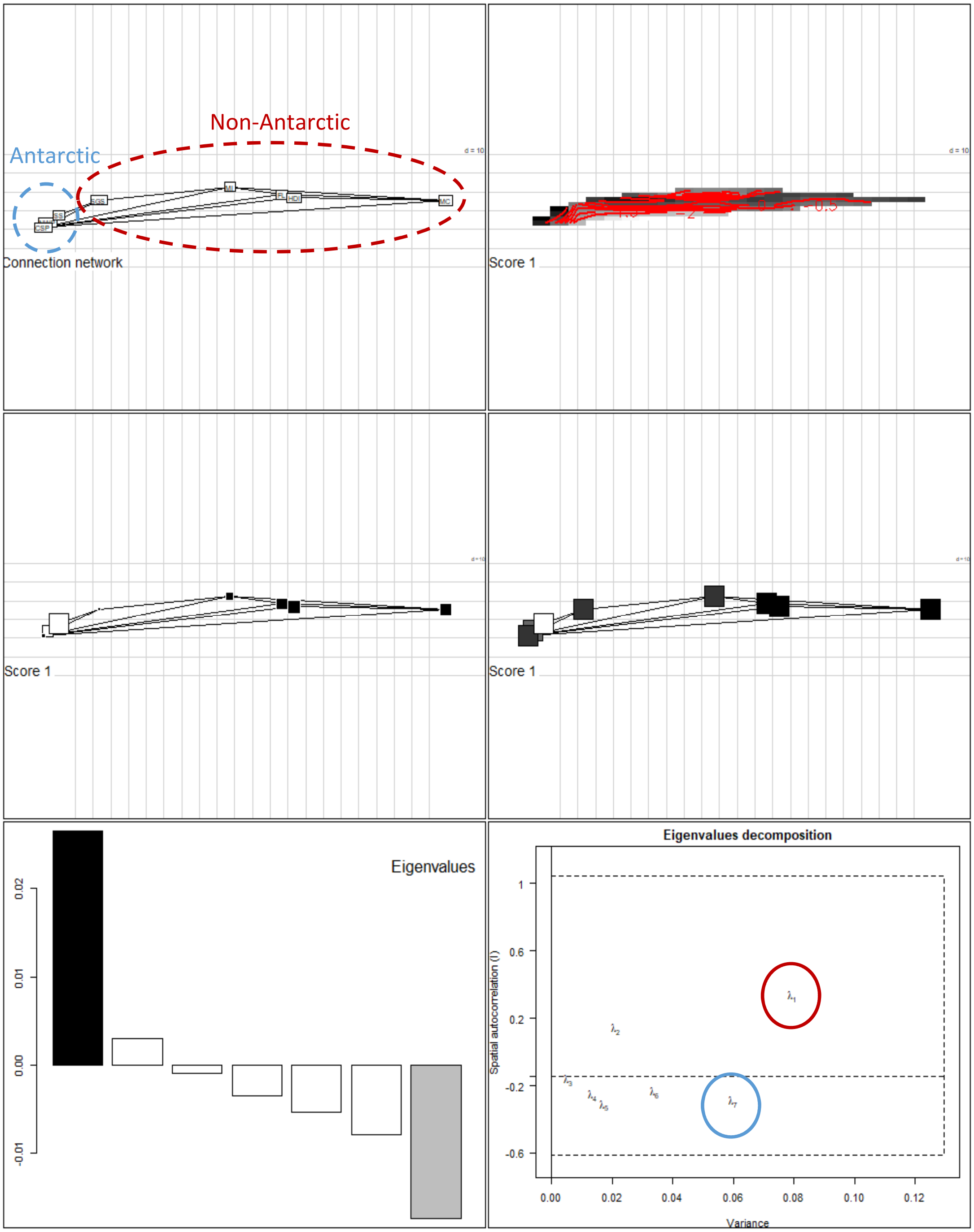


Figure S2. Results from Spatial Components Analysis (sPCA) of *Halozetes* spp. Plot a defines spatial weightings of regions through connection network. Plot b shows local interpolation of scores with distances of counter lines representing genetic differentiation (steeper differentiation, closer lines). In plot c, sizes of squares represent size of genetic differentiation, while colours represent two groups of regions by genetic differences. Plot d shows genetic differentiation by grey levels. Plots e and f represent global (positive spatial autocorrelation using Moran's index) and local (negative spatial autocorrelation) scores of PCA eigenvalues. In plot f, λ_1 (red circle) represents the highest positive score while λ_7 (blue circle) represents the highest negative score.

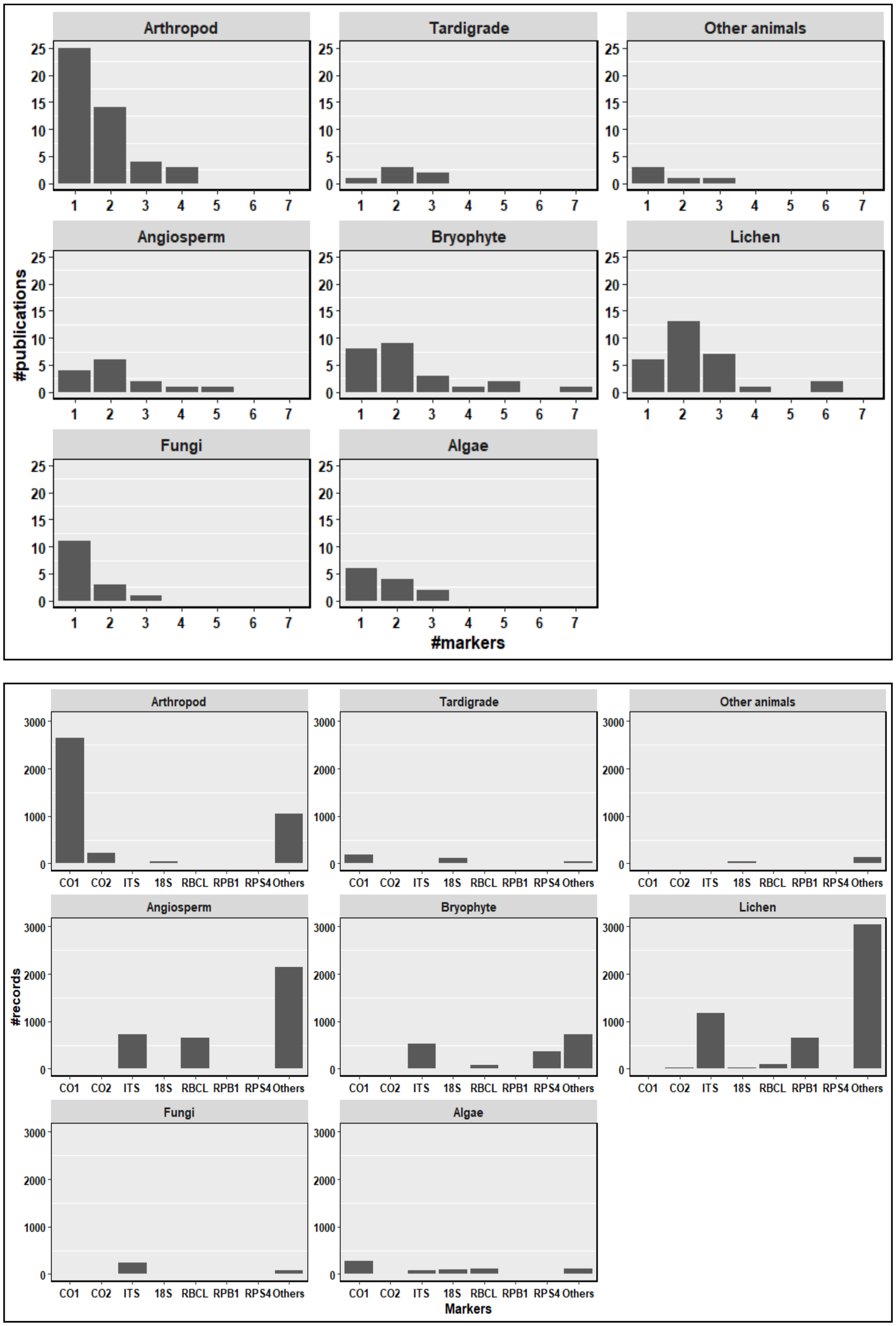
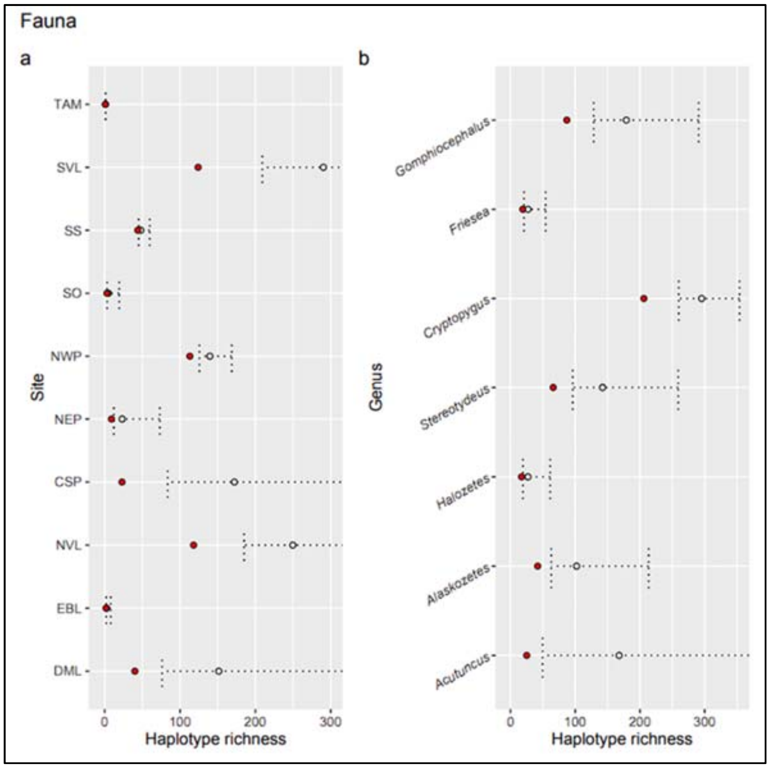


Figure S3. Bar graphs showing number of genetic markers and number of publications in each Antarctic terrestrial taxon among 153 studies (upper), as well as number of different marker types in each Antarctic terrestrial taxon among 7222 records of a total of 71 genetic different genetic regions (lower).



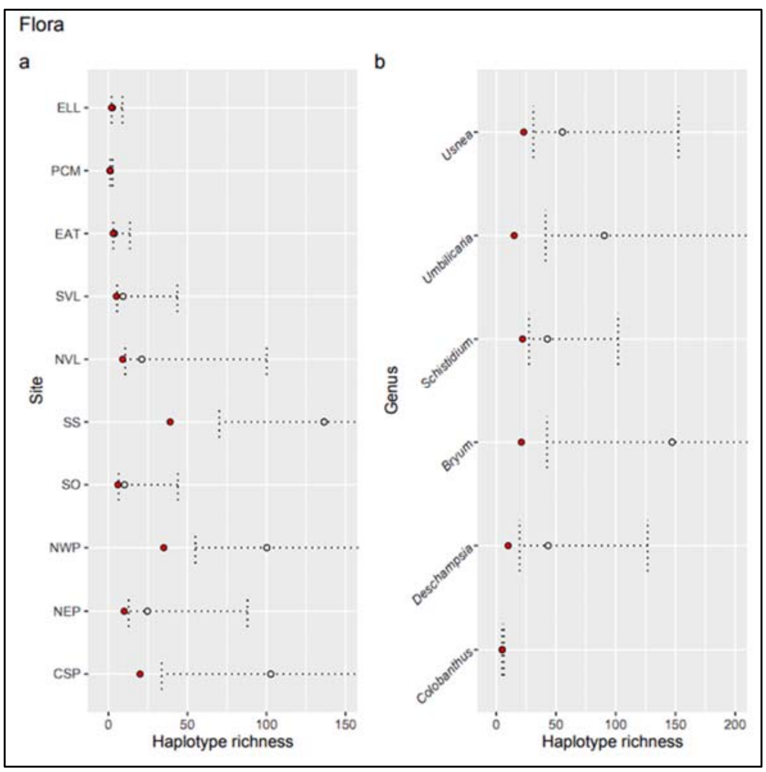


Figure S4. Plots showing rarefied haplotype richness of major taxa of Antarctic terrestrial fauna (upper) and flora (lower) by population regions (a) and genus (b). Red circles were observed haplotype richness, white circles were estimated haplotype richness. Lines were lower and upper confidence limits of estimated richness.