

Supplementary material

Table S1. Values for models fitted for the relationship between latitudinal centre and log10(area). Observed values are calculated as coefficients from the model area vs. linear and squared term of latitudinal centre. P values indicate if the slopes of the terms were significant. For reptiles, since the quadratic term was not significant, area was fitted to the linear term of latitudinal centre only. R² values indicate the explained variance for the full models. For the setup of null model simulations, see text.

	Observed values						Null model simulations		
	Intercept	Slope	p	Slope ^{2*}	p ^{2*}	R ²	Intercept	Slope	Slope ^{2*}
Fishes	-14.7	0.76	<0.001	-0.0067	<0.001	0.43	-5.14	0.41	-0.0037
Amphibians	-9.12	0.59	0.015	-0.0056	0.003	0.25	-6.61	0.47	-0.0042
Reptiles	1.79	0.099	<0.001			0.58	-5.02	0.41	-0.0037
Mammals	-14	0.75	0.009	-0.0068	0.003	0.42	-5.03	0.41	-0.0037
Mammals and birds	-15.3	0.8	<0.001	-0.0073	<0.001	0.52	-3.83	0.36	-0.0032
Birds	-17.1	0.89	<0.001	-0.0085	<0.001	0.34	-3.94	0.36	-0.0032

* Values for the squared term of latitudinal centre.

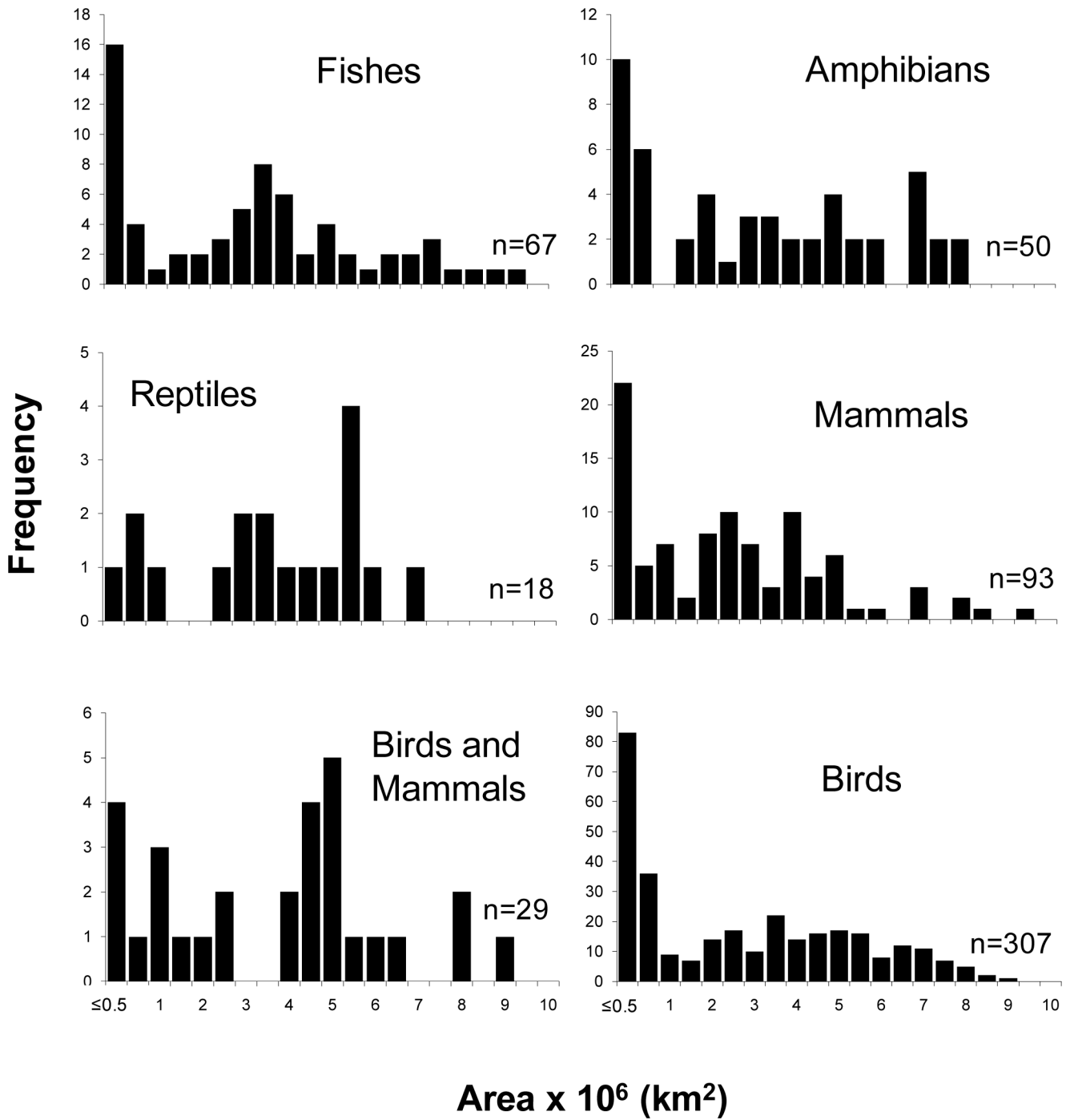


Figure S1. Frequency distribution of range sizes (area) of European freshwater trematodes utilising different types of definitive hosts. Numbers of trematode species in each host group are shown.

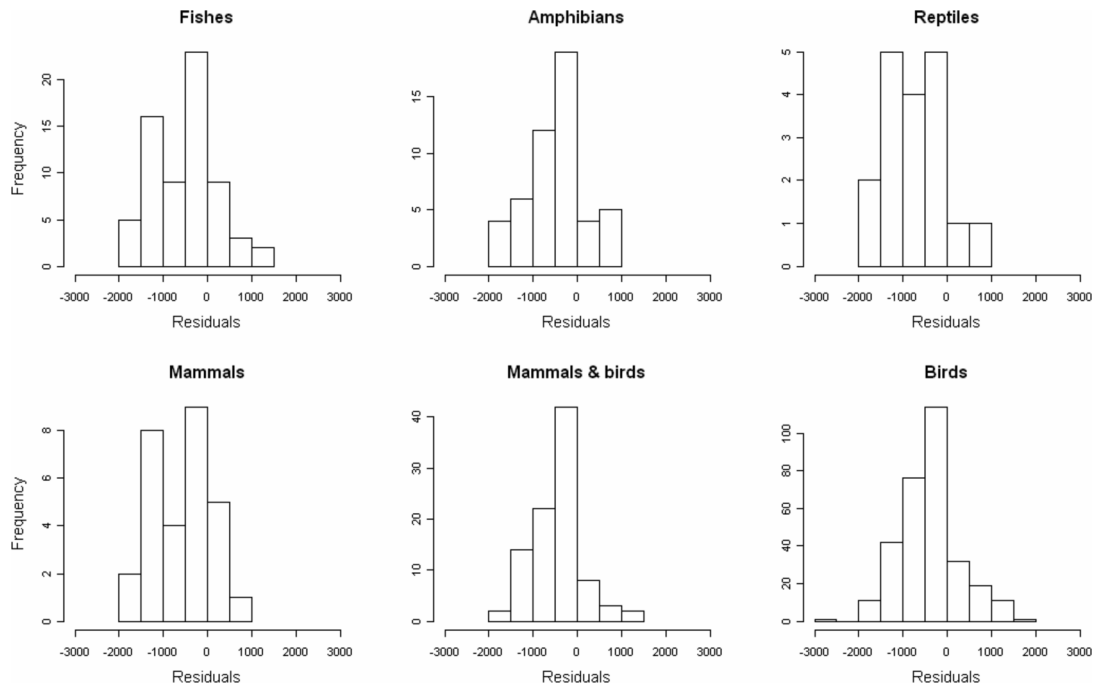


Figure S2. Frequency distributions of the residuals of the observed values of north-south vs east-west extent against the line fitted from the null model simulations. Negative values are those that fall below the null model line, i.e. that have a larger east-west than north-south extent than expected from the geographic shape and extent of the European continent and the biogeographic regions. Positive values are those that fall above the null model line