

Appendix: GLMM Model Results

The following are the model average outputs from model.avg call of the MUMIn package in R software, as described in the text. For each averaged model, we report the parameter estimates, their standard errors, Z values and corresponding p-values. Bolded entries in the tables were reported in the text. Asterisks indicate level of significance: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

S3 Table. Proportion of arthropod biomass.

	Estimate	Std. Error	Adjusted SE	z value	Pr(> z)
(Intercept)	0	0	0	NA	NA
Trap_heightmid	-0.284	0.4206	0.4238	0.67	0.50279
Trap_heighthigh	-1.1949	0.4438	0.4471	2.672	0.00753 **
Rat_Removaluntreated:Trap_heightlow	-0.3952	0.2988	0.3011	1.312	0.18935
Rat_Removaluntreated:Trap_heightmid	-0.6393	0.3609	0.3631	1.761	0.07825 .
Rat_Removaluntreated:Trap_heighthigh	1.035	0.5908	0.5922	1.748	0.08052 .
Rat_Removaluntreated	-0.332	0.2515	0.2534	1.31	0.19016
Rat_Removaltreated:Trap_heightmid	-0.1354	0.2007	0.2022	0.67	0.50299
Rat_Removaltreated:Trap_heighthigh	-0.599	0.2224	0.2241	2.673	0.00752 **
log(Area_ha)	-0.0388	0.1457	0.1468	0.264	0.79157

Relative variable importance: Rat_Removal:Trap_height Rat_Removal Trap_height log(Area_ha)

Importance:	1	0.73	0.64	0.19
N containing models:	5	5	4	3

*Trap height: categorical variable with 3 levels ("low" used as reference level). Rat_Removal: categorical variable with 2 levels ("untreated" used as reference level).