

Supplementary Information

Appendix S1: Summary of abundance for each invertebrate family observed for all combinations of study site and habitat type: D = Douglas fir plantation; D/BI = Douglas fir/beech interface; B = beech forest.

Order	Family	Rankleburn Forest			Burnt Face			Hira Forest		
		B	D	D/BI	B	D	D/BI	B	D	D/BI
Amphipoda	Talitridae	34	105	21	0	0	0	55	58	36
Crassiclitellata	Megascolecidae	0	1	1	3	2	0	1	0	0
Araneae	Agelenidae	0	0	2	0	0	0	0	0	0
Araneae	Amphinectidae	16	17	14	4	4	5	29	7	13
Araneae	Clubionidae	0	1	1	0	0	1	0	0	0
Araneae	Cycloctenidae	11	21	12	7	1	7	35	18	27
Araneae	Huttonidae	0	1	1	0	0	0	0	0	0
Araneae	Linyphiidae	0	0	0	3	0	15	0	0	0
Araneae	Micropholcommatidae	0	1	1	0	0	1	4	2	3
Araneae	Nemesiidae	0	0	2	0	0	0	0	0	0
Araneae	Salticidae	0	0	0	1	0	0	0	0	0
Blattodea	Blattidae	0	0	0	0	0	1	0	0	0
Chilopoda	Chilopoda	0	0	1	0	0	0	1	1	0
Coleoptera	Carabidae	12	31	21	1	3	3	50	3	28
Coleoptera	Clambidae	0	0	0	0	0	0	1	0	0
Coleoptera	Curculionidae	0	5	1	2	0	1	1	2	5
Coleoptera	Elateridae	0	0	0	0	0	1	0	0	0
Coleoptera	Erotylidae	0	0	0	0	0	0	0	1	0
Coleoptera	Hydrophilidae	0	0	0	0	1	4	9	1	3
Coleoptera	Latridiidae	0	0	0	0	0	2	0	2	1
Coleoptera	Leiodidae	0	0	0	1	0	4	2	4	4
Coleoptera	Lucanidae	0	1	1	1	0	0	0	0	0
Coleoptera	Melandryidae	0	0	0	0	0	0	0	1	0
Coleoptera	Nitidulidae	0	0	0	0	0	0	0	1	0
Coleoptera	Scarabaeidae	0	1	0	1	2	1	22	0	4
Coleoptera	Staphylinidae	2	2	1	4	0	9	4	4	1
Coleoptera	Zopheridae	0	0	0	0	0	0	0	2	1
Collembola	Onychiuridae	52	30	7	46	1	78	38	88	373
Collembola	Sminthuridae	0	0	1	2	4	0	7	4	1
Collembola	Tomoceridae	11	10	12	21	13	87	40	39	38
Diplopoda	Dalodesmidae	1	1	1	12	14	7	4	5	2
Diplopoda	Sphaerotheriidae	0	1	0	0	0	0	4	0	3
Diplopoda	Spirobolidae	1	1	0	0	3	2	0	0	0
Diptera	Calliphoridae	0	0	0	0	1	1	0	0	0
Diptera	Chironomidae	0	0	0	1	0	0	0	0	0
Diptera	Mycetophilidae	0	0	0	0	1	0	0	0	0
Diptera	Sciaridae	2	0	0	6	2	7	0	0	0
Diptera	Simuliidae	0	0	0	11	1	25	4	19	2
Diptera	Syrphidae	0	0	0	0	0	0	12	165	9
Diptera	Tanyderidae	0	0	0	0	0	0	0	1	0
Diptera	Tipulidae	11	0	6	5	8	12	8	21	0
Hemiptera	Lygaeidae	0	0	0	4	0	8	0	0	0
Hymenoptera	Braconidae	1	0	0	10	1	24	1	2	1
Hymenoptera	Diapriidae	0	0	0	0	0	3	0	0	0
Hymenoptera	Formicidae	2	0	0	1	0	0	11	0	3
Hymenoptera	Ichneumonidae	2	0	0	0	0	5	0	0	0
Hymenoptera	Pteromalidae	1	0	0	0	0	0	0	0	0
Isopoda	Oniscidae	0	2	1	0	0	0	0	0	0
Isopoda	Styloniscidae	1	2	1	0	0	0	2	2	13
Stylommatophora	Punctidae	1	1	0	0	1	0	1	3	0
Opiliones	Triaenonychidae	1	0	0	3	3	8	7	1	5
Orthoptera	Gyrillidae	1	0	0	0	0	1	0	0	1
Orthoptera	Stenopelmatidae	1	2	2	1	1	0	3	0	0
Orthoptera	Anostostomatidae	4	3	0	0	0	0	0	0	0
Pseudoscorpionida	Neobisiidae	0	0	0	0	0	0	1	0	0

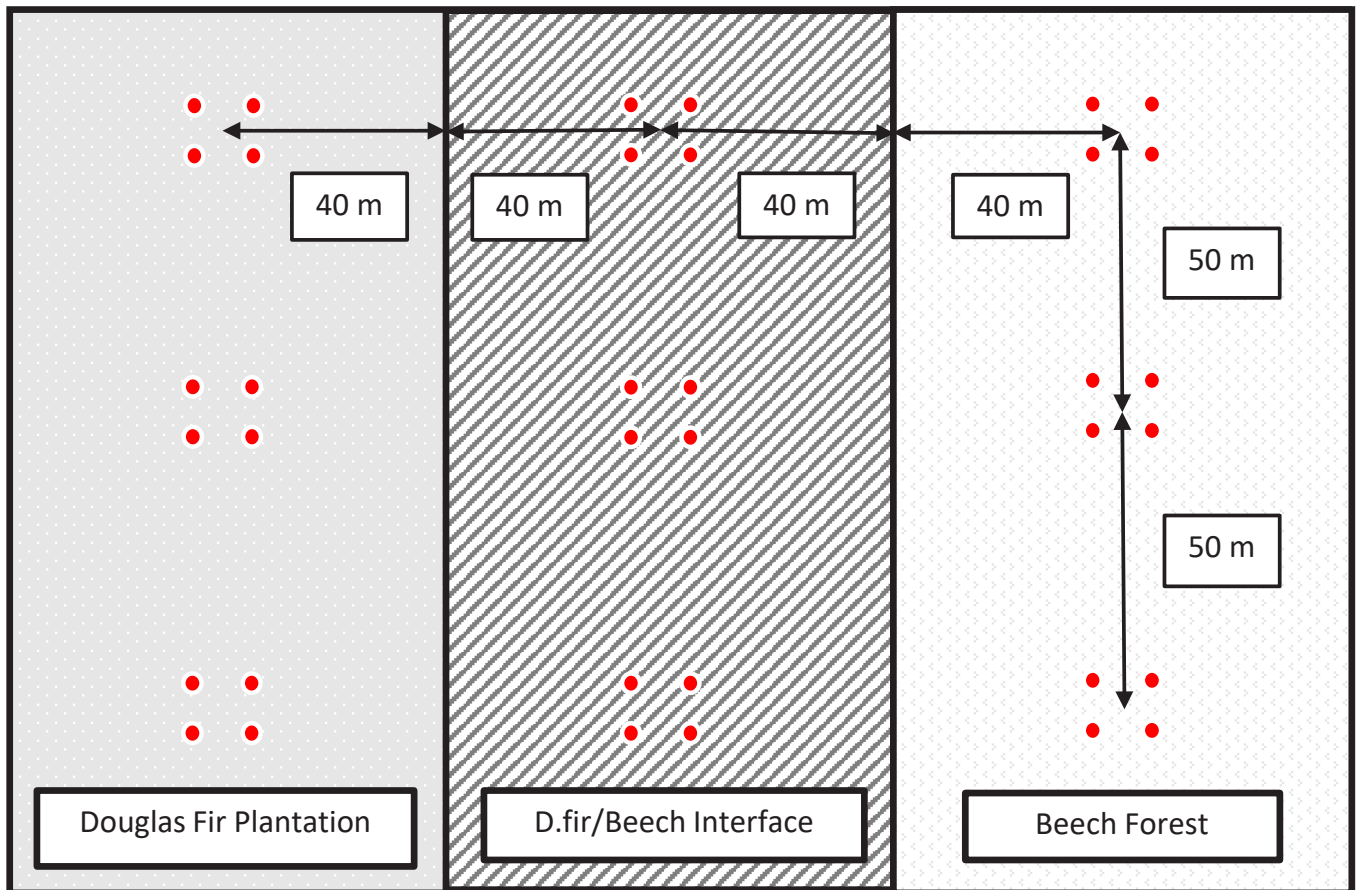
Appendix S2: Coefficients of three generalized linear mixed-effects models used to determine changes in the abundance, richness (number of families) and diversity (Shannon-Wiener family diversity) of invertebrates across habitat types (Douglas fir plantation, Douglas fir/beech forest interface, beech forest). All models included site as a random factor. We used a negative binomial error distribution for the invertebrates' abundance model (Z-values), Poisson error distribution for the richness model (Z-values) and Gaussian for the diversity model (t-value). Bold values indicate significant results ($\alpha = 0.05$).

Response variable	Predictors	Estimate \pm SE	Z/t-value	P value
Abundance	Intercept	5.413 \pm 0.345	15.581	< 0.001
	Douglas fir/beech interface	0.312 \pm 0.384	0.813	0.416
	Beech forest	-0.07 \pm 0.375	-0.188	0.851
Family richness	Intercept	3.135 \pm 0.120	26.045	< 0.001
	Douglas fir/beech interface	0.070 \pm 0.167	0.418	0.676
	Beech forest	0.056 \pm 0.168	0.336	0.737
Diversity	Intercept	2.191 \pm 0.216	10.136	< 0.001
	Douglas fir/beech interface	-0.067 \pm 0.304	-0.221	0.833
	Beech forest	0.266 \pm 0.304	0.876	0.415

Appendix S3: Coefficients of six generalized linear mixed-effects models used to determine changes in the abundance, family richness (number of families) and Shannon-Wiener family diversity of predators and parasitoids across habitat types (Douglas fir plantation, Douglas fir/beech interface, beech forest). All models included site as a random factor. We used Poisson error distribution for the abundance and richness models (Z-values), and Gaussian error distribution for the diversity models (t-value). ^a = indicates that negative binomial distribution (Z-values) was used instead of Poisson distribution, to account for over dispersion. Bold values indicate significant results ($\alpha = 0.05$).

Trophic group	Response variable	Predictors	Estimate \pm SE	Z/t-value	P value
Predators	Abundance ^a	Intercept	3.436 \pm 0.428	8.021	< 0.001
		Douglas fir/beech interface	0.478 \pm 0.413	1.158	0.247
		Beech forest	0.428 \pm 0.416	1.030	0.303
	Richness	Intercept	1.540 \pm 0.267	5.764	< 0.001
		Douglas fir/beech interface	0.305 \pm 0.352	0.867	0.386
		Beech forest	$-1.2 \times 10^{-15} \pm 0.378 \times 10^{-15}$	0.000	1.000
	Diversity	Intercept	1.127 \pm 0.094	11.946	< 0.001
		Douglas fir/beech interface	0.265 \pm 0.133	1.987	0.094
		Beech forest	0.111 \pm 0.133	0.833	0.436
Parasitoids	Abundance	Intercept	-0.639 \pm 0.890	-0.718	0.473
		Douglas fir/beech interface	2.398 \pm 0.596	4.023	< 0.001
		Beech forest	1.609 \pm 0.625	2.575	0.010
	Richness	Intercept	-0.405 \pm 0.707	-0.573	0.566
		Douglas fir/beech interface	0.693 \pm 0.866	0.800	0.423
		Beech forest	0.916 \pm 0.837	1.095	0.273
	Diversity	Intercept	0.000 \pm 0.244	0.000	1.000
		Douglas fir/beech interface	0.243 \pm 0.345	0.702	0.509
		Beech forest	0.347 \pm 0.345	1.003	0.354

Appendix S4: Schematic diagram of each sampling site. Each site (three sites in total sampled across the South Island of New Zealand) comprised a Douglas fir plantation adjacent to a native beech forest. To sample invertebrate communities across the gradient from Douglas fir to native beech forest interior, twelve pitfall traps (arranged in 3 groups of 4 pitfall traps each identified by a red circle) were placed in each of three habitat types: Douglas fir plantation, Douglas fir/beech interface and beech forest).



Appendix S5: Abundance of predator and parasitoid taxa across habitat types: D = Douglas fir forest; D/BI = Douglas fir/ beech interface; B = beech forest.

