A

Aphis farinosa abundance vs. Willow genotype (G, U, S, X, J, I, F, L, T, W)

B

Formica obscuripes abundance vs. Aphid treatment (Aphids, None)

C

Plant height (cm) vs. Willow genotype (G, U, S, X, J, I, F, L, T, W)

D

Trichome density (no. cm^{-2}) vs. Aphid treatment (Aphids, None)

A

Arthropod richness
$R^2 = 0.14$

Trait PC2
$R^2 = 0.23$

Trait PC1
$R^2 = 0.12$

Willow genotype

-0.10
0.36
0.38
0.23
0.47
0.39

B

Arthropod abundance
$R^2 = 0.06$

F. obscuripes abund.
$R^2 = 0.18$

Trait PC2
$R^2 = 0.23$

Trait PC1
$R^2 = 0.12$

A. farinosa abund.
$R^2 = 0.19$

Aphid treatment

Ant mound distance

Willow genotype

0.13
0.19
0.43
0.19
0.28
0.47
0.44
0.23
0.39

C

Rarefied richness
$R^2 = 0.01$

F. obscuripes abund.
$R^2 = 0.18$

A. farinosa abund.
$R^2 = 0.19$

Aphid treatment

-0.10
0.43
-0.18
0.44

D

RDA 2 (1%)

RDA 1 (2%)

Cicadellidae
Trait_PC1
Trait_PC2
Spider
Tortricidae
Gelechiidae
Miridae
Gracillariidae
F_obscuripes_abund
Orthoptera
Syrphidae
Aphididae
A_farinosa_abund
Formica_ant

0.8
0.4
0.0
-0.4
-0.5
0.0
0.5
1.0

A Arthropods

B Mycorrhiza

C Bacteria

Figure Legends

Figure 1. Responses of the arthropod community to genetic variation within the willow *Salix hookeriana*, the addition of the aphid *Aphis farinosa*, and proximity to mounds of the ant *Formica obscuripes*. We found that willow genotype influenced both the total richness (A) and abundance (B) of arthropods. Arthropod abundance was also influenced by the addition of aphids, but only at the furthest distances from ant mounds (C). The addition of aphids reduced the probability of encountering a different arthropod species (rarefied richness) by 16% across all treatments (D). We also found that the addition of aphids modified the effect of willow genotype on the composition of the arthropod community (E). This interaction between willow genotype and aphid treatment was solely due to the differential effect of genotype J on the abundance of non-*A. farinosa*

aphids in the aphid treatment (F). Symbols and error bars correspond to the response variable's mean ± 95% confidence interval. We calculated mean and confidence intervals based on the full models (Table 1) using the '*effects*' package in R. Black squares correspond to the effect of willow genotype after controlling for other treatments, while grey diamonds and white circles represent the aphid treatment and control, respectively.

Figure 2. Variability in ant-aphid interactions and plant traits explained by genetic variation within the willow *Salix hookeriana*, the addition of the aphid *Aphis farinosa*, and distance from mounds of the ant *Formica obscuripes*. In the aphid treatment, we found that willow genotype influenced the abundance of the aphid *Aphis farinosa* (A). The effect of willow genotype on *A. farinosa* resulted in willow genotype determining the abundance of the ant *Formica obscuripes*, but only in the aphid treatment (B). Plant height was solely determined by willow genetic variation (C). In contrast, the aphid treatment modified the effect of willow genotype on leaf trichome density (D). Symbols and error bars correspond to the response variable's mean ± 95% confidence interval. We calculated mean and confidence intervals based on the full models (Table 1) using the '*effects*' package in R. Black squares correspond to the effect of willow genotype after controlling for other treatments, while grey diamonds and white circles represent the aphid treatment and control, respectively.

Figure 3. Statistical models of the processes mediating arthropod community assembly in the ant-aphid experiment. Piecewise structural equation models of arthropod richness (A), abundance (B), and rarefied richness (C). Colored and white boxes represent exogenous

and endogenous variables, respectively. Solid, single-headed arrows correspond to modeled pathways between predictor and response variables, and may be either positive (black) or negative (red). Grey, double-headed arrows denote variables with no direct relationship and that we assumed to be driven by the same underlying factor. For clarity, we only plotted paths with standardized coefficients > 0.10. Numbers next to all arrows represent the standardized path coefficient, which also corresponds to the thickness of arrows. (B) Redundancy analysis illustrating the effect of plant traits (Trait PC1 & PC2) on arthropod community composition (Hellinger-transformed = square root of proportional abundances of species found on each willow). Black and blue arrows correspond to plant traits and species, respectively, while grey dots represent the position of individual willow communities.

Figure 4. Arthropod community responses to wind exposure and genetic variation within the willow *Salix hookeriana*. We found that both wind exposure and willow genotype had strong, but independent effects on the arthropod community. Specifically, arthropod communities on wind-exposed willows had lower richness (A), abundance (C), and rarefied richness (E) compared to unexposed willows. Willow genotype had a strong effect on the richness (B) and abundance (D) of arthropods, but only a marginal effect on rarefied richness (F). Points and error bars correspond to the response variable's mean ± 95% confidence interval. We calculated mean and confidence intervals based on the full models (Table 2) using the '*effects*' package in R.

Figure 5. Community dissimilarity of foliar arthropods (A) as well as root-associated ectomycorrhiza (B) and bacteria (C) in response to wind exposure and genetic variation within the willow *Salix hookeriana*. Black text and grey ellipses correspond to the community centroid ± 95% confidence interval. Grey numbers denote blocks and each unique number is the community centroid for the plot within each block. Grey circles mark the location of individual willow communities in multivariate space. We calculated the locations of centroids ± 95% confidence interval and individual samples using redundancy analysis on Hellinger-transformed community data.

Figure 6. Variability in soil characteristics and plant traits explained by wind exposure and genetic variation within the willow *Salix hookeriana*. Wind exposure had marginal effects on both soil moisture (A) and Nitrogen availability (B). The negative effect of wind exposure on plant height was magnified in the second year of the experiment (C); however, plant height still varied ~2-fold among the most disparate willow genotypes (D). Willow genotype was a good predictor of leaf C:N (E), but a poor predictor of root C:N (F). Symbols and error bars correspond to the response variable's mean ± 95% confidence interval. We calculated mean and confidence intervals based on the full models (Table 2) using the '*effects*' package in R.

Figure 7. Statistical models of the processes mediating community assembly in the wind experiment. (A) Piecewise structural equation model of the richness of foliar arthropods as well as root-associated ectomycorrhiza and bacteria. Colored and white boxes represent exogenous and endogenous variables, respectively. Solid, single-headed arrows

correspond to modeled pathways between predictor and response variables, and may be either positive (black) or negative (red). Grey, double-headed arrows denote variables with no direct relationship and that we assumed to be driven by the same underlying factor. For clarity, we only plotted paths with standardized coefficients > 0.10. Numbers next to all arrows represent the standardized path coefficient, which also corresponds to the thickness of arrows. (D) Redundancy analysis illustrating the effect of plant traits (Trait PC1 & PC2) on arthropod community composition (Hellinger-transformed = square root of proportional abundances of species found on each willow). Black and blue arrows correspond to plant traits and species, respectively, while grey dots represent the position of individual willow communities.