Supplementary Figure S1: Sampling sites in Canada; a) West Coast, b) the Atlantic Region, and c) Eastern Canada. Adapted from Google Earth.
Supplementary Figure S2: Upset plot to visualize a few types of trees that surrounded the sample traps (including the trees from which traps were suspended). The intersection size number represents the number of times a specific tree combination was found (similar to a Venn diagram), and the set size number corresponds to the number of samples surrounded by a specific type of tree. Most samples were collected from traps placed in forested areas comprising more than one tree species.
Supplementary Figure S3: Fungal species a) evenness (Shannon) and b) true diversity (Shannon) by semiochemical type, and oomycete species c) evenness (Shannon) and d) true diversity (Shannon) by semiochemical type. The ITS1 sequences were used. Pairwise comparison significance calculated with t tests (P value < 0.05 (α)). Different letters (wxy) show a significant difference between the boxplots compared whereas shared letters represent non-significantly different boxplots.

Supplementary Figure S4: Venn diagram of a) fungal species shared or unique to the semiochemical type employed in insect traps prior to species subtraction and b) oomycete species shared or unique to the semiochemical type employed in insect traps prior to species subtraction. All were obtained by amplifying the ITS1 genic region.

Supplementary Material S1: Semiochemicals' composition and additional details.
Each lure set (i.e., C₆C₈, UHR_E_AP, General Longhorn, and Pine Sawyer) was placed on separate traps.

First semiochemical set: C₆C₈.

The first combination (C₆C₈) consisted of racemic 3-hydroxyhexan-2-one (C₆) (Bedoukian Research Inc., Danbury, CT, USA), racemic 3-hydroxyoctan-2-one (C₈) (Bedoukian Research Inc.), and ultra-high release ethanol (UHR EtoH), where each chemical was placed within individual release devices. C₆ and C₈ were verified 99% pure by gas chromatography–mass spectrometry (GC-MS) by the Canadian Forest Service, and loaded into polyethylene pouches by Contech Inc (Delta, BC, Canada). Each pouch contained 1.4 g of either C₆ or C₈. The release rates (at 20°C) were 20 mg/d for C₆, and 25 mg/d for C₈. Two C₆ and two C₈ pouches (semiochemicals) were both placed on a trap to obtain cumulative release rates of 40 to 50 mg/d.

Second semiochemical set: UHR_E_AP.

The second semiochemical set (UHR_E_AP) consisted of UHR EtoH and UHR alpha-pinene. The two chemicals were loaded into separate release devices and placed on an insect trap. The UHR ethanol (95% purity, 121.5 g loaded/pouch) and UHR alpha-pinene [95% (+) enantiomer, 172 g/pouch] lures (Contech Inc., Delta, BC, Canada) had release rates (at 20°C) of 275 mg/d and 2 g/d, respectively. The UHR ethanol and UHR alpha-pinene chemicals were exactly the same throughout this project.

Third semiochemical set: General Longhorn.

The lure set consisted of UHR EtoH, (E)-6,10-dimethyl-5,9-undecadien-2-ol (E-fuscumol) and (E)-6,10-dimethyl-5,9-undecadien-2-yl (E-fuscumol acetate). Both E-fuscumol and E-fuscumol acetate were synthesized by Bedoukian Research Inc. and placed into polyethylene bubble caps by Contech Inc.; 130 mg/bubble cap of E-fuscumol (release rate = 1 mg/d), and 200 mg/bubble cap of E-fuscumol acetate (release rate = 2 mg/d).

Fourth semiochemical set: Pine Sawyer.

The Pine Sawyer lure set included four separate components consisting of 2-undecyloxy-1-ethanol (monochamol), UHR EtoH, UHR alpha-pinene and racemic 2-methyl-6-methylene-7-octen-4-ol (ipsenol). Monochamol (99.3% purity, 0.025 g/bubble cap) and racemic ipsenol (>99% purity, 0.04 g/bubble cap) were also purchased from Contech Inc. and had release rates (20°C) of 0.2 mg/d and 0.4 mg/d, respectively.

Supplementary Material S2: Fungal OTU, prior to species subtraction.

The most abundant fungi for all semiochemical treatments at the phylum, genus and species (top 10 per semiochemical) taxonomic levels are listed in Supplementary Table S4.

From the 2439 different species OTU detected prior to the species subtraction, 1057 (43%) were common to all semiochemical types, 228 species (9%) were unique to the UHR_E_AP semiochemical, 112 (4.6%) were unique to General Longhorn, 105 (4.3%) were unique to Pine Sawyer, and 118 (4.8%) were unique to the C₆C₈ semiochemical (Supplementary Figure S4a).
To visualize sampling depth, examples of the rarefaction curves obtained for the spore traps (negative control) and their respective original insect dataset, and subtracted insect dataset are shown in Supplementary Figure S5. The spore trap data demonstrated the highest sequencing depth as saturation was obtained for all of the samples tested with a sequence number per species ranging between approximately 5,000 and 25,000 (sequences). The lowest species number obtained by all samples tested was just below 150. In contrast, only part of the samples from both the original insect and the subtracted data reached saturation in their respective rarefaction curves.

**Supplementary Material S3: Oomycetes OTU, prior to species subtraction.**

The most abundant oomycetes for all semiochemical treatments at the phylum, genus and species (top 10 per semiochemical) taxonomic levels can be found in Supplementary Table S6. Prior to species subtraction, of the total 54 different OTU, there were 21 species detected in all semiochemical types but few were unique to each treatment (Supplementary Figure S4b). *Pythium monospermum* was unique to traps baited with the UHR_E_AP semiochemical. *Pythium oligandrum* was unique to traps baited with the Pine Sawyer semiochemical. Five species were unique to traps baited with the General Longhorn semiochemical (*Peronospora* sp. UPS F-119986, *P. flava*, *P. sparsa*, *Pythium carolinianum*, and *Phytophthora* spp.). No unique species were recovered from traps baited with the C6C8 semiochemical. Within the top ten most abundant species identified, all semiochemicals except C6C8 (0.67%) had a high percentage of *Peronospora manshurica* (Supplementary Table S6). The UHR_E_AP (26.1%) and C6C8 (26.6%) semiochemicals had a considerably higher number of OTU unclassified below genus compared with General Longhorn (traces) and Pine Sawyer (3.02%). Additionally, ATP9-NAD9 OTU from the original dataset generated prior to the species subtraction could only recover *Phytophthora* spp. from traps baited with the C6C8 and UHR_E_AP semiochemicals. *Phytophthora cryptogea* could only be detected from traps baited with the UHR_E_AP semiochemical, whereas *P. foliorum*, *Phytophthora* sp. “kelmania” [87] and *P. syringae* were associated with both C6C8 and UHR_E_AP lures.
### Supplementary Table S1: Summary of the samples collected from 2013 to 2015. Specific details associated with samples available upon request.

| Semiochemical<sup>a</sup>   | Year | Number of samples | Canadian provinces                                                                 |
|---------------------------|------|-------------------|------------------------------------------------------------------------------------|
| UHR_E_AP                  | 2013 | 13                | British Columbia, New Brunswick, Newfoundland and Labrador, Ontario and Quebec       |
|                           | 2014 | 26                | Ontario and Quebec                                                                 |
| CaCs                      | 2013 | 13                | British Columbia, New Brunswick, Newfoundland and Labrador, Ontario and Quebec       |
|                           | 2014 | 23                |                                                                                   |
| General Longhorn          | 2015 | 17                | British Columbia, New Brunswick, Newfoundland and Labrador, Ontario and Quebec       |
| Pine Sawyer               |      | 16                |                                                                                   |
| **Total:**                | 3    | **108**           | 5 Canadian provinces                                                               |

<sup>a</sup>UHR_E_AP = Combination of two semiochemicals (ultra-high release (UHR) ethanol and UHR alpha-pinene) that attract a wide range of bark and wood-boring insects [50,56,57].

CaCs = Combination of three semiochemicals (racemic 3-hydroxyhexan-2-one, racemic 3-hydroxyoctan-2-one, and UHR ethanol). The first two chemicals are aggregation pheromones of some longhorned beetles in the Cerambycinae subfamily [55] but, the addition of UHR ethanol increases attraction to other wood-boring insects.

**General Longhorn** = Combination of three semiochemicals (UHR ethanol, (E)-6,10-dimethyl-5,9-undecadien-2-ol (E-fuscumol), and (E)-6,10-dimethyl-5,9-undecadien-2-yl (E-fuscumol acetate)) used to attract Spondylidinae, Lamiinae, and Scolytinae beetles [58,59,72].

**Pine Sawyer** = Combination of four semiochemicals (2-undecyloxy-1-ethanol (monochamol), UHR ethanol, UHR alpha-pinene, and racemic 2-methyl-6-methylene-7-octen-4-ol (ipsenol)) used to attract longhorned beetles (*Monochamus*) and bark and ambrosia beetles due to the added ethanol and alpha-pinene [48,60,61].
**Supplementary Table S2:** Presence or absence of amplification as detected by gel electrophoreses using barcoded bidirectional PCR products from 108 environmental insect samples by targeted organisms, and the percentages of positive reactions obtained respectively with each bidirectional primer used.

| Primer used to append barcodes | Organism   | Target region | Positive PCR | Total PCR | Positive (%) |
|--------------------------------|------------|---------------|--------------|-----------|--------------|
| ITS1-Forward                   | Fungi      | ITS1          | 90           | 108       | 84           |
| ITS1-Reverse                   | Fungi      |               | 98           | 108       | 91           |
| ITS1-Forward                   | Oomycete   |               | 12           | 108       | 11           |
| ITS1-Reverse                   | Oomycete   |               | 12           | 108       | 11           |
| ATP9-NAD9- forward             | *Phytophthora* sp. | ATP9-NAD9 | 8            | 20        | 40           |
| **Total**                      | ...        | ...           | 220          | 452       | **Average: 47** |

*Each PCR included a set of primers but, as presented by Tremblay et al. [62], bidirectional sequencing required one primer per direction to append the sample and organism index (i.e., barcode).

*ITS1 = internal transcribed spacer 1 and ATP9-NAD9 = adenosine triphosphate synthase subunit 9-nicotinamide adenine dinucleotide dehydrogenase subunit 9 spacer.

*Percentage of the number of positive PCR over the total number of reactions done.
**Supplementary Table S3**: Exotic and native fungal species of interest that are unique to a semiochemical (i.e., post species subtraction), and grouped by the potential damage (= trophic status of concern) associated with those fungi. Also included is a risk level scale in terms of virulence. Identifications based on the ITS1 sequences obtained.

| Species                      | Known damage                           | Semiochemicals | Presence status | Risk level | Known host(s)                  | References |
|------------------------------|----------------------------------------|----------------|-----------------|------------|-------------------------------|------------|
| *Ambrosiella ferruginea*     | galleries and wounds caused by insect vector (mycangia) | x              | N, C            | 2          | conifers and deciduous trees  | [135]      |
| *Ciborisia whetzelii*        | anthracnose and ink spot disease       | x              | N, C            | 2          | aspen and cottonwood          | [136-138]  |
| *Colletotrichum fructi*      | anthracnose                            | x              | N               | 2          | grapevine, pepper, black locust, strawberry, water lily, apple, crab apple and protea | [139,140]  |
| *Colletotrichum nymphaeae*   | anthracnose, leaf spot, and bitter rot | x              | N               | 2          | citrus orthezia               | [141-144]  |
| *Devriesia americana*        | insect pathogen unknown                | x              | N               | 2[^1]      | citrus orthezia               | [145]      |
| *Devriesia strelitziiola*    | death of leaves                        | x              | E               | 2          | Strelitzia spp.               | [146,147]  |
| *Erysiphe adunca*            | death of leaves                        | x              | N, C            | 2          | Populus spp. and willow       | [148-151]  |
| *Erysiphe convolvuli*        | powdery mildew                         | x              | N, C            | 2          | Calystegia spp. and Convolvulus spp. | [94,152]  |
**Erysiphe cruciferarum** x N, C 2 mustard, cabbage, bok choy, and turnip soybean and legumes [153]

**Erysiphe diffusa** x N 2 flowering trees [154,155]

**Erysiphe elevata** x N 2 numerous plants in the Asteraceae family [156,157]

**Golovinomyces depressus** x E 2 wild basil, nettle, white turtlehead, and mint serviceberry, hawthorn, purple loosestrife, crab apple, apricot, cherry, plum, peach and spirea apple, and crab [102,136,158]

**Neoerysiphe galeopsidis** x N, C 2 [136,153,158,159]

**Podosphaera clandestina** x N, C 2 [102,136,158]

**Podosphaera leucotricha** x N, C 2 [102,136,153]

**Podosphaera lini** x E 2 flowering shrubs [127,152,160]

**Podosphaera negeri** x E 2 [127,152,161]

**Echinodontium tinctorium** heart rot and brown stringy rot blue stain and sapstain x N, C 3 hemlock, fir, and cedar [102,136,162,163]

**Leptographium sp.** needle cast x N, C 1? conifer and hardwood [104-108,164]

**Lirula macrosora** eyespot of cereal areolate mildew x N, C 3 spruce [136,165]

**Meria laricis** x N, C 3 larch [102,166]

**Mollisia dextrinospora** Mycosphaerella areola eyespot of cereal areolate mildew x E 2 cereals [167-169]

**Phaeoacremonium inflatipes** wilt and decline x N 1? [19,127,171-173]

**Phoma glomerata** blight, leaf spots, and fruit rot x N, C 2 cotton [127,170]

**Quercus spp., Nectandra spp., whitebeam, vine, and quince over 80 different plants** [127,136,174-176]
| Organism | Disease | Host | Source Codes |
|----------|---------|------|--------------|
| **Pucciniastrum circaeae** | rust | E | 2 | shrubs, fir and **Circaea** spp. | [127,177] |
| **Septoria gladioli** | leaf spot and hard rot | x | N, C | 2 | flowers and corn | [102,136,178] |
| **Siroccoccus conigenus** | shoot blight | x | N, C | 2 | pine, spruce, fir, and hemlock | [102,179,180] |
| **Siroccoccus piceicola** | shoot blight | x | N, C | 2 | spruce | [180,181] |
| **Stagonospora pseudopaludosa** | leaf spot | x | E | 3 | grass | [182] |
| **Teratosphaeria xenocryptica** | leaf spot | x | E | 2 | eucalyptus | [183,184] |
| **Phyllosticta minima** | sooty blotch | x | E | 3 | apple and vine | [187-189] |
| **Sirococcus conigenus** | sooty blotch | x | E | 3 | cherry | [190-192] |
| **Strelitziana mali** | sooty blotch | x | E | 3 | artichoke, tomato, spinach, lettuce, cauliflower, eggplant, pepper, and strawberry | [118,193] |
| **Verticillium isaacii** | sooty blotch | x | N | 2 | handsome fungus beetle | [194] |

**Loss of wood value**

| Organism | Disease | Host | Source Codes |
|----------|---------|------|--------------|
| **Donkioporia albidofusca** | white rot | x | U | 5 | decaying wood | [94,195] |
| **Melastiza chateri** | white rot | x | U | 5 | decaying wood | [94] |
| **Perenniporia luteola** | white rot | x | U | 5 | decaying wood | [196] |
| **Phlebiopsis sp.** | white rot | x | N, C | 5 | decaying wood | [197,198] |
| **Pleurotus ostreatus** | white rot | x | N, C | 5 | decaying wood | [102,136,138,158,199] |
| **Pluteus eludens** | white rot | x | U | 5 | decaying wood | [94] |
| **Pluteus phlebophorus** | white rot | x | U | 5 | decaying wood | [94] |
| **Ramaria pinicola** | white rot | x | U | 5 | decaying wood | [94] |
| **Steccherinum oreophilum** | white rot | x | N, C | 5 | decaying wood | [136,200] |
| **Trametes cubensis** | white rot | x | N | 5 | decaying wood | [94,201-203] |
| **Antrodia albobrunnea** | white rot | x | N, C | 5 | decaying wood | [204,205] |
| **Sidera lunata** | white rot | x | E | 5 | decaying wood | [94,206] |
| **Species**                      | **Common Name**          | **Status** | **VIRULENCE** | **Hosts**         | **Reference** |
|---------------------------------|--------------------------|------------|---------------|------------------|---------------|
| *Diatrype disciformis*          | beech barkspot           | x          | N, C          | 3                | [136,158,207] |
| *Hyphodontia microspora*        | other wood rots          | x          | E             | 5                | [208,209]     |
| *Phellinus ferruginovelutinus*   |                          |            | N, C          | 3                | [102,210,211] |

*C.Cs* = Racemic 3-hydroxyhexan-2-one (K6), racemic 3-hydroxyoctan-2-one (K8), and ultra-high release ethanol.

**General Longhorn** = Ultra-high release ethanol, (E)-6,10-dimethyl-5,9-undecadien-2-ol (E-fascumol), and (E)-6,10-dimethyl-5,9-undecadien-2-y1 (E-fascumol acetate).

**Pine Sawyer** = 2-undecyloxy-1-ethanol (monocharol), ultra-high release ethanol, ultra-high release alpha-pinene, and racemic 2-methyl-6-methylene-7-octen-4-ol (ipsenol).

b N = the organism is native or reported to be present in North America, C = the organism is native or reported to be present in Canada, E = the organism is not reported or present in North America (exotic), and U = unknown status because information is lacking for Canada and North America.

c Risk associated with the organism on a 1 to 5 scale. 5 = a riskless saprophyte fungus, 4 = a saprophyte fungus capable of causing damages to plants 3 = a weakly-virulent pathogenic fungus, 2 = a moderate virulent pathogenic fungus but common in Canada, and 1 = a highly-virulent pathogenic fungus.

d Assumption based on the impact of species within the same genus.

e Not applicable.

*UHR_E_AP* = Ultra-high release ethanol and ultra-high release alpha-pinene.
**Supplementary Table S4**: Operational Taxonomic Units: fungal identification proportion (%) by semiochemical type at the phylum, genus and species (Top 10) taxonomic level using the ITS1 genic region. Data obtained prior to species subtraction.

| Semiochemicala | UHR_E_AP | CsCs | General Longhorn | Pine Sawyer |
|----------------|----------|------|------------------|-------------|
| **Phylum**     |          |      |                  |             |
| Ascomycota     | 39.6     | 41.6 | 63.9             | 68.5        |
| Basidiomycota  | 39.5     | 40.9 | 24.2             | 23.0        |
| Unidentified OTU | 17.5  | 14.2 | 9.3              | 5.6         |
| OTU unclassified below |    |      |                  |             |
| kingdom        | 3.1      | 3.1  | 2.4              | 2.4         |
| Chytridiomycota | 0.3   | 0.1  | 0.1              | 0.2         |
| Zygomycota     | 0.1      | 0.1  | 0.1              | 0.2         |
| Glomeromycota  | tracesb  | 1.0  | traces           | traces      |
| Rozellomyctota | traces   | 0.5  | absent           | traces      |
| **Genus**      |          |      |                  |             |
| Unidentified OTU | 40.5  | 34.2 | 29.5             | 30.0        |
| Rhodotorula    | 10.0     | 11.0 | traces           | 3.2         |
| Cystobasidium  | 7.5      | 5.5  | traces           | traces      |
| Cryptococcus   | 4.3      | 4.1  | 5.5              | 6.1         |
| OTU unclassified below |    |      |                  |             |
| family         | 3.1      | 3.1  | 2.4              | 2.4         |
| Alternaria     | 2.9      | traces| traces          | traces      |
| Epicoccum      | 2.5      | 5.2  | 3.3              | 2.2         |
| Phoma          | 2.2      | 3.2  | traces           | traces      |
| Scopuloides    | 1.8      | traces| traces          | traces      |
| Verticillium   | 1.8      | 2.2  | traces           | traces      |
| Hannaella      | traces   | 2.3  | traces           | traces      |
| Wickerhamomyces | traces | 1.8  | traces           | traces      |
| Aureobasidium  | traces   | traces| 5.3             | traces      |
| Leptographium  | traces   | traces| 5.2             | 4.4         |
| Cladosporium   | traces   | traces| 3.9             | 7.3         |
| Neurospora     | traces   | traces| 3.2             | traces      |
| Kluyveromyces  | absent   | traces| 3.0             | traces      |
| Torulaspora    | traces   | traces| 2.3             | traces      |
| Candida        | traces   | traces| traces          | 8.0         |
| Mycosphaerella | traces   | traces| traces          | 3.1         |
| Geopyxis       | traces   | traces| traces          | 2.0         |
| **Species**    |          |      |                  |             |
| fungi sp.      | 17.5     | 14.2 | 9.3              | 5.6         |
| Rhodotorula mucilaginosa | 8.2   | 8.5  | tracesb          | 2.7         |
| Cystobasidium slooffiae | 6.4   | 3.3  | traces           | traces      |
| Species                        | C6C8 | C6C8 and General Longhorn |
|-------------------------------|------|---------------------------|
| **Ascomycota sp.**            | 5.3  | 4.5                       |
| OTU unclassified below genus  | 9.6  | 3.1                       |
| **Epicoccum nigrum**          | 2.5  | 5.2                       |
| **Alternaria alternata**      | 2.5  | traces                    |
| **Scopuloides hydnoides**     | 1.8  | traces                    |
| **Verticillium dahliae**      | 1.8  | 2.2                       |
| **Cystobasidium pinicola**    | traces| 2.2                       |
| **Hannaella luteola**         | traces| 1.9                       |
| **Wickerhamomyces anomalus**  | traces| 1.8                       |
| **Leptographium piriiforme**  | traces| traces                    |
| **Aureobasidium pullulans**   | traces| traces                    |
| **Cladosporium exasperatum**  | traces| traces                    |
| **Neurospora terricola**      | traces| traces                    |
| **Kluyveromycetes wickerhamii**| absent | absent | 2.9 | traces |
| **Torulaspora delbrueckii**   | absent| absent | 2.3 | traces |
| **Candida sp.**               | traces| traces                    |
| **Mycosphaerellaceae sp.**    | traces| traces                    |

\*UHR_E_AP – Ultra-high release ethanol and ultra-high release alpha-pinene.\n
\*C6C8 = Racemic 3-hydroxyhexan-2-one (K6), racemic 3-hydroxyoctan-2-one (K8), and ultra-high release ethanol.\n
**General Longhorn** – Ultra-high release ethanol, (E)-6,10-dimethyl-5,9-undecadien-2-ol (E-fuscumol), and (E)-6,10-dimethyl-5,9-undecadien-2-yl (E-fuscumol acetate).\n
**Pine Sawyer** – 2-undecyloxy-1-ethanol (monochamol), ultra-high release ethanol, ultra-high release alpha-pinene, and racemic 2-methyl-6-methylene-7-octen-4-ol (ipsenol).\n
\*Below 0.01% or not in the top 10 for this semiochemical.

**Supplementary Table S5**: Unique oomycete species detected in the different semiochemicals after proceeding with species subtraction and using the ITS1 genic region.

| Semiochemical\* | General Longhorn | C6C8 | C6C8 and General Longhorn |
|-----------------|------------------|------|---------------------------|
| Species         |                  |      |                           |
| **Peronospora farinosa** | **Pythium sp. CAL-2011e** | **Pythium sp. BG01** | |
| **Peronospora sp. isolate 079405,59** | | | **Pythium sp. P3862** |
| **Peronospora sp. UPS F-119986** | | | No blast hit |
| **Peronospora sparsa** | | | |
**Peronospora viciae**

**Pythium aff. hypogynum**

**Pythium sp. AvdB-2012**

**Pythium sp. BP2013k**

**Pythium sp. CAL-2011f**

**Pythium sp. P19300/1/3**

**Saprolegnia sp. SAP1**

| Total:        | 11 | 1 | 3 |
|---------------|----|---|---|

*a General Longhorn* = Ultra-high release ethanol, (E)-6,10-dimethyl-5,9-undecadien-2-ol (E-fuscumol), and (E)-6,10-dimethyl-5,9-undecadien-2-yl (E-fuscumol acetate).

CcCs = Racemic 3-hydroxyhexan-2-one (K6), racemic 3-hydroxyoctan-2-one (K8), and ultra-high release ethanol.

**Supplementary Table S6:** Operational taxonomic units: oomycete identification proportion (%) by semiochemical type at the phylum, genus and species (top 10) taxonomic levels using the ITS1 genic region.

| Semiochemicala | UHR_E_AP | CcCs | General Longhorn | Pine Sawyer |
|----------------|----------|------|------------------|------------|
| **Phylum**     |          |      |                  |            |
| Oomycota       | 73.9     | 73.4 | 99.9             | 96.9       |
| OTU unclassified | below kingdom | 26.1 | 26.6 | 0.01 | 3.02 |

| **Genus**      |          |      |                  |            |
| Peronospora    | 38.7     | 8.55 | 64.1             | 9.39       |
| OTU unclassified | below family | 26.1 | 26.6 | 0.01 | 0.30 |
| Phytophthora    | 18.4     | 46.5 | 16.3             | absent     |
| Pythium         | 13.1     | 14.4 | 17.5             | 0.14       |
| Hyaloperonospora| 1.90    | 2.68 | 0.87             | 0.15       |
| Plasmopara      | 1.72     | absent | 0.13          | absent     |
| Basidiophora    | 0.13     | 1.34 | 1.07             | 0.01       |
| Saprolegnia     | absent   | absent | tracesb         | traces     |

| **Species**    |          |      |                  |            |
| Peronospora    |          |      |                  |            |
| manshurica     | 26.7     | 0.67 | 61.3             | 84.9       |
| OTU unclassified | below genus | 26.1 | 26.6 | tracesb | 3.02 |
| Phytophthora sp. | 18.04 | 46.2 | 16.3             | traces     |
| Peronospora aestivalis | 8.20 | 2.82 | 1.36             | 1.47       |
| Species                        | C6    | C8    | C9    | C10   | C11   |
|-------------------------------|-------|-------|-------|-------|-------|
| Pythium sp. CAL-2011e         | 4.61  | 11.4  | NA$^c$| NA    | NA    |
| Pythium hypogynum             | 4.14  | 1.63  | traces| traces| traces|
| Peronospora alta              | 2.11  | 4.59  | 0.002 | 3.16  |       |
| Pythium sp. BG01              | 1.80  | NA    | 17.1  | NA    |       |
| Plasmopara viticola           | 1.72  | NA    | traces| traces| traces|
| Hyaloperonospora brassicae    | 1.42  | traces| 0.75  | 0.39  |       |
| Hyaloperonospora parasitica   | traces| 2.43  | 0.001 | 1.10  |       |
| Basidiophora entospora        | traces| 1.34  | 1.07  | traces|       |
| Pythium catenulatum           | NA    | 0.32  | 0.23  | traces|       |
| Peronospora polygoni          | 0.01  | traces| 0.49  | 2.95  |       |
| Peronospora variabilis        | traces| traces| 0.40  | 0.83  |       |
| Peronospora sepium            | traces| traces| 0.19  | traces|       |
| Pythium sp. 3862              | traces| traces| traces| 0.96  |       |
| Peronospora arthuri           | traces| NA    | traces| 0.29  |       |

$^a$UHR_E_AP = Ultra-high release ethanol and ultra-high release alpha-pinene.

$^b$GCs = Racemic 3-hydroxyhexan-2-one (K6), racemic 3-hydroxyoctan-2-one (K8), and ultra-high release ethanol.

$^c$General Longhorn = Ultra-high release ethanol, (E)-6,10-dimethyl-5,9-undecadien-2-ol (E-fuscumol), and (E)-6,10-dimethyl-5,9-undecadien-2-yl (E-fuscumol acetate).

$^d$Pine Sawyer = 2-undecyloxy-1-ethanol (monochamol), ultra-high release ethanol, ultra-high release alpha-pinene, and racemic 2-methyl-6-methylene-7-octen-4-ol (ipsenol).

$^e$Below 0.01% or not in the top 10 for this semiochemical.

$^f$Not applicable or not in the top 10 for this semiochemical.

Supplementary Figure S5: Rarefaction curves (number of sequences obtained for each species) for a) spore trap samples and their respective b) insect trap samples (original data), and c) insect trap samples (subtracted data) to visualize sequencing depth.