Supplementary Information for

The genome sequence of the grape phylloxera provides insights into the evolution, adaptation and invasion routes of an iconic pest

Claude Rispe*$, Fabrice Legeai*$, Paul Nabity, Rosa Fernández, Arinder K. Arora, Patrice Baa-Puyoulet, Celeste R. Banfill, Leticia Bao, Miquel Barberà, Maryem Bouallègue, Anthony Bretaudeau, Jennifer A. Brisson, Federica Calevro, Pierre Capy, Olivier Catrice, Thomas Chertemps, Carole Couture, Laurent Delière, Angela E. Douglas, Keith Dufault-Thompson, Paula Escuer, Honglin Feng, Astrid Forneck, Toni Gabaldón, Roderic Guigó, Frédérique Hilliou, Silvia Hinojosa-Alvarez, Yi-min Hsiao, Sylvie Hudaverdian, Emmanuelle Jacquin-Joly, Edward B. James, Spencer Johnston, Benjamin Joubard, Gaëlle Le Goff, Gaël Le Trionnaire, Pablo Librado, Shanlin Liu, Eric Lombaert, Hsiao-ling Lu , Martine Maïbèche, Mohamed Makni, Marina Marcet-Houben, David Martínez-Torres, Camille Meslin, Nicolas Montagné, Nancy A. Moran, Daciana Papura, Nicolas Parisot, Yvan Rahbé, Mélanie Ribeiro Lopes, Aida Ripoll-Cladellas, Stéphanie Robin, Céline Roques, Pascale Roux, Julio Rozas, Alejandro Sánchez-Gracia, J11ose F. Sánchez-Herrero, Didac Santesmasses, Iris Scatoni, Rémy-Félix Serre, Ming Tang, Wenhua Tian, Paul A. Umina, Manuella van Munster, Carole Vincent-Monégat, Joshua Wemmer, Alex C. C. Wilson, Ying Zhang, Chaoyang Zhao, Jing Zhao, Serena Zhao, Xin Zhou, **François Delmotte*£, Denis Tagu*£**

*: corresponding authors, $: co-first authors, £: co-last authors

Additional files

Additional File 1: Figures S1-S22, Table S1-S20, Methods and Results. **FigS1.** Mitochondrial genome view of grape phylloxera. **FigS2.** Proportion of transposable elements (TE) in the genome. **FigS3.** GO terms of phylloxera-specific genes. **FigS4.** Enriched GO terms in the phylloxera genome with and without TEs. **FigS5.** Gene gain/loss at different nodes or branches. **FigS6.** Species phylogenetic tree based on insect genomes and the transcriptomes of *Planoccoccus citri* and *Adelges tsugae*. **FigS7.** Diagram of the gap-filling and annotation process. **FigS8.** Urea cycle in *D. vitifoliae* and *A. pisum*. **FigS9.** IMD immune pathway in *D. vitifoliae.* **FigS10.** Phylogenetic tree of RR-1 cuticular proteins. **FigS11.** Phylogenetic tree of RR-2 cuticular proteins. **FigS12.** Comparison of miRNAs in *D. vitifoliae* and other insect genomes. **FigS13.** Phylogenetic tree of aquaporin protein sequences. **FigS14.** Comparison of the phylloxera PER protein with other insects. **FigS15.** Amino acid alignment of PTTH amino acid sequences. **FigS16.** Phylogeny of hemipteran ORs. **FigS17.** Phylogeny of hemipteran GRs. **FigS18.** Phylogenetic analysis of OBPs. **FigS19.** Phylogenetic analysis of CSPs. **FigS20.** Phylogenetic analysis of NPC2s. **FigS21.** Distribution of cluster sizes of putative effectors. **FigS22.** Physical distribution of the three largest clusters of effectors. **TabS1.** Genes of bacterial and fungal origin.**TabS2.** Statistics on TEs. **TabS3.** GO enrichment of genes duplicated at different ancestral nodes. **TabS4.** Metabolic gaps in the D. vitifoliae reaction network. **TabS5.** Functional annotation of metabolic genes. **TabS6.** Genes of the TOLL pathway. **TabS7.** Genes of the IMD pathway. **TabS8.** Statistics on cuticular proteins. **TabS9.** Developmental genes in *D. vitifoliae* and *A. pisum*. **TabS10.** miRNAs. **TabS11.** Clock-related genes. **TabS12.** List of ORs and GRs. **TabS13.** Number of OBPs, CSPs and NPC2s. **TabS14.** List of Cytochromes P450. **TabS15.** List of genes involved in detoxification. **TabS16.** Effector genes with predicted domains and their corresponding functions. **TabS17.** Statistics on sequence reads and SRA accessions used for the reference genome. **TabS18.** List of species used to study gene expansions. **TabS19.** Sampling sites and SRA used for population genomics analyses. **TabS20.** Prior distribution of parameters used for ABC modelling of invasion routes.

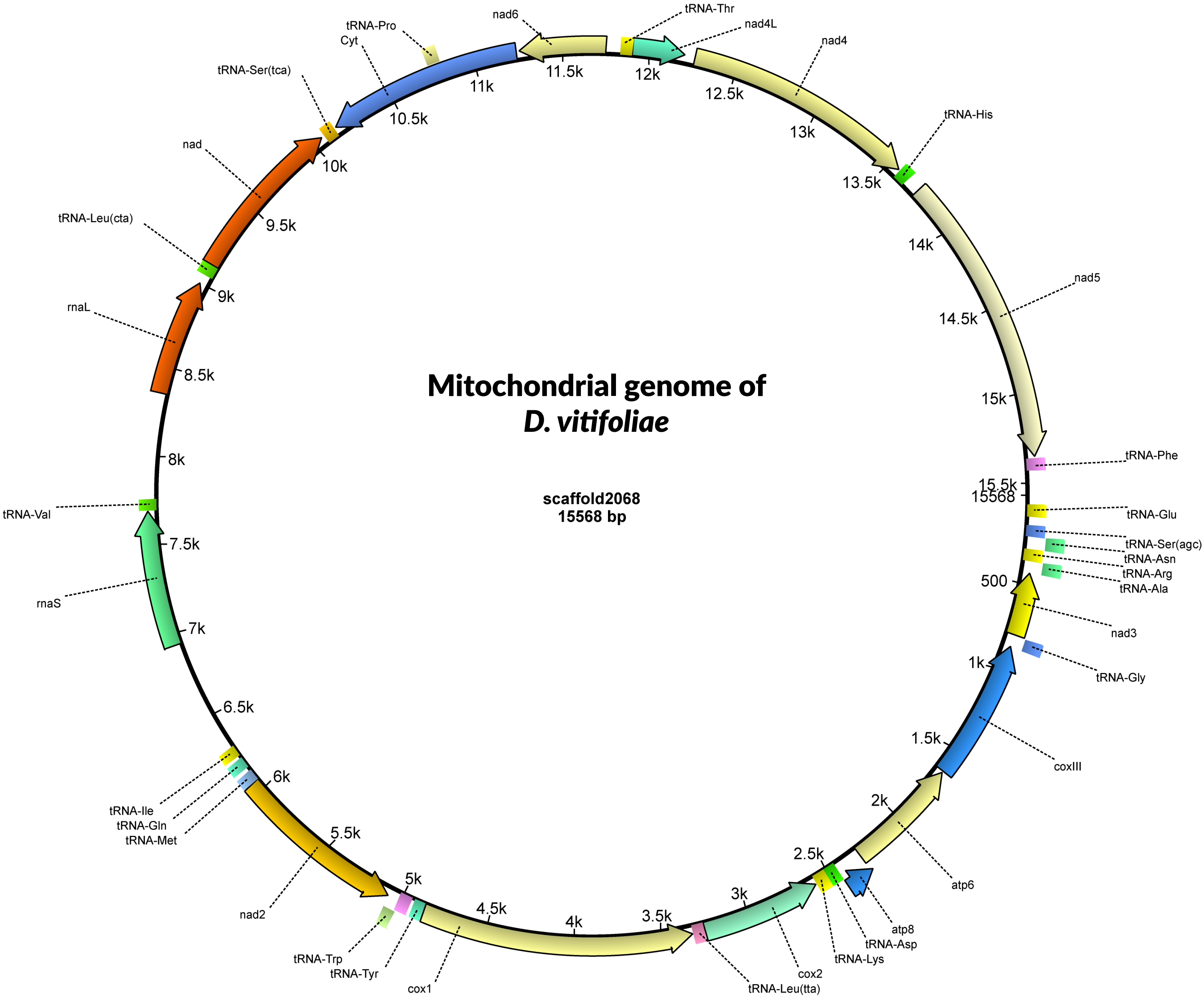


Figure S1. Mitochondrial genome view after editing of the Nd5 gene. The contig is shown in its circular form. The phylloxera mitochondrial scaffold is slightly smaller (15568 bp) than the mitochondrial genomes from *A. pisum* (16971 bp) and *D. melanogaster* (19517 bp) but has similar GC content to both other species (15.5% vs 15.2% and 17.8% respectively). The protein sequences shared an average of 78% identity with their homologs in *A. pisum* (ranging between 53% and 94%); average identity with *D. melanogaster* homologs was 49% (ranging between 31% and 72%).

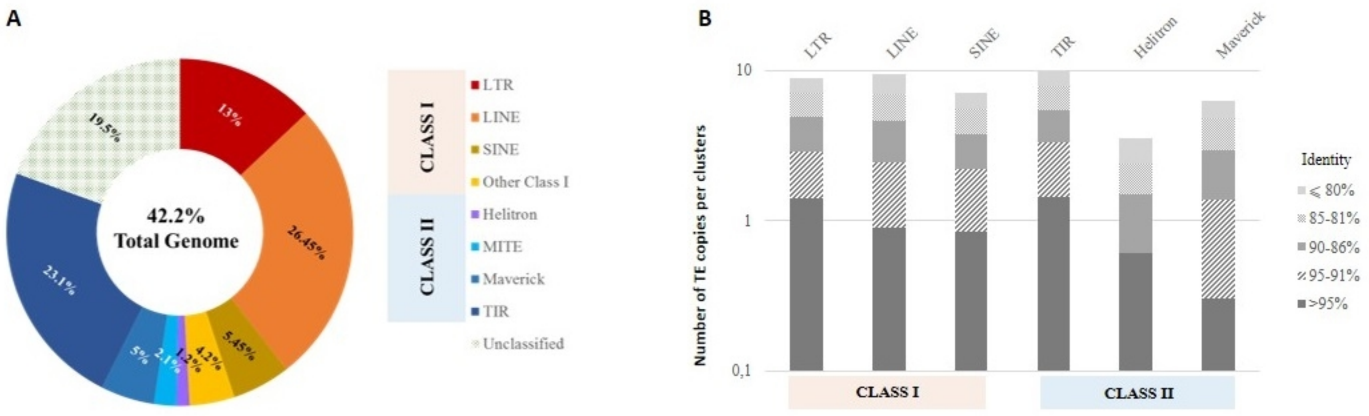


Figure S2. Proportion of transposable elements (TE) in the phylloxera draft genome. A. ercentage of the phylloxera genome occupied by the main Orders of TE (according to the classification of Wicker et al. [18]). Long interspersed elements (LINE) and Terminal Inverted Repeats (TIR) are the most frequent elements. Unclassified elements (according to REPET) have no structural features or similarity with other known TEs. B. Identity levels between TE of the different clusters defined by REPET. Identities are calculated from pairwise comparison between all TE of a cluster. The clusters are grouped according to the main Orders of TE. The y-axis is a log scale. Clusters with a high level of identity probably correspond to the recently expanded TE family. On the contrary, clusters with low identity values are probably old families. Repeat Orders previously named ‘‘Other Class I”, “MITE’’ and “Unclassified” are not shown included in this analysis.

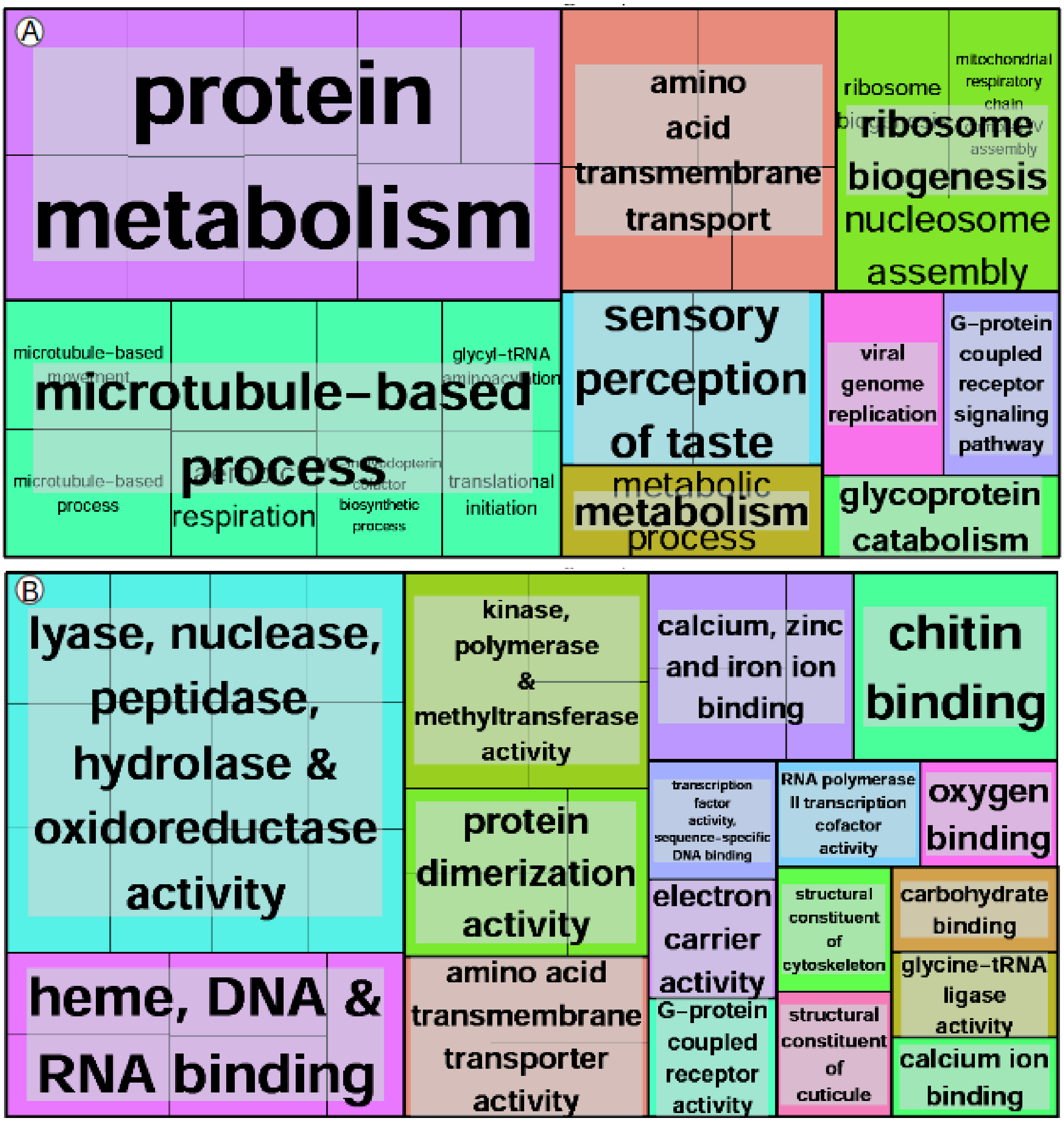


Figure S3. REVIGO tree maps summarizing GO terms in the 363 lineage-specific genes in phylloxera genome at the biological process level (A) and molecular function level (B). The size of each square is related to the uniqueness of each category.

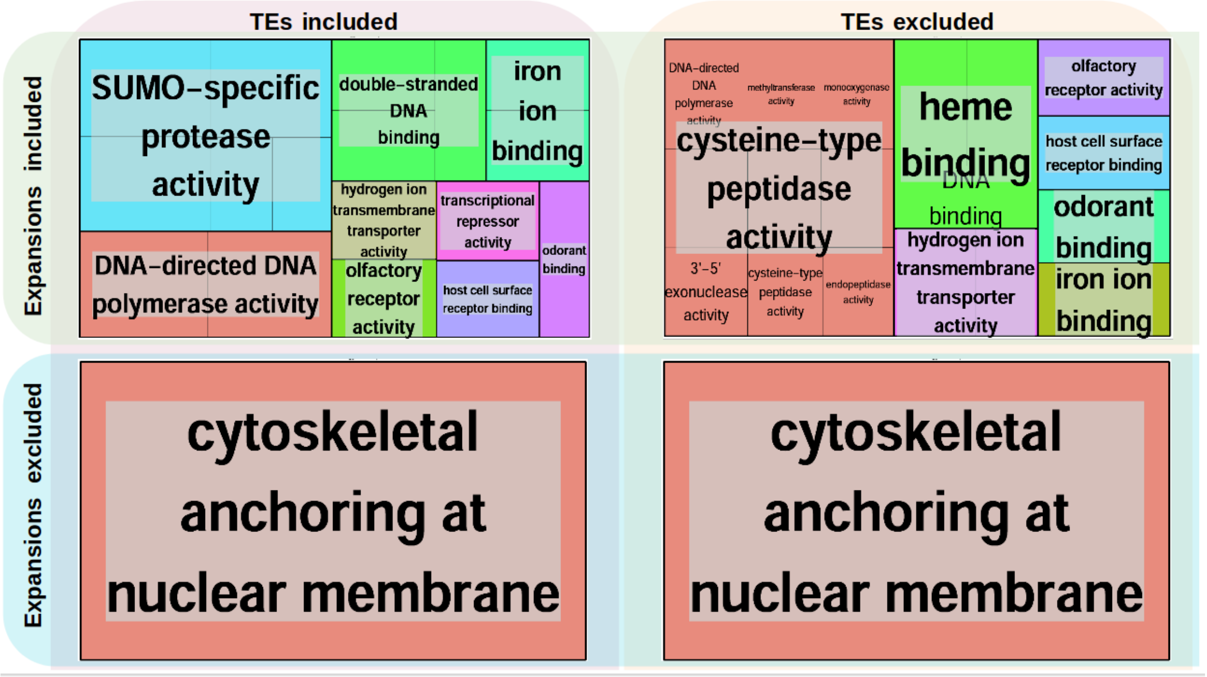


Figure S4. REVIGO tree maps summarizing enriched GO terms in the phylloxera genome (molecular function). The effect of inclusion and exclusion of expansions and TEs in the enrichment analysis is shown by the different composition of terms in the treemaps. The size of each square is related to the significance of p-values in the enrichment analyses.

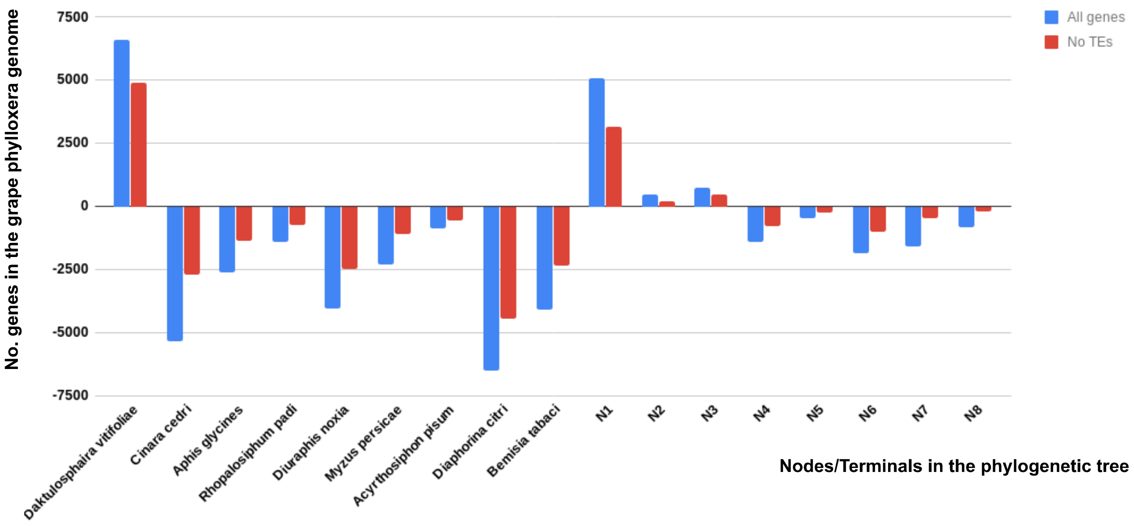
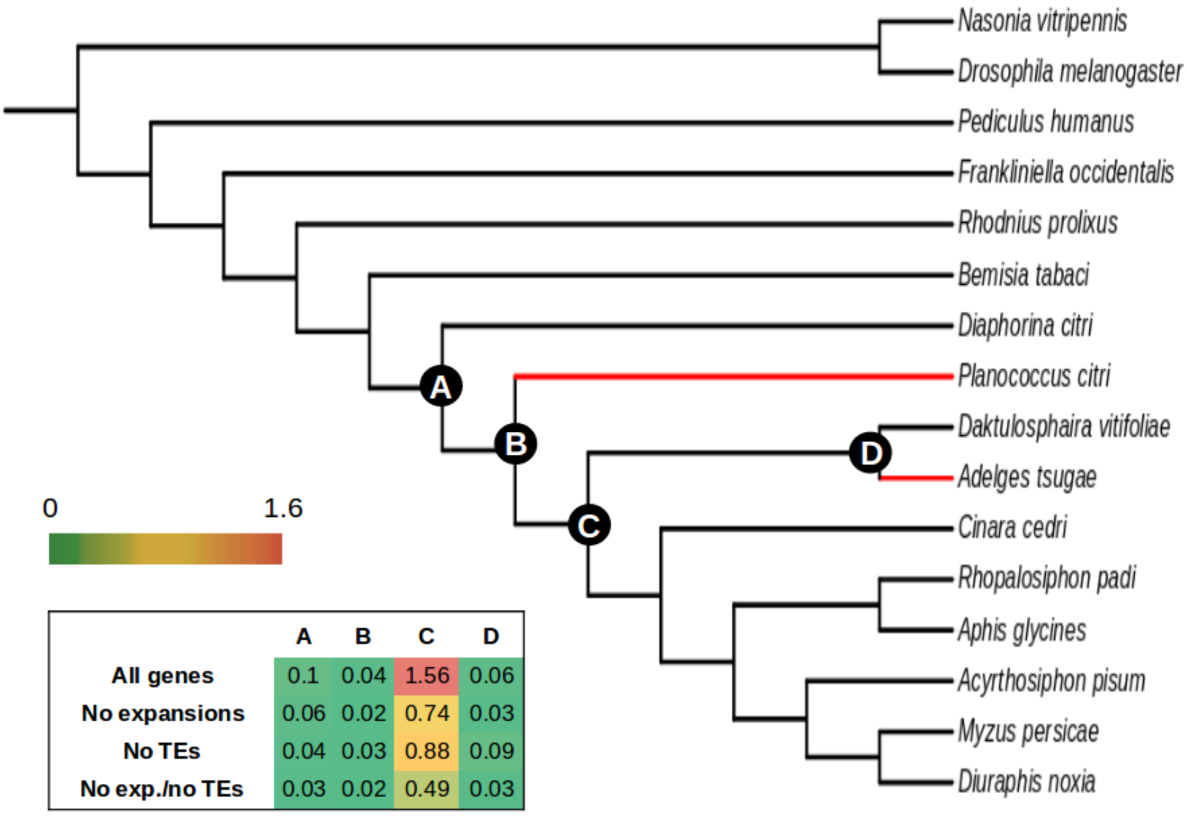


Figure S5. Histogram of gene gain/loss reference to the gene content of *D. vitifoliae*. Values represent the number of genes of the genome of the grape phylloxera that have been gained or lost in each taxon or nodes. Note that genes can only be gained at nodes previous to or during the split of phylloxera (*i.e.*, phylloxera-specific genes), and only be lost at nodes before or after any splits not involving phylloxera (*i.e.*, the remaining clades in the tree). Node numbers refer to a phylogenetic study based on the complete genomes of 14 different species of insects (Figure 3).



	A	B	C	D
All genes	0.1	0.04	1.56	0.06
No expansions	0.06	0.02	0.74	0.03
No TEs	0.04	0.03	0.88	0.09
No exp./no TEs	0.03	0.02	0.49	0.03

Figure S6. Species tree based on one-to-one orthologs inferred in the data set after inclusion of *Planococcus citri* (Coccoidea) and *Adelges tsugae* (Adelgidae) (branches highlighted in red). All nodes were highly supported (>0.95 SH-like support). Duplication ratios considering all genes and excluding proteins encoded by transposable elements (TE), as well as including and excluding phylloxera-specific expansions, are indicated for the three most basal nodes of Sternorrhyncha and Hemiptera (A, B and C), and the node of Phylloxeridae and Adelgidae (D).

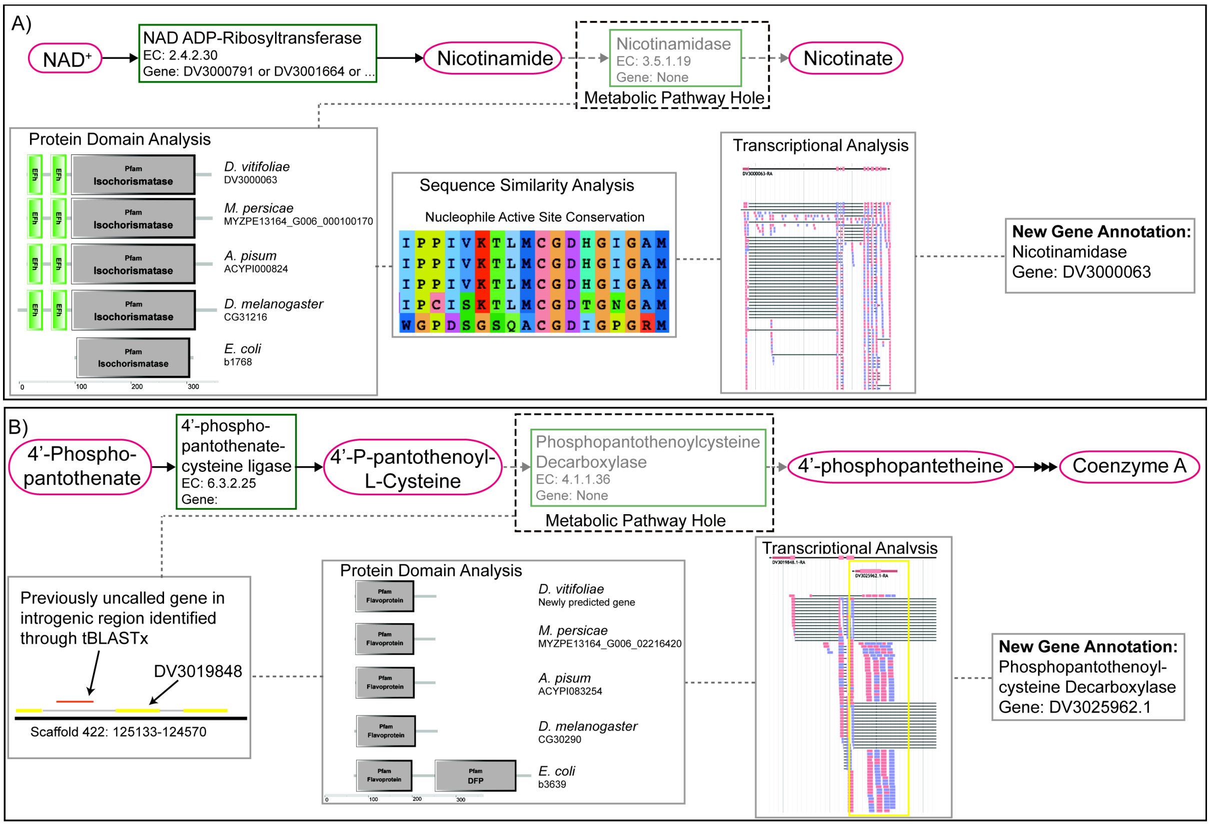


Figure S7. A diagrammatic representation of the metabolic gap-filling and annotation process. Pathway gaps are shown as faded reaction boxes in the pathway diagram. Visual representations of the evidence used during the gene annotation process for DV3000063 (A) and DV3025962.1 (B) are shown in boxes below the pathway diagrams.

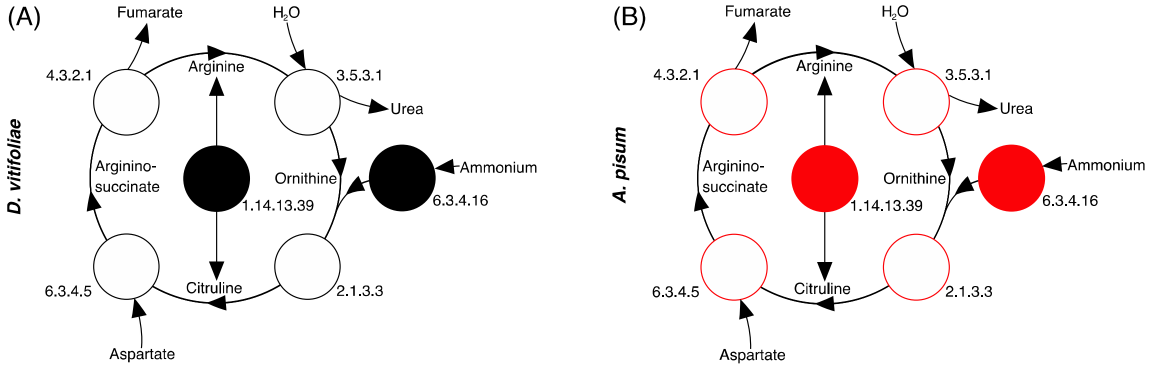


Figure S8. A comparison of the urea cycle between *D. vitifoliae* (left cycle, with enzymes shown by black circles and the aphid *A. pisum* (right cycle, with enzymes shown by red circles). The presence of an enzyme in the cycle is shown by a filled circle, and absence by an empty circle. Enzymes are identified by EC number. All annotations are from Dakvicyc and gap-filling analysis, except for 1.14.13.39, which was annotated via blastp and HMM searches based on KEGG.

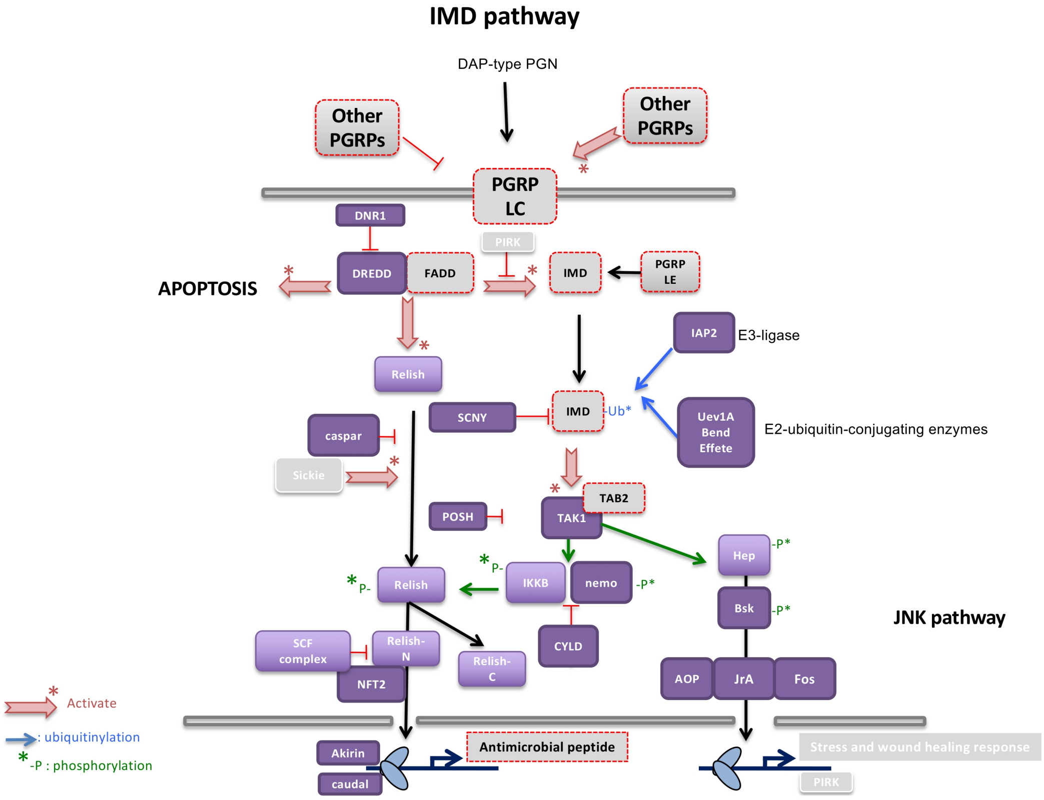


Figure S9. Schematic representation of the putative IMD immune pathway in *D. vitifoliae*. All the proteins present in the reference pathway (*D. melanogaster*) are indicated. Phylloxera proteins with high similarity scores are shown in purple boxes. Proteins with lower similarity scores are shown in clear purple boxes. Missing proteins are shown in gray boxes highlighted in red. Light gray boxes contain proteins that were not searched for. Red arrows show the potential to activate a target protein. Ubiquitinylation targets are represented by blue arrows and phosphorylation by green arrows, respectively.

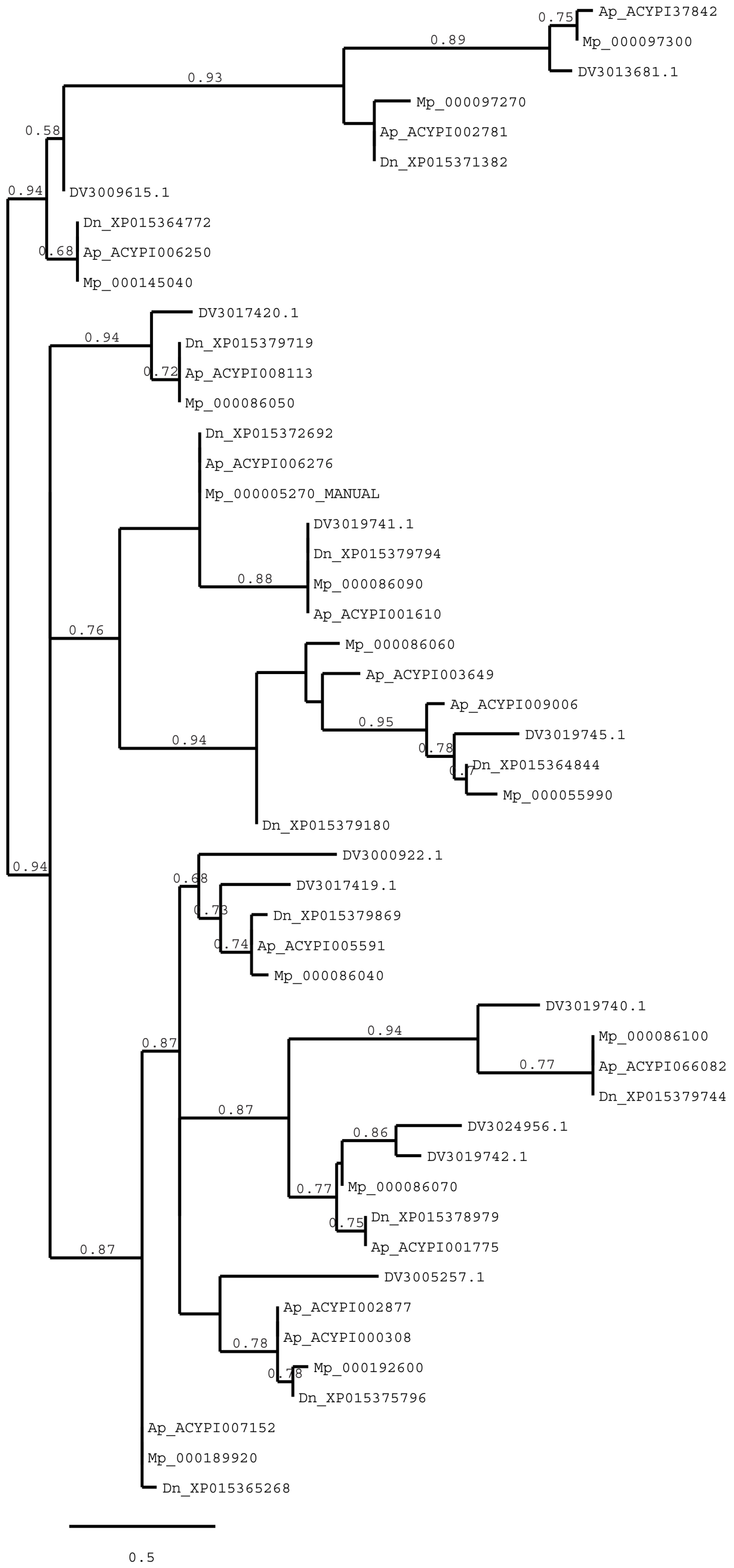
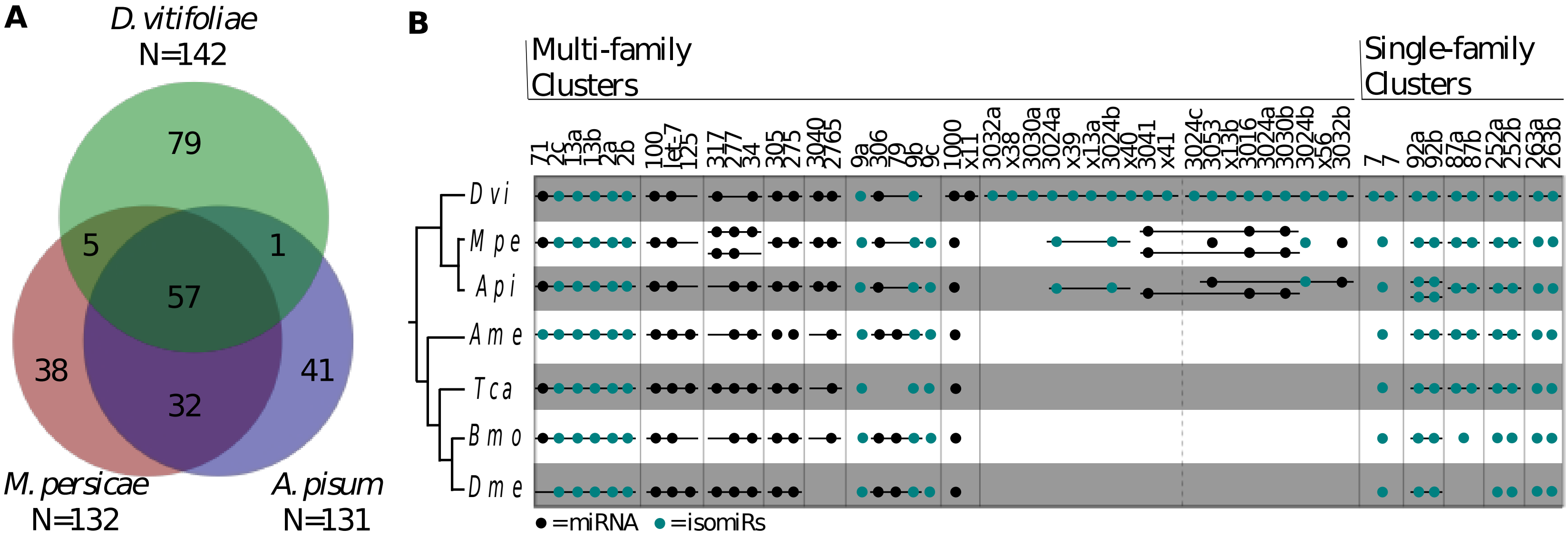


Figure S10. Phylogenetic relationships of full RR-1 proteins of *D. vitifoliae*, *D. noxia*, *A. pisum* and *M. persicae*. Phylogenetic reconstruction was performed using an updated list of RR-1 proteins of the different aphid species and *D. vitifoliae* as described in Material & Methods section. Numbers at nodes indicate the aLRT value that supports each node. The scale represents probabilities of change from one amino acid to another in terms of a unit, which is an expected 1 % change between two amino acid sequences.

Figure S11. Phylogenetic relationships of the core RR-2 proteins of *D. vitifoliae* and three aphid species, *D. noxia* , *A. pisum* and *M. persicae.* Phylogenetic reconstruction was performed using the extended domain of 69 amino acids specific of RR2-proteins. Selected numbers at nodes indicate the percentage of 1000 bootstrap replicates. Groups of one-to-one orthologs among the four species are shaded in blue and numbered (CcOG), as well as clades showing expansions in aphids only (Clade A) or in both aphids and phylloxera.



Supplementary Figure S12. Comparison of miRNAs in *D. vitifoliae* and other insect genomes. (A) Overlap of mature miRNAs between the genomes of *D. vitifoliae* (green), *A. pisum* (blue) and *M. persicae* (red). (B) Genomic clusters of miRNAs. Similar to other insect taxa that include *M. periscae (Mpe), A. pisum (Api), Aphis mellifera* (*Ame*), *Tribolium castaneum* (*Tca*), *Bombyx mori* (*Bmo*), *Drosophila melanogaster* (*Dme*), 31% (i.e. 47/150 miRNA precursors) of *D. vitifoliae* miRNAs are arranged in 14 genomic clusters. The majority of those miRNA clusters are deeply conserved across different insect taxa. Two large clusters: 3032a/x38/3030a/3024a/x39/x13a/3024b/x40/3041/x41 and 3024c/3053/x13b/3016/3024a/3030b/3024b/x56/3032b share some orthology with aphids. Multi-family clusters are composed of miRNAs from different miRNA families, while single-family clusters are composed of duplicated members of the same miRNA. Each circle marks an individual miRNA; teal circles highlight isomiRs, anciently duplicated miRNAs that share identical seed regions but diverge in sequence of non-seed regions. miRNA names are abbreviated and full names are available by appending "Dvit-miR-" to each of the abbreviated names.

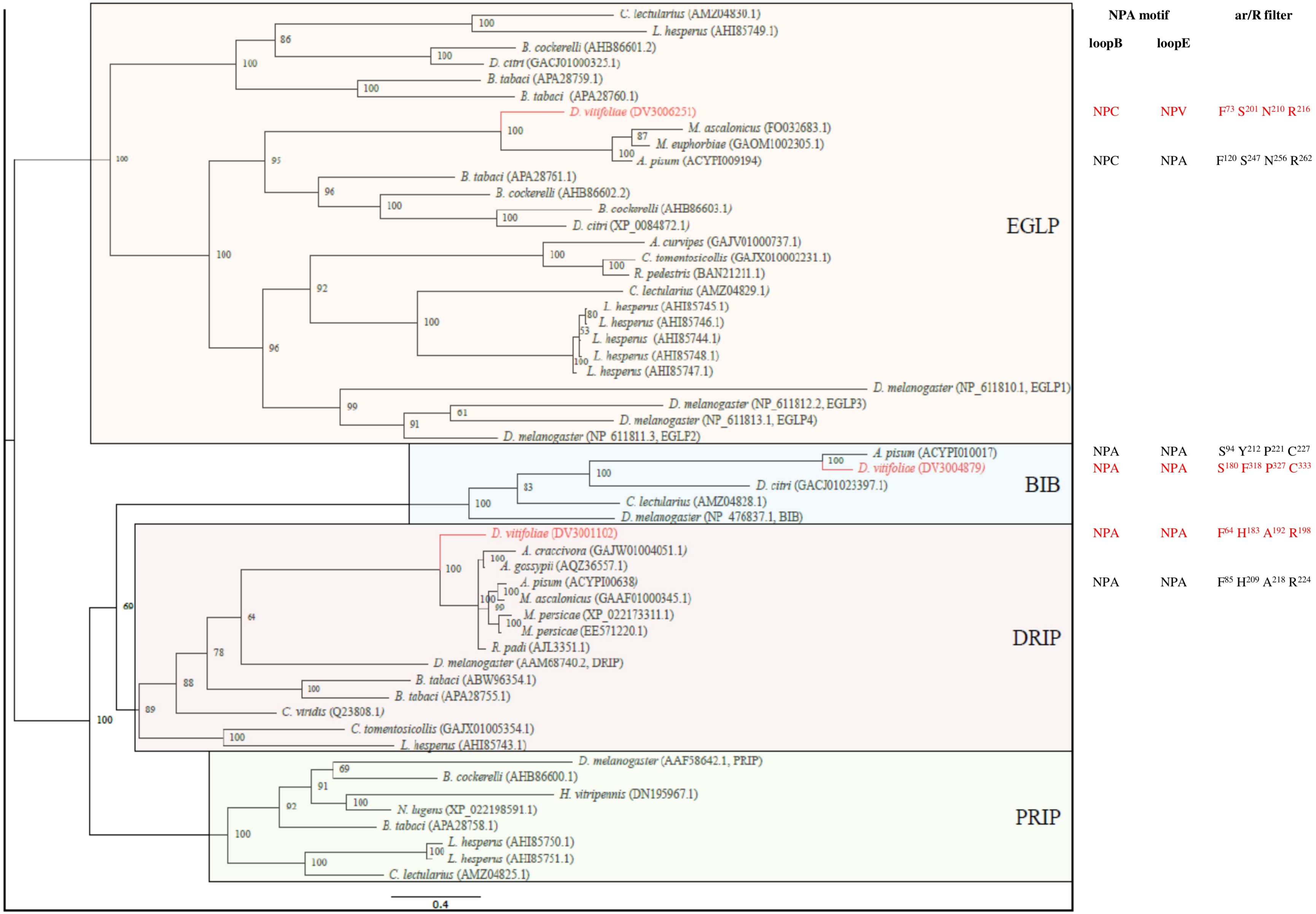
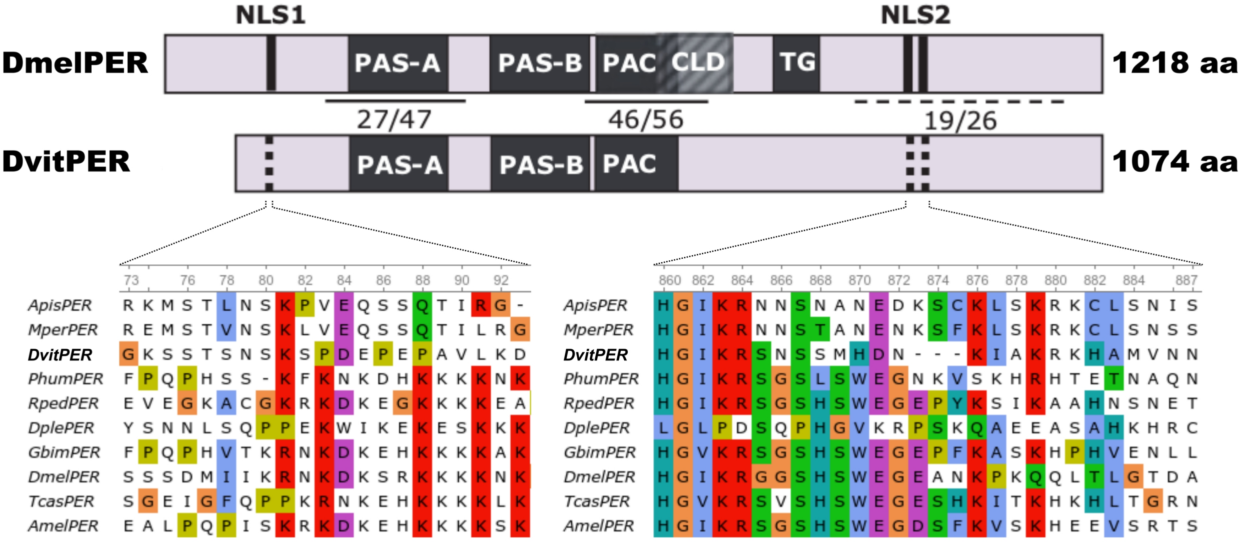

C. lectularius (AMZ04830.1)
L. hesperus (AHI85749.1)
B. cockerelli (AHB86601.2)
D. citri (GACJ01000325.1)
B. tabaci (APA28759.1)
B. tabaci (APA28760.1)
D. vitifoliae (DV3006251)
M. ascalonicus (FO032683.1)
M. euphorbiae (GAOM1002305.1)
A. pisum (ACYPI009194)
B. tabaci (APA28761.1)
B. cockerelli (AHB86602.2)
B. cockerelli (AHB86603.1)
D. citri (XP_0084872.1)
A. curvipes (GAJV01000737.1)
C. tomentosicollis (GAJX010002231.1)
R. pedestris (BAN21211.1)
C. lectularius (AMZ04829.1)
L. hesperus (AHI85745.1)
L. hesperus (AHI85746.1)
L. hesperus (AHI85744.1)
L. hesperus (AHI85748.1)
L. hesperus (AHI85747.1)
D. melanogaster (NP_611810.1, EGLP1)
D. melanogaster (NP_611812.2, EGLP3)
D. melanogaster (NP_611813.1, EGLP4)
D. melanogaster (NP_611811.3, EGLP2)
EGLP
A. pisum (ACYPI010017)
D. vitifoliae (DV3004879)
D. citri (GACJ01023397.1)
C. lectularius (AMZ04828.1)
D. melanogaster (NP_476837.1, BIB)
BIB
D. vitifoliae (DV3001102)
A. craccivora (GAJW01004051.1)
A. gossypii (AQZ36557.1)
A. pisum (ACYPI00638)
M. ascalonicus (GAAF01000345.1)
M. persicae (XP_022173311.1)
M. persicae (EE571220.1)
R. padi (AJL3351.1)
D. melanogaster (AAM68740.2, DRIP)
B. tabaci (ABW96354.1)
B. tabaci (APA28755.1)
C. viridis (Q23808.1)
C. tomentosicollis (GAJX01005354.1)
L. hesperus (AHI85743.1)
DRIP
D. melanogaster (AAF58642.1, PRIP)
B. cockerelli (AHB86600.1)
H. vitripennis (DN195967.1)
N. lugens (XP_022198591.1)
B. tabaci (APA28758.1)
L. hesperus (AHI85750.1)
L. hesperus (AHI85751.1)
C. lectularius (AMZ04825.1)
PRIP
100
86
100
100
100
100
100
87
100
95
96
100
100
100
100
100
92
100
80
53
100
96
99
61
91
100
100
83
100
100
60
100
100
100
99
100
64
78
88
100
89
100
69
91
92
100
100
100
100
0.4
NPA motif
loopB
loopE
ar/R filter
NPC
NPV
F^{73} S^{201} N^{210} R^{216}
NPC
NPA
F^{120} S^{247} N^{256} R^{262}
NPA
NPA
S^{94} Y^{212} P^{221} C^{227}
NPA
NPA
S^{180} F^{318} P^{327} C^{333}
NPA
NPA
F^{64} H^{183} A^{192} R^{198}
NPA
NPA
F^{85} H^{209} A^{218} R^{224}

Figure S13 (above). Bayesian phylogenetic tree of aquaporin protein sequences identified in *D. vitifoliae*. Percent posterior probabilities are given on the branches. All sequences were downloaded from NCBI except for *A. pisum*, which was downloaded from AphidBase, as its BIB sequence is not available on NCBI. Abbreviations: DRIP, *Drosophila* integral protein family; PRIP, *Pyrocoelia rufa* integral protein family; EGLP, *Entomoglyceroporin*; BIB, *Drosophila* big brain; *C. lectularius, Cimex lectularius; L. hesperus, Lygus hesperus; B. cockerelli, Bactericera cockerelli*; *D. citri, Diaphorina citri; B. tabaci, Bemisia tabaci; D. vitifoliae, Daktulosphaira vitifoliae; M. ascalonicus, Myzus ascalonicus; M. euphorbiae, Macrosiphum euphorbiae; A. pisum, Acyrthosiphon pisum; A. curvipes, Anoplocnemis curvipes; C. tomentosicollis, Clavigralla tomentosicollis; R. pedestris, Riptortus pedestris; D. melanogaster, Drosophila melanogaster; A. craccivora, Aphis craccivora; R. padi, Rhopalosiphum padi*); *C. viridis, Cicadella viridis*; *H. vitripennis, Homalodisca vitripennis; N. lugens, Nilaparvata lugens*. The amino acids comprising NPA boxes and ar/R selectivity filter of *D. vitifoliae* and *A. pisum* AQPs are displayed in red and black, respectively.

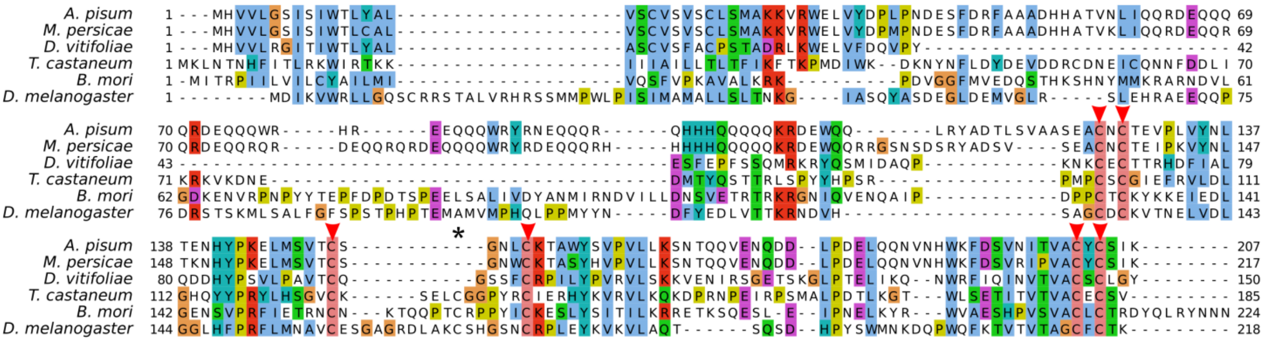


```
         73    76  78  80  82  84  86  88  90  92
ApisPER  R K M S T L N S K P V E Q S S Q T I R G -
MperPER  R E M S T V N S K L V E Q S S Q T I L R G
DvitPER  G K S S T S N S K S P D E P E P A V L K D
PhumPER  F P Q P H S S - K F K N K D H K K K K N K
RpedPER  E V E G K A C G K R K D K E G K K K K E A
DplePER  Y S N N L S Q P P E K W I K E K E S K K K
GbimPER  F P Q P H V T K R N K D K E H K K K K A K
DmelPER  S S S D M I I K R N K D K S R K K K K N K
TcasPER  S G E I G F Q P P K R N K E H K K K K L K
AmelPER  E A L P Q P I S K R K D K E H K K K K S K
```

```
         860 862 864 866 868 870 872 874 876 878 880 882 884   887
ApisPER  H G I K R N N S N A N E D K S C K L S K R K C L S N I S
MperPER  H G I K R N N S T A N E N K S F K L S K R K C L S N S S
DvitPER  H G I K R S N S S M H D N - - - K I A K R K H A M V N N
PhumPER  H G I K R S G S L S W E G N K V S K H R H T E T N A Q N
RpedPER  H G I K R S G S H S W E G E P Y K S I K A A H N S N E T
DplePER  L G L P D S Q P H G V K R P S K Q A E E A S A H K H R C
GbimPER  H G V K R S G S H S W E G E P F K A S K H P H V E N L L
DmelPER  H G I K R G G S H S W E G E A N K P K Q Q L T L G T D A
TcasPER  H G V K R S V S H S W E G E S H K I T K H K H L T G R N
AmelPER  H G I K R S G S H S W E G D S F K V S K H E E V S R T S
```

Figure S14. Comparison of the phylloxera PER protein with other insects. Top: schematic representation of the whole protein in Drosophila and phylloxera. Bottom: detail of the alignment of PER proteins from different insect species including two aphid species. Note that in the two regions shown (otherwise highly conserved), aphids and phylloxera are both rather divergent from other insects. Accession numbers of sequences used in the alignment are as follows: Apis (*A. pisum*, XP_029344821.1); Mper (*M. persicae*, XP_022163848.1); Phum (*P. humanus*, XP_002426301.1); Rped (R. pedestris, BAG07407.1); Dple (*D plexippus*, AAO48719.1); Gbim (*G. bimaculatus*, BAG48878.1); Dmel (*D. melanogaster*, XP_003399949.1); Tcas (*T. castaneum*, EFA04566.2); Amel (*A. mellifera*, ARB43935.1).

PTTH



```
       A. pisum   1 ---MHVVLGSISIWTLYAL--------------------VSCVSVSCLSMAKKVRWELVYDPLPNDESFDRFAAADHHATVNLIQQRDEQQQ 69
    M. persicae   1 ---MHVVLGSISIWTLCAL--------------------VSCVSVSCLSMAKKVRWELVYDPMPNDESFDRFAAADHHATVKLIQQRDEQQR 69
  D. vitifoliae   1 ---MHVVLRGITIWTLYAL--------------------ASCVSFACPSTADRLKWELVFDQVPY--------------------------- 42
   T. castaneum   1 MKLNTNHFITLRKWIRTKK--------------------IIIAILLTLTFIKFTKPMDIWK--DKNYNFLDYDEVDDRCDNEICQNNFDDLI 70
        B. mori   1 -MITRPIILVILCYAILMI--------------------VQSFVPKAVALKRK----------PDVGGFMVEDQSTHKSHNYMMKRARNDVL 61
D. melanogaster   1 --------MDIKVWRLLGQSCRRSTALVRHRSSMMPWLPISIMAMALLSLTNKG----IASQYASDEGLDEMVGLR-----SLEHRAEEQQP 75

       A. pisum  70 QRDEQQQWR-----HR------EEQQQWRYRNEQQQR------QHHHQQQQQKRDEWQQ-------LRYADTLSVAASEACNCTEVPLVYNL 137
    M. persicae  70 QRDEQQRQR-----DEQQRQRDEQQQQWRYRDEQQQRH-----HHHHQQQQQKRDEWQQRRGSNSDSRYADSV----SEACNCTEIPKVYNL 147
  D. vitifoliae  43 -------------------------------------------ESFEPFSSQMRKRYQSMIDAQP------------KNKCECTTRHDFIAL 79
   T. castaneum  71 KRKVKDNE-----------------------------------DMTYQSTTRLSPYYHPSR----------------PMPCSCGIEFRVLDL 111
        B. mori  62 GDKENVRPNPYYTEPFDPDTSPEELSALIVDYANMIRNDVILLDNSVETRTRKRGNIQVENQAIP------------DPPCTCKYKKEIEDL 141
D. melanogaster  76 DRSTSKMLSALFGFSPSTPHPTEMAMVMPHQLPPMYYN-----DFYEDLVTTKRNDVH-------------------SAGCDCKVTNELVDL 143

                                             *
       A. pisum 138 TENHYPKELMSVTCS------------GNLCKTAWYSVPVLLKSNTQQVENQDD--LPDELQQNVNHWKFDSVNITVACYCSIK-------- 207
    M. persicae 148 TKNHYPKELMSVTCS------------GNWCKTASYHVPVLLKSNTQQVENQDD--LPDELQQNVNHWKFDSVRIPVACYCSIK-------- 217
  D. vitifoliae  80 QDDHYPSVLPAVTCQ-----------GSSFCRPILYPVRVLSKKVENIRSGETSKGLPTELIKQ--NWRFIQINVTVACSCLGY-------- 150
   T. castaneum 112 GHQYYPRYLHSGVCK------SELCGGPYRCIERHYKVRVLKQKDPRNPEIRPSMALPDTLKGT---WLSETITVTVACECSV--------- 185
        B. mori 142 GENSVPRFIETRNCN---KTQQPTCRPPYICKESLYSITILKRRETKSQESL-E--IPNELKYR---WVAESHPVSVACLCTRDYQLRYNNN 224
D. melanogaster 144 GGLHFPRFLMNAVCESGAGRDLAKCSHGSNCRPLEYKVKVLAQT------SQSD--HPYSWMNKDQPWQFKTVTVTAGCFCTK--------- 218
```

Figure S15. Amino acid alignment of PTTH amino acid sequences of different insect species, including aphids and the putative PTTH of *D. vitifoliae*. Conserved cysteine residues are indicated with red arrowheads. The cysteine conserved in all insects except Aphidomorpha is indicated by an asterisk.

Phylogenetic tree of ORs

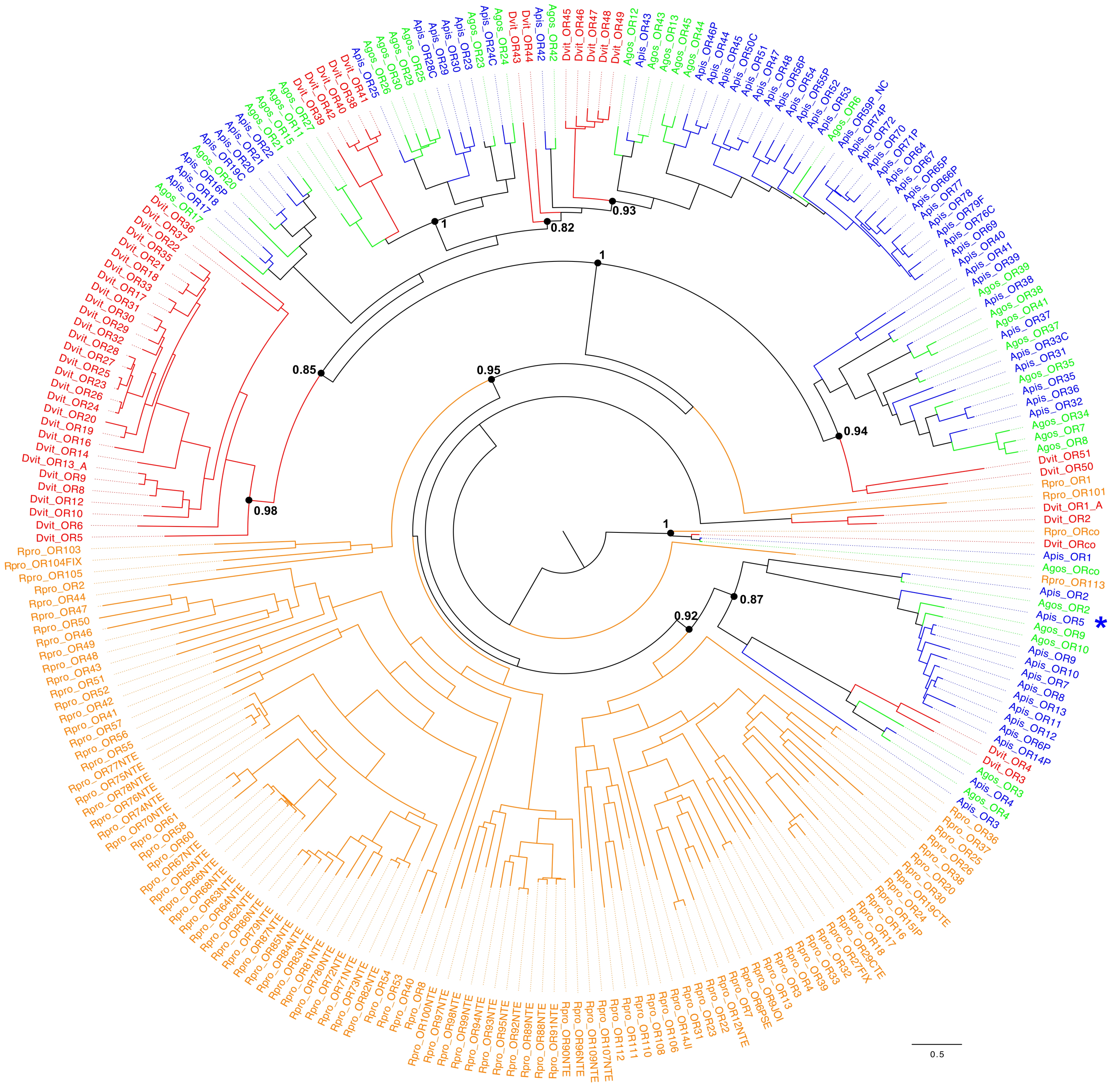


Figure S16. Maximum likelihood phylogeny of hemipteran ORs. The amino acid dataset included OR sequences from *D. vitifoliae* (Dvit), *A. pisum* (Apis), *A. gossypii* (Agos) and *R. prolixus* (Rpro). The tree was rooted using the OR co-receptor (ORco) clade as the outgroup. The scale bar indicates the expected number of amino acid substitutions per site. Support values indicated on the nodes by a black circle correspond to the result of the likelihood ratio-test (aLRT values). An asterisk indicates the only hemipteran receptor that was deorphanized so far, the receptor to the *A. pisum* alarm pheromone.

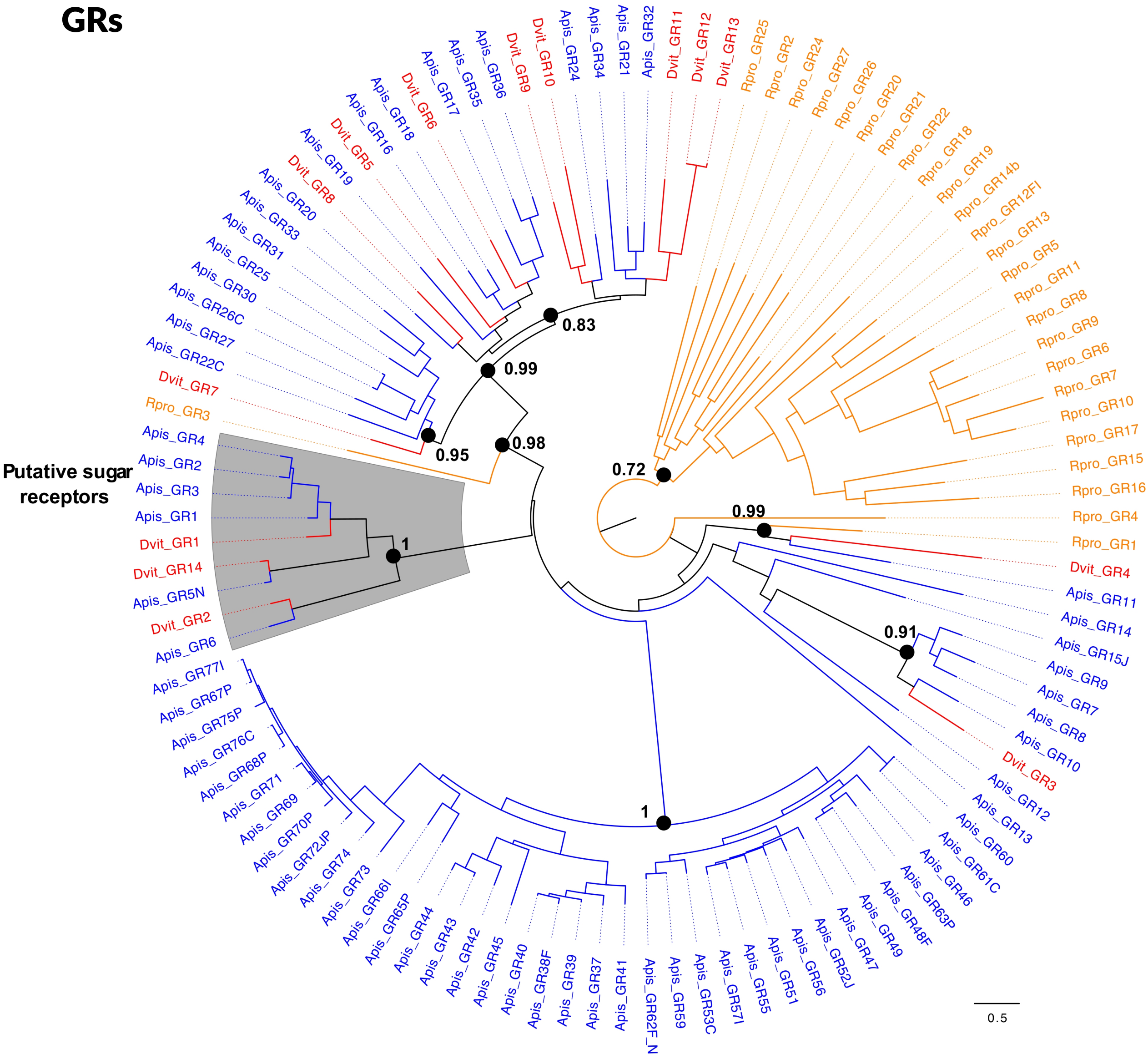


Figure S17. Maximum likelihood phylogeny of hemipteran GRs. The amino acid dataset included OR sequences from *D. vitifoliae* (Dvit), *R. prolixus* (Rpro) [34] and *A. pisum* (Apis) [35]. The tree was mid-point rooted. The scale bar indicates the expected number of amino acid substitutions per site. Support values indicated on the nodes by a black circle correspond to the result of the likelihood ratio-test (aLRT values). The gray clade indicates putative sugar receptors [35].

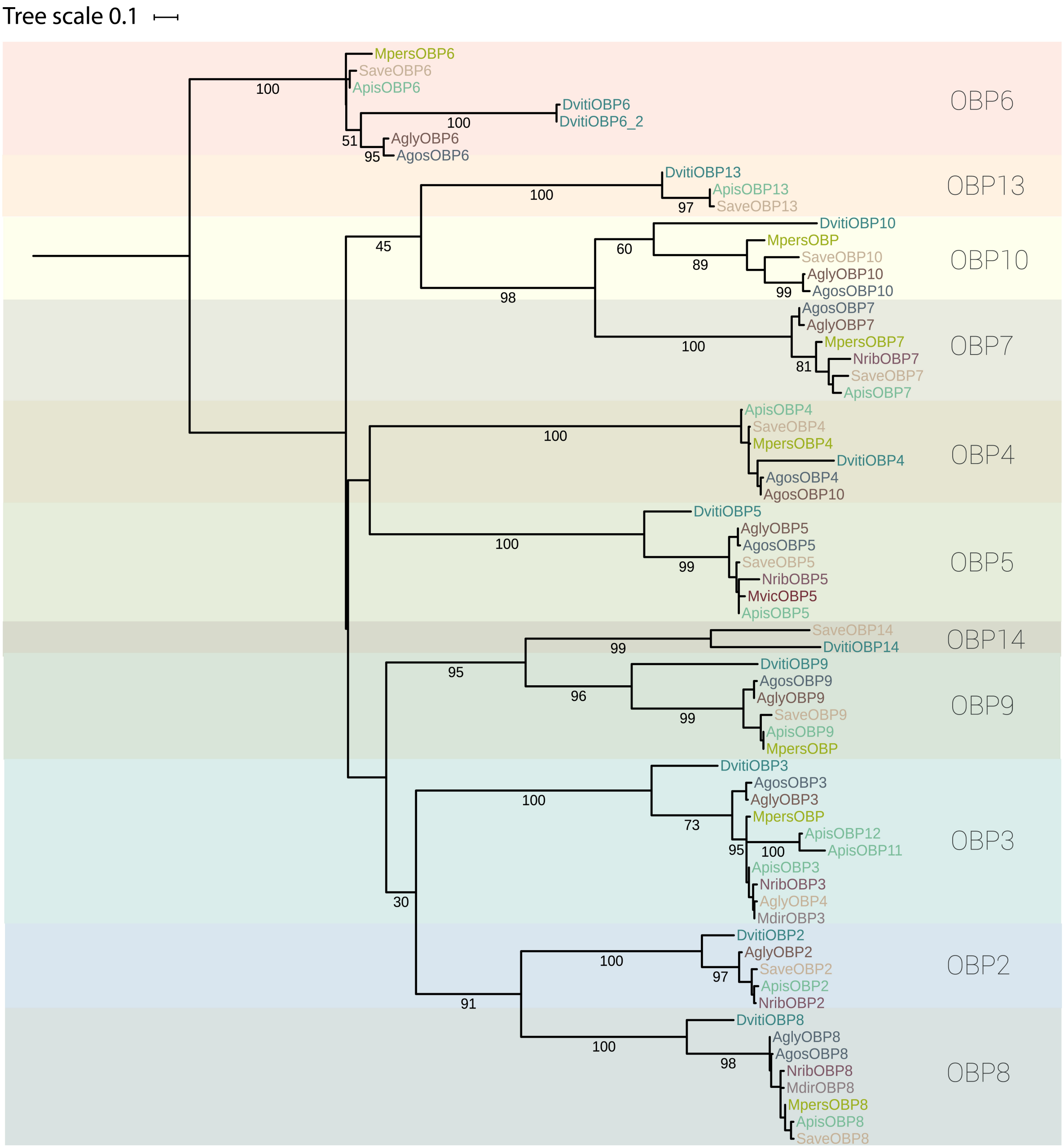


Figure S18. Phylogenetic analysis of the full length OBPs from phylloxera and representative aphid species. Each orthogroup is shaded in a different colour.

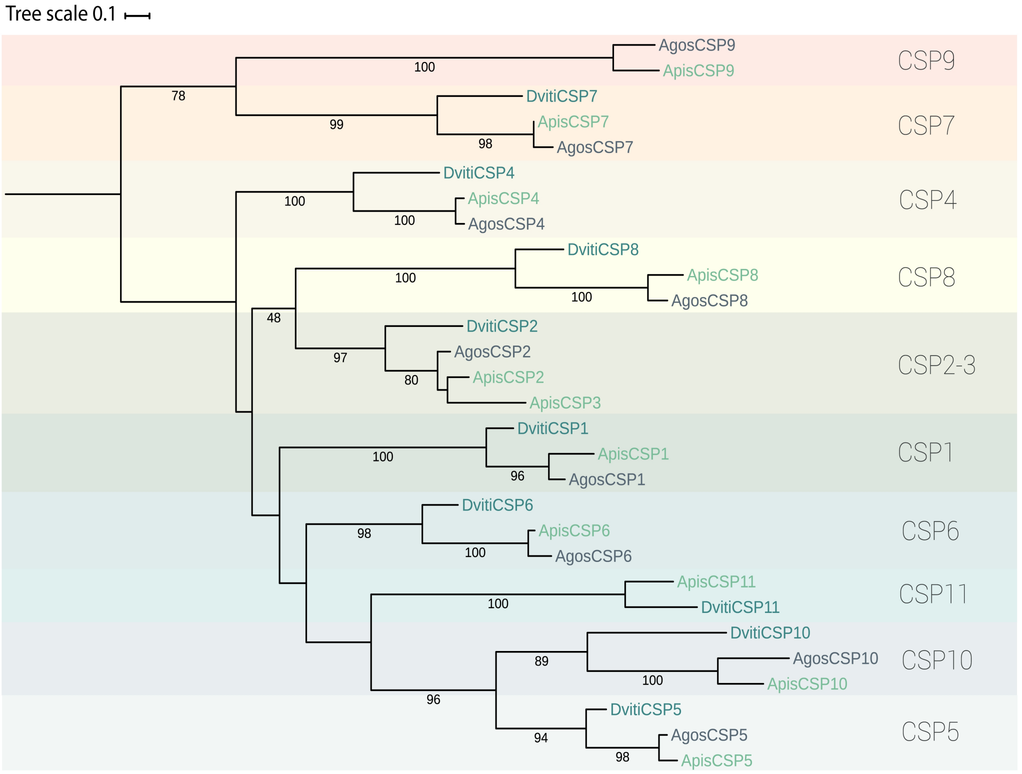


Figure S19. Phylogenetic relationships of the full length CSPs identified in phylloxera and some representative aphid species. Each orthogroup is shaded in a different colour.

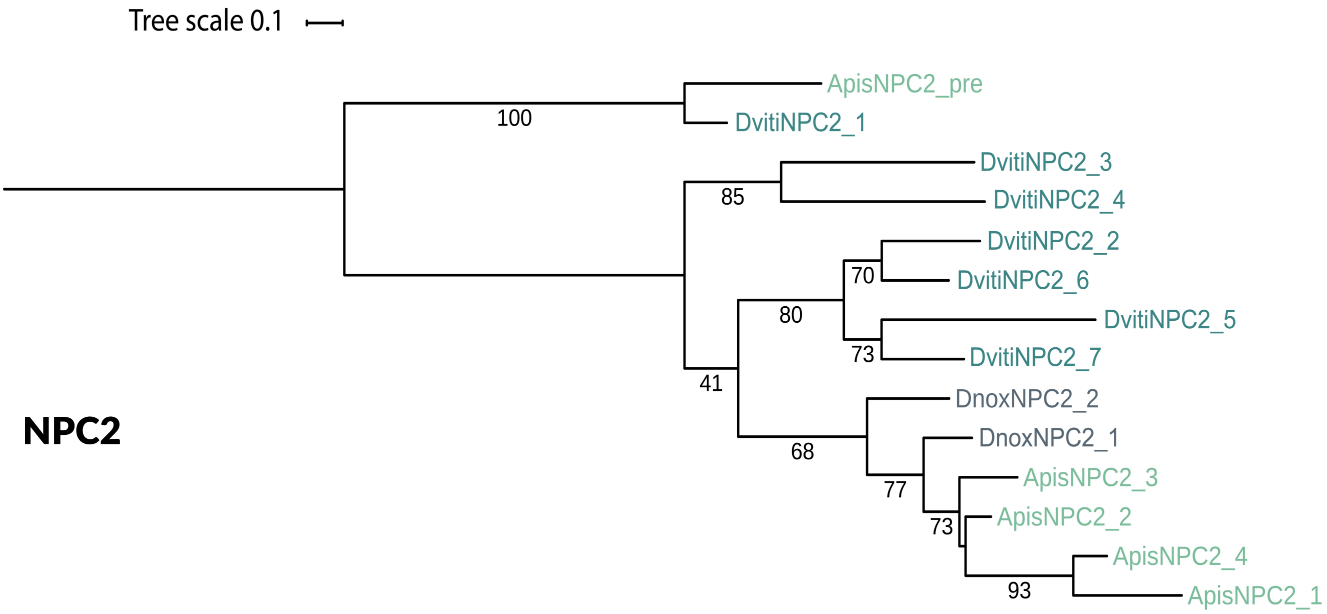


Figure S20. Phylogenetic relationships of the full length NPC2s identified in phylloxera and some representative aphid species.

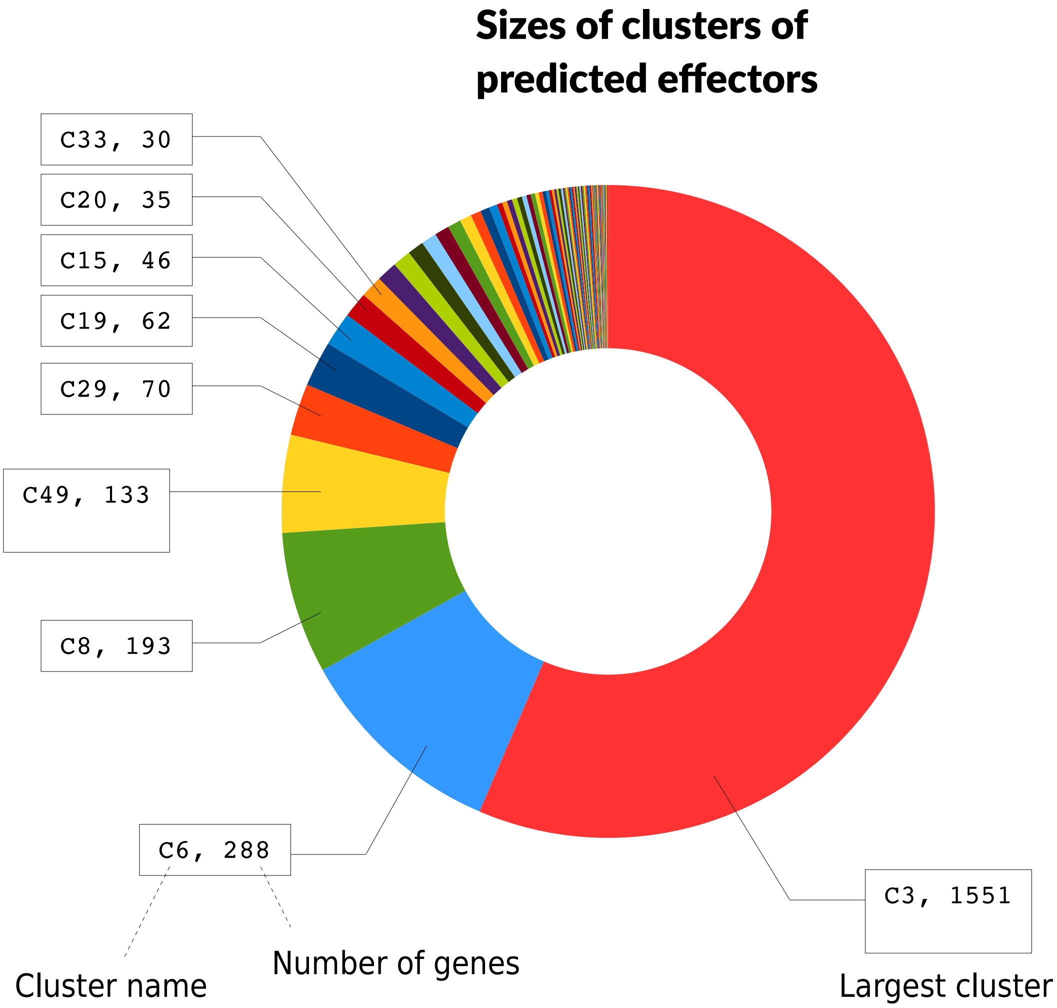


Figure S21. Distribution of siezs of clusters for putative effectors. Surface is proportional to cluster size, n=78 clusters. Details are given for the largest clusters (≥ 30 members), which totalize 87.6% of predicted effectors: cluster number and cluster size, separated by commas.

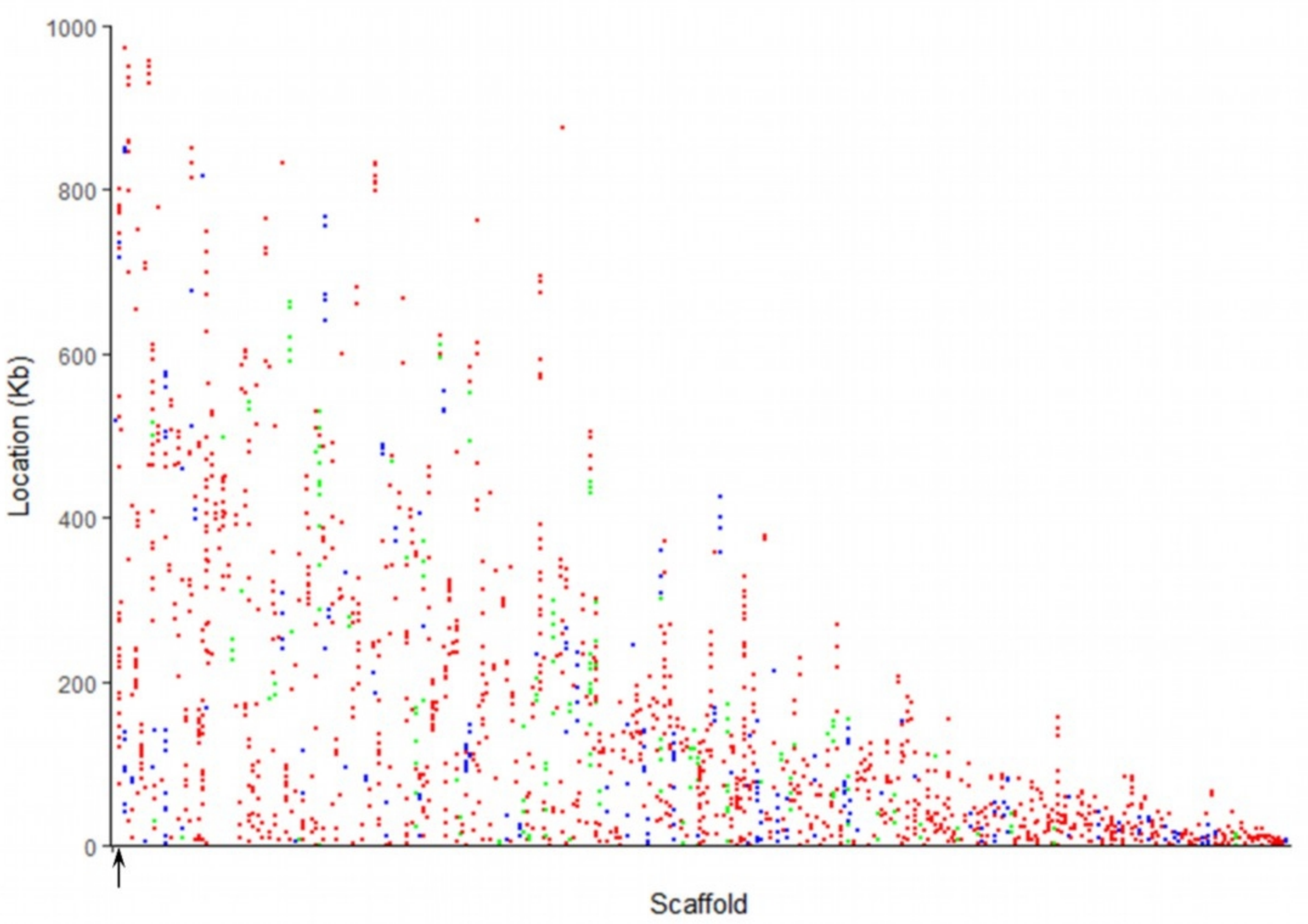


Figure S22. Predicted effectors of the three largest clusters (cluster numbers 3, 6, and 8) form tandem arrays on scaffolds. Each dot represents one gene. Only scaffolds (n=351) with ≥2 genes from a same cluster are shown (X-axis), and the scaffold length, if longer, is shown to the first 1000-kb (Y-axis). The arrow points to Scaffold #2 where 24 genes from the largest cluster (cluster 3) are located within an 800-kb region. Colors are coded such that cluster 3=red, 6=blue and 8=green.

Table S1. Genes of bacterial and fungal origin in *D. vitifoliae* and other insects. Horizontally transferred genes in *D. vitifoliae* and other insects [16,17]

Taxonomical group	**Species**	**Genome DB**	**LD-carboxypeptidase (*LdcA*)**[1]	**Rare lipoprotein A (*rlpA*)**[1]	**N-acetylmuramoyl-L-alanine amidase (*amiD*)**[1]	**Phytoene desaturase**[2]	**Lycopene cyclase/ Phytoene synthase**[2]
Aphididae	*Acyrthosiphon pisum*	NCBI	100168405	100163669, 100570300, 100167729, 100165005, 100570509	103308396	100169245	100161104
	Myzus persicae	NCBI	111041263	111033601, 111033591, 111033602, 111033592	111040498	111035763	111035746
	Diuraphis noxia	NCBI	107162751	107165933, 107165935	107164800	107165446	107165458
	Aphis glycines	Aphidbase	AG000567	AG002737, AG002738, AG002739	no hit	AG002135	AG002132
	Rhopalosipum padi	Aphidbase	Rpa16117	Rpa06900, Rpa06899, Rpa06898	no hit	no hit	Rpa14780
Phylloxeridae	*Daktulosphaira vitifoliae*	Aphidbase	no hit	no hit	no hit	DV3003641	DV3003639
Adelgidae	*Adelges cooleyi, Adelges laricis*	NA	NA	NA	NA	JN022785, JN022784	not confirmed
Psyllidae	*Diaphorina citri*	NCBI	no hit	no hit	103506806	no hit	no hit
Aphalaridae	*Pachypsylla venusta*	NCBI	no hit	no hit	no hit	no hit	no hit
Aleyrodidae	*Bemisia tabaci*	NCBI	no hit	no hit	no hit	no hit	no hit
Other insects	*Habropoda spp, Rhodnius prolixus, Blatella germanica, Drosophila spp.*	i5K	no hit	inconclusive	no hit	no hit	no hit

Putative homologs to genes of bacterial and fungal origin found by BLAST: [1] Gene of bacterial origin, [2] Gene of fungal origin , NA: no published genome

Table S2. Statistic results of the major superfamilies belonging to long terminal repeats (LTR) and terminal inverted repeats (TIR) orders. *Gypsy* and *hAT* elements are the most represented LTR and TIR superfamilies, respectively.

Classes	**Order**	**Super-families**	**Number of clusters**	**Total copy number**	**Coverage (% of the Genome)**
Class I	LTR	*Copia*	10	857	0.13
		Gypsy	259	14.577	2.88
		Bel/Pao	128	9.305	1.25
		ERV	10	519	0.12
Class II	TIR	*Tc1-mariner*	111	5.996	0.71
		piggyBac	21	1.268	0.14
		hAT	370	23.003	3.25
		CACTA	23	1672	0.18
		Merlin	1	42	0.004
		Transib	13	1.057	0.11
		PIF-Harbinger	20	1.506	0.19
		P	10	889	0.1
		Mutator	17	1.053	0.17

Table S3. GO enrichment of genes duplicated at different ancestral nodes on the branch leading to graphe phylloxera (Aphidomorpha; Phylloxeroidea). From more basal to more terminal, Sternorrhyncha, Psyllidae + Aphidomorpha, and Aphidomorpha. Node, GO category (biological process, molecular function and cellular component), GO term, p-value of enrichment and putative functions are indicated.

GO enrichment genes duplicated at different nodes

Node	#overlist	term	term_level	adj. pvalue	name
1. Sternorrhyncha					
Molecular_function	2	GO:0005515	1	5.54E-14	structural constituent of ribosome
Cellular_component	2	GO:0005737	1	6.96E-04	cytoplasm
2. Psyllidae + Aphidomorpha					
Molecular_function	2	GO:0003964	1	1.95E-04	RNA-directed DNA polymerase activity
3. Aphidomorpha					
Molecular_function	2	GO:0003735	1	2.13E-04	structural constituent of ribosome
	2	GO:0005488	1	2.47E-08	binding
	2	GO:0005515	1	7.86E-83	protein binding
Cellular_component	2	GO:0005622	1	3.49E-06	intracellular
	2	GO:0005634	1	1.66E-09	nucleus
	2	GO:0005737	1	1.51E-28	cytoplasm
	2	GO:0005739	1	2.60E-07	mitochondrion
	2	GO:0005783	1	7.63E-04	ndoplasmic reticulum
	2	GO:0005811	1	1.37E-05	lipid droplet
	2	GO:0005829	1	1.93E-10	cytosol
	2	GO:0005875	1	2.44E-06	microtubule associated complex
	2	GO:0005886	1	2.37E-07	plasma membrane
	2	GO:0005887	1	6.65E-06	integral component of plasma membrane
	2	GO:0012505	1	1.75E-04	endomembrane system
	2	GO:0016020	1	5.11E-05	membrane
Biological Process	2	GO:0006350	1	5.85E-05	transcription, DNA-templated
	2	GO:0006355	1	1.61E-04	regulation of transcription, DNA-templated
	2	GO:0006412	1	1.61E-04	translation
	2	GO:0006468	1	1.37E-05	protein phosphorylation
	2	GO:0006508	1	9.79E-09	proteolysis
	2	GO:0019233	1	4.41E-11	sensory perception
	2	GO:0022008	1	1.49E-11	neurogenesis
	2	GO:0048477	1	5.42E-04	oogenesis
	2	GO:0055114	1	4.34E-06	oxidation-reduction process

Table S4. Metabolic gaps in the *D. vitifoliae* reaction network. EC number, Gene ID, and type of annotation. Gene ID's linked by "and" are all required for function. Annotation categories are defined as follows: (i) *New gene prediction*: the gene was not called as part of the initial set of gene predictions. The gene was called, annotated, and is now part of the new official gene set, (ii) *New gene annotation*: The gene was called in the initial set of gene prediction but was not assigned any function by automated annotation. Function was assigned as a result of gap filling, and (iii) *Modified existing gene association*: the gene was called and assigned a function, gap filling identified an additional or alternative gene function.

Enzyme Name	EC Number	Gene ID(s)	Annotation Category
4-phosphopantotheoylcysteine decarboxylase	4.1.1.36	DV3025962.1	New gene prediction
nicotinamidase	3.5.1.19	DV3000063	New gene annotation
L-serine ammonia-lyase	4.3.1.17	DV3002372	Modified existing gene association
cysteine synthase	2.5.1.47	DV3002954	Modified existing gene association
glycerate 3-kinase	2.7.1.31	DV3011431	Modified existing gene association
glycine hydroxymethyltransferase	2.1.2.1	DV3018664	Modified existing gene association
glutamine—fructose-6-phosphate transaminase (isomerizing)	2.6.1.16	DV3002742	Modified existing gene association
enoyl-CoA hydratase	4.2.1.17	DV4015045	Modified existing gene association
2-(1,2-epoxy-1,2-dihydrophenyl) acetyl-CoA isomerase	5.3.3.18	DV3008326	Modified existing gene association
3-oxo-5,6-didehydrosuberyl-CoA thiolase	2.3.1.223	DV3017937	Modified existing gene association
spermine synthase	2.5.1.22	DV3017954	Modified existing gene association
3-hydroxybutyryl-CoA epimerase	5.1.2.3	DV3015045	Modified existing gene association
dodecenoyl-CoA isomerase	5.3.3.8	DV3015045	Modified existing gene association
fatty-acyl-CoA synthase	2.3.1.86	DV3018512, DV3000627, DV3004693	Modified existing gene association
nicotinamide phosphoribosyltransferase	2.4.2.12	DV3004539	Modified existing gene association
dihydropyrimidine dehydrogenase	1.3.1.1	DV3010281	Modified existing gene association
pimelyl-ACP methyl ester esterase	3.1.1.85	DV3004923	Modified existing gene association
dihydropyrimidine dehydrogenase	1.3.1.1	DV3010281	Modified existing gene association
ditrans,polycis-undecaprenyl-diphosphate synthase	2.5.1.31	DV3017386	Modified existing gene association
oxoglutarate dehydrogenase	1.2.4.2	DV3002078 and (DV3009715-PA or DV3006787) and DV3008581	Modified existing gene association
tripeptide aminopeptidase	3.4.11.4	DV3012927	Modified existing gene association
glycine dehydrogenase	1.4.4.2	DV3008581 and DV3001871 and DV3000698 and (DV3005511 or DV3020276)	Modified existing gene association
NADPH dehydrogenase	1.6.99.1	DV3017563	Modified existing gene association
protein phosphatase methylesterase-1	3.1.1.89	DV3009888	Modified existing gene association
versatile peroxidase	1.11.1.16	DV3001833, DV3001185, DV3010201, DV3000879	Modified existing gene association
acetaldehyde dehydrogenase	1.2.1.10	DV3000458, DV3009670, DV3010601, DV3008252	Modified existing gene association
acetaldehyde dehydrogenase	1.2.1.10	DV3000458, DV3009670, DV3010601, DV3008252	Modified existing gene association
glycerol-3-phosphate dehydrogenase	1.1.5.3	DV3012446	Modified existing gene association
1-pyrroline-5-carboxylate dehydrogenase	No EC	DV3010601	Modified existing gene association

Table S5. Functional annotation of metabolic genes in the Phylloxera, *Myzus persicae* and *Acyrthosiphon pisum* genomes. [1] Number of unique and complete numerical designations within the Enzyme Commission (EC) classification system for enzymes and their catalytic reactions. [2] comparison among the three species (Phylloxera, *Myzus persicae* and *Acyrthosiphon pisum*).

Species	***Daktulosphaira vitifoliae***	***Myzus persicae (G006)***	***Acyrthosiphon pisum***
Gene set ID	OGS v3.2	TGAC Annotation 1.0	OGS v2.1b
CycADS Database ID	DakviCyc	MyzpeCyc	AcypiCyc
Polypeptides	25840	24849	36228
Pathways	319	319	307
Enzymatic reactions	2377	2384	2339
Enzymes	3182	4646	5087
Compounds	1598	1603	1637
EC[1] present in the genome	1097	1115	1169
EC unique to this genome[2]	66	34	116
EC missing only in this genome[2]	71	21	49

Table S6. Identification of genes belonging to the TOLL pathway in *D. vitifoliae* based on the annotation available for *D. melanogaster.*

UniProt ID	**Flybase ID**	**name**	**Sequences producing best significant alignments**	**E-value**	**score**
Q03017	FBgn0000250	cact	DV3003678.2-PA gene=Cactus	118	2.00E-29
P98149	FBgn0011274	dif	DV3014881.2-PA gene=Dorsal	271	1.00E-79
P15330	FBgn0260632	dl	DV3014881.2-PA gene=Dorsal	454	3.00E-144
Q9VVR4	FBgn0040322	gnbp2	DV3010589-PA gene=DV3010589	125	2.00E-30
Q7K105		myd88	DV3005273.2-PA gene=myeloid differentiation primary response 88	141	3.00E-37
Q05652	FBgn0010441	pll	DV3016029-PA gene=DV3016029	296	5.00E-92
Q9VWU1	FBgn0030926	psh	DV3022332.2-PA gene=predicted effector 1928-5000	166	1.00E-46
Q9VCJ8		Spe	DV3019909-PA gene=DV3019909	177	9.00E-51
P48607		Spz	DV3006862.2-PA gene=spatzle	87	1.00E-19
P08953	FBgn0262473	toll	DV3003707.2-PA gene=Toll	435	1.00E-134
P22812		tube	DV3008856-PA gene=DV3008856	67.8	3.00E-12

Table S7. Identification of genes belonging to the IMD pathway in *D. vitifoliae* based on the annotation available for *D. melanogaster* (except for no-hit genes, e.g. Q8IPC3).

UniProt ID	**Flybase ID**	**name**	**in/out**	**Sequences producing best alignments**	**E-value**	**score**
Q9VS59	FBgn0082598	akirin	in	DV3005216-PA gene=DV3005216	108	5.00E-29
P35128	FBgn0000173	ben	in	DV3001602-PA gene=DV3001602	285	6.00E-99
P92208	FBgn0000229	bsk	in	DV3005807-PA gene=DV3005807	648	0.00E+00
P09085	FBgn0000251	cad	in	DV3019704.2-PA gene=caudal-3	135	5.00E-36
Q7JUP3	FBgn0034068	casp	in	DV3001972-PA gene=DV3001972	385	5.00E-124
Q24311	FBgn0015509	Cul1	in	DV3006657-PA gene=DV3006657	963	0
Q8IPC3	FBgn0032210	CYLD	out			
P36192	FBgn0010385	def	out			
Q24307	FBgn0015247	Diap2	in	DV3009949-PA gene=DV3009949	228	6.00E-68
Q8SWW8	FBgn0260866	dnr1	in	DV3014323.2-PA gene=E3 ubiquitin-protein ligase MYLIP	207	5.00E-59
Q8IRY7	FBgn0020381	Dredd	in	DV3011341-PA gene=DV3011341	80.1	4.00E-16
P25867	FBgn0011217	eff	in	DV3012664-PA gene=DV3012664	258	4.00E-89
Q9V3B4	FBgn0038928	fadd	out			
Q23977		hep	in	DV3010686-PA gene=DV3010686	430	6.00E-136
Q9VEZ5	FBgn0024222	ikkb	in	DV3002191-PA gene=DV3002191	111	2.00E-25
Q7K4Z4.1	FBgn0013983	IMD	out			
P18289		jra	in	DV3016658-PA gene=DV3016658	158	5.00E-46
P21525	FBgn0001297	kay	in	DV3008765-PA gene=DV3008765	60.1	2.00E-09
NP_729319	FBgn0011817	nemo	in	DV3004747.2-PA gene=serine/threonine-protein kinase NLK	650	0.00E+00
NP_608422	FBgn0031145	ntf2	in	DV3003037-PA gene=DV3003037	183	9.00E-160
Q9GNK5	FBgn0035976	PGRP-LC	out			
NP_523776	FBgn0040294	posh	in	DV3011697-PA gene=DV3011697	180	2.00E-47
Q94527	FBgn0014018	Rel	in	DV3014881.2-PA gene=Dorsal	162	5.00E-41
Q9VRP5	FBgn0260936	scny	in	DV3005278.2-PA gene=ubiquitin carboxyl-terminal hydrolase 36	344	5.00E-102
NP_730815.2	FBgn0037236	skp2	in	DV3014210-PA gene=DV3014210	150	1.00E-39
Q4TZQ4		tab2	out			
Q9V3Q6	FBgn0026323	tak1	in	DV3004556.1-PA gene=TGF-beta activated kinase 1	333	1.00E-105
NP_001286940.1	FBgn0035601	Uev1A	in	DV3004034-PA gene=DV3004034	231	5.00E-78

Table S8. Number of genes for different cuticular proteins sub-groups in *D. vitifoliae* (manual curation) and three aphid species. * Automatic annotation using CutProtFramPred, no manual curation.

CP sub-groups	***D. vitifoliae***	***M. persicae***	***A. pisum***	***D. noxia****
CPAP1	10	6	10	10
CPAP3	8	5	8	9
CPCFC	1	1	1	1
CPF	0	0	2	1
Tweedle	3	1	3	3
RR-1	11	13	14	12
RR-2	61	65	98	57
Total	**94**	**91**	**137**	**93**

Table S9. List and comparison of developmental genes in the *D. vitifoliae* and *A. pisum* genomes. In blue: genes not found. Part1:

Classes	Gene Name	Number of copies	symbol	scaffold	start	end	strand
1. Anterior-posterior axis formation	*bicoid*	0	-				
	exuperantia	1	*exu*	495	1614	6788	-
	torso	0	-				
	torso-like protein	2	*tsl-1*	153	30556	46072	+
			tsl-2	409	270198	274152	-
	staufen	1	*stau*	163	172837	182839	+
	nos, vas, pum, tud (in germ-cell development)						
	cad (in Gap genes)						
2. Dorsal-ventral axis formation	*snail*	0	-				
	short gastrulation	1	*sog*	144	447524	458891	-
	twist	1	*twi*	177	236031	240028	+
	crossveinless	1	*cv*	544	39992	44630	+
	dorsal	1	*dl*	329	120811	127888	-
	cactus	1	*cact*	184	424807	430798	-
	Drop	1	*Dr*	186	378388	382070	-
	pannier	1	*pnr*	13	82138	91739	-
	ventral nervous system defective	1	*vnd*	215	353543	360483	-
	gurken	0	-				
	intermediate neuroblasts defective	1	*ind*	4	738487	741356	+
	dachshund	2	*dac-1*	453	181439	209658	+
			dac-2	555	96556	116284	-
	tolloid	1	*tld*	35	713694	736887	-
	Race	0	-				
	zen (in Hox genes)						
	dpp,tkv and *tgfbr1* (in TGF-beta signaling)						
3. Hox genes	*labial*	1	*lab*	879	5876	25628	-
	proboscipedia	1	*pb*	612	11216	47474	+
	zerknüllt	0	-				
	Deformed	1	*Dfd*	218	54308	64316	-
	Sex combs reduced	1	*Scr*	218	193293	211340	-
	fushi tarazu	1	*ftz*	218	218666	220045	-
	Antennapedia	1	*Antp*	218	347931	363442	-
	Ultrabithorax	1	*Ubx*	737	138256	215533	+
	abdominal-A	1	*abd-A*	205	209056	235709	+
	Abdominal-B	1	*Abd-B*	1302	25688	30488	+
4. Segmentation - Gap genes	*Kruppel*	2	*Kr-2*	39	370715	377549	+
			Kr-1	185	101941	105133	+
	knirps	1	*kni*	324	58057	68980	-
	hunchback	1	*hb*	54	438888	443102	+
	tailless	1	*tll*	542	90047	94834	-
	empty spiracles	1	*ems*	449	88454	101741	+
	orthodenticle	1	*otd*	491	76397	102830	-
	Otx	0	-				
	cap-n-collar	1	*cnc*	257	154479	208718	+
	caudal	3	*cad-1*	1046	6086	8793	+
			cad-2	2021	4829	6030	-
			cad-3	860	28796	43916	-
	knot	1	*kn*	26	46250	79571	+
	giant	0	-				
	huckebein	0	-				
	buttonhead	0	-				

Table S9. Legend in the preceding page. Part2:

Classes	**Gene Name**	**Number of copies**	**symbol**	**scaffold**	**start**	**end**	**strand**
5. Segmentation - pair-rule genes	*hairy*	1	*h*	507	43994	47821	+
	even skipped	1	*eve*	198	199497	207954	-
	runt	2	*run-1*	355	196452	205877	-
			run-2	937	5530	10812	+
	ftz (in Hox genes)						
	odd skipped	2	*odd-1*	7	975573	978345	+
			odd-2	7	963819	965051	-
	sloppy paired	1	*slp*	534	181714	183575	+
	paird	0	-				
6. Segmentation - segment polartiy genes	*engrailed*	2	*en-1*	198	390864	402479	-
			en-2	198	318773	349713	+
	fused	1	*fu*	128	147432	155857	-
	gooseberry	1	*gsb-1*	433	215455	223347	+
			gooseberry-p1	2833	1243	2220	+
	Wg, arm, pan (in Wnt signaling)						
	hh, ptc, ci (in Hh signaling)						
7. Eye development	*twin of eyeless*	1	*toy*	145	350880	378445	-
	eyeless	2	*ey-1*	1555	1383	15325	-
			ey-2	928	37512	64135	+
	eyes absent	1	*eya*	50	376877	400438	-
	twin of eyegone	1	*toe*	1685	1339	2238	+
	eyegone	1	*eyg*	10314	116	317	-
	sine oculis	1	*so*	499	121303	141266	+
	Optix	1	*Optix*	268	250760	268797	-
	lozenge	1	*lz*	289	178730	205388	-
	sevenless	1	*sev*	273	158483	174481	-
	bride of sevenless	1	*boss*	105	230184	235144	+
	Son of sevenless	1	*Sos*	289	311036	314711	+
	downstream of receptor kinase	1	*drk*	338	440240	444008	+
	atonal	1	*ato*	77	694066	694585	+
	pointed	1	*pnt*	361	52652	75745	-
	hh (in Hh signaling)						
	Wg, dpp (in Wnt signaling)						
	dac (in Dorsal-Ventral axis formation)						
	Dl, ser (in Notch signaling)						
	Egfr (in EGF signaling)						
8. Salivary gland genes	*fork head*	1	*fkh*	26	453100	455934	-
	saliva	1	*slv*	83	278720	287383	+
	extradenticle	1	*exd*	1003	3191	27638	-
	homothorax	3	*hth-1*	277	99537	106214	+
			hth-2	143	163637	179124	+
			hth-3	143	189823	214685	+
9. Appendage developmental genes	*apterous*	2	*ap-1*	98	599879	614498	-
			ap-2	98	670044	698588	-
	Distal-less	1	*Dll*	392	315693	354992	-
	dpp (in Wnt signaling)						
	hh (in Hh signaling)						
	en (in segment polarity)						

Table S9. Legend in the preceding pages. Part3:

Classes	Gene Name	Number of copies	symbol	scaffold	start	end	strand
10. Nurogenesis and muscle	*nautilus*	0	-				
	nubbin	1	*nub*	134	572199	601225	+
	castor	1	*cas*	137	587896	638128	-
	achaete	0	-				
	scute	0	-				
	asense	0	-				
	lethal of scute	0	-				
	ato (in eye development)						
	Dl and N (in Notch signalling)						
11. Gem-cell development	*armitage*	1	*armi*	7	347915	357173	-
	bruno 1	0	-				
	cappuccino	1	*capu*	184	385770	404785	+
	cup	0	-				
	mago nashi	2	*mago-1*	523	24376	27222	+
			mago-2	190	50787	55999	+
	oo18 RNA-binding protein	0	-				
	spire	1	*spir*	49	567784	586723	-
	oskar	0	-				
	valois	0	-				
	vasa	4	*vas-1*	102	336827	346608	-
			vas-2	102	274123	283160	-
			vas-3	60	454821	463448	-
			vas-4	95	671350	676692	+
	tuder	1	*tud*	401	37741	41026	+
	stau (in Anterior-posterior axis formation)						
	germ cell-less	0	-				
	gustavus	1	*gus*	468	16847	33631	-
	pipsqueak	1	*psq*	25	668106	680064	+
	nanos	3	*nos-1*	389	136705	138652	-
			nos-2	43	211197	215297	+
			nos-3	300	209744	215053	+
	wunen	0	-				
	wunen-2	0	-				
	HMG Coenzyme A reductase	1	*Hmgcr*	61	204652	219637	+
	argonaute-3	2	*ago-3-a*	392	6496	23191	+
			ago-3-b	440	3272	26332	-
	aubergine	0	-				
	piwi	2	*piwi-1*	227	119927	157232	-
			piwi-2	227	186276	215905	-
	pumilio	1	*pum*	120	907333	912298	+
	Tropomyosin 1	1	*Tm1*	35	143676	153089	+
	par-1	0	-				
	zero population growth	0	-				
	swallow	0	-				
	polar granule component	0	-				
	spindle E	1	*spn-E*	248	49438	77571	+

Table S10, part1. miRNAs predicted by miRDeep2 (Part1, 'known' miRNAs, Part2, 'novel' miRNAs). 'Known' miRNAs are miRNAs with orthologs reported from other species, while 'novel' miRNAs are specific to *D. vitifoliae*. Clusters were assigned based on sorted scaffold numbers while the number of each cluster member is assigned based on its position. Duplications were assigned based on the sorted given miRNA names and duplicates were assigned based on genomic position. Pairs of miRNAs encoded from both strands at the same genomic location are named Both# and the numbers are assigned based on the sorted given miRNA names; + and - is in reference to the scaffold in the assembly. Part1.

miRNA name	provisional id	miRDeep2 score	total read count	mature read count	loop read count	star read count	significant randfold p-value	consensus mature sequence	consensus star sequence	consensus precursor sequence	precursor coordinate	Clusters (distance < 10 kb)	Duplications	Encoded by both strands	Topology
Dvit-bantam	scaffold200_11861	462260.7	906698	905984	25	689	yes	ugagaucauugugaaagcuaau	ugguuuucacuuugaucugucaga	ugguuuucacuuugaucugucagauuuauguuuugccuuuucugagaucauugugaaagcuaau	scaffold200:126202..126266:+				IGR (Between DV3005276.2 and DV3005280.2)
Dvit-let-7	scaffold30_3527	8998.2	17642	17512	1	129	yes	ugagguaguugguuguauagu	cuauacaaucggcuaacuuuucu	ugagguaguugguuguauaguaccauauaaucaauuuggaacguacuauacaaucggcuaacuuuucu	scaffold30:608779..608847:-	Cluster7-1			Exon (of DV3002867)
Dvit-miR-10	scaffold218_12729	2865228	5620020	5538002	0	82018	yes	uacccuguagauccgaauuugu	caaauucgguucuagagagguuu	uacccuguagauccgaauuuguuugaaaaacggcgacaaauucgguucuagagagguuu	scaffold218:95780..95839:-				3UTR&Exon Conjunction (of DV3014923.2)
Dvit-miR-100	scaffold30_3529	382.5	751	732	0	19	no	gacccguagauccgaacuugug	caaguacgguucuagaggaca	gacccguagauccgaacuugugucguaaaauuuagcaucgcaaguacgguucuagaggaca	scaffold30:612021..612082:-	Cluster7-2			Intron (of DV3002867)
Dvit-miR-1000	scaffold280_15631	5	7063	7011	28	24	yes	auauuguccugucacagcag	cugcuguugcgggacauuuuca	auauuguccugucacagcaguaaugucacauuuaugaaucguacugcuguugcgggacauuuuca	scaffold280:208680..208745:-	Cluster5-1			IGR (Between DV3014985 and DV3014989.1)
Dvit-miR-124*	scaffold116_8112	984.2	1935	1426	0	509	no	cgcauucuccguuggucaauuaug	uaaggcacgcggugaaugcca	cgcauucuccguuggucaauuauguguaaaauuauucuucauaaggcacgcggugaaugcca	scaffold116:76333..76395:+				Intron&Exon Conjunction (of DV3008513)
Dvit-miR-137	scaffold88_7006	1002.5	1969	1639	0	330	yes	uuauugcuugagaauacacguag	ccgcguauucuugggacauaaca	ccgcguauucuugggacauaacacauauuuaagacuguuauugcuugagaauacacguag	scaffold88:195796..195856:-				IGR (Between DV3000981.2 and DV3000984.2)
Dvit-miR-13a	scaffold690_30149	65869.6	129194	128581	0	613	yes	uaucacagccacuuugaugagc	caucaaaauggaugugaagug	caucaaaauggaugugaaguguacauuacaauauucauaucacagccacuuugaugagc	scaffold690:75678..75737:+	Cluster12-3	Duplication1-1		Intron (of DV3017631)
Dvit-miR-13b	scaffold690_30151	1041823.9	2043496	2042694	0	802	no	uaucacagccguuuuugacaauu	uggucaaaucggaugugacgug	uggucaaaucggaugugacguguugauaugucuauucauaucacagccguuuuugacaauu	scaffold690:76517..76578:+	Cluster12-4	Duplication1-2		Intron (of DV3017631)
Dvit-miR-14	scaffold368_19305	218285.6	428151	423581	61	4509	yes	ucagucuuuuucucucuccuau	cggagagaguuaacaggcuuuggcu	cggagagaguuaacaggcuuuggcuguuuacauguuugucauuagucagucuuuuucucucuccuau	scaffold368:38036..38103:+				IGR (At scaffold end before DV3025882.1)
Dvit-miR-184a	scaffold1_17	179121.7	351332	349682	0	1650	yes	uggacggagaacugauaagggc	ccuuaucauucuucgccuugu	ccuuaucauucuucgccuugugugcauuuuaaacaacuggacggagaacugauaagggc	scaffold1:352628..352687:+		Duplication2-1		IGR (Between DV3002342 and DV3002343)
Dvit-miR-184b	scaffold360_19068	59781	117250	116837	0	413	yes	uggacggagaacugauaaaggu	cuuuaucauucucuugucuugu	cuuuaucauucucuugucuuguguguauguuaaacuacuggacggagaacugauaaaggu	scaffold360:52323..52383:-		Duplication2-2		Intron (of DV3010567)
Dvit-miR-190	scaffold339_18126	5318.9	10425	10248	0	177	yes	agauauguuugauauucuugguug	accgggaaucagacauauugua	agauauguuugauauucuugguuguaauauuugaaaucgaccgggaaucagacauauugua	scaffold339:80816..80877:+				Intron (of DV3005333)
Dvit-miR-252a	scaffold89_7026	3087	6049	6041	2	6	yes	cuaaguacuagugccgcgggag	ccugcagcucaagugcuuauca	cuaaguacuagugccgcgggagugguuuccuauuuuguaucuccugcagcucaagugcuuauca	scaffold89:496123..496187:+	Cluster13-2	Duplication3-1		IGR (Between DV3005002 and DV3005004)
Dvit-miR-252b-1	scaffold110_7879	16987.4	33320	32955	9	356	yes	uaaguaguagcgccaacgguga	accugcguacuacugcuuacc	uaaguaguagcgccaacggugaauugaauuuaaauaugucaccugcguacuacugcuuacc	scaffold110:207217..207278:-		Duplication3-2		IGR (At scaffold end after DV3015934
Dvit-miR-252b-2	scaffold89_7024	16987.8	33320	32955	9	356	yes	uaaguaguagcgccaacgguga	accugcguacuacugcuuacc	uaaguaguagcgccaacggugaauuguauuuaaauaugucaccugcguacuacugcuuacc	scaffold89:488252..488313:+	Cluster13-1	Duplication3-3		IGR (Between DV3005002 and DV3005004)
Dvit-miR-263a	scaffold162_10057	80164.1	157230	152905	75	4250	yes	aauggcacugaaagaauucacggg	cguaauucuucugugccgugcu	aauggcacugaaagaauucacggguacucacauuuuuauaccgcccguaauucuucugugccgugcu	scaffold162:230133..230201:-	Cluster3-2	Duplication4-1		IGR (Between DV3007646 and DV3007648)
Dvit-miR-263b	scaffold162_10055	704.2	1376	1325	7	44	yes	cuuggcacuggaagaauucacaga	gugagucucucggugucaauua	cuuggcacuggaagaauucacagacugaauguuauaaagaucgugagucucucggugucaauua	scaffold162:221202..221266:-	Cluster3-1	Duplication4-2		IGR (Between DV3007646 and DV3007648)
Dvit-miR-275	scaffold59_5347	17100.7	33534	31009	66	2459	yes	ucagguaccugaaguagcgcg	ggcugcugcaggcacuuuuagacu	ggcugcugcaggcacuuuuagacucuguauuguuugaugaagucagguaccugaaguagcgcg	scaffold59:130977..131040:+	Cluster10-1			IGR (Between DV3009288 and DV3009292)
Dvit-miR-2765	scaffold109_7852	16999.3	33336	31358	146	1832	yes	ugguaacuccaaaccauugccgg	cgcaaugguuggaaguuccuca	ugguaacuccaaaccauugccggugucuuguaauucuuuuguaucccgcaaugguuggaaguuccuca	scaffold109:139874..139942:+	Cluster1-1			IGR (Between DV3012389 and DV3012392.2)
Dvit-miR-276a	scaffold25_3139	1240309.1	2432805	2427679	72	5054	yes	uaggaacuucauaccgugcucu	agcgagguauagaguuccuacg	agcgagguauagaguuccuacguucaaaauauuucauuauucguaggaacuucauaccgugcucu	scaffold25:160833..160899:+			Both1 +	IGR (Between DV3025716.1 and DV3004263)
Dvit-miR-276b	scaffold25_3174	4.7	20	18	0	2	yes	uaggaacucuauaccucgcuag	cacgguaugaaguuccuacgaau	cacgguaugaaguuccuacgaauaaugaaauauuuuugaacguaggaacucuauaccucgcuag	scaffold25:160831..160895:-			Both1 -	IGR (Between DV3004260 and DV3004265)
Dvit-miR-278	scaffold18_2623	12978.5	25448	19802	12	5634	yes	ucggugggacuuucguucguuu	acgggcgaagguuucaucaauc	acgggcgaagguuucaucaaucguguuacauuaagcgugucggucggugggacuuucguucguuu	scaffold18:449212..449277:+				IGR (Between DV3011526 and DV3011528)
Dvit-miR-279a	scaffold505_24573	153621.8	301315	295123	46	6146	yes	ugacuagauccacacucaucc	augggugugcgucuugugacaug	augggugugcgucuugugacaugcuuuuuauauuuauucgacaugacuagauccacacucaucc	scaffold505:59622..59686:+		Duplication5-1		Exon (of DV3017081)
Dvit-miR-279b	scaffold250_14514	68331.5	134024	129264	118	4642	yes	ugacuagaucuacacucauca	cguggguguucuucuagucuaca	cguggguguucuucuagucuacacuaaguaaauaaguuugugacuagaucuacacucauca	scaffold250:223628..223689:-		Duplication5-2		Intron (of DV3016322.1)
Dvit-miR-281	scaffold277_15541	129064.9	253155	246494	1	6660	yes	aagagagcuauccgucgacagu	ugucauggaguugcucucuu	aagagagcuauccgucgacaguauaaugauugacuacacugucauggaguugcucucuu	scaffold277:112571..112630:-				3UTR (of DV3015052)
Dvit-miR-29	scaffold281_15796	7141.8	14003	13684	39	280	yes	uagcaccauuugaaaccaguac	acugguuuuuuuuggugguaga	acugguuuuuuuuggugguagacuaaaauguugaacucaucuagcaccauuugaaaccaguac	scaffold281:267179..267244:-				Intron (of DV3006964)
Dvit-miR-2a	scaffold690_30153	79686.9	156302	156243	0	59	yes	ucacagccagcuuugaugagcg	cucacaaagcaacugugaaaug	cucacaaagcaacugugaaauguagauauugaagaaucauaucacagccagcuuugaugagcg	scaffold690:76626..76689:+	Cluster12-5	Duplication6-1		Intron (of DV3017631)
Dvit-miR-2b	scaffold690_30155	51584.7	101174	101079	92	3	yes	uaucacagccagcuuuguaug	aucaaagugguagugaaac	aucaaagugguagugaaacguucuauuuucuuaauuauacauuaauucguaucacagccagcuuuguaug	scaffold690:76757..76827:+	Cluster12-6	Duplication6-2		Intron (of DV3017631)
Dvit-miR-2c	scaffold690_30147	77807.6	152615	147957	24	4634	yes	ucacagccagcuuugaugagca	cgucaaagcgggcugucguaga	cgucaaagcgggcugucguagaguguuaacuguguuugacuaucacagccagcuuugaugagca	scaffold690:75558..75622:+	Cluster12-2	Duplication6-3		Intron (of DV3017631)
Dvit-miR-3016	scaffold57_5279	148603.9	291474	289467	55	1952	yes	auugguaacacucaacgucuuuag	aaagauguuuuuguugccuuug	auugguaacacucaacgucuuuagcauguuauuaaugaaagccuaaagauguuuuuguugccuuug	scaffold57:345463..345529:-	Cluster9-4			IGR (Between DV3005077.2 and DV3005080.2)
Dvit-miR-3024a-1	scaffold299_16540	4.5	101774	101774	0	0	yes	ucuuugggauuuaagagagc	uaucuagaauuccaaaau	ucuuugggauuuaagagagcagguuuagauaauuaauaaaauuaauuaccagcuaucuagaauuccaaaau	scaffold299:20950..21021:+	Cluster6-4	Duplication7-1		IGR (Between DV3005472 and DV3005476)
Dvit-miR-3024a-2	scaffold57_5281	4.2	101774	101774	0	0	yes	ucuuugggauuuaagagagc	uaucuugaauuucaaaau	ucuuugggauuuaagagagcagguuuuaaguuugaaauaccagcuaucuugaauuucaaaau	scaffold57:345578..345640:-	Cluster9-5	Duplication7-4		IGR (Between DV3005077.2 and DV3005080.2)
Dvit-miR-3024b	scaffold299_16546	1.4	64	64	0	0	yes	ucuuugggauuuccagcgagcug	gcucuuuuaaauuccaagaua	ucuuugggauuuccagcgagcuggucaaaauuaaauuaaauuaucagcucuuuuaaauuccaagaua	scaffold299:21931..21998:+	Cluster6-7	Duplication7-2		IGR (Between DV3005472 and DV3005476)
Dvit-miR-3024c	scaffold57_5273	4.4	24628	24079	124	425	yes	ucuuugggauuucuagugggcu	aguuccuuagaaucccaggaua	ucuuugggauuucuagugggcugguauaaagaguauaaauugaccaguuccuuagaaucccaggaua	scaffold57:344857..344924:-	Cluster9-1	Duplication7-3		IGR (Between DV3005077.2 and DV3005080.2)
Dvit-miR-3027-1	scaffold3852_48070	40707.4	79838	63755	5	16078	yes	ccagucuugcauuuauuccacu	ggggauaauuguagggcuuacu	ggggauaauuguagggcuuacuguucccuuuaaauacagccagucuugcauuuauuccacu	scaffold3852:363..424:-		Duplication8-1		IGR (At scaffold end before DV3023864)
Dvit-miR-3027-2	scaffold750_31842	40707.4	79838	63755	5	16078	yes	ccagucuugcauuuauuccacu	ggggauaauuguagggcuuacu	ggggauaauuguagggcuuacuguucccuuuaaauacagccagucuugcauuuauuccacu	scaffold750:19392..19453:-		Duplication8-2		Intron (of DV3018158.2)
Dvit-miR-3030a	scaffold299_16538	89043.7	174659	173621	81	957	yes	agguaacggauuugcuguggga	ccaagcgaauuucgauacccu	agguaacggauuugcugugggauuauggacguuuaaauucccaagcgaauuucgauacccu	scaffold299:20846..20907:+	Cluster6-3	Duplication9-1		IGR (Between DV3005472 and DV3005476)
Dvit-miR-3030b	scaffold57_5283	99367.1	194904	180125	39	14740	yes	agguaacggauuugcuauggga	ccaagcgaauccuguacccug	agguaacggauuugcuaugggaaagaucauguuaaauaucccaagcgaauccuguacccug	scaffold57:345705..345766:-	Cluster9-6	Duplication9-2		IGR (Between DV3005077.2 and DV3005080.2)
Dvit-miR-3032a*	scaffold299_16533	233.7	452	331	1	120	yes	ugacuagaauuauacuagca	guuaguauuguucuuaguaacg	guuaguauuguucuuaguaacgcgugaaaauuuaauucgugacuagaauuauacuagca	scaffold299:20327..20386:+	Cluster6-1	Duplication10-1		IGR (Between DV3005472 and DV3005476)
Dvit-miR-3032b*	scaffold57_5288	2.5	62216	60811	39	1366	yes	ugacuagaauuuauacuacu	gguaguauaauucuuaguaaca	gguaguauaauucuuaguaacauugauuauuuaaguacugugacuagaauuuauacuacu	scaffold57:346050..346110:-	Cluster9-8	Duplication10-2		IGR (Between DV3005077.2 and DV3005080.2)
Dvit-miR-3038*	scaffold226_12999	101.9	199	178	0	21	yes	caaugcccuuagaaaucccaug	ugggguuucgauaggcauuuacc	ugggguuucgauaggcauuuaccuuguagauuaaaauggcaaugcccuuagaaaucccaug	scaffold226:166057..166118:+				IGR (Between DV3012084 and DV3012092)
Dvit-miR-3040*	scaffold109_7854	16709.1	32767	25694	12	7061	yes	ugguaacuccaccaccgauugcg	cagccgguggugacuguucccaca	ugguaacuccaccaccgauugcguuuuuuuuuuguuucaaaaauuguuuugaacucgcagccgguggugacuguucccaca	scaffold109:140047..140131:+	Cluster1-2			IGR (Between DV3012389 and DV3012392.2)
Dvit-miR-3041	scaffold299_16549	15253.1	29910	23520	0	6390	yes	uuaaagcuuugaugacgggau	ucccgaucgucaaguuuuaggu	ucccgaucgucaaguuuuagguuuuaauaauuuuacaauacuuaaagcuuugaugacgggau	scaffold299:25866..25930:+	Cluster6-9			IGR (Between DV3005472 and DV3005476)
Dvit-miR-3049a	scaffold294_16228	654.6	1275	1134	0	141	yes	ucgggaaggcaguugcggcggacu	uccguccaacuccuuuccguuu	ucgggaaggcaguugcggcggacugugugcuaauauauuaguccguccaacuccuuuccguuu	scaffold294:138647..138710:+			Both2 +	IGR (Between DV3017398 and DV3017399)
Dvit-miR-3049b	scaffold294_16237	17.8	34	33	0	1	yes	acggaaaggaguuggacggacu	uccgccgcaacugccuucccgauu	acggaaaggaguuggacggacuaauauauuagcacacaguccgccgcaacugccuucccgauu	scaffold294:138645..138708:-			Both2 -	IGR (Between DV3017397 and DV3017401.2)
Dvit-miR-305	scaffold59_5350	42485.1	83333	83327	0	6	yes	auuguacuucaucaggugcu	acuuguuggagugcaauu	auuguacuucaucaggugcucugguaaugcugaaaucccggcacuuguuggagugcaauu	scaffold59:131209..131270:+	Cluster10-2			IGR (Between DV3009288 and DV3009292)
Dvit-miR-3053	scaffold57_5275	38108.8	74741	74637	0	104	yes	agguaacuuauucacugugga	cacgggagaaugggggaccccg	agguaacuuauucacugugggagugauauuaaauaucccacgggagaaugggggaccccg	scaffold57:345100..345160:-	Cluster9-2			IGR (Between DV3005077.2 and DV3005080.2)
Dvit-miR-306	scaffold118_8162	14123.3	27695	27580	0	115	yes	ccagguacuaagugacuucug	aguuggcucuaaguaccucuaac	ccagguacuaagugacuucugagugaaauuaaaaauuauacaucaguuggcucuaaguaccucuaac	scaffold118:4838..4905:+	Cluster2-2			Intron (of DV3008114)
Dvit-miR-317	scaffold223_12925	80142.2	157188	156710	0	478	yes	ugaacacagcugguguaucucagu	ugggaaccccgcgguguuaacu	ugggaaccccgcgguguuaacuugucauaauauuucgaugcauuauucgauaaaucagagugaacacagcugguguaucucagu	scaffold223:172812..172897:+	Cluster4-1			IGR (Between DV3010857 and DV3010858)
Dvit-miR-34	scaffold223_12930	3937.3	7715	6972	7	736	yes	uggcagugugauuagcugguugug	cgaccacuaaacacauuccacu	uggcagugugauuagcugguuguguacaauaauuaauuuacuacucacgaccacuaaacacauuccacu	scaffold223:182494..182563:+	Cluster4-2			IGR (Between DV3010858 and DV3010861)
Dvit-miR-375	scaffold466_23533	39629	77730	77479	0	251	yes	uuuguucguucggcucgaguca	ccuugagccuagaggacaaau	ccuugagccuagaggacaaauuuguucauuauucgaaaaucaauuuguucguucggcucgaguca	scaffold466:36696..36761:+				IGR (Between DV3015519 and DV3015520)
Dvit-miR-7-1	scaffold419_21829	3.6	3875	3870	3	2	yes	uggaagacuagugauuuuguu	caagaagucucuagucuucuua	uggaagacuagugauuuuguuguuuuaauguaaaucuuccuaacaagaagucucuagucuucuua	scaffold419:248568..248633:-	Cluster14-1	Duplication11-1		IGR (Between DV3009493 and DV3009494)
Dvit-miR-7-2	scaffold419_21831	3.6	3875	3870	3	2	yes	uggaagacuagugauuuuguu	caagaagucucuagucuucuua	uggaagacuagugauuuuguuguuuuaauguaaaucuuccuaacaagaagucucuagucuucuua	scaffold419:331200..331265:-	Cluster14-2	Duplication11-2		Intron (of DV3009500)
Dvit-miR-71	scaffold690_30145	247771.7	485993	476228	0	9765	yes	ucucacuaucuugucuuucaug	ugaaagacaugggguagugagaug	ugaaagacauggguagugagauguaaaauugaaaccuaucucacuaucuugucuuucaug	scaffold690:75442..75502:+	Cluster12-1			Intron (of DV3017631)
Dvit-miR-8	scaffold51_4888	2.9	1858877	1855094	0	3783	yes	uaauacugucagguaaugaug	cgucuuacuuuggcaggauuaga	cgucuuacuuuggcaggauuagagugaauuaaaaugucuaauacugucagguaaugaug	scaffold51:268769..268828:-				IGR (Between DV3006020.1 and DV3006022.1)
Dvit-miR-87a	scaffold61_5431	6612.8	12963	12225	0	738	yes	gugagcaaaguuucaggugugc	gggccugacucguugcucaaccu	gggccugacucguugcucaaccugugcauuuauuauuaggugagcaaaguuucaggugugc	scaffold61:746000..746061:+	Cluster11-1	Duplication12-1		IGR (Between DV3002239 and DV3002243)
Dvit-miR-87b*	scaffold61_5434	5436.3	10662	5494	5	5163	yes	cgccugaaacuugcuuugaccu	gugagcaaaguuucaggcgugu	cgccugaaacuugcuuugaccucgauuuauuuacgguaaggugagcaaaguuucaggcgugu	scaffold61:746138..746200:+	Cluster11-2	Duplication12-2		IGR (Between DV3002239 and DV3002243)
Dvit-miR-927a	scaffold232_13115	9268.2	18173	16703	3	1467	yes	uuuagaauuccuacgcuuuacc	caaagcguuugaauuuuaaac	uuuagaauuccuacgcuuuaccuauacuuuaucaaaauggcaaagcguuugaauuuuaaac	scaffold232:92765..92827:-			Both3 -	IGR (Between DV3017604 and DV3017608)
Dvit-miR-927b	scaffold232_13107	262.7	515	510	0	5	yes	uaaagcguaggaauucuaaaau	uuuaaaauucaaacgcuuugcc	uuuaaaauucaaacgcuuugccauuuugauaaaguauagguaaagcguaggaauucuaaaau	scaffold232:92767..92829:+			Both3 +	IGR (Between DV3017605 and DV3017606)
Dvit-miR-929	scaffold219_12752	272.9	527	517	0	10	yes	aaauugacucuaguagggagu	cucucuaaugggggucagauuga	aaauugacucuaguagggaguccuucuauuuaaugugacucucuaaugggggucagauuga	scaffold219:138982..139042:+			Both4 +	Intron (of DV3017036.2)
Dvit-miR-929*	scaffold219_12777	103.7	208	206	1	1	yes	aaucugaccccauuagagaguc	cucccuacuagagucaauuug	aaucugaccccauuagagagucacauuaaauagaaggacucccuacuagagucaauuug	scaffold219:138981..139040:-			Both4 -	IGR (Between DV3017031 and DV3017045)
Dvit-miR-92a	scaffold394_20958	17301	33929	30562	0	3367	yes	uauugcacaugucccggccaau	cggucgaugaccuguguaacuauu	cggucgaugaccuguguaacuauuguauaaauucgacaaauauugcacaugucccggccaau	scaffold394:30892..30954:-	Cluster8-2	Duplication13-1		IGR (Between DV3012759 and DV3012761)
Dvit-miR-92b	scaffold394_20956	44458	87196	86355	18	823	yes	uauugcacuugacccagccugc	agguuguguugugugcaaugug	agguuguguugugugcaaugugcguuuguucaauuaguauguuauuuucauauugcacuugacccagccugc	scaffold394:30727..30799:-	Cluster8-1	Duplication13-2		IGR (Between DV3012759 and DV3012761)
Dvit-miR-971	scaffold228_13039	4.5	264	151	0	113	yes	uugguguucaaccuuacagu	acuuuaaguuugaucaccaagc	acuuuaaguuugaucaccaagccucagugcuaaauuguuugguguucaaccuuacagu	scaffold228:213624..213682:+				IGR (Between DV3006987 and DV3006988)
Dvit-miR-981	scaffold511_24787	174.8	336	300	2	34	yes	uucguuguugaugaaaccuuga	uggguuucucaauagcagaacc	uggguuucucaauagcagaaccuugacacagaauuaauaugguucguuguugaugaaaccuuga	scaffold511:140527..140591:+				IGR (At scaffold end after DV3014771)
Dvit-miR-993-1	scaffold300_16668	7141	13998	6409	29	7560	yes	gaagcucgucucuacagguaucu	cuacccuguagauccgggcu	cuacccuguagauccgggcuuuuguagaauaaugauuugcauuucagaagcucgucucuacagguaucu	scaffold300:336013..336082:-		Duplication14-1		IGR (Between DV3010119 and DV3010120.2)
Dvit-miR-993-2	scaffold7361_49118	7141	13998	6409	29	7560	yes	gaagcucgucucuacagguaucu	cuacccuguagauccgggcu	cuacccuguagauccgggcuuuuguagaauaaugauuugcauuucagaagcucgucucuacagguaucu	scaffold7361:265..334:-		Duplication14-2		IGR (no genes predicted on this scaffold)
Dvit-miR-996*	scaffold58_5324	16730.6	32815	20917	0	11898	yes	acggguguagucuuuagugcacg	ugacuagaguuacacucguca	acggguguagucuuuagugcacguugauuuugaaauucgugacuagaguuacacucguca	scaffold58:495924..495984:+				Intron (of DV3006260.1)
Dvit-miR-998	scaffold120_8289	169262.5	332007	331566	1	440	no	uagcaccauggaauucagcug	acugaauuuuacgagugccgca	acugaauuuuacgagugccgcauguaauguaugucuuguagcaccauggaauucagcug	scaffold120:822838..822897:+				Intron (of DV3002008)
Dvit-miR-9a	scaffold138_9000	57466.7	112710	112447	202	61	yes	ucuuugguuaucuagcuguauga	auaggucuaggugaccgaaguu	ucuuugguuaucuagcuguaugaguguaacguuucauugauucucauaggucuaggugaccgaaguu	scaffold138:295939..296006:+		Duplication15-1		Intron (of DV3016190)
Dvit-miR-9b	scaffold118_8160	10193.5	19989	19824	2	163	yes	ucuuugguacucuagcuguagg	uaaagcuuuuguaccuaaguga	ucuuugguacucuagcuguagguauauuauaaguuggccuaaagcuuuuguaccuaaguga	scaffold118:3269..3330:+	Cluster2-1	Duplication15-2		IGR (At scaffold end before DV3008114)
Dvit-miR-iab-4	scaffold205_12089	3.9	138	126	0	12	yes	acguauacuaaauguauccug	cgguauaccuucaguauacguaac	acguauacuaaauguauccugagugcauuauaaacuguccgguauaccuucaguauacguaac	scaffold205:114943..115006:-			Both5 -	IGR (At scaffold end after DV3021311)
Dvit-miR-iab-4*	scaffold205_12082	356.8	698	491	0	207	yes	uuacguauacugaagguauaccgga	aggauacauuuaguauacguaca	uuacguauacugaagguauaccggacaguuuauaaugcacucaggauacauuuaguauacguaca	scaffold205:114944..115009:+			Both5 +	IGR (At scaffold after DV3025607.1)

Table S10, part2. See preceding page for the legend.

miRNA name	provisional id	miRDeep2 score	total read count	mature read count	loop read count	star read count	significant randfold p-value	consensus mature sequence	consensus star sequence	consensus precursor sequence	precursor coordinate	Clusters (distance < 10 kb)	Duplications	Encoded by both strands	Topology
Dvit-miR-x1	scaffold10_1850	0.7	1289	1216	0	73	yes	acugaucuguuuucuuacuuacu	uaaguaaggaaauggguaucu	uaaguaaggaaauggguaucuauuguuucuuuguuuguaacaacugaucuguuuucuuacuuacu	scaffold10:1340790..1340856:-		Duplication16-1		Intron (of DV3000834)
Dvit-miR-x2	scaffold436_22300	3.3	8	4	0	4	yes	auaagaaaacugguuucuauuguu	caauugaccuauuuccuuauuu	auaagaaaacugguuucuauuguuauuauuuauaacaauugaccuauuuccuuauuu	scaffold436:115648..115705:-		Duplication16-2		IGR (Between DV3012678 and DV3012680.2)
Dvit-miR-x3a	scaffold335_18052	0.3	2718	2717	1	0	yes	auugaccuguuuacuuacuuacu	uaaggaagaaagcagguuucaauug	uaaggaagaaagcagguuucaauuguucuuauuguuuguauuaauugaccuguuuacuuacuuacu	scaffold335:51676..51742:-		Duplication16-3		IGR (Between DV3017612.2 and DV3017615)
Dvit-miR-x3b	scaffold451_22682	2	7137	7061	5	71	yes	auugaccuguuuccuuacuuacu	uaaggaaacggauucuauuguu	uaaggaaacggauucuauuguucucauuguuuauaacaauugaccuguuuccuuacuuacu	scaffold451:116515..116576:+		Duplication16-4		IGR (At scaffold end after DV3019074)
Dvit-miR-x3c	scaffold1069_39320	1569.4	3079	3023	0	56	yes	auugaccuguuugcuuacuuacu	uaaguuaggaaauggguuucu	uaaguuaggaaauggguuucuauuggucucauuauuuauaacaauugaccuguuugcuuacuuacu	scaffold1069:4840..4906:-		Duplication16-5		IGR (At scaffold end before DV3021221)
Dvit-miR-x3d	scaffold46_4463	1.6	807	800	0	7	yes	auugaccuguuuuguuacuuacu	aauaaggaaauggguuuuaauu	aauaaggaaauggguuuuaauuguuuugauuguaacaauugaccuguuuuguuacuuacu	scaffold46:592274..592334:+		Duplication16-6		IGR (Between DV3007574.2 and DV3007576)
Dvit-miR-x4	scaffold699_30519	2429.6	4764	4745	0	19	yes	auuuaccuguuuccuuacuuacu	caagcaaggaaacagguuuuuauug	caagcaaggaaacagguuuuuauuguuuuaauuguaacaauuuaccuguuuccuuacuuacu	scaffold699:44868..44930:-		Duplication16-7		Intron (of DV3018739)
Dvit-miR-x5	scaffold165_10150	1406.9	2758	2699	38	21	yes	ccuauuuccuuacuuacugaaca	uucaguaaguaaguaaauaggu	uucaguaaguaaguaaauagguuucuauuguucucauuguuuguaacaaucuaccuauuuccuuacuuacugaaca	scaffold165:169283..169359:-		Duplication16-8		IGR (Between DV3013994.2 and DV3024789.2)
Dvit-miR-x6a	scaffold14_2490	981.3	1923	1908	0	15	yes	ccuguuuccuuacauacugaaca	uucuguaaguaaggaaaugggu	uucuguaaguaaggaaauggguucuauuguucucauaguuuuaacaauggaccuguuuccuuacauacugaaca	scaffold14:435049..435124:-		Duplication16-9		IGR (Between DV3005850 and DV3005853)
Dvit-miR-x6b	scaffold196_11780	2491	4885	4763	0	122	yes	ccuguuuccuuacuuacugaaca	uucaguaaguaaggaaaugggu	uucaguaaguaaggaaauggguaucuaucguucuuauuguaaccuguuuccuuacuuacugaaca	scaffold196:524887..524952:+		Duplication16-10		IGR (Between DV3006661 and DV3006666)
Dvit-miR-x6c	scaffold620_28468	1.2	3051	2739	3	309	yes	ccuguuuccuuauuuacugaaca	uguucaguaaguaaggaaac	uguucaguaaguaaggaaacgaguuucuauuguacuuauuauuuauaacaauucaccuguuuccuuauuuacugaaca	scaffold620:36783..36861:-		Duplication16-11		Intron (of DV3017172)
Dvit-miR-x6d	scaffold255_14755	1.3	963	941	22	0	yes	cuguuuucuuacuuacugaaca	uucagaaaguaagcaaacgau	uucagaaaguaagcaaacgauuucuauuguuuucauuguuuguaacaauuuaucuguuuucuuacuuacugaaca	scaffold255:521703..521778:+		Duplication16-12		Intron (of DV3006307.1)
Dvit-miR-x7	scaffold38_4013	329.4	646	580	0	66	yes	uuuccucacuuacugaacacc	uguucaguaaguaaggaaaa	uguucaguaaguaaggaaaaugguaaauuauuacaaacaauagaaauguguuuccucacuuacugaacacc	scaffold38:272660..272731:+		Duplication17-1		Intron (of DV3014139)
Dvit-miR-x8a	scaffold257_14807	1354.2	2657	2625	28	4	yes	cccguuuccuuacuuacugaaca	uuuaguaagucaggacac	uuuaguaagucaggacacaggucaauuauuauaaacaaugaaaacaauagagacccguuuccuuacuuacugaaca	scaffold257:54910..54986:+		Duplication17-2		IGR (Between DV3014080 and DV3014083.1)
Dvit-miR-x8b	scaffold454_22782	177.1	348	159	0	189	yes	ccguuuccuuaauuacugaaca	aucaguaaguaaggaaacagguc	aucaguaaguaaggaaacaggucagcuguuacaaacaauuacgauaauauaagaccguuuccuuaauuacugaaca	scaffold454:38274..38350:-		Duplication17-3		Intron (of DV3013567)
Dvit-miR-x9	scaffold75_6251	594.4	1167	1134	19	14	yes	cuguuucuuuacuuacugaaca	uucaguaaguuuugaaauaggu	uucaguaaguuuugaaauagguaaauuguuauaaacaaugagaacauuagaaaucuguuucuuuacuuacugaaca	scaffold75:216285..216361:-		Duplication17-4		IGR (Between DV3000430 and DV3000431)
Dvit-miR-x10	scaffold2620_47495	9	53	51	0	2	yes	guaaauaucaugauuguaaua	auuacgaaaucauuuauuuacag	guaaauaucaugauuguaauauuuuugaaacaauuaucaaauuacgaaaucauuuauuuacag	scaffold2620:1949..2012:-		Duplication18-1		IGR (no genes predicted in this scaffold)
Dvit-miR-x10*	scaffold492_24214	37.2	90	39	0	51	yes	uuaugaaaucauuuuauuuacag	guaaauaucaugauuguaaua	guaaauaucaugauuguaauauuuuugaaaaauuaugaaauuaugaaaucauuuuauuuacag	scaffold492:232164..232228:+		Duplication18-2		Intron (of DV3011756.1)
Dvit-miR-x11	scaffold280_15616	4748.2	9314	8921	0	393	yes	auugggacaauggauuuauaauu	cuauaaauccauugucccaau	auugggacaauggauuuauaauucgguuuaaaauguacaacuauaaauccauugucccaau	scaffold280:218020..218081:+			Both6 +	IGR (Between DV3014987 and DV3014988.2)
Dvit-miR-x11*	scaffold280_15634	7160.7	14044	4897	0	9147	yes	uuauaaauccauugucccaaucg	auugggacaauggauuuauaguu	auugggacaauggauuuauaguuguacauuuuaaaccgaauuauaaauccauugucccaaucg	scaffold280:218018..218081:-	Cluster5-2		Both6 -	IGR (Between DV3014985 and DV3014989.1)
Dvit-miR-x12-1	scaffold644_29283	43.7	83	79	0	4	yes	auggcaucugugaucgaaugaa	ucauucgaucacagaugccaua	ucauucgaucacagaugccauaaaguuuuauacuuuauggcaucugugaucgaaugaa	scaffold644:56377..56435:+			Both7 +	IGR (Between DV3019244 and DV3019248.2)
Dvit-miR-x12-2	scaffold644_29288	43.8	83	79	0	4	yes	auggcaucugugaucgaaugaa	ucauucgaucacagaugccaua	ucauucgaucacagaugccauaaaguauaaaacuuuauggcaucugugaucgaaugaa	scaffold644:56376..56434:-			Both7 -	IGR (Between DV3019246 and DV30192470
Dvit-miR-x13a	scaffold299_16543	59387.5	116490	115890	0	600	yes	guaaagauguuuuaacuacua	aguagcauaaaauaucuuuagc	aguagcauaaaauaucuuuagcuaguuaaaaguaucaaccuaguaaagauguuuuaacuacua	scaffold299:21511..21574:+	Cluster6-6	Duplication19-1		IGR (Between DV3005472 and DV3005476)
Dvit-miR-x13b	scaffold57_5278	61177.6	119996	118629	1	1366	yes	guaaagauguuuuaacuacuc	aguagcaaaaagcaucuuuaacu	aguagcaaaaagcaucuuuaacuaguauauuauaguaaucuaguaaagauguuuuaacuacuc	scaffold57:345274..345337:-	Cluster9-3	Duplication19-2		IGR (Between DV3005077.2 and DV3005080.2)
Dvit-miR-x14a	scaffold766_32636	2132.4	4183	4073	0	110	yes	uguucuauaguuuuggcugcu	acagccagaucuguagaauaau	uguucuauaguuuuggcugcuuuacauguuaauaagaaacagccagaucuguagaauaau	scaffold766:35440..35500:+		Duplication20-1	Both8 +	IGR (Between DV3015639 and DV3015640)
Dvit-miR-x14b	scaffold766_32637	7.1	23	17	0	6	yes	uauucuacagaucuggcuguuu	gcagccaaaacuauagaacagc	uauucuacagaucuggcuguuucuuauuaacauguaaagcagccaaaacuauagaacagc	scaffold766:35438..35498:-		Duplication20-2	Both8 -	IGR (Between DV3015638 and DV3015641)
Dvit-miR-x15-1	scaffold103_7495	104.8	206	203	0	3	yes	ucaagaucguaauacaccggccg	ccuggguauuaccaucggcuga	ccuggguauuaccaucggcugauuuugauaccacucgaaucaagaucguaauacaccggccg	scaffold103:371948..372010:+		Duplication21-1		IGR (Between DV3006426.2 and DV3006430)
Dvit-miR-x15-2	scaffold103_7497	104.8	206	203	0	3	yes	ucaagaucguaauacaccggccg	ccuggguauuaccaucggcuga	ccuggguauuaccaucggcugauuuugauaccacucgaaucaagaucguaauacaccggccg	scaffold103:394935..394997:+		Duplication21-2		IGR (Between DV3006426.2 and DV3006430)
Dvit-miR-x16-1	scaffold10_1455	94.2	189	79	0	110	yes	guaaguaaaaauucaauuauug	auaguugaauuuuuauuuauuag	guaaguaaaaauucaauuauuguuuaaauaaauaauauaaaaauauuaauaguaauaauaguugaauuuuuauuuauuag	scaffold10:447718..447798:-		Duplication22-1		Intron (of DV3000764)
Dvit-miR-x16-2	scaffold891_35621	79.5	161	79	0	82	yes	guaaguaaaaauucaauuauug	auaguugaauuuuuauuuaauag	guaaguaaaaauucaauuauuguuuaaauaaauaauaugaaaauauuaauaguaauaauaguugaauuuuuauuuaauag	scaffold891:16595..16675:-		Duplication22-2		IGR (Between DV3019959 and DV3019961)
Dvit-miR-x17	scaffold115_8091	462	904	406	0	498	yes	uguuccaccgucauuuacuaauu	uuaguaaaucacgguggacacu	uguuccaccgucauuuacuaauuuuaacauuaguuuauauagucaaauuaguaaaucacgguggacacu	scaffold115:333811..333881:-		Duplication23-1		IGR (Between DV3025277.1 and DV3002415.2)
Dvit-miR-x17*	scaffold88_7010	69.7	142	141	0	1	yes	uuaguaaaucacagugggaca	acccacuaagauuuaccaauuu	acccacuaagauuuaccaauuuuaacauuauuuuauauuaucaaauuaguaaaucacagugggaca	scaffold88:629867..629933:-		Duplication23-2		3UTR (of DV3001018)
Dvit-miR-x18	scaffold1_33	9.6	18	16	0	2	yes	uuaaguauagcuauucauagga	uaugcauaaguuuuacuuaagca	uaugcauaaguuuuacuuaagcauguuguuuagauagcuuaaguauagcuauucauagga	scaffold1:698629..698689:+				Intron (of DV3002368)
Dvit-miR-x19	scaffold1_47	68.2	133	78	0	55	yes	acuuaaucccuuuagcucuga	agugcuaaaaggugauuaagucc	agugcuaaaaggugauuaaguccuuucaaauuacauggacuuaaucccuuuagcucuga	scaffold1:878591..878651:+				IGR (Between DV3002371.2 and DV3002376)
Dvit-miR-x20	scaffold10_1058	252.8	497	492	0	5	yes	ugauuuucuuuuucaauugggc	cccaauugaaaaagaaguucaua	ugauuuucuuuuucaauugggcauaauaauaauuucuucuacccaauugaaaaagaaguucaua	scaffold10:1288659..1288723:+				Intron (of DV3000829)
Dvit-miR-x21	scaffold116_8129	39.1	80	40	0	40	yes	aucgcucacgaaaggauguaag	uacauccauucaugagcaauuu	uacauccauucaugagcaauuucauuaagcauauuuaaaucgcucacgaaaggauguaag	scaffold116:323231..323293:+				Intron (of DV3008536)
Dvit-miR-x22	scaffold120_8346	4322	8476	8306	0	170	yes	cggacagacugaguauggaccac	guucauacucagucuguucug	guucauacucagucuguucugaauuuucuuuucuauccggacagacugaguauggaccac	scaffold120:759788..759848:-				IGR (Between DV3002003 and DV3002004)
Dvit-miR-x23	scaffold1264_41708	2808.8	5508	5071	0	437	yes	uacugauuuauguuggugguaga	accaccaacauaauucgggggg	accaccaacauaauucgggggggcauacuuucuuugccuacugauuuauguuggugguaga	scaffold1264:22211..22272:-				IGR (Between DV3021919 and DV3021920.2)
Dvit-miR-x24	scaffold155_9831	54.9	109	71	0	38	yes	ugccuugaugacgacuguaaucg	uaugcgucguaaucaaguuaga	ugccuugaugacgacuguaaucgacguacauucucucaaggucauaugcgucguaaucaaguuaga	scaffold155:268368..268434:-				Exon (of DV3009437)
Dvit-miR-x25	scaffold158_9935	34.8	65	54	0	11	yes	ucauuguuaugggccauauga	cuuauggcccauaccaaugaag	ucauuguuaugggccauaugagcguuaaaaagaauacauguauauaugugcucuuauggcccauaccaaugaag	scaffold158:122824..122898:-				Intron (of DV3004923)
Dvit-miR-x26	scaffold187_11467	88.9	178	169	0	9	yes	aaaguuaauaguaauacggaacu	uucaaaauacuauuaauuuagu	aaaguuaauaguaauacggaacuguuucuucuccauuuucuuacaguucaaaauacuauuaauuuagu	scaffold187:125884..125952:-				Intron (of DV3012210.1)
Dvit-miR-x27	scaffold19_2729	14.2	32	28	0	4	yes	ucuguccauuuuucauacccauu	gugggaauguagaacgggcacagcucau	gugggaauguagaacgggcacagcucauacuuguguacguauacucuguccauuuuucauacccauu	scaffold19:630363..630430:+				Intron (of DV3006837)
Dvit-miR-x28	scaffold194_11717	47.1	88	87	0	1	yes	gggaauguuuguaaaaugucaa	aauauuuuacaaauauuuuuu	aauauuuuacaaauauuuuuuguaaaaaaaaaaagggaauguuuguaaaaugucaa	scaffold194:190056..190114:+				IGR (Between DV3010043 and DV3010044)
Dvit-miR-x29	scaffold2_214	155.1	311	266	0	45	yes	uaauucuuauauugucgguuuug	aaacugacacuguaauuauuaaa	aaacugacacuguaauuauuaaauucuauauuuauuuuuaauucuuauauugucgguuuug	scaffold2:544098..544159:-				5UTR(of DV3002152)
Dvit-miR-x30	scaffold208_12251	14.3	39	37	0	2	yes	uauuugagauuauuaaaacugga	uaguuuuaguuuuucaucaaua	uaguuuuaguuuuucaucaauaaauugucaauaaaauuuauuugagauuauuaaaacugga	scaffold208:9877..9938:+				Iintron (of DV3018694)
Dvit-miR-x31	scaffold210_12323	9.1	20	19	0	1	yes	aauugacagaauaucguggaac	cccacaauguucugacaaauu	cccacaauguucugacaaauucacauucuuucuuuauggugaauugacagaauaucguggaac	scaffold210:57152..57215:+				IGR (Between DV3014482.2 and DV3014487)
Dvit-miR-x32	scaffold216_12627	2901.4	5690	5106	0	584	yes	aggcaagaugaggcaaagcug	agcuauggaucaucaggccacu	aggcaagaugaggcaaagcuguaguaauugcauugugcaaaguuuaaauuacagcuauggaucaucaggccacu	scaffold216:195981..196055:-				IGR (Between DV3001277 and DV3001279)
Dvit-miR-x33	scaffold222_12894	112.5	219	157	1	61	yes	ucauuuucuuaguuggaucauu	ugauuuuacuaagaaaaugacu	ugauuuuacuaagaaaaugacugaucgauaacaauuuucaaccagauguuguugacuagucauuuucuuaguuggaucauu	scaffold222:65323..65404:+				IGR (Between DV3008972 and DV3008975)
Dvit-miR-x34	scaffold223_12954	31.7	60	22	0	38	yes	aagaugauggaaauuugagagc	ucucaaauuuccaucgucuuacg	ucucaaauuuccaucgucuuacgaccauacuugguguugaccauacuuaaagguccuuaagaugauggaaauuugagagc	scaffold223:135979..136059:-				Intron (of DV30108520)
Dvit-miR-x35	scaffold25_3191	109	218	201	0	17	yes	uuuauaauuaucaguuguaug	guuaaucugguaauuauuugug	uuuauaauuaucaguuguaugaugugauuuucuaauugcgcuaauguuauuuaucguuaaucugguaauuauuugug	scaffold25:575027..575104:-				Intron (of DV3004307)
Dvit-miR-x36	scaffold252_14588	136.5	270	266	0	4	yes	uugaacccugacaaaaugaaaa	uuuuguuuuggguggguuc	uugaacccugacaaaaugaaaauagcguuuuguugaaaaauacuugauuauucguuauuuuguuuuuguuuuggguggguuc	scaffold252:100095..100177:+				Intron (of DV3013673)
Dvit-miR-x37	scaffold291_15962	136.6	268	244	0	24	yes	cuguuucucuacuuacugaaca	uuuaguaagugaggaaacgg	uuuaguaagugaggaaacggauauuguucucuuuacuuuuuacaaucgaccuguuucucuacuuacugaaca	scaffold291:49815..49887:-				IGR (Between DV3016942 and DV3025780.1)
Dvit-miR-x38	scaffold299_16535	14593.5	28626	28500	5	121	yes	uuaaaacuaggugggcgggcu	ccuguuucaucuaguuuugugu	ccuguuucaucuaguuuuguguuugauuguugaacauacuuaaaacuaggugggcgggcu	scaffold299:20498..20558:+	Cluster6-2			IGR (Between DV3005472 and DV3005476)
Dvit-miR-x39	scaffold299_16542	17319.9	33966	30390	7	3569	yes	auugguaacauguaacaucuuuag	aaagauguuuuuguugccuguau	auugguaacauguaacaucuuuaguaguaaauauauuaaucuaaagauguuuuuguugccuguau	scaffold299:21069..21134:+	Cluster6-5			IGR (Between DV3005472 and DV3005476)
Dvit-miR-x40	scaffold299_16547	4.1	1182	1173	7	2	yes	ugacuagaaguuauacuacaa	uaguauaauuuacuagauacauu	uaguauaauuuacuagauacauuaagugaaacaaauaucuaugugacuagaaguuauacuacaa	scaffold299:25709..25773:+	Cluster6-8			IGR (Between DV3005472 and DV3005476)
Dvit-miR-x41	scaffold299_16557	5004.6	9819	9756	0	63	yes	ucacuggugacaauuuaugaag	cugugaauuguuuccaguugau	cugugaauuguuuccaguugauacuaguauuuaauaguuaucacuggugacaauuuaugaag	scaffold299:27851..27913:+	Cluster6-10			IGR (Between DV3005472 and DV3005476)
Dvit-miR-x42	scaffold302_16701	3.8	10	9	0	1	yes	cgugcauuuuaacacauuggcug	cucuauguauuaaaaugcuugu	cgugcauuuuaacacauuggcuguuguuuauuuauacuccaaucacguuauauacucacucuauguauuaaaaugcuugu	scaffold302:59904..59984:-				Intron (of DV3016241)
Dvit-miR-x43	scaffold316_17173	5480.6	10750	10631	0	119	yes	ucccaccgugauuuacugauug	auugguaaaucacguuggcaca	ucccaccgugauuuacugauuguaauaauuguucauauauucaaauugguaaaucacguuggcaca	scaffold316:246716..246782:-				Intron (of DV3014120)
Dvit-miR-x44	scaffold32_3617	158.9	321	180	0	141	yes	cgcucuuuuuuuggucuucuaac	uagcugccuaaaaaagaguuau	cgcucuuuuuuuggucuucuaacauucaauuauuauaguuagcugccuaaaaaagaguuau	scaffold32:126829..126890:-				IGR (Between DV3006152 and DV3006154.2)
Dvit-miR-x45	scaffold328_17850	12.6	26	16	0	10	yes	uaccgauucauaacaugacagg	cgucauuuuaugaaucgauagc	uaccgauucauaacaugacaggguguauaguaucugucgucauuuuaugaaucgauagc	scaffold328:276118..276177:+				Intron (of DV3010320)
Dvit-miR-x46	scaffold35_3781	12.7	31	29	0	2	yes	aauuucguuaaaauaaaaggga	uccuuuauucuaaugaaaguuggu	uccuuuauucuaaugaaaguugguaugaaaacuuacgaauuucguuaaaauaaaaggga	scaffold35:269494..269554:+				IGR (Between DV3003411 and DV3003415)
Dvit-miR-x47	scaffold37_3973	3642.6	7143	3218	6	3919	yes	agacgaggugguuguuacauuaa	uuaauguaauaaccacucgucu	uuaauguaauaaccacucgucuuuuggaucuguuguugaagacgaggugguuguuacauuaa	scaffold37:281232..281294:+				Intron (of DV3005042)
Dvit-miR-x48	scaffold398_21234	16.7	53	50	0	3	yes	cauaaaucguuuuuuaagaaaug	uuucuuuuaaaugauuuguuaa	cauaaaucguuuuuuaagaaaugauguuuguaaaaaauauuucuuuuaaaugauuuguuaa	scaffold398:47857..47918:+				IGR (Between DV3025926.1 and DV3016862.2)
Dvit-miR-x49	scaffold4_334	494.7	969	964	0	5	yes	uuuguacaucagagguaaacu	uuuaccucagguguacgguaua	uuuguacaucagagguaaacuaaguuacauuuuuugaaaauuugucuuguaaaaguuuaccucagguguacgguaua	scaffold4:1000891..1000969:+				Intron (of DV3001120)
Dvit-miR-x50	scaffold40_4175	115.3	223	149	0	74	yes	uaagacuaaguguuaaucggacc	uucgauuaacacuuagucuuaug	uucgauuaacacuuagucuuauguaagacuaauaggaacuuauaagacuaaguguuaaucggacc	scaffold40:354930..354995:+				IGR (Between DV3003900 and DV3003901)
Dvit-miR-x51	scaffold40_4221	0.4	69	49	0	20	yes	aggacaguaauauucaaauuuga	ucacuuuuaaauauuacugcca	aggacaguaauauucaaauuugacguuuggggucacuuuuaaauauuacugcca	scaffold40:597130..597184:-				Intron (of DV3025931.1)
Dvit-miR-x52	scaffold465_23530	173.3	338	316	0	22	yes	ucuagcuaggccuuauuacc	uaauaaggccuugcuaagcuu	uaauaaggccuugcuaagcuuguauuagauuuugcauaaagucuagcuaggccuuauuacc	scaffold465:60474..60535:-				IGR (Between DV3015083 and DV3015085)
Dvit-miR-x53	scaffold476_23777	16.1	32	21	1	10	yes	caaagguguaaugauauuuggc	caaauucaauuacaccauugac	caaagguguaaugauauuuggcauauaauaauaauugucuagcgucaaauucaauuacaccauugac	scaffold476:63725..63792:-				Intron (of DV3017856)
Dvit-miR-x54	scaffold48_4598	234.5	466	465	0	1	yes	aaauauuguuuuaguaggucu	agcccuaguaacacaauauauc	aaauauuguuuuaguaggucuuuuaauaacuaagcccuaguaacacaauauauc	scaffold48:271712..271767:+				Intron (of DV3001386)
Dvit-miR-x55	scaffold515_24882	22147.6	43441	40590	1	2850	yes	ugugauguguuugugagccacu	uggcccacaaccacagaacuuc	ugugauguguuugugagccacugugauauuauauaauaguuaguggcccacaaccacagaacuuc	scaffold515:101561..101626:+				IGR (Between DV3013911 and DV3013912)
Dvit-miR-x56	scaffold57_5285	15766.4	30927	28396	25	2506	yes	uaaagauguuuacuacucu	ggguagaauaaacgucuuuugc	ggguagaauaaacgucuuuugcuaguuuaagcuauuuuucaauauucugcuaaagauguuuacuacucu	scaffold57:345834..345903:-	Cluster9-7			IGR (Between DV3005077.2 and DV3005080.2)
Dvit-miR-x57	scaffold586_28079	7.6	17	16	0	1	yes	uaaucaauuacuuuuauuagcu	uaauagguggauugauuaca	uaaucaauuacuuuuauuagcuacuuuagauaacgcaacaguguuaaaagcacagcuaauagguggauugauuaca	scaffold586:35158..35235:-				Exon (of DV3017763)

Table S11. List of clock-related genes searched for in the genome of *D. vitifoliae*.

Genes	Symbol	Prediction[1]	Scaffold number	*A. pisum homolog(s)*	Comments
Input-related					
long wavelength opsin	Dvit*LWO*	DV3019248	644	ACYPI009332	
short wavelength opsin	Dvit*SWO*	DV3010484	153	ACYPI004442 ACYPI002544	Duplicated in *A. pisum*
Arthropsin	Dvit*arthrops*	DV3009221	308	ACYPI32968	
C-opsin	Dvit*C-ops*	DV3010731	104	ACYPI009397	
Rhodopsin 7	Dvit*Rh7*	DV3008393	648	ACYPI001006 ACYPI005074	Duplicated in *A. pisum*
cryptochrome 1	Dvit*cry1*	DV3005203	141	ACYPI005757	
Core					
period	Dvit*per*	DV3009458	378	ACYPI47669	
timeless	Dvit*tim*	DV3010827 [2]	270	ACYPI36439	Manually annotated (absent in the gene predictions set)
Clock	Dvit*Clk*	DV3008870	180	ACYPI004812	
cycle	Dvit*cyc*	DV3002036	95	ACYPI004686	
PAR-domain protein 1	Dvit*Pdp1*	DV3000657	27	ACYPI004812	
vrille	Dvit*vri*	DV3002370	1	ACYPI008851	
cryptochrome 2	Dvit*cry2*	DV3016418	579	ACYPI006584 ACYPI004197	Duplicated in *A. pisum*
Output-related					
arylalkylamine N-acetyltransferase 1	Dvit*aanat1*	DV3007886	29	ACYPI002543	*aanat1* and *aanat2* genes in tandem in the genome, as observed in *A. pisum*.
arylalkylamine N-acetyltransferase 2	Dvit*aanat2*	DV3007886	29	ACYPI000655	*aanat1* and *aanat2* genes in tandem in the genome, as observed in *A. pisum*.
arylalkylamine N-acetyltransferase 3	Dvit*aanat3*			ACYPI000856	absent in *D. vitifoliae*
arylalkylamine N-acetyltransferase 4	Dvit*aanat4*			ACYPI060713	absent in *D. vitifoliae*
Prothoracicotropic hormone	Dvit*Ptth*	DV3024948 [2]	43	ACYPI37989	Manually annotated (absent in the gene predictions set)
Ancillary and related genes					
Photolyase 6-4	Dvit*Ph6-4*	DV3000677	27	ACYPI003810	
timeless2/timeout	Dvit*tim2/timeout*	DV3016946	291	ACYPI001257	
clockwork orange	Dvit*cwo*	DV3001859	12	ACYPI24234	
doubletime/casein kinase	Dvit*dbt/CKI*	DV3003852	168	ACYPI008162	
supernumerary limbs	Dvit*slmb*	DV3004609	15	ACYPI006874	
casein kinase II α	Dvit*CKIIα*	DV3013255	327	ACYPI002006	
casein kinase II β	Dvit*CKIIβ*	DV3005119	56	ACYPI000089	
twins	Dvit*tws*	DV3002660	53	ACYPI009741	
widerborst	Dvit*wdb*	DV3002950	50	ACYPI000666	
shaggy/glycogen synthase kinase 3	Dvit*sgg/GSK3*	DV3017481	678	ACYPI009257	Absent both in *A. pisum* and *D. vitifoliae*

---

[1] Assigned gene name in the *D. vitifoliae* database (http://bipaa.genouest.org/sp/daktulosphaira_vitifoliae/)

[2] Gene initially not annotated (no gene model in automatic predictions). This gene was identified manually.

Table S12. List of OR and GR annotated genes. Part1 (OR):

Name	**Symbol**	**Scaffold number**	**Complete?**	**Notes**
Olfactory receptor co-receptor	ORco	54	complete	
Olfactory receptor 1 allele A	OR1_A	109	complete	
Olfactory receptor 1 allele B	OR1_B	4219	partial	lacks Nter
Olfactory receptor 2	OR2	425	complete	
Olfactory receptor 3	OR3	523	partial	lacks Nter
Olfactory receptor 4	OR4	403	partial	lacks Nter
Olfactory receptor 5	OR5	244	partial	Model corrected, lacks N-ter.
Olfactory receptor 6	OR6	428	complete	
Olfactory receptor 7	OR7	259	partial	lacks N-ter, beginning of scaffold
Olfactory receptor 8	OR8	259	complete	
Olfactory receptor 9	OR9	259	complete	
Olfactory receptor 10	OR10	259	partial	one exon/intron junction is not good but N in sequence
Olfactory receptor 11	OR11	259	partial	N-ter only, end of scaffold
Olfactory receptor 12	OR12	380	complete	
Olfactory receptor 13 allele A	OR13_A	179	complete	
Olfactory receptor 13 allele B	OR13_B	8233	partial	small fragment
Olfactory receptor 14	OR14	289	complete	
Olfactory receptor 15	OR15	229	partial	C-ter only
Olfactory receptor 16	OR16	229	complete	
Olfactory receptor 17	OR17	15	complete	abnormal intron-exon boundary
Olfactory receptor 18	OR18	15	complete	STOP codon in 1st exon
Olfactory receptor 19	OR19	15	complete	abnormal intron-exon boundary
Olfactory receptor 20	OR20	15	partial	lack C-ter
Olfactory receptor 21	OR21	15	complete	
Olfactory receptor 22	OR22	15	partial	readthrough stop codon, pseudogene?, lacks C-ter
Olfactory receptor 23	OR23	186	complete	
Olfactory receptor 24	OR24	186	partial	1 exon lacking
Olfactory receptor 25	OR25	186	partial	1 exon lacking
Olfactory receptor 26	OR26	186	complete	
Olfactory receptor 27	OR27	186	partial	1 exon lacking
Olfactory receptor 28	OR28	186	partial	
Olfactory receptor 29	OR29	711	complete	
Olfactory receptor 30	OR30	711	partial	1 exon lacking
Olfactory receptor 31	OR31	711	partial	lacks Nter
Olfactory receptor 32	OR32	682	complete	
Olfactory receptor 33	OR33	66	complete	
Olfactory receptor 34	OR34	66	partial	N-ter only, no clue for C-ter
Olfactory receptor 35	OR35	973	partial	c-ter missing
Olfactory receptor 36	OR36	237	complete	
Olfactory receptor 37	OR37	679	complete	
Olfactory receptor 38	OR38	293	complete	
Olfactory receptor 39	OR39	293	complete	
Olfactory receptor 40	OR40	1209	complete	
Olfactory receptor 41	OR41	1209	complete	
Olfactory receptor 42	OR42	861	complete	
Olfactory receptor 43	OR43	460	complete	
Olfactory receptor 44	OR44	11	complete	
Olfactory receptor 45	OR45	39	complete	readthrough stop codon
Olfactory receptor 46	OR46	183	complete	
Olfactory receptor 47	OR47	933	complete	
Olfactory receptor 48	OR48	614	complete	
Olfactory receptor 49	OR49	761	complete	
Olfactory receptor 50	OR50	86	complete	
Olfactory receptor 51	OR51	16	partial	N-ter missing,
Olfactory receptor 52	OR52	168	partial	
Olfactory receptor 53	OR53	1845	partial	N-ter only
Olfactory receptor 54	OR54	328	partial	N-ter only, putative pseudo-gene ? (STOP codon)
Olfactory receptor 55	OR55	3666	partial	
Olfactory receptor 56	OR56	507	partial	C-ter only
Olfactory receptor 57	OR57	7347	partial	C-ter only
Olfactory receptor 58	OR58	740	partial	small fragment
Olfactory receptor 59	OR59	7822	partial	small fragment
Olfactory receptor 60	OR60	800	partial	C-ter only, putative pseudo-gene ? (STOP codon)

Table S12. Legend in the preceding page. Part2 (GR).

Name	**Symbol**	**Scaffold number**	**Complete?**	**Notes**
Gustatory receptor 1	GR1	scaffold13	complete	
Gustatory receptor 2	GR2	scaffold596	partial	lack terminal exon in C-ter
Gustatory receptor 3	GR3	scaffold63	partial	
Gustatory receptor 4	GR4	scaffold41	partial	
Gustatory receptor 5	GR5	scaffold344	complete	
Gustatory receptor 6	GR6	scaffold344	complete	
Gustatory receptor 7	GR7	scaffold106	partial	
Gustatory receptor 8	GR8	scaffold106	partial	very end of C-ter is missing
Gustatory receptor 9	GR9	scaffold42	complete	
Gustatory receptor 10	GR10	scaffold308	complete	
Gustatory receptor 11	GR11	scaffold50	complete	
Gustatory receptor 12	GR12	scaffold939	partial	
Gustatory receptor 13	GR13	scaffold939	partial	
Gustatory receptor 14	GR14	scaffold506	partial	N-ter is missing
Gustatory receptor 15	GR15	scaffold1390	partial	
Gustatory receptor 16	GR16	scaffold54	partial	
Gustatory receptor 17	GR17	scaffold39	partial	
Gustatory receptor 18	GR18	scaffold144	partial	predicted partial gene model

Table S13, Part1. Number of OBP (A), CSP (B) and NPC2 (C) members identified in *D. vitifoliae* and *A. pisum* (known orthologous relationships are specified). Th gene DvitCSP11 was found in the grape phylloxera genome by using exhaustive searches performed by the BITACORA pipeline (http://www.ub.edu/softevol/bitacora/) [36]. In gene names, a and b refer to paralogs.

A)

	D. vitifoliae		***A. pisum***	
Orthogroup	**Number of genes**	**Gene Name**	**Number of genes**	**Gene Name**
OBP2	1	DvitiObp2	1	ApisObp2
OBP3	1	DvitiObp3	3	ApisObp3, ApisObp11, ApisObp12
OBP4	1	DvitiObp4	1	ApisObp4
OBP5	1	DvitiObp5	1	ApisObp5
OBP6	2	DvitiObp6a, DvitiObp6b	1	ApisObp6
OBP7	0		1	ApisObp7
OBP8	2	DvitiObp8a, DvitiObp8b[1,2]	1	ApisObp8
OBP9	1	DvitiObp9	1	ApisObp9
OBP10	1	DvitiObp10	1	ApisObp10
OBP13	1	DvitiObp13	1	ApisObp13
OBP14	1	DvitiObp14	1	ApisObp14
Not assigned	1	DvitiObpU[1,2,3]	0	
Total	**13**		13	

[1] partial genes, [2] not included in the phylogenetic analysis, [3] dubious model

B)

	D. vitifoliae		***A. pisum***	
Orthogroup	**Number of genes**	**Gene Name**	**Number of genes**	**Gene Name**
CSP1	3	DvitiCsp1a, DvitiCsp1b[1,2], DvitiCsp1c	2	ApisCsp1
CSP2-3	1	DvitiCsp2	3	ApisCsp2, ApisCsp3, ApisCsp3_2
CSP4	1	DvitiCsp4	1	ApisCsp4
CSP5	1	DvitiCsp5	1	ApisCsp5
CSP6	1	DvitiCsp6	1	ApisCsp6
CSP7	1	DvitiCsp7	1	ApisCsp7
CSP8	1	DvitiCsp8	1	ApisCsp8
CSP9	0		1	ApisCsp9
CSP10	2	DvitiCsp10a, Csp10b	1	ApisCsp10
CSP11	1	DvitiCsp11 [3]	1	ApisCsp11
Total	**12**		13	

[1] partial gene, [2] not included in the phylogenetic analysis, [3] named DviCSP9 in the study of [37].

Table S13, Part2. Legend in the preceding page. Since homologous relationships among NPC2 could not be unambigously determined, we used numbered suffixes to name the different copies.

C)

	D. vitifoliae		*A. pisum*	
Orthogroup	**Number of genes**	**Gene Name**	**Number of genes**	**Gene Name**
NPC2_1	1	DvitiNpc2_1	1	ApisNpc2_pre
	1	DvitiNpc2_2		
	1	DvitiNpc2_3		
	1	DvitiNpc2_4		
	1	DvitiNpc2_5		
	1	DvitiNpc2_6		
	1	DvitiNpc2_7		
	1	DvitiNpc2_8		
			1	ApisNpc2_1
			1	ApisNpc2_3
			1	ApisNpc2_4
			1	ApisNpc2_5
			1	ApisNpc2_6
			1	ApisNpc2_7
Total	**8**		**7**	

Table S14. List of genes for Cytochromes P450, UDP-glycosyl transferases, Glutathione S-transferases, Carboxylesterases and ABC transporters annotated in the genome of grape phylloxera. Scaffold= scaffold number of the gene; position or transcript name= Position of the gene on the scaffold or transcript name given by the automatic annotation; Strand= Strand on which the gene has been annotated; size (aa)= Number of amino-acids of the corresponding protein; detox family= Cytochrome P450 (CYP), UDP-glucosyl transferase (UGT), Glutathione S-transferase (GST), Carboxylesterase (CCE) and ABC transporter; name_ID= Unique ID given by the annotator for CYP and display on the genome browser; Classification=Clan 2, 3 or 4 or mitochondrial clan for CYP; Glutathione S-transferase delta, omega, sigma, or theta for GST; family number for UGT; Pheromone/hormone processing, Neuro/developmental, Detoxification/dietary class for CCE; ABC A, B, C, D, E, F ,G, and H for ABC transporter. Name= Unique ID given by the annotators for UGTs, GSTs, CCEs and ABC transporters and by D. Nelson for CYP genes. Comments= Contain additional information on gene structures or transcripts names.

Table S14, Part1. See above the Legend.

scaffold number	position or transcript name	strand	size (aa)	Number of exons	detox family	name_ID	classification	name
89	DV3004986-RA-00001	minus	238	6	GST		Glutathione S-transferase omega	GSTo1
140	DV3010592-RA-00001	minus	244	6	GST		Glutathione S-transferase omega	GSTo2
421	DV3016774-RA	plus	203	4	GST		Glutathione S-transferase sigma	GSTs1
421	DV3016773-RA	plus	205	4	GST		Glutathione S-transferase sigma	GSTs2
44	DV3004805-RA-00001	minus	201	4	GST		Glutathione S-transferase sigma	GSTs3
77	DV3003239-RA-00001	plus	214	5	GST		Glutathione S-transferase delta	GSTd1
77	DV3003238-RA-00001	plus	217	5	GST		Glutathione S-transferase delta	GSTd2
416	DV3008706-RA-00001	minus	233	5	GST		Glutathione S-transferase theta	GSTt1
283	DV3007510-RA-00001	minus	149	3	GST		Glutathione S-transferase microsomal	MGST1
283	DV3007514-RA-00001	minus	161	3	GST		Glutathione S-transferase microsomal	MGST2
35	DV3003399-RA-00001	minus	158	3	GST		Glutathione S-transferase microsomal	MGST3
6	DV3000285-RA-00001	plus	529	6	UGT		350C1	UGT_1
19	DV3006825-RA-00001	minus	509	5	UGT		343B	UGT_2
30	DV3002826-RA-00001	plus	514	4	UGT		329A	UGT_3
61	DV3002241-RA-00001	minus	531	5	UGT		350C3	UGT_4
61	DV3002242-RA-00001	minus	530	6	UGT		350C2	UGT_5
101	DV3005994-RA-00001	minus	523	4	UGT		344N1	UGT_6
137	DV3003766-RAa-00001	plus	489	4	UGT		329B	UGT_7
198	DV3008018-RA-00001	minus	513	4	UGT		344N5	UGT_8
294	DV3017396-RA-00001	minus	517	6	UGT		330A	UGT_9
344	DV301262+B258-RA-00001	plus	508	4	UGT		348A1	UGT_10
354	DV3007831-RA-00001	plus	423	2	UGT		349A1	UGT_11
398	DV3016865-RA-00001	plus	509	4	UGT		339A	UGT_12
424	DV3008618-RA-00001	minus	517	5	UGT		349A3	UGT_13
424	DV3008619-RAaa-00001	minus	512	5	UGT		349A4	UGT_14
424	DV3008619-RAa-00002	minus	510	5	UGT		349A5	UGT_15
424	DV3008619-RA-00002	minus	515	5	UGT		342A	UGT_16
424	DV3008628-RA-00001	plus	517	5	UGT		349A2	UGT_17
431	blast_result_XP_003245050_scaffold431_-00001	plus	502	4	UGT		348A2	UGT_18
443	DV3014656-RAa-00001	minus	517	5	UGT		343C4	UGT_19
510	DV3009069-RA-00001	plus	525	8	UGT		341A	UGT_20
519	DV3019637-RA-00001	plus	244	4	UGT		344M1	UGT_21
565	DV3015063-RA-00001	minus	547	5	UGT		351A	UGT_22
572	DV3016285-RAaaa-00001	minus	525	4	UGT		344N2	UGT_23
572	DV3016285-RAaa-00002	minus	507	6	UGT		344N3	UGT_24
572	DV3016285-RAa-00002	minus	512	4	UGT		344N9	UGT_25
572	DV3016285-RA-00001	minus	538	5	UGT		344N10	UGT_26
572	DV3016286-RA-00001	minus	489	5	UGT		344N7	UGT_27
572	DV3016290-RAa-00001	minus	505	4	UGT		344N8	UGT_28
572	DV3016290-RA-00001	minus	520	4	UGT		344N6	UGT_29
572	DV3016291-RAa-00001	minus	278	1	UGT		344N4	UGT_30
572	DV3016291-RA-00001	minus	472	4	UGT		344M2	UGT_31
766	DV3015648-RA-00001	plus	517	5	UGT		343C1	UGT_32
766	DV3015649-RA-00001	plus	517	5	UGT		343C3	UGT_33
1238	DV3021594-RA-00001	plus	520	5	UGT		343C2	UGT_34
4315	blast_result_XP_016661510_scaffold4315_-00001	minus	231	1	UGT		344F	UGT_35
212	11667-20901	minus	*562*	7	CCE		Pheromone/hormone processing	CCE-1
212	31598-38026	minus	*558*	7	CCE		Pheromone/hormone processing	CCE-2
212	46944-50145	minus	560	7	CCE		Pheromone/hormone processing	CCE-3
212	60220-74779	minus	576	7	CCE		Pheromone/hormone processing	CCE-4
114	260409-273625	minus	603	9	CCE		Pheromone/hormone processing	CCE-5
114	220014-226309	minus	579	8	CCE		Pheromone/hormone processing	CCE-6
114	278979-295821	minus	604	11	CCE		Pheromone/hormone processing	CCE-7
1086	27800-31467	plus	687	6	CCE		Neuro/developmental (clade J)	CCE-8
118	274871-303671	plus	654	11	CCE		Neuro/developmental (clade J)	CCE-9
27	1062697-1067673	minus	559	8	CCE		Pheromone/hormone processing	CCE-10
195	144240-148535	minus	584	10	CCE		Pheromone/hormone processing	CCE-11
195	150860-157187	plus	572	8	CCE		Pheromone/hormone processing	CCE-12
13	333949-356626	minus	757	9	CCE		Neuro/developmental (clade L)	CCE-13
20	391435-589634	minus	968	10	CCE		Neuro/developmental (clade L)	CCE-14
134	191123-197284	minus	828	13	CCE		Neuro/developmental (clade K)	CCE-15
146	545984-560565	plus	755	12	CCE		Neuro/developmental (clade H)	CCE-16
191	59224-78875	minus	553	11	CCE		Detoxification/dietary class	CCE-17
191	80077-88986	minus	568	11	CCE		Detoxification/dietary class	CCE-18
334	35419-56136	plus	1153	11	CCE		Neuro/developmental (clade L)	CCE-19
775	11760-34482	plus	649	3	CCE		Neuro/developmental (unknown)	CCE-20

Table S14, Part2. See above for Legend.

scaffold number	position or transcript name	strand	size (aa)	Number of exons	detox family	classification	name	comments
447	35973-26849	minus	1633	24	ABC transporter	ABCA	ABCA1	DV3016087-RA
391	15026-0	minus	1744	21	ABC transporter	ABCA	ABCA2	DV3013382-RA
2301	10497-6026	minus	820	12	ABC transporter	ABCA	ABCA3partial	DV3022439-RA
502	129486-160967	plus	1556	19	ABC transporter	ABCA	ABCA4	DV3011141-RA
249	32974-50780	plus	1307	27	ABC transporter	ABCB	ABCB1	DV3010127-RA
126	191664-172277	minus	1432	27	ABC transporter	ABCB	ABCB2	DV3007299-RA
3	586320-591820	plus	670	14	ABC transporter	ABCB	ABCB3	DV3008235-RA
330	11089-6571	minus	644	10	ABC transporter	ABCB	ABCB4	DV3003320-RA
168	730217-737766	plus	1048	12	ABC transporter	ABCB	ABCB5	DV3003862-RA
288	187905-174604	minus	839	14	ABC transporter	ABCB	ABCB6	DV3014308-RA
27	639228-605373	minus	1514	29	ABC transporter	ABCC	ABCC1	DV3000687-RA
82	365312-326212	minus	1344	27	ABC transporter	ABCC	ABCC2	DV3006329-RA
82	286282-256234	minus	1361	25	ABC transporter	ABCC	ABCC3	DV3006327-RA DV3006328-RA
159	25553-1974	minus	1493	20	ABC transporter	ABCC	ABCC4	DV3008821-RA DV3008819-RA
8	1078397-1070560	minus	1657	26	ABC transporter	ABCC	ABCC5	DV3000399-RA
106	284926-273707	minus	664	11	ABC transporter	ABCD	ABCD1	DV3007820-RA
294	20415-10029	minus	721	11	ABC transporter	ABCD	ABCD2	DV3017393-RA
1331	19105-17036	minus	333	7	ABC transporter	ABCD	ABCD3partial	DV3022459-RA
93	29750-33773	plus	608	7	ABC transporter	ABCE	ABCE1	DV3002710-RA
500	40965-55584	plus	870	17	ABC transporter	ABCF	ABCF1	DV3014627-RA
188	52100-56606	plus	618	13	ABC transporter	ABCF	ABCF2	DV3007322-RA
144	121311-127307	plus	716	13	ABC transporter	ABCF	ABCF3	DV3011964-RA
88	798381-788310	minus	695	13	ABC transporter	ABCG	ABCG1	DV3001032-RA
329	172411-185492	plus	619	12	ABC transporter	ABCG	ABCG2	DV3014885-RA
40	189294-204850	plus	615	11	ABC transporter	ABCG	ABCG3	DV3003887-RA
88	759119-752052	minus	639	10	ABC transporter	ABCG	ABCG4	DV3001031-RA
88	727736-743252	plus	610	11	ABC transporter	ABCG	ABCG5	DV3001029-RA
200	30922-24199	minus	570	10	ABC transporter	ABCG	ABCG6	DV3005271-RA
215	164774-181479	plus	693	11	ABC transporter	ABCG	ABCG7	DV3008090-RA
763	83551-73607	minus	617	9	ABC transporter	ABCG	ABCG8	DV3019657-RA
40	228657-245631	plus	915	11	ABC transporter	ABCG	ABCG9	DV3003890-RA
40	248917-259465	plus	599	12	ABC transporter	ABCG	ABCG10	DV3003891-RA
101	157821-150312	minus	564	11	ABC transporter	ABCG	ABCG11	DV3005975-RA
213	592317-579236	minus	657	13	ABC transporter	ABCG	ABCG12	DV3007427-RA
213	577596-569977	minus	594	12	ABC transporter	ABCG	ABCG13	DV3007427-RA
213	562729-556488	minus	601	12	ABC transporter	ABCG	ABCG14	DV3007426-RA
427	317312-310519	minus	595	13	ABC transporter	ABCG	ABCG15	DV3013094-RA
289	299381-308640	plus	677	14	ABC transporter	ABCG	ABCG16	DV3013706-RA
101	273872-264989	minus	649	13	ABC transporter	ABCG	ABCG17 white	DV3005986-RA
20	729099-737489	plus	623	14	ABC transporter	ABCG	ABCG18 scarlet	DV3007978-RA
358	142642-148216	plus	613	15	ABC transporter	ABCG	ABCG19 scarlet-like	DV3015962-RA
206	127698-115445	minus	688	18	ABC transporter	ABCG	ABCG20 scarlet-like	DV3013197-RA
31	347058-356851	plus	638	9	ABC transporter	ABCG	ABCG21	DV3006727-RA
31	335858-331537	minus	915	14	ABC transporter	ABCG	ABCG22	DV3006726-RA
607	18050-4589	minus	760	14	ABC transporter	ABCH	ABCH1	DV3019319-RA
231	63052-40478	minus	778	16	ABC transporter	ABCH	ABCH2	DV3018892-RA
1067	16890-29348	plus	443	10	ABC transporter	ABCH	ABCH3partial	DV3022536-RA
1882	12035-5705	minus	406	9	ABC transporter	ABCH	ABCH4partial	DV3022675-RA
581	69870-61307	minus	692	14	ABC transporter	ABCH	ABCH5	DV3015611-RA
97	283470-265140	minus	711	15	ABC transporter	ABCH	ABCH6	DV3008435-RA
184	285728-267463	minus	700	16	ABC transporter	ABCH	ABCH7	DV3003665-RA
184	338036-326250	minus	645	15	ABC transporter	ABCH	ABCH8	DV3003667-RA DV3003668-RA DV3003669-RA
246	89338-96515	plus	681	15	ABC transporter	ABCH	ABCH9	DV3013023-RA
454	192106-196822	plus	541	11	ABC transporter	ABCH	ABCH10	DV3013584-RA
36	300462-281066	minus	676	15	ABC transporter	ABCH	ABCH11	DV3002992-RA
36	317234-303419	minus	675	15	ABC transporter	ABCH	ABCH12	DV3002993-RA
36	279955-272244	minus	687	15	ABC transporter	ABCH	ABCH13	DV3002991-RA
994	32446-12015	minus	678	15	ABC transporter	ABCH	ABCH14	DV3021404-RA
489	4240-37038	plus	528	11	ABC transporter	ABCH	ABCH15	DV3020532-RA
129	456698-481297	plus	832	17	ABC transporter	ABCH	ABCH16	DV3004573-RA
129	484158-504969	plus	675	15	ABC transporter	ABCH	ABCH17	DV3004574-RA
129	514068-538944	plus	677	15	ABC transporter	ABCH	ABCH18	DV3004576-RA
129	547700-560694	plus	677	15	ABC transporter	ABCH	ABCH19	DV3004577-RA
36	336129-324463	minus	678	15	ABC transporter	ABCH	ABCH20	DV3002994-RA
184	301929-295340	minus	680	15	ABC transporter	ABCH	ABCH21	DV3003666-RA
184	312226-306759	minus	679	15	ABC transporter	ABCH	ABCH22	DV3003666-RA
184	324319-315890	minus	691	15	ABC transporter	ABCH	ABCH23	DV3003666-RA

Table S14, Part3. See above for Legend.

scaffold number	position or transcript name	strand	size (aa)	Number of exons	detox family	name_ID	classification	name
1012	20126-42066	minus	466	8	P450	CYP041	CLAN4	CYP4LS2
1034	9378-19878	minus	454	7 PARTIAL	P450	CYP044	CLAN4	CYP4CH4
107	293519-310023	plus	533	11	P450	CYP052	CLAN4	CYP380C36
109	329252-335722	plus	499	8	P450	CYP017	CLAN2	CYP15A1
11	255781-279372	plus	520	12	P450	CYP078	CLAN4	CYP380A1
11	208753-214325	plus	528	13	P450	CYP077	CLAN4	CYP380B1
1161	24968-25683	plus	109	2 PARTIAL	P450	CYP051	CLAN4	CYP4CH4-fragment1
1233	5936-14055	minus	455	11	P450	CYP060	CLAN4	CYP380C25
1376	15259-16173	minus	233	3 PARTIAL	P450	CYP073	CLAN4	CYP4CH-fragment1
146	427199-432200	minus	474	7 PARTIAL	P450	CYP081	CLANM	CYP302A1
156	377098-383366	plus	512	4	P450	CYP036	CLAN3	CYP6CY25
156	384366-387202	plus	513	5	P450	CYP035	CLAN3	CYP6CZ2
156	392333-392932	plus	297	2 PARTIAL	P450	CYP088	CLAN3	CYP6CZ-fragment2
156	373687-375534	plus	515	5	P450	CYP037	CLAN3	CYP6NZ1
1566	12225-13139	plus	304	1 PARTIAL	P450	CYP089	CLAN3	CYP6CY28-fragment
1566	2887-9927	plus	483	5	P450	CYP033	CLAN3	CYP6PC2
158	232454-247451	minus	536	7	P450	CYP031	CLAN3	CYP6DD2
16	586876-598356	minus	512	11	P450	CYP032	CLAN4	CYP4CJ9
168	65191-85724	minus	564	13	P450	CYP054	CLAN4	CYP380C20
168	93228-115677	minus	537	12	P450	CYP055	CLAN4	CYP380C21
172	292652-296571	minus	500	7	P450	CYP034	CLAN2	CYP303A1
1808	5015-5602	minus	170	2 PARTIAL	P450	CYP050	CLAN4	CYP4CH4-fragment2
183	286-1245	plus	234	5 PARTIAL	P450	CYP053	CLAN4	CYP380C-fragment3
184	99346-103193	plus	499	5	P450	CYP038	CLAN3	CYP6CZ3
184	96231-97503	plus	296	2 PARTIAL	P450	CYP039	CLAN3	CYP6CZ3-fragment
184	28545-35027	plus	507	5	P450	CYP040	CLAN3	CYP6CZ4
184	367-5588	plus	477	10	P450	CYP004	CLAN3	CYP6CZ-fragment1
188	183722-196207	minus	524	7 PARTIAL	P450	CYP049	CLAN4	CYP4LM2
19	255459-265708	minus	495	7	P450	CYP075	CLAN4	CYP4LS1
190	108980-118256	plus	444	8 PARTIAL	P450	CYP048	CLAN4	CYP4CK1
204	367140-392225	plus	458	5 PARTIAL	P450	CYP082	CLAN3	CYP3323B1
214	189191 .. 198508	plus	517	7	P450	CYP007	CLAN4	CYP4LP1
218	142145-148270	plus	514	7	P450	CYP071	CLAN4	CYP4LM1
218	149202-171616	plus	517	7	P450	CYP072	CLAN4	CYP4LN1
2347	497-2152	plus	250	4 PARTIAL	P450	CYP080	CLANM	CYP315A1
26	22157-24425	minus	512	4	P450	CYP020	CLAN3	CYP6CY27
26	2450-5282	minus	508	4	P450	CYP019	CLAN3	CYP6CY29
26	15981-19024	minus	498	5	P450	CYP021	CLAN3	CYP6CY30
26	540670-544976	minus	498	4	P450	CYP023	CLAN3	CYP6PD1
26	617688-618155	minus	118	2 PARTIAL	P450	CYP026	CLAN3	CYP6PD-fragment1
26	673887-673976	minus	74	1 PARTIAL	P450	CYP024	CLAN3	CYP6PD-fragment2
26	695303-695530	minus	76	1 PARTIAL	P450	CYP025	CLAN3	CYP6PD-fragment3
26	713826-718215	minus	324	5 PARTIAL	P450	CYP022	CLAN3	CYP6PD-fragment4
28	1045765-1056041	plus	524	3	P450	CYP027	CLAN2	CYP307A2
28	905594-907642	minus	510	3	P450	CYP042	CLAN2	CYP307C1
2952	1-1805	plus	381	4 PARTIAL	P450	CYP029	CLAN3	CYP6PA1-partial
308	327774-331448	plus	476	9 PARTIAL	P450	CYP083	CLANM	CYP314A1
315	498486-514286	minus	532	12	P450	CYP062	CLAN4	CYP380C23
315	425673-443577	minus	507	11	P450	CYP006	CLAN4	CYP380C26
315	473863-489932	minus	538	12	P450	CYP061	CLAN4	CYP380C28
315	528653-529786	minus	267	6 PARTIAL	P450	CYP063	CLAN4	CYP380C-fragment1
327	135796-139332	minus	211	4 PARTIAL	P450	CYP079	CLAN4	CYP4LS-fragment1
3321	79-838	minus	196	3 PARTIAL	P450	CYP070	CLAN4	CYP4G196-fragment
3560	114-686	plus	139	2 PARTIAL	P450	CYP028	CLAN3	CYP6PB1-fragment
36	710865-711305	minus	118	2 PARTIAL	P450	CYP018	CLAN2	CYP15A1-fragment
375	12670-14928	plus	505	4	P450	CYP086	CLAN3	CYP6CY26
375	37240-40488	plus	508	4	P450	CYP010	CLAN3	CYP6CY28
375	48361-50517	plus	525	4	P450	CYP069	CLAN3	CYP6PA1
375	18841-22424	plus	510	4	P450	CYP009	CLAN3	CYP6PB1
375	1961-5015	plus	374	3 PARTIAL	P450	CYP087	CLAN3	CYP6PB2
375	25442-32804	plus	511	4	P450	CYP008	CLAN3	CYP6PC1
376	177366-187275	minus	553	9	P450	CYP074	CLAN4	CYP3373A1
379	222828-234500	plus	566	11	P450	CYP066	CLAN4	CYP4G194
379	250528-256115	plus	567	11	P450	CYP068	CLAN4	CYP4G195
379	239779-247927	plus	507	10	P450	CYP067	CLAN4	CYP4G196
386	105783-131499	plus	537	13	P450	CYP059	CLAN4	CYP380C22
386	45513-83895	minus	525	13	P450	CYP056	CLAN4	CYP380C24
386	2621-12905	minus	462	11	P450	CYP058	CLAN4	CYP380C27
386	27230-27907	minus	183	3 PARTIAL	P450	CYP057	CLAN4	CYP380C-fragment4
39	142340-146225	plus	541	7	P450	CYP005	CLAN3	CYP6DB6
400	29114-42861	minus	463	10	P450	CYP065	CLAN4	CYP380C29
400	4589-7415	minus	129	3 PARTIAL	P450	CYP090	CLAN4	CYP380C-fragment6
4382	36-615	plus	195	1 PARTIAL	P450	CYP043	CLAN3	CYP6CZ4-fragment
52	348966-353080	plus	511	5	P450	CYP012	CLAN2	CYP18A1
52	357022-361531	minus	496	6	P450	CYP011	CLAN2	CYP306A1
5421	36-859	plus	235	3 PARTIAL	P450	CYP045	CLAN3	CYP6NZ1-fragment
55	16484-18043	minus	293	7 PARTIAL	P450	CYP064	CLAN4	CYP380C-fragment2
64	129440-134687	plus	448	6 PARTIAL	P450	CYP076	CLAN4	CYP4LR1
717	47078..50042	plus	447	8 PARTIAL	P450	CYP001	CLANM	CYP353B1
72	282286..285221	plus	522	9	P450	CYP002	CLANM	CYP301A1
72	289352..293786	plus	515	9	P450	CYP003	CLANM	CYP301B1
742	59376-67317	minus	183	5 PARTIAL	P450	CYP084	CLAN4	CYP380C-fragment5
82	166802-181391	plus	488	8	P450	CYP047	CLAN2	CYP305E1
82	154525-162736	minus	549	7	P450	CYP046	CLAN4	CYP4CH5
89	108086-113372	minus	522	11	P450	CYP085	CLAN4	CYP4CJ6
89	39494-51729	minus	518	11	P450	CYP013	CLAN4	CYP4CJ7
89	58439-69871	minus	383	9 PARTIAL	P450	CYP016	CLAN4	CYP4CJ8
89	72157-86667	minus	412	10 PARTIAL	P450	CYP015	CLAN4	CYP4LQ1
89	29291-38034	minus	513	11	P450	CYP014	CLAN4	CYP4LQ2
9715	252-530	plus	93	1 PARTIAL	P450	CYP030	CLAN3	CYP6PC-fragment

Table S15. Number of genes in detoxification families found in different insects and arthropods genomes. ND: not determined, **=ABC transporter numbers from *A. pisum* were obtained by automatic analysis. *= numbers based on EST data from [38]; *A. pisum* UGT sequences were reanalysed based on the latest genome release (AphidBase). Numbers in brackets are the numbers of previously described UGTs in [38,39]. CYP numbers for CYP from *Tetranychus urticae* were obtained from [40]. CYP data from *B. mori*, *T. castaneum*, *A. mellifera*, *N. vitripenis*, *D. melanogaster*, *A. gambiae*, and *A. pisum* from [41]. Data for *Bemisia tabaci* were obtained from [42].

Table S15, continued.

Order	Hemiptera					Diptera		Lepidoptera	Hymenoptera		Coleoptera	Phthiraptera	Arachnid
Species	*Daktulosphaira vitifoliae*	*Acyrthosiphon pisum*	*Rhodnius prolixus*	*Bemisia tabaci*	*Myzus persicae**	*Drosophila melanogaster*	*Anopheles gambiae*	*Bomby mori*	*Apis mellifera*	*Nasonia vitripennis*	*Tribolium castaneum*	*Pediculus humanus*	*Tetranychus urticae*
Glutathione S-transferase													
Glutathione S-transferase omega	2	2	1	ND	1 (0)	4	1	4	2	2	3	ND	ND
Glutathione S-transferase epsilon	0	0	0	ND	0	14	8	8	0	0	19	ND	ND
Glutathione S-transferase sigma	3	5	6(7)	ND	7 (8)	1	1	2	4	8	7	ND	ND
Glutathione S-transferase delta	2	11	1	ND	3 (2)	11	17	5	2	5	3	ND	ND
Glutathione S-transferase theta	1	2	2(4)	ND	2 (0)	4	2	1	1	3	1	ND	ND
Glutathione S-transferase Zeta	0	2(0)	1	ND	0	2	1	2	1	1	1	ND	ND
Glutathione S-transferase unknown	0	1 (3)	0	ND	0	1	2	1	1	0	2	ND	ND
Glutathione S-transferase microsomal	3	2	1	ND	2	3	3	0	2	0	5	ND	ND
Total	**11**	**25**	**13**	**ND**	**14**	**40**	**35**	**23**	**13**	**19**	**41**	ND	ND
Uridine diphosphate-GlycosylTransferase (UGT)													
UGTs	**35**	**55**	**ND**	**ND**	**38**	**34**	**26**	**45**	**12**	**22**	**43**	**ND**	**ND**
Carboxyl/Cholinesterase (CCE)													
Detoxification/dietary class	2	5	22	ND	5	13	16	55	8	13	26	3	0
Pheromone/hormone processing	10	18	9	ND	12	8	14	8	5	17	11	2	2
Neuro/developmental (total)	8	8	12	ND	5	14	20	13	11	11	12	12	10
clade H - Glutactin	1	1	2	ND	0	5	10	0	1	1	1	0	2
clade J - Acetylcholinesterase	2	2	2	ND	3	1	2	2	2	2	2	2	1
clade K - Gliotactin	1	1	1	ND	1	1	1	1	1	1	1	1	1
clade L - neuroligins	3	3	4	ND	0	4	5	6	5	5	5	5	5
clade M - neurotactine	0	0	1	ND	0	2	2	2	1	1	2	3	1
Unknown function	1	1	2	ND	1	1	1	2	1	1	1	1	0
Acari specific-class													59
Total CCEs	**20**	**31**	**43**	**51**	**22**	**35**	**51**	**76**	**24**	**41**	**49**	**17**	**71**
ABC sub-family													
A	4	11	ND	8	ND	10	9	9	3	ND	10	2	9
B	6	9	ND	3	ND	8	5	9	5	ND	6	6	4
C	5	16	ND	6	ND	14	13	15	9	ND	35	5	39
D	3	2	ND	2	ND	2	2	2	2	ND	2	2	2
E	1	1	ND	1	ND	1	1	1	1	ND	1	1	1
F	3	4	ND	3	ND	3	3	3	3	ND	3	3	3
G	22	19	ND	23	ND	15	16	13	15	ND	13	13	23
H	23	9	ND	9	ND	3	3	3	3	ND	3	2	22
Total	**67**	**71****	**ND**	**55**		**56**	**52**	**55**	**41**		**73**	**40**	**103**
Cytochrome P450 (CYP)													
clan2	7	10	5	10	9	7	10	7	8	7	8	8	48
clanmito	6	8	6	7	7	11	9	12	6	7	9	8	5
clan3	27	23	50	57	25	36	40	30	28	48	72	11	10
clan4	41	23	23	56	19	32	46	34	4	30	45	9	23
Total	**86**	**64**	**84**	**130**	**60**	**88**	**105**	**83**	**46**	**92**	**134**	**36**	**86**

Table S16. Effector genes with predicted domains and their corresponding functions. The number of proteins with InterPro hits belonging to each cluster are indicated in parentheses.

InterPro entry	**Name**	**Function**	**Genes with IPR hits**	**Cluster number (IPR hits)**
IPR001841 /IPR013083	Zinc finger, RING-type	Mediating protein-protein interactions	144	1(2), 3(37), 5(19), 15(45), 17(1), 18(13), 19(18), 38(2), 50(4), 67(1), 69(1), 78(1)
IPR020683 /IPR036770	Ankyrin repeat-containing domain	Mediating protein-protein interactions	133	49(133)
IPR002048 /IPR011992	EF-hand domain	Calcium binding	56	2(2), 7(11), 16(17), 29(22), 36(3), 44(1)
IPR019080 /IPR011335	YqaJ viral recombinase	Processive alkaline exonuclease activity	27	33(27)
IPR003172 /IPR036846	MD-2-related lipid-recnition domain	Lipid recognition	15	14(15)
IPR003323 /IPR038765	OTU domain	Cysteine protease activity	15	19(15)
IPR014044 /IPR035940	CAP domain	Regulation extracellular matrix and branching morphogenesis, ion channel regulation, tumor suppressor, cell-cell adhesion	14	13(14)
IPR001254 /IPR009003	Serine proteases, trypsin domain	Serine protease activity	6	23(6)
IPR032675	Leucine-rich repeat domain	Mediating protein-protein interactions	3	49(3)
IPR002350 /IPR036058	Kazal domain	Proteinase inhibitor	2	11(2)
IPR000971	Globin	Binding and/or transporting oxygen	1	3(1)
IPR007099	RNA-directed RNA polymerase, negative-strand RNA virus	Catalyzing RNA synthesis	1	3(1)
IPR009056	Cytochrome c-like domain	Electron transfer activity, heme binding	1	3(1)
IPR016024	Armadillo-type fold	Protein/nucleic acid binding	1	29(1)

Table S17. Statistics on raw sequences used for assembling the complete genome of *D. vitifoliae*, with SRA accessions. Details are given for each type of library. Calculation of depth based on a genome size of 294 Mb. For PacBio, mean read length.

Experiment (SRA Id)	**type**	**Insert size**	**Read length**	**# bases sequenced**	**Depth**
SRX7110322	Illumina Paired Ends	250	148	17.3G	57.1
SRX7110323	Illumina Paired Ends	500	150	7.7G	25.7
SRX7110324	Illumina Paired Ends	800	100	15.6G	53.1
SRX7110325	Illumina Mate Pairs	2000	100	5.4G	18.3
SRX7110326	Illumina Mate Pairs	5000	100	5.3G	18
SRX7110327	PacBio	-	6792	17.1G	58

Table S18. List of taxa included in the study of gene expansions. Genome source (NCBI accessions or other databases) and number of predicted proteins are indicated for each taxon.

Taxon	Source	No. predicted proteins
Diaphorina citri	PRJNA29447	19681
Myzus persicae	PRJEB11304 (clone O), PRJNA319804 (clone G006)	18378
Diuraphis noxia	PRJNA296778	15072
Aphis glycines	AphidBase	18984
Rhopalosiphum padi	AphidBase	27554
Cinara cedri	ongoing sequencing project	16933
Daktulosphaira vitifoliae	this study	25567
Acyrthosiphon pisum	PRJNA13657	23886
Bemisia tabaci	PRJNA352527	19320

Table S19. Details on the sampling of phylloxera populations used for population genomics analyses. Populations corresponds to pools of insects collected in geographically close sites or to ‘lineages’ maintained in laboratory conditions as precised (comment column). SRA accession of each sequenced library in the population genomics study.

Continent of origin	Country	Population (Pool) Name	SRA Accession	region/town	Native/introduced	nb of ind.	nb of sites/lineages pooled	GA/RA	Host plant	comment	cv.
North America	California	CA	SRX7116434	-	native	30	2	Radicicole	*rootstock*	lineages maintained on 1103P	-
North America	Washington	WA	SRX7116435	-	native	50	2	Radicicole	*Vitis labrusca*		Concord
North America	Arizona	AR	SRX7116444	-	native	80	5	Gallicole	*Vitis arizonica*		-
North America	Wisconsin	WI	SRX7116445	-	native	60	3	Gallicole	*Vitis riparia*		-
North America	Ilinois	IL	SRX7116446	-	native	85	3	Gallicole	*Vitis riparia*		-
North America	New York	NY	SRX7116447	-	native	100	7	Gallicole	*Vitis riparia*		-
North America	Pennsylvania	PA	SRX7116448	-	native	37	1	Gallicole	*Vitis vulpina*		-
North America	Virginia	VA1	SRX7116449	-	native	100	5	Gallicole	*Vitis vulpina*		-
North America	Virgnia	VA2	SRX7116450	-	native	35	1	Gallicole	interspecific hybrid		Chambourcin
North America	West Virginia	WV	SRX7116451	-	native	31	2	Gallicole	*Vitis aestivalis*		-
North America	Massachusetts	MA	SRX7116436	-	native	20	1	Gallicole	*Vitis labrusca*		-
Europe	France	France	SRX7116437	South-west	introduced	100	6	Gallicole	savaged rootstock		-
Europe	Germany	Germany	SRX7116438	Palatinat	introduced	70	3	Gallicole	savaged rootstock, *V. vinifera*	insects maintained on SO4	Muscat Ottonel, Sylvaner
Europe	Austria	Austria	SRX7116439	Vienna	introduced	32	3	Gallicole	*V. vinifera*		Zweigelt, Cabernet
Europe	Romania	Romania	SRX7116440	na	introduced	100	4	Gallicole	*V. vinifera*		na
Europe	Armenia	Armenia	SRX7116441	na	introduced	40	1	Gallicole	*V. vinifera*		Rkatsiteli
South America	Uruguay	Uruguay	SRX7116442	Montevideo	introduced	100	2	Gallicole	*V. vinifera*		Marselan, Chardonnay
Australia	Australia	Australia	SRX7116443	Victoria	introduced	20	1 (G4)	Gallicole	*V. vinifera*	lineage maintained on 3309C	-

Table S20. Prior distribution of parameters used for modelling the different scenarios of invasion routes (ABC methods). A) List of parameters and their characteristics. FR, IL and NY are the French, Illinois and New-York populations, respectively. B) Summary statistics: for all statistics, Mean and variance non-zero values and Mean of complete distribution were computed.

A. Parameter	**Interpretation**	**Distribution**	**Range**	**Conditions**
Introduction in France				
N0	Effective size of the FR founder population	Uniform	[10-10000]	N0<N2,N0<N3
N1	Effective size of the FR population	Uniform	[10-10000]	
N2	Effective size of the IL population	Uniform	[10-10000]	
N3	Effective size of the NY population	Uniform	[10-10000]	
N4	Effective size of the original US population	Uniform	[10-10000]	
N5	Effective size of founder from IL population	Uniform	[10-10000]	N5<N2
N6	Effective size of founder from NY population	Uniform	[10-10000]	N6<N3
t0	Time to invasion	Uniform	[10-10000]	
tn	Time to merge event between original population and NY population	Uniform	[10-10000]	tn>t5,tn>tf
ti	Time to merge event between original population and IL population	Uniform	[10-10000]	ti>t6
tf	Time to merge event between the FR population and the invasive population	Uniform	[10-10000]	tf<ti,tf>t0
t5,t6	Time to merge between the invasive population coming founder population and their respective origin populations	Uniform	[10-10000]	t5>tf,t6>tf
ra	ratio of admixture	Uniform	[0.001-0.999]	
Introduction in Germany (after France)				
N1	Effective size of the FR population	Uniform	[10-10000]	
N2	Effective size of the German population	Uniform	[10-10000]	
N3	Effective size of the IL population	Uniform	[10-10000]	
N3b	Effective size of the German founder population from IL	Uniform	[10-10000]	N3b<N2,N3b<N3
N4	Effective size of the original NY population	Uniform	[10-10000]	N4b<N4,N4b<N2
N4b	Effective size of German founder population from NY	Uniform	[10-10000]	
N5	Effective size of FR founder population from IL	Uniform	[10-10000]	N5<N3,N5<N1
N6	Effective size of FR founder population from NY	Uniform	[10-10000]	N6<N4,N6<N1
N7	Effective size of the original US population	Uniform	[10-10000]	
N8	Effective size of German founder population from IL	Uniform	[10-10000]	N8<N3,N8<N2
N9	Effective size of German founder population from NY	Uniform	[10-10000]	N9<N4,N9<N2
tg	Time to merge event between the German founder and its ancestral population	Uniform	[10-10000]	tg>tg1
tg1	Time to merge event between the German opulation and its founder population	Uniform	[10-10000]	
tf	Time to split event between the FR population and the invasive population	Uniform	[10-10000]	tf<tg
t5,t6, t8, t9	Time to merge between the invasive populations coming founder population and their respective origin populations	Uniform	[10-10000]	t5>tf,t6>tf,t8>tg,t9>tg,
tn	Time to merge event between original population and NY population	Uniform	[10-10000]	tn>t5,tn>t6,tn>t8,tn>tg
ti	Time to merge event between original population and IL population	Uniform	[10-10000]	ti>t9,ti>t6,ti>tg,ti>t5,ti>t8
ra, rb	ratio of admixture	Uniform	[0.001-0.999]	

B. Summary statistics used for all scenarios	
One sample statistics	Genetic Diversities
Pairwise statistics	FST distances
	Nei's distances
Admixture statistics	All estimates

Supplementary Methods and Results

microRNAs

Methods: Total RNA was isolated from a whole colony of the isofemale INRA-Pcf7 clone using the MirVana kit (Ambion) that allows to enrich the preparation for small RNAs shorter than 200 nucleotides. Small RNAs were sequenced at the IGBMC laboratory (Illkirch, France) by 50 bp single reads, with the Illumina TruSeq technology on a HiSeq4000,. The 188 millions reads, after clipping adapters (with clip_adapters.pl from mirDeep2 TGGAATTCTCGGGTGCCAAGG) were mapped to the genome with and collapsed with the mapper.pl script from mirDeep2 with the options “-j -l 18 -m”. Finally, the resulting arf file was processed with miRDeep2.pl with the *A. pisum* mature sequences from miRBase as reference. The structures of precursor sequences returned from miRDeep2 were manually inspected. Any predicted miRNAs that lacked significant support for a hairpin structure, or candidate star and loop sequences were excluded. The predicted precursors and mature sequences of miRNAs were blasted against miRBase v21 using miRBase implemented blastn to assign known miRNAs and novel miRNAs [43]. miRNA duplications were analyzed with CodonCode Aligner v.5.1.5 (CodonCode Corporation: http://www.codoncode.com/aligner/index.htm), while miRNA clusters were manually annotated.

Results: Using small RNA-Seq data, and after automatic prediction and manual curations, 150 miRNA precursors encoding 142 unique mature miRNAs were identified (Figure S12); of these 69 (49%) were homologous to miRNAs previously reported in other species, while 73 (51%) were novel (Table S10). 31% (*i.e.* 47/150) of miRNA precursors were arranged in 14 genomic clusters and 42% percent (*i.e.* 63/150) were derived from 23 miRNA duplications, with one group containing 12 duplicates (Table S10). With respect to genomic localization, 63% (*i.e.* 95/150) of miRNA precursors were found in intergenic regions (IGR), 31% (*i.e.* 46/150) were in introns, and 6% (*i.e.* 9/150) were in exons, UTRs, or UTR/exon junctions. Lastly, eight genomic sites expressed miRNAs from both +/- DNA strands.

Aquaporins

Methods: Aquaporins (AQPs) function as a channel for the passage of water and other small molecules across cell membranes [44]. These genes vary considerably in numbers and sequence identity among phloem sap-feeding insect groups [45]. The amino acid sequences of aquaporins were obtained from AphidBase for *A. pisum* and from Genbank for other species. Aquaporins of phylloxera were identified by blastp against the predicted phylloxera proteome, with *A. pisum* and *D. melanogaster* aquaporins as queries, and gene models were manually curated. Amino acid sequences were aligned using MAFFT [46] and trimmed using TrimAl [47]. A Bayesian analysis was conducted with MrBayes 3.2.6 using the model LG+I+G [48]. The Bayesian Inference (BI) model was determined using ProtTest 3.4.1 [49]. In total, 10,000 trees were obtained (ngen= 1,000,000; samplefreq=100) and the first 25% were discarded as burn-in. The average split frequencies were < 0.01. The consensus phylogenetic tree was visualized with FigTree.

Results: We found three *AQP* genes in the genome of grape phylloxera, with one in each of three clades: *Drosophila* integral protein (*DRIP*), entomoglyceroporin (*EGLP*) and big brain (*BIB*). These sequences had the expected canonical amino acid residues, indicating that the proteins are functional. We found these three genes to have 1:1 orthologs in *A. pisum* (Figure S13), suggesting that they have not been duplicated. By contrast, Aleyrodoidea (whiteflies) and Psylloidea have multiple genes in the different aquaporin gene families, including PRIP-aquaporins [45] which are absent from both phylloxera and *A. pisum*.

Methylation

Methods: Putative DNA methylation-related genes were discovered using tblastn queries from pea aphid and *Apis mellifera* sequences. Pea aphid sequences used were Dnmt1 (ACYPI073296), Dnmt2 (ACYPI00794), Dnmt3 (ACYPI29975), methyl-CpG-binding protein (ACYPI004592), and Dnmt1-associated protein (ACYPI004738). Corresponding *Apis mellifera* sequences used were XP_026298868, XP_006563008, XP_026302148, XP_003250633, and XP_392117, respectively. Hits above 1e-50 were reverse blasted back to the pea aphid genome for verification. Identification of homologs was followed by manual curation of gene models.

Results: The DNA methylation machinery consists of proteins such as Dnmt1, Dnmt2, Dnmt3, methyl-CpG-binding protein, and Dnmt1-associated protein. Genes coding for these proteins were found in the grape phylloxera genome, each with only a single copy. The grape phylloxera thus has genes necessary for DNA methylation.

Circadian clock and related genes

Methods: Annotation of circadian clock genes was performed using the corresponding protein sequences from *Acyrthosiphon pisum* (Table S11) as blastp or tblastn queries against *Phylloxera* predicted transcripts or genome (e-value threshold, 1e-6). This was followed by manual curation of gene models for hits.

Results: The circadian clock mechanism which is conserved among different taxa, consists of two interlocked feedback loops of transcription factors [50], organised into three groups of elements: the input, core and output of the clock. Based on the sequences of the *A. pisum* circadian clock genes [51-52] (Table S11), we found that these three groups are conserved in the phylloxera in terms of presence or absence of their members. The circadian clock of grape phylloxera belongs to the insect ancestral type [53], which is mainly characterized by the presence of two different types of cryptochromes (CRY): a *Drosophila*-like CRY (d-CRY or CRY1) and a vertebrate-like CRY (v-CRY or CRY2). Phylloxeran circadian clock genes are highly similar to those found in *A*. *pisum*. As in *A. pisum*, some of them seem to have experienced accelerated evolutionary rates especially Dvit*per* (Figure S14), Dvit*tim* and Dvit*cry2 (not shown)*. A gene encoding the prothoracicotropic hormone (PTTH) was also identified which, as in aphids [54] was characterized by the presence of six cysteine residues rather than the more typical seven (Figure S15). While several elements of the circadian clock appear to be duplicated in the *A. pisum* genome, we found fewer or no duplications in phylloxera (e.g. no duplication of *cry2*, or *Rhodopsin 7*, and two instead of four copies of *iAANAT* and *SWO*).

Adaptation to biotic and abiotic environment

Methods:

i) Odorant and gustatory receptors: OR and GR sequences (ORs: 599 sequences, GRs: 190 sequences) from other hemipteran species were retrieved from the nr database (July 2017) and used against the grape phylloxera genome using tblastn. Respectively 46 and 13 scaffolds presented a hit with OR or GR query sequences. Hemipteran chemoreceptor amino acid sequences (ORs and GRs) were aligned on these scaffolds using Scipio [55], Exonerate [56] and Genewise [57]. These alignments were used to generate gene models using Apollo [58] which were manually curated based on sequence similarity with other species and on RNAseq data. To build a phylogeny, amino acid sequences of candidate ORs and GRs of phylloxera were added to sequences from other Hemiptera: *A. pisum* (Apis, ORs and GRs) [35], *R. prolixus* (Rpro, ORs and GRs) [34] and *A. gossypii* (Agos, ORs only) [59]. Sequences with less than 300 amino acids were removed from the data sets. Sequences were aligned using MAFFT [60] and a phylogeny was built using PhyML 3.0 [61] . The best-fit model of protein evolution was determined using SMS [62]. Node support was assessed by carrying out an approximate likelihood-ratio test aLRT [63]

ii) Odorant, gustatory ligand-binding and extracellular-binding families: We first examined preliminary annotations of the phylloxera genome to assign genes to odorant, gustatory ligand-binding and extracellular-binding families based on the detection of a Pfam domain for OBPs, CSPs and NPC2s [64]. Then we built a protein database containing all protein sequences of this first set completed by members of these families previously characterized in the genome of *A. pisum* [65] . Using this collection as query sequences, we searched the genome sequence using tblastn (*E*-value $< 10^{-3}$) to find additional members. All new annotations were visually checked using RNA-Seq data and SNP coverage density curves. We then conducted a phylogenetic analysis of the three principal families (OBP, CSP and NPC2 families) including only full-length proteins for phylloxera, and a set of representative sequences from aphid species - a different set of species was used in each of the three analyses. Overall this list of species comprised *A. pisum* (Apis), *A. gossypii*

(Agos), *D. noxia* (Dnox), *M. persicae* (Mper), *Sitobion avenae* (Save), *A. glycines* (Agly), *Nasonovia ribisnigri* (Nrib) *and Metopolophium dirhodum* (Mdir). Protein sequences were aligned using MAFFT v7.273 [66] and RAxMLHPC-AVX v8.2.4 [67] was used to obtain the maximum likelihood phylogenetic relationships within each family. Node support was calculated using 500 bootstrap replicates. An analysis of gene conversion across paralogues was carried out using GeneConv [68] . The resulting trees were edited using iTOLv3.5.4 [69].
iii) Detoxification genes: We first analyzed Cytochrome P450 (CYP) proteins, a group in which sequence identity can be as low as 25 percent, but where conserved motifs allows assignment to CYP sequences [70]. The phylloxera genome was searched for P450 genes by tblastn against the whole genome sequence, using annotated CYP protein sequences from *A. pisum* and *M. persicae* as queries. Candidate genomic regions containing CYPs were manually annotated to confirm or correct gene models with the help of RNA-Seq data when available (these curation steps were also done in the next groups of detoxification genes). Protein CYP sequences were sent to D. Nelson for name attribution. For GSTs and UGTs, we used sets of Hemiptera proteins to search the phylloxera genome by tblastn using Galaxy [71], and then Exonerate and Scipio to align protein sequences on the genome and to define intron/exon boundaries [55]. The classification of deduced proteins and their integrity were verified using blastp against the non-redundant (nr) GenBank database. When genes were suspected to split in different scaffolds, protein sequences were merged for further analyses. All active sites were confirmed using the NCBI CD-search program. CCE genes were searched by tblastn against the whole genome assembly using CCE proteins sequences from *N. vitripennis*, *R. prolixus*, *A. pisum* and *M. persicae* collected from the latest NCBI release. Then CCE sequences were analyzed as described above for UGTs/GSTs. ABC transporters genes were searched by tblastn against the genome sequence using ABC transporter proteins sequences from *D. melanogaster* and *A. mellifera*.

Results: Sensing and reacting to the biotic and abiotic environment involves chemical senses, as well as detoxification and secretion of effectors. Genes associated with these functions often evolve rapidly, allowing adaptation to new environments. Although little is known about the chemical ecology of grape phylloxera, it has been shown that this species exhibits selectivity to grape rootstocks and cultivars that produce different volatile organic compounds [72]. This suggests that phylloxera uses chemical cues, as suggested above by the GO term enrichment seen in the phylloxera lineage-specific set of genes. We annotated odorant (ORs) and gustatory (GRs) receptors in the phylloxera genome, this being the first time for a root-feeding herbivore. We annotated 60 OR genes (Dvit_OR), plus one gene encoding the co-receptor ORco (Table 12). While *ORco* sequences are highly conserved, other hemipteran ORs are very divergent (Figure 16). Our phylogenetic analysis suggests that evolution of the ORs is mostly characterized by lineage-specific expansions. In particular, almost half of Dvit_ORs (29 out of 60) belong to a well supported clade containing no aphid OR. We found no ortholog of *Apis_OR5*, underlying production of the alarm pheromone of *A. pisum* [73]. This fits with the absence in phylloxera of both alarm pheromones and cornicles, the organs that emit pheromones in aphids. A total of 18 GRs (Dvit_GRs) were annotated, less than in other Hemiptera species (*A. pisum*: n=70, *R. prolixus*: n=26). Three Dvit_GRs belonged to a clade including putative *A. pisum* sugar receptors [35] (Figure 17). While CO_2 may be one of the volatile cues for root detection, no candidate CO_2 receptor could be found, just as in the *A. pisum* and *R. prolixus* genomes.

We also identified a total of 13 odorant-binding (*Obp*), 12 chemosensory (*Csp*) and 8 Niemann-Pick (*Npc2*) genes, encoding soluble proteins regarded as possible carriers of sensory cues in insect chemoreception [74] (Table 13). These numbers are very similar to those found in *A. pisum* (13, 12 and 7, respectively) and in other aphids [37,65,75]. We did not find members of the CheA/B superfamily in the phylloxera genome. Our phylogenetic analysis of the OBP gene family (Figure 18) identified 11 orthogroups. Grape phylloxera was represented in every orthogroup except OBP7, and aphid species were represented in all of them, suggesting that the diversification of this gene family preceded the divergence between phylloxera and aphids. Some orthogroups (e.g. OBP14) were missing from one or a few species, indicating gene turnover during the evolution of this family. The CSP tree (Figure 19) shows a similar picture to that of the OBP tree, although, in this case, the lower number of species available for the analysis precluded clear conclusions about gene turnover dynamics. The phylogenetic tree of the NPC2 proteins presented a different aspect, with multiple copies from the same species clustering together, with no clear orthogroups (Figure 20). As we did not detect evidence of gene conversion between paralogs, we suggest that the NPC2 family is highly dynamic both in aphids and phylloxera, with multiple lineage-specific duplications in each group. Concerning the detoxification function, the genome of grape phylloxera contained 86 cytochrome P450s (CYPs), 35 UDP-glycosyltransferases (UGTs), 11 glutathione S-transferases (GSTs), 20 carboxylesterases (CCEs) and 67 ABC transporters (Table 14, Table 15). We found that these five classes of genes have seen duplication events both preceding and following the divergence between phylloxera and aphids. Compared to aphids, phylloxera generally had a reduced number of copies though it did show expansion of particular clusters. In the case of the CYPome, a very dynamic gene family [41], two CYP families, *CYP6CZ* and *CYP380C*, were expanded in phylloxera while the CYP6CY family comprised only six members compared to 16 and 12 in *A. pisum* and *M. persicae*, respectively. Finally, a new *CYP* family, *CYP3373*, was found in the phylloxera genome.