TABLE S1 Bioinformatics analysis in figures.

Parameter	**Number**
Contigs *de novo* assembled by Trinity and clustered by CD-Hit (≥98% identity)	134911
ORFs predicted by TransDecoder (cutoff: protein length ≥ 100 aa)	66919
ORFs with Pfam annotation	31535
Single 'best' ORF per transcript according to pfam results and sequence length, with longer ORFs preferred	36951
with orthologous group (according to eggNOG)	28305
Proteins with at least one blastp hit (cutoff: E-value ≤1-04)	39179
Proteins with an arthropod sequence as first blastp hit	17916
with GO Annotation (according to blast2GO)	10871
with predicted signal peptide and without transmembrane domains (according to InterPRO)	1362

TABLE S2 Blastp 5 top-hit species distribution.

Species	**Number of blast top-hits**
Zootermopsis nevadensis	3368
Cimex lectularius	2336
Halyomorpha halys	2156
Tribolium castaneum	903
Acyrthosiphon pisum	824

TABLE S3 Overview of *Euscelidius variegatus* transcripts up-regulated during chrysanthemum yellows (CYp) infection, compared with insects infected by Flavescence dorée (FDp) phytoplasmas. Transcripts were classified into functional categories according to the putative identification assigned by a blastx search.

Contig accession*	Eva transcript ID	Sequence description	Hit Accession	Organism	E-Value
Immune response					
GFTU01010641.1	TR70079_c0_g2_i1	PREDICTED: serpin B3-like	XP_014246505.1	*Cimex lectularius*	3E-45
GFTU01009442.1	TR59420_c0_g3_i1	hypothetical protein g.45731 (Protein Disulfide Isomerase (PDIa) family, redox active TRX domains)	JAT21035.1	*Graphocephala atropunctata*	0
GFTU01009443.1	TR59420_c0_g3_i5	PREDICTED: uncharacterized protein LOC109042410 isoform X4 (Protein Disulfide Isomerase (PDIa) family, redox active TRX domains)	XP_018914663.1	*Bemisia tabaci*	0
GFTU01009445.1	TR59420_c0_g3_i8	PREDICTED: uncharacterized protein LOC106678838 isoform X8 (Protein Disulfide Isomerase (PDIa) family, redox active TRX domains)	XP_014273104.1	*Halyomorpha halys*	0
GFTU01009444.1	TR59420_c0_g3_i7	hypothetical protein g.45731 (Protein Disulfide Isomerase (PDIa) family, redox active TRX domains)	JAT21035.1	*Graphocephala atropunctata*	0
GFTU01012880.1	TR94789_c0_g1_i1	PREDICTED: protein disulfide-isomerase A6	XP_011301143.1	*Fopius arisanus*	1E-15
GFTU01010415.1	TR68562_c5_g1_i1	PREDICTED: gamma-interferon-inducible lysosomal thiol reductase-like	XP_008190385.1	*Tribolium castaneum*	2E-13
GFTU01003389.1	TR10030_c0_g1_i1	hypothetical protein g.13589 (Single domain von Willebrand factor type C)	JAS60102.1	*Cuerna arida*	2E-12
GFTU01000362.1	TR17520_c1_g1_i2	PREDICTED: hexamerin 4 isoform X1	XP_008197349.1	*Tribolium castaneum*	9E-25
GFTU01005409.1	TR25619_c0_g1_i1	chitinase	AJO25038.1	*Nilaparvata lugens*	0
GFTU01006368.1	TR33965_c0_g1_i1	PREDICTED: E3 ubiquitin-protein ligase HUWE1 isoform X5	XP_005162339.1	*Danio rerio*	0
Movement and energy metabolism					
GFTU01004258.1	TR16310_c0_g1_i4	PREDICTED: troponin I-like isoform X2	XP_015117836.1	*Diachasma alloeum*	3E-50
GFTU01000669.1	TR32741_c1_g2_i1	PREDICTED: maltase A1-like	XP_003703631.1	*Megachile rotundata*	1E-42
GFTU01001629.1	TR82415_c2_g3_i8	PREDICTED: twitchin isoform X25	XP_015599633.1	*Cephus cinctus*	0
GFTU01012455.1	TR82415_c2_g3_i13	PREDICTED: twitchin isoform X19	XP_015599627.1	*Cephus cinctus*	0
GFTU01012453.1	TR82415_c2_g3_i1	PREDICTED: twitchin isoform X23	XP_015599631.1	*Cephus cinctus*	0
GFTU01001631.1	TR82415_c2_g3_i21	PREDICTED: twitchin isoform X1	XP_012289119.1	*Orussus abietinus*	0
GFTU01001630.1	TR82415_c2_g3_i20	PREDICTED: twitchin isoform X1	XP_012289119.1	*Orussus abietinus*	0
GFTU01001638.1	TR82415_c2_g3_i40	PREDICTED: twitchin isoform X1	XP_012289119.1	*Orussus abietinus*	0
GFTU01001632.1	TR82415_c2_g3_i24	PREDICTED: twitchin isoform X1	XP_012289119.1	*Orussus abietinus*	0
GFTU01001635.1	TR82415_c2_g3_i31	PREDICTED: twitchin isoform X1	XP_012289119.1	*Orussus abietinus*	0
GFTU01001634.1	TR82415_c2_g3_i30	PREDICTED: twitchin isoform X23	XP_015599631.1	*Cephus cinctus*	0
GFTU01001636.1	TR82415_c2_g3_i37	PREDICTED: twitchin isoform X25	XP_015599633.1	*Cephus cinctus*	0
GFTU01001637.1	TR82415_c2_g3_i39	PREDICTED: twitchin isoform X25	XP_015599633.1	*Cephus cinctus*	0
GFTU01001633.1	TR82415_c2_g3_i27	PREDICTED: twitchin isoform X24	XP_015599632.1	*Cephus cinctus*	0
GFTU01012458.1	TR82415_c2_g3_i38	PREDICTED: twitchin isoform X16	XP_014256281.1	*Cimex lectularius*	0
GFTU01012456.1	TR82415_c2_g3_i28	PREDICTED: twitchin isoform X13	XP_018903677.1	*Bemisia tabaci*	0
GFTU01001910.1	TR201186_c0_g1_i1	PREDICTED: arginine kinase	XP_014239180.1	*Cimex lectularius*	0
GFTU01009195.1	TR57237_c0_g1_i1	PREDICTED: myosin light chain alkali	XP_014291721.1	*Halyomorpha halys*	6E-48
GFTU01001677.1	TR83034_c0_g1_i1	PREDICTED: myosin heavy chain, muscle isoform X30	XP_016656804.1	*Acyrthosiphon pisum*	0
GFTU01002981.1	TR6028_c0_g1_i11	PREDICTED: PDZ and LIM domain protein 3 isoform X3	XP_014283142.1	*Halyomorpha halys*	6E-102
GFTU01000140.1	TR6028_c0_g1_i10	PREDICTED: PDZ and LIM domain protein 3 isoform X4	XP_014283149.1	*Halyomorpha halys*	9E-89
GFTU01012488.1	TR82451_c1_g1_i1	PREDICTED: sarcalumenin isoform X2	XP_014255390.1	*Cimex lectularius*	0
GFTU01006510.1	TR34691_c1_g3_i2	actin muscle	XP_002426688.1	*Acyrthosiphon pisum*	0
GFTU01009078.1	TR56715_c0_g1_i1	PREDICTED: muscle M-line assembly protein unc-89 isoform X1	XP_018906227.1	*Bemisia tabaci*	0
GFTU01012457.1	TR82415_c2_g3_i29	PREDICTED: muscle M-line assembly protein unc-89-like	XP_014256262.1	*Cimex lectularius*	0

GFTU01012454.1	TR82415_c2_g3_i11	PREDICTED: muscle M-line assembly protein unc-89-like	XP_014256262.1	*Cimex lectularius*	0
GFTU01001628.1	TR82415_c2_g3_i7	PREDICTED: muscle M-line assembly protein unc-89-like	XP_014256262.1	*Cimex lectularius*	0
GFTU01007383.1	TR44181_c1_g1_i1	PREDICTED: titin isoform X2	XP_014261219.1	*Cimex lectularius*	0
GFTU01010045.1	TR65388_c0_g1_i1	PREDICTED: titin-like, partial	XP_015517479.1	*Neodiprion lecontei*	0
GFTU01008365.1	TR51524_c0_g1_i5	PREDICTED: ryanodine receptor	XP_014270803.1	*Halyomorpha halys*	0
GFTU01008363.1	TR51524_c0_g1_i1	PREDICTED: ryanodine receptor	XP_014270803.1	*Halyomorpha halys*	0
GFTU01002369.1	TR1465_c0_g1_i1	D-beta-hydroxybutyrate dehydrogenase, putative	XP_002430627.1	*Pediculus humanus corporis*	3E-155
GFTU01014213.1	TR172637_c0_g1_i1	PREDICTED: calcium-transporting ATPase sarcoplasmic/endoplasmic reticulum type isoform X3 (SERCA)	XP_014240091.1	*Cimex lectularius*	0
GFTU01010911.1	TR71289_c0_g1_i1	PREDICTED: dynein beta chain, ciliary-like	XP_014246445.1	*Cimex lectularius*	0
Proteases					
GFTU01004471.1	TR18473_c0_g1_i1	PREDICTED: cathepsin L1	XP_015592402.1	*Cephus cinctus*	2E-55
GFTU01003425.1	TR10248_c0_g2_i1	hypothetical protein g.35645 (Peptidase M1 Aminopeptidase N)	JAS50411.1	*Cuerna arida*	2E-148
GFTU01001733.1	TR147669_c0_g1_i1	hypothetical protein g.22606 (Peptidase M1 Aminopeptidase N family)	JAS92288.1	*Homalodisca liturata*	0.0
GFTU01012473.1	TR82434_c0_g6_i2	PREDICTED: prostatic acid phosphatase-like	XP_014279962.1	*Halyomorpha halys*	2E-101
GFTU01013458.1	TR135531_c0_g1_i1	hypothetical protein g.31954 (Chitin-binding domain type 2, Peptidase M1 Aminopeptidase N family)	JAT07207.1	*Homalodisca liturata*	5E-51
GFTU01002473.1	TR2416_c0_g1_i1	PREDICTED: neprilysin isoform X1 (membrane metallo-endopeptidase)	XP_015600086.1	*Cephus cinctus*	0
GFTU01016619.1	TR222575_c0_g1_i1	PREDICTED: leucyl-cystinyl aminopeptidase-like	XP_014296891.1	*Microplitis demolitor*	1E-31
GFTU01003281.1	TR9182_c0_g1_i2	PREDICTED: membrane metallo-endopeptidase-like 1 isoform X3	XP_012244761.1	*Bombus impatiens*	1E-170
GFTU01012719.1	TR83509_c2_g2_i1	hypothetical protein g.32075 (invasion associated secreted endopeptidase; Provisional)	JAT00648.1	*Homalodisca liturata*	0
Extracellular matrix					
GFTU01000571.1	TR27727_c2_g1_i1	PREDICTED: neurogenic locus notch homolog protein 3-like, partial	XP_015378277.1	*Diuraphis noxia*	0
GFTU01005879.1	TR28949_c0_g1_i1	PREDICTED: neurogenic locus notch homolog protein 1	XP_001944803.2	*Acyrthosiphon pisum*	2E-175
GFTU01007832.1	TR47223_c0_g1_i4	PREDICTED: membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3-like	XP_015370062.1	*Diuraphis noxia*	1E-32
GFTU01007834.1	TR47223_c0_g1_i6	PREDICTED: membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3-like	XP_015370062.1	*Diuraphis noxia*	1E-32
GFTU01007833.1	TR47223_c0_g1_i5	PREDICTED: membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3-like	XP_015370062.1	*Diuraphis noxia*	1E-32
GFTU01007831.1	TR47223_c0_g1_i3	PREDICTED: membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3-like	XP_015370062.1	*Diuraphis noxia*	1E-32
GFTU01011451.1	TR76061_c1_g1_i13	hypothetical protein g.48125 (Calcium-binding EGF-like domain)	JAT25493.1	*Graphocephala atropunctata*	0
GFTU01001449.1	TR76061_c1_g1_i15	PREDICTED: uncharacterized protein LOC658528 (Calcium-binding EGF-like domain)	XP_015839066.1	*Tribolium castaneum*	0
GFTU01001450.1	TR76061_c1_g1_i25	PREDICTED: uncharacterized protein LOC106669909 (Calcium-binding EGF-like domain)	XP_014255247.1	*Cimex lectularius*	0
GFTU01001448.1	TR76061_c1_g1_i3	PREDICTED: uncharacterized protein LOC658528 (Calcium-binding EGF-like domain)	XP_015839066.1	*Tribolium castaneum*	0
GFTU01011448.1	TR76061_c1_g1_i4	PREDICTED: uncharacterized protein LOC106669909 (Calcium-binding EGF-like domain)	XP_014255247.1	*Cimex lectularius*	0
GFTU01009271.1	TR58448_c2_g2_i8	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X19	XP_011265246.1	*Camponotus floridanus*	0
GFTU01009275.1	TR58448_c2_g2_i17	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X7	XP_011864488.1	*Vollenhovia emeryi*	0
GFTU01001084.1	TR58448_c2_g2_i10	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X8	XP_016918284.1	*Apis cerana*	0
GFTU01009272.1	TR58448_c2_g2_i9	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X6	XP_014478061.1	*Dinoponera quadriceps*	0

GFTU01009276.1	TR58448_c2_g2_i18	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X13	XP_011864494.1	*Vollenhovia emeryi*	0
GFTU01009270.1	TR58448_c2_g2_i7	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X21	XP_015835390.1	*Tribolium castaneum*	0
GFTU01009274.1	TR58448_c2_g2_i14	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein isoform X15	XP_011864496.1	*Vollenhovia emeryi*	0
GFTU01009267.1	TR58448_c2_g2_i2	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein	XP_011054372.1	*Acromyrmex echinatior*	0
GFTU01003839.1	TR13893_c7_g1_i1	PREDICTED: protein mesh isoform X2	XP_015366076.1	*Diuraphis noxia*	0
Nucleic acid binding					
GFTU01010183.1	TR67138_c1_g2_i1	PREDICTED: piggyBac transposable element-derived protein 4-like	XP_014676879.1	*Priapulus caudatus*	1E-59
GFTU01001044.1	TR56227_c8_g1_i4	PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like	XP_015438077.1	*Dufourea novaeangliae*	0
GFTU01010403.1	TR68543_c0_g1_i1	PREDICTED: retrovirus-related Pol polyprotein from transposon 17.6	XP_015840034.1	*Tribolium castaneum*	6E-173
GFTU01004281.1	TR16696_c1_g2_i2	PREDICTED: uncharacterized protein K02A2.6-like (2 integrases)	XP_014262899.1	*Maylandia zebra*	0
GFTU01004309.1	TR16773_c1_g1_i2	Hypothetical protein g.15643 (integrase)	JAT29099.1	*Graphocephala atropunctata*	4E-112
GFTU01007993.1	TR48210_c0_g1_i1	PREDICTED: nuclear factor interleukin-3-regulated protein	XP_014273353.1	*Halyomorpha halys*	1E-126
Detoxification					
GFTU01009741.1	TR61468_c0_g1_i1	PREDICTED: venom carboxylesterase-6	XP_012275036.1	*Orussus abietinus*	2E-170
GFTU01002688.1	TR3320_c0_g1_i1	PREDICTED: cytochrome P450 4C1-like	XP_008482780.1	*Diaphorina citri*	0
GFTU01002689.1	TR3320_c0_g1_i2	PREDICTED: cytochrome P450 4C1-like	XP_008482780.1	*Diaphorina citri*	4E-162
GFTU01000057.1	TR2236_c0_g2_i1	PREDICTED: gamma-aminobutyric acid receptor subunit alpha-6-like	XP_014254948.1	*Cimex lectularius*	3E-48

* Contig Accessions correspond to BioProject PRJNA393620.

TABLE S4 Overview of *Euscelidius variegatus* transcripts down-regulated during chrysanthemum yellows (CYp) infection, compared with insects infected by Flavescence dorée (FDp) phytoplasmas. Transcripts were classified into functional categories according to the putative identification assigned by a blastx search.

Contig accession*	Eva transcript ID	Sequence description	Hit Accession	Organisms	E-Value
Immune response					
GFTU01001177.1	TR64039_c0_g1_i3	PREDICTED: mitogen-activated protein kinase kinase kinase 12 isoform X2	XP_012256857.1	*Athalia rosae*	0
GFTU01016523.1	TR220860_c1_g1_i1	PREDICTED: serine protease snake-like isoform X2	XP_014259171.1	*Cimex lectularius*	2E-99
GFTU01005213.1	TR23882_c3_g1_i1	hypothetical protein g.9121 (Kazal-type 1 serine protease inhibitor-like protein type gamma)	JAT33323.1	*Graphocephala atropunctata*	3E-37
GFTU01006779.1	TR39162_c0_g1_i1	hypothetical protein g.7830 (Kazal-type 1 serine protease inhibitor-like protein type gamma)	JAS84502.1	*Homalodisca liturata*	9E-24
GFTU01007903.1	TR47813_c0_g1_i1	PREDICTED: protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	XP_015511043.1	*Neodiprion lecontei*	1E-119
GFTU01003663.1	TR12299_c0_g1_i3	PREDICTED: Kruppel-like factor 10	XP_008469759.1	*Diaphorina citri*	8E-72
GFTU01003662.1	TR12299_c0_g1_i1	PREDICTED: Kruppel-like factor 10	XP_008469759.1	*Diaphorina citri*	8E-71
GFTU01005275.1	TR25275_c0_g1_i1	PREDICTED: circadian clock-controlled protein-like	XP_014245484.1	*Cimex lectularius*	6E-92
GFTU01002709.1	TR3427_c0_g2_i1	PREDICTED: heat shock protein 68-like	XP_013201116.1	*Amyelois transitella*	0
GFTU01007012.1	TR40569_c0_g1_i1	PREDICTED: pancreatic triacylglycerol lipase-like	XP_014247562.1	*Cimex lectularius*	3E-60
Movement and energy metabolism					
GFTU01009515.1	TR59721_c0_g2_i6	dihydropyridine-sensitive l-type calcium channel (DHPR)	XP_014253595.1	*Cimex lectularius*	1.20E-06
Proteases					
GFTU01013038.1	TR105022_c0_g1_i1	PREDICTED: cathepsin D-like	XP_014270708.1	*Halyomorpha halys*	9E-29

Detoxification					
GFTU01002121.1	TR236_c1_g2_i1	PREDICTED: probable cytochrome P4506a14	XP_008192267.1	*Tribolium castaneum*	1E-147

* Contig Accessions correspond to BioProject PRJNA393620.

TABLE S5 qPCR Validation. Mean normalized relative quantities ± standard error of each gene in the category healthy (H), infected by chrysanthemum yellows (CYp) or by Flavescence dorée (FDp) phytoplasmas. Within the same category (H, CY, FD), asterisks indicate significant differences between female and male of each category. Within the same gender, different letters indicate significant differences among the categories (capitalized for females and small for males). Whenever no sex-related differences were recorded within the same category, female and male data were pooled.

Mechanism	Gene	Female			Male		
		H	CY	FD	H	CY	FD
Immune response	phenoloxidase	1.41^{A} ± 0.35 (N=7)	1.42^{A} ± 0.21 (N=7)	2.02^{A} ± 0.83 (N=7)	1.22^{a} ± 0.23 (N=6)	1.44^{a} ± 0.35 (N=6)	1.25^{a} ± 0.15 (N=7)
	sex pooled	**H**		**CY**		**FD**	
		1.32^{a} ± 0.21 (N=13)		1.43^{a} ± 0.19 (N=13)		1.64^{a} ± 0.42 (N=14)	
	Kazal type 1	0.91^{A*} ± 0.17 (N=7)	0.79^{A*} ± 0.13 (N=7)	0.73^{A} ± 0.13 (N=7)	0.47^{ab*} ± 0.05 (N=6)	0.41^{a*} ± 0.08 (N=7)	0.71^{b} ± 0.09 (N=7)
Movement and energy metabolism	myosin	0.42^{A*} ± 0.11 (N=7)	0.40^{A*} ± 0.03 (N=7)	0.32^{A*} ± 0.01 (N=7)	0.97^{a*} ± 0.20 (N=6)	1.22^{a*} ± 0.131 (N=7)	0.89^{a*} ± 0.11 (N=7)
	tropomyosin	1.09^{A} ± 0.28 (N=7)	1.67^{A*} ± 0.19 (N=7)	1.31^{A*} ± 0.21 (N=7)	1.98^{a} ± 0.56 (N=6)	6.00^{b*} ± 1.01 (N=7)	2.48^{ab*} ± 0.41 (N=7)
	arginine kinase	0.72^{AB} ± 0.11 (N=7)	0.96^{A*} ± 0.06 (N=7)	0.64^{B*} ± 0.06 (N=7)	1.59^{a} ± 0.38 (N=6)	3.59^{b*} ± 0.32 (N=7)	1.51^{a*} ± 0.13 (N=7)
	maltase	0.39^{A*} ± 0.07 (N=7)	0.68^{A*} ± 0.21 (N=7)	1.26^{A*} ± 0.36 (N=7)	2.85^{a*} ± 0.85 (N=6)	5.72^{a*} ± 1.55 (N=7)	3.48^{a*} ± 0.71 (N=7)
Proteases	cathepsin L_92i3	0.67^{AB} ± 0.07 (N=7)	0.97^{A} ± 0.08 (N=7)	0.56^{B*} ± 0.08 (N=7)	0.96^{a} ± 0.15 (N=6)	1.11^{a} ± 0.10 (N=7)	0.82^{a*} ± 0.08 (N=7)
	cathepsin L_92i4	0.57^{AB} ± 0.19 (N=7)	0.67^{A} ± 0.14 (N=7)	0.30^{B} ± 0.05 (N=7)	0.31^{a} ± 0.04 (N=6)	0.37^{a} ± 0.05 (N=7)	0.33^{a} ± 0.03 (N=7)
	sex pooled	**H**		**CY**		**FD**	
		0.46^{a} ± 0.11 (N=13)		0.52^{a} ± 0.08 (N=14)		0.32^{a} ± 0.03 (N=14)	
	cathepsin L_92i6	0.61^{A} ± 0.13 (N=7)	0.64^{A} ± 0.10 (N=7)	0.45^{A*} ± 0.06 (N=7)	0.56^{a} ± 0.05 (N=6)	0.57^{a} ± 0.23 (N=7)	0.70^{a*} ± 0.06 (N=7)
	cathepsin L_473	0.75^{A*} ± 0.18 (N=7)	1.97^{B*} ± 0.30 (N=7)	1.01^{A*} ± 0.14 (N=7)	0.19^{a*} ± 4.0E-03 (N=6)	0.22^{a*} ± 0.04 (N=7)	0.17^{a*} ± 0.03 (N=7)

TABLE S6 Phenoloxidase activity. Mean enzymatic activity (U) ± standard error (SEM) of phenoloxidase (PO) and prophenoloxidase (ProPO) measured in *Euscelidius variegatus* haemolymph samples (plasma and haemocyte lysate supernatant, HLS, fractions) in healthy (H), chrysanthemum yellows (CYp) infected, or Flavescence dorée (FDp) infected insects. Duration (final time in minutes) and slope of exponential linear phase of the reaction are also indicated. Within the same category (H, CY, FD), asterisks indicate significant differences between female and male of each category. Within the same gender, different letters indicate significant differences among the categories (capitalized for females and small for males). Whenever no sex-related differences were recorded within the same category, female and male data were pooled. As similar PO activities were recorded in HLS fraction either in the presence and in the absence of the specific inhibitor phenylthiourea, comparison between gender and among categories was not performed and no slope was calculated.

Haemolymph fraction	**Enzyme**	**Measured parameter**	**Female**			**Male**		
			H	**CY**	**FD**	**H**	**CY**	**FD**
Plasma	PO	Activity	0.17^{A} ± 0.03	0.14^{A} ± 0.02	0.13^{A} ± 0.02	0.12^{a} ± 0.02	0.12^{a} ± 0.02	0.13^{a} ± 0.02
		(U ± SEM, N)	(N=5)	(N=7)	(N=8)	(N= 5)	(N= 6)	(N= 5)
		Final time		570 min			570 min	
		Slope	2.0E-04	2.0E-04	2.0E-04	1.0E-04	1.0E-04	1.0E-04
	ProPO	Activity	2.83^{A*}± 0.50	2.86^{A*}± 0.51	4.18^{A*}± 0.64	0.63^{ab*}± 0.09	0.55^{a*}± 0.17	1.12^{b*}± 0.14
		(U ± SEM, N)	(N=5)	(N=7)	(N=7)	(N= 4)	(N= 6)	(N= 5)
		Final time		150 min			330 min	
		Slope	2.8E-03	2.8E-03	4.1E-03	6.0E-04	6.0E-04	1.2E-03
HLS	PO	Activity	0.02 ± 0.01	-1E-03 ± 0.01	0.01 ± 0.01	0.02 ± 0.01	0.02 ± 0.01	0.03 ± 0.02
		(U ± SEM, N)	(N=5)	(N=7)	(N=8)	(N=5)	(N=6)	(N=5)
		Final time		570 min			570	
	ProPO	Activity	0.21^{A} ± 0.05	0.15^{A} ± 0.02	0.35^{A} ± 0.09	0.13^{a} ± 0.03	0.10^{a} ± 0.02	0.17^{a} ± 0.01
		(U ± SEM, N)	(N=4)	(N=6)	(N=6)	(N= 5)	(N= 6)	(N= 5)
		Final time		390 min			270 min	
		Slope	2.0E-04	2.0E-04	4.0E-04	1.0E-04	9.0E-05	2.0E-04
		Sex pooled	**H**		**CY**		**FD**	
		Activity	0.17^{ab} ± 0.03 (N=9)		0.13^{a} ± 0.01 (N=12)		0.27^{b} ± 0.05 (N=11)	

TABLE S7 Pigmentation and immunocompetence assays. Pigmentation assay: mean degree of grey intensity ± standard error (SEM) calculated for body (dorsal side) and forewing of insects healthy (H), infected by chrysanthemum yellows (CYp) or by Flavescence dorée (FDp) phytoplasmas. The pigmentation is expressed as a numerical reading ranging from 0 for black to 255 for white. Within the same category (H, CY, FD), asterisks indicate significant differences between female and male of each category. Within the same gender, different letters indicate significant differences among the categories (capitalized for females and small for males).

For the immunocompetence assay, nylon threads were implanted in *Euscelidius variegatus* healthy (H) and infected by chrysanthemum yellows (CYp) or Flavescence dorée (FDp) phytoplasmas. Mean melanization index (MI) of the nylon thread implants and mean number of adherent cells were determined (± standard error of the means). MI was the ratio between the Integrated Density/surface unit of nylon portions inside and outside the body of each H, CY and FD infected insect. Mean number of cells adherent to the surface of each nylon thread was calculated following DAPI staining and confocal microscopy observations. Whenever no sex-related differences were recorded within the same category, female and male data were pooled. Within each line, different letters indicate significant differences among the categories (H, CY, FD).

Assay	**Measured parameter**	**Female**			**Male**		
		H	**CY**	**FD**	**H**	**CY**	**FD**
Pigmen- tation	Body (dorsal side)	94.24^{A*} ± 1.09 (N=36)	92.56^{A*} ± 1.53 (N=30)	84.66^{B*} ± 1.06 (N=36)	88.18^{a*} ± 1.95 (N=23)	83.83^{a*} ± 1.63 (N=23)	75.06^{b*} ± 1.62 (N=20)
	Forewing	200.79^{A*} ± 2.28 (N=36)	202.66^{A*} ± 3.46 (N=30)	197.20^{A*} ± 1.95 (N=36)	181.53^{a*} ± 3.34 (N=22)	182.04^{a*} ± 2.97 (N=30)	183.00^{a*} ± 3.30 (N=20)
Immuno- competence	Sex pooled	**H**		**CY**		**FD**	
	Melanization Index	0.90^{a} ± 0.03 (N=11)		0.72^{b} ± 0.04 (N=12)		0.79^{ab} ± 0.03 (N=23)	
	Number of adherent cells	57.10^{a} ± 10.33 (N=10)		184.42^{b} ± 29.41 (N=12)		36.00^{a} ± 8.15 (N=18)	

TABLE S8 MOVEMENT AND RESPIRATION ASSAYS. Movement assay: mean time (seconds) required to leave the 1st and the 2nd circles and mean number of jumps ± standard error (SEM), measured observing for 300 sec single insect of the category healthy (H), infected by chrysanthemum yellows (CYp) or by Flavescence dorée (FDp) phytoplasmas. Within the same gender, different letters indicate significant differences among the categories (capitalized for females and small for males).

Respiration assay: mean CO_2 production (µl/h per single insect) ± standard error (SEM), as recorded by gas exchange chamber for insect of the category healthy (H), infected by chrysanthemum yellows (CYp) or by Flavescence dorée (FDp) phytoplasmas. Whenever no sex-related differences were recorded within the same category, female and male data were pooled. Different letters indicate significant differences among the categories.

Assay	**Measured parameter**	**Female**			**Male**		
		H	**CY**	**FD**	**H**	**CY**	**FD**
Movement	Total observed insects	22	24	24	22	23	23
	Time within 1st circle (s)	47.60^{A} ± 11.20 (N=15)	65.25^{A} ± 17.41 (N=20)	41.89^{A} ± 5.38 (N= 18)	64.65^{a} ± 11.13 (N= 17)	36.86^{a} ± 5.83 (N= 21)	50.55^{a} ± 7.41 (N= 20)
	Time within 2nd circle (s)	44.71^{A} ± 10.65 (N=14)	70.56^{A} ± 16.75 (N=18)	53.82^{A} ± 7.35 (N=17)	65.93^{a} ± 12.61 (N= 15)	40.78^{a} ± 6.33 (N= 18)	69.85^{a} ± 12.68 (N= 20)
	Number of jumps	1.41^{A} ± 0.28 (N=22)	1.83^{A} ± 0.33 (N=24)	1.79^{A} ± 0.36 (N=24)	1.55^{a} ± 0.39 (N= 22)	2.35^{a} ± 0.46 (N= 23)	1.65^{a} ± 0.25 (N=23)
Respiration	Sex pooled	**H**		**CY**		**FD**	
	CO_2 production	0.90^{a} ± 0.05 (N=8)		1.52^{b} ± 0.14 (N=8)		1.09^{a} ± 0.12 (N=8)	

TABLE S9 Genes analyzed in qRT-PCR and corresponding specific primers. Efficiency (E%) of qPCR reaction, Correlation coefficient (R2) of standard curve and Melting peak temperature (Melt Peak T) were calculated by CFX Software Manager ver. 3.1 (Bio-Rad).

Metabolism	Gene	Eva transcript ID	Primer name	Primer sequence 5’-3’	Amplicon length (bp)	qPCR Parameters		
						E%	R^2	Melt Peak T (°C)
Immune response	phenoloxidase	TR176219_c0_g1_i1	PO2_F1020	CAATGTGGTTCCCTCAGGAT	115	103.0	0.997	74.5
			PO2_R1085	TCTGCGAGGTCTCATTTCTGT				
	Kazal type 1 serine protease inhibitor	TR23882_c3_g1_i1	kaz1_F70	CTGGTTCGCAGGCAAATACC	103	110.3	0.997	80.0
			kaz1_R172	GGCATGACACTCGGTACACT				
Movement and energy metabolism	myosin	TR57237_c0_g1_i1	MYO-L1_F138	CCAGTGTGAAGGGAGCGATT	126	95.0	0.993	80.5
			MYO-L1_R263	CATGTAGACGTGGTGGAGCT				
	tropomyosin	TR11297_c7_g1_i2	Tm1Fw783	GGTGGAGAAGGAACGTTATCG	78	92.0	0.997	77.0
			Tm1Rv860	GCAGATTAGTATCCGTATAACTCTA				
	arginine kinase	TR201186_c0_g1_i1	ArgKin_F793	CTGGGCTTCCTCACCTTCTG	121	99.6	1.000	83.5
			ArgKin_R913	TGAACTTTCCAGCGACCTCC				
	maltase	TR70195_c0_g1_i2	MALT1_F1345	CAATAAGCGCTGGTTTCTCC	90	94.0	0.993	79.0
			MALT1_R1434	CATTTCTTTGGGCCTCCAC				
Proteases	cathepsin L_92i3	TR22292_c3_g1_i3	CATH-L_F1065	GCATCACACGAGTCCTTCCA	156	93.0	0.996	82.5
			CATH-L_R1220	CGTTGTGGCCCATGAGTTCT				
	cathepsin L_92i4	TR22292_c3_g1_i4	CathL92_i4-6F	CATTAAGATGGCCCGGAACAAAG	170	88.7	0.992	83.0
			CathL92_i4R	AAGACAATTTAGCACTGTCGGT				
	cathepsin L_92i6	TR22292_c3_g1_i6	CathL92_i4-6F	CATTAAGATGGCCCGGAACAAAG	166	85.7	0.990	83.5
			CathL92_i6R	AAGTTTGGCACTGTCGGTAAGG				
	cathepsin L_473	TR18473_c0_g1_i1	CathL473_F	CGTCAAGAAGCAGGGCCAAT	92	92.8	0.999	82.0
			CathL473_R	CCAGCTTGCCAGACTTGAGG				

TABLE S10 List of candidate reference genes and corresponding specific primers evaluated for stability in RT-qPCR. Efficiency (E%) of qPCR reaction, Correlation coefficient (R2) of standard curve, Melting peak temperature (Melt Peak T), Coefficient of Variation (CV) and expression stability value (M) were calculated by CFX Software Manager ver. 3.1 (Bio-Rad). In bold: selected reference genes for this study.

Gene	**Eva transcript ID**	**Primer name**	**Primer sequence 5'-3'**	**Amplicon length (bp)**	**qPCR Parameters**			**Reference gene stability values**	
					E%	**R^2**	**Melt Peak T (°C)**	**CV**	**M**
elongation factor-1α	TR29211_ c0_g2_i1	EF1-α_F215	CCATCGACATTGCCCTGTGG	111	87.9	0.997	78.5	0.144	0.51
		EF1-α_R325	CCTGTGAGGTTCCAGTGATCATG						
glutathione S-transferase	TR32009_ c0_g1_i1	GST1_F257	CCAAGGACCCCAAGAAGCGA	113	87.3	0.997	79.0	0.260	0.60
		GST1_R369	TGGCGCTCCTCCAAACATCA						
heat shock protein 70-1	TR176296_ c0_g1_i1	HSP70_F808	CGCACCTTGTCATCCAGCAC	115	88.1	0.998	83.0	0.299	0.65
		HSP70_R922	ACAGGTCGGAGCACAGTTCC						
ATP synthase-beta	TR146391_ c0_g1_i1	ATPβFw622	CGCTTTACTCAGGCTGGTTC	171	100.0	0.995	83.5	0.329	0.697
		ATPβRv792	GTCATCAGCTGGCACGTAGA						
succinate dehydrogenase	TR217947_ c0_g1_i1	SDHubi_F338	AGGAGGACAACTGGCAGTGG	58	98.1	0.998	77.0	0.330	0.672
		SDHubi_R395	CCCAGCCAATCAGAACCCTTT						
glyceraldehyde 3-phosphate dehydrogenase	JX273239	GAPFw632	ATCCGTCGTCGACCTTACTG	51	99.0	0.998	77.5	0.452	0.776
		GAPRv682	TCATCGTAGCTGGCTTCCTTG						

TABLE S11 Statistical analysis used for different assays: t-test or non parametric Mann-Whitney test were used to compare female and male insects of different experimental categories (healthy- H, chrysanthemum yellows-CYp- or flavescence dorée-FDp- infected insects); One way analysis of variance (ANOVA) or non parametric Kruskal-Wallis test were used to compare H, CY and FD category, generally by separating insects for different sex, and in some cases by pooling insects together regardless the gender, when no significant differences were found between sex. Significant differences are in bold.

Assay	**Parameter**	**Female vs. Male**	**H vs. CY vs. FD**	
			Female	**Male**
qPCR validation	phenoloxidase	Mann-Whitney	Kruskal-Wallis, P=0.989	Kruskal-Wallis, P=0.731
	Kazal type 1	Mann-Whitney	ANOVA, P=0.689	**ANOVA, P=0.019**
	myosin	Two-tailed t-test	ANOVA, P=0.569	ANOVA, P=0.198
	tropomyosin	Mann-Whitney	ANOVA, P=0.216	**Kruskal-Wallis, P=0.015**
	arginine kinase	Two-tailed t-test	**ANOVA, P=0.025**	**ANOVA, P<0.001**
	maltase	Two-tailed t-test	Kruskal-Wallis, P=0.128	ANOVA, P=0.197
	cathepsin L_473	Mann-Whitney	**ANOVA, P=0.002**	Kruskal-Wallis, P= 0.437
	cathepsin L_92i3	Two-tailed t-test	**Kruskal-Wallis, P=0.014**	ANOVA, P=0.203
	cathepsin L_92i4	Two-tailed t-test	**Kruskal-Wallis, P=0.028**	ANOVA, P=0.618
	cathepsin L_92i6	Mann-Whitney	ANOVA, P=0.382	Kruskal-Wallis, P= 0.446
Phenoloxidase activity	Plasma PO	Two-tailed t-test	ANOVA, P=0.551	ANOVA, P=0.857
	Plasma ProPO	Two-tailed t-test	Kruskal-Wallis, P=0.192	**ANOVA, P=0.045**
	HLS ProPO	Two-tailed t-test	**Kruskal-Wallis (pooled), P=0.021**	
Pigmentation	Body	Two-tailed t-test	**ANOVA, P<0.001**	**ANOVA, P<0.001**
	Forewing	Two-tailed t-test	Kruskal-Wallis, P=0.163	ANOVA, P=0.954
Immuno-competence	Melanization Index	Two-tailed t-test	**ANOVA (pooled), P=0.007**	
	Number of nuclei	Two-tailed t-test	**Kruskal-Wallis (pooled), P<0.001**	
Movement	Time in 1st circle	Mann-Whitney	Kruskal-Wallis, P=0.857	Kruskal-Wallis, P=0.063
	Time in 2nd circle	Mann-Whitney	Kruskal-Wallis, P=0.406	Kruskal-Wallis, P=0.176
	Number of jumps	Mann-Whitney	Kruskal-Wallis, P=0.704	Kruskal-Wallis, P=0.365
Respiration	CO_2 production	Two-tailed t-test	**ANOVA (pooled), P=0.002**	

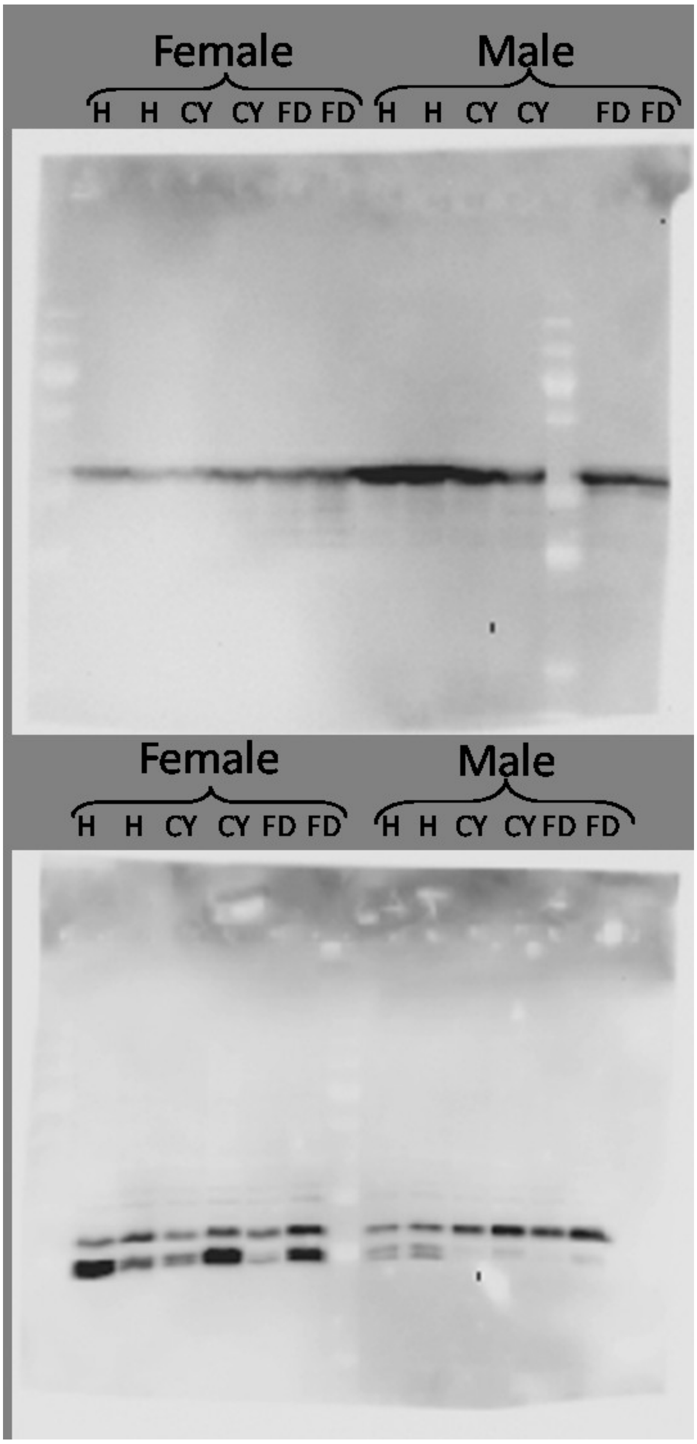

FIG S1 Full length original blots presented in Figure 3I and Figure 4G. Two biological replicates of each sample were loaded in adjacent lanes and only one was presented in final figures 3I (upper panel) and 4G (lower panel). Prestained Protein SHARPMASS™ VPlus (Euroclone) was used as protein MW marker.