Table S1. Sequence Read Archive accession numbers used to predict piRNA clusters in each respective population.

SRA Accession #	**D. citri population**	**Source**	**Publication**
SRX8463967	CRF-UY	Whole body	Nigg *et al.* 2020
SRX8463959	CRF-TW	Whole body	Nigg et al. 2020
SRX8463965	CRF-TW	Whole body	Nigg et al. 2020
SRX8463966	CRF-TW	Whole body	Nigg et al. 2020
SRX8463936	CRF-CA	Whole body	Nigg et al. 2020
SRX8463937	CRF-CA	Whole body	Nigg et al. 2020
SRX8463948	CRF-CA	Whole body	Nigg et al. 2020

Table S2. Accession numbers used for constructing full mitochondrial coding sequence TCS haplotype network.

NCBI Accession #	Locality	Haplotype	Publication Source
OM181945.1	CRF-CA	1	This study
OM181946.1	CRF-TW	16	This study
OM181947.1	CRF-UY	17	This study
KY426014	California, USA	1	Wu *et al.* 2017
KY426015	Florida, USA	1	Wu *et al.* 2017
MF614803	Shaoguan, Guangdong, Chi	2	Wu *et al.* 2018
MF614804	Huizhou, Guangdong, Chin	2	Wu *et al.* 2018
MF614805	Yangchun, Guangdong, Chi	2	Wu *et al.* 2018
MF614806	Jieyang, Guangdong, China	3	Wu *et al.* 2018
MF614807	Xiamen, Fujian, China	3	Wu *et al.* 2018
MF614808	Fuzhou, Fujian, China	4	Wu *et al.* 2018
MF614809	Ji'an, Jiangxi, China	2	Wu *et al.* 2018
MF614810	Guangchang, Jiangxi, China	2	Wu *et al.* 2018
MF614811	Hainan, China	2	Wu *et al.* 2018
MF614812	Yulin, Guangxi, China	5	Wu *et al.* 2018
MF614813	Nanning, Guangxi, China	6	Wu *et al.* 2018
MF614814	Zhejiang, China	4	Wu *et al.* 2018
MF614815	Yizhang, Hunan, China	7	Wu *et al.* 2018
MF614816	Miyi, Sichuan, China	8	Wu *et al.* 2018
MF614817	Ningnan, Sichuan, China	9	Wu *et al.* 2018
MF614818	Wangmo, Guizhou, China	10	Wu *et al.* 2018
MF614819	Bingchuan, Yunnan, China	9	Wu *et al.* 2018
MF614820	Jianshui, Yunnan, China	9	Wu *et al.* 2018
MF614821	Ruili, Yunnan, China	11	Wu *et al.* 2018
MF614822	Baoshao, Yunnan, China	11	Wu *et al.* 2018
MF614823	Taiwan	3	Wu *et al.* 2018
MF614824	Cambodia	12	Wu *et al.* 2018
MF614825	Malaysia	13	Wu *et al.* 2018
MF614826	Vietnam	3	Wu *et al.* 2018
MF614827	Indonesia	14	Wu *et al.* 2018
MF614828	Pakistan	15	Wu *et al.* 2018

Table S3. Accession numbers used for constructing partial mitochondrial CO1 sequence TCS haplotype network.

NCBI Accession	Locality	Haplotype	Publication Source
FJ190321.1	Brazil	1	Boykin et al. 2012
FJ190322.1	Brazil	1	Boykin et al. 2012
FJ190323.1	Brazil	1	Boykin et al. 2012
FJ190324.1	Brazil	1	Boykin et al. 2012
KY426014.1	California	1	Wu et al. 2017
OM181945.1	CRF-CA	1	This study
FJ190167.1	Florida	1	Boykin et al. 2012
FJ190168.1	Florida	1	Boykin et al. 2012
FJ190169.1	Florida	1	Boykin et al. 2012
FJ190170.1	Florida	1	Boykin et al. 2012
FJ190171.1	Florida	1	Boykin et al. 2012
FJ190172.1	Florida	1	Boykin et al. 2012
FJ190173.1	Florida	1	Boykin et al. 2012
FJ190174.1	Florida	1	Boykin et al. 2012
FJ190175.1	Florida	1	Boykin et al. 2012
FJ190176.1	Florida	1	Boykin et al. 2012
FJ190182.1	Florida	1	Boykin et al. 2012
FJ190183.1	Florida	1	Boykin et al. 2012
FJ190184.1	Florida	1	Boykin et al. 2012
FJ190185.1	Florida	1	Boykin et al. 2012
FJ190186.1	Florida	1	Boykin et al. 2012
FJ190187.1	Florida	1	Boykin et al. 2012
FJ190188.1	Florida	1	Boykin et al. 2012
FJ190189.1	Florida	1	Boykin et al. 2012
FJ190190.1	Florida	1	Boykin et al. 2012
FJ190191.1	Florida	1	Boykin et al. 2012
FJ190192.1	Florida	1	Boykin et al. 2012
FJ190193.1	Florida	1	Boykin et al. 2012
FJ190194.1	Florida	1	Boykin et al. 2012
FJ190195.1	Florida	1	Boykin et al. 2012
FJ190196.1	Florida	1	Boykin et al. 2012
FJ190197.1	Florida	1	Boykin et al. 2012
FJ190198.1	Florida	1	Boykin et al. 2012
FJ190199.1	Florida	1	Boykin et al. 2012
FJ190200.1	Florida	1	Boykin et al. 2012
FJ190201.1	Florida	1	Boykin et al. 2012
FJ190202.1	Florida	1	Boykin et al. 2012
FJ190203.1	Florida	1	Boykin et al. 2012
FJ190204.1	Florida	1	Boykin et al. 2012
FJ190205.1	Florida	1	Boykin et al. 2012
FJ190206.1	Florida	1	Boykin et al. 2012
FJ190207.1	Florida	1	Boykin et al. 2012
FJ190208.1	Florida	1	Boykin et al. 2012

FJ190209.1	Florida	1	Boykin et al. 2012
FJ190210.1	Florida	1	Boykin et al. 2012
FJ190211.1	Florida	1	Boykin et al. 2012
FJ190212.1	Florida	1	Boykin et al. 2012
FJ190213.1	Florida	1	Boykin et al. 2012
FJ190214.1	Florida	1	Boykin et al. 2012
FJ190215.1	Florida	1	Boykin et al. 2012
FJ190216.1	Florida	1	Boykin et al. 2012
FJ190217.1	Florida	1	Boykin et al. 2012
FJ190218.1	Florida	1	Boykin et al. 2012
FJ190219.1	Florida	1	Boykin et al. 2012
FJ190220.1	Florida	1	Boykin et al. 2012
FJ190221.1	Florida	1	Boykin et al. 2012
FJ190222.1	Florida	1	Boykin et al. 2012
FJ190223.1	Florida	1	Boykin et al. 2012
FJ190224.1	Florida	1	Boykin et al. 2012
FJ190225.1	Florida	1	Boykin et al. 2012
FJ190226.1	Florida	1	Boykin et al. 2012
FJ190227.1	Florida	1	Boykin et al. 2012
FJ190232.1	Florida	1	Boykin et al. 2012
FJ190233.1	Florida	1	Boykin et al. 2012
FJ190234.1	Florida	1	Boykin et al. 2012
FJ190235.1	Florida	1	Boykin et al. 2012
FJ190236.1	Florida	1	Boykin et al. 2012
FJ190237.1	Florida	1	Boykin et al. 2012
FJ190238.1	Florida	1	Boykin et al. 2012
FJ190239.1	Florida	1	Boykin et al. 2012
FJ190240.1	Florida	1	Boykin et al. 2012
FJ190241.1	Florida	1	Boykin et al. 2012
FJ190242.1	Florida	1	Boykin et al. 2012
FJ190243.1	Florida	1	Boykin et al. 2012
FJ190244.1	Florida	1	Boykin et al. 2012
FJ190245.1	Florida	1	Boykin et al. 2012
FJ190246.1	Florida	1	Boykin et al. 2012
FJ190247.1	Florida	1	Boykin et al. 2012
FJ190249.1	Florida	1	Boykin et al. 2012
FJ190250.1	Florida	1	Boykin et al. 2012
FJ190251.1	Florida	1	Boykin et al. 2012
FJ190252.1	Florida	1	Boykin et al. 2012
FJ190254.1	Florida	1	Boykin et al. 2012
FJ190255.1	Florida	1	Boykin et al. 2012
FJ190256.1	Florida	1	Boykin et al. 2012
FJ190257.1	Florida	1	Boykin et al. 2012
FJ190258.1	Florida	1	Boykin et al. 2012
FJ190259.1	Florida	1	Boykin et al. 2012
FJ190277.1	Florida	1	Boykin et al. 2012
FJ190278.1	Florida	1	Boykin et al. 2012

FJ190310.1	Florida	1	Boykin et al. 2012
FJ190311.1	Florida	1	Boykin et al. 2012
FJ190372.1	Florida	1	Boykin et al. 2012
FJ190373.1	Florida	1	Boykin et al. 2012
FJ190374.1	Florida	1	Boykin et al. 2012
FJ190375.1	Florida	1	Boykin et al. 2012
FJ190376.1	Florida	1	Boykin et al. 2012
FJ190377.1	Florida	1	Boykin et al. 2012
KY426015.1	Florida	1	Wu et al. 2017
FJ190342.1	India	1	Boykin et al. 2012
FJ190343.1	India	1	Boykin et al. 2012
FJ190344.1	India	1	Boykin et al. 2012
FJ190345.1	India	1	Boykin et al. 2012
FJ190336.1	Indonesia	1	Boykin et al. 2012
FJ190306.1	Mexico	1	Boykin et al. 2012
FJ190307.1	Mexico	1	Boykin et al. 2012
FJ190308.1	Mexico	1	Boykin et al. 2012
FJ190309.1	Mexico	1	Boykin et al. 2012
FJ190290.1	Pakistan	1	Boykin et al. 2012
FJ190291.1	Pakistan	1	Boykin et al. 2012
FJ190292.1	Pakistan	1	Boykin et al. 2012
MF614828.1	Pakistan	1	Wu et al. 2018
FJ190318.1	Reunion	1	Boykin et al. 2012
FJ190337.1	Saudi Arab	1	Boykin et al. 2012
FJ190338.1	Saudi Arab	1	Boykin et al. 2012
FJ190339.1	Saudi Arab	1	Boykin et al. 2012
FJ190340.1	Saudi Arab	1	Boykin et al. 2012
FJ190341.1	Saudi Arab	1	Boykin et al. 2012
FJ190177.1	Texas	1	Boykin et al. 2012
FJ190178.1	Texas	1	Boykin et al. 2012
FJ190179.1	Texas	1	Boykin et al. 2012
FJ190180.1	Texas	1	Boykin et al. 2012
FJ190181.1	Texas	1	Boykin et al. 2012
MF614822.1	Baoshao, Y	2	Wu et al. 2018
MF614819.1	Bingchuan,	2	Wu et al. 2018
FJ190228.1	Brazil	2	Boykin et al. 2012
FJ190229.1	Brazil	2	Boykin et al. 2012
FJ190230.1	Brazil	2	Boykin et al. 2012
FJ190231.1	Brazil	2	Boykin et al. 2012
FJ190325.1	Brazil	2	Boykin et al. 2012
FJ190326.1	Brazil	2	Boykin et al. 2012
FJ190327.1	Brazil	2	Boykin et al. 2012
FJ190328.1	Brazil	2	Boykin et al. 2012
FJ190329.1	Brazil	2	Boykin et al. 2012
FJ190330.1	Brazil	2	Boykin et al. 2012
FJ190331.1	Brazil	2	Boykin et al. 2012
FJ190332.1	Brazil	2	Boykin et al. 2012

FJ190333.1	Brazil	2	Boykin et al. 2012
MF614824.1	Cambodia	2	Wu et al. 2018
FJ190357.1	China	2	Boykin et al. 2012
FJ190358.1	China	2	Boykin et al. 2012
FJ190359.1	China	2	Boykin et al. 2012
FJ190360.1	China	2	Boykin et al. 2012
FJ190361.1	China	2	Boykin et al. 2012
FJ190362.1	China	2	Boykin et al. 2012
FJ190363.1	China	2	Boykin et al. 2012
FJ190364.1	China	2	Boykin et al. 2012
FJ190366.1	China	2	Boykin et al. 2012
FJ190368.1	China	2	Boykin et al. 2012
FJ190369.1	China	2	Boykin et al. 2012
OM181946.1	CRF-TW	2	This study
OM181947.1	CRF-UY	2	This study
MF614808.1	Fuzhou, Fu	2	Wu et al. 2018
MF614810.1	Guangcha	2	Wu et al. 2018
MF614811.1	Hainan, Ch	2	Wu et al. 2018
MF614804.1	Huizhou, G	2	Wu et al. 2018
FJ190263.1	Indonesia	2	Boykin et al. 2012
FJ190264.1	Indonesia	2	Boykin et al. 2012
FJ190265.1	Indonesia	2	Boykin et al. 2012
FJ190266.1	Indonesia	2	Boykin et al. 2012
FJ190267.1	Indonesia	2	Boykin et al. 2012
FJ190268.1	Indonesia	2	Boykin et al. 2012
FJ190269.1	Indonesia	2	Boykin et al. 2012
FJ190270.1	Indonesia	2	Boykin et al. 2012
FJ190271.1	Indonesia	2	Boykin et al. 2012
FJ190279.1	Indonesia	2	Boykin et al. 2012
FJ190280.1	Indonesia	2	Boykin et al. 2012
FJ190281.1	Indonesia	2	Boykin et al. 2012
FJ190282.1	Indonesia	2	Boykin et al. 2012
MF614827.1	Indonesia	2	Wu et al. 2018
MF614809.1	Ji'an, Jiang	2	Wu et al. 2018
MF614820.1	Jianshui, Y	2	Wu et al. 2018
MF614806.1	Jieyang, G	2	Wu et al. 2018
MF614825.1	Malaysia	2	Wu et al. 2018
FJ190312.1	Mauritius	2	Boykin et al. 2012
FJ190314.1	Mauritius	2	Boykin et al. 2012
FJ190315.1	Mauritius	2	Boykin et al. 2012
FJ190316.1	Mauritius	2	Boykin et al. 2012
MF614816.1	Miyi, Sichu	2	Wu et al. 2018
MF614813.1	Nanning, G	2	Wu et al. 2018
MF614817.1	Ningnan, S	2	Wu et al. 2018
FJ190317.1	Reunion	2	Boykin et al. 2012
FJ190319.1	Reunion	2	Boykin et al. 2012
FJ190320.1	Reunion	2	Boykin et al. 2012

MF614821.1	Ruili, Yunn	2	Wu et al. 2018
MF614803.1	Shaoguan,	2	Wu et al. 2018
FJ190284.1	Taiwan	2	Boykin et al. 2012
FJ190285.1	Taiwan	2	Boykin et al. 2012
FJ190286.1	Taiwan	2	Boykin et al. 2012
FJ190287.1	Taiwan	2	Boykin et al. 2012
MF614823.1	Taiwan	2	Wu et al. 2018
FJ190293.1	Thailand	2	Boykin et al. 2012
FJ190294.1	Thailand	2	Boykin et al. 2012
FJ190295.1	Thailand	2	Boykin et al. 2012
FJ190296.1	Thailand	2	Boykin et al. 2012
FJ190272.1	Vietnam	2	Boykin et al. 2012
FJ190273.1	Vietnam	2	Boykin et al. 2012
FJ190274.1	Vietnam	2	Boykin et al. 2012
FJ190275.1	Vietnam	2	Boykin et al. 2012
FJ190276.1	Vietnam	2	Boykin et al. 2012
FJ190378.1	Vietnam	2	Boykin et al. 2012
FJ190379.1	Vietnam	2	Boykin et al. 2012
FJ190380.1	Vietnam	2	Boykin et al. 2012
FJ190381.1	Vietnam	2	Boykin et al. 2012
FJ190382.1	Vietnam	2	Boykin et al. 2012
MF614826.1	Vietnam	2	Wu et al. 2018
MF614818.1	Wangmo, (	2	Wu et al. 2018
MF614807.1	Xiamen, Fu	2	Wu et al. 2018
MF614805.1	Yangchun,	2	Wu et al. 2018
MF614815.1	Yizhang, Hu	2	Wu et al. 2018
MF614812.1	Yulin, Guar	2	Wu et al. 2018
MF614814.1	Zhejiang, C	2	Wu et al. 2018
FJ190248.1	Florida	3	Boykin et al. 2012
FJ190346.1	Guadeloup	4	Boykin et al. 2012
FJ190347.1	Guadeloup	4	Boykin et al. 2012
FJ190348.1	Guadeloup	4	Boykin et al. 2012
FJ190349.1	Guadeloup	4	Boykin et al. 2012
FJ190350.1	Guadeloup	4	Boykin et al. 2012
FJ190351.1	Guadeloup	4	Boykin et al. 2012
FJ190352.1	Guadeloup	4	Boykin et al. 2012
FJ190353.1	Guadeloup	4	Boykin et al. 2012
FJ190354.1	Guadeloup	4	Boykin et al. 2012
FJ190355.1	Guadeloup	4	Boykin et al. 2012
FJ190356.1	Guadeloup	4	Boykin et al. 2012
FJ190260.1	Puerto Rico	4	Boykin et al. 2012
FJ190261.1	Puerto Rico	4	Boykin et al. 2012
FJ190262.1	Puerto Rico	4	Boykin et al. 2012
FJ190288.1	Pakistan	5	Boykin et al. 2012
FJ190289.1	Pakistan	5	Boykin et al. 2012
FJ190297.1	China	6	Boykin et al. 2012
FJ190298.1	China	6	Boykin et al. 2012

FJ190299.1	China	6	Boykin et al. 2012
FJ190300.1	Mexico	6	Boykin et al. 2012
FJ190301.1	Mexico	6	Boykin et al. 2012
FJ190302.1	Mexico	6	Boykin et al. 2012
FJ190303.1	Mexico	6	Boykin et al. 2012
FJ190304.1	Mexico	6	Boykin et al. 2012
FJ190305.1	Mexico	6	Boykin et al. 2012
FJ190367.1	China	7	Boykin et al. 2012
FJ190313.1	Mauritius	2	Boykin et al. 2012

Table S4. Putative endogenous viral elements (EVEs) identified by BLASTx and filtering with custom Python scripts. Each *Diaphorina citri* population is in its own sheet.

Table S4.1 – CRF-CA *D. citri* EVEs

sequence	length (aa)	perc identity (aa)	gaps	frame	position on hit start (aa)	position on hit stop (aa)	position on query start (nt)	position on query stop (nt)	evalue	score	query id
gnl|BL ORD ID|32373 QLJ83484.1 ORF3 [Broome densovirus 1]	98	50.00	5	-3	5	102	12508560	12508838	7.46E-17	238	HiC_scaffold_3
gnl|BL ORD ID|23226 YP 009336527.1 hypothetical protein 4 [Beihai tombus-like virus 12]	165	24.85	0	3	288	452	1586568	1587062	0.000152793	147	HiC_scaffold_3
gnl|BL ORD ID|33449 QTW97811.1 hypothetical protein [Mononegavirales sp.]	373	38.61	11	2	7	375	2496674	2497771	5.15E-109	726	HiC_scaffold_4
gnl|BL ORD ID|107580 QEM39187.1 glycoprotein [Aedes aegypti anphevirus]	261	34.10	7	3	389	643	2497773	2498552	1.37E-104	412	HiC_scaffold_4
gnl|BL ORD ID|92059 QEM39034.1 nonstructural protein [Bactericera trigonica densovirus]	237	32.91	25	-2	202	433	21314350	21315000	2.61E-17	255	HiC_scaffold_5
gnl|BL ORD ID|75136 AMK09235.1 nucleocapsid protein [Drosophila busckii rhabdovirus]	186	26.88	2	-3	206	389	3951989	3952546	4.89E-08	175	HiC_scaffold_6
gnl|BL ORD ID|124979 AJG39051.1 polymerase [Lishi spider virus 1]	553	27.49	16	3	1624	2168	1989807	1991441	1.21E-39	449	HiC_scaffold_6
gnl|BL ORD ID|23226 YP 009336527.1 hypothetical protein 4 [Beihai tombus-like virus 12]	144	27.78	11	-1	309	441	17305897	17306328	0.000387531	143	HiC_scaffold_7
gnl|BL ORD ID|24043 QPB73984.1 glycoprotein [Megalopteran chu-related virus OKIAV119]	228	21.05	21	-3	90	315	4998933	4999559	8.19E-09	183	HiC_scaffold_8
gnl|BL ORD ID|19408 YP 009259672.1 polyprotein [Diaphorina citri flavi-like virus]	929	77.07	38	-2	1687	2607	16531627	16534323	0	3476	HiC_scaffold_9
gnl|BL ORD ID|21035 QMP82317.1 nucleocapsid protein [Hemipteran orthomyxo-related virus OKIAV188]	101	39.60	4	3	1	97	831489	831791	0.000184381	144	HiC_scaffold_9
gnl|BL ORD ID|48377 QMI58129.1 putative capsid protein, partial [Verdadero virus]	400	34.50	45	-2	53	433	12948882	12950003	1.30E-37	408	HiC_scaffold_12
gnl|BL ORD ID|92059 QEM39034.1 nonstructural protein [Bactericera trigonica densovirus]	183	30.60	9	-1	203	385	12964144	12964665	4.72E-13	217	HiC_scaffold_12
gnl|BL ORD ID|12538 YP 009256211.1 putative nonstructural protein NS1 [Diaphorina citri densovirus]	87	42.53	6	-3	251	332	12948368	12948625	1.67E-06	162	HiC_scaffold_12

gnl|BL ORD ID|72222 AVK59491.1 coat protein [Wuhan fly virus 6]	317	36.59	9	2	98	410	5353295	5354230	1.44E-48	487	HiC_scaffold_12
gnl|BL ORD ID|16485 QIJ56918.1 RNA-directed RNA polymerase [Scaphoideus titanus-associated partiti-like virus 1]	167	51.50	0	-2	298	464	1444757	1445257	1.24E-46	475	HiC_scaffold_13
gnl|BL ORD ID|92059 QEM39034.1 nonstructural protein [Bactericera trigonica densovirus]	306	33.01	29	-2	202	499	1445741	1446595	5.01E-33	359	HiC_scaffold_13
gnl|BL ORD ID|92059 QEM39034.1 nonstructural protein [Bactericera trigonica densovirus]	108	37.04	4	-1	222	329	1484910	1485221	4.49E-09	183	HiC_scaffold_13
gnl|BL ORD ID|110597 ASA47282.1 RdRp [Culex mononega-like virus 1]	196	34.18	6	-2	140	330	1144889	1145473	8.10E-33	330	HiC_scaffold_13
gnl|BL ORD ID|12538 YP 009256211.1 putative nonstructural protein NS1 [Diaphorina citri densovirus]	27	48.15	0	-1	505	531	1445589	1445669	3.84E-30	81	HiC_scaffold_13
gnl|BL ORD ID|12538 YP 009256211.1 putative nonstructural protein NS1 [Diaphorina citri densovirus]	115	33.91	17	-2	177	287	1461323	1461628	5.69E-11	159	HiC_scaffold_13
gnl|BL ORD ID|12538 YP 009256211.1 putative nonstructural protein NS1 [Diaphorina citri densovirus]	59	38.98	1	-1	309	366	1461099	1461275	5.69E-11	81	HiC_scaffold_13
gnl|BL ORD ID|79329 QBK47204.1 RdRP [Anopheles darlingi virus]	210	33.81	6	-2	91	295	1144886	1145512	1.00E-27	309	HiC_scaffold_13
gnl|BL ORD ID|41450 YP 009256210.1 putative nonstructural protein [Diaphorina citri densovirus]	160	35.00	2	3	274	432	6375405	6375881	4.36E-20	178	HiC_scaffold_13
gnl|BL ORD ID|113173 QEM39033.1 nonstructural protein [Bactericera trigonica densovirus]	128	26.56	4	2	137	263	6374999	6375373	2.63E-19	156	HiC_scaffold_13
gnl|BL ORD ID|124979 AJG39051.1 polymerase [Lishi spider virus 1]	97	53.61	3	-3	1180	1274	9565156	9565443	2.64E-18	264	HiC_scaffold_13
gnl|BL ORD ID|48377 QMI58129.1 putative capsid protein, partial [Verdadero virus]	265	33.58	30	1	103	356	2371903	2372640	1.08E-17	251	HiC_scaffold_13
gnl|BL ORD ID|31292 QMP82337.1 RNA-dependent RNA polymerase, partial [Coleopteran chu-related virus OKIAV151]	101	36.63	0	-1	896	996	9564369	9564671	1.50E-07	171	HiC_scaffold_13
gnl|BL ORD ID|24376 QMP82266.1 hemagglutinin, partial [Hemipteran orthomyxo-related virus OKIAV188]	142	28.17	8	-2	292	426	9556193	9556615	1.15E-09	186	HiC_scaffold_13
gnl|BL ORD ID|116272 AYP67573.1 PB1 [Old quarry swamp virus]	45	60.00	0	-1	656	700	1462839	1462973	0.000116508	145	HiC_scaffold_13

Table S4.2 – CRF-TW EVEs

sequence	length (aa)	perc identity (aa)	gaps	frame	position on hit start (aa)	position on hit stop (aa)	position on query start (nt)	position on query stop (nt)	evalue	score	query id
gnl|BL ORD ID|54230 QRD99908.1 capsid [Dragana partiti-like virus]	183	29.51	15	-2	225	407	24205312	24205815	1.23E-26	200	HiC_scaffold_2
gnl|BL ORD ID|32373 QLJ83484.1 ORF3 [Broome densovirus 1]	98	50.00	5	-1	5	102	12636371	12636649	4.24E-17	240	HiC_scaffold_3
gnl|BL ORD ID|24043 QPB73984.1 glycoprotein [Megalopteran chu-related virus OKIAV119]	228	21.05	21	-2	90	315	8847055	8847681	1.05E-08	183	HiC_scaffold_3
gnl|BL ORD ID|33835 YP 004063985.1 non-structural polyprotein [Mud crab virus]	125	28.80	25	-3	1297	1396	24144576	24144950	0.000918	142	HiC_scaffold_4
gnl|BL ORD ID|12538 YP 009256211.1 putative nonstructural protein NS1 [Diaphorina citri densovirus]	110	35.45	9	-1	190	299	21640971	21641273	2.05E-05	154	HiC_scaffold_5
gnl|BL ORD ID|23226 YP 009336527.1 hypothetical protein 4 [Beihai tombus-like virus 12]	146	34.93	0	-1	314	459	682286	682723	2.39E-05	154	HiC_scaffold_6
gnl|BL ORD ID|124979 AJG39051.1 polymerase [Lishi spider virus 1]	489	36.81	12	3	1087	1566	2218230	2219687	2.81E-76	763	HiC_scaffold_6
gnl|BL ORD ID|124979 AJG39051.1 polymerase [Lishi spider virus 1]	238	31.09	3	2	1711	1947	2220776	2221483	1.29E-25	291	HiC_scaffold_6
gnl|BL ORD ID|43041 QPL15312.1 RNA-dependent RNA polymerase [Orthopteran chu-related virus OKIAV152]	111	45.95	0	3	355	465	2216754	2217086	5.06E-38	290	HiC_scaffold_6
gnl|BL ORD ID|43041 QPL15312.1 RNA-dependent RNA polymerase [Orthopteran chu-related virus OKIAV152]	48	60.42	0	2	496	543	2217170	2217313	5.06E-38	162	HiC_scaffold_6
gnl|BL ORD ID|75136 AMK09235.1 nucleocapsid protein [Drosophila busckii rhabdovirus]	109	34.86	6	-2	287	389	4333312	4333638	0.000484	142	HiC_scaffold_6
gnl|BL ORD ID|19408 YP 009259672.1 polyprotein [Diaphorina citri flavi-like virus]	929	77.07	38	-1	1687	2607	15741407	15744103	0	3476	HiC_scaffold_7
gnl|BL ORD ID|19408 YP 009259672.1 polyprotein [Diaphorina citri flavi-like virus]	929	77.07	38	-2	1687	2607	15456873	15459569	0	3476	HiC_scaffold_9
gnl|BL ORD ID|54230 QRD99908.1 capsid [Dragana partiti-like virus]	264	33.33	7	2	54	316	12950432	12951205	1.65E-39	423	HiC_scaffold_11
gnl|BL ORD ID|100122 QEM39036.1 VP4 [Bactericera trigonica densovirus]	217	37.33	27	3	334	535	13377762	13378376	5.53E-25	314	HiC_scaffold_12
gnl|BL ORD ID|23242 YP 009336731.1 hypothetical protein 1 [Shuangao toti-like virus]	201	24.88	17	-1	548	740	13388967	13389542	9.37E-07	165	HiC_scaffold_12
gnl|BL ORD ID|12538 YP 009256211.1 putative nonstructural protein NS1 [Diaphorina citri densovirus]	484	42.15	11	-3	196	675	13378672	13380102	2.2E-102	917	HiC_scaffold_12
gnl|BL ORD ID|12538 YP 009256211.1 putative nonstructural protein NS1 [Diaphorina citri densovirus]	87	42.53	6	-1	251	332	13365708	13365965	8.42E-07	165	HiC_scaffold_12

gnl|BL ORD ID|48377 QMI58129.1 putative capsid protein, partial [Verdadero virus]	409	33.99	47	-3	53	442	13366195	13367337	2.37E-36	398	HiC_scaffold_12
gnl|BL ORD ID|92059 QEM39034.1 nonstructural protein [Bactericera trigonica densovirus]	108	37.04	4	3	222	329	1678965	1679276	4.88E-09	183	HiC_scaffold_13
gnl|BL ORD ID|2569 QRW42585.1 polymerase PA [Guadeloupe mosquito quaranja-like virus 1]	54	53.70	0	2	10	63	1716941	1717102	2.18E-06	160	HiC_scaffold_13
gnl|BL ORD ID|116272 AYP67573.1 PB1 [Old quarry swamp virus]	45	60.00	0	1	656	700	1706170	1706304	0.000127	145	HiC_scaffold_13
gnl|BL ORD ID|109953 APG79108.1 RNA-dependent RNA polymerase [Hubei lepidoptera virus 4]	247	35.63	9	-2	428	668	1436258	1436989	2.4E-107	354	HiC_scaffold_13
gnl|BL ORD ID|102424 APG79114.1 RdRp [Hubei reo-like virus 12]	153	47.06	0	-3	691	843	1435798	1436256	3.8E-98	267	HiC_scaffold_13
gnl|BL ORD ID|124979 AJG39051.1 polymerase [Lishi spider virus 1]	237	46.84	9	1	1139	1369	11336422	11337123	1.29E-45	498	HiC_scaffold_13
gnl|BL ORD ID|124979 AJG39051.1 polymerase [Lishi spider virus 1]	133	33.83	2	2	1356	1487	11337086	11337481	1.42E-11	206	HiC_scaffold_13
gnl|BL ORD ID|26364 QRW41688.1 RNA-dependent RNA polymerase [Lasigmu virus]	424	32.31	20	-3	10	428	1436953	1438179	3.45E-45	492	HiC_scaffold_13
gnl|BL ORD ID|48377 QMI58129.1 putative capsid protein, partial [Verdadero virus]	295	33.22	30	2	73	356	2505944	2506771	4.08E-20	270	HiC_scaffold_13
gnl|BL ORD ID|48377 QMI58129.1 putative capsid protein, partial [Verdadero virus]	299	32.78	30	2	73	360	2507429	2508268	4.23E-20	270	HiC_scaffold_13
gnl|BL ORD ID|48377 QMI58129.1 putative capsid protein, partial [Verdadero virus]	207	36.71	22	3	103	300	2504721	2505302	1.12E-17	251	HiC_scaffold_13
gnl|BL ORD ID|113173 QEM39033.1 nonstructural protein [Bactericera trigonica densovirus]	128	26.56	4	1	137	263	6506233	6506607	2.96E-19	156	HiC_scaffold_13
gnl|BL ORD ID|12538 YP 009256211.1 putative nonstructural protein NS1 [Diaphorina citri densovirus]	169	36.69	2	1	259	426	6506632	6507135	1.24E-15	238	HiC_scaffold_13
gnl|BL ORD ID|12538 YP 009256211.1 putative nonstructural protein NS1 [Diaphorina citri densovirus]	115	33.91	17	2	177	287	1707515	1707820	4.2E-11	159	HiC_scaffold_13
gnl|BL ORD ID|12538 YP 009256211.1 putative nonstructural protein NS1 [Diaphorina citri densovirus]	59	40.68	1	1	309	366	1707868	1708044	4.2E-11	82	HiC_scaffold_13
gnl|BL ORD ID|33449 QTW97811.1 hypothetical protein [Mononegavirales sp.]	604	35.43	12	-3	7	605	21147	22937	1.1E-129	1101	HiC_scaffold_24
gnl|BL ORD ID|92059 QEM39034.1 nonstructural protein [Bactericera trigonica densovirus]	77	35.06	3	2	252	328	28637	28858	1.15E-05	134	HiC_scaffold_25
gnl|BL ORD ID|35151 YP 009179392.1 hypothetical protein [Shuangao insect virus 7]	109	33.03	8	2	29	135	30992	31300	2.59E-05	121	HiC_scaffold_25
gnl|BL ORD ID|41450 YP 009256210.1 putative nonstructural protein [Diaphorina citri densovirus]	108	35.19	6	2	150	251	23621	23944	0.000712	118	HiC_scaffold_25
gnl|BL ORD ID|92059 QEM39034.1 nonstructural protein [Bactericera trigonica densovirus]	108	37.04	4	1	222	329	24670	24981	2.3E-11	183	HiC_scaffold_25
gnl|BL ORD ID|33449 QTW97811.1 hypothetical protein [Mononegavirales sp.]	604	35.43	12	-3	7	605	41871	43661	9.5E-130	1101	HiC_scaffold_31

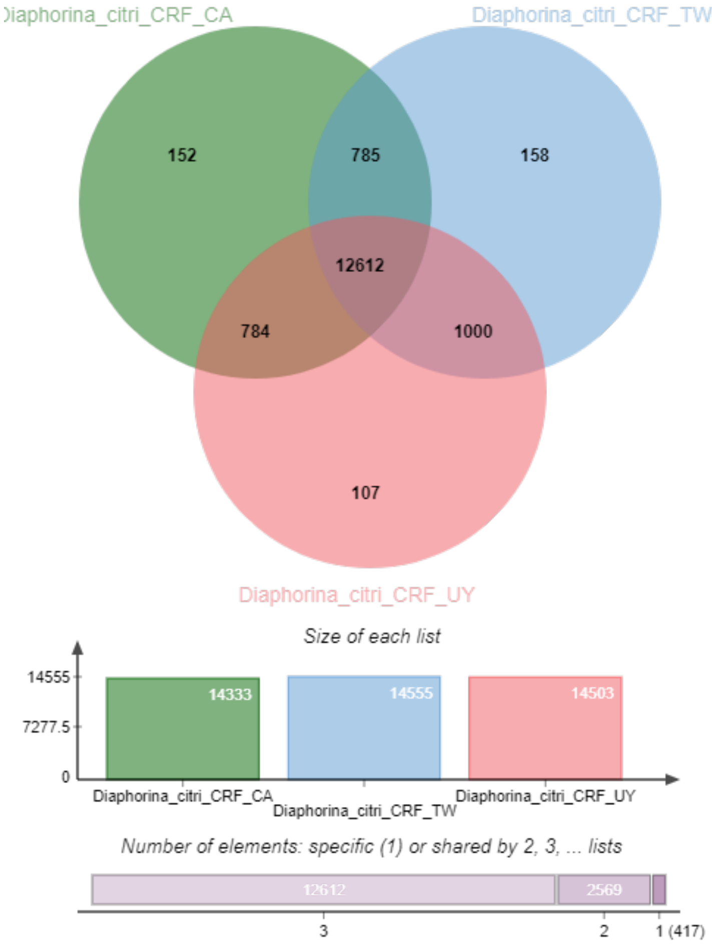
Table S4.3 – CRF-UY EVEs

sequence	length (aa)	perc identity (aa)	gaps	frame	position on hit start (aa)	position on hit stop (aa)	position on query start (nt)	position on query stop (nt)	evalue	score	query id
gnl|BL ORD ID|32373 QLJ83484.1 ORF3 [Broome densovirus 1]	98	50.00	5	-1	5	102	12112354	12112632	4.09E-17	240	HiC_scaffold_3
gnl|BL ORD ID|33449 QTW97811.1 hypothetical protein [Mononegavirales sp.]	604	35.43	12	3	7	605	2344587	2346377	4.6E-127	1101	HiC_scaffold_4
gnl|BL ORD ID|43041 QPL15312.1 RNA-dependent RNA polymerase [Orthopteran chu-related virus OKIAV152]	111	45.95	0	3	355	465	1938036	1938368	4.87E-38	290	HiC_scaffold_6
gnl|BL ORD ID|43041 QPL15312.1 RNA-dependent RNA polymerase [Orthopteran chu-related virus OKIAV152]	48	60.42	0	2	496	543	1938452	1938595	4.87E-38	162	HiC_scaffold_6
gnl|BL ORD ID|102284 API61887.1 RNA-directed RNA polymerase [Chuvirus Mos8Chu0]	286	25.87	21	3	1735	2010	1942059	1942883	1.21E-12	218	HiC_scaffold_6
gnl|BL ORD ID|75136 AMK09235.1 nucleocapsid protein [Drosophila busckii rhabdovirus]	186	26.88	2	-1	206	389	3885142	3885699	4.88E-08	175	HiC_scaffold_6
gnl|BL ORD ID|23226 YP 009336527.1 hypothetical protein 4 [Beihai tombus-like virus 12]	137	36.50	0	-1	314	450	583633	584043	7.5E-07	166	HiC_scaffold_6
gnl|BL ORD ID|124979 AJG39051.1 polymerase [Lishi spider virus 1]	489	36.81	12	3	1087	1566	1939512	1940969	2.69E-76	763	HiC_scaffold_6
gnl|BL ORD ID|124979 AJG39051.1 polymerase [Lishi spider virus 1]	206	33.98	3	3	1743	1947	1942155	1942766	2.99E-26	294	HiC_scaffold_6
gnl|BL ORD ID|75720 AXQ04844.1 hypothetical protein, partial [Bidnavirus-like Culex mosquito virus]	395	31.14	38	-3	259	622	1765894	1767057	6.45E-31	365	HiC_scaffold_8
gnl|BL ORD ID|19408 YP 009259672.1 polyprotein [Diaphorina citri flavi-like virus]	929	77.07	38	-3	1687	2607	14631711	14634407	0	3476	HiC_scaffold_10
gnl|BL ORD ID|54230 QRD99908.1 capsid [Dragana partiti-like virus]	264	33.33	7	-2	54	316	2337676	2338449	1.47E-39	423	HiC_scaffold_11
gnl|BL ORD ID|12538 YP 009256211.1 putative nonstructural protein NS1 [Diaphorina citri densovirus]	484	42.15	11	-3	196	675	11964921	11966351	2E-102	917	HiC_scaffold_12
gnl|BL ORD ID|23242 YP 009336731.1 hypothetical protein 1 [Shuangao toti-like virus]	201	24.88	17	-3	548	740	11975217	11975792	8.5E-07	165	HiC_scaffold_12
gnl|BL ORD ID|12538 YP 009256211.1 putative nonstructural protein NS1 [Diaphorina citri densovirus]	87	42.53	6	-2	251	332	11951968	11952225	7.64E-07	165	HiC_scaffold_12
gnl|BL ORD ID|48377 QMI58129.1 putative capsid protein, partial [Verdadero virus]	409	33.99	47	-1	53	442	11952455	11953597	2.15E-36	398	HiC_scaffold_12
gnl|BL ORD ID|72222 AVK59491.1 coat protein [Wuhan fly virus 6]	215	38.14	6	2	184	393	4546442	4547083	1.12E-30	351	HiC_scaffold_12
gnl|BL ORD ID|100122 QEM39036.1 VP4 [Bactericera trigonica densovirus]	217	37.33	27	2	334	535	11964011	11964625	5.02E-25	314	HiC_scaffold_12

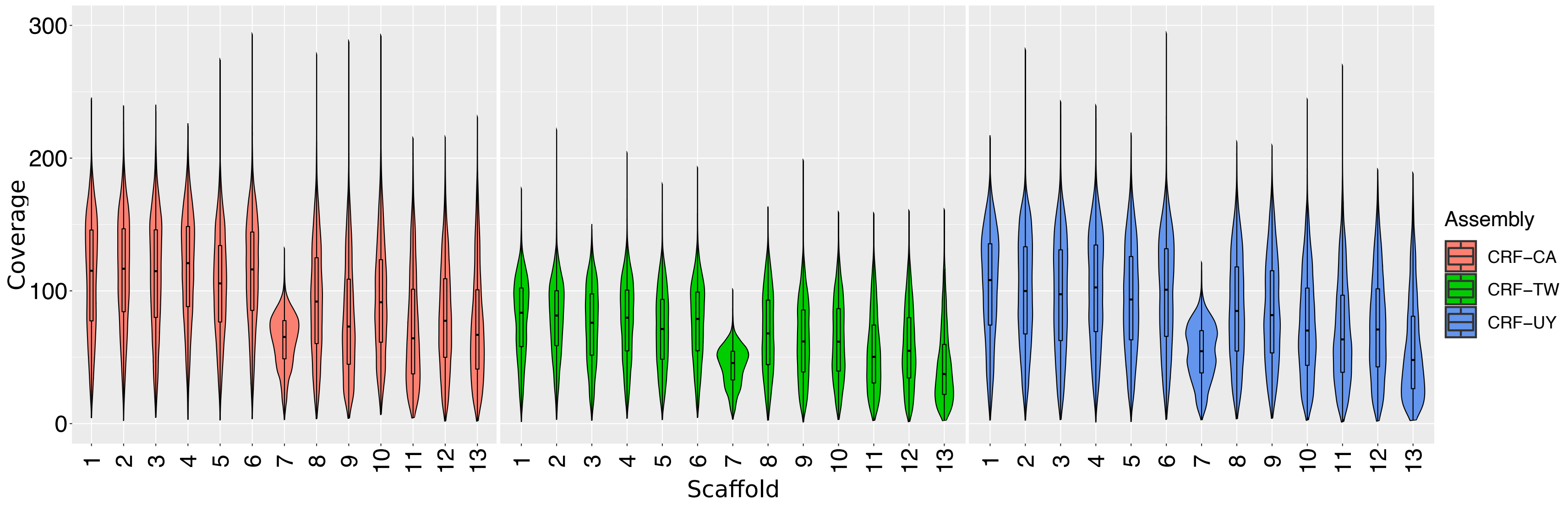
gnl|BL ORD ID|12538 YP 009256211.1 putative nonstructural protein NS1 [Diaphorina citri densovirus]	27	48.15	0	-3	505	531	1368365	1368445	2.9E-30	81	HiC_scaffold_13
gnl|BL ORD ID|12538 YP 009256211.1 putative nonstructural protein NS1 [Diaphorina citri densovirus]	115	33.91	17	-1	177	287	1384099	1384404	5.05E-11	159	HiC_scaffold_13
gnl|BL ORD ID|12538 YP 009256211.1 putative nonstructural protein NS1 [Diaphorina citri densovirus]	59	38.98	1	-3	309	366	1383875	1384051	5.05E-11	81	HiC_scaffold_13
gnl|BL ORD ID|116272 AYP67573.1 PB1 [Old quarry swamp virus]	45	60.00	0	-3	656	700	1385615	1385749	0.000103	145	HiC_scaffold_13
gnl|BL ORD ID|48377 QMI58129.1 putative capsid protein, partial [Verdadero virus]	265	33.58	30	3	103	356	2126178	2126915	9.57E-18	251	HiC_scaffold_13
gnl|BL ORD ID|24376 QMP82266.1 hemagglutinin, partial [Hemipteran orthomyxo-related virus OKIAV188]	435	20.46	26	-1	1	426	9451357	9452610	1.82E-11	200	HiC_scaffold_13
gnl|BL ORD ID|102424 APG79114.1 RdRp [Hubei reo-like virus 12]	153	47.06	0	-1	691	843	1135378	1135836	3.21E-98	267	HiC_scaffold_13
gnl|BL ORD ID|16485 QIJ56918.1 RNA-directed RNA polymerase [Scaphoideus titanus-associated partiti-like virus 1]	167	51.50	0	-1	298	464	1367533	1368033	1.09E-46	475	HiC_scaffold_13
gnl|BL ORD ID|26364 QRW41688.1 RNA-dependent RNA polymerase [Lasigmu virus]	424	32.31	20	-1	10	428	1136533	1137759	2.81E-45	492	HiC_scaffold_13
gnl|BL ORD ID|92059 QEM39034.1 nonstructural protein [Bactericera trigonica densovirus]	306	33.01	29	-1	202	499	1368517	1369371	4.44E-33	359	HiC_scaffold_13
gnl|BL ORD ID|92059 QEM39034.1 nonstructural protein [Bactericera trigonica densovirus]	108	37.04	4	-1	222	329	1410475	1410786	3.97E-09	183	HiC_scaffold_13
gnl|BL ORD ID|124979 AJG39051.1 polymerase [Lishi spider virus 1]	56	41.07	0	-3	1432	1487	166	333	7.04E-11	130	HiC_scaffold_234
gnl|BL ORD ID|31292 QMP82337.1 RNA-dependent RNA polymerase, partial [Coleopteran chu-related virus OKIAV151]	69	36.23	7	-3	957	1018	199	405	8.49E-05	114	HiC_scaffold_234
gnl|BL ORD ID|124979 AJG39051.1 polymerase [Lishi spider virus 1]	195	45.13	5	-1	1178	1369	891	1469	3.74E-45	413	HiC_scaffold_319

Table S5. Mitochondrial CO1 haplotypes by locality.

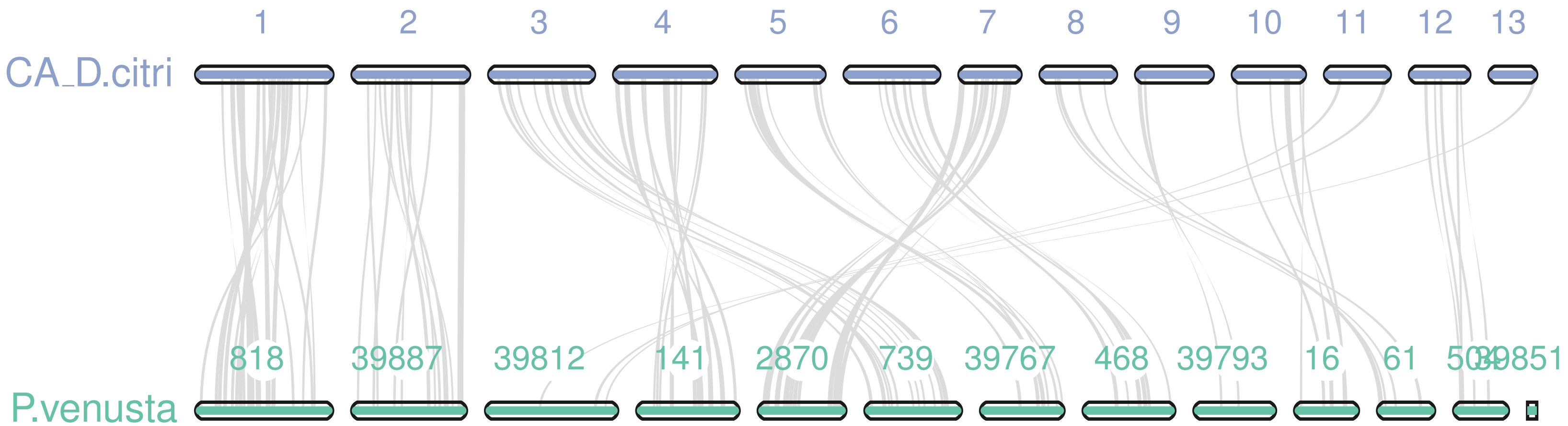
		mtDNA CO1 Haplotypes							
	Locality	1	2	3	4	5	6	7	Total
SEA Asia	China	0	31	0	0	0	3	1	35
	Taiwan	0	5	0	0	0	0	0	5
	Vietnam	0	11	0	0	0	0	0	11
	Cambodia	0	1	0	0	0	0	0	1
	Indonesia	1	14	0	0	0	0	0	15
	Malaysia	0	1	0	0	0	0	0	1
	Thailand	0	4	0	0	0	0	0	4
South Asia	India	4	0	0	0	0	0	0	4
	Pakistan	4	0	0	0	2	0	0	6
	Saudi Arabia	5	0	0	0	0	0	0	5
Indian Ocean Isles	Mauritius	0	5	0	0	0	0	0	5
	Reunion	1	3	0	0	0	0	0	4
	Brazil	4	13	0	0	0	0	0	17
Caribbean	Guadeloupe	0	0	0	11	0	0	0	11
	Puerto Rico	0	0	0	3	0	0	0	3
	Florida	93	0	1	0	0	0	0	94
	Texas	5	0	0	0	0	0	0	5
	Mexico	4	0	0	0	0	6	0	10
	California	1	0	0	0	0	0	0	1
	CRF-CA	1	0	0	0	0	0	0	1
	CRF-UY	0	1	0	0	0	0	0	1
	CRF-TW	0	1	0	0	0	0	0	1
	Total	123	90	1	14	2	9	1	240



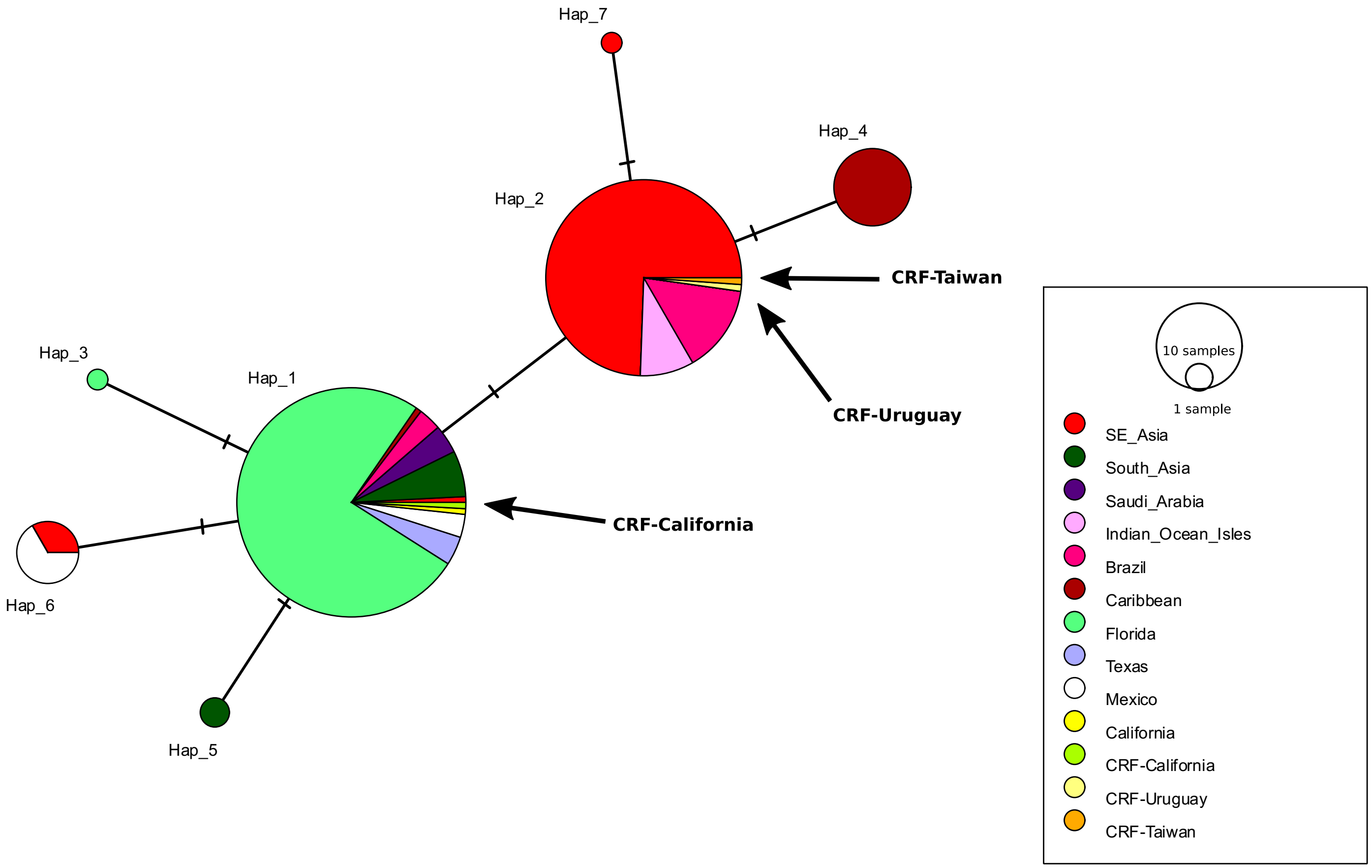
Supplemental Figure 1. OrthoVenn2 orthologous protein-clustering Venn diagram. Numbers within circles are protein ortholog group numbers. Numbers within overlapping regions of circles represent the number of shared ortholog clusters between each protein set: CRF-CA *D. citri* (green); CRF-TW *D. citri* (blue); CRF-UY *D. citri* (pink).



Supplemental Figure 2. Male-only, ultra-low input HiFi PacBio sequencing average coverage per superscaffold (chromosome) across 10 Kb sliding windows of CRF-CA, CRF-TW, and CRF-UY.



Supplemental Figure 3. Genome synteny plot highlighting syntenic blocks between CRF-CA *D. citri* and *Pachypsylla venusta* (hackberry petiole gall psyllid). Bars represent chromosomes. Numbers above bars refer to the chromosome's scaffold number in the assembly. Lines between bars represent syntenic links. *P. venusta* scaffold 2870 is the X chromosome in that species.



Supplemental Figure 4. Partial cytochrome *c* oxidase I (*COI*) TCS haplotype network coded by geographic region. Circle size is scaled to the number of haplotypes. Hatch marks represent single nucleotide substitutions. CRF-CA is in haplotype 1. CRF-TW and CRF-UY are in haplotype 2. Arrows added for emphasis. Haplotype 1 is most common (n = 123). Localities have been collapsed into broad geographic regions. Region labelled "California" represents a mitogenome downloaded from NCBI. Accession numbers available in Table S1. Specific locality and haplotype information available in Table S6.