

Diversity of insect-specific viruses in *Culex* mosquitoes from Papua New Guinea

Supplementary tables

Supplementary Table 1a: Site details of mosquito collection locations.

Province	Collection dates	Site location details	Site code in map	No of mosquitoes collected
Central	26/11/2019–20/12/2019	City Mission farm	C1	392
		Boroma Piggery	C2	420
		Eden Green farm	C3	435
Morobe	20/9/2020–16/10/2020	EBC Farm	MO1	3100
		Rumion Ltd Farm	MO2	1217
Western	19/7/2021–20/8/2021	Kilo 1	W1	61
		Kilo 8	W2	910
		Kilo 6	W3	769
		Peter's Pig farm	W4	738
		Broken Hill	W5	52
		Mepu Village	W6	37
		Maprik	ES1	629
Madang	August to September 2019	Bogia	MA1	4779

Supplementary Table 1b: Sample details.

SAN No	Pooling	Collection dates	Feeding status	Province	Mosquito species	Mosquitoes in the pool	Average size in bp	Raw read pairs	Filtered read pairs	Viral read pairs	% Viral read out of filtered reads	ISV read pairs	% ISV read out of viral reads
23-00945-0001	Pool	2019-11-26/2019-12-20	Unfed	Central	<i>Cx. annulirostris</i>	135	467	6.95E+06	4.84E+06	3.59E+05	7.410	1.81E+05	50.42
23-00945-0002	Pool	2019-11-26/2019-12-19	Unfed	Central	<i>Cx. gelidus</i>	198	491	1.58E+07	1.51E+07	2.76E+05	1.822	1.43E+05	51.70
23-00945-0004	Pool	2019-11-28/2019-12-07	Unfed	Central	<i>Cx. quinquefasciatus</i>	164	456	1.85E+07	1.77E+07	4.21E+04	0.238	2.15E+04	51.03
23-00945-0005	Pool	2019-11-26/2019-12-20	Unfed	Central	<i>Cx. sitiens</i>	145	454	1.32E+07	1.06E+07	2.05E+05	1.937	1.03E+05	50.09
23-00945-0008	Pool	2019-04-03/2019-04-15	Unfed	East Sepik	<i>Cx. annulirostris</i>	190	502	1.66E+07	1.50E+07	1.03E+05	0.684	5.67E+04	55.20
23-00945-0009	Pool	2019-03-04/2019-04-19	Unfed	East Sepik	<i>Cx. quinquefasciatus</i>	439	448	1.98E+07	1.89E+07	2.96E+05	1.566	1.60E+05	54.07
23-00945-0011	Pool	2019-03-02/2019-07-22	Unfed	Madang	<i>Cx. annulirostris</i>	73	494	2.26E+07	2.19E+07	2.47E+06	11.279	1.24E+06	50.01
23-00945-0012	Pool	2019-10-28/2020-02-20	Unfed	Madang	<i>Cx. gelidus</i>	13	631	1.10E+07	9.23E+06	1.22E+04	0.132	6.05E+03	49.70
23-00945-0013	Pool	2019-06-27/2019-07-22	Unfed	Madang	<i>Cx. quinquefasciatus</i>	481	481	1.27E+07	1.12E+07	9.50E+05	8.497	4.73E+05	49.86
23-00945-0018	Pool	2020-05-04/2020-05-21	Unfed	Madang	<i>Cx. quinquefasciatus</i>	362	464	1.86E+07	1.67E+07	3.03E+06	18.118	1.51E+06	49.96
23-00945-0019	Pool	2019-08-24/2019-09-12	Unfed	Madang	<i>Cx. annulirostris</i>	466	457	1.16E+07	9.89E+06	3.10E+05	3.136	1.54E+05	49.75
23-00945-0020	Pool	2019-09-04/2019-09-12	Unfed	Madang	<i>Cx. quinquefasciatus</i>	40	436	5.00E+06	2.72E+06	5.73E+04	2.105	2.86E+04	50.00
23-00945-0021	Pool	2020-09-22/2020-10-16	Unfed	Morobe	<i>Cx. annulirostris</i>	59	456	2.92E+07	2.86E+07	6.00E+05	2.102	2.99E+05	49.75
23-00945-0024	Pool	2020-10-06	Unfed	Morobe	<i>Cx. gelidus</i>	471	432	2.22E+07	1.60E+07	2.90E+05	1.816	1.43E+05	49.35
23-00945-0035	Pool	2020-09-21/2020-10-16	Unfed	Morobe	<i>Cx. gelidus</i>	442	511	1.74E+07	1.55E+07	6.69E+05	4.327	3.32E+05	49.67
23-00945-0037	Pool	2020-09-21/2020-10-16	Unfed	Morobe	<i>Cx. quinquefasciatus</i>	472	474	2.99E+07	2.50E+07	1.87E+06	7.473	9.29E+05	49.75
23-00945-0039	Pool	2020-09-21/2020-10-03	Unfed	Morobe	<i>Cx. quinquefasciatus</i>	270	533	3.41E+07	2.73E+07	9.20E+05	3.374	4.47E+05	48.56
23-00945-0040	Pool	2020-09-25/2020-10-03	Unfed	Morobe	<i>Cx. sitiens</i>	21	515	1.57E+07	1.43E+07	1.59E+05	1.113	6.56E+04	41.34
23-00945-0041	Pool	2021-07-20/2021-08-20	Unfed	Western	<i>Cx. annulirostris</i>	476	484	1.40E+07	1.27E+07	1.19E+05	0.941	5.79E+04	48.44
23-00945-0046	Pool	2021-07-20/2021-08-19	Unfed	Western	<i>Cx. gelidus</i>	484	462	1.82E+07	1.63E+07	1.64E+05	1.003	8.12E+04	49.63
23-00945-0050	Pool	2021-08-06/2021-08-08	Unfed	Western	<i>Cx. pulk</i>	109	399	1.99E+07	1.34E+07	4.10E+05	3.065	2.05E+05	49.96
23-00945-0051	Pool	2021-07-20/2021-08-20	Unfed	Western	<i>Cx. quinquefasciatus</i>	439	433	6.45E+06	4.28E+06	5.48E+05	12.805	2.70E+05	49.28
23-00945-0052	Pool	2021-07-20/2021-08-08	Unfed	Western	<i>Cx. sitiens</i>	7	412	1.56E+07	9.36E+06	4.81E+05	5.134	2.36E+05	49.06
23-00945-0053	Single	2019-12-03	Blood-fed	Central	<i>Cx. annulirostris</i>	1	663	1.52E+07	1.39E+07	2.07E+03	0.015	1.01E+03	48.84
23-00945-0057	Single	2019-12-05	Blood-fed	Central	<i>Cx. annulirostris</i>	1	547	1.78E+07	1.64E+07	1.83E+03	0.011	9.05E+02	49.40
23-00945-0058	Single	2019-12-04	Blood-fed	Central	<i>Cx. gelidus</i>	1	552	1.61E+07	1.46E+07	4.64E+02	0.003	8.40E+01	18.10
23-00945-0064	Single	2019-12-16	Blood-fed	Central	<i>Cx. quinquefasciatus</i>	1	484	2.63E+07	2.33E+07	4.17E+05	1.790	2.01E+05	48.20
23-00945-0065	Single	2019-12-16	Blood-fed	Central	<i>Cx. quinquefasciatus</i>	1	529	1.82E+07	1.76E+07	2.75E+05	1.559	1.37E+05	50.01
23-00945-0068	Single	2019-10-03	Blood-fed	Madang	<i>Cx. annulirostris</i>	1	667	1.90E+07	1.85E+07	3.83E+04	0.207	1.91E+04	49.85
23-00945-0071	Single	2020-02-13	Blood-fed	Madang	<i>Cx. annulirostris</i>	1	502	1.81E+07	1.75E+07	7.14E+03	0.041	3.57E+03	50.00
23-00945-0075	Single	2019-08-12	Blood-fed	Madang	<i>Cx. quinquefasciatus</i>	1	634	1.67E+07	1.63E+07	7.04E+02	0.004	3.52E+02	50.00
23-00945-0076	Single	2019-08-12	Blood-fed	Madang	<i>Cx. quinquefasciatus</i>	1	591	1.76E+07	1.71E+07	5.56E+03	0.033	2.81E+03	50.47
23-00945-0085	Single	2019-08-25	Blood-fed	Madang	<i>Cx. quinquefasciatus</i>	1	493	1.42E+07	1.34E+07	1.52E+05	1.131	0.00E+00	0.00
23-00945-0088	Single	2019-08-25	Blood-fed	Morobe	<i>Cx. annulirostris</i>	1	582	2.09E+07	2.04E+07	4.09E+04	0.200	2.01E+04	49.15
23-00945-0089	Single	2019-09-01	Blood-fed	Morobe	<i>Cx. annulirostris</i>	1	550	1.49E+07	1.37E+07	2.86E+04	0.209	1.25E+02	0.44
23-00945-0096	Single	2019-09-07	Blood-fed	Morobe	<i>Cx. gelidus</i>	1	534	2.23E+07	2.18E+07	3.28E+02	0.002	1.50E+02	45.73
23-00945-0099	Single	2019-09-26	Blood-fed	Morobe	<i>Cx. quinquefasciatus</i>	1	578	2.02E+07	1.95E+07	3.02E+03	0.016	3.05E+02	10.10
23-00945-0100	Single	2019-09-26	Blood-fed	Morobe	<i>Cx. quinquefasciatus</i>	1	549	3.61E+07	3.34E+07	9.28E+03	0.028	1.31E+02	1.41
23-00945-0102	Single	2020-10-14	Blood-fed	Western	<i>Cx. annulirostris</i>	1	631	2.07E+07	2.02E+07	3.37E+03	0.017	1.93E+02	5.73
23-00945-0105	Single	2020-10-14	Blood-fed	Western	<i>Cx. annulirostris</i>	1	600	2.16E+07	2.10E+07	2.83E+04	0.135	1.39E+04	49.12
23-00945-0108	Single	2020-09-22	Blood-fed	Western	<i>Cx. gelidus</i>	1	485	1.76E+07	1.70E+07	6.79E+03	0.040	8.28E+02	12.19
23-00945-0113	Single	2021-07-29	Blood-fed	Western	<i>Cx. quinquefasciatus</i>	1	445	2.12E+07	1.86E+07	2.24E+05	1.205	1.11E+05	49.67
23-00945-0115	Single	2021-07-29	Blood-fed	Western	<i>Cx. quinquefasciatus</i>	1	469	4.24E+07	4.11E+07	9.32E+05	2.268	1.35E+05	14.51
23-00945-0122	Single	2021-07-28	Blood-fed	Madang	<i>Cx. annulirostris</i>	1	643	1.92E+07	1.85E+07	4.54E+03	0.025	2.48E+03	54.71
23-00945-0124	Single	2021-07-28	Blood-fed	Madang	<i>Cx. annulirostris</i>	1	536	1.63E+07	1.55E+07	1.56E+03	0.010	1.12E+02	7.19
23-00945-0127	Pool	2019-07-01/2020-05-04	Blood-fed	Madang	<i>Cx. quinquefasciatus</i>	499	531	2.70E+07	2.64E+07	1.46E+05	0.553	7.27E+04	49.90
23-00945-0128	Pool	2020-05-07/2020-05-11	Blood-fed	Madang	<i>Cx. quinquefasciatus</i>	52	384	2.21E+07	1.97E+07	1.51E+05	0.767	7.52E+04	49.81
23-00945-0129	Pool	2019-08-29/2019-09-09	Blood-fed	Madang	<i>Cx. annulirostris</i>	27	552	1.60E+07	1.56E+07	2.96E+04	0.190	1.43E+04	48.28
23-00945-0130	Pool	2019-11-26/2019-12-18	Blood-fed	Central	<i>Cx. annulirostris</i>	5	756	1.22E+07	1.18E+07	1.25E+04	0.106	6.12E+03	48.87
23-00945-0131	Pool	2019-11-29/2019-12-19	Blood-fed	Central	<i>Cx. gelidus</i>	49	552	2.17E+07	2.10E+07	6.32E+03	0.030	2.16E+03	34.12
23-00945-0132	Pool	2019-11-26/2019-12-20	Blood-fed	Central	<i>Cx. quinquefasciatus</i>	86	696	2.79E+04	2.58E+04	0.00E+00	0.000	0.00E+00	0.00
23-00945-0133	Pool	2019-11-29/2019-12-16	Blood-fed	Central	<i>Cx. sitiens</i>	22	519	1.52E+07	1.46E+07	8.03E+04	0.548	4.02E+04	49.99
23-00945-0134	Pool	2020-10-07/2020-10-08	Blood-fed	Morobe	<i>Cx. gelidus</i>	495	487	3.80E+07	3.70E+07	6.06E+04	0.164	2.53E+04	41.67
23-00945-0135	Pool	2020-10-08/2020-10-10	Blood-fed	Morobe	<i>Cx. gelidus</i>	498	473	2.22E+07	2.18E+07	1.52E+04	0.070	5.61E+03	36.90

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Supplementary Table 1b continued.

SAN No	Pooling	Collection dates	Feeding status	Province	Mosquito species	Mosquitoes in the pool	Average size in bp	Raw read pairs	Filtered read pairs	Viral read pairs	% Viral read pairs out of filtered reads	ISV read pairs	% ISV read pairs out of viral reads
23-00945-0136	Pool	2020-10-10/2020-10-15	Blood-fed	Morobe	<i>Cx. gelidus</i>	500	485	1.55E+07	1.52E+07	2.20E+04	0.145	1.04E+04	47.21
23-00945-0137	Pool	2020-09-21/2020-10-16	Blood-fed	Morobe	<i>Cx. gelidus</i>	244	572	2.01E+07	1.95E+07	3.69E+04	0.189	1.15E+04	31.29
23-00945-0138	Pool	2020-09-21/2020-10-10	Blood-fed	Morobe	<i>Cx. quinquefasciatus</i>	272	581	1.94E+07	1.87E+07	1.97E+04	0.105	9.56E+03	48.48
23-00945-0139	Pool	2020-09-28/2020-10-08	Blood-fed	Morobe	<i>Cx. sitiens</i>	17	519	1.83E+07	1.75E+07	6.49E+04	0.371	3.23E+04	49.81
23-00945-0140	Pool	2021-07-20/2021-08-19	Blood-fed	Western	<i>Cx. annulirostris</i>	449	705	1.86E+07	1.80E+07	1.57E+04	0.087	7.60E+03	48.53
23-00945-0141	Pool	2021-07-20/2021-08-17	Blood-fed	Western	<i>Cx. gelidus</i>	147	532	2.75E+07	2.67E+07	2.99E+04	0.112	1.34E+04	45.03
23-00945-0142	Pool	2021-07-30	Blood-fed	Western	<i>Cx. pullus</i>	1	447	2.51E+07	2.44E+07	6.19E+03	0.025	2.51E+03	40.58
23-00945-0143	Pool	2021-07-21/2021-08-14	Blood-fed	Western	<i>Cx. quinquefasciatus</i>	11	500	1.69E+07	1.62E+07	4.29E+05	2.645	2.15E+05	49.98
23-00945-0144	Pool	2021-07-21	Blood-fed	Western	<i>Cx. sitiens</i>	1	421	2.45E+07	2.39E+07	1.63E+04	0.068	6.79E+03	41.76
23-00945-0145	Pool	2019-08-24/2019-09-12	Blood-fed	Madang	<i>Cx. annulirostris</i>	42	566	1.96E+07	1.91E+07	4.14E+04	0.217	2.09E+04	50.50
23-00945-0146	Pool	2019-09-07/2019-09-10	Blood-fed	Madang	<i>Cx. quinquefasciatus</i>	5	489	2.46E+07	2.34E+07	1.29E+05	0.550	6.46E+04	50.09
23-00945-0147	Pool	2020-02-20/2020-05-07	Blood-fed	Madang	<i>Cx. annulirostris</i>	166	610	1.72E+07	1.67E+07	9.45E+05	5.669	4.72E+05	50.02
23-00945-0148	Pool	2020-02-13	Blood-fed	Madang	<i>Cx. gelidus</i>	2	513	1.33E+07	1.30E+07	3.66E+02	0.003	2.15E+02	58.74
23-00945-0149	Pool	2019-07-04/2019-07-22	Blood-fed	Madang	<i>Cx. quinquefasciatus</i>	496	663	1.36E+07	1.01E+07	6.41E+03	0.064	3.49E+03	54.51
23-00945-0150	Pool	2019-07-22/2019-07-29	Blood-fed	Madang	<i>Cx. quinquefasciatus</i>	498	501	2.30E+07	2.23E+07	1.13E+05	0.509	5.56E+04	49.01
23-00945-0151	Pool	2019-07-29/2019-08-08	Blood-fed	Madang	<i>Cx. quinquefasciatus</i>	493	669	2.23E+07	2.18E+07	1.76E+05	0.807	8.16E+04	46.42
23-00945-0152	Pool	2019-08-08/2019-10-14	Blood-fed	Madang	<i>Cx. quinquefasciatus</i>	499	434	1.64E+07	1.37E+07	4.82E+04	0.352	2.49E+04	51.72
23-00945-0153	Pool	2019-10-14/2019-10-28	Blood-fed	Madang	<i>Cx. quinquefasciatus</i>	495	603	2.60E+07	1.32E+07	3.19E+03	0.024	1.89E+03	59.26
23-00945-0154	Pool	2019-07-22/2019-10-31	Blood-fed	Madang	<i>Cx. quinquefasciatus</i>	395	591	2.24E+07	7.47E+06	9.79E+03	0.131	5.18E+03	52.88
23-00945-0155	Pool	2019-11-26/2019-12-19	Blood-fed	Central	<i>Cx. annulirostris</i>	66	437	3.38E+06	2.94E+06	2.90E+03	0.099	1.64E+03	56.44
23-00945-0156	Pool	2019-12-03/2019-12-16	Blood-fed	Central	<i>Cx. gelidus</i>	47	465	1.56E+07	1.51E+07	7.10E+02	0.005	3.53E+02	49.72
23-00945-0157	Pool	2019-11-26/2019-12-20	Blood-fed	Central	<i>Cx. quinquefasciatus</i>	258	347	2.22E+07	1.58E+07	5.50E+04	0.348	2.72E+04	49.43
23-00945-0158	Pool	2019-11-26/2019-12-19	Blood-fed	Central	<i>Cx. sitiens</i>	67	447	3.67E+06	3.08E+06	1.33E+04	0.431	6.21E+03	46.78
23-00945-0160	Pool	2020-09-21/2020-10-09	Blood-fed	Morobe	<i>Cx. annulirostris</i>	10	475	1.69E+07	1.65E+07	1.35E+05	0.822	6.69E+04	49.41
23-00945-0161	Pool	2020-09-24/2020-10-16	Blood-fed	Morobe	<i>Cx. gelidus</i>	344	630	1.80E+07	1.74E+07	5.29E+04	0.304	1.83E+04	34.61
23-00945-0162	Pool	2020-09-24/2020-10-16	Blood-fed	Morobe	<i>Cx. quinquefasciatus</i>	189	388	1.39E+07	1.27E+07	1.92E+04	0.152	9.72E+03	50.48
23-00945-0163	Pool	2020-10-03	Blood-fed	Morobe	<i>Cx. sitiens</i>	8	486	1.63E+07	1.58E+07	2.16E+05	1.370	1.08E+05	50.01
23-00945-0164	Pool	2021-07-22/2021-08-17	Blood-fed	Western	<i>Cx. annulirostris</i>	224	691	1.50E+07	1.45E+07	1.43E+05	0.981	7.15E+04	50.06
23-00945-0165	Pool	2021-07-21/2021-08-15	Blood-fed	Western	<i>Cx. gelidus</i>	78	415	2.66E+07	2.51E+07	5.74E+04	0.228	7.82E+03	13.63
23-00945-0166	Pool	2021-07-20/2021-08-19	Blood-fed	Western	<i>Cx. pullus</i>	49	563	1.70E+07	1.66E+07	1.32E+05	0.796	6.50E+04	49.28
23-00945-0167	Pool	2021-07-20/2021-08-20	Blood-fed	Western	<i>Cx. quinquefasciatus</i>	85	520	2.23E+07	2.17E+07	1.92E+05	0.886	9.51E+04	49.53
23-00945-0168	Pool	2021-08-07	Blood-fed	Western	<i>Cx. sitiens</i>	2	505	1.92E+07	1.87E+07	4.22E+03	0.023	2.06E+03	48.86
											Variance		216.081
											SD	3.006	14.700

Supplementary Table 1c: Alpha diversity metrics of insect-specific virus communities according to province, mosquito species, and feeding status.

Variable	Category	n	Shannon (mean $\pm$ SD)	p-value (Shannon)	Simpson (mean $\pm$ SD)	p-value (Simpson)	Chao1 (mean $\pm$ SD)	p-value (Chao1)
Province	Central	17	0.858 $\pm$ 0.540	0.3860	0.476 $\pm$ 0.235	0.166	9.118 $\pm$ 8.609	0.1980
	East Sepik	2	1.447 $\pm$ 0.190		0.655 $\pm$ 0.005		26.000 $\pm$ 14.142	
	Madang	26	1.123 $\pm$ 0.554		0.568 $\pm$ 0.220		14.577 $\pm$ 13.085	
	Morobe	21	0.992 $\pm$ 0.695		0.448 $\pm$ 0.292		14.810 $\pm$ 10.685	
	Western	20	1.417 $\pm$ 0.696		0.610 $\pm$ 0.225		17.200 $\pm$ 14.137	
Mosquito species	<i>Cx. annulirostris</i>	24	1.077 $\pm$ 0.692	0.4580	0.504 $\pm$ 0.269	0.727	13.167 $\pm$ 12.727	0.9100
	<i>Cx. gelidus</i>	18	1.136 $\pm$ 0.565		0.533 $\pm$ 0.220		13.167 $\pm$ 10.656	
	<i>Cx. pullus</i>	3	1.073 $\pm$ 0.621		0.523 $\pm$ 0.176		16.667 $\pm$ 15.177	
	<i>Cx. quinquefasciatus</i>	32	1.163 $\pm$ 0.644		0.580 $\pm$ 0.242		16.125 $\pm$ 13.045	
	<i>Cx. sitiens</i>	9	1.014 $\pm$ 0.745		0.444 $\pm$ 0.280		13.556 $\pm$ 11.609	
Feeding status	Blood-fed	63	1.058 $\pm$ 0.651	0.2990	0.522 $\pm$ 0.256	0.565	12.222 $\pm$ 12.474	0.0003*
	Unfed	23	1.270 $\pm$ 0.589		0.561 $\pm$ 0.219		20.478 $\pm$ 9.184	

Mean $\pm$ standard deviation values are shown for Shannon, Simpson, and Chao1 diversity indices. P-values were calculated using Kruskal–Wallis tests. * $p < 0.05$ indicates a statistically significant difference.

Supplementary Table 2a: *Partitiviridae* ISVs detected in the PNG samples. Putative Broome partiti-like virus 1 RdRP and capsid sequences.

Sample No	Feeding status	Province	Mosquito species	Mosquitoes in pool	Total reads for <i>Partitiviridae</i>	RdRp length (Reference: 1484 bp)	RdRp depth	RdRp best match	Capsid length (Reference: 1494 bp)	Capsid depth	Capsid best match*
23-00945-0005	UF	Central	<i>Cx. sitiens</i>	145	2,222	1,463	119	Broome partiti-like virus 1 (100% ID; 99.2% cov)	1,224	128	Aedes partiti-like virus 1 (31% ID; 71% cov)
23-00945-0008	UF	East Sepik	<i>Cx. annulirostris</i>	190	46,634	1,468	3,131	Broome partiti-like virus 1 (84% ID; 98.9% cov)	1,223	2,151	Aedes partiti-like virus 1 (31% ID; 71% cov)
23-00945-0011	UF	Madang	<i>Cx. annulirostris</i>	73	712,382	1,464	44,384	Broome partiti-like virus 1 (86% ID; 100% cov)	1,367	31,504	Aedes partiti-like virus 1 (31% ID; 49% cov)
23-00945-0013	UF	Madang	<i>Cx. quinquefasciatus</i>	481	409,574	1,489	28,438	Broome partiti-like virus 1 (100% ID; 100% cov)	1,267	16,891	Aedes partiti-like virus 1 (32% ID; 20% cov)
23-00945-0021	UF	Morobe	<i>Cx. annulirostris</i>	59	244,646	1,486	15,900	Broome partiti-like virus 1 (100% ID; 100% cov)	1,239	10,783	Aedes partiti-like virus 1 (31% ID; 40% cov)
23-00945-0039	UF	Morobe	<i>Cx. quinquefasciatus</i>	270	14,466	1,484	955	Broome partiti-like virus 1 (100% ID; 99.9% cov)	1,221	669	Aedes partiti-like virus 1 (31% ID; 71% cov)
23-00945-0040	UF	Morobe	<i>Cx. sitiens</i>	21	51,132	1,487	3,587	Broome partiti-like virus 1 (100% ID; 99.9% cov)	1,231	2,167	Aedes partiti-like virus 1 (31% ID; 72% cov)
23-00945-0041	UF	Western	<i>Cx. annulirostris</i>	476	6,772	1,475	217	Broome partiti-like virus 1 (95.9% ID; 99.4% cov)	1,089	137	Aedes partiti-like virus 1 (31% ID; 73% cov)
23-00945-0051	UF	Western	<i>Cx. quinquefasciatus</i>	439	1,808	1,463	124	Broome partiti-like virus 1 (100% ID; 98.9% cov)	1,223	82	Aedes partiti-like virus 1 (31% ID; 71% cov)
23-00945-0052	UF	Western	<i>Cx. sitiens</i>	7	10,424	1,486	755	Broome partiti-like virus 1 (100% ID; 99.9% cov)	1,226	424	Aedes partiti-like virus 1 (30% ID; 70% cov)
23-00945-0071	BF	Madang	<i>Cx. annulirostris</i>	1	1,844	1,486	86	Broome partiti-like virus 1 (98% ID; 99.9% cov)	1,198	116	Aedes partiti-like virus 1 (31% ID; 72% cov)
23-00945-0139	BF	Morobe	<i>Cx. sitiens</i>	17	17,004	1,490	721	Broome partiti-like virus 1 (100% ID; 100% cov)	1,220	1,118	Aedes partiti-like virus 1 (31% ID; 71% cov)
23-00945-0140	BF	Western	<i>Cx. annulirostris</i>	449	2,222	1,468	132	Broome partiti-like virus 1 (69% ID; 99.9% cov)	1,290	104	Aedes partiti-like virus 1 (31% ID; 71% cov)
23-00945-0147	BF	Madang	<i>Cx. annulirostris</i>	99	350,476	1,506	21,504	Broome partiti-like virus 1 (100% ID; 100% cov)	1,231	17,299	Aedes partiti-like virus 1 (31% ID; 53% cov)
23-00945-0151	BF	Madang	<i>Cx. quinquefasciatus</i>	493	413	1,462	25	Broome partiti-like virus 1 (100% ID; 98.5% cov)	1,194	19	Aedes partiti-like virus 1 (31% ID; 72% cov)
23-00945-0164	BF	Western	<i>Cx. annulirostris</i>	224	40,666	1,492	2,449	Broome partiti-like virus 1 (100% ID; 100% cov)	1,225	1,654	Aedes partiti-like virus 1 (31% ID; 70% cov)

Abbreviations: BF, Blood fed; UF, Unfed; Cx, *Culex*; ID, identity; cov, coverage.

The % identity and coverage of the consensus sequences for the respective reference genome are included.

Reference virus RdRP/capsid nucleotide lengths are provided for comparative purposes with PNG-derived sequences and represent approximate values derived from the closest BLAST-matched GenBank genomes.

Broome partiti-like virus 1 RdRP, 1,484 bp; Aedes partiti-like virus 1 capsid, 1,494 bp.

*No capsid reference is available for the Broome virus. ID is assumed based on co-detection of the RdRP and capsid.

Supplementary Table 2b: Other *Partitiviridae* ISVs detected in the PNG samples.

Sample No	Feeding status	Province	Mosquito species	Mosquitoes in pool	Total reads for <i>Partitiviridae</i>	Species from NCBI with the highest BLAST match	Largest contig	RdRp			Capsid			Hypothetical Protein		
								% ID	% Coverage	Reads	% ID	% Coverage	Reads	% ID	% Coverage	Reads
23-00945-0018	UF	Madang	<i>Cx. quinquefasciatus</i>	362	5,018	Chaq-like virus	1,426							93.8	99.8	1,145
						Verdadero virus	1,687	99	100	739	99	100	3,109			
23-00945-0021	UF	Morobe	<i>Cx. annulirostris</i>	59	244,646	Wyndham partiti-like virus 1	878	85	91.7	207						
23-00945-0035	UF	Morobe	<i>Cx. gelidus</i>	442	18,316	Osugoroshi virus HP-LC597875.1	1,369 (DN90455)							73.7	99.7	15,322
						Osugoroshi virus HP-LC597877.1	1,313 (DN3043)							71.6	98	
						Osugoroshi virus HP-LC597882.1	1,293 (DN3)							63.8	100	
						Osugoroshi virus HP-LC597884.1	1,280 (DN87122)							76	98.8	
						Osugoroshi virus HP-LC597890.1	1,307 (DN304)							67	100	
						Osugoroshi virus HP-LC597891.1	1,262 (DN3896)							73.4	99	
						Osugoroshi virus HP-LC597894.1	1,233 (DN113037)							60.9	94.2	
						Osugoroshi virus HP-LC597895.1	1,258 (DN304)							76.1	98.6	
						Osugoroshi virus HP-LC597896.1	1,289 (DN294)							58.6	98.7	
						Partitiviridae sp. PPYX/3609	1,294	47	92	2,743						
23-00945-0037	UF	Morobe	<i>Cx. quinquefasciatus</i>	472	4,672	Sonnbo virus	1,732	99.7	99.7	1,311						
						Zeya Brook partiti-like virus 1	1,638				50.8	97.8	3,164			
23-00945-0041	UF	Western	<i>Cx. annulirostris</i>	476	6,772	Inari deltapartitivirus	1,497	80	99.4	3,837						
23-00945-0129	BF	Madang	<i>Cx. annulirostris</i>	27	79	Wyndham partiti-like virus 1	579	94.3	32.4	16						
23-00945-0140	BF	Western	<i>Cx. annulirostris</i>	449	2,222	Verdadero virus	432	93.9	32.9							
23-00945-0154	BF	Madang	<i>Cx. quinquefasciatus</i>	130	26	Verdadero virus	661				77.5	49.9	26			
23-00945-0160	BF	Morobe	<i>Cx. annulirostris</i>	10	326	Wyndham partiti-like virus 1	1,794	92.4	100	179						
						Wyndham partiti-like virus 3	1,624	66.2	79.9	64						
23-00945-0164	BF	Western	<i>Cx. annulirostris</i>	224	40,666	Atrato Partiti-like virus 1	1,614				62	97	2,696			
							1,498 (DN1119)							(HP1)	100	685
							1,591 (DN183)							(HP2)	100	787
														54.5		

The % identity and coverage of the consensus sequences for the respective reference genome are included.

Abbreviations: BF, Blood fed; UF, Unfed; Cx, *Culex*; ID, identity; HP, hypothetical protein.

Reference virus RdRP/capsid/HP nucleotide lengths are provided for comparative purposes with PNG-derived sequences and represent approximate values derived from the closest BLAST-matched GenBank genomes. Chaq-like virus: HP, 1,415 bp; Atrato Partiti-like virus 1: RdRP, 1,610 bp, capsid, 1,564 bp, HP, 1,414 bp; Inari deltapartitivirus: RdRP, 1,726 bp; Osugoroshi virus: RdRP, 1,497 bp, HP, 1,266 bp; Partitiviridae sp. PPYX/3609: RdRP, 1,371 bp; Sonnbo virus: RdRP, 1,737 bp; Verdadero virus: RdRP, 1,628 bp, capsid, 1,497 bp; Wyndham partiti-like virus 1: RdRP, 1,794 bp; Wyndham partiti-like virus 3: RdRP, 1,622 bp; Zeya Brook partiti-like virus 1: capsid, 1,597 bp.

Supplementary Table 3: *Birnaviridae* ISVs detected in the PNG samples.

Sample No	Feeding status	Province	Mosquito species	Mosquitoes in pool	Total reads for <i>Birnaviridae</i>	Species from NCBI with the highest BLAST match	Largest contig	RdRp			Polyprotein		
								% ID	% Coverage	Reads	% ID	% Coverage	Reads
23-00945-0002	UF	Central	<i>Cx. gelidus</i>	198	760	Cambodia Culex birnavirus	353	98.9	26	202	98.8	38.2	556
23-00945-0004	UF	Central	<i>Cx. quinquefasciatus</i>	164	694	Cambodia Culex birnavirus	3,047	98.6	95.2	378	98.4	93.7	316
23-00945-0009	UF	East Sepik	<i>Cx. quinquefasciatus</i>	439	32	Cambodia Culex birnavirus	149	0	0	0	99.8	4.3	32
23-00945-0011	UF	Madang	<i>Cx. annulirostris</i>	73	6,170	Cambodia Culex birnavirus	3,429	98.8	97.4	3,633	98.8	98.9	2,528
23-00945-0013	UF	Madang	<i>Cx. quinquefasciatus</i>	481	23,956	Cambodia Culex birnavirus	3,416	93.4	97.5	14,254	95.2	98.5	10,576
23-00945-0018	UF	Madang	<i>Cx. quinquefasciatus</i>	362	452,122	Cambodia Culex birnavirus	3,468	93.7	99.3	242,644	95.4	99.6	208,351
23-00945-0024	UF	Morobe	<i>Cx. gelidus</i>	471	13,522	Cambodia Culex birnavirus	3,444	94.3	97.9	6,571	95.1	99.3	6,904
23-00945-0035	UF	Morobe	<i>Cx. gelidus</i>	442	314,598	Cambodia Culex birnavirus	3,221	93.7	100	178,729	95.6	99.7	134,269
23-00945-0037	UF	Morobe	<i>Cx. quinquefasciatus</i>	472	193,954	Cambodia Culex birnavirus	3,435	95.7	99.3	123,611	92.8	99.1	69,257
23-00945-0039	UF	Morobe	<i>Cx. quinquefasciatus</i>	270	112,716	Cambodia Culex birnavirus	3,488	93.6	98.9	76,831	95.9	99.6	35,018
23-00945-0050	UF	Western	<i>Cx. pullus</i>	109	158	Cambodia Culex birnavirus	258	93.6	36.1	70	96	38.9	88
23-00945-0051	UF	Western	<i>Cx. quinquefasciatus</i>	439	13,996	Cambodia Culex birnavirus	3,434	94.5	98.1	8,296	95.3	99.3	5,629
23-00945-0052	UF	Western	<i>Cx. sitiens</i>	7	11,192	Cambodia Culex birnavirus	3,380	94.1	97.6	7,091	95	97.5	4,048
23-00945-0127	BF	Madang	<i>Cx. quinquefasciatus</i>	499	9,798	Cambodia Culex birnavirus	3,444	98.9	98.2	6,108	98.8	99.3	3,658
23-00945-0128	BF	Madang	<i>Cx. quinquefasciatus</i>	52	4,418	Cambodia Culex birnavirus	3,329	94.7	97.8	2,769	95.2	96	1,619
23-00945-0130	BF	Central	<i>Cx. annulirostris</i>	5	20	Cambodia Culex birnavirus	437	97.3	51	18	96.8	7.6	20
23-00945-0134	BF	Morobe	<i>Cx. gelidus</i>	495	4,465	Cambodia Culex birnavirus	3,385	98.5	96.6	2,591	98.9	97.6	1,909
23-00945-0135	BF	Morobe	<i>Cx. gelidus</i>	498	272	Cambodia Culex birnavirus	783	97.2	92	173	97.1	80.1	94
23-00945-0136	BF	Morobe	<i>Cx. gelidus</i>	500	434	Cambodia Culex birnavirus	2,073	97.1	95.9	285	97.3	91	136
23-00945-0137	BF	Morobe	<i>Cx. gelidus</i>	244	7,046	Cambodia Culex birnavirus	3,427	98.8	98.9	4,148	99	98.8	2,832
23-00945-0138	BF	Morobe	<i>Cx. quinquefasciatus</i>	272	64	Cambodia Culex birnavirus	519	98.5	59.5	42	95.5	28.2	22
23-00945-0146	BF	Madang	<i>Cx. quinquefasciatus</i>	5	20	Cambodia Culex birnavirus	267	98.1	12	4	97.5	17.9	16
23-00945-0147	BF	Madang	<i>Cx. annulirostris</i>	99	374	Cambodia Culex birnavirus	2,479	93.2	95.1	256	98	93.6	120
23-00945-0148	BF	Madang	<i>Cx. gelidus</i>	2	18	Cambodia Culex birnavirus	471	96.5	16.5	6	95.9	31.9	12
23-00945-0149	BF	Madang	<i>Cx. quinquefasciatus</i>	496	2,226	Cambodia Culex birnavirus	1,375	99.1	96.5	1,597	99.1	88.5	227
23-00945-0150	BF	Madang	<i>Cx. quinquefasciatus</i>	498	15,854	ambodia Culex birnavirus	3,433	99.1	97.5	11,178	99.1	99	4,629
23-00945-0151	BF	Madang	<i>Cx. quinquefasciatus</i>	493	53,192	Cambodia Culex birnavirus	3,441	99	99.5	35,314	98.9	99.8	17,812
23-00945-0152	BF	Madang	<i>Cx. quinquefasciatus</i>	499	1,328	Cambodia Culex birnavirus	1,139	98.9	90.5	890	99.2	62	432
23-00945-0153	BF	Madang	<i>Cx. quinquefasciatus</i>	495	132	Cambodia Culex birnavirus	468	98	9.9	106	98.9	41.3	26
23-00945-0154	BF	Madang	<i>Cx. quinquefasciatus</i>	130	1,522	Cambodia Culex birnavirus	2,181	99.1	93.7	978	99.2	77	544
23-00945-0161	BF	Morobe	<i>Cx. gelidus</i>	344	13,208	Cambodia Culex birnavirus	3,432	98.8	98.2	8,421	99	99	4,688
23-00945-0162	BF	Morobe	<i>Cx. quinquefasciatus</i>	189	5,642	Cambodia Culex birnavirus	3,386	99	98	4,390	99.1	97.6	1,234

The % identity and coverage of the consensus sequences for the respective reference genome are included.

Abbreviations: BF, Blood fed; UF, Unfed; Cx, *Culex*; ID, identity.

Reference virus RdRp and polyprotein nucleotide lengths are provided for comparative purposes with PNG-derived sequences and represent approximate values derived from the closest BLAST-matched GenBank genomes.

Cambodia Culex birnavirus reference sequence RdRP gene length in nucleotides – 3,233.

Supplementary Table 4a: *Rhabdoviridae* ISVs detected in the PNG samples.

Sample No	Feeding status	Province	Mosquito species	Mosquitoes in pool	Total reads for <i>Rhabdoviridae</i>	Species from NCBI with the highest BLAST match	Longest contig	Total reads	Whole genome	
									% ID	% Coverage
23-00945-0001	UF	Central	<i>Cx. annulirostris</i>	135	2,860	Merida virus	843	2,860	98.8	87.9
23-00945-0002	UF	Central	<i>Cx. gelidus</i>	198	117,520	Merida virus	6,450	117,445	98.7	100
23-00945-0004	UF	Central	<i>Cx. quinquefasciatus</i>	164	4,010	Merida virus	6,453	4,010	98.7	100
23-00945-0005	UF	Central	<i>Cx. sitiens</i>	145	895	Merida virus	1,063	719	98	96.3
						Guadeloupe Culex rhabdovirus	675	128	99.2	38.5
23-00945-0009	UF	East Sepik	<i>Cx. quinquefasciatus</i>	439	12,519	Merida virus	807	12,519	98.6	92.9
23-00945-0018	UF	Madang	<i>Cx. quinquefasciatus</i>	362	2,226	Merida virus	2,601	2,226	94.5	100
23-00945-0041	UF	Western	<i>Cx. annulirostris</i>	476	15,625	Merida virus	2,699	3,675	95.4	48.4
						Guadeloupe Culex rhabdovirus	4,457	11,950	95.7	100
23-00945-0050	UF	Western	<i>Cx. pullus</i>	109	29,190	Guadeloupe Culex rhabdovirus	6,870	29,190	95	100
23-00945-0051	UF	Western	<i>Cx. quinquefasciatus</i>	439	57,777	Merida virus	4,988	31,738	95.3	100
						Guadeloupe Culex rhabdovirus	6,870	26,039	95.2	100
23-00945-0052	UF	Western	<i>Cx. sitiens</i>	7	54,321	Merida virus	6,195	29,727	95	100
						Guadeloupe Culex rhabdovirus	5,227	24,594	94.8	100
23-00945-0064	BF	Central	<i>Cx. quinquefasciatus</i>	1	198,159	Merida virus	6,195	198,159	96	100
23-00945-0065	BF	Central	<i>Cx. quinquefasciatus</i>	1	112,198	Merida virus	6,453	112,198	98.8	100
23-00945-0113	BF	Western	<i>Cx. quinquefasciatus</i>	1	25,967	Guadeloupe Culex rhabdovirus	3,751	25,967	95.7	100
23-00945-0115	BF	Western	<i>Cx. quinquefasciatus</i>	1	120,013	Merida virus	6,408	99,806	99	100
						Grenada mosquito rhabdovirus 1	6,870	20,207	99.5	100
23-00945-0134	BF	Morobe	<i>Cx. gelidus</i>	495	45	Bat sobemo virus	372	12	96.4	37.8
23-00945-0140	BF	Western	<i>Cx. annulirostris</i>	449	178	Merida virus	440	135	98	46
						Guadeloupe Culex rhabdovirus	468	43	98.4	31.4
23-00945-0143	BF	Western	<i>Cx. quinquefasciatus</i>	11	583,113	Merida virus	6,453	106,063	98.7	100
						Guadeloupe Culex rhabdovirus	2,903	477,050	98.8	100
23-00945-0150	BF	Madang	<i>Cx. quinquefasciatus</i>	498	62	Merida virus	447	62	98	23.2
23-00945-0151	BF	Madang	<i>Cx. quinquefasciatus</i>	493	91	Merida virus	470	91	97.5	57.5
23-00945-0157	BF	Central	<i>Cx. quinquefasciatus</i>	258	15,026	Merida virus	3,989	14,620	98.8	100
						Guadeloupe Culex rhabdovirus	463	406	99.2	69.6
23-00945-0164	BF	Western	<i>Cx. annulirostris</i>	224	3,651	Merida virus	1,361	2,690	98.6	98.3
						Guadeloupe Culex rhabdovirus	1,152	961	98.8	85
23-00945-0167	BF	Western	<i>Cx. quinquefasciatus</i>	85	69,119	Merida virus	6,453	45,476	98.7	100
						Guadeloupe Culex rhabdovirus	6,870	23,643	98.4	100

The % identity and the coverage of the consensus sequences for the respective reference genome are included.

Abbreviations: BF, Blood fed; UF, Unfed; Cx, *Culex*; ID, identity.

Reference virus whole-genome nucleotide lengths are provided for comparative purposes with PNG-derived sequences and represent approximate values based on the closest BLAST-matched GenBank genomes.

Reference sequence lengths in nucleotides: Grenada mosquito rhabdovirus 1, 14,420; Guadeloupe Culex rhabdovirus, 14,362; Merida virus, 11,798.

Supplementary Table 4b: *Culex tritaeniorhynchus* rhabdovirus detected in the PNG samples.

Sample No	Feeding status	Province	Mosquito species	Mosquitoes in pool	Total reads for <i>Rhabdoviridae</i>	Species from NCBI with the highest BLAST match	Longest contig	Total reads	Whole genome		N gene		
									% ID	% Coverage	% ID	% Coverage	Reads
23-00945-0011	UF	Madang	<i>Cx. annulirostris</i>	73	48	<i>Culex tritaeniorhynchus</i> rhabdovirus	621	48	74.6	7.3	74.6	57.7	19
23-00945-0021	UF	Morobe	<i>Cx. annulirostris</i>	59	68	<i>Culex tritaeniorhynchus</i> rhabdovirus	1407	68	68.3	13.8	70.6	98.7	68
23-00945-0053	BF	Central	<i>Cx. annulirostris</i>	1	106	<i>Culex tritaeniorhynchus</i> rhabdovirus	624	106	64.1	13.6	71	87.5	101
23-00945-0089	BF	Morobe	<i>Cx. annulirostris</i>	1	54	<i>Culex tritaeniorhynchus</i> rhabdovirus	550	54	74.2	7.7	74.2	60.7	45
23-00945-0122	BF	Madang	<i>Cx. annulirostris</i>	1	212	<i>Culex tritaeniorhynchus</i> rhabdovirus	329	212	75.1	5.7	75.1	44.7	212
23-00945-0129	BF	Madang	<i>Cx. annulirostris</i>	27	99	<i>Culex tritaeniorhynchus</i> rhabdovirus	643	56	70	10.9	70	84.4	54
23-00945-0130	BF	Central	<i>Cx. annulirostris</i>	5	56	<i>Culex tritaeniorhynchus</i> rhabdovirus	1291	56	69.8	11.4	70.8	88.4	55
23-00945-0145	BF	Madang	<i>Cx. annulirostris</i>	42	198	<i>Culex tritaeniorhynchus</i> rhabdovirus	2093	135	60.1	17.9	70.07	100	141
23-00945-0147	BF	Madang	<i>Cx. annulirostris</i>	99	22	<i>Culex tritaeniorhynchus</i> rhabdovirus	668	22	76.3	5.9	76.3	46.6	20

The % identity and the coverage of the consensus sequences for the respective reference genome for the nucleoprotein gene (N gene) are included.

Abbreviations: BF, Blood fed; UF, Unfed; Cx, *Culex*; ID, identity; N gene, nucleoprotein gene.

Reference virus N gene nucleotide lengths are provided for comparative purposes with PNG-derived sequences and represent approximate values derived from the closest BLAST-matched GenBank genomes.

Reference sequence lengths in nucleotides: *Culex tritaeniorhynchus* rhabdovirus, 1,500.

Supplementary Table 5: *Iflaviridae* ISVs detected in the PNG samples.

Sample No	Feeding status	Province	Mosquito species	Mosquitoes in pool	Total reads for <i>Iflaviridae</i>	Species from NCBI with the highest BLAST match	Longest contig	RdRp/Polypeptide*		
								% ID	% Coverage	Reads
23-00945-0008	UF	East Sepik	<i>Cx. annulirostris</i>	190	4,484	Isahaya Culex iflavirus	549	97.7	78.2	4,484
23-00945-0009	UF	East Sepik	<i>Cx. quinquefasciatus</i>	439	1,096	Isahaya Culex iflavirus	307	98.5	17.9	526
23-00945-0011	UF	Madang	<i>Cx. annulirostris</i>	73	153	Yongsan iflavirus 1	509	98.9	12.6	570
						Yongsan iflavirus 1	486	97.5	46.1	124
23-00945-0018	UF	Madang	<i>Cx. quinquefasciatus</i>	362	14,990	Culex Iflavi-like virus 4	225	97.6	16	29
						Culex Iflavi-like virus 4	9,180	96.4	100	7,362
23-00945-0021	UF	Morobe	<i>Cx. annulirostris</i>	59	354	Yongsan iflavirus 1	8,274	94	100	7,425
						Isahaya Culex iflavirus	989	96.4	85.9	354
23-00945-0037	UF	Morobe	<i>Cx. quinquefasciatus</i>	472	342,186	Culex Iflavi-like virus 4	8,857	95	100	337,969
						Aedes Ifla-like virus	552	93.1	25.1	2,579
23-00945-0039	UF	Morobe	<i>Cx. quinquefasciatus</i>	270	329,214	Culex Iflavi-like virus 4	6,082	96.5	100	326,288
						Isahaya Culex iflavirus	362	94	78.7	336
23-00945-0040	UF	Morobe	<i>Cx. sitiens</i>	21	4,508	Isahaya Culex iflavirus	449	95.1	90.6	4,508
23-00945-0041	UF	Western	<i>Cx. annulirostris</i>	476	806	Isahaya Culex iflavirus	297	96.6	50.9	806
23-00945-0050	UF	Western	<i>Cx. pullus</i>	109	8,252	Yongsan iflavirus 1	2,020	94.1	100	7,193
						Isahaya Culex iflavirus	428	94.2	70.7	966
23-00945-0051	UF	Western	<i>Cx. quinquefasciatus</i>	439	9,644	Yongsan iflavirus 1	3,622	94.7	100	8,746
						Culex Iflavi-like virus 4	844	94.8	8.3	827
23-00945-0052	UF	Western	<i>Cx. sitiens</i>	7	5,670	Yongsan iflavirus 1	2,528	94.8	75.5	4,838
						Culex Iflavi-like virus 4	844	93.4	75.5	768
23-00945-0088	BF	Morobe	<i>Cx. annulirostris</i>	1	20,206	Isahaya Culex iflavirus	8,607	98.8	100	20,206
23-00945-0127	BF	Madang	<i>Cx. quinquefasciatus</i>	499	16,768	Yongsan iflavirus 1	8,274	98.7	100	16,234
						Culex Iflavi-like virus 4	2,044	97.9	85	441
23-00945-0129	BF	Madang	<i>Cx. annulirostris</i>	27	266	Isahaya Culex iflavirus	863	97.1	64.4	248
23-00945-0134	BF	Morobe	<i>Cx. gelidus</i>	495	302	Culex Iflavi-like virus 4	734	97.8	75.5	298
23-00945-0137	BF	Morobe	<i>Cx. gelidus</i>	244	42	Isahaya Culex iflavirus	501	89.5	37.1	42
23-00945-0138	BF	Morobe	<i>Cx. quinquefasciatus</i>	272	4,372	Culex Iflavi-like virus 4	9,399	98.1	100	4,359
23-00945-0139	BF	Morobe	<i>Cx. sitiens</i>	17	3,330	Isahaya Culex iflavirus	7,241	97.3	100	3,308
23-00945-0142	BF	Western	<i>Cx. pullus</i>	1	868	Isahaya Culex iflavirus	1,429	97.8	96.2	861
23-00945-0147	BF	Madang	<i>Cx. annulirostris</i>	99	10,652	Culex Iflavi-like virus 4	9,399	99.1	100	10,641
23-00945-0149	BF	Madang	<i>Cx. quinquefasciatus</i>	496	55	Culex Iflavi-like virus 4	250	96.9	41.4	55
23-00945-0150	BF	Madang	<i>Cx. quinquefasciatus</i>	498	2,740	Yongsan iflavirus 1	1,247	98.7	98.8	2,415
						Culex Iflavi-like virus 4	883	98.7	77	318
23-00945-0151	BF	Madang	<i>Cx. quinquefasciatus</i>	493	11,506	Yongsan iflavirus 1	8,274	98.4	100	7,183
						Culex Iflavi-like virus 4	9,399	98.8	100	4,271
23-00945-0152	BF	Madang	<i>Cx. quinquefasciatus</i>	499	218	Culex Iflavi-like virus 4	348	98.9	45.5	218
23-00945-0153	BF	Madang	<i>Cx. quinquefasciatus</i>	495	74	Culex Iflavi-like virus 4	287	98.6	16.3	74
23-00945-0154	BF	Madang	<i>Cx. quinquefasciatus</i>	130	550	Culex Iflavi-like virus 4	621	98.2	61	325
						Yongsan iflavirus 1	471	98.6	47.7	224
23-00945-0157	BF	Central	<i>Cx. quinquefasciatus</i>	258	2,472	Culex Iflavi-like virus 4	2,361	99.2	99.9	2,469
23-00945-0162	BF	Morobe	<i>Cx. quinquefasciatus</i>	189	3,622	Culex Iflavi-like virus 4	2,744	98.7	100	3,617
23-00945-0164	BF	Western	<i>Cx. annulirostris</i>	224	776	Isahaya Culex iflavirus	804	91.7	98.8	576
						Pityohyphantes rubrofasciatus iflavirus	553	91.6	47.2	66
23-00945-0165	BF	Western	<i>Cx. gelidus</i>	78	750	Isahaya Culex iflavirus	642	96	84.6	584
23-00945-0167	BF	Western	<i>Cx. quinquefasciatus</i>	85	36	Isahaya Culex iflavirus	345	86.7	36.9	32

The % identity and the coverage of the consensus sequences for the respective reference genome are included.

Abbreviations: BF, Blood fed; UF, Unfed; Cx, *Culex*; ID, identity.

Reference virus RdRp/polypeptide nucleotide lengths are provided for comparative purposes with PNG-derived sequences and represent approximate values derived from the closest BLAST-matched GenBank genomes.

Reference sequence lengths in nucleotides: Aedes Ifla-like virus, 9,666; Culex Iflavi-like virus 4, 10,319; Isahaya Culex iflavirus, 9,491; Pityohyphantes rubrofasciatus iflavirus, 9,834; Yongsan iflavirus 1, 8,971.

*The RdRp/polypeptide region annotated in this table corresponds to the polypeptide of *Iflaviridae* members; however, for Isahaya Culex iflavirus, the polypeptide is annotated as "RdRp" in the NCBI database (<https://www.ncbi.nlm.nih.gov/nucleotide/?term=Isahaya+Culex+iflavirus;Faizah+et+al.+2020>).

Supplementary Table 6: Top ISVs unassigned to a taxonomic virus family.

Unclassified virus	Read number	Relative abundance (%) among unclassified ISVs
Hubei virga-like virus 2	2,059,852	53.7
Broome luteo-like virus 1	382,273	10
Culex-associated Luteo-like virus	163,136	4.2
Hubei partiti-like virus 22	126,176	3.3
Old Port virus	109,643	2.9
Culex pseudovishnui negev-like virus	102,035	2.7
Culex mononega-like virus 1	86,821	2.3
Hubei mosquito virus 4	85,021	2.2
Yongsan picorna-like virus 3	49,802	1.3
Atrato Retro-like virus	31,582	0.8
Others	642,405	16.7
Total ISVs unassigned to a taxonomic virus family	3,838,746	100

Supplementary Table 7: Hubei virga-like virus 2 detected in the PNG samples.

Sample No	Feeding status	Province	Mosquito species	Mosquitoes in pool	Total reads for Hubei virga-like virus 2	Species from NCBI with the highest BLAST match	Longest contig	Whole genome	
								% ID	% Coverage
23-00945-0001	UF	Central	<i>Cx. annulirostris</i>	135	153,000	Hubei virga-like virus 2	911	84.7	32
23-00945-0002	UF	Central	<i>Cx. gelidus</i>	198	7,110	Hubei virga-like virus 2	547	98.3	78.8
23-00945-0004	UF	Central	<i>Cx. quinquefasciatus</i>	164	1,263	Hubei virga-like virus 2	2,122	98.7	90
23-00945-0005	UF	Central	<i>Cx. sitiens</i>	145	144	Hubei virga-like virus 2	406	98.2	58.4
23-00945-0011	UF	Madang	<i>Cx. annulirostris</i>	73	410,247	Hubei virga-like virus 2	1,849	98.8	97.3
23-00945-0013	UF	Madang	<i>Cx. quinquefasciatus</i>	481	41	Hubei virga-like virus 2	255	94.6	44.6
23-00945-0018	UF	Madang	<i>Cx. quinquefasciatus</i>	362	1,010,983	Hubei virga-like virus 2	2,571	95.2	99.8
23-00945-0020	UF	Madang	<i>Cx. quinquefasciatus</i>	40	27	Hubei virga-like virus 2	327	95.2	27.2
23-00945-0037	UF	Morobe	<i>Cx. quinquefasciatus</i>	472	386,748	Hubei virga-like virus 2	5,895	98.5	100
23-00945-0051	UF	Western	<i>Cx. quinquefasciatus</i>	439	672	Hubei virga-like virus 2	617	97.2	86.1
23-00945-0052	UF	Western	<i>Cx. sitiens</i>	7	458	Hubei virga-like virus 2	383	97.4	79.6
23-00945-0064	BF	Central	<i>Cx. quinquefasciatus</i>	1	9,469	Hubei virga-like virus 2	9,948	98	92
23-00945-0068	BF	Madang	<i>Cx. annulirostris</i>	1	19,047	Hubei virga-like virus 2	9,948	99	94.7
23-00945-0127	BF	Madang	<i>Cx. quinquefasciatus</i>	499	34,743	Hubei virga-like virus 2	1,883	98.7	98.5
23-00945-0128	BF	Madang	<i>Cx. quinquefasciatus</i>	52	12,452	Hubei virga-like virus 2	914	97.5	91.7
23-00945-0134	BF	Morobe	<i>Cx. gelidus</i>	495	7	Hubei virga-like virus 2	185	91.7	5.8
23-00945-0138	BF	Morobe	<i>Cx. quinquefasciatus</i>	272	2,197	Hubei virga-like virus 2	814	98.4	53.9
23-00945-0147	BF	Madang	<i>Cx. annulirostris</i>	99	110	Hubei virga-like virus 2	545	97.9	58.4
23-00945-0149	BF	Madang	<i>Cx. quinquefasciatus</i>	496	54	Hubei virga-like virus 2	399	98.5	22
23-00945-0150	BF	Madang	<i>Cx. quinquefasciatus</i>	498	4,573	Hubei virga-like virus 2	816	98.4	82.4
23-00945-0151	BF	Madang	<i>Cx. quinquefasciatus</i>	493	920	Hubei virga-like virus 2	3,070	98.9	88.8
23-00945-0154	BF	Madang	<i>Cx. quinquefasciatus</i>	130	92	Hubei virga-like virus 2	525	98.7	29.1
23-00945-0157	BF	Central	<i>Cx. quinquefasciatus</i>	258	771	Hubei virga-like virus 2	1,049	99.1	79.2
23-00945-0161	BF	Morobe	<i>Cx. gelidus</i>	344	77	Hubei virga-like virus 2	765	98.4	35.5
23-00945-0162	BF	Morobe	<i>Cx. quinquefasciatus</i>	189	54	Hubei virga-like virus 2	531	99.3	25.4
23-00945-0167	BF	Western	<i>Cx. quinquefasciatus</i>	85	4,545	Hubei virga-like virus 2	5,088	99.1	92.2

The % identity and the coverage of the consensus sequences for the respective reference genome are included.

Abbreviations: BF, Blood fed; UF, Unfed; Cx, *Culex*; ID, identity.

Reference virus whole genome nucleotide lengths are provided for comparative purposes with PNG-derived sequences and represent approximate values derived from the closest BLAST-matched GenBank genomes.

Reference sequence lengths in nucleotides: Hubei virga-like virus 2, 10,650.

Supplementary Table 8: Broome luteo-like virus 1 detected in the PNG samples.

Sample No	Feeding status	Province	Mosquito species	Mosquitoes in pool	Total reads for Broome luteo-like virus 1	Species from NCBI with the highest BLAS match	Longest contig	Segment 1			Segment 2		
								% ID	% Coverage	Reads	% ID	% Coverage	Reads
23-00945-0001	UF	Central	<i>Cx. annulirostris</i>	135	662	Broome luteo-like virus 1	539	98.7	64.8	402	96.6	59.2	260
23-00945-0005	UF	Central	<i>Cx. sitiens</i>	145	74,588	Broome luteo-like virus 1	1,320	98.2	100	50,196	86	16.6	24,331
23-00945-0008	UF	East Sepik	<i>Cx. annulirostris</i>	190	122	Broome luteo-like virus 1	268	98.8	17.7	108	98.2	8.6	14
23-00945-0011	UF	Madang	<i>Cx. annulirostris</i>	73	1,548	Broome luteo-like virus 1	1,331	98.3	99.9	1,117	97.7	100	430
23-00945-0013	UF	Madang	<i>Cx. quinquefasciatus</i>	481	532	Broome luteo-like virus 1	267	92.9	84.2	279	95.6	73.2	249
23-00945-0019	UF	Madang	<i>Cx. annulirostris</i>	466	22,658	Broome luteo-like virus 1	1,123	93.8	99.9	14,946	94.6	100	7,594
23-00945-0021	UF	Morobe	<i>Cx. annulirostris</i>	59	40,900	Broome luteo-like virus 1	1,320	98.3	100	29,026	77.2	8.1	11,830
23-00945-0037	UF	Morobe	<i>Cx. quinquefasciatus</i>	472	2,404	Broome luteo-like virus 1	1,306	95.4	99.9	1,774	95.2	100	621
23-00945-0039	UF	Morobe	<i>Cx. quinquefasciatus</i>	270	276	Broome luteo-like virus 1	718	96	78.1	110	94.5	100	163
23-00945-0040	UF	Morobe	<i>Cx. sitiens</i>	21	7,152	Broome luteo-like virus 1	571	94.5	100	5,114	94.8	100	2,003
23-00945-0041	UF	Western	<i>Cx. annulirostris</i>	476	514	Broome luteo-like virus 1	279	94.4	55.8	384	94.6	66.1	124
23-00945-0050	UF	Western	<i>Cx. pullus</i>	109	2,916	Broome luteo-like virus 1	1,276	95.6	99.6	2,068	93.6	100	837
23-00945-0051	UF	Western	<i>Cx. quinquefasciatus</i>	439	214	Broome luteo-like virus 1	338	94.9	80.1	140	93.3	99.7	74
23-00945-0052	UF	Western	<i>Cx. sitiens</i>	7	2,186	Broome luteo-like virus 1	867	94.6	99.9	1,567	93.5	100	606
23-00945-0053	BF	Central	<i>Cx. annulirostris</i>	1	452	Broome luteo-like virus 1	717	96.1	81.4	319	94.5	88.3	132
23-00945-0057	BF	Central	<i>Cx. annulirostris</i>	1	796	Broome luteo-like virus 1	562	95.6	82.6	417	96.3	100	377
23-00945-0129	BF	Madang	<i>Cx. annulirostris</i>	27	436	Broome luteo-like virus 1	647	99.4	96.8	368	98.3	99.3	68
23-00945-0130	BF	Central	<i>Cx. annulirostris</i>	5	5,066	Broome luteo-like virus 1	1,320	98.7	100	3,254	62.5	9.7	1,590
23-00945-0133	BF	Central	<i>Cx. sitiens</i>	22	36,014	Broome luteo-like virus 1	1,334	98.5	99.9	27,479	95.9	3.2	8,457
23-00945-0134	BF	Morobe	<i>Cx. gelidus</i>	495	14	Broome luteo-like virus 1	429	92	16.9	4	97.1	21.2	10
23-00945-0139	BF	Morobe	<i>Cx. sitiens</i>	17	5,782	Broome luteo-like virus 1	1,320	98.6	99.9	4,384	98.1	100	1,384
23-00945-0140	BF	Western	<i>Cx. annulirostris</i>	449	14	Broome luteo-like virus 1	208	95.8	18.5	12	95.7	11.9	2
23-00945-0145	BF	Madang	<i>Cx. annulirostris</i>	42	1,638	Broome luteo-like virus 1	1,295	98.4	99.8	1,296	97.7	100	324
23-00945-0147	BF	Madang	<i>Cx. annulirostris</i>	99	2,550	Broome luteo-like virus 1	1,345	98.2	100	1,715	98.1	100	830
23-00945-0155	BF	Central	<i>Cx. annulirostris</i>	66	1,168	Broome luteo-like virus 1	805	98.4	96.7	744	97.8	98.2	422
23-00945-0157	BF	Central	<i>Cx. quinquefasciatus</i>	258	242	Broome luteo-like virus 1	387	98.6	71.3	170	97.8	77.7	72
23-00945-0158	BF	Central	<i>Cx. sitiens</i>	67	1,242	Broome luteo-like virus 1	663	98.6	81.1	684	98.3	99.7	556
23-00945-0160	BF	Morobe	<i>Cx. annulirostris</i>	10	56,702	Broome luteo-like virus 1	1,320	99.2	100	43,568	64.9	6.5	12,927
23-00945-0161	BF	Morobe	<i>Cx. gelidus</i>	344	132	Broome luteo-like virus 1	571	98	79.7	98	97.1	75.7	34
23-00945-0163	BF	Morobe	<i>Cx. sitiens</i>	8	108,428	Broome luteo-like virus 1	1,320	99	100	82,506	66.6	18.3	25,768
23-00945-0164	BF	Western	<i>Cx. annulirostris</i>	224	7,560	Broome luteo-like virus 1	1,320	98.6	100	5,142	97.7	100	2,379
23-00945-0165	BF	Western	<i>Cx. gelidus</i>	78	782	Broome luteo-like virus 1	831	99.2	99.6	532	95.6	90.4	244
23-00945-0167	BF	Western	<i>Cx. quinquefasciatus</i>	85	578	Broome luteo-like virus 1	670	99.5	94.4	474	99	93.3	104

The % identity and the coverage of the consensus sequences for the respective reference genome are included.

Abbreviations: BF, Blood fed; UF, Unfed; Cx, *Culex*; ID, identity.

Reference virus segment 1/segment 2 nucleotide lengths are provided for comparative purposes with PNG-derived sequences and represent approximate values derived from the closest BLAST-matched GenBank genomes.

Reference sequence lengths in nucleotides: Broome luteo-like virus 1, segment 1, 3,239; segment 2, 1,532.

Supplementary Table 9: Culex-associated Luteo-like virus detected in the PNG samples.

Sample No	Feeding status	Province	Mosquito species	Mosquitoes in pool	Total reads for <i>Culex-associated</i> Luteo-like virus	Species from NCBI with the highest BLAST match	Longest contig	RNA 1			RNA 2		
								% ID	% Coverage	Reads	% ID	% Coverage	Reads
23-00945-0002	UF	Central	<i>Cx. gelidus</i>	198	1,510	Culex-associated Luteo-like virus	840	98.7	68.6	1,327	98.7	30.2	182
23-00945-0008	UF	East Sepik	<i>Cx. annulirostris</i>	190	200	Culex-associated Luteo-like virus	247	93.5	24.6	62	98.9	19.8	138
23-00945-0009	UF	East Sepik	<i>Cx. quinquefasciatus</i>	439	37,816	Culex-associated Luteo-like virus	2,786	96.6	98.9	28,862	96.6	99.1	9,680
23-00945-0011	UF	Madang	<i>Cx. annulirostris</i>	73	5,524	Culex-associated Luteo-like virus	2,792	98	99	3,834	98.5	98	1,686
23-00945-0013	UF	Madang	<i>Cx. quinquefasciatus</i>	481	1,142	Culex-associated Luteo-like virus	1,809	92.9	55.3	1,020	90.1	88.0	118
23-00945-0018	UF	Madang	<i>Cx. quinquefasciatus</i>	362	25,054	Culex-associated Luteo-like virus	2,791	93.9	100	22,626	92.1	97.8	2,327
23-00945-0019	UF	Madang	<i>Cx. annulirostris</i>	466	1,280	Culex-associated Luteo-like virus	859	90	39.4	329	94.8	98.1	950
23-00945-0020	UF	Madang	<i>Cx. quinquefasciatus</i>	40	1,406	Culex-associated Luteo-like virus	2,089	95.2	86.9	1,376	0	0	0
23-00945-0037	UF	Morobe	<i>Cx. quinquefasciatus</i>	472	1,406	Culex-associated Luteo-like virus	2,785	92	99	1,366	88.9	49	28
23-00945-0127	BF	Madang	<i>Cx. quinquefasciatus</i>	499	2,880	Culex-associated Luteo-like virus	1,338	93.4	44.1	21	98.1	99.9	2,856
23-00945-0128	BF	Madang	<i>Cx. quinquefasciatus</i>	52	1,410	Culex-associated Luteo-like virus	2,784	93.9	99	1,080	92.4	77.8	323
23-00945-0136	BF	Morobe	<i>Cx. gelidus</i>	500	10	Culex-associated Luteo-like virus	261	87.1	28.3	10	0	0	0
23-00945-0138	BF	Morobe	<i>Cx. quinquefasciatus</i>	272	96	Culex-associated Luteo-like virus	990	92.3	69.5	66	83.3	72.2	29
23-00945-0143	BF	Western	<i>Cx. quinquefasciatus</i>	11	4,762	Culex-associated Luteo-like virus	2,739	97.6	99.2	2,829	0	0	0
23-00945-0146	BF	Madang	<i>Cx. quinquefasciatus</i>	5	61,868	Culex-associated Luteo-like virus	2,784	99	100	38,519	99.2	100	23,215
23-00945-0147	BF	Madang	<i>Cx. annulirostris</i>	99	230	Culex-associated Luteo-like virus	1,871	97.9	87	173	98.4	88.2	59
23-00945-0149	BF	Madang	<i>Cx. quinquefasciatus</i>	496	92	Culex-associated Luteo-like virus	557	96.8	50	72	97.6	60.9	20
23-00945-0150	BF	Madang	<i>Cx. quinquefasciatus</i>	498	1,378	Culex-associated Luteo-like virus	2,785	97.1	100	1,317	97.1	16.1	63
23-00945-0151	BF	Madang	<i>Cx. quinquefasciatus</i>	493	7,522	Culex-associated Luteo-like virus	2,784	96.8	100	7,256	97.2	83.1	262
23-00945-0152	BF	Madang	<i>Cx. quinquefasciatus</i>	499	80	Culex-associated Luteo-like virus	304	88.9	19.2	6	97.7	15.4	74
23-00945-0154	BF	Madang	<i>Cx. quinquefasciatus</i>	130	146	Culex-associated Luteo-like virus	462	97.7	74.8	110	97.7	74.8	36
23-00945-0157	BF	Central	<i>Cx. quinquefasciatus</i>	258	511	Culex-associated Luteo-like virus	1,320	98	53.5	510	0	0	0
23-00945-0161	BF	Morobe	<i>Cx. gelidus</i>	344	26	Culex-associated Luteo-like virus	372	96.3	24	16	94.3	40.2	10
23-00945-0162	BF	Morobe	<i>Cx. quinquefasciatus</i>	189	92	Culex-associated Luteo-like virus	780	84.4	65	80	99.5	19.8	12

The % identity and the coverage of the consensus sequences for the respective reference genome are included.

Abbreviations: BF, Blood fed; UF, Unfed; Cx, *Culex*; ID, identity.

Reference virus RNA1/RNA2 nucleotide lengths are provided for comparative purposes with PNG-derived sequences and represent approximate values derived from the closest BLAST-matched GenBank genomes.

Reference sequence lengths in nucleotides: Culex-associated Luteo-like virus, RNA1, 2,794; RNA2, 1,610.

Supplementary Table 10: GenBank accession numbers for viral genome sequences generated from Papua New Guinea *Culex* mosquito samples.

Sample ID	Virus name	Family	Genome segment	Genome status	Length (nt)	GenBank accession number
23-00945-0018	Culex Iflavi-like virus 4	<i>Iflaviridae</i>	Polyprotein	complete	9,718	PZ253856
23-00945-0037	Culex Iflavi-like virus 4	<i>Iflaviridae</i>	Polyprotein	complete	9,766	PZ253857
23-00945-0039	Culex Iflavi-like virus 4	<i>Iflaviridae</i>	Polyprotein	complete	9,829	PZ253858
23-00945-0138	Culex Iflavi-like virus 4	<i>Iflaviridae</i>	Polyprotein	complete	9,679	PZ253859
23-00945-0147	Culex Iflavi-like virus 4	<i>Iflaviridae</i>	Polyprotein	complete	9,773	PZ253860
23-00945-0151	Culex Iflavi-like virus 4	<i>Iflaviridae</i>	Polyprotein	complete	9,686	PZ253861
23-00945-0157	Culex Iflavi-like virus 4	<i>Iflaviridae</i>	Polyprotein	partial	9,729	PZ253862
23-00945-0162	Culex Iflavi-like virus 4	<i>Iflaviridae</i>	Polyprotein	complete	9,730	PZ253863
23-00945-0040	Isahaya Culex iflavivirus	<i>Iflaviridae</i>	Polyprotein	partial	8,698	PZ253864
23-00945-0088	Isahaya Culex iflavivirus	<i>Iflaviridae</i>	Polyprotein	complete	9,760	PZ253865
23-00945-0139	Isahaya Culex iflavivirus	<i>Iflaviridae</i>	Polyprotein	complete	9,687	PZ253866
23-00945-0142	Isahaya Culex iflavivirus	<i>Iflaviridae</i>	Polyprotein	partial	9,254	PZ253867
23-00945-0164	Isahaya Culex iflavivirus	<i>Iflaviridae</i>	Polyprotein	partial	9,382	PZ253868
23-00945-0018	Yongsan iflavivirus 1	<i>Iflaviridae</i>	Polyprotein	complete	9,139	PZ253869
23-00945-0050	Yongsan iflavivirus 1	<i>Iflaviridae</i>	Polyprotein	complete	9,121	PZ253870
23-00945-0051	Yongsan iflavivirus 1	<i>Iflaviridae</i>	Polyprotein	complete	9,147	PZ253871
23-00945-0127	Yongsan iflavivirus 1	<i>Iflaviridae</i>	Polyprotein	complete	9,137	PZ253872
23-00945-0150	Yongsan iflavivirus 1	<i>Iflaviridae</i>	Polyprotein	partial	9,026	PZ253873
23-00945-0151	Yongsan iflavivirus 1	<i>Iflaviridae</i>	Polyprotein	complete	9,139	PZ253874
23-00945-0005	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,472	PZ253875
23-00945-0008	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,477	PZ253876
23-00945-0011	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,691	PZ253877
23-00945-0013	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,489	PZ253878
23-00945-0021	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,550	PZ253879
23-00945-0039	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,647	PZ253880
23-00945-0040	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,818	PZ253881
23-00945-0041	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,493	PZ253882
23-00945-0051	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,494	PZ253883
23-00945-0052	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,592	PZ253884
23-00945-0071	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,482	PZ253885
23-00945-0139	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,484	PZ253886
23-00945-0140	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,468	PZ253887
23-00945-0147	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,557	PZ253888
23-00945-0151	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,462	PZ253889
23-00945-0164	Broome partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,497	PZ253890
23-00945-0005	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,224	PZ253891
23-00945-0008	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,224	PZ253892
23-00945-0011	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,278	PZ253893
23-00945-0013	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,248	PZ253894
23-00945-0021	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,266	PZ253895
23-00945-0039	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,221	PZ253896
23-00945-0040	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,231	PZ253897
23-00945-0041	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,173	PZ253898
23-00945-0051	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,223	PZ253899
23-00945-0052	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,240	PZ253900
23-00945-0071	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,198	PZ253901
23-00945-0139	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,222	PZ253902
23-00945-0140	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,219	PZ253903
23-00945-0147	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,240	PZ253904
23-00945-0151	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,194	PZ253905
23-00945-0164	Broome partiti-like virus 1	<i>Partitiviridae</i>	Putative capsid protein	complete	1,226	PZ253906
23-00945-0018	Verdadero virus	<i>Partitiviridae</i>	RdRP	complete	1,628	PZ253907
23-00945-0021	unclassified Partitiviridae	<i>Partitiviridae</i>	RdRP	complete	1,791	PZ253908
23-00945-0035	Partitiviridae sp.	<i>Partitiviridae</i>	RdRP	complete	1,365	PZ253909
23-00945-0037	Sonnbo virus	<i>Partitiviridae</i>	RdRP	complete	1,762	PZ253910
23-00945-0041	unclassified Deltapartitivirus	<i>Partitiviridae</i>	RdRP	complete	1,716	PZ253911
23-00945-0160	Wyndham partiti-like virus 1	<i>Partitiviridae</i>	RdRP	complete	1,645	PZ253912
23-00945-0160	unclassified Partitiviridae	<i>Partitiviridae</i>	no ORF detected in this sequence	partial	1,296	PZ253913
23-00945-0018	Verdadero virus	<i>Partitiviridae</i>	Capsid protein	complete	1,498	PZ253914
23-00945-0037	Sonnbo virus	<i>Partitiviridae</i>	Putative capsid protein	complete	1,675	PZ253915
23-00945-0164	unclassified Partitiviridae	<i>Partitiviridae</i>	Capsid protein	complete	1,505	PZ253916

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Supplementary Table 10 (continued)

Sample ID	Virus name	Family	Genome segment	Genome status	Length (nt)	GenBank accession number
23-00945-0035	unclassified Partitiviridae	<i>Partitiviridae</i>	Hypothetical protein	complete	1,369	PZ253917
23-00945-0035	unclassified Partitiviridae	<i>Partitiviridae</i>	Hypothetical protein	complete	1,313	PZ253918
23-00945-0035	unclassified Partitiviridae	<i>Partitiviridae</i>	Hypothetical protein	complete	1,306	PZ253919
23-00945-0035	unclassified Partitiviridae	<i>Partitiviridae</i>	Hypothetical protein	complete	1,280	PZ253920
23-00945-0035	unclassified Partitiviridae	<i>Partitiviridae</i>	Hypothetical protein	complete	1,307	PZ253921
23-00945-0035	unclassified Partitiviridae	<i>Partitiviridae</i>	Hypothetical protein	complete	1,262	PZ253922
23-00945-0035	unclassified Partitiviridae	<i>Partitiviridae</i>	Hypothetical protein	complete	1,233	PZ253923
23-00945-0035	unclassified Partitiviridae	<i>Partitiviridae</i>	Hypothetical protein	complete	1,258	PZ253924
23-00945-0035	unclassified Partitiviridae	<i>Partitiviridae</i>	Hypothetical protein	complete	1,289	PZ253925
23-00945-0018	Chaq-like virus	<i>Partitiviridae</i>	Hypothetical protein	complete	1,426	PZ253926
23-00945-0164	unclassified Partitiviridae	<i>Partitiviridae</i>	Hypothetical protein	complete	1,498	PZ253927
23-00945-0164	unclassified Partitiviridae	<i>Partitiviridae</i>	Hypothetical protein	complete	1,591	PZ253928
23-00945-0004	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,250	PZ253929
23-00945-0011	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,426	PZ253930
23-00945-0013	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,416	PZ253931
23-00945-0018	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,300	PZ253932
23-00945-0024	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,444	PZ253933
23-00945-0035	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,459	PZ253934
23-00945-0037	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,697	PZ253935
23-00945-0039	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,606	PZ253936
23-00945-0051	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,443	PZ253937
23-00945-0052	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,380	PZ253938
23-00945-0127	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,444	PZ253939
23-00945-0128	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,331	PZ253940
23-00945-0134	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,385	PZ253941
23-00945-0136	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,163	PZ253942
23-00945-0137	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,427	PZ253943
23-00945-0150	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,433	PZ253944
23-00945-0151	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,515	PZ253945
23-00945-0161	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,432	PZ253946
23-00945-0162	Cambodia Culex birnavirus	<i>Birnaviridae</i>	Polyprotein	complete	3,386	PZ253947
23-00945-0004	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,065	PZ253948
23-00945-0011	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,134	PZ253949
23-00945-0013	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,142	PZ253950
23-00945-0018	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,176	PZ253951
23-00945-0024	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,151	PZ253952
23-00945-0035	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,541	PZ253953
23-00945-0037	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,520	PZ253954
23-00945-0039	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,266	PZ253955
23-00945-0051	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,171	PZ253956
23-00945-0052	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,141	PZ253957
23-00945-0127	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,195	PZ253958
23-00945-0128	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,149	PZ253959
23-00945-0134	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,109	PZ253960
23-00945-0135	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	2,964	PZ253961
23-00945-0136	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,088	PZ253962
23-00945-0137	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,291	PZ253963
23-00945-0147	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,061	PZ253964
23-00945-0149	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,106	PZ253965
23-00945-0150	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,140	PZ253966
23-00945-0151	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,236	PZ253967
23-00945-0152	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	2,915	PZ253968
23-00945-0154	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,021	PZ253969
23-00945-0161	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,300	PZ253970
23-00945-0162	Cambodia Culex birnavirus	<i>Birnaviridae</i>	RdRP	complete	3,156	PZ253971
23-00945-0002	Merida virus	<i>Rhabdoviridae</i>	Whole genome	complete	11,786	PZ253972
23-00945-0004	Merida virus	<i>Rhabdoviridae</i>	Whole genome	complete	11,775	PZ253973
23-00945-0005	Merida virus	<i>Rhabdoviridae</i>	Whole genome	partial	11,350	PZ253974
23-00945-0009	Merida virus	<i>Rhabdoviridae</i>	Whole genome	partial	10,929	PZ253975
23-00945-0018	Merida virus	<i>Rhabdoviridae</i>	Whole genome	complete	11,764	PZ253976
23-00945-0051	Merida virus	<i>Rhabdoviridae</i>	Whole genome	complete	11,788	PZ253977
23-00945-0052	Merida virus	<i>Rhabdoviridae</i>	Whole genome	complete	11,804	PZ253978
23-00945-0064	Merida virus	<i>Rhabdoviridae</i>	Whole genome	complete	11,805	PZ253979

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Supplementary Table 10 (continued)

Sample ID	Virus name	Family	Genome segment	Genome status	Length (nt)	GenBank accession number
23-00945-0065	Merida virus	<i>Rhabdoviridae</i>	Whole genome	complete	11,781	PZ253980
23-00945-0115	Merida virus	<i>Rhabdoviridae</i>	Whole genome	complete	11,815	PZ253981
23-00945-0143	Merida virus	<i>Rhabdoviridae</i>	Whole genome	complete	11,877	PZ253982
23-00945-0157	Merida virus	<i>Rhabdoviridae</i>	Whole genome	complete	11,776	PZ253983
23-00945-0164	Merida virus	<i>Rhabdoviridae</i>	Whole genome	partial	11,567	PZ253984
23-00945-0167	Merida virus	<i>Rhabdoviridae</i>	Whole genome	complete	11,870	PZ253985
23-00945-0041	Guadeloupe Culex rhabdovirus	<i>Rhabdoviridae</i>	Whole genome	complete	14,400	PZ253986
23-00945-0050	Guadeloupe Culex rhabdovirus	<i>Rhabdoviridae</i>	Whole genome	complete	14,669	PZ253987
23-00945-0051	Guadeloupe Culex rhabdovirus	<i>Rhabdoviridae</i>	Whole genome	complete	14,712	PZ253988
23-00945-0052	Guadeloupe Culex rhabdovirus	<i>Rhabdoviridae</i>	Whole genome	complete	14,399	PZ253989
23-00945-0113	Guadeloupe Culex rhabdovirus	<i>Rhabdoviridae</i>	Whole genome	complete	14,403	PZ253990
23-00945-0143	Guadeloupe Culex rhabdovirus	<i>Rhabdoviridae</i>	Whole genome	complete	14,637	PZ253991
23-00945-0167	Guadeloupe Culex rhabdovirus	<i>Rhabdoviridae</i>	Whole genome	complete	14,514	PZ253992
23-00945-0115	Grenada mosquito rhabdovirus 1	<i>Rhabdoviridae</i>	Whole genome	complete	14,394	PZ253993
23-00945-0004	Hubei virga-like virus 2	Unclassified	Whole genome	partial	10,592	PZ253994
23-00945-0011	Hubei virga-like virus 2	Unclassified	Whole genome	partial	11,713	PZ253995
23-00945-0018	Hubei virga-like virus 2	Unclassified	Whole genome	partial	11,917	PZ253996
23-00945-0037	Hubei virga-like virus 2	Unclassified	Whole genome	complete	10,869	PZ253997
23-00945-0064	Hubei virga-like virus 2	Unclassified	Whole genome	complete	10,821	PZ253998
23-00945-0068	Hubei virga-like virus 2	Unclassified	Whole genome	complete	10,865	PZ253999
23-00945-0127	Hubei virga-like virus 2	Unclassified	Whole genome	partial	10,942	PZ254000
23-00945-0128	Hubei virga-like virus 2	Unclassified	Whole genome	partial	10,794	PZ254001
23-00945-0167	Hubei virga-like virus 2	Unclassified	Whole genome	complete	10,847	PZ254002
23-00945-0005	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,251	PZ254003
23-00945-0011	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,241	PZ254004
23-00945-0019	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,247	PZ254005
23-00945-0021	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,250	PZ254006
23-00945-0037	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,246	PZ254007
23-00945-0040	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,252	PZ254008
23-00945-0050	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,249	PZ254009
23-00945-0052	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,248	PZ254010
23-00945-0129	Broome luteo-like virus 1	Unclassified	Segment 1	partial	3,140	PZ254011
23-00945-0130	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,251	PZ254012
23-00945-0133	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,250	PZ254013
23-00945-0139	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,250	PZ254014
23-00945-0145	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,242	PZ254015
23-00945-0147	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,252	PZ254016
23-00945-0155	Broome luteo-like virus 1	Unclassified	Segment 1	partial	3,143	PZ254017
23-00945-0160	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,250	PZ254018
23-00945-0163	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,250	PZ254019
23-00945-0164	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,251	PZ254020
23-00945-0165	Broome luteo-like virus 1	Unclassified	Segment 1	complete	3,235	PZ254021
23-00945-0167	Broome luteo-like virus 1	Unclassified	Segment 1	partial	3,067	PZ254022
23-00945-0011	Broome luteo-like virus 1	Unclassified	Segment 2	complete	1,547	PZ254023
23-00945-0019	Broome luteo-like virus 1	Unclassified	Segment 2	complete	1,587	PZ254024
23-00945-0037	Broome luteo-like virus 1	Unclassified	Segment 2	complete	1,559	PZ254025
23-00945-0039	Broome luteo-like virus 1	Unclassified	Segment 2	complete	1,545	PZ254026
23-00945-0040	Broome luteo-like virus 1	Unclassified	Segment 2	complete	1,550	PZ254027
23-00945-0050	Broome luteo-like virus 1	Unclassified	Segment 2	complete	1,555	PZ254028
23-00945-0051	Broome luteo-like virus 1	Unclassified	Segment 2	complete	1,454	PZ254029
23-00945-0052	Broome luteo-like virus 1	Unclassified	Segment 2	complete	1,547	PZ254030
23-00945-0057	Broome luteo-like virus 1	Unclassified	Segment 2	complete	1,550	PZ254031
23-00945-0129	Broome luteo-like virus 1	Unclassified	Segment 2	complete	1,527	PZ254032
23-00945-0139	Broome luteo-like virus 1	Unclassified	Segment 2	complete	1,635	PZ254033
23-00945-0145	Broome luteo-like virus 1	Unclassified	Segment 2	complete	1,545	PZ254034
23-00945-0147	Broome luteo-like virus 1	Unclassified	Segment 2	complete	1,583	PZ254035
23-00945-0155	Broome luteo-like virus 1	Unclassified	Segment 2	partial	1,539	PZ254036
23-00945-0158	Broome luteo-like virus 1	Unclassified	Segment 2	partial	1,567	PZ254037
23-00945-0164	Broome luteo-like virus 1	Unclassified	Segment 2	complete	1,600	PZ254038
23-00945-0165	Broome luteo-like virus 1	Unclassified	Segment 2	partial	1,401	PZ254039
23-00945-0167	Broome luteo-like virus 1	Unclassified	Segment 2	partial	1,437	PZ254040
23-00945-0009	Culex-associated Luteo-like virus	Unclassified	RNA 1	complete	2,786	PZ254041
23-00945-0011	Culex-associated Luteo-like virus	Unclassified	RNA 1	complete	2,792	PZ254042

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Supplementary Table 10 (continued)

Sample ID	Virus name	Family	Genome segment	Genome status	Length (nt)	GenBank accession number
23-00945-0018	Culex-associated Luteo-like virus	Unclassified	RNA 1	complete	2,791	PZ254043
23-00945-0037	Culex-associated Luteo-like virus	Unclassified	RNA 1	complete	2,785	PZ254044
23-00945-0128	Culex-associated Luteo-like virus	Unclassified	RNA 1	complete	2,784	PZ254045
23-00945-0143	Culex-associated Luteo-like virus	Unclassified	RNA 1	complete	2,739	PZ254046
23-00945-0146	Culex-associated Luteo-like virus	Unclassified	RNA 1	complete	2,784	PZ254047
23-00945-0150	Culex-associated Luteo-like virus	Unclassified	RNA 1	complete	2,785	PZ254048
23-00945-0151	Culex-associated Luteo-like virus	Unclassified	RNA 1	complete	2,784	PZ254049
23-00945-0009	Culex-associated Luteo-like virus	Unclassified	RNA 2	complete	1,587	PZ254050
23-00945-0011	Culex-associated Luteo-like virus	Unclassified	RNA 2	complete	1,542	PZ254051
23-00945-0018	Culex-associated Luteo-like virus	Unclassified	RNA 2	complete	1,570	PZ254052
23-00945-0019	Culex-associated Luteo-like virus	Unclassified	RNA 2	complete	1,571	PZ254053
23-00945-0127	Culex-associated Luteo-like virus	Unclassified	RNA 2	complete	1,605	PZ254054
23-00945-0146	Culex-associated Luteo-like virus	Unclassified	RNA 2	complete	1,610	PZ254055

Abbreviations: nt, nucleotides; RdRP, RNA-dependent RNA polymerase.