

**Supplementary Table 3:** List of viruses from this study with their associated sample and NCBI GenBank accession numbers. Genome length, assembling software used for the specific genome's assembly, the number of reads involved in the assembly, as well as the average coverage and the percentage of total reads, are also presented. AgTV – Agapanthus tungro virus; AgVV – Agapanthus velarivirus, AgVA – Agapanthus virus A, ClCVA – Clivia carlavirus A, NeLV – Nerine latent virus, HiMV – Hippeastrum mosaic virus, ScCRV – Scadoxus chlorotic ringspot virus

Sample number	Virus name with strain number where applicable	NCBI GenBank accession number	Genome length (bp/nt), excluding poly-A-tract	Software used for assembly <sup>1</sup>	Number of mapped reads	Average coverage (X)	Percent base contribution <sup>2</sup> (%)	Percent plant virus base contribution <sup>3</sup> (%)
19-3001	AgTV 1	MT501685	7942	CLC	841862	12512	7.5	100
19-3004	AgTV 1	MT501686	7956	CLC	51335	763	3.5	71
19-3005	AgTV 2	MT501687	7953	CLC	54547	810	2.9	97.6
19-3006	AgTV 1	MT579870	7935	CLC	70888	1055	6.8	89.3
19-3007	AgTV 1	MT501688	7953	CLC	34517	506	3.6	93.1
19-3010	AgTV 2	MT501689	8061	CLC	12670	184	1.4	85.8
19-3013	AgTV 2	MT501690	7965	SPAdes	n/a	9	0.1	6.8
19-3013	AgTV 1	MT501691	8061	SPAdes	n/a	35	0.34	26.9
19-3017	AgTV 1	MW080813	8013	SPAdes	n/a	165	1.1	58.8
19-3021	AgTV 1	MW080814	7991	SPAdes	n/a	173	0.74	1.9
19-3004	AgVV 3	MT533600	17479	SPAdes	n/a	33	0.33	6.8
19-3005	AgVV 2	MT533601	17635	SPAdes	n/a	9	0.07	2.4
19-3006	AgVV 3	MT533602	17575	CLC	3457	23	0.33	4.3
19-3007	AgVV1	MW080811	17544	SPAdes	n/a	5	0.08	2
19-3007	AgVV3	MW080812	17598	SPAdes	n/a	12	0.19	4.9
19-3008	AgVV 1	MT533603	17523	SPAdes	n/a	34	0.36	100
19-3009	AgVV 1	MT533604	17492	SPAdes	n/a	17	0.21	44.4
19-3010	AgVV 1	MT533605	17526	SPAdes	n/a	14	0.23	14.2
19-3013	AgVV 1	MT533606	17521	SPAdes	n/a	9	0.19	15
19-3017	AgVV 1	MT533607	17492	CLC	7723	53	0.7	41.2
19-3004	AgVA	MT533608	7116	CLC	15948	268	1.1	22.2
19-3006	AgVA	MT533609	7109	SPAdes	n/a	85	0.5	6.4
19-3035	AgCVB	MW303999	8727	SPAdes	n/a	193	0.53	100
19-3040	ClCVA	MT533598	8412	SPAdes	n/a	2700	6.7	100
19-3009	NeLV	MT536155	8282	SPAdes	n/a	45	0.26	56.6
19-3013	NeLV	MT536156	8409	SPAdes	n/a	64	0.64	51.3
19-3019	NeLV	MT536157	8282	SPAdes	n/a	102	0.66	100
19-3029	NeLV	MT536158	8338	SPAdes	n/a	1478	3.6	11.7
19-3029	NeLV	MT536159	8321	SPAdes	n/a	3255	7.8	25.7
19-3044	NeLV	MT536160	8275	SPAdes	n/a	1228	3.4	100
19-3026	ClYSV	MT533610	9800	SPAdes	n/a	385	2.9	100
19-3027	ClYSV	MT533611	9800	CLC	138660	1689	6.9	100

MT533599	HiMV	19-3029	9722	CLC	566211	6777	19	62.6
MW080808	ScCRV	19-3032	8915	SPAdes	n/a	476	2.7	100
MW080809	ScCRV	19-3032	4885	SPAdes	n/a	776	n/a	n/a
MW080810	ScCRV	19-3032	3406	SPAdes	n/a	848	n/a	n/a

<sup>1</sup>CLC refers to CLC Genomics Workbench version 9 and SPAdes refers to metaSPAdes version 3.14.0, with n/a indicating: Not available when using metaSPAdes assembler.

<sup>2</sup> Base contribution refers to the percentage of bases involved in the assembly of a specific viral genome, calculated by multiplying coverage by genome length, divided by the total number of bases in the dataset, multiplied by 100.

<sup>3</sup> Plant virus base contribution refers to the percentage of bases associated with a specific virus from a metavirome, divided by the total number of plant virus reads, multiplied by 100.