

Table S2: Cassava common mosaic virus (CsCMV) complete genome sequences used to infer phylogenetics. The complete genome sequences were retrieved from the National Center for Biotechnology Information (NCBI). *M. esculenta*: *Manihot esculenta*, *N. Benthamiana*: *Nicotiana benthamiana*

Name	Isolate	Size (bp)	Host	Location	Accession number
CsCMV	BR-21GS-C3-251-6	6398	<i>M. esculenta</i>	Brazil	PQ497977
	BGM0087	6395	<i>M. esculenta</i>	Brazil	PQ497976
	Hainan-CM	6398	<i>M. esculenta</i>	China	MW175326
	LG	6397	<i>M. esculenta</i>	China	MT038420
	China	6395	<i>M. esculenta</i>	China	MN428639
	Hainan-DZ	6395	<i>M. esculenta</i>	China	MN243731
	pCsCMV-28, pCsCMV-X7, pCsCMV-SP2, pCsCMV-64	6376	<i>M. esculenta</i>	Brazil	NC_001658, U23414
	DSMZ PV-0723	6398	<i>N. benthamiana</i>	Argentina	PQ341268
	JB017_ApX	6403	Unknown		OM927720
	BR	6373	<i>M. esculenta</i>	Brazil	MT279196
	PisVera	4635	<i>Pistacia vera</i> (unverified)	Iran	MT334616
	Arg127_1	6407	<i>M. esculenta</i>	Argentina	KT002439
	Mcol22_1	6392	<i>M. esculenta</i>	Colombia	KT002435