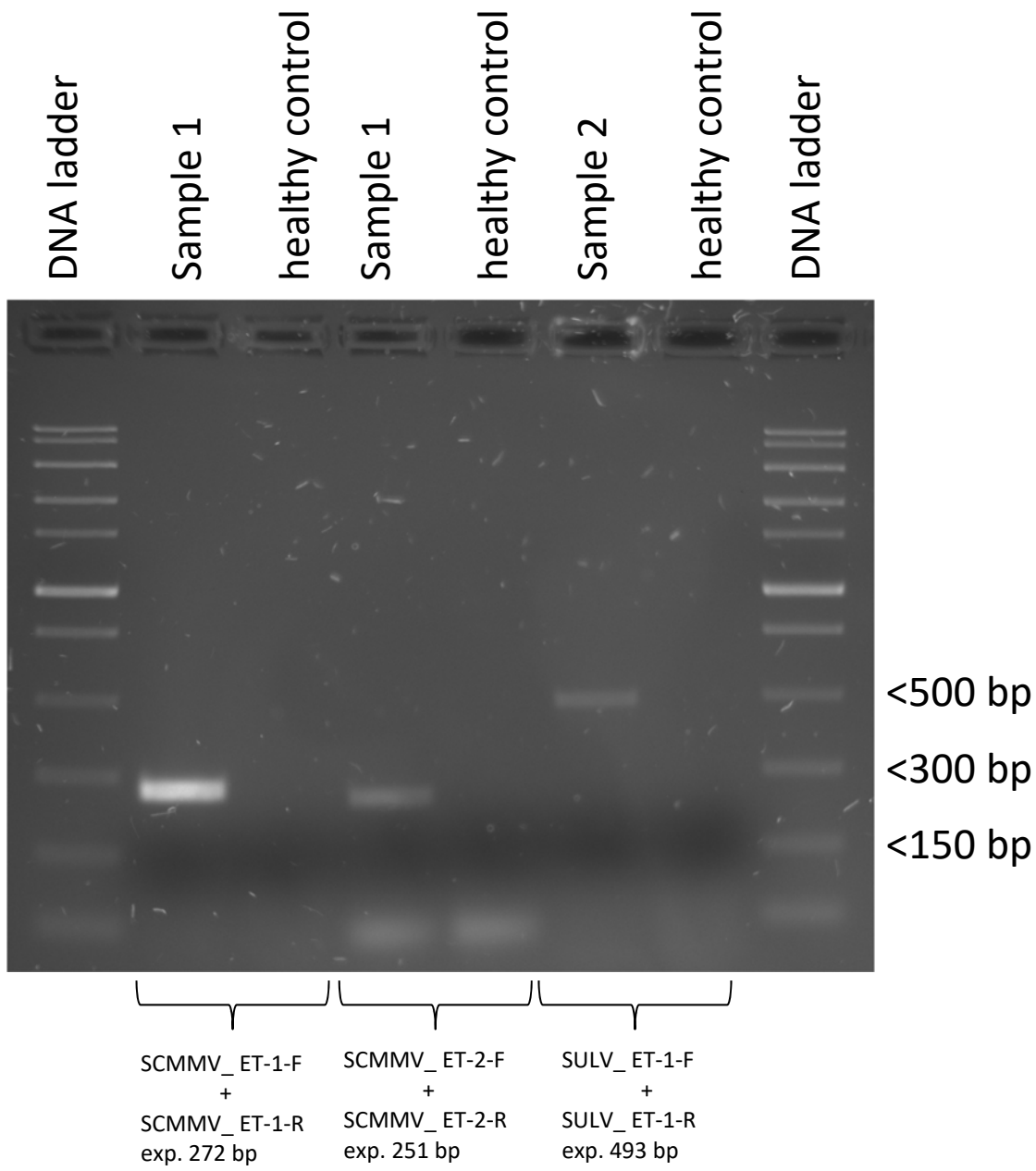


**Figure S1.** Different virus-like symptoms (A) dwarf and yellowing; (B) leaf yellowing; (C) leaf fleck; (D) yellowing and chlorosis



**Figure S2:** RT-PCR amplification result for HTS data verification

**TableS1:** Overview of the number of raw reads generated per library, and of the reads at different steps of the bioinformatic analysis conducted in GeneiousPrime software

<b>Sample/Library</b>	<b>Raw reads</b>	<b>Trimmed reads</b>	<b>Normalized reads</b>	<b>Unmapped reads</b>	<b>Virus</b>	<b>Mapped reads*</b>
Sugarcane sample 1	24,366,538	21,275,638	2,631,026	469.817	SCMMV (isolate ET-1)	2.271
					SCMMV (isolate ET-2)	1.554
Sugarcane sample 2	32,838,040	29,575,906	2,617,240	438.538	SULV	136

\*Number of reads mapped to the final virus sequences

**Table S2:** Primers used to amplify identified genome

Primers	Sequences
SCMMV_ET-1-F	TCGGTGATGTTCCAGTGAAGG
SCMMV_ET-1-R	TTTGCCGCTATCTCCTTTCGT
SCMMV_ET-2-F	GTGTGAAACCGTCCAGACAGA
SCMMV_ET-2-R	CTGAATGAGCCGTCTGTGTCT
SULV_ET-1-F	GATGCTCTGCGCTTCACTCA
SULV_ET-1-R	ATCCTGACTGCATGCGGTA