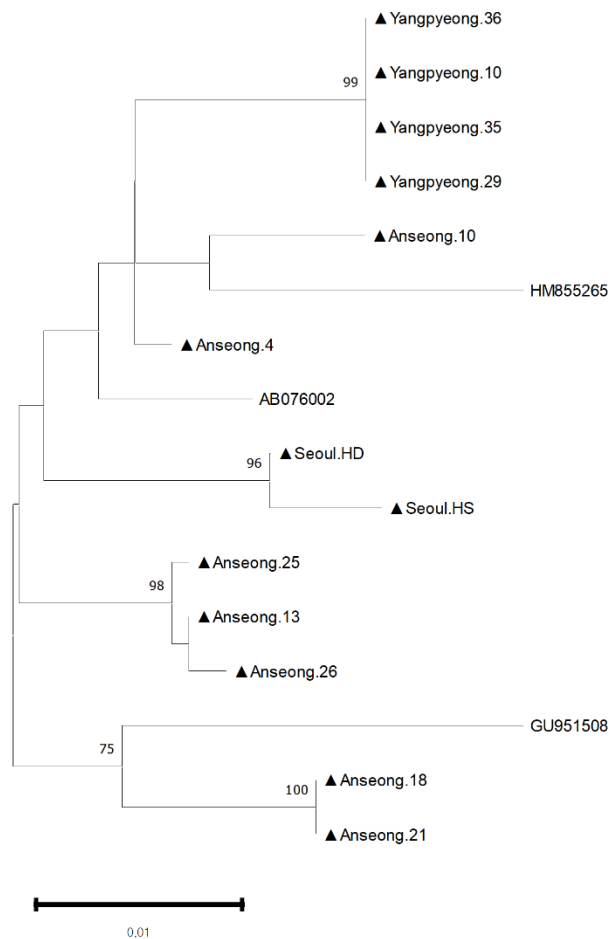


Figure S1. Phylogenetic tree generated using the partial sequences of TTCaV amplified by primer set 1 and the reference strains. The 13 TTCaV-positive samples identified in this study are marked with closed triangles



**Table S1. Recombination region identified in MZ503912**

Recombinant	Parental virus		Breakpoints <sup>a</sup>		Score for the seven detection methods in RDP4 <sup>b</sup>						
Virus	Major	Minor	Begin	End	RDP	GENECONV	BootScan	MaxChi	Chimaera	SiScan	3Seq
MZ503912	KX827768	MZ503910	40	985	1.3 x 10 <sup>-224</sup>	1.1 x 10 <sup>-226</sup>	5.5 x 10 <sup>-223</sup>	1.2 x 10 <sup>-60</sup>	3.6 x 10 <sup>-42</sup>	4.8 x 10 <sup>-83</sup>	6.3 x 10 <sup>-14</sup>

<sup>a</sup>The breakpoints are based on the locations in the genome of MZ503912.

<sup>b</sup>The *p* value cut-off was 0.05. *p* < 0.05 indicated that the recombination events were significant.