**New Phytologist Supporting Information**

Article title: Terpene synthases in cucumber (*Cucumis sativus*) and their contribution to herbivore-induced volatile terpenoid emission  
Authors: Jun He, Francel Verstappen, Ao Jiao, Marcel Dicke, Harro J. Bouwmeester, Iris F. Kappers  
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**Table S6** CARE motif analysis

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**Fig. S1** Distribution of *CsTPS* genes in the cucumber genome. The location of all *CsTPS* genes is indicated at the relative position in seven artificial chromosomes (white bars); the loci harbouring *CsTPS* genes are enlarged, and gene models are shown in black (*CsTPS* genes) or white (non-*CsTPS* genes), with the point representing the orientation of the genes and the Kb number indicating the position in the artificial chromosomes.
Fig. S2 Phylogenetic relationship of full length CsTPSs from Cucumis sativus. CsTPSs with putative full-length sequences are sub-grouped into TPS-a through TPS-f according to their sequence similarity to reported TPSs in Arabidopsis.
Fig. S3 Quantitative RT-PCR analysis of gene expression in two *Cucumis sativus* genotypes ('Chinese Long, Cl' and 'Corona, Co') upon herbivory. A, relative expression of selected DXS and HMGR genes in cucumber leaves that were infested with spider mites for three days; B, relative expression of *CsTPS2*, *CsTPS9* and *CsTPS19* genes in cucumber leaves that were infested with spider mites (green bars), thrips (blue bars) or aphids (yellow bars) for three days. Bars represent the expression relative to that in control leaves. Expression was normalized to the expression of reference gene *CsACTIN*. Data are means of 5 independent biological replicates ± SD.
Fig. S4 GCMS chromatograms showing product profiles of heterologous CsTPS2, CsTPS9 & CsTPS19 upon incubation with GPP, NPP, e,e-FPP, z,z-FPP and GGPP
Fig. S5 Arabidopsis reporter plants harbouring GUS::ffLUC driven by the Cucumber pTPS9 promotor

Gene expression in non-stressed cucumber organs