

Table S1 Number of analyzed clones and phylotypes (defined with 99.0% identity) of 16S rRNA pseudogenes.

	Total number of clones	Total number of phylotypes	Number of K1-type ^b clones	Number of K1-type ^b phylotypes	Number of K2-type ^b clones	Number of K2-type ^b phylotypes	Reverse primer for PCR
Nucleus-1 ^a	48	13	48	13	0	0	1492R
Nucleus-2 ^a	42	9	35	7	7	2	1492R
Nucleus-3 ^a	22	2	7	1	15	1	1492R
Nucleus-6 ^a	14	12	14	12	0	0	1390R
Nucleus-9 ^a	14	6	14	6	0	0	1492R
Nucleus-10 ^a	16	8	15	8	0	0	1492R
total	156	47	133	44	22	3	

^a The identifiers 1–6, 9 and 10 correspond to the clone codes RsTaN1–6 and RsTaN-A, B in Supplementary Figure S2, respectively. Each of the nuclei 1–6 was subjected to WGA, and after that, PCR was performed. For the nuclei 9 and 10, PCR was performed directly, without the WGA step.

^b K1 and K2 indicate phylotypes RsTaN-K1 and RsTaN-K2 in Figure 2.

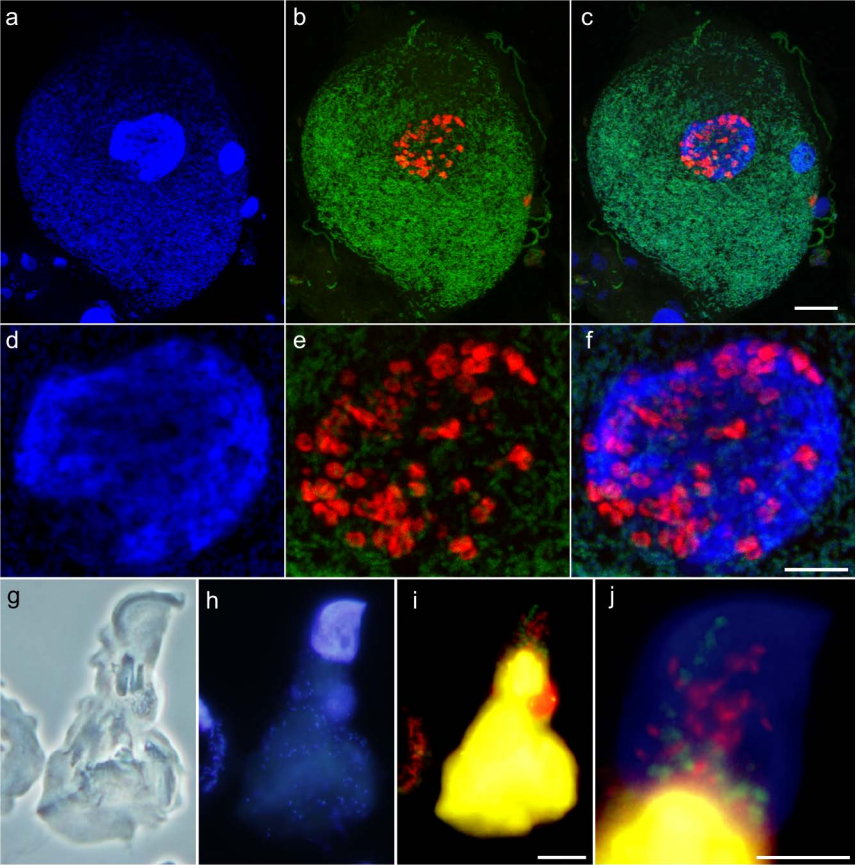


Figure S1 Detection of verrucomicrobial intranuclear symbionts by FISH. (a–c) Detection in a *Trichonympha agilis* cell and (d–f) its nucleus, observed under a laser scanning microscope. (a, d) DAPI images. (b, e) Merged images of FISH analyses using the Texas-red labeled *Verrucomicrobia*-specific probe EUB338-III (red) or the 6FAM-labeled probe EUB338 specific to *Bacteria* except *Verrucomicrobia* and several other taxa (green). (c, f) DAPI images merged with the FISH signals. (g–j) Detection in a *Pyronympha grandis* cell. (g) Phase contrast image. (h) DAPI-stained image. (i) Merged image of FISH analyses using the Texas-red labeled *Verrucomicrobia*-specific probe EUB338-III (red) or the 6FAM-labeled *Bacteria*-specific probe EUB338 (green). (j) Magnified merged image of panels (h) and (i). Bars represent 10 μm (c, i); 5 μm (f, j).

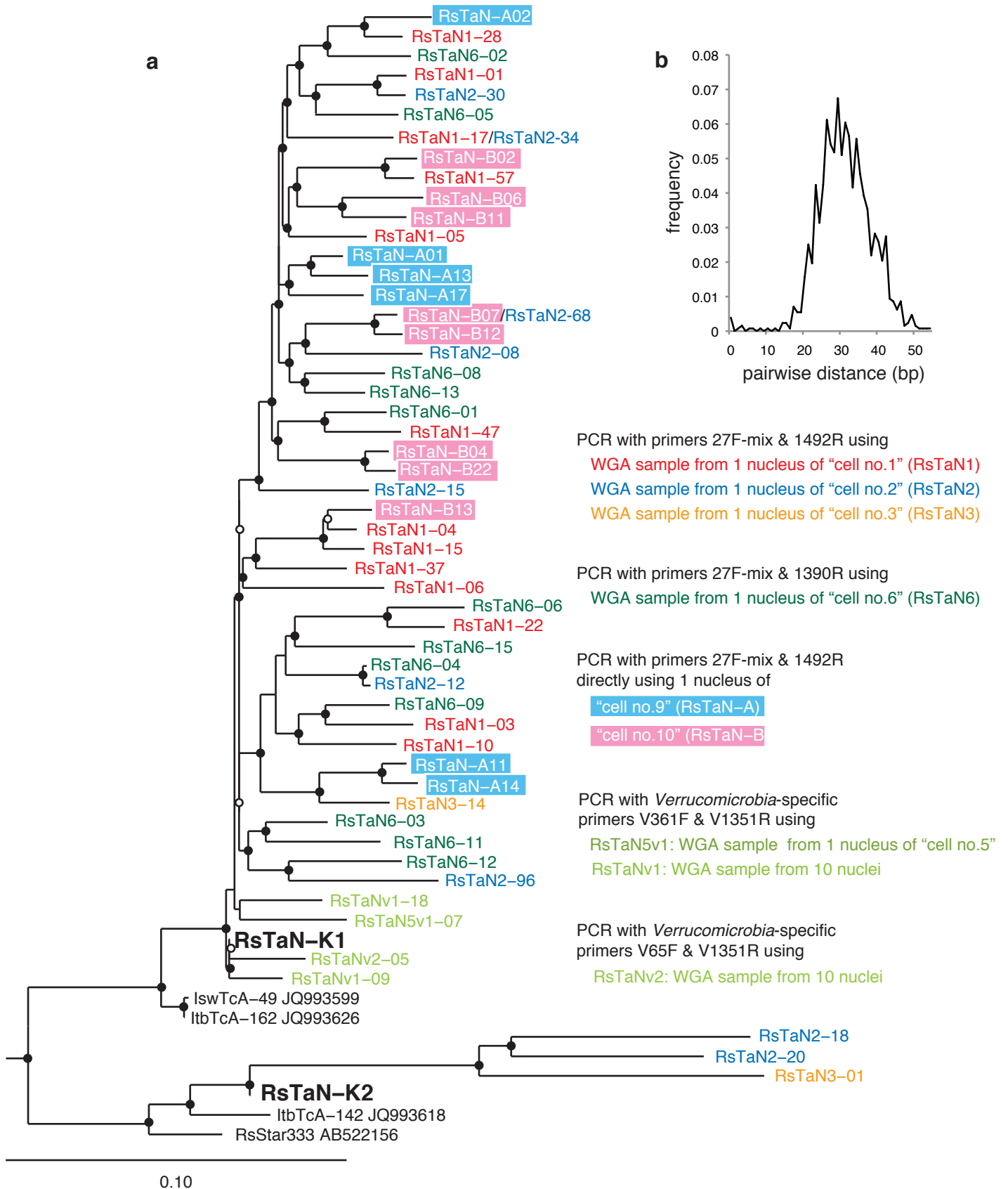


Figure S2 Phylogenetic relationships among the phylotypes of 16S rRNA pseudogenes. The phylotype was defined with 99.0% sequence identity. **(a)** A maximum likelihood tree. Clones CsOx50 (FN37791), ItbTcA-159 (JQ993624), and CsOx25 (FN37789) were used as outgroups. Open and closed circles at the nodes indicate the bootstrap confidence values of 70–94% and 95–100%, respectively. **(b)** The frequency of pairs of RsTaN-K1-related pseudogene phylotypes with the genetic distances.