

Legends to Supplemental Figures:

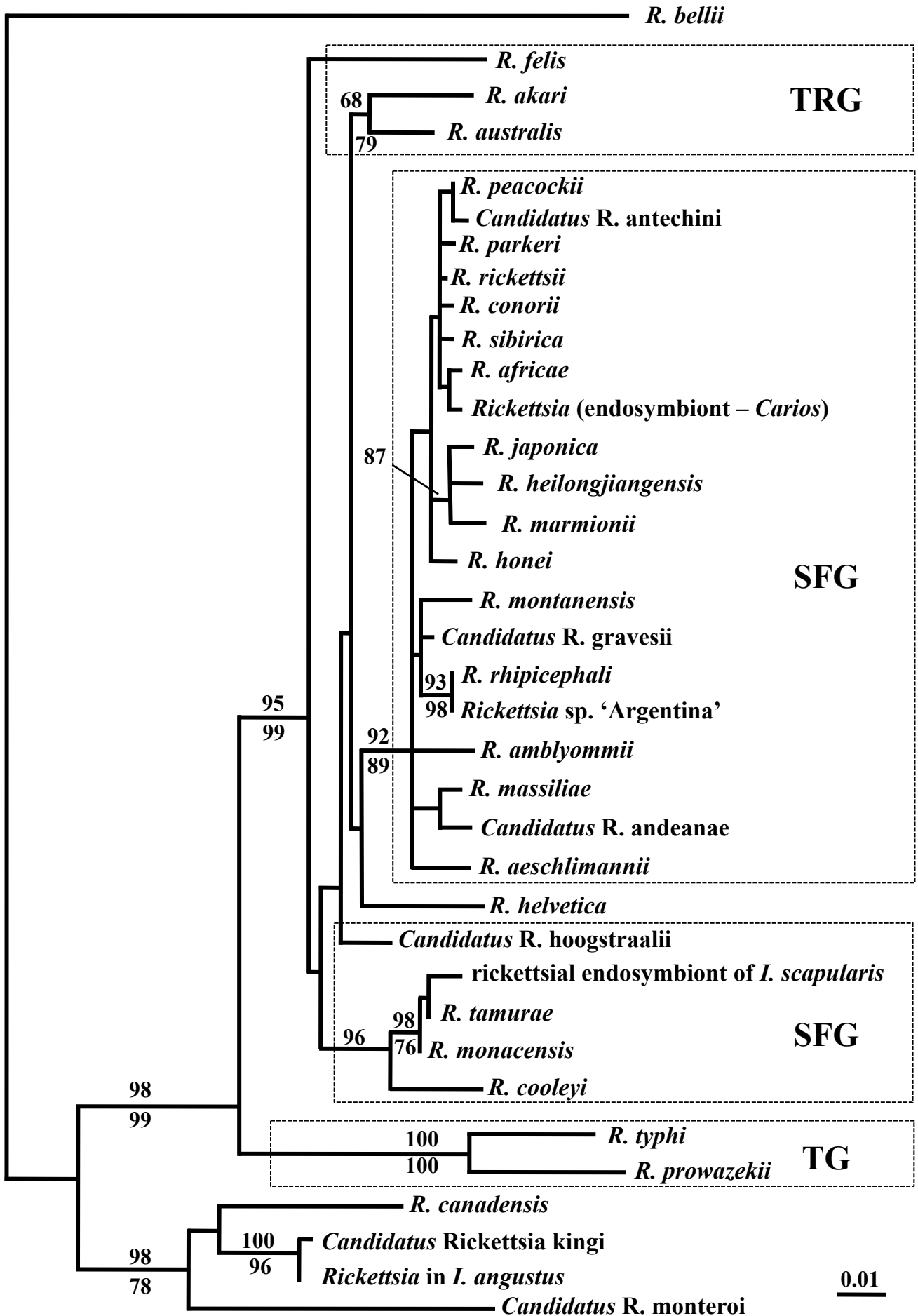
Figure S1. Neighbor-joining tree depicting the relationships of the sequences for the rickettsial 17-kDa gene of the rickettsiae in *Ixodes angustus* and those of other *Rickettsia* species. SFG, TRG and TG refer to the spotted fever group, transitional group and typhus group of *Rickettsia*, respectively. We have not included *R. helvetica* within the SFG based on the findings of a recent study [11] that considered the position of this species within the genus *Rickettsia* as *incertae sedis*. The scale bar represents the inferred substitutions per nucleotide site. The relative support for clades in the tree produced from the NJ and MP analyses are indicated above and below branches, respectively. The MP analysis of the same data set (i.e., 117 cladistically informative characters) produced over 1000 equally most-parsimonious trees (strict consensus tree not shown), with a length of 365, a CI of 0.69 and a RI of 0.73.

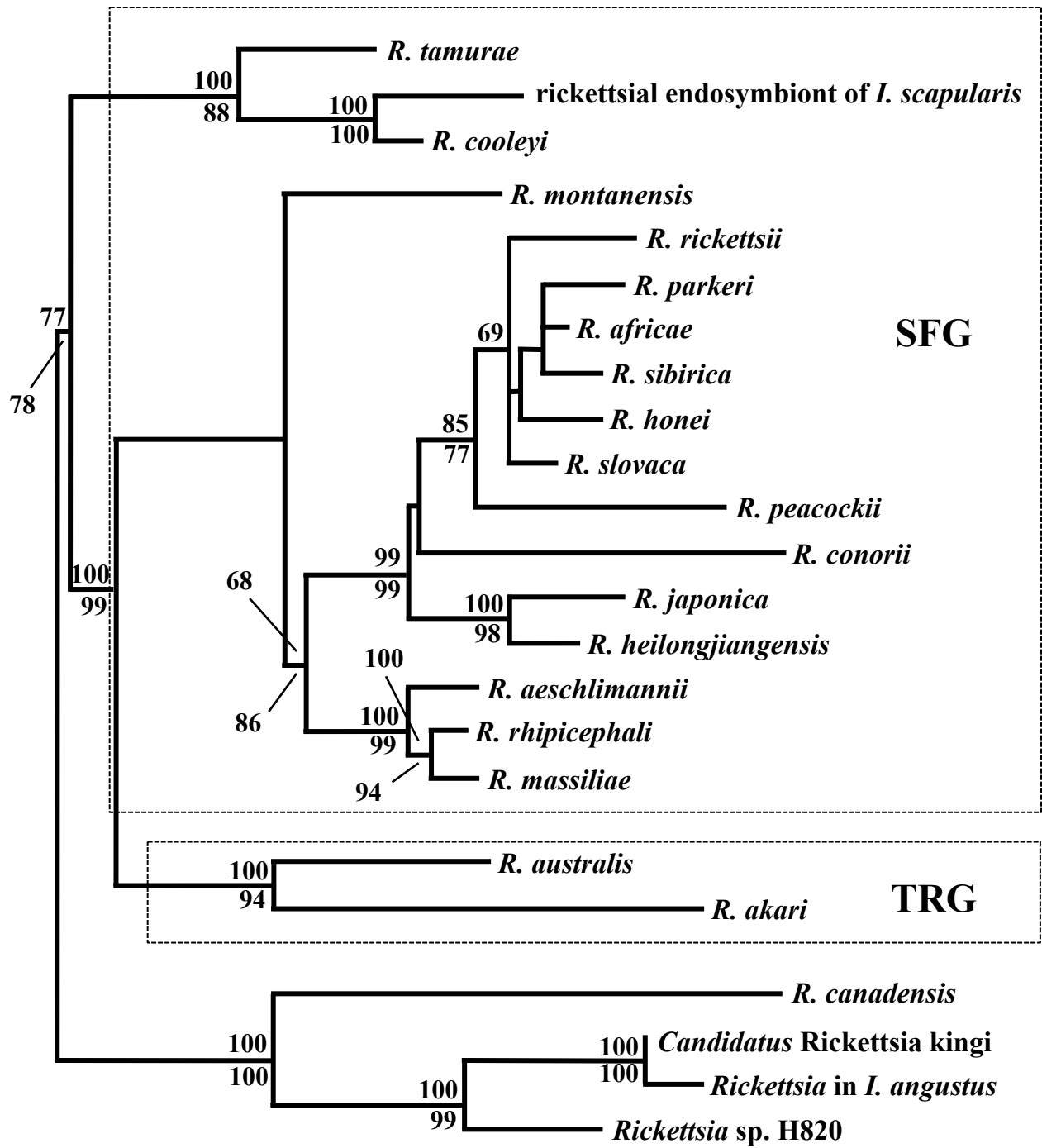
Figure S2. Neighbor-joining tree depicting the relationships of the outer membrane protein A gene (*ompA*) sequences for the rickettsiae in *Ixodes angustus* and those of other *Rickettsia* species. SFG and TRG refers to the spotted fever group and transitional group of *Rickettsia*, respectively. We have not included *R. helvetica* within the SFG based on the findings of a recent study [11] that considered the position of this species within the genus *Rickettsia* as *incertae sedis*. Representatives of the TG rickettsiae are not included because there are no *ompA* sequences for these taxa. The scale bar represents the inferred substitutions per nucleotide site. The relative support for clades in the tree produced from the NJ and MP analyses are indicated above and below branches, respectively. This clade also had 100% statistical support in the 30 equally most-parsimonious trees (length of 462, a CI of 0.67 and a RI of 0.77) based on 149 cladistically informative characters (tree not shown).

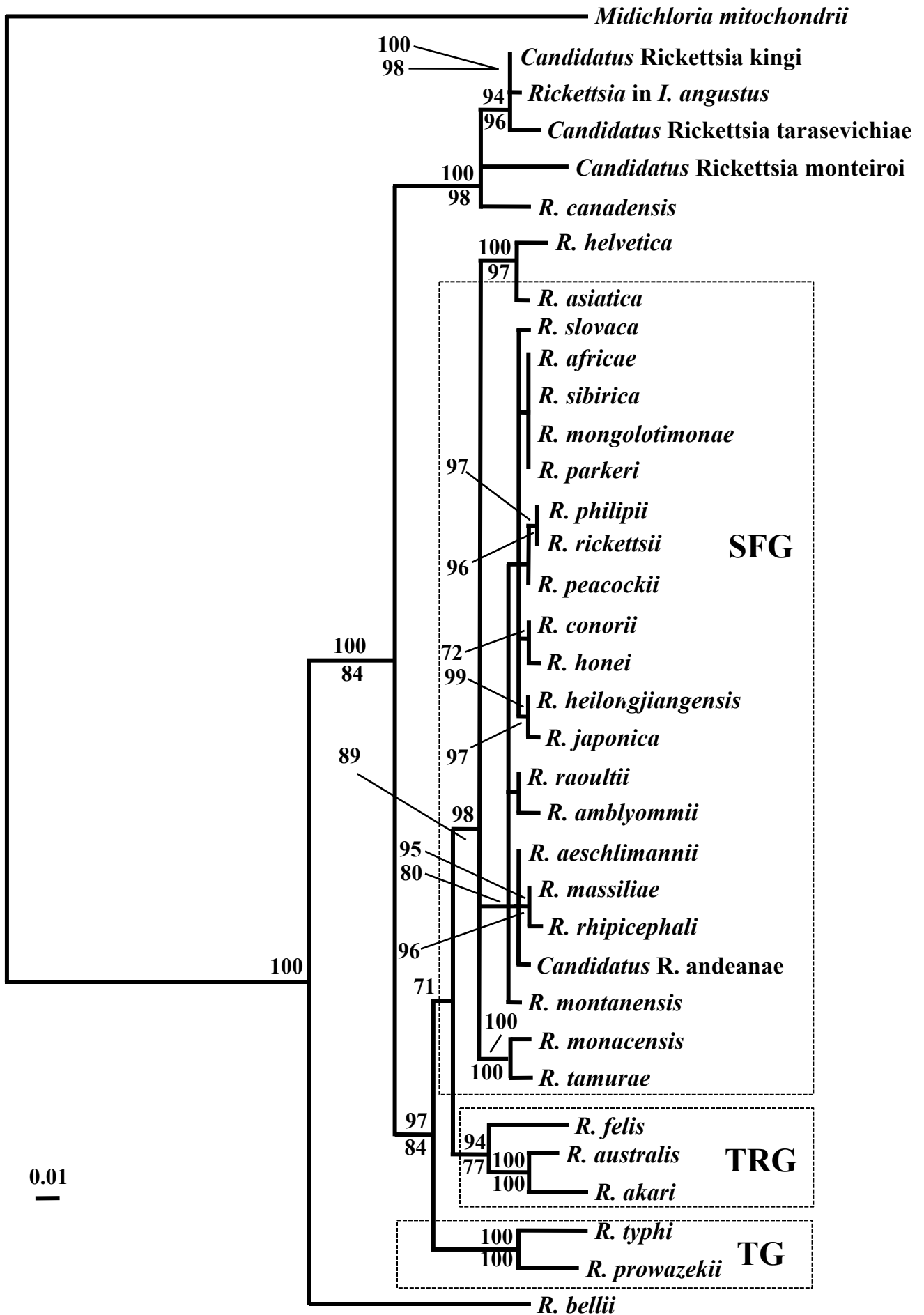
Figure S3. Neighbor-joining tree depicting the relationships of the citrate synthase gene (*gltA*) sequences for the rickettsiae in *Ixodes angustus* and those of other *Rickettsia* species. SFG, TRG and TG refer to the spotted fever group, transitional group and typhus group of *Rickettsia*, respectively. We have not included *R. helvetica* within the SFG based on the findings of a recent study [11] that considered the position of this species within the genus *Rickettsia* as *incertae sedis*. The scale bar represents the inferred substitutions per nucleotide site. The relative support for clades in the tree produced from the NJ and MP analyses are indicated above and below branches, respectively. The same clade was also strongly supported (98%) by the bootstrap analyses of the 84 equally most-parsimonious trees (length of 829, a CI of 0.71 and a RI of 0.73) based on 219 cladistically informative characters (tree not shown).

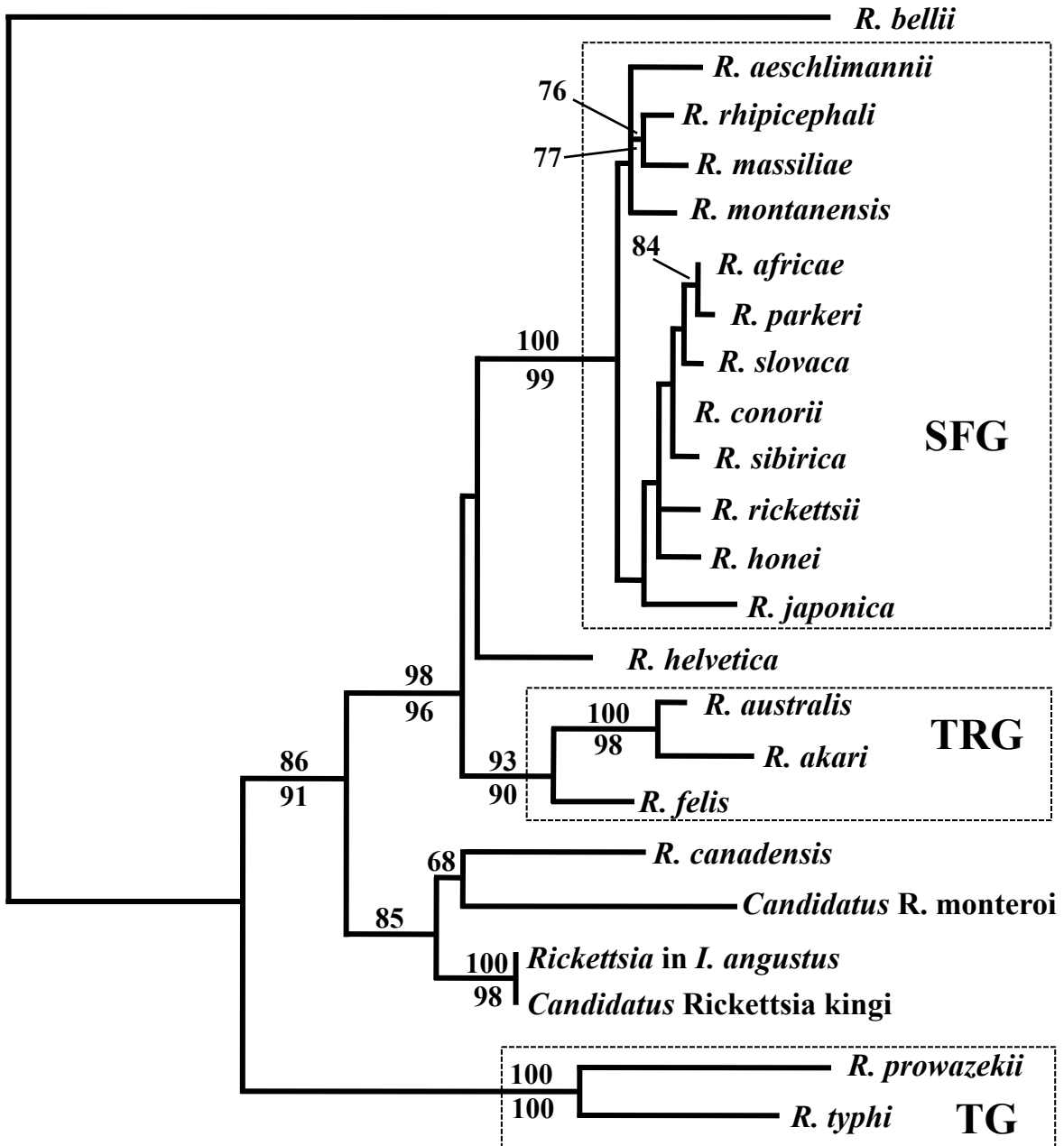
Figure S4. Neighbor-joining tree depicting the relationships of the surface cell antigen 1 gene (*sca1*) sequences for the rickettsiae in *Ixodes angustus* and those of other *Rickettsia* species. SFG, TRG and TG refer to the spotted fever group, transitional group and typhus group of *Rickettsia*, respectively. We have not included *R. helvetica* within the SFG based on the findings of a recent study [11] that considered the position of this species within the genus *Rickettsia* as *incertae sedis*. The scale bar represents the inferred substitutions per nucleotide site. The relative support for clades in the tree produced from the NJ and MP analyses are indicated above and below branches, respectively. The same clade was not supported by the bootstrap analyses of the 60 equally most-parsimonious trees (length of 262, a CI of 0.63 and a RI of 0.59) based on 85 cladistically informative characters (data not shown).

Figure S5. Neighbor-joining tree depicting the relationships of the sequences for the 16S-rRNA gene of the rickettsiae in *Ixodes angustus* and those of other *Rickettsia* species. SFG, TRG and TG refer to the spotted fever group, transitional group and typhus group of *Rickettsia*, respectively. We have not included *R. helvetica* within the SFG based on the findings of a recent study [11] that considered the position of this species within the genus *Rickettsia* as *incertae sedis*. The scale bar represents the inferred substitutions per nucleotide site. The relative support for clades in the tree produced from the NJ and MP analyses are indicated above and below branches, respectively.



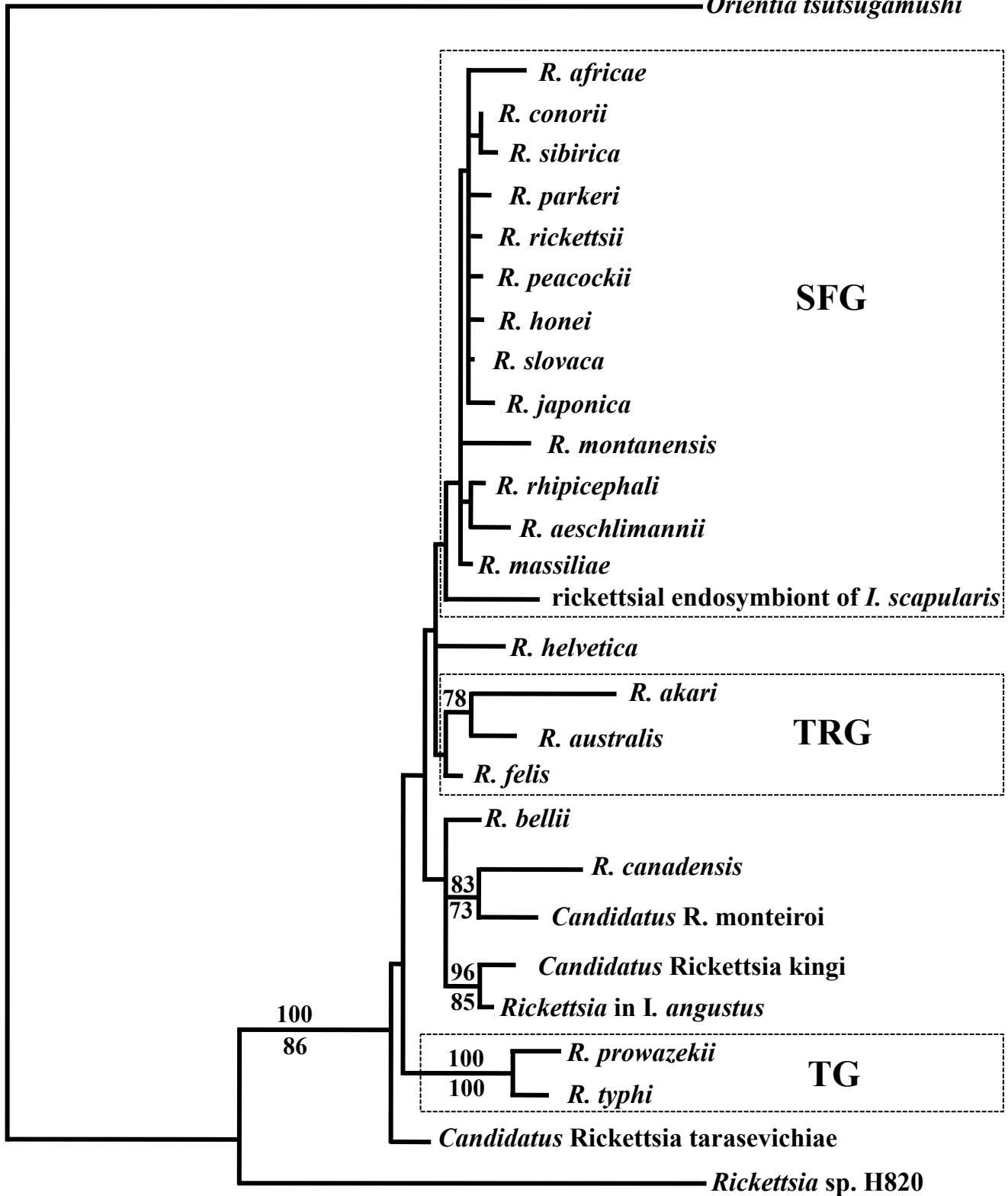






0.01

Orientia tsutsugamushi



0.01

Supplemental TABLE 1: The GenBank accession numbers of the rickettsial DNA sequences used in phylogenetic analyses.

Taxon	16S rRNA	17-kDa	Gene <i>gltA</i>	<i>ompA</i>	<i>sca1</i>
<i>R. aeschlimannii</i>	U74757	DQ3799979	AY259084	U43800	DQ306900
<i>R. africanae</i>	L36098	CP001612	U59733	U43790	DQ306901
<i>R. akari</i>	L36099	CP000847	U59717	CP000847	DQ306902
<i>R. amblyommii</i>	-	AY375162	-	-	-
<i>R. australis</i>	L36101	M74042	U59718	AF149108	DQ306903
<i>R. bellii</i>	L36103	AF445380	U59716	-	DQ306904
<i>R. canadensis</i>	L36104	CP000409	U59713	CP000409	DQ306905
<i>R. conorii</i>	L36105	AE006914	U59730	U43806	DQ306906
<i>R. cooley</i>	-	AF031534	-	-	-
<i>R. felis</i>	L28944	CP000053	AF210692	-	DQ306907
<i>R. heilongjiangensis</i>	-	AB473988	AY280709	AY280711	-
<i>R. helvetica</i>	L36212	AF181036	U59723	-	DQ306908
<i>R. honei</i>	L36220	AF027124	U59726	U43809	DQ306909
<i>R. japonica</i>	L36213	D16515	U59724	U43795	DQ306910
<i>R. marmionii</i>	-	AY737683	-	-	-
<i>R. massiliae</i>	L36214	CP000683	U59719	U43799	DQ306911
<i>R. monacensis</i>	-	EF380355	-	-	-
<i>R. montanensis</i>	L36215	U11017	U74756	U43801	DQ306912
<i>R. parkeri</i>	L36673	EF102237	U59732	U43802	DQ306913
<i>R. peacocki</i>	DQ062433	CP001227	DQ100162	AY357766	-
<i>R. prowazekii</i>	M21789	CP001584	M17149	-	DQ306914
<i>R. rhipicephali</i>	L36216	DQ865207	U59721	U43803	DQ306915
<i>R. rickettsii</i>	L36217	AY281069	U59729	U43804	DQ306916
<i>R. sibirica</i>	L36218	AF445384	U59734	U43807	DQ306918
<i>R. slovacae</i>	L36224	-	-	U43808	DQ306917
<i>R. tamurae</i>	-	AB114825	AY394896	AB114823	-
<i>R. typhi</i>	L36221	AE017197	U59714	-	DQ306919
<i>R. endosymbiont of Ixodes scapularis</i>	D84558	EF689734	-	EF689735	-
<i>R. endosymbiont of Carios kelleyi</i>	-	AY763102	-	-	-
<i>Rickettsia</i> sp. 'Argentina'	-	EU826507	-	-	-
<i>Candidatus R. andreanae</i>	-	GU395295	-	-	-
<i>Candidatus R. antechini</i>	-	DQ372953	-	-	-
<i>Candidatus R. gravesii</i>	-	DQ269436	-	-	-
<i>Candidatus R. hoogstraalii</i>	-	EF629538	-	-	-
<i>Candidatus R. kingi</i>	HF935068	HF935071	HF935074	HF935077	HF935080
<i>Candidatus R. monteiroi</i>	FJ269037	FJ269036	FJ269035	-	JF734727
<i>Candidatus R. tarasevichiae</i>	AF503168	-	AF503167	-	-
Undescribed <i>Rickettsia</i> sp. 'H820'	JF714221	-	-	JF714220	-