Figure Legends for Supplementary Figures

Supplementary Fig. S1 Phylogenetic tree of alpha-Proteobacteria based on the 16S rRNA sequences.

A phylogenetic tree based on the 16S rRNA sequences was constructed for selected members of alpha-Proteobacteria using the neighbor-joining method with the Kimura two-parameter model for nucleotide change.⁵³

Supplementary Fig. S2 Comparison of the restriction enzyme-digestion patterns deduced from the assembled sequence of *O. tsutsugamushi* strain Ikeda and those observed in the PFGE analysis.

The predicted lengths of each DNA fragment to be generated by the *EagI*, *SmaI* or *EagI-SmaI* digestion are shown. The fragment lengths observed in the PFGE analysis are given in parentheses.

Supplementary Fig. S3 Conventional and cumulative GC skew diagrams of the O. tsutsugamushi genome.

Red and black lines represent the results of cumulative and conventional GC skew analyses of the *O. tsutsugamushi* genome, respectively (sliding window size, 10

kb; step size, 500 bp). Based on the cumulative GC skew analysis, we defined the putative origin of replication (around the position of base pair 1). In this analysis, the maximum value was observed at the 1.37-Mb position, which may correspond to the replication terminus of the *O. tsutsugamushi* genome.

Supplementary Fig. S4 Genome comparison of *O. tsutsugamushi* with four sequenced *Rickettsia* species.

Red dots represent homologous CDSs identified by the BLASTP program (threshold: \geq 30% amino-acid sequence identity and \geq 60% coverage of the query sequence). The results of GC skew (pink) and G+C content (dark blue) analyses for each genome are also shown.

Supplementary Fig. S5 Amplification of repetitive sequences in the genomes of W. pipientis, A. phagocytophilum, R. bellii and O. tsutsugamushi.

The repetitive sequences and their positions and repetition rates were determined as described in the legend for Fig. 1. The vertical axes represent the repetition rates. *W. pipientis, A. phagocytophilum* and *R. bellii* are the obligate intracellular bacteria known to contain a large amount of repetitive sequences.

Supplementary Fig. S6 Extensive degradation of IS elements and MITEs in the O. *tsutsugamushi* genome.

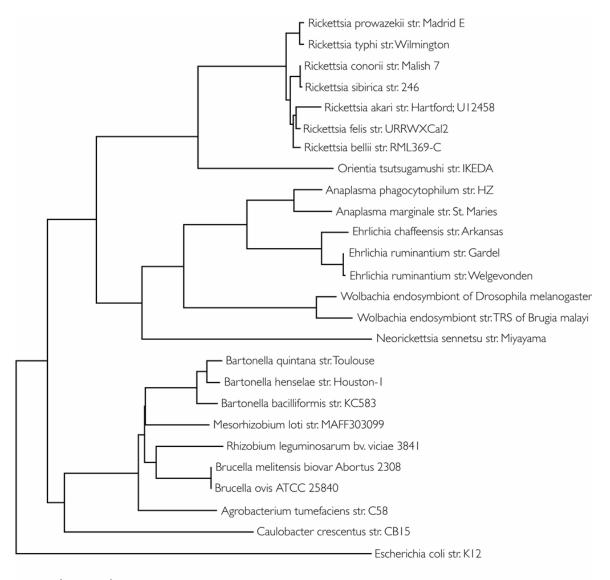
The size distributions of each IS element and MITE identified in the *O*. *tsutsugamushi* genome are shown. The length of the intact copy was rated as 100%. Extensive degradation has taken place in all types of elements, except for three small MITEs (mIS*Ot1*, mIS*Ot2*a and mIS*Ot2*a). The number of copies of each element is shown in parentheses.

Supplementary Fig. S7 Possible involvement of ISs/MITEs and/or OtAGEs in the gene amplification.

Ten patterns of positional relationship between the three types of mobile genetic elements and repeated genes belonging to 31 OtRG families (from OtRG55 to OtRG85, excluding repeated genes belonging to the families for the core components of the OtAGE, IS transposases and reverse transcriptase) are shown. The number of copies of the repeated genes exhibiting each pattern is shown for each OtRG family. IS elements and MITEs are not distinguished in this figure. Among the 85 repeated genes belonging to the 31 OtRG families, 69 (81.2%) are located adjacent to the mobile genetic elements.

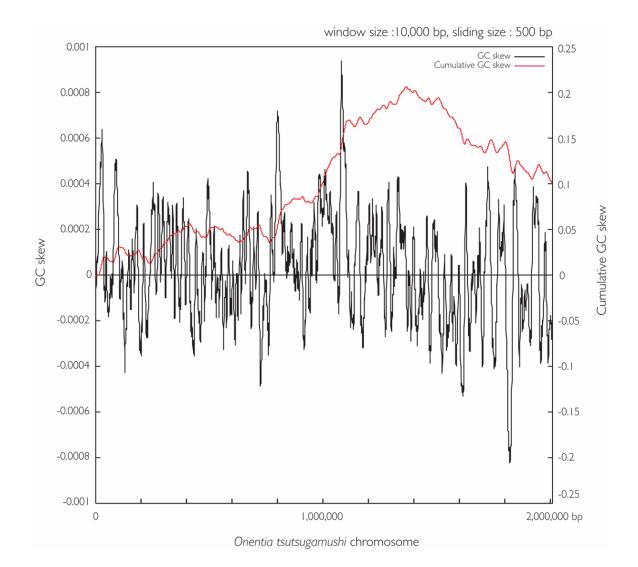
Supplementary Fig. S8 Organization of T4SS-related genes in the genomes of obligate intracellular bacteria belonging to the order *Rickettsiales*.

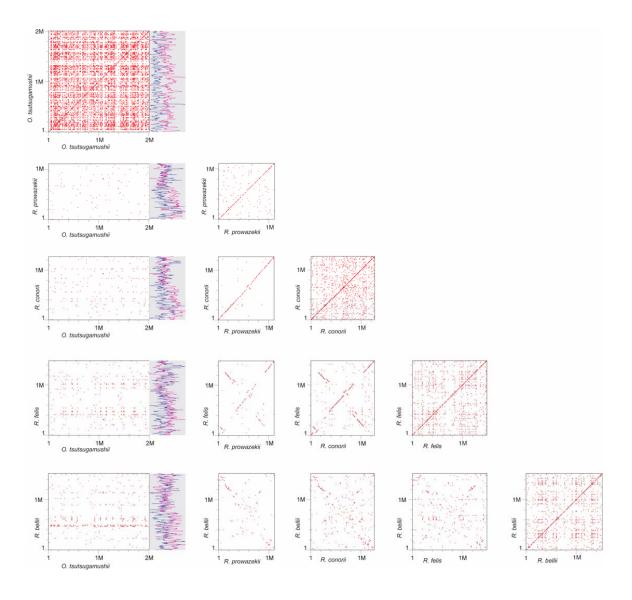
The relative locations of T4SS-related genes in the genomes are shown for 14 obligate intracellular bacteria belonging to the order *Rickettsiales*. The CDS ID of each gene is indicated by a red number.

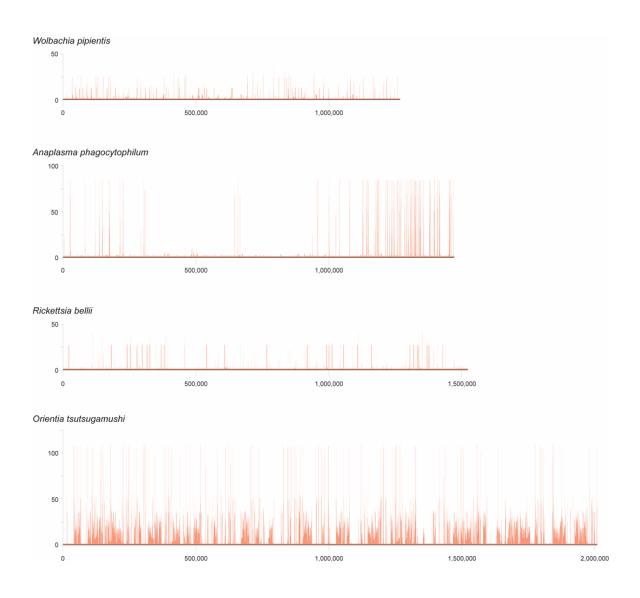


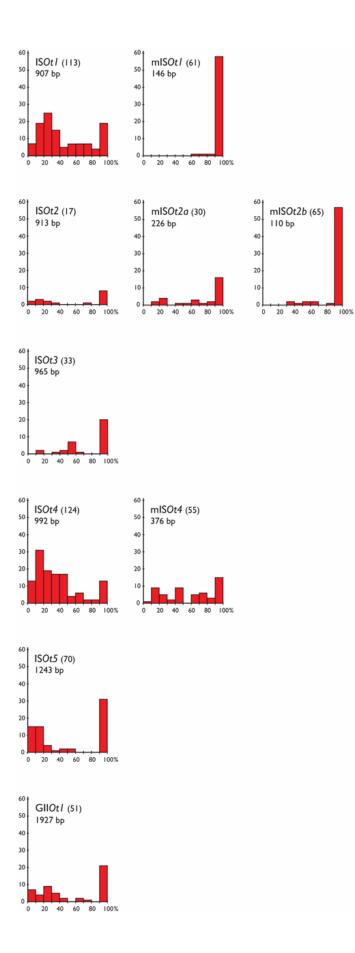
0.02

[l		238.6 137 (245) (14		355.2 (365)	151.2 148.3 (160) (155)	777.2 (770)	kb
Eagl							
Smal	552.5 (560)	22.2 (-)	705.1 (690)		294.3 (305)	434.8 (445)	kb
Eagl & Smal	346.9 (350)	205.6 10.8 13 (215) (-) (14		355.2 (365)	0.6 150.5 143.8 4.5 (-) (160) (150) (-)	430.2 (440)	kb
Lugi & Sindi		22.2					









	OtRG#	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85
Т	OtAGE_a OtRG OtAGE_a				4			3				I		I							Ι							2			2	1
2	OtAGE_a IS OtRG OtAGE_a	I																														
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<u></u>	virB3	vir84	vir86	virBó	virBó	virB6	virB8 trbG	vi86 viD4 vi811 vi810 vi88 vi84
Orientia tsutsugamushi	0769	0770	0771	0772	0773	0774	1077 1078	1404 1567 1568 1569 1370 1371 0002
Rickettsia bellii	vir83	virB4-1	vir86-	vir86-2	vir86-3	vir86-4	vir86-5	vir89-1 vir88-2 vir89-1 vir88-1 vir89-2 vir810 vir811 virD4 vir84-2
hickettsiu beii	1275	1266	1265	1264	1263	1262	1261	1012 1013 1014 1015 1016 1017 1018 0080 RP288 RP290
Rickettsia prowazekii		RPI03	RP104	RP105	RP106	RP107	RP108	RP285 RP287 RP289 RP291 RP292 RP293 RP784
		103	104	105	106	167	108	285 287 288 289 270 291 292 293 784 RF_0464 vir69_2
Rickettsia felis		virB4	vi66_1	virB6_2	vir86_3	vir86_4	vir86_5	vi88_1 vi88_1 vi88_2 vi810 vi811 vi04 vi84_2
	0087	COBB	0089	00%0	0091	0092	0093	0462 0463 0464 0465 0466 0467 0468 0469 1250 RC0387
Rickettsia conori	RC0140	virB4	RC0142	RC0143	11	RC0145	RC0146	105 vit88 RC0386 vit89 vit810 vit811 vit24 vit84
	0140 vir83	virB4a	0142 RT0032	0143 RT0031	RT0030	0145 RT0029	0146 RT0028	0384 0385 0384 0387 0388 0389 0390 0391 1217 RT0279 vi499 vi491 trsG RT0279 RT0280 vi4810 vi4811 vi404 vi4945
Rickettsia typhi		0033	0032	0031	0000	0029	0038	
	virB3	w84-1	virB6	APH_0375	APH_0376		APH_0377	مرتح مرتق مرتف APH_0417 APH_0419 - ش64-2 - ش104 - ش1811 - ش1810 - ش189-2 - ش184 - ش19
Anaplasma phagocytophilum	0372	0373	0374	0375	0376		0377	
Anoplasma marginale St. Maries	vieB.)	virB4	vir86	AM812	AMBII	-	AMBID	A11757 0-bG wills wills will will will will will a start and a sta
Phoposina marginale Sc. Maries	#<5 w#83	uir84	#1) virB6	B12 ERUPH5230	ERUM(5220		ERUM5210	757 097 1316 1315 1314 (31) 1313 wi88 wi89 wi810 wi811 wiQ4
hrlichia ruminantium Welgevonden	100	3250	1240	500	1330		5210	ERU/M410 CON 0200 CON 0200 CON
	virB3	wB4-1	vir86	ECH_0497	ECH_0498		ECH_0499	+++0 000 000 000 000 000 000 7330 w988.1 we88.2 we84.2 we04 we811 we80 w9811
Ehrlichia chaffeensis Arkansas	0494	-5415	OTH.	ORI	ONDE		. ORM	
		ECAL0523	ECAL_0532	ECAL_0531	ECAL0530		ECAL 0529	ECAL,0448 ECAL,0021 ECAL,0019 ECAL,0018 ECAL,0787
Ehrlichia canis Jake	05.94	(633	6532	(653)	0530		0529	0446 0022 0021 0020 0019 0014 076
Wolbachia endosymbiont		WBM0797	W8M0796	WBM0795	W9M0294	WBM0793	W8M0641 W8M0591	WBH0282 WBH0380 WBH0283 WBH0281 WBH0279
strain TRS of Brugia malayi	6/790	0.797	0.79%	ens	0.94	Q793		UIRE COR COR COR COR
Wolbachia pipientis wMel		WCX0858	WD0857	WD0856	WD0855	WD0854	1010	WD0007 WD0005 WD1104
	0859	NSE_0863	0817 NSE_0862	NSE_0861	NSE_0860	NSE_0859	NSE_0743 NSI	
Neorickettsia sennetsu Miyayama	П						NSE_0742	