

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 (mISOt1, mISOt2a and mISOt2a). The number of copies of each element is shown in parentheses.

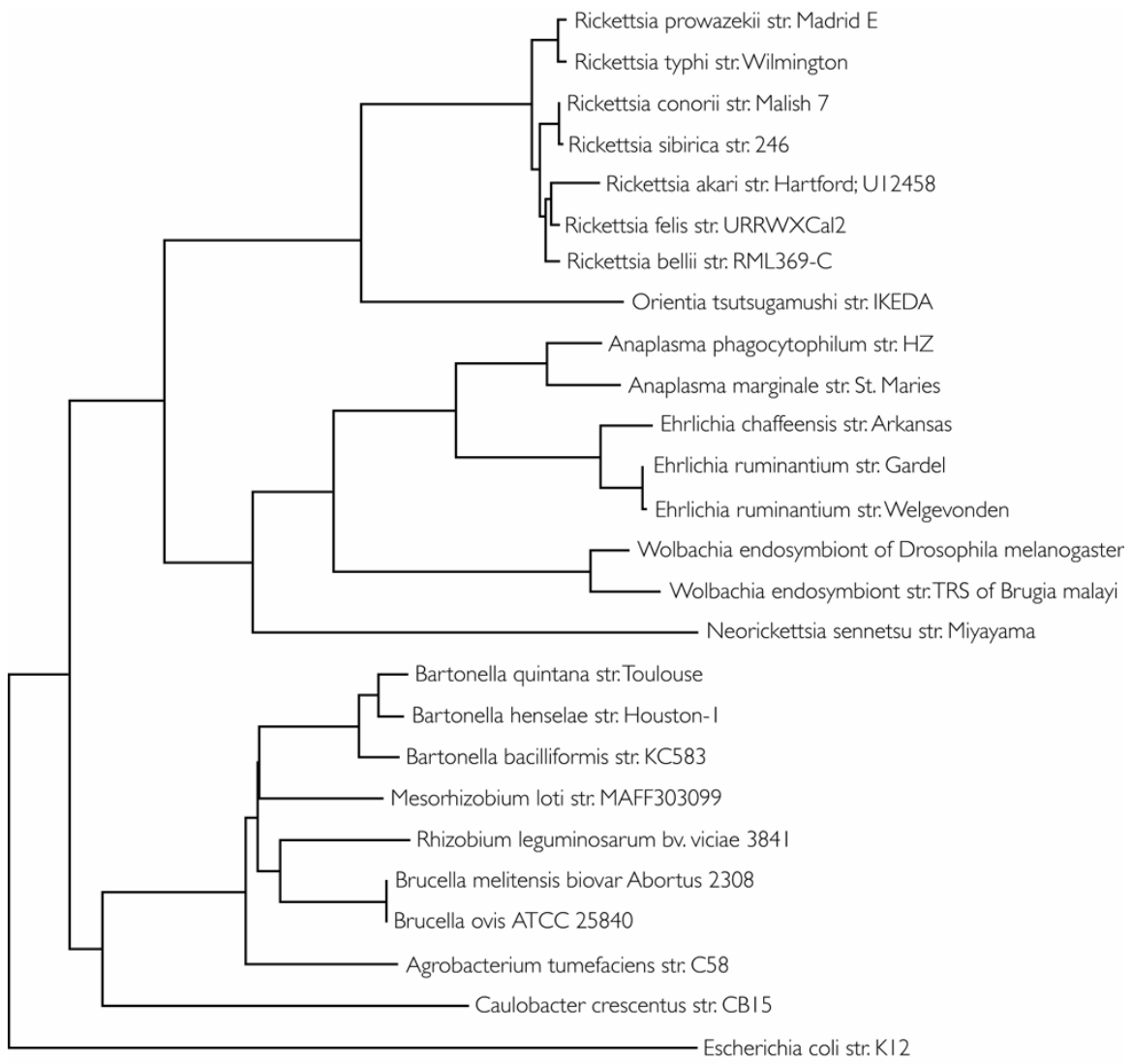
Supplementary Fig. S7 Possible involvement of ISs/MITEs and/or OtAGEs in the gene amplification.

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

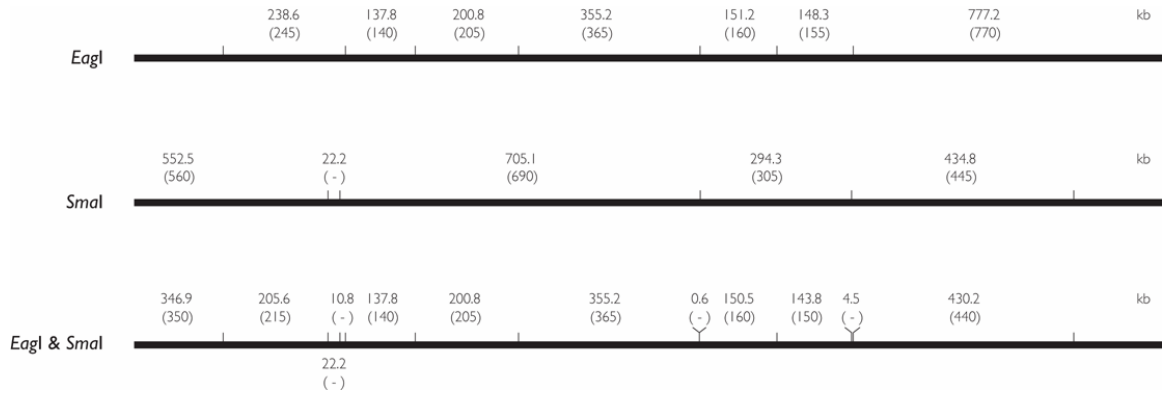
genetic elements.

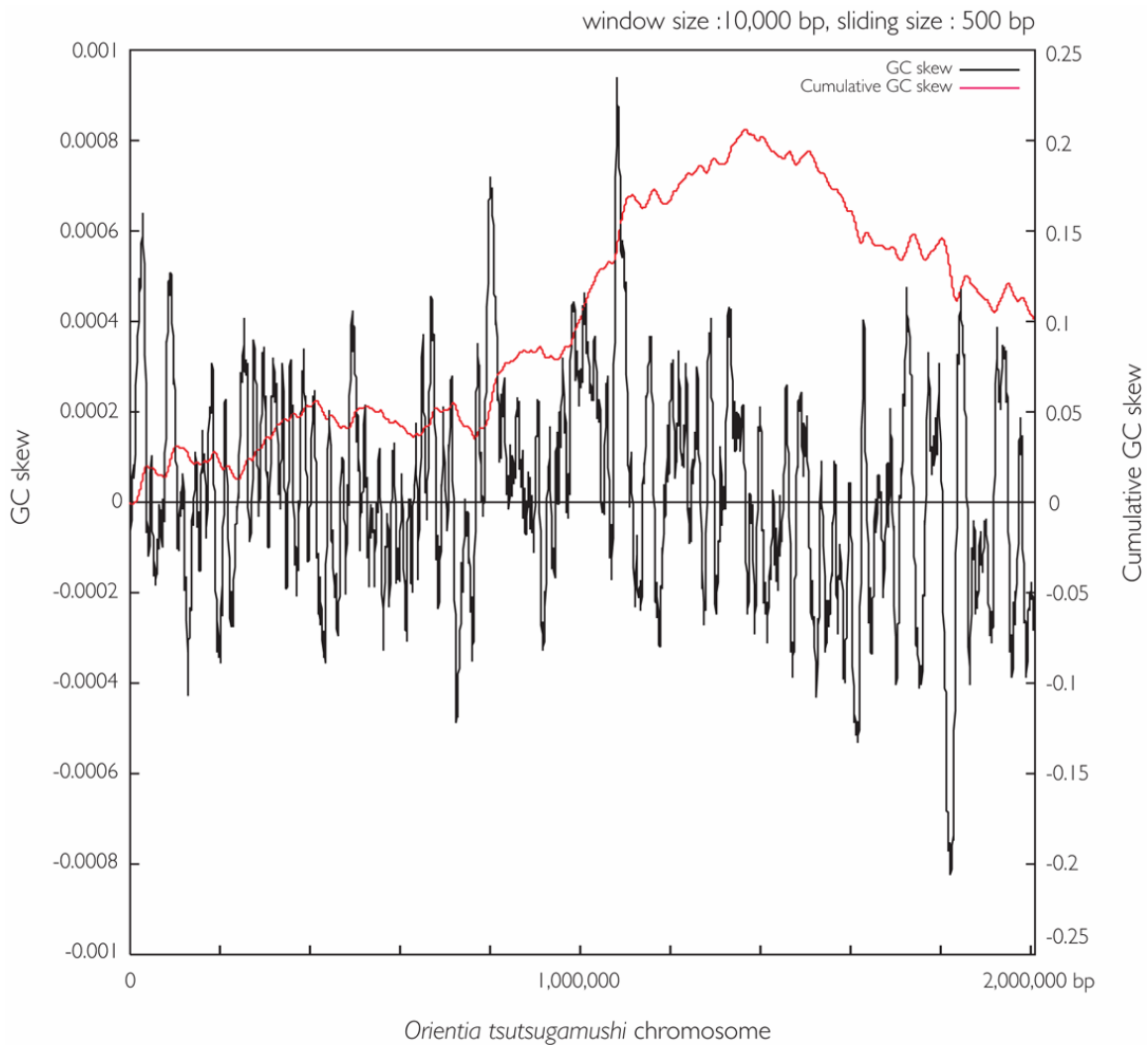
Supplementary Fig. S8 Organization of T4SS-related genes in the genomes of obligate intracellular bacteria belonging to the order *Rickettsiales*.

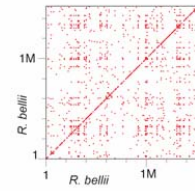
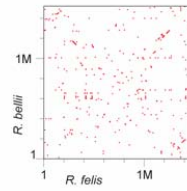
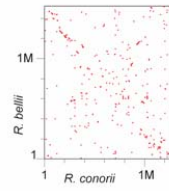
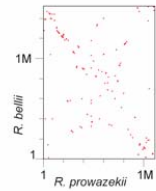
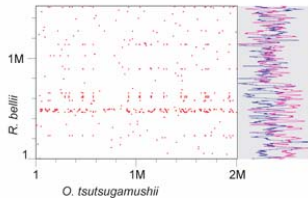
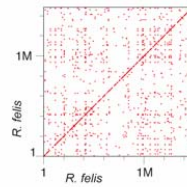
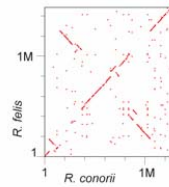
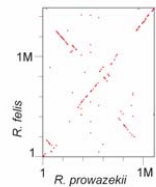
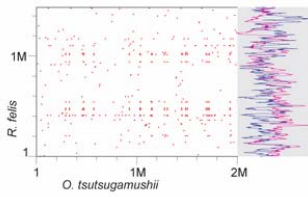
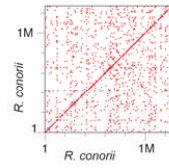
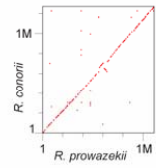
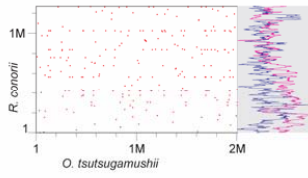
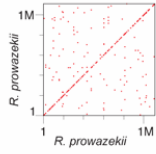
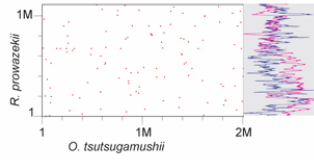
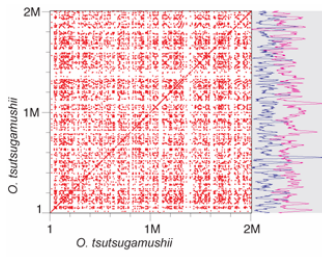
The relative locations of T4SS-related genes in the genomes are shown for 14 obligate intracellular bacteria belonging to the order *Rickettsiales*. The CDS ID of each gene is indicated by a red number.



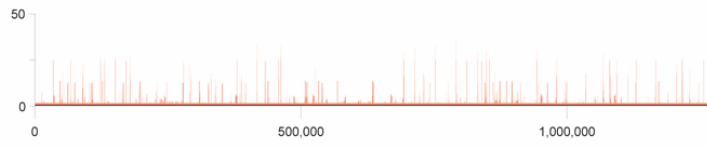
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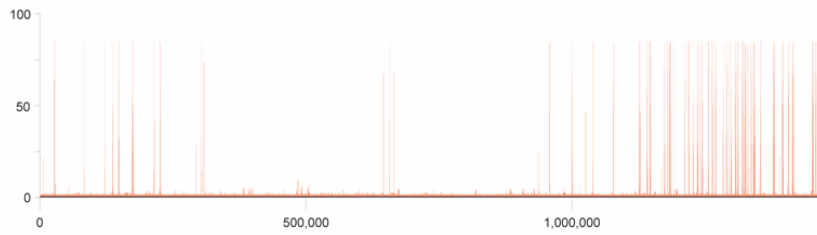




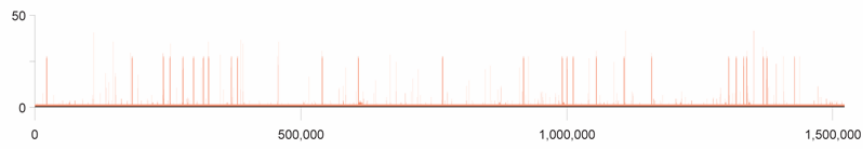
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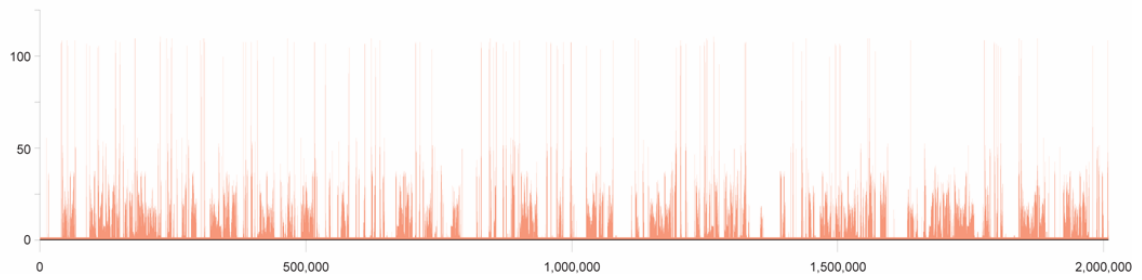
Anaplasma phagocytophilum

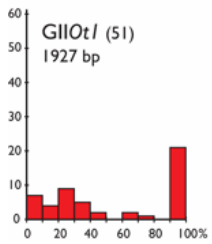
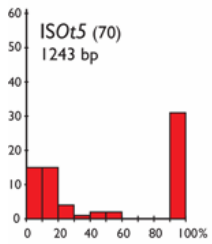
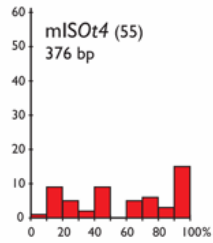
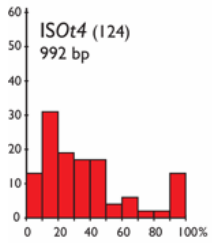
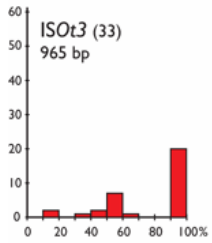
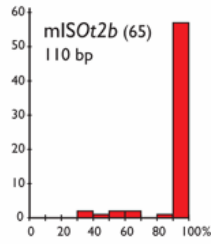
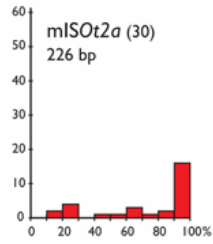
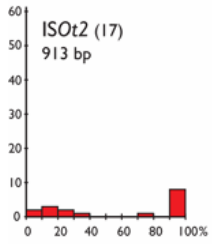
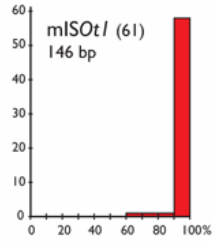
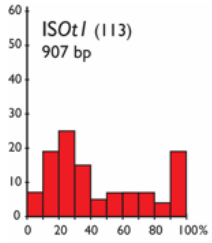


Rickettsia bellii



Orientia tsutsugamushi





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
1	OtAGE_a OtRG OtAGE_a			4		3					1	1								1							2		2	1	
2	OtAGE_a IS OtRG OtAGE_a			1																											
3	OtAGE_a OtRG OtAGE_b			1		1		2		1	1									1											
4	OtAGE_a IS OtRG IS OtAGE_b			1																											
5	OtAGE_a IS OtRG OtAGE_b															1															
6	OtAGE_a IS OtRG IS			2															1												
7	OtAGE_a OtRG IS			1	1		1				1	1												1							
8	OtAGE_a OtRG			2	4	4	1	2	1	1	1	1	1	1							2	2						1	1		
9	IS OtRG			3						1	1				1	1	1	1						1			2	1			
10	OtRG			1					1	1	1	1	1	1	1	1			2		2				2	2					

