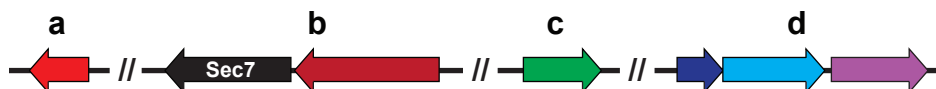
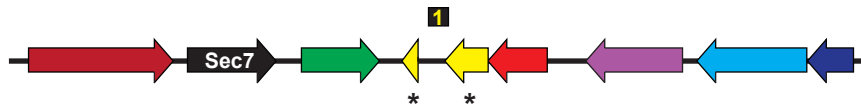
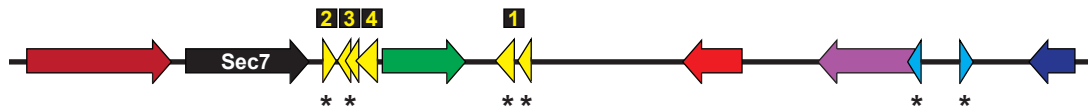
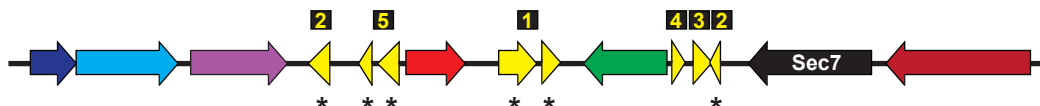
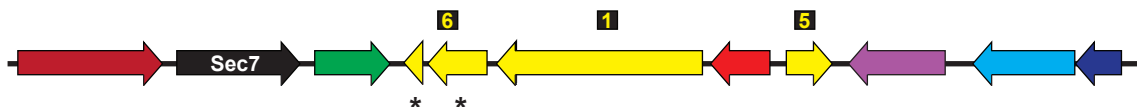
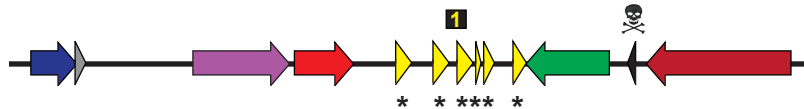
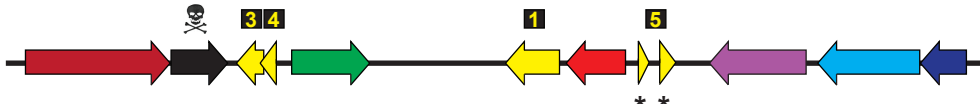
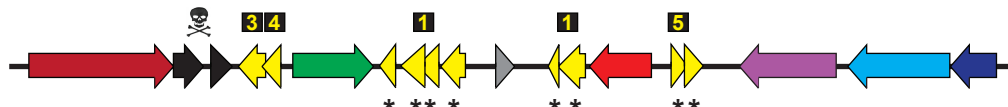
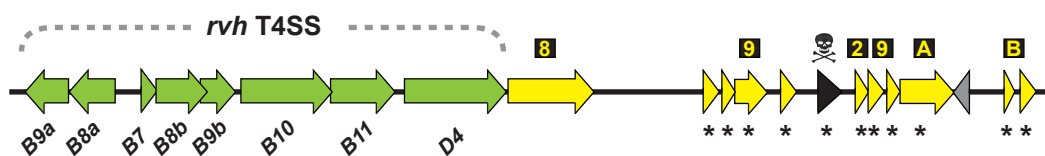


S5 Fig. Genome synteny analysis across the *raIF_R* loci from select *Rickettsia* genomes.

For select *Rickettsia* genomes, gene neighborhood models were constructed using the Kyoto Encyclopedia of Genes and Genomes (KEGG) database [1], with manual adjustment to gene annotations. Genome coordinates are provided for each species, except for *R. bellii*, for which four separate loci are shown that contain genes found in the single *raIF* loci of all other *Rickettsia* species. The genome coordinates for these separate loci are as follows: a, 714015-714959; b, 955271-959620; c, 1037705-1038928; d, 1082690-1086679. These separate loci reflect the substantial gene rearrangement in *R. bellii* genomes relative to all other *Rickettsia* species [2]. (A) *raIF* gene neighborhood models for ten *Rickettsia* species. The six species at top contain genes encoding full-length RaIF proteins (noted with 'Sec7' on the *raIF* gene model). The remaining four species contain *raIF* genes that lack the regions encoding the S7D and SCD. (B) The genome of *R. akari* is unique in that it contains a second *raIF* locus, which is found within a highly pseudogenized region that flanks a cluster of *rvh* (*Rickettsiales vir* homolog) type IV secretion systems genes.

References

1. Ogata H, Goto S, Sato K, Fujibuchi W, Bono H, Kanehisa M. KEGG: Kyoto encyclopedia of genes and genomes. *Nucleic Acids Research*. 1999. pp. 29–34. doi:10.1093/nar/27.1.29
2. Gillespie JJ, Williams K, Shukla M, Snyder EE, Nordberg EK, Ceraul SM, et al. *Rickettsia* phylogenomics: Unwinding the intricacies of obligate intracellular life. *PLoS One*. 2008;3. doi:10.1371/journal.pone.0002018

A*R. bellii* RML369-C
(four separate loci)*R. typhi* Wilmington
(455946-469200)*R. prowazekii* p22
(454330-467529)*R. akari* Hartford
(501203-517955)*R. australis* Cutlack
(926889-942964)*R. felis* URRWxCal2
(622072-639690)*R. canadensis* McKiel
(728159-740397)*R. montanensis* OSU 85-930
(1213647-1228762)*R. conorii* Malish 7
(500323-514926)*R. rickettsii* Sheila Smith
(503544-519015)**B***R. akari* Hartford
(382294-398684)

■ Malic enzyme oxidoreductase/phosphotransacetylase (MaeB)

■ Sec7 domain containing protein (RalF)

■ Proline/betaine transporter (ProP3)

■ Malate dehydrogenase (Mdh)

■ ATP/ADP translocase (Tlc2)

■ CTP synthase (PyrG)

■ 3-deoxy-manno-octulosonate cytidyltransferase (KdsB)

■ Hypothetical protein (HP)

☠ RalF ORFs lacking at least the Sec7 domain. Other truncated or split ORFs are noted with an asterisk.

■ Other genes, which encode:

1 HP with SMC_prok_B domain (TIGR02168)

2 Transposase IS200-family protein

3 Toxin of T-AT module; PIN_VapC-like

4 Antitoxin of T-AT module; MazeE-like

5 Ankyrin repeat-containing protein

6 Transposase, Mutator family; cl19537

7 HP containing RPE4

8 guanosine pentaphosphate phosphohydrolase

9 Surface cell antigen 7 (Sca7)

A Surface cell antigen 3 (Sca3)

B Putative transposase, YhgA-like; pfam04754