

Supplemental file 3

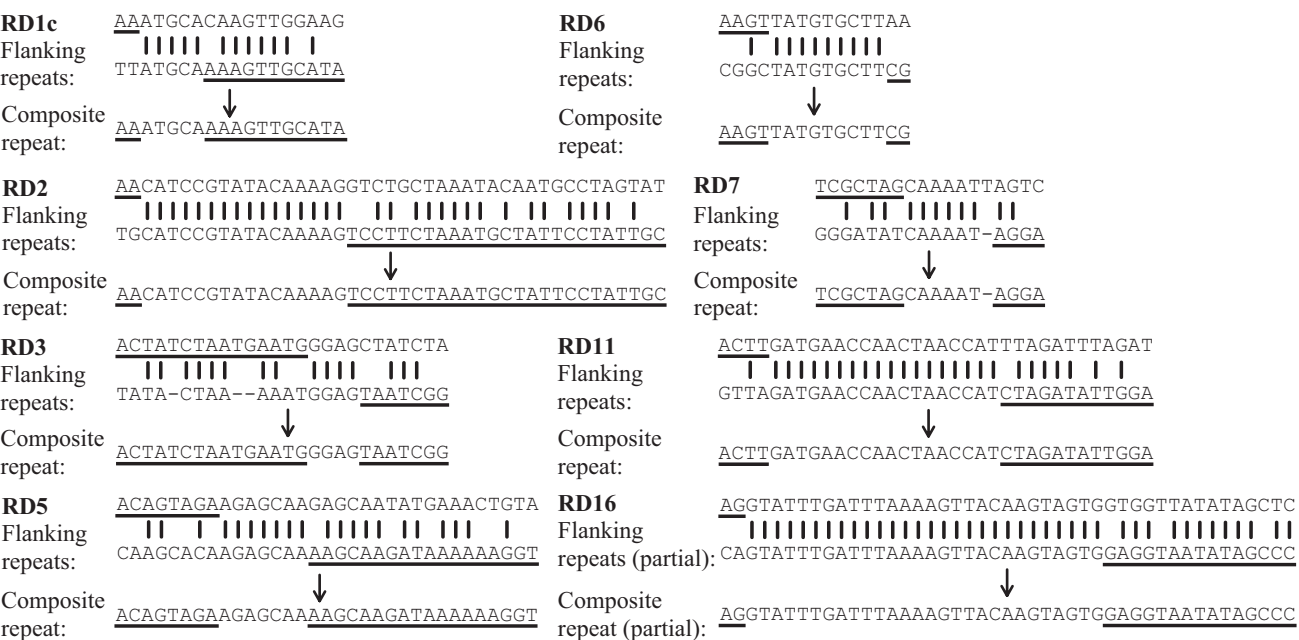


FIGURE S1. Alignment of direct repeated sequences that define the RDs analyzed in the present study. The arrow indicates the evolutionary direction of a deletion event. Nucleotide sequences are shown before (flanking repeats) and after (composite repeat) the deletion of intervening sequence. Flanking repeat sequences were extracted from the *F. tularensis* strain SCHU S4 genome sequence (13). Composite repeat sequences were derived from *F. tularensis* strains exhibiting deletion.

<i>F. tularensis</i> subspecies	Isolate	Nucleotide and amino acid substitution (gene and position)																																						
<i>novicida</i>	FSC040	C	C	A	C	C	G	G	G	C	C	C	C	C	C	C	C	C	T	T	C	G	G	C	G	C	C	C	G	T	G	T	C	T	C	G	C	A		
<i>tularensis</i> (Type A)	FSC041	C	A	A	C	C	G	G	G	C	C	C	C	C	C	C	C	A	C	C	T	T	C	G	G	C	G	C	T	C	G	T	G	C	C	T	C	G	C	G
	FSC198	C	A	A	C	C	G	G	G	C	C	C	C	C	C	C	C	A	C	C	T	T	C	G	G	C	G	C	T	C	G	T	G	C	C	T	C	G	C	G
	FSC237	C	A	A	C	C	G	G	G	C	C	C	C	C	C	C	C	A	C	C	T	T	C	G	G	C	G	C	T	C	G	T	G	C	C	T	C	G	C	G
	FSC230	C	C	A	C	C	G	G	G	C	C	C	C	C	C	C	C	G	C	C	T	T	C	G	G	C	G	C	T	C	G	T	G	T	C	T	T	A	C	A
	FSC054	C	C	A	C	C	G	G	G	C	C	C	C	C	C	C	C	G	C	C	T	T	C	G	G	C	G	C	T	C	G	T	G	T	C	T	T	A	C	A
<i>mediasiatica</i>	FSC147	C	C	G	C	C	G	A	G	C	C	C	C	C	C	C	C	G	C	C	T	C	G	A	C	G	C	T	C	A	C	A	T	T	T	C	G	C	A	
	FSC148	C	C	G	C	C	G	A	G	C	C	C	C	C	C	C	C	G	C	C	T	C	G	A	C	G	C	T	C	A	C	A	T	T	T	C	G	C	A	
<i>holarctica</i> from Japan	FSC021	C	C	A	C	T	A	G	T	C	C	C	C	A	C	G	C	T	C	G	T	G	G	C	A	C	T	T	G	T	G	T	C	A	C	G	C	A		
	FSC022	T	C	A	C	T	A	G	T	C	C	C	C	A	C	G	C	T	C	G	T	G	G	C	A	C	T	T	G	T	G	T	C	A	C	G	C	A		
<i>holarctica</i> (Type B)	FSC035	C	C	A	T	T	A	G	G	T	T	T	C	A	T	G	A	T	C	G	T	T	G	T	A	A	T	T	G	T	G	T	C	A	C	G	T	A		
	FSC150	C	C	A	T	T	A	G	G	T	T	T	C	A	T	G	A	T	C	G	T	T	G	T	A	A	C	T	G	T	G	T	C	A	C	G	T	A		
	FSC155	C	C	A	T	T	A	G	G	T	T	T	C	A	T	G	A	T	C	G	T	T	G	T	A	A	C	T	G	T	G	T	C	A	C	G	T	A		
	FSC200	C	C	A	T	T	A	G	G	T	T	T	C	A	T	G	A	T	C	G	T	T	G	T	A	A	C	T	G	T	G	T	C	A	C	G	T	A		
	FSC257	C	C	A	T	T	A	G	G	T	T	T	C	A	T	G	A	T	C	G	T	T	G	T	A	A	C	T	G	T	G	T	C	A	C	G	T	A		
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FIGURE S2. Single nucleotide variations in seven genes and fifteen strains of *F. tularensis*. Nucleotide variation (gray shading) and predicted amino acid substitution are indicated in reference to *F. tularensis* subsp. *novicida* (FSC040). Nucleotide sites that were unique to *F. tularensis* subsp. *novicida* (41 / 3135 base pairs) are not shown. Single nucleotide variations (37 / 3135 base pairs) of *F. tularensis* subsp. *tularensis*, *mediasiatica* and *holarctica* are shown. Nucleotide position refers to the genome of *F. tularensis* strain SCHU S4 (13).

SNVs in seven genes. Six SNVs divided type A isolates into two distinct groups. By showing seven unique sites, isolates of subspecies *mediasiatica* were distinct from other subspecies. Isolates from Japan showed only two unique SNVs and appeared intermediate to subspecies *tularensis* and Eurasian/North American subsp. *holarctica* isolates insofar they shared SNVs with both groups. Among Eurasian/North American subsp. *holarctica* isolates, 12 SNVs were unique to the subspecies. The single North American representative was distinct from Eurasian isolates at three sites. Two of the loci (*aroA*, *tpiA*) appeared to be under strong stabilizing selection pressure with a high proportion of synonymous nucleotide substitutions, while other loci showed many non-synonymous substitutions.