

	<i>F. tularensis</i> subsp <i>holarctica</i> LVS bS21-1	<i>F. tularensis</i> subsp <i>holarctica</i> LVS bS21-3	<i>F. tularensis</i> subsp <i>holarctica</i> LVS bS21-2	<i>E. coli</i> bS21
<i>F. tularensis</i> subsp <i>holarctica</i> LVS bS21-1	100.0	72.3	54.0	50.8
<i>F. tularensis</i> subsp <i>holarctica</i> LVS bS21-3		100.0	47.6	48.5
<i>F. tularensis</i> subsp <i>holarctica</i> LVS bS21-2			100.0	60.0
<i>E. coli</i> bS21				100.0

Figure S2. The three bS21 homologs in *F. tularensis* are distinct. Percent identities of amino acid sequences for *F. tularensis* LVS bS21-1, bS21-2, bS21-3, and *E. coli* bS21 were calculated using the multiple sequence alignment tool ClustalOmega (2). The bS21 homologs in *F. tularensis* are similar to each other, particularly bS21-1 and bS21-3 which are 72% identical at the amino acid level. bS21-2, encoded by the *rpsU* homolog gene syntenic to the single *E. coli* *rpsU* gene, is also the most similar to *E. coli* bS21, with 60% amino acid identity.