

Table S7: Mean percentage of trimmed paired-end reads aligning to *Yersinia entomophaga* MH96 reference genome, including protein-coding, tRNA and non-coding regions (*in vivo*: n = 4, *in vitro*: n = 2).

Infection-stage / growth-phase	Total alignments	Protein coding region	Anti-sense protein coding region	tRNA	Non-annotated regions
<i>In vivo</i>					
Early infection	9 %	77 %	2 %	1 %	22 %
Middle infection	58 %	74 %	2 %	1 %	24 %
Late infection	59 %	75 %	1 %	0 %	24 %
<i>In vitro</i>					
Lag	93 %	84 %	2 %	1 %	14 %
Exponential	84 %	83 %	1 %	1 %	15 %
Stationary	93 %	85 %	1 %	0 %	14 %