



Figure S2. Mean proportion of paired-end reads attributed to host and pathogen based on average percent alignment to *Galleria mellonella* rRNA and EST sequence or *Yersinia entomophaga* MH96 genome or rRNA sequence (*in vivo*: n = 4, *in vitro*: n = 2). The growth phase and estimated cell number (CFU g⁻¹ and CFU ml⁻¹ for *in vivo* and *in vitro*, respectively) are provided in Table 1). Only percentages of 4 % and greater are shown.