

Fig S1 Preparation of macrophage-released *E. tarda*.

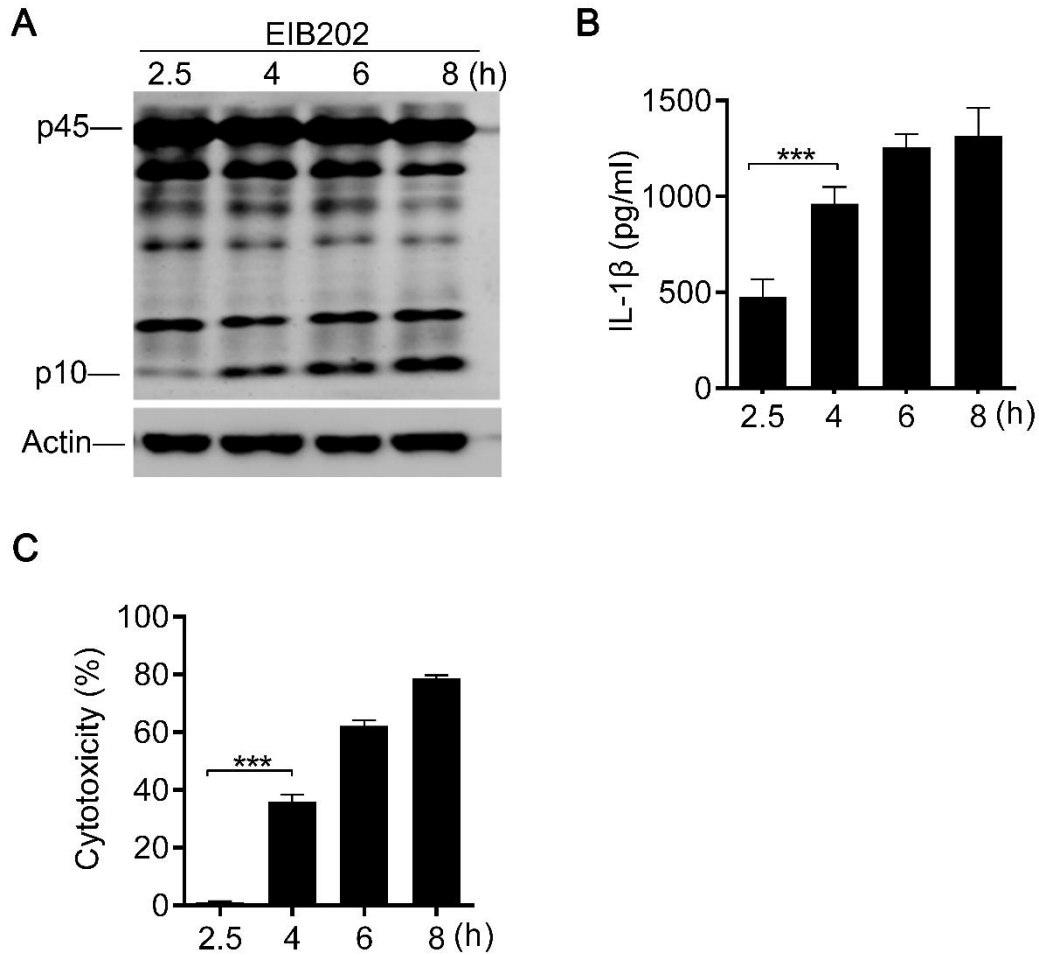


Fig S2 Activation of inflammasome in bone-marrow-derived macrophages (BMDMs) by *E. tarda*. (A) Caspase-1 activation in *E. tarda*-infected BMDMs was measured by immunoblotting. p45, procaspase-1; p10, the processed mature form of caspase-1. (B) Content of IL-1 $\beta$  in the supernatant of *E. tarda*-infected BMDMs was measured by ELISA. Error bar represents SEM \*\*\* $P < 0.001$ , test. (C) Cell death of *E. tarda*-infected BMDMs was assessed as release of lactate dehydrogenase released from *E. tarda*-infected BMDMs, detected at certain time intervals.

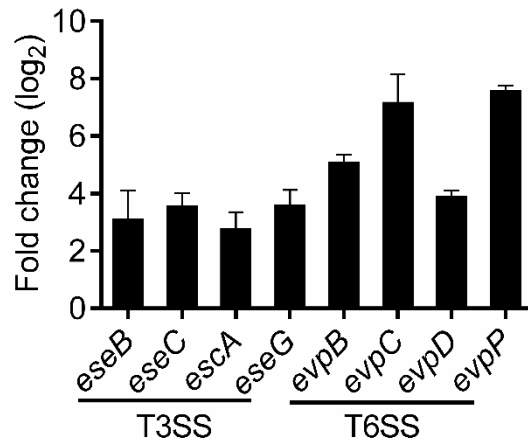


Fig S3 Real Time-PCR for indicated genes belongs to T3SS and T6SS of BMDM-released and DMEM-cultured *E. tarda*. Data are representative of at least 3 experiments. Graphs show mean  $\pm$ SD of triplicate cultures. \* $p < 0.05$ , \*\* $p < 0.01$ .

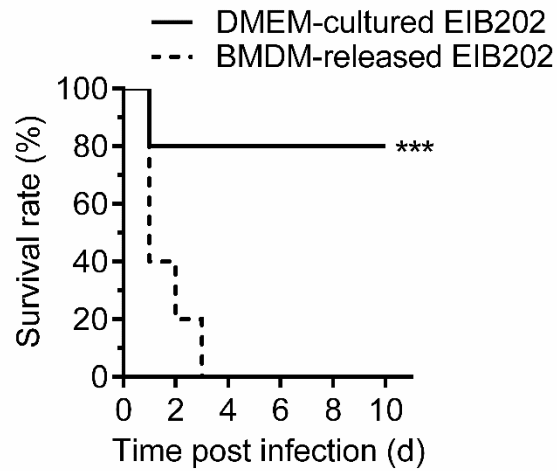


Fig S4 *E. tarda* released from BMDM cells exhibits enhanced virulence *in vivo*. Survival rate of C57BL/6 mice by intraperitoneally infected with BMDM-released or DMEM-cultured *E. tarda* ( $1.5 \times 10^6$  CFU/g, n=5 mice per group). \*\*\* $p < 0.001$ , Log-Rank test.

Table S1 Genes involved in stress response and adaptation.

Gene	Function	Log <sub>2</sub> (fold_change)
<b>Oxidative stress</b>		
ETAE_2186	thioredoxin (H-type, TRX-H)	7.581313435
ETAE_0271	coproporphyrinogen III oxidase and related Fe-S oxidoreductases	2.135055216
ETAE_3142	oxidoreductase molybdopterin binding	3.065059011
ETAE_2070	NADH dehydrogenase, FAD-containing subunit	2.205477572
ETAE_2373	NADH:ubiquinone oxidoreductase subunit 2 (chain N)	2.004362629
ETAE_2375	NADH:ubiquinone oxidoreductase subunit 5 (chain L)/multisubunit Na <sup>+</sup> /H <sup>+</sup> antiporter, MnhA subunit	2.01233935
ETAE_2378	formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I)	2.060150407
ETAE_2379	NADH:ubiquinone oxidoreductase subunit 1 (chain H)	2.828952088
ETAE_2380	NADH dehydrogenase/NADH:ubiquinone oxidoreductase 75 kD subunit (chain G)	2.250371121
<b>Acid tolerance</b>		
ETAE_0756	lysine/cadaverine transporter	2.213365971
ETAE_1884	lysine/cadaverine transport protein (APC family)	2.922141541