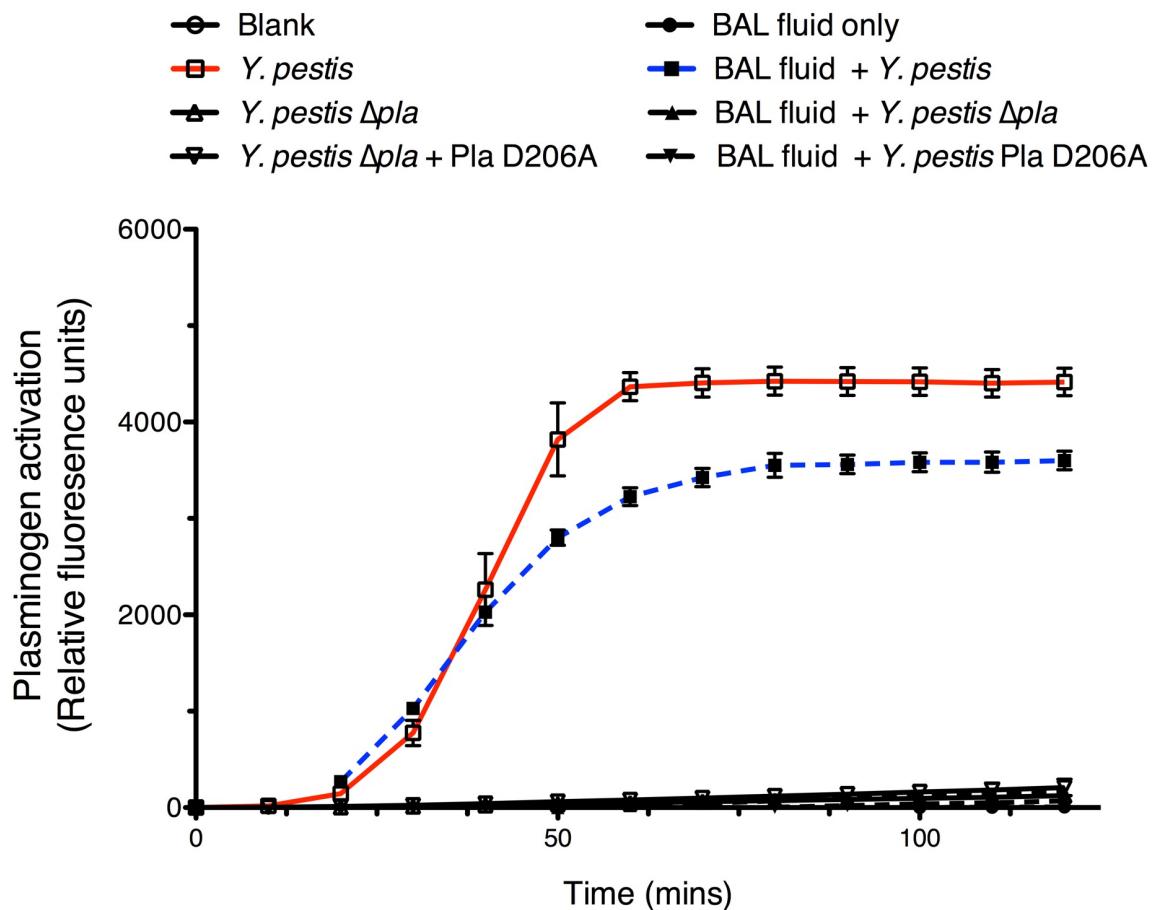
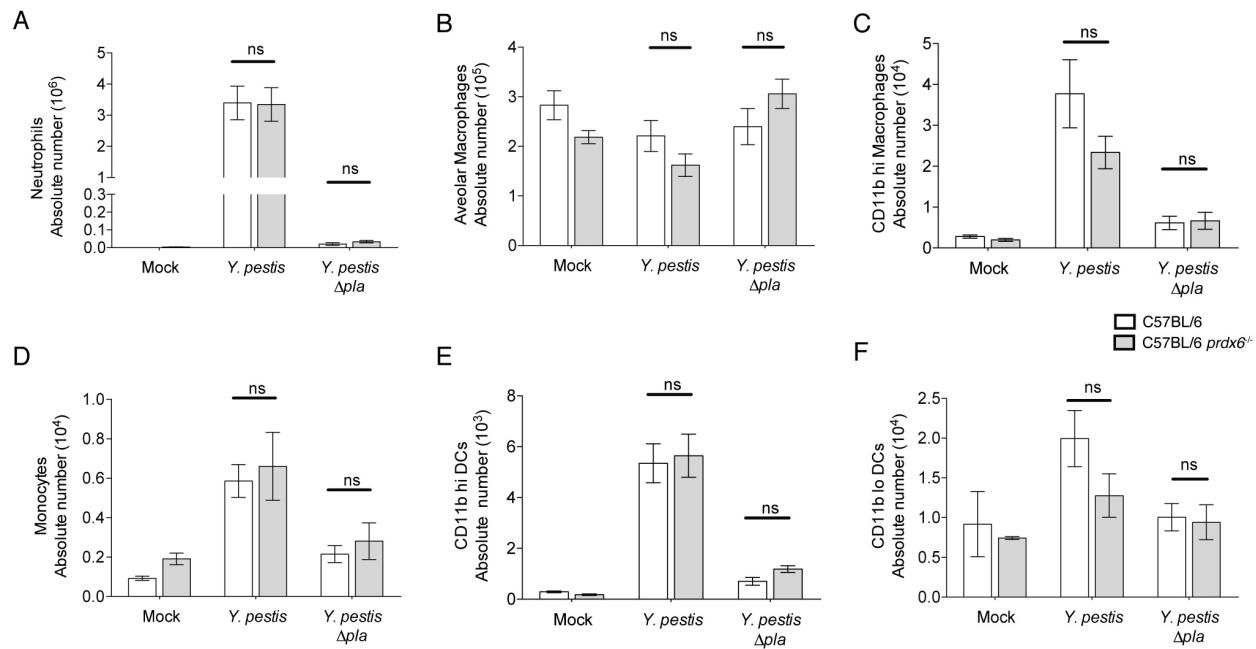


## SUPPLEMENTARY MATERIALS



**Fig. S1. Protease activity of Pla following *Y. pestis* incubation in BALF.** *Y. pestis*, *Y. pestis Δpla*, and *Y. pestis* Pla D206A were incubated in BHI (solid lines) or BALF (dashed lines) for 6 hours at 37°C. Bacteria were separated from the media and the plg-activating ability of the strains was determined by incubating with purified human glu-plasminogen and a fluorescent substrate of plasmin. Data are representative of 3 independent experiments performed in triplicate; error bars represent the s.e.m.



**Fig. S2. Prdx6 does not affect immune cell populations in the airspace following *Y. pestis* infection.** C57BL/6 or C57BL/6 *prdx6*<sup>-/-</sup> mice were inoculated with PBS (mock),  $10^4$  CFU of *Y. pestis*, or  $10^4$  CFU *Y. pestis* Δ*pla*, and after 48 hours BAL was performed to recover immune cells. Flow cytometry was performed to determine the percentages and absolute numbers of (A) neutrophils, (B) alveolar macrophages, (C) CD11b hi macrophages, (D) monocytes, (E) CD11b hi dendritic cells (DCs), and (F) CD11b lo DCs recruited to the lungs. Data are combined from 2 independent experiments ( $n=10$  for each group); error bars represent the s.e.m. (One-way ANOVA with Bonferroni's Multiple Comparison test, ns = not significant).

**Table S1. Bacterial strains and plasmids used in this study.**

Strain or plasmid	Designation	Relevant characteristics*	Source/reference
<i>Y. pestis</i> strains			
CO92	SAN2	pCD1 <sup>+</sup> , pMT1 <sup>+</sup> , pPCP1 <sup>+</sup> , pgm <sup>+</sup>	(1); Lab stock
CO92 Δ <i>pla</i>	SAN6	Δ <i>pla</i> ; pCD1 <sup>+</sup> , pMT1 <sup>+</sup> , pPCP1 <sup>+</sup> , pgm <sup>+</sup>	(2)
CO92 LCR <sup>-</sup>	PAN259	pCD1 <sup>-</sup> , pMT1 <sup>+</sup> , pPCP1 <sup>+</sup> , pgm <sup>+</sup>	(2); Lab stock
CO92 LCR <sup>-</sup> Δ <i>pla</i>	PAN314	Δ <i>pla</i> ; pCD1 <sup>-</sup> , pMT1 <sup>+</sup> , pPCP1 <sup>+</sup> , pgm <sup>+</sup>	(2)
CO92 LCR <sup>-</sup> Pla D206A	PAN163	Δ <i>pla</i> + <i>pla</i> D206A; pCD1 <sup>-</sup> , pMT1 <sup>+</sup> , pPCP1 <sup>+</sup> , pgm <sup>+</sup>	(2)
<i>E. coli</i> strains			
BL21	LAN211	pSE380; Ap <sup>R</sup>	(3)
BL21	LAN212	pMRK1; Ap <sup>R</sup>	(3)
BL21	LAN213	pMRK1206; Ap <sup>R</sup>	(3)
Plasmids			
pSE380	expression vector		Invitrogen
pMRKI	<i>pla</i> in pSE380		(4)
pMRK1206	<i>pla</i> D206A in pSE380		(4)

\* Ap<sup>R</sup>, ampicillin resistance

**Table S2. *Ex vivo* effect of proteolytically active Pla on protein abundance in mouse BALF.**

Protein name	Biological Function/Process <sup>a</sup>	Accession number	Size (AA)	<i>Y. pestis</i> /BAL <sup>b</sup>	pval <sup>c</sup>	<i>Y. pestis</i> Pla D206A /BAL <sup>b</sup>	pval <sup>c</sup>	<i>Y. pestis</i> / <i>Y. pestis</i> Pla D206A <sup>b</sup>	pval <sup>c</sup>
Glutathione S-transferase A3	immune system process; ROS metabolic process	sp P30115	220	0.395	0.022	0.751	0.019	0.610	0.031
Glutathione peroxidase 3	immune system process; response to toxin	sp P46412	226	0.386	0.001	0.804	0.044	0.526	0.002
Tubulin polymerization-promoting protein family	cell component; structure	sp Q8CRB6	176	0.464	0.000	0.892	0.734	0.619	0.000
Pigment epithelium-derived factor	protein binding; proteolysis	sp P97298	417	0.449	0.039	0.972	0.829	0.385	0.010
Alpha-2-HS-glycoprotein	protein binding; immune system process; proteolysis	sp P29699	345	0.561	0.000	0.888	0.002	0.642	0.000
Glutathione S-transferase Mu 1	immune system process; transferase activity	sp P10649	218	0.621	0.000	0.803	0.022	0.797	0.012
BPI fold-containing family A member 1 (sPlunc)	immune system response	sp P97361	278	0.653	0.007	0.772	0.072	0.906	0.397
Carboxypeptidase N subunit 2	immune system process; cytokine-mediated signaling	sp Q9DBB9	547	0.655	0.000	0.974	0.432	0.655	0.000
Sulfated glycoprotein 1	protein binding; lipid transport	sp Q61207	557	0.659	0.001	0.959	0.342	0.691	0.000
BPI fold-containing family B member 1 (Lplunc1)	MAC activation, response to stress	sp Q61114	474	0.669	0.057	0.832	0.175	0.817	0.069
Complement C3	cytokine activity; complement activation	sp P01027	1663	0.670	0.000	0.906	0.000	0.754	0.000
Vinculin	actin binding; cell adhesion	sp Q64727	1065	0.688	0.001	1.916	0.934	0.232	0.000
Plasminogen	serine-type peptidase activity; proteolysis	sp P20918	812	0.714	0.000	0.970	0.317	0.747	0.000
Actin Gamma	cell component; structure	sp P63260	375	0.724	0.000	0.819	0.000	0.893	0.031
Plastin-2	structure; actin binding	sp Q61233	626	0.739	0.001	0.823	0.003	0.919	0.169
Lipoprotein lipase	lipase activity; lipid transport	sp P11152	474	0.743	0.000	0.942	0.892	0.777	0.000
Peroxiredoxin 6	immune system process; ROS metabolic process	tr Q6GT24	223	0.746	0.000	1.012	0.958	0.782	0.071
Phosphoglycerate mutase 1	glycolysis	sp Q9DBJ1	253	0.756	0.001	0.804	0.532	0.917	0.000
Complement C4-B	complement activation; signal transduction	sp P01029	1738	0.775	0.069	0.873	0.313	0.939	0.244
Hypoxanthine-guanine phosphoribosyltransferase	monosaccharide metabolic process	sp P00493	219	0.798	0.000	0.914	0.234	1.019	0.000
Calmodulin	Ca <sup>2+</sup> binding	sp P62204	149	0.830	0.080	0.749	0.014	1.179	0.032
Apolipoprotein A-IV	lipid transporter activity; blood circulation	sp P06728	395	0.842	0.000	0.973	0.000	0.885	0.014
Alpha-2-antiplasmin	proteolysis	sp Q61247	491	0.847	0.022	0.972	0.523	0.881	0.034

a. Biological function are based on Uniprot (<http://www.uniprot.org>).

b. Average relative protein expression level ratio in sample and control, quantified by Protein Pilot 4.0 software (ABSciex).

c. Determined by Student's *t* test.

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