Supporting Information Figure Legends

Figure S1. Negative ion mode MALDI TOF/TOF tandem mass spectrum of *m/z* 1688 of lipid A from Wt Lo bacteria.

Figure S2. Negative ion mode MALDI TOF/TOF tandem mass spectrum of *m/z* 1448 of lipid A from Wt Lo bacteria.

Figure S3. Positive ion mode MALDI TOF/TOF tandem mass spectrum of *m/z* 1378 (*m/z* 1368 cluster) of lipid A from Wt Lo bacteria.

Figure S4. Negative ion mode MALDI TOF/TOF tandem mass spectrum of *m/z* 1448 of lipid A from Wt Hi bacteria.

Figure S5. Positive ion mode MALDI TOF/TOF tandem mass spectrum of *m/z* 1378 (*m/z* 1368 cluster) of lipid A from Wt Hi bacteria.

Figure S6. Thin layer chromotography indicating the major phosphorylated lipid A structures present in Wt and phosphatase-deficient *P. gingivalis.* Non-phosphorylated lipid A was detected in the solvent front of Wt samples, but not samples derived from PG1587-deficient strains.

Figure S7. Amino acid sequence alignments of putative lipid A phosphatases identified in *P. gingivalis* and known lipid A phosphatases from *F. novicida*. (A) Sequence alignment comparing PG1587 and *F. novicida* LpxF amino acid sequences. (B) Sequence alignment comparing PG1773 and *F. novicida* LpxE amino acid sequences. Red letters and yellow background indicate amino acid identity. Underline indicates the novel carboxy-terminal domain of PG1773.

Figure S8. *P. gingivalis* deficient in lipid A 4'- and 1-phosphate activities exhibit hemin-independent lipid A structural profiles. Lipid A derived from 1587KO and 1773KO bacteria that were grown in the presence of either (1 μg ml^{-1}) hemin (Lo) or (10 μg ml^{-1}) hemin (Hi) were examined by MALDI-TOF MS to elucidate their structural content. Lipid A samples were examined in the negative ion mode (A, C, E, G) or the positive ion mode (B, D, F, H). (A and B) 1587KO Lo bacteria. (C and D) 1587KO Hi bacteria. (E and F) 1773KO Lo bacteria. (G and H) 1773KO Hi bacteria.

Figure S9. Negative ion mode MALDI TOF/TOF tandem mass spectrum of *m/z* 1448 of lipid A from 1773KO bacteria.

Figure S10. Negative ion mode MALDI TOF/TOF tandem mass spectrum of *m/z* 1688 of lipid A from 1587KO bacteria.

Figure S11. Negative ion mode MALDI TOF/TOF tandem mass spectrum of *m/z* 1768 of lipid A from 73.87DKO bacteria. Both bis-phosphate and 1-pyrophosphate lipid A structures are detected in this sample.

Figure S12. Negative ion mode MALDI TOF/TOF tandem mass spectrum of *m/z* 1688 of lipid A from 73.87DKO bacteria.

Figure S13. Lipid A phosphatases are required for *P. gingivalis* to evade TLR4-dependent activation of E-selectin expression in human endothelial cells. Human umbilical vein endothelial cells were stimulated for 4 hours with the indicated types and doses of (A) LPS or (B) intact *P. gingivalis* bacteria. ELISA assay was performed to detect TLR4-dependent E-selectin expression.