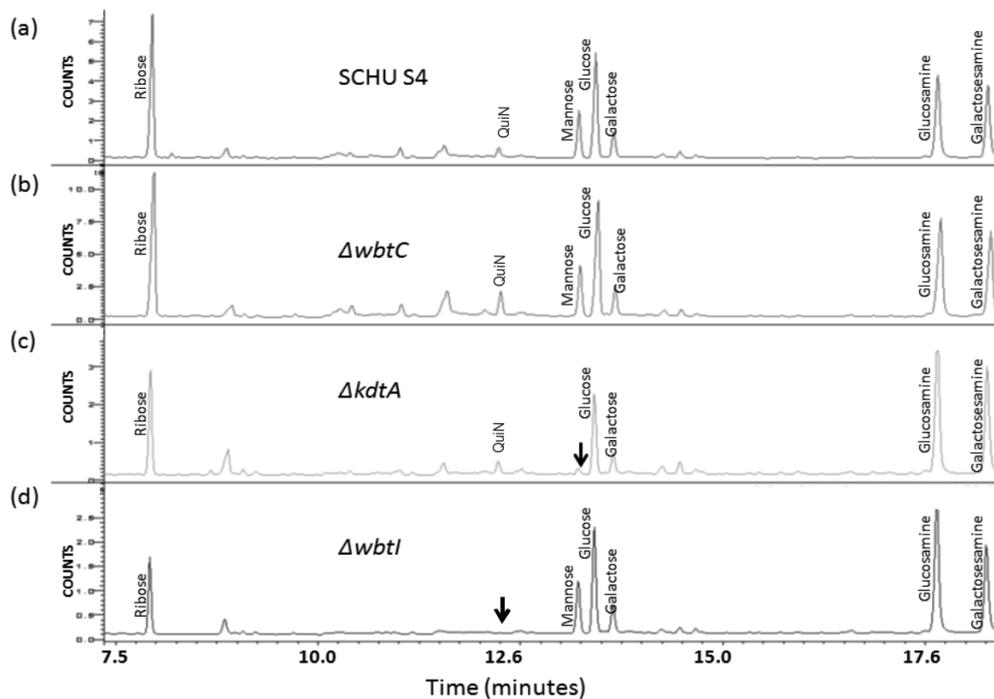
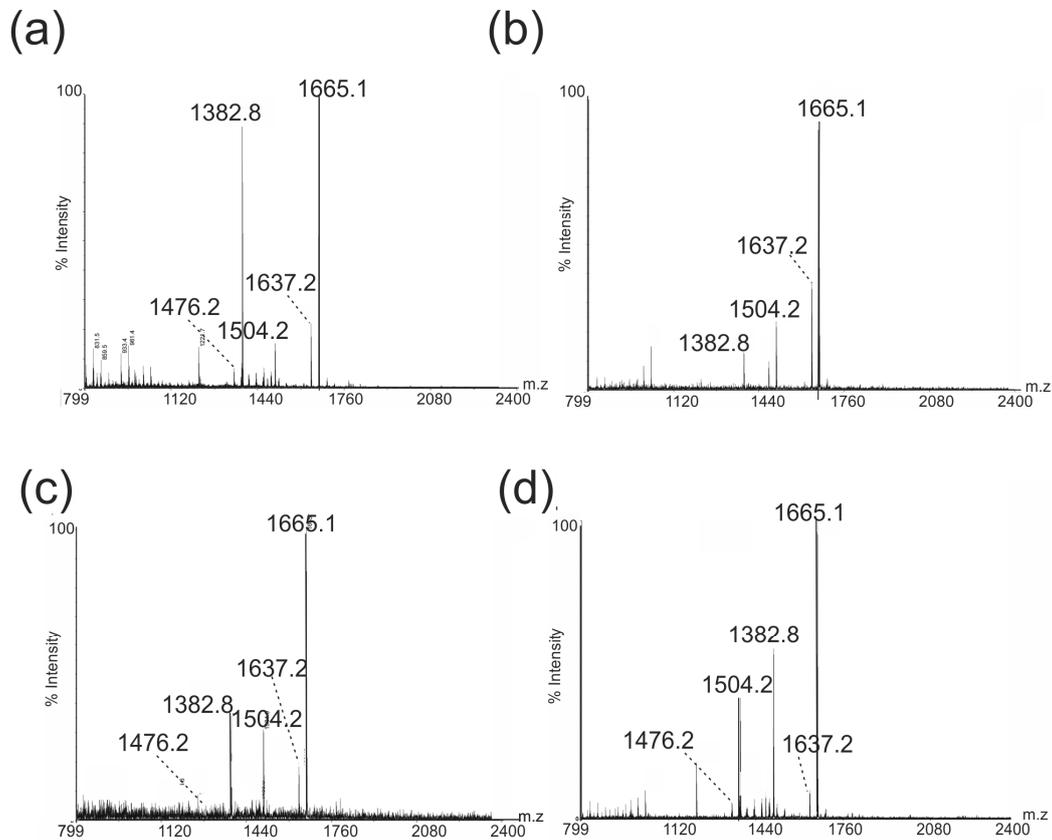


## Supplementary Materials

**Figure S1.** GC-MS analysis of alditol acetates of (a) SCHU S4, (b)  $\Delta wbtC$ , (c)  $\Delta kdtA$  and (d)  $\Delta wbtI$ , obtained after hydrolysis of material remaining after treatment of whole killed bacteria with DNase, RNase and proteinase K. The  $\Delta wbtC$  spectrum was similar to wild type *F. tularensis*. Of note the  $\Delta kdtA$  mutant had low levels of the LPS core sugar mannose, evidence that this mutant does not elaborate a core structure. An arrow on panel (c) shows the absence of mannose in the  $\Delta kdtA$  mutant. The  $\Delta wbtI$  mutant had levels of the mannose comparable to those observed in the wild type strain, however did not have detectable levels of other sugars, such as QuiN. These data are similar to those obtained from GC-MS analyses of material isolated by LPS preparations.



**Figure S2.** MALDI-TOF analysis of purified lipid A from (a) SCHU S4, (b)  $\Delta kdtA$ , (c)  $\Delta wbtC$  and (d)  $\Delta wbtI$ . As reported by others (Schilling, McLendon et al. 2007), species were observed at  $m/z$  1665.3 and 1504.2, with a putative composition of  $C_{16:0}$ , 3  $\times$   $C_{18:0}(3-OH)$ , phosphate and  $GalN_{n=1/0}$ . No differences in the fragment ion profiles of lipid A isolated from wild type and each mutant was observed.



**Figure S3.** 1D-PAGE of killed whole bacterial cells treated with DNase, RNase and proteinase K, visualised with periodic acid based glycostain. Candy Cane marker (Lane 1), SCHU S4 (lane 1),  $\Delta wbtC$  (lane 2),  $\Delta wbtI$  (lane 3)  $\Delta kdtA$  (lane 4). The LPS and unconjugated lipid or carbohydrate portions of cells were visualised using a commercial glycostaining kit, based upon traditional periodic acid chemistry, and a fluorescent marker group. O-antigen banding pattern was observed in cell extracts of wild type and  $\Delta wbtC$  only.

