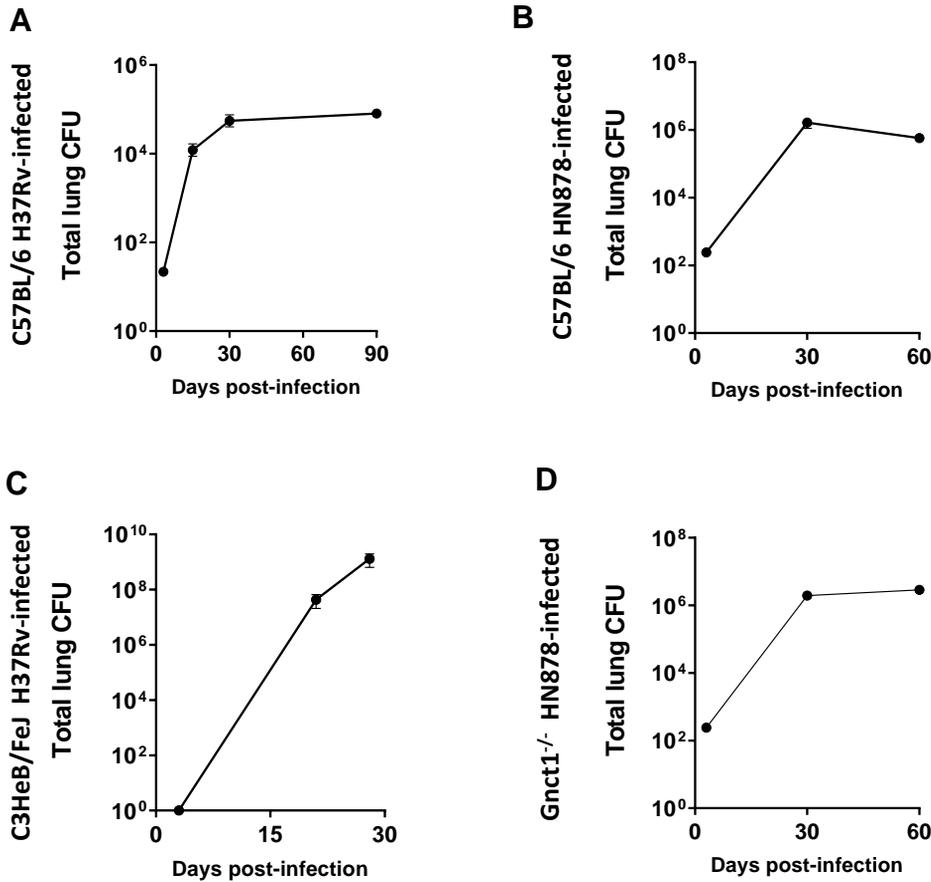


Supplementary Figure 1

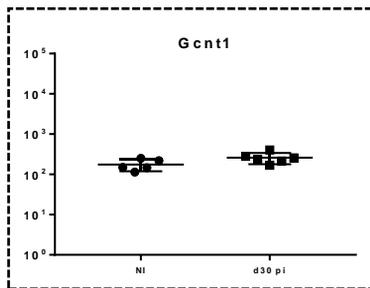


Supplementary Figure 1. Lung bacterial burdens obtained for the different experimental infections used in this study.

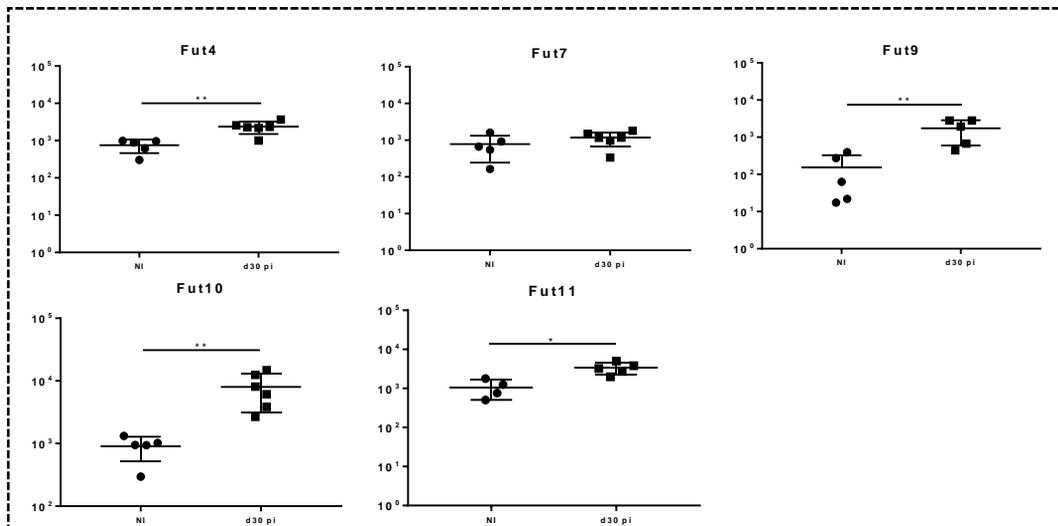
C57BL/6 mice were infected by aerosol with a low dose of *M. tuberculosis* strain H37Rv (A) or HN878 (B). C3HeB/FeJ mice were infected intravenously with H37Rv strain (C). *Gcmt1*^{-/-} mice were infected by aerosol with a low dose of *M. tuberculosis* strain HN878 (D). At the indicated time-points post-infection, the lungs of infected mice were collected and the bacteria burden determined by CFU enumeration. Represented is the Mean \pm SEM for at least 5 mice per time point.

Supplementary Figure 2

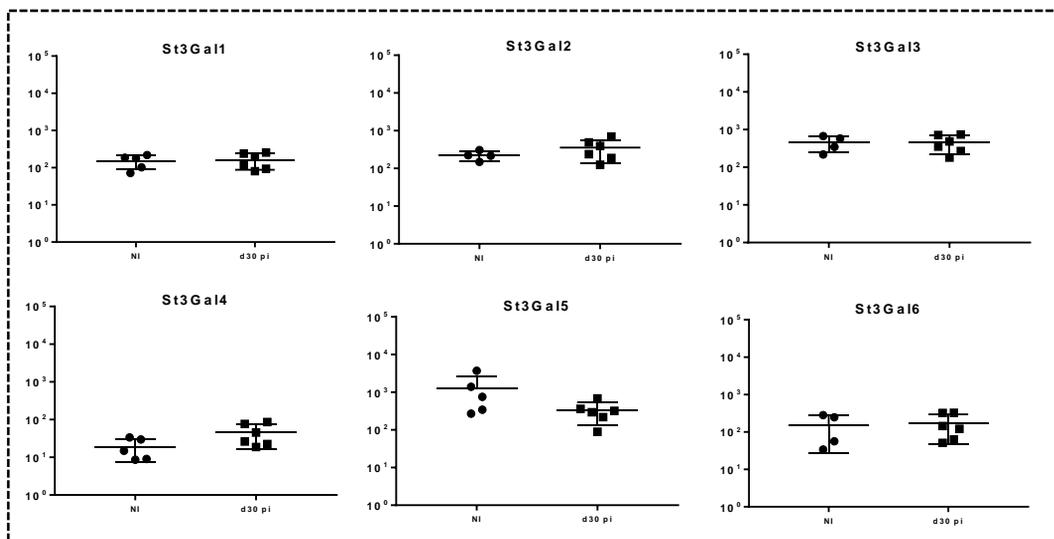
Core2-GlcNAcT



α 1,3FucTs



α 2,3SialylTs



Supplementary Figure 2. Transcriptomic analysis of glycosyltransferase-encoding genes on C57BL/6 mice infected with H37Rv *M. tuberculosis* strain.

The expression of several glycosyltransferases involved on the SLeX biosynthetic pathways (Core 2-GlcNAcT, α 2,3SialylTs and α 1,3FucosylTs) was measured by real-time PCR in lungs of C57BL/6 mice infected via aerosol with a low dose of *M. tuberculosis* strain H37Rv on days 15, 30 and 90 post-infection. Non-infected animals (NI) are shown as controls. Each dot represents one mouse of a total of 6-8 from 2 independent experiments. Statistical analysis was performed using one-way ANOVA with Tukey's test for multiple comparisons. *, $p < 0.05$; **, $p < 0.01$.