Early Salmonella Typhimurium infection in pigs disrupts Microbiome composition and functionality principally at the ileum mucosa.

AUTHORS

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Figure S1a

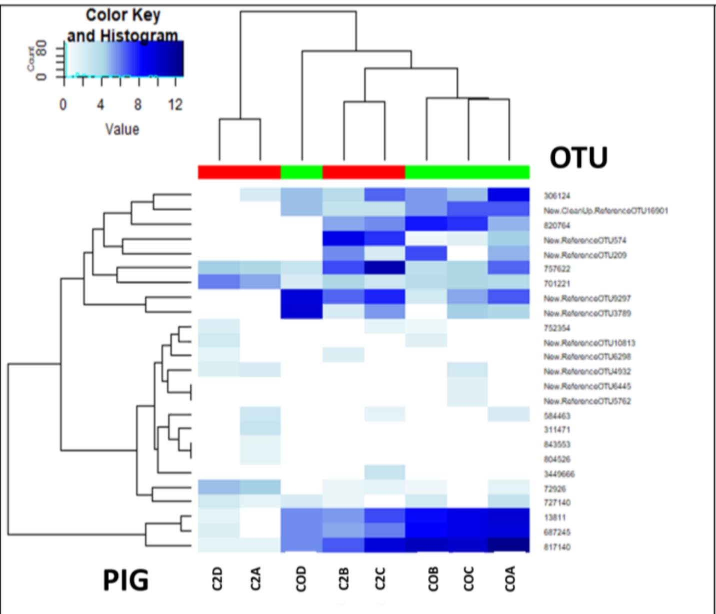
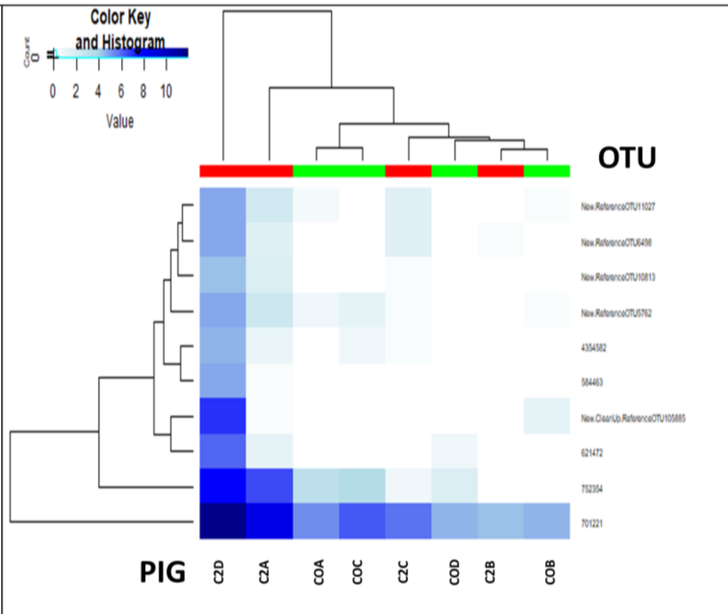
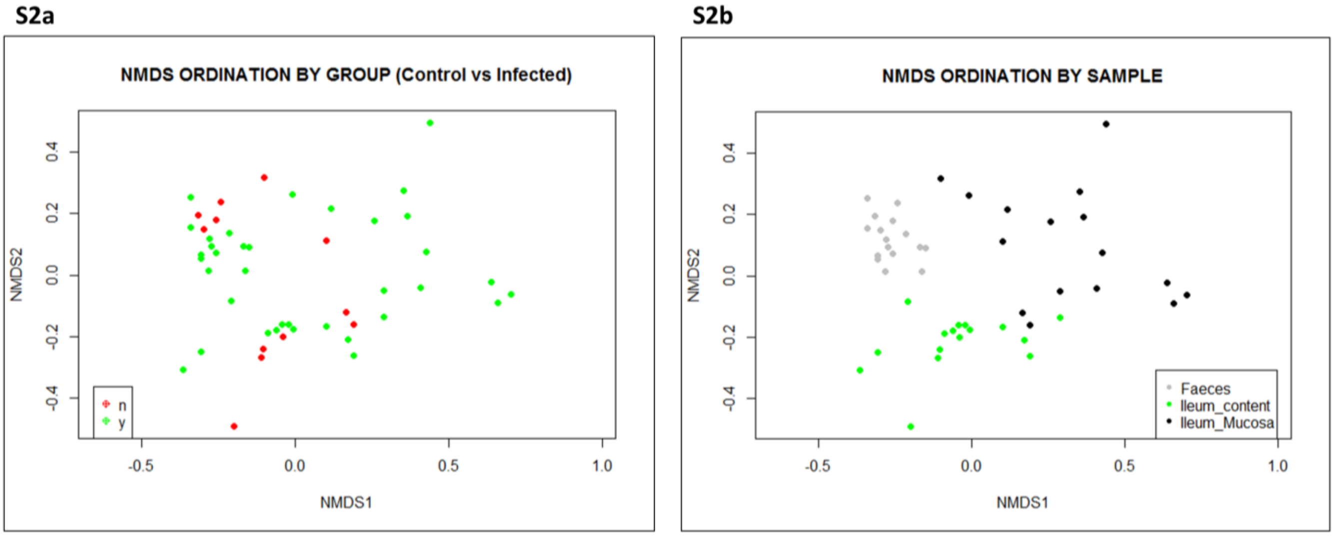


Figure S1b

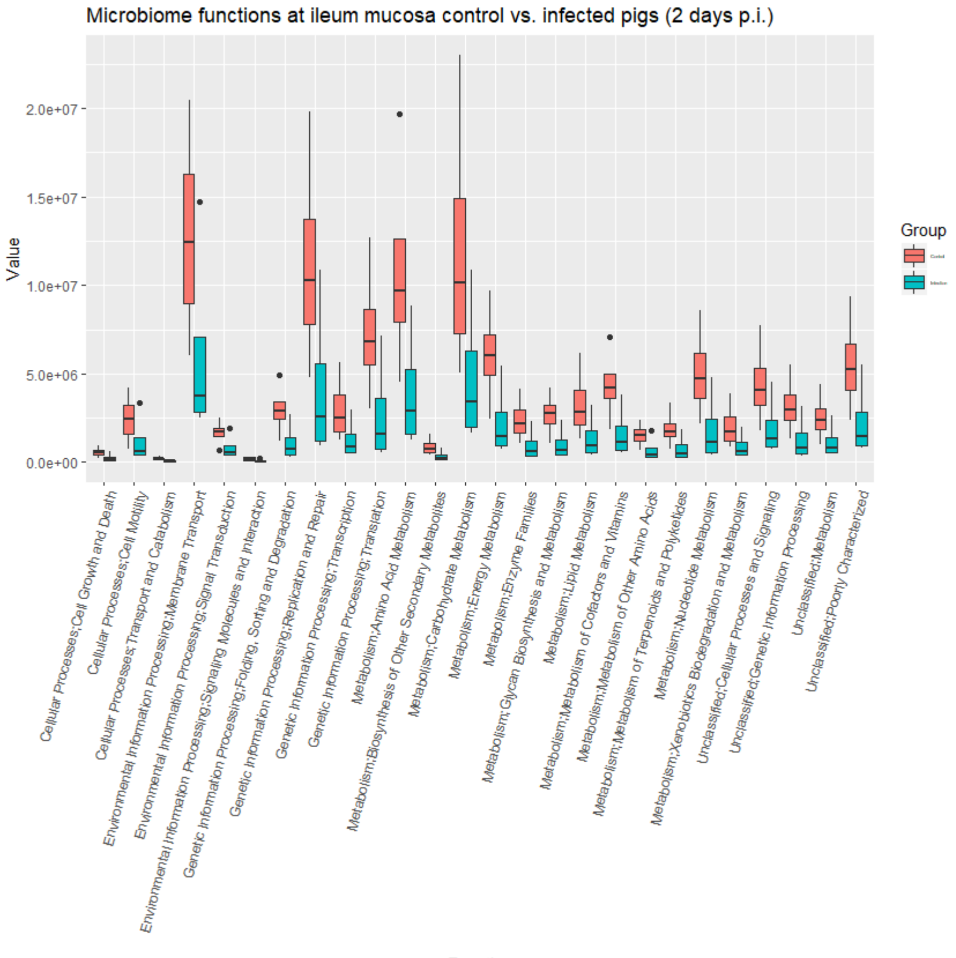


Supplementary Figure S1. *Salmonella* Typhimurium infection affects the relative abundance of OTUs at the ileum content and faeces. Heatmap illustrating the mean relative abundance of multiple OTUs at the ileum content (Figure S1a) and faeces (Figure S1b) of non-infected control pigs (green) and Day 2 p.i. infected pigs (red). White colour indicates low abundance while dark blue high values of abundance. Dendrogram was built using hierarchical cluster analysis with Bray-Curtis dissimilarity indices.


S2a

S2b

Supplementary Figure S2. Ordination analysis of the functions predicted by (PICRUSt) in samples obtained through the time-course of a *S.* Typhimurium infection in pigs. Figure S2A represents the ordination using Bray-Curtis dissimilarity index and plot by Non-metric Multidimensional Scaling (NMDS) of samples split by infection group. Figure S2B represent Bray-Curtis dissimilarity by NMDS of samples by type of sample factor.



Supplementary Figure S3. Boxplot representation of logarithm of abundance of detected KEGG level 2 functions in the ileum mucosa from control pigs (non-infected) and S. Typhimurium infected pigs at 2 days post infection. Significant differences are expressed by (*) in those functions with a *p*<0.05).