



Figure S1: Statistics and sample grouping of *H. contortus* adult males exposed to the vaccine response, or the control group's de novo transcriptome assemblies. Raw counts (A) were normalized (B) by a variance stabilizing transformation (D), and profiles are outlined using principal component analyses (PCA) of the normalized transcript counts measured in worms collected from vaccinated or control sheep (C). Volcano plot of significantly differentially expressed (DE) genes, determined using DESeq2 (E).