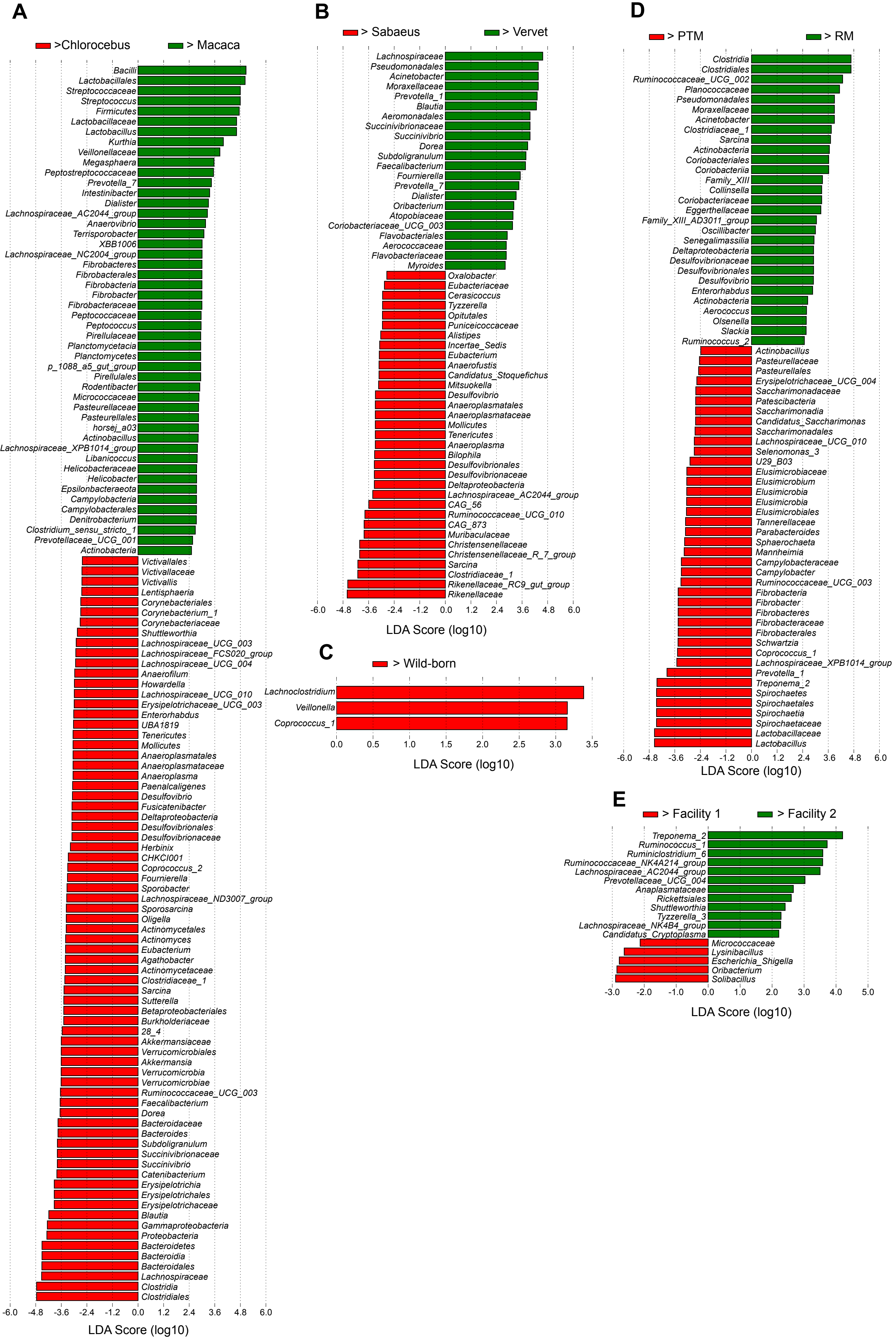

FIG S1

LEfSe Results, Expanded. All differentially abundant taxa – from phylum level to genus level - with associated LDA scores in the GI microbiome that were significantly different (A) between the NHP genera Chlorocebus and Macaca, (B) between sabaeus monkeys and vervets, (C) between captive-born and wild-born vervets, (D) between PTM and RM, and (E) between RM in facility 1 and facility 2.