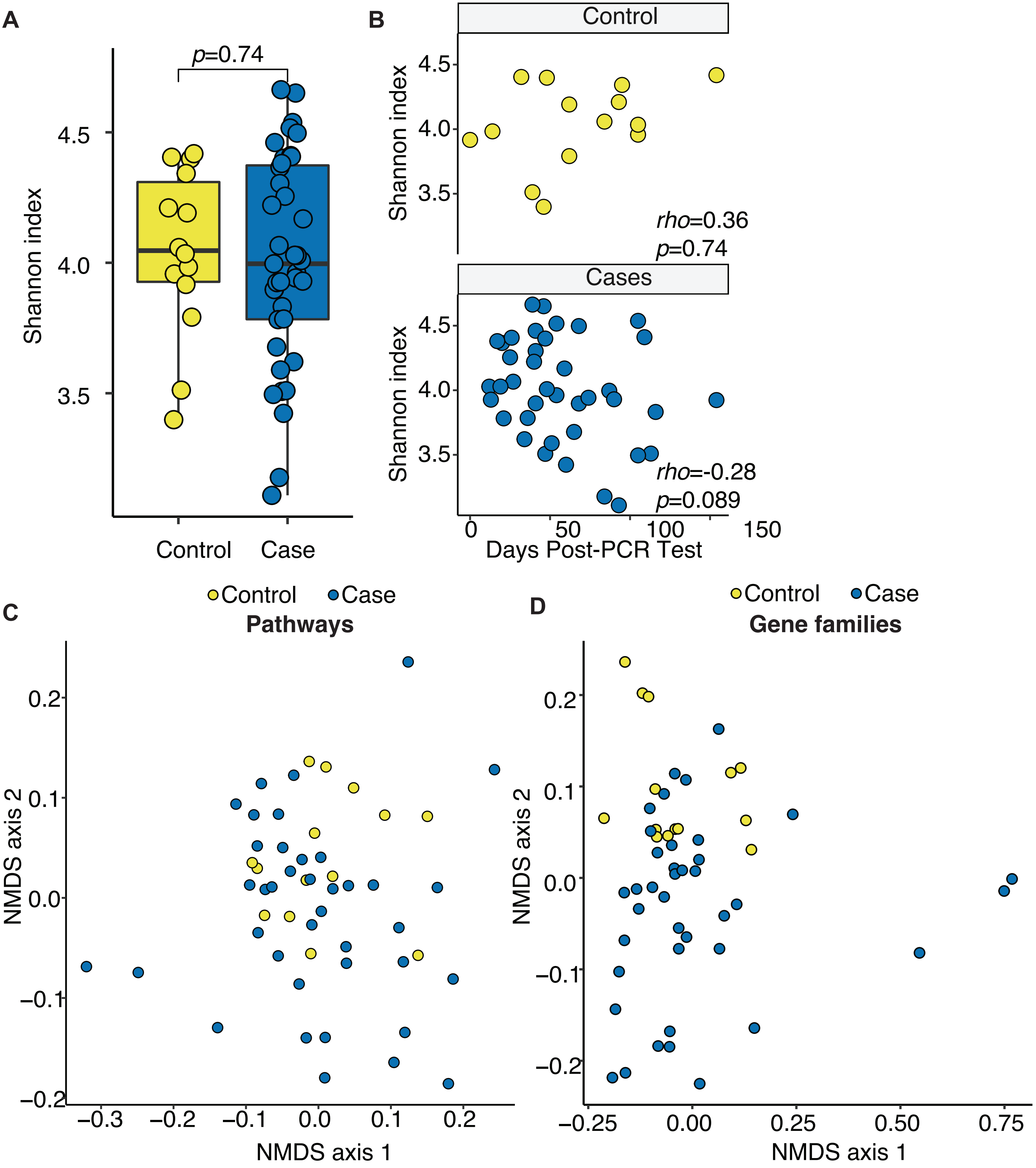

FIG S2 Lack of a consistent signature of mild SARS-CoV-2 infection based on 16S-seq and metagenomic data. (A-B) 16S-Seq data. **(C-D)** MGS data. **(A)** Microbial diversity was comparable between groups based on the Shannon Index (*p*-value, Student's *t* test) and **(B)** was not significantly associated with time post-PCR test (Spearman correlations shown). **(C-D)** MGS unstratified pathway data **(C)** and gene families **(D)** were not significantly different between Cases and Controls (PERMANOVA p_{adj}=1, both panels, n=18 subjects, 53 samples).