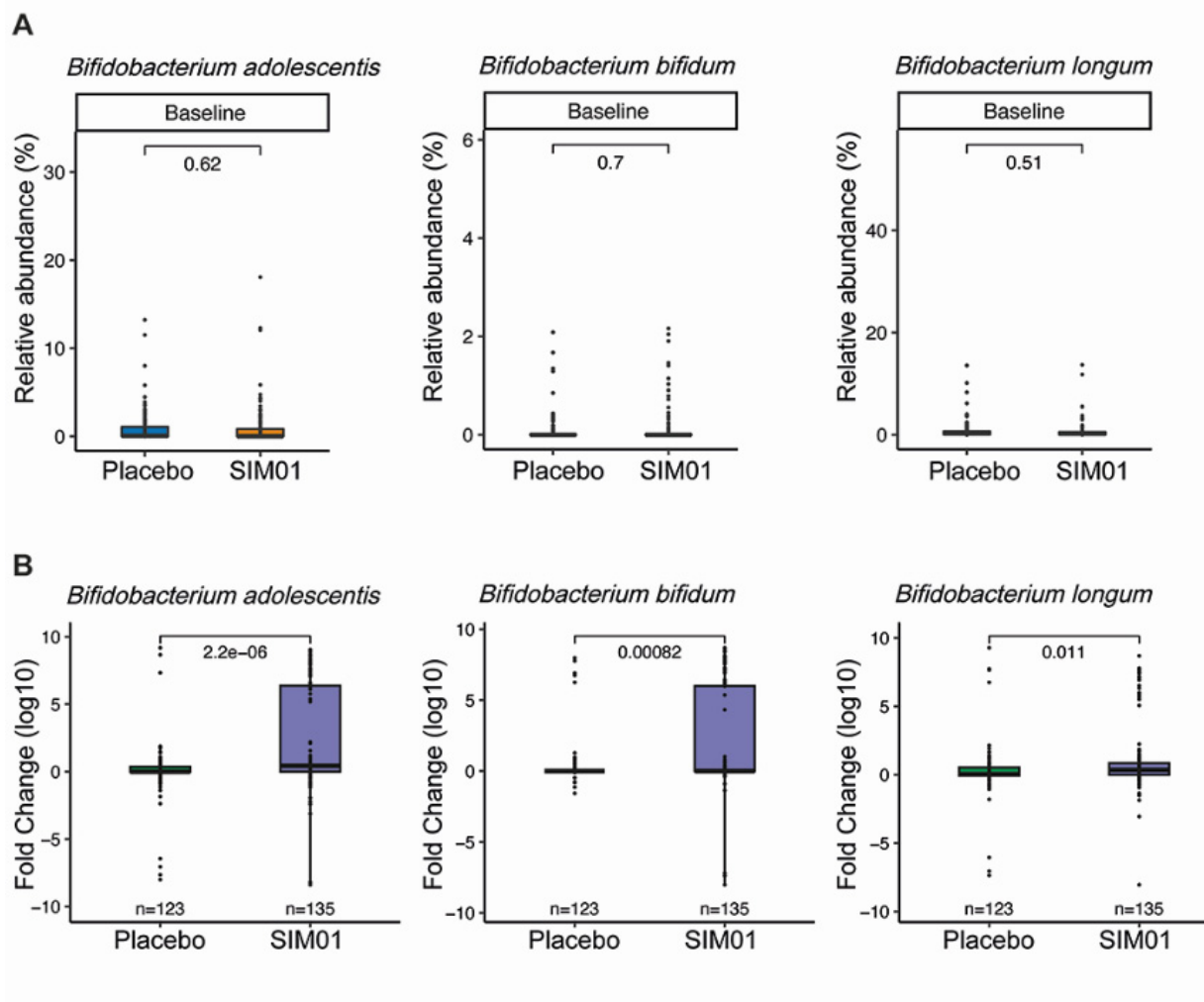


Table S1. Grouping of pathogenic bacteria according to the faecal metagenomic analysis of microbial profile

Species	Group	Publication
<i>s__Bifidobacterium_adolescentis</i>	Covid_Negative_Cor	Yeoh Y K, et al. Gut, 2021, 70(4): 698-706.
<i>s__Bifidobacterium_pseudocatenulatum</i>	Covid_Negative_Cor	
<i>s__Collinsella_aerofaciens</i>	Covid_Negative_Cor	
<i>s__Bacteroides_caccae</i>	Covid_Positive_Cor	
<i>s__Bacteroides_dorei</i>	Covid_Positive_Cor	
<i>s__Bacteroides_ovatus</i>	Covid_Positive_Cor	
<i>s__Bacteroides_vulgatus</i>	Covid_Positive_Cor	
<i>s__Blautia_obeum</i>	Covid_Negative_Cor	
<i>s__Ruminococcus_gnavus</i>	Covid_Positive_Cor	
<i>s__Ruminococcus_torques</i>	Covid_Positive_Cor	
<i>s__Coprococcus_comes</i>	Covid_Negative_Cor	
<i>s__Dorea_formicigenerans</i>	Covid_Negative_Cor	
<i>s__Dorea_longicatena</i>	Covid_Negative_Cor	
<i>s__Eubacterium_rectale</i>	Covid_Negative_Cor	
<i>s__Faecalibacterium_prausnitzii</i>	Covid_Negative_Cor	
<i>s__Ruminococcus_bromii</i>	Covid_Negative_Cor	
<i>s__Ruminococcus_obeum_CAG_39</i>	Covid_Negative_Cor	
<i>s__Akkermansia_muciniphila</i>	Covid_Positive_Cor	Su Q, Lau R I, Liu Q, et al.. Gut, 2022.
<i>s__Bacteroides_fragilis</i>	Long_covid_Positive_Cor	
<i>s__Bacteroides_salysiae</i>	Long_covid_Positive_Cor	
<i>s__Blautia_hansenii</i>	Long_covid_Positive_Cor	
<i>s__Blautia_sp_CAG_257</i>	Long_covid_Positive_Cor	
<i>s__Ruminococcus_gnavus</i>	Long_covid_Positive_Cor	
<i>s__Clostridium_bolteae</i>	Long_covid_Positive_Cor	
<i>s__Coprobacillus_cateniformis</i>	Long_covid_Positive_Cor	
<i>s__Erysipelatoclostridium_amosum</i>	Long_covid_Positive_Cor	
<i>s__Parasutterella_excrementihominis</i>	Long_covid_Positive_Cor	
<i>s__Sutterella_parvirubra</i>	Long_covid_Positive_Cor	
<i>s__Bifidobacterium_adolescentis</i>	Long_covid_Negative_Cor	
<i>s__Bifidobacterium_pseudocatenulatum</i>	Long_covid_Negative_Cor	
<i>s__Bacteroides_dorei</i>	Long_covid_Negative_Cor	
<i>s__Eubacterium_hallii</i>	Long_covid_Negative_Cor	
<i>s__Blautia_obeum</i>	Long_covid_Negative_Cor	
<i>s__Blautia_wexlerae</i>	Long_covid_Negative_Cor	
<i>s__Roseburia_hominis</i>	Long_covid_Negative_Cor	
<i>s__Gemmiger_formicilis</i>	Long_covid_Negative_Cor	
<i>s__Firmicutes_bacterium_CAG_83</i>	Long_covid_Negative_Cor	
<i>s__Megamonas_funiformis</i>	Long_covid_Negative_Cor	



Supplementary Figure S1. (A) There is no difference in the relative abundance of three species (*Bifidobacterium adolescentis*, *Bifidobacterium bifidum*, and *Bifidobacterium longum*) contained in SIM01 between the placebo and SIM01 groups at baseline. (B) Oral SIM01 treatment significant increase in the fold change (month 3/baseline) of three probiotic species contained in SIM01 compared with the placebo arm. *p* values were given by the Wilcoxon rank-sum test (two-sided). Elements on boxplots: centre line, median; box limits, upper and lower quartiles; points, each sample.