Supplementary Figure 1. Relative abundance of probiotic species contained in SIM01

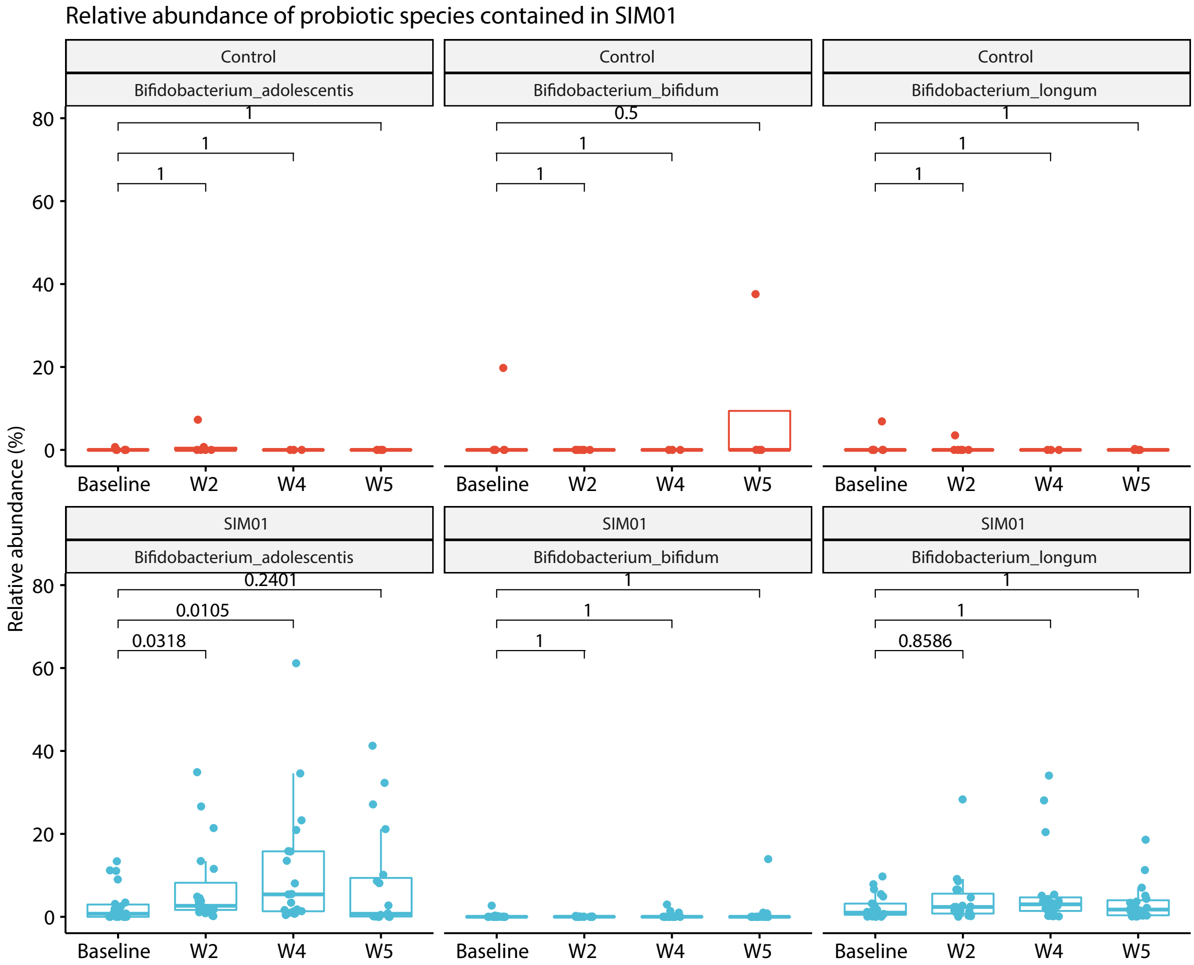

Figure legend: Relative abundance of three probiotic species (*B. adolescentis*, *B. bifidum*, *B. longum*) contained in SIM01 at baseline, week 2, week 4 and week 5 in the control (upper panel) and SIM01 (lower panel) groups. P values were determined by Friedman test, Post-hoc: Wilcoxon signed-rank test with Bonferroni correction.

Supplementary Figure 2. The impact of SIM01 on the gut microbial diversity at phylum and order level

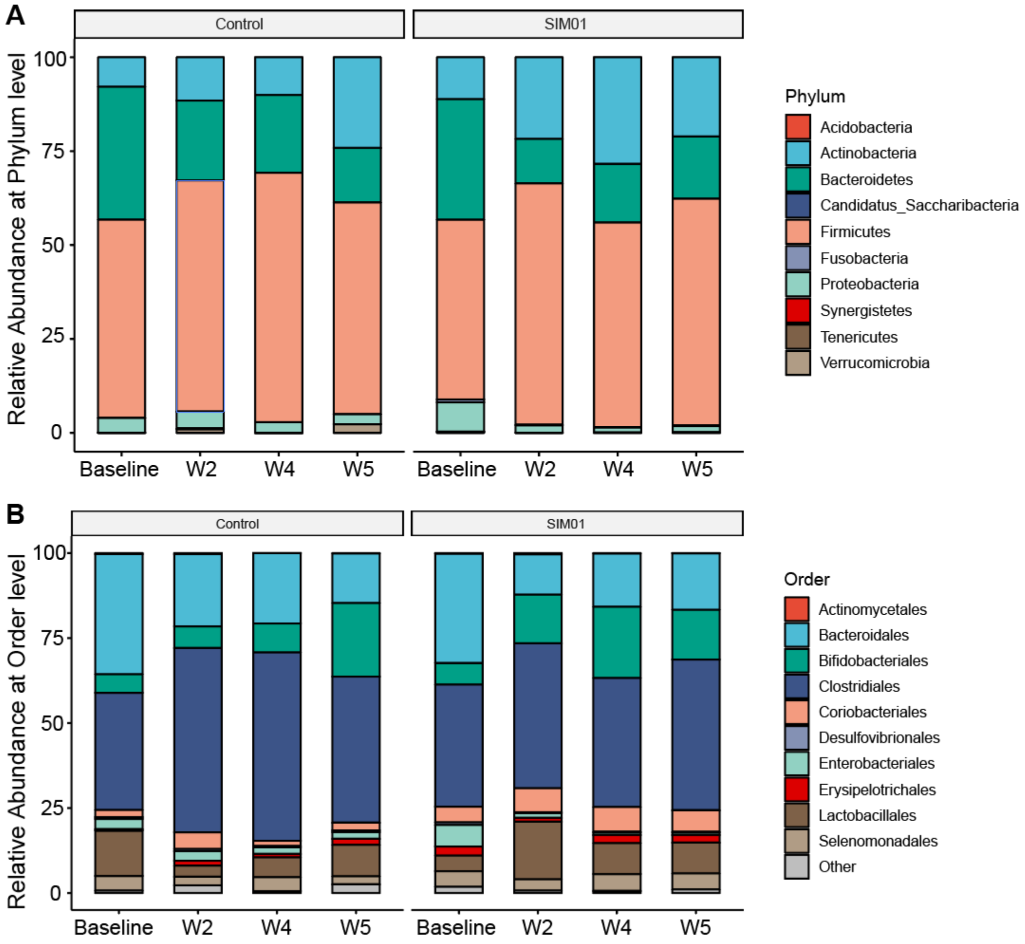

Figure legend: A. Mean relative at Relative abundance at phylum level at baseline, week 2, week 4 and week 5 in the SIM01 and control groups. **B.** Mean relative at Relative abundance at order level at baseline, week 2, week 4 and week 5 in the SIM01 and control groups.

Supplementary Figure 3. Mean and 95% CI for 100 times of subsampling

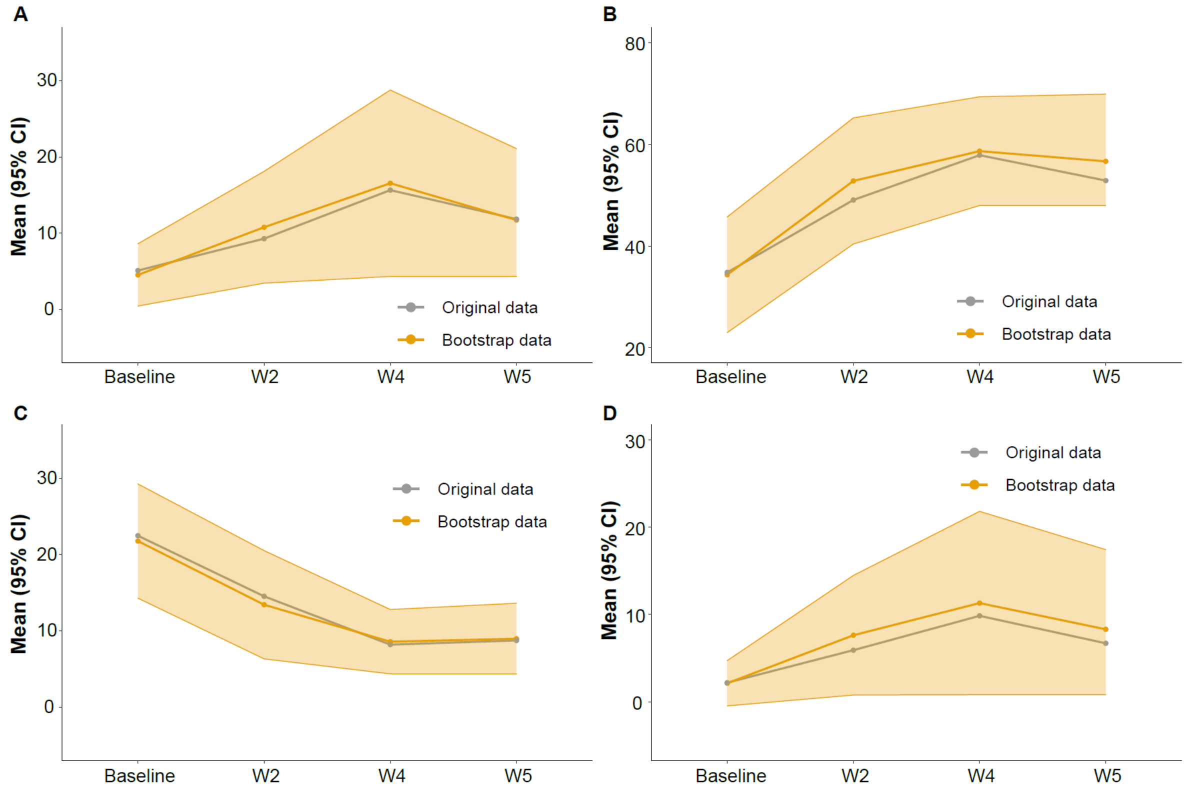

Figure legend: Mean and 95% CI for 100 times of subsampling are depicted. **A.** Bootstrap data for total abundance of probiotic species in SIM01. B. Bootstrap data for total abundance of bacterial species depleted in COVID−19 patients. **C.** Bootstrap data for total abundance of bacterial species enriched in COVID−19 patients. **D.** Bootstrap data for abundance of B. *adolescentis* after SIM01 treatment. Grey line (original data); orange line (bootstrap data).

Supplementary Table 1. The impact of SIM01 on the gut microbiota at species level at Week 5

Species		log2FoldChange	Adjusted p value
Fusobacterium_varium	Decreased at week 5	-13.55215521	7.44E-05
Veillonella_parvula	Decreased at week 5	-6.068494877	3.44E-04
Escherichia_coli	Decreased at week 5	-4.182168969	5.48E-05
Clostridium_bolteae	Decreased at week 5	-2.962670134	2.02E-04
Clostridium_hathewayi	Decreased at week 5	-2.651254916	0.0323593
Bacteroides_caccae	Decreased at week 5	-1.774449533	0.00244275
Bacteroides_xylanisolvens	Decreased at week 5	-1.586831898	0.029841257
Bacteroides_thetaiotaomicron	Decreased at week 5	-1.017302515	0.039582649
Parabacteroides_distasonis	Decreased at week 5	-0.936770137	0.040365898
Faecalibacterium_prausnitzii	Increased at week 5	1.772224535	0.017780547
Bifidobacterium_longum	Increased at week 5	1.857775702	0.029841257
Gordonibacter_pamelaeae	Increased at week 5	2.038224315	0.039582649
Collinsella_aerofaciens	Increased at week 5	2.262809793	2.36E-04
Dorea_longicatena	Increased at week 5	2.299855058	7.44E-05
Ruminococcus_sp_5_1_39BFAA	Increased at week 5	2.334996081	0.0323593
Streptococcus_salivarius	Increased at week 5	2.396230537	0.009991312
Streptococcus_parasanguinis	Increased at week 5	2.449409466	0.004014728
Eubacterium_hallii	Increased at week 5	2.501266794	1.01E-04
Eubacterium_ramulus	Increased at week 5	2.563473563	0.040097587
Ruminococcus_obeum	Increased at week 5	2.591205871	3.27E-09
Adlercreutzia_equolifaciens	Increased at week 5	2.631502419	0.048330022
Dorea_formicigenerans	Increased at week 5	2.649581947	0.017747723
Coprococcus_catus	Increased at week 5	2.774034238	0.017636927
Lachnospiraceae_bacterium_5_1_63FAA	Increased at week 5	2.818095129	0.005917225

Eubacterium_rectale	Increased at week 5	3.786915702	0.002114212
Bifidobacterium_adolescentis	Increased at week 5	3.872783933	0.015540752
Coprococcus_comes	Increased at week 5	4.260491064	0.001608894
Bifidobacterium_pseudocatenulatum	Increased at week 5	4.513841999	1.17E-04
Clostridium_leptum	Increased at week 5	4.728114182	0.002166021
Clostridium_bartlettii	Increased at week 5	9.186039416	3.42E-09
Lactococcus_garvieae	Increased at week 5	16.35294196	8.63E-07

Supplementary Table 2. Correlations between microbial functions and plasma inflammation markers

Plasma inflammation markers	Gut microbial functions	R	P value
MCP1	PWY-6590: superpathway of Clostridium acetobutylicum acidogenic fermentation	-0.4661001	0.01120384
IL6	PWY-5941: glycogen degradation II (eukaryotic)	-0.45657183	0.03246406
IL6	PWY-6507: 4-deoxy-L-threo-hex-4-enopyranuronate degradation	-0.43863075	0.04746892
IL6	P162-PWY: L-glutamate degradation V (via hydroxyglutarate)	0.086904296	5.08E-04
IL6	PWY0-1479: tRNA processing	0.145415568	3.61E-04
IL6	PWY-7198: pyrimidine deoxyribonucleotides de novo biosynthesis IV	0.156946565	0.04389681
IL6	PWY-7210: pyrimidine deoxyribonucleotides biosynthesis from CTP	0.184185225	0.03408422
MCP1	NAGLIPASYN-PWY: lipid IVA biosynthesis	0.193627451	0.04860949
IL18	PWY-6936: seleno-amino acid biosynthesis	0.252605811	0.0191918
MCP1	P162-PWY: L-glutamate degradation V (via hydroxyglutarate)	0.302212214	0.03116647
IL18	PWY66-398: TCA cycle III (animals)	0.336217397	0.01405937
MCP1	PWY0-862: (5Z)-dodec-5-enoate biosynthesis	0.345800188	0.04860654
IL6	PWY-6284: superpathway of unsaturated fatty acids biosynthesis (E. coli)	0.347624154	0.00299421
MCP1	PWY-7388: octanoyl-[acyl-carrier protein] biosynthesis (mitochondria, yeast)	0.348252671	0.04142349
MCSF	PWY-6531: mannitol cycle	0.357217254	0.02542461
MCSF	PWY0-845: superpathway of pyridoxal 5'-phosphate biosynthesis and salvage	0.357217254	0.02254836
MCSF	PYRIDOXSYN-PWY: pyridoxal 5'-phosphate biosynthesis I	0.357217254	0.02085337
MCSF	PWY-5971: palmitate biosynthesis II (bacteria and plants)	0.357436339	0.01254865
MCSF	PWY-7388: octanoyl-[acyl-carrier protein] biosynthesis (mitochondria, yeast)	0.357436339	0.02342056
MCSF	PWY-7664: oleate biosynthesis IV (anaerobic)	0.357436339	0.02392005
MCSF	PWY0-862: (5Z)-dodec-5-enoate biosynthesis	0.357436339	0.02690538
MCP1	PWY-5971: palmitate biosynthesis II (bacteria and plants)	0.360515089	0.04522212
MCP1	PWY-6282: palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate)	0.360515089	0.04822185
MCP1	PWY-7664: oleate biosynthesis IV (anaerobic)	0.360515089	0.04388111

IL1RA	PWY-6138: CMP-N-acetylneuraminate biosynthesis I (eukaryotes)	0.367798958	0.02848334
IL6	PWY-7003: glycerol degradation to butanol	0.381699329	0.04434183
IL6	PWY-7196: superpathway of pyrimidine ribonucleosides salvage	0.390756601	0.02792876
MCSF	NAGLIPASYN-PWY: lipid IVA biosynthesis	0.40824829	0.00493903
MCSF	PWY-4984: urea cycle	0.40824829	0.00170098
MCP1	PWY-5179: toluene degradation V (aerobic) (via toluene-cis-diol)	0.40824829	0.04070735
CXCL10	PWY-5179: toluene degradation V (aerobic) (via toluene-cis-diol)	0.40824829	3.87E-04
MCP1	PWY-5180: toluene degradation I (aerobic) (via o-cresol)	0.40824829	0.04070735
CXCL10	PWY-5180: toluene degradation I (aerobic) (via o-cresol)	0.40824829	3.87E-04
MCP1	PWY-5182: toluene degradation II (aerobic) (via 4-methylcatechol)	0.40824829	0.04070735
CXCL10	PWY-5182: toluene degradation II (aerobic) (via 4-methylcatechol)	0.40824829	3.87E-04
MIG	PWY-5509: adenosylcobalamin biosynthesis from cobyrinate a,c-diamide I	0.40824829	8.82E-04
MIG	PWY-5871: ubiquinol-9 biosynthesis (eukaryotic)	0.40824829	8.82E-04
MIG	PWY-5873: ubiquinol-7 biosynthesis (eukaryotic)	0.40824829	8.82E-04
MCSF	PWY-7003: glycerol degradation to butanol	0.40824829	0.03262827
IL18	PWY-5509: adenosylcobalamin biosynthesis from cobyrinate a,c-diamide I	0.408498673	8.74E-04
IL18	PWY-5871: ubiquinol-9 biosynthesis (eukaryotic)	0.408498673	8.74E-04
IL18	PWY-5873: ubiquinol-7 biosynthesis (eukaryotic)	0.408498673	8.74E-04
MCSF	PWY-6282: palmitoleate biosynthesis I (from (5Z)-dodec-5-enoate)	0.408498673	0.00995845
MCSF	PWY-6284: superpathway of unsaturated fatty acids biosynthesis (E. coli)	0.408498673	3.47E-04
IL1RA	PWY-7374: 1,4-dihydroxy-6-naphthoate biosynthesis I	0.408498673	0.0013775
MCSF	P162-PWY: L-glutamate degradation V (via hydroxyglutarate)	0.409252593	0.00288907
MCSF	PWY-7198: pyrimidine deoxyribonucleotides de novo biosynthesis IV	0.409252593	0.04930692
MCSF	PWY-7210: pyrimidine deoxyribonucleotides biosynthesis from CTP	0.409252593	0.04460937
MCSF	PWY0-1479: tRNA processing	0.413345221	8.11E-07
IL6	NAGLIPASYN-PWY: lipid IVA biosynthesis	0.43345517	0.01257136
CXCL10	PWY66-409: superpathway of purine nucleotide salvage	0.450980392	0.03171542

MCP1	PWY-6126: superpathway of adenosine nucleotides de novo biosynthesis II	0.463235294	0.03770801
CXCL10	NAD-BIOSYNTHESIS-II: NAD salvage pathway II	0.473039216	0.01491173
MCP1	PWY-7220: adenosine deoxyribonucleotides de novo biosynthesis II	0.473039216	0.03988149
MCP1	PWY-7222: guanosine deoxyribonucleotides de novo biosynthesis II	0.473039216	0.03988149
IL6	PWY-6318: L-phenylalanine degradation IV (mammalian, via side chain)	0.475873693	0.01417966
MCP1	PWY-7229: superpathway of adenosine nucleotides de novo biosynthesis I	0.477941176	0.03291406
IL6	PROTOCATECHUATE-ORTHO-CLEAVAGE-PWY: protocatechuate degradation II (ortho-cleavage pathway)	0.496876075	0.0303078
IL6	PWY-7117: C4 photosynthetic carbon assimilation cycle, PEPCK type	0.503325555	0.01264789
IL1RA	PWY-622: starch biosynthesis	0.525427083	4.51E-04
MCP1	PWY-2941: L-lysine biosynthesis II	0.575980392	0.03196995
MIG	PWY-6936: seleno-amino acid biosynthesis	0.590686275	2.2E-04
MCP1	PWY66-409: superpathway of purine nucleotide salvage	0.593137255	0.00615523
CXCL10	P562-PWY: myo-inositol degradation I	0.606173878	8.61E-04
MCP1	PWY-7187: pyrimidine deoxyribonucleotides de novo biosynthesis II	0.632352941	0.01441646
MCP1	PWY-6123: inosine-5'-phosphate biosynthesis I	0.644607843	0.02566031
CXCL10	PWY-6270: isoprene biosynthesis I	0.647058824	0.00231275
CXCL10	PWY-7560: methylerythritol phosphate pathway II	0.659313725	0.00177093