**Table S1**.List of bacterial taxa used in PMP™ panels.

|  |  |  |  |
| --- | --- | --- | --- |
| **Acidaminococcus intestini** | **Bifidobacterium angulatum** | **Eggerthella lenta** | **Parabacteroides goldsteinii** |
| Akkermansia muciniphila | Bifidobacterium animalis subsp. lactis | Enterococcus faecalis | Parabacteroides merdae |
| Akkermansia muciniphila AmI | Bifidobacterium bifidum | Erysipelatoclostridium ramosum | Paraprevotella clara |
| Alistipes communis | Bifidobacterium catenulatum | Escherichia coli | Parasutterella excrementihominis |
| Alistipes finegoldii | Bifidobacterium longum | Eubacterium eligens | Parvimonas micra |
| Alistipes onderdonkii | Bifidobacterium longum subsp. longum | Eubacterium rectale | Phascolarctobacterium faecium |
| Alistipes putredinis | Bifidobacterium pseudocatenulatum | Eubacterium siraeum | Phocaeicola dorei |
| Alistipes senegalensis | Bilophila wadsworthia | Eubacterium ventriosum | Phocaeicola massiliensis |
| Alistipes shahii | Blautia hydrogenotrophica | Faecalibacterium cf. prausnitzii KLE1255 | Phocaeicola vulgatus |
| Anaerostipes hadrus | Blautia obeum | Faecalibacterium prausnitzii | Prevotella copri |
| Bacteroides caccae | Blautia wexlerae | Faecalibacterium prausnitzii A2-165 | Roseburia hominis |
| Bacteroides cellulosilyticus | Butyrivibrio crossotus | Faecalibacterium prausnitzii AHMP21 | Roseburia intestinalis |
| Bacteroides coprocola | Christensenella minuta | Faecalibacterium prausnitzii CNCM4575 | Roseburia inulinivorans |
| Bacteroides eggerthii | Clostridium bolteae | Faecalibacterium prausnitzii L2-6 | Ruminococcus albus |
| Bacteroides faecis | Clostridium citroniae | Faecalibacterium prausnitzii M21/2 | Ruminococcus bicirculans |
| Bacteroides finegoldii | Clostridium leptum | Flavonifractor plautii | Ruminococcus bromii |
| Bacteroides fragilis | Clostridium nexile | Gemmiger formicilis | Ruminococcus gnavus |
| Bacteroides intestinalis | Clostridium scindens | Gordonibacter pamelaeae | Ruminococcus lactaris |
| Bacteroides nordii | Clostridium spiroforme | Haemophilus parainfluenzae | Ruminococcus torques |
| Bacteroides ovatus | Clostridium symbiosum | Holdemanella biformis | Streptococcus thermophilus |
| Bacteroides plebeius | Collinsella aerofaciens | Holdemania filiformis | Subdoligranulum sp. (group 2) |
| Bacteroides stercoris | Coprococcus catus | Hungatella hathewayi | Subdoligranulum sp. (group 3) |
| Bacteroides thetaiotaomicron | Coprococcus comes | Intestinibacter bartlettii | Subdoligranulum sp. (group 4) |
| Bacteroides uniformis | Desulfovibrio piger | Malassezia (genus) | Subdoligranulum variabile |
| Bacteroides xylanisolvens | Dialister invisus | Methanobrevibacter smithii | Sutterella wadsworthensis |
| Barnesiella intestinihominis | Dorea formicigenerans | Odoribacter splanchnicus | Veillonella atypica |
| Bifidobacterium adolescentis | Dorea longicatena | Parabacteroides distasonis |  |

**Figure S1.** Principal component analysis of SARS-CoV-2 positive and negative participants at baseline.

A graph with red and blue dots

Description generated with high confidence

**Figure S2.** Boxplot of bacterial richness between SARS-CoV-2 positive and negative participants at baseline.

