

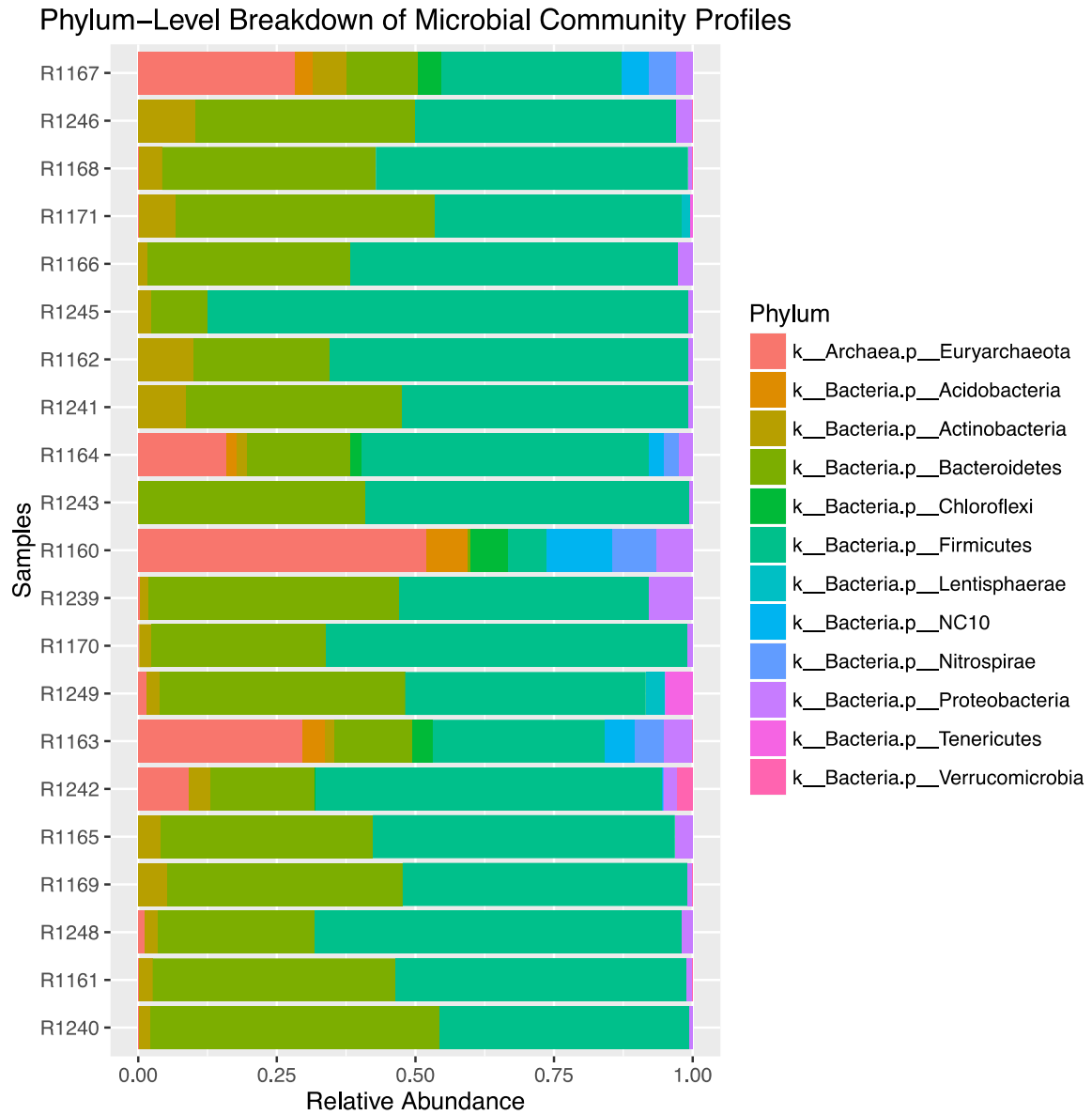
Table S1. The top 100 bacterial species identified in Fecal samples by metagenomic sequencing.

| Rank | Bacterial species identified |
|------|--------------------------------|
| 1 | <u>Bacteroides vulgatis</u> |
| 2 | Prevotella copri |
| 3 | Bacteroides uniformis |
| 4 | Novel species |
| 5 | Bacteroides stercoris |
| 6 | Escherichia coli |
| 7 | Faecalibacterium prausnitzii_A |
| 8 | Novel species |
| 9 | Agathobacter rectalis |
| 10 | Blautia wexlerae |
| 11 | Novel species |
| 12 | Bacteroides ovatus |
| 13 | Faecalibacterium prausnitzii_C |
| 14 | Novel species |
| 15 | Novel species |
| 16 | Faecalibacterium prausnitzii_B |
| 17 | Novel species |
| 18 | Alistipes putredinis |
| 19 | CAG37 sp1 |
| 20 | Novel species |
| 21 | CAG94 sp1 |
| 22 | Parabacteroides distasonis |
| 23 | Novel species |
| 24 | Roseburia intestinalis |
| 25 | Subdoligranulum sp2 |
| 26 | Novel species |
| 27 | Roseburia inulinivorans |
| 28 | Collinsella aerofaciens |
| 29 | Novel species |
| 30 | Ruminococcus_E bromii |
| 31 | Anaerostipes hadrus |
| 32 | UBA11524 sp1 |
| 33 | Ruminococcus_B faecis |
| 34 | CAG24 sp1 |
| 35 | Blautia sp2 |
| 36 | Novel species |
| 37 | Oscillibacter sp4 |
| 38 | Novel species |
| 39 | CAG180 sp2 |
| 40 | Agathobacter faecis |
| 41 | Novel species |
| 42 | Novel species |
| 43 | Bacteroides intestinalis |
| 44 | Novel species |
| 45 | Eubacterium_K siraeum |
| 46 | Novel species |

| | |
|----|-------------------------------------|
| 47 | <i>Lachnospira eligens</i> |
| 48 | Novel species |
| 49 | Novel species |
| 50 | <i>Bacteroides fragilis</i> |
| 51 | <i>Dialister</i> sp1 |
| 52 | <i>Bacteroides caccae</i> |
| 53 | Novel species |
| 54 | Novel species |
| 55 | <i>Barnesiella intestinihominis</i> |
| 56 | <i>Akkermansia muciniphila</i> |
| 57 | <i>Bifidobacterium longum</i> |
| 58 | <i>Ruminococcus_D bicirculans</i> |
| 59 | Novel species |
| 60 | CAG349 sp1 |
| 61 | Novel species |
| 62 | CAG217 sp1 |
| 63 | <i>Sutterella</i> |
| 64 | <i>Alistipes shahii</i> |
| 65 | Novel species |
| 66 | Novel species |
| 67 | Novel species |
| 68 | Novel species |
| 69 | <i>Bifidobacterium adolescentis</i> |
| 70 | Novel species |
| 71 | F23-B02 sp3 |
| 72 | <i>Phascolarctobacterium</i> |
| 73 | Novel species |
| 74 | <i>Oscillibacter</i> sp6 |
| 75 | Novel species |
| 76 | <i>Ruminococcus_E</i> sp1 |
| 77 | Novel species |
| 78 | Novel species |
| 79 | Novel species |
| 80 | <i>Bacteroides finegoldii</i> |
| 81 | PeH17 sp1 |
| 82 | Novel species |
| 83 | Novel species |
| 84 | Novel species |
| 85 | Novel species |
| 86 | CAG177 sp1 |
| 87 | <i>Ruminococcus_B lactaris</i> |
| 88 | Novel species |
| 89 | <i>Catenibacterium mitsuokai</i> |
| 90 | CAG279 sp1 |
| 91 | Novel species |
| 92 | Novel species |
| 93 | Novel species |
| 94 | Novel species |
| 95 | Novel species |

| | |
|-----|-----------------------|
| 96 | Roseburia hominis |
| 97 | CAG510 sp1 |
| 98 | Bilophila wadsworthia |
| 99 | Novel species |
| 100 | Prevotella sp13 |

Figure S1: Phylum – level breakdown of microbial community profiles expressed as relative abundance. The key code indicates whether the sample was pre or post supplementation.



| <u>Before</u> | <u>After</u> |
|---------------|--------------------|
| <u>R1160</u> | <u>R1239</u> |
| <u>R1161</u> | <u>R1240</u> |
| <u>R1162</u> | <u>R1241</u> |
| <u>R1163</u> | <u>R1242</u> |
| <u>R1164</u> | <u>R1243</u> |
| <u>R1165</u> | <u>dropped out</u> |

| | |
|--------------|------------------|
| <u>R1166</u> | <u>R1245</u> |
| <u>R1167</u> | <u>R1246</u> |
| <u>R1168</u> | <u>Low reads</u> |
| <u>R1169</u> | <u>R1248</u> |
| <u>R1170</u> | <u>R1249</u> |
| <u>R1171</u> | <u>R1250</u> |

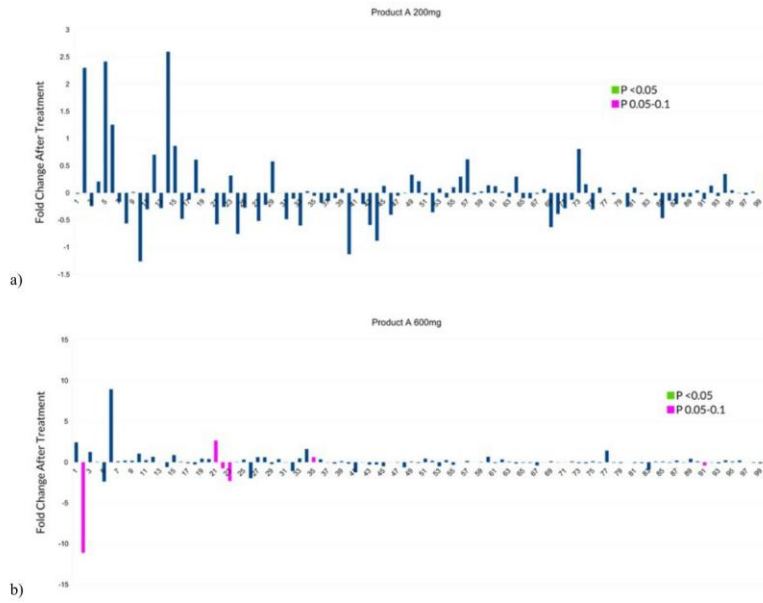


Figure S24. Fold changes in top 100 bacterial species for a) Product A dose 200mg, and b) Product A 600mg.



Figure S32. Fold changes in top 100 bacterial species for a) Product B dose 200mg, and b) Product B 600mg).

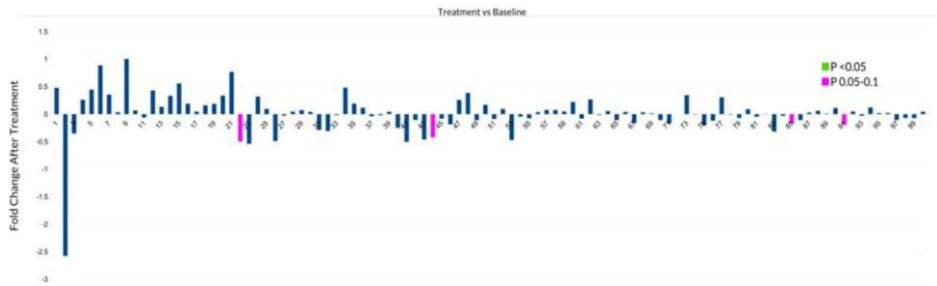


Figure S43. Fold changes in the top 100 bacterial species. Pooled data for both products.