

Supplementary Table 5 List of contrasted MSP species and Spearman correlations with MD index by time point. Reporting of contrasted MSP between ConD and MedD groups at each timepoint (after 20% occurrence filter) with their enrichment status, pvalues from Wilcoxon rank sum tests (pvalue_w) and after adjustment for multiple comparisons using the Benjamini-Hochberg procedure (qvalue_w), Spearman Rho and pvalue_{s_p} calculated with MD index score and the respective status based on Venn diagram results (status VD).

| MSP | Phylum | Species annotation | Baseline | | | | | Status VD |
|----------|----------------|--|-------------|---------------------|---------------------|--------|---------------------------------|---------------------|
| | | | Enriched in | pvalue _w | qvalue _w | Rho | pvalue _{s_p} | |
| msp_0713 | Firmicutes | <i>Clostridium citroniae</i> | ConD | 0,001 | 0,19 | -0,007 | 0,96 | baseline and 4w |
| msp_0056 | Firmicutes | <i>unclassified Clostridiales</i> | ConD | 0,002 | 0,19 | 0,015 | 0,90 | baseline, 4w and 8w |
| msp_0172 | Firmicutes | <i>Ruthenibacterium lactatiformans</i> | ConD | 0,002 | 0,19 | 0,138 | 0,29 | baseline, 4w and 8w |
| msp_0066 | Firmicutes | <i>Clostridium</i> sp. AT4 | ConD | 0,003 | 0,19 | -0,183 | 0,15 | baseline, 4w and 8w |
| msp_0009 | Firmicutes | <i>Clostridium bolteae</i> | ConD | 0,009 | 0,35 | 0,015 | 0,91 | baseline |
| msp_0335 | Bacteroidetes | <i>unclassified Alistipes</i> | ConD | 0,011 | 0,39 | -0,262 | 0,04 | baseline, 4w and 8w |
| msp_0263 | Actinobacteria | <i>Bifidobacterium adolescentis</i> | ConD | 0,017 | 0,49 | -0,066 | 0,61 | baseline and 8w |
| msp_1541 | Firmicutes | <i>unclassified Clostridiales</i> | ConD | 0,021 | 0,49 | 0,016 | 0,90 | baseline and 4w |
| msp_0020 | Firmicutes | <i>Clostridium clostridioforme</i> 1 | ConD | 0,022 | 0,49 | -0,174 | 0,18 | baseline and 4w |
| msp_0014 | Firmicutes | <i>Eisenbergiella tayi</i> | ConD | 0,028 | 0,51 | 0,153 | 0,24 | baseline, 4w and 8w |
| msp_0318 | Bacteroidetes | <i>Alistipes indistinctus</i> | ConD | 0,043 | 0,61 | -0,027 | 0,84 | baseline and 4w |
| msp_0164 | Firmicutes | <i>Ruminococcus</i> sp. | MedD | 0,003 | 0,19 | 0,140 | 0,28 | baseline, 4w and 8w |
| msp_0979 | NA | NA | MedD | 0,004 | 0,19 | 0,244 | 0,06 | baseline, 4w and 8w |
| msp_0265 | Firmicutes | <i>unclassified Faecalibacterium</i> | MedD | 0,004 | 0,19 | -0,004 | 0,97 | baseline, 4w and 8w |
| msp_0586 | Firmicutes | <i>Clostridium</i> sp. CAG:343 | MedD | 0,004 | 0,19 | 0,306 | 0,02 | baseline |
| msp_0285 | Firmicutes | <i>Clostridium</i> sp. CAG:217 | MedD | 0,022 | 0,49 | 0,009 | 0,95 | baseline, 4w and 8w |
| msp_0133 | Firmicutes | <i>Coprococcus</i> sp. | MedD | 0,022 | 0,49 | 0,149 | 0,25 | baseline and 4w |
| msp_0820 | Firmicutes | <i>unclassified Clostridiales</i> | MedD | 0,023 | 0,49 | 0,277 | 0,03 | baseline, 4w and 8w |
| msp_0679 | Firmicutes | <i>unclassified Firmicutes</i> | MedD | 0,024 | 0,49 | 0,040 | 0,76 | baseline, 4w and 8w |
| msp_0906 | Firmicutes | <i>Clostridium</i> sp. | MedD | 0,025 | 0,49 | 0,041 | 0,75 | baseline, 4w and 8w |
| msp_0189 | Firmicutes | <i>Blautia</i> sp. CAG:237 | MedD | 0,029 | 0,51 | 0,166 | 0,20 | baseline, 4w and 8w |
| msp_0893 | Firmicutes | <i>Faecalibacterium prausnitzii</i> 2 | MedD | 0,032 | 0,51 | 0,034 | 0,79 | baseline |
| msp_0087 | Firmicutes | <i>Lactobacillus rogosae</i> | MedD | 0,033 | 0,51 | 0,264 | 0,04 | baseline |

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|-----------|------------|---------------------------------------|------|-------|------|-------|------|---------------------|
| msp_0639 | Firmicutes | <i>Faecalibacterium prausnitzii</i> 6 | MedD | 0,034 | 0,51 | 0,096 | 0,46 | baseline, 4w and 8w |
| msp_1428 | Firmicutes | <i>unclassified Clostridiales</i> | MedD | 0,047 | 0,61 | 0,155 | 0,23 | baseline |
| msp_1643c | Firmicutes | <i>Ruminococcus</i> sp. JC304 | MedD | 0,048 | 0,61 | 0,258 | 0,04 | baseline, 4w and 8w |
| msp_0153 | Firmicutes | <i>Erysipelatoclostridium ramosum</i> | MedD | 0,048 | 0,61 | 0,146 | 0,26 | baseline |

Total Number MSP species at baseline= 1065

4w

| MSP | Phylum | Species annotation | Enriched in | pvaluew | qvaluew | Rho | pvaluesp | Status VD |
|----------|---------------|---|-------------|---------|---------|-------|----------|---------------------|
| msp_0172 | Firmicutes | <i>Ruthenibacterium lactatiformans</i> | ConD | 0,00016 | 0,019 | -0,44 | 0,0004 | baseline, 4w and 8w |
| msp_0066 | Firmicutes | <i>Clostridium</i> sp. AT4 | ConD | 0,00481 | 0,10 | -0,35 | 0,0058 | baseline, 4w and 8w |
| msp_0024 | Firmicutes | <i>Hungatella hathewayi</i> 2 | ConD | 0,00559 | 0,10 | -0,34 | 0,0066 | 4w |
| msp_0249 | Firmicutes | <i>unclassified Firmicutes</i> | ConD | 0,00665 | 0,10 | -0,23 | 0,0695 | 4w |
| msp_0335 | Bacteroidetes | <i>unclassified Alistipes</i> | ConD | 0,00681 | 0,10 | -0,38 | 0,0026 | baseline, 4w and 8w |
| msp_0619 | NA | NA | ConD | 0,00895 | 0,12 | -0,31 | 0,0155 | 4w |
| msp_0058 | Firmicutes | <i>Ruminococcus gnavus</i> | ConD | 0,00939 | 0,12 | -0,23 | 0,0734 | 4w and 8w |
| msp_0707 | Firmicutes | <i>unclassified Firmicutes</i> | ConD | 0,01057 | 0,12 | -0,24 | 0,0614 | 4w and 8w |
| msp_0713 | Firmicutes | <i>Clostridium citroniae</i> | ConD | 0,01088 | 0,12 | -0,43 | 0,0005 | baseline and 4w |
| msp_0056 | Firmicutes | <i>unclassified Clostridiales</i> | ConD | 0,01270 | 0,13 | -0,42 | 0,0008 | baseline, 4w and 8w |
| msp_0052 | Firmicutes | <i>Blautia</i> sp. CAG:257 | ConD | 0,01368 | 0,13 | -0,28 | 0,0296 | 4w and 8w |
| msp_0317 | Firmicutes | <i>unclassified Clostridiales</i> | ConD | 0,01368 | 0,13 | -0,13 | 0,3082 | 4w |
| msp_0331 | Firmicutes | <i>Oscillibacter</i> sp. | ConD | 0,01379 | 0,13 | -0,33 | 0,0085 | 4w |
| msp_0271 | Firmicutes | <i>Eubacterium</i> sp. CAG:180 | ConD | 0,01420 | 0,13 | -0,28 | 0,0299 | 4w |
| msp_0126 | Firmicutes | <i>Ruminococcus torques</i> | ConD | 0,01453 | 0,13 | -0,34 | 0,0063 | 4w and 8w |
| msp_0621 | Firmicutes | <i>Intestinibacter bartlettii</i> | ConD | 0,01563 | 0,13 | -0,14 | 0,2883 | 4w |
| msp_0027 | Bacteroidetes | <i>Parabacteroides merdae</i> | ConD | 0,01625 | 0,13 | -0,17 | 0,1937 | 4w |
| msp_1090 | NA | NA | ConD | 0,01640 | 0,13 | -0,25 | 0,0528 | 4w |
| msp_0132 | Firmicutes | <i>Coprobacillus cateniformis</i> | ConD | 0,01734 | 0,14 | -0,26 | 0,0425 | 4w and 8w |
| msp_0318 | Bacteroidetes | <i>Alistipes indistinctus</i> | ConD | 0,01862 | 0,14 | -0,23 | 0,0765 | baseline and 4w |
| msp_0014 | Firmicutes | <i>Eisenbergiella tayi</i> | ConD | 0,01883 | 0,14 | -0,32 | 0,0115 | baseline, 4w and 8w |
| msp_0510 | Firmicutes | <i>Clostridium glycyrrhizinilyticum</i> | ConD | 0,02199 | 0,16 | -0,35 | 0,0056 | 4w |
| msp_1315 | Firmicutes | <i>unclassified Firmicutes</i> | ConD | 0,02687 | 0,17 | -0,21 | 0,0981 | 4w |
| msp_0364 | Firmicutes | <i>Intestinimonas butyriciproducens</i> | ConD | 0,02694 | 0,17 | -0,23 | 0,0675 | 4w |
| msp_0442 | Firmicutes | <i>unclassified Flavonifractor</i> | ConD | 0,02787 | 0,17 | -0,33 | 0,0089 | 4w |
| msp_0861 | Firmicutes | <i>unclassified Oscillibacter</i> | ConD | 0,03166 | 0,19 | -0,30 | 0,0164 | 4w |
| msp_0230 | Bacteroidetes | <i>Alistipes inops</i> | ConD | 0,03206 | 0,19 | -0,18 | 0,1559 | 4w |
| msp_1012 | Firmicutes | <i>Intestinimonas massiliensis</i> | ConD | 0,03310 | 0,19 | -0,32 | 0,0109 | 4w |
| msp_0833 | Firmicutes | <i>Streptococcus thermophilus</i> | ConD | 0,03320 | 0,19 | -0,30 | 0,0166 | 4w |

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|-----------|----------------|--|------|---------|-------|-------|---------|---------------------|
| msp_0522 | Firmicutes | <i>Anaerotruncus colihominis</i> | ConD | 0,03393 | 0,19 | -0,40 | 0,0012 | 4w |
| msp_0103 | Firmicutes | <i>Clostridium innocuum</i> | ConD | 0,03433 | 0,19 | -0,30 | 0,0190 | 4w and 8w |
| msp_0020 | Firmicutes | <i>Clostridium clostridioforme</i> 1 | ConD | 0,03648 | 0,20 | -0,33 | 0,0080 | baseline and 4w |
| msp_0353 | NA | NA | ConD | 0,04238 | 0,20 | -0,31 | 0,0157 | 4w |
| msp_1541 | Firmicutes | <i>unclassified Clostridiales</i> | ConD | 0,04247 | 0,20 | -0,34 | 0,0074 | baseline and 4w |
| msp_1724 | Firmicutes | <i>Phoceea massiliensis</i> | ConD | 0,04435 | 0,21 | -0,27 | 0,0327 | 4w and 8w |
| msp_0213 | Firmicutes | <i>Flavonifractor plautii</i> | ConD | 0,04472 | 0,21 | -0,23 | 0,0679 | 4w and 8w |
| msp_0881 | Proteobacteria | <i>Haemophilus parainfluenzae</i> | MedD | 0,00001 | 0,003 | 0,55 | 4,0E-06 | 4w and 8w |
| msp_0388 | Firmicutes | <i>Faecalibacterium prausnitzii</i> 3 (L2-6) | MedD | 0,00010 | 0,017 | 0,24 | 0,0614 | 4w and 8w |
| msp_0884 | Firmicutes | <i>Veillonella atypica</i> | MedD | 0,00023 | 0,02 | 0,32 | 0,0104 | 4w |
| msp_1641 | Firmicutes | <i>unclassified Lachnospiraceae</i> | MedD | 0,00037 | 0,03 | 0,35 | 0,0049 | 4w and 8w |
| msp_1643c | Firmicutes | <i>Ruminococcus</i> sp. JC304 | MedD | 0,00052 | 0,03 | 0,28 | 0,0277 | baseline, 4w and 8w |
| msp_0979 | NA | NA | MedD | 0,00156 | 0,08 | 0,37 | 0,0030 | baseline, 4w and 8w |
| msp_0906 | Firmicutes | <i>Clostridium</i> sp. | MedD | 0,00188 | 0,08 | 0,40 | 0,0013 | baseline, 4w and 8w |
| msp_0285 | Firmicutes | <i>Clostridium</i> sp. CAG:217 | MedD | 0,00207 | 0,08 | 0,10 | 0,4188 | baseline, 4w and 8w |
| msp_0164 | Firmicutes | <i>Ruminococcus</i> sp. | MedD | 0,00238 | 0,08 | 0,34 | 0,0077 | baseline, 4w and 8w |
| msp_0313 | Firmicutes | <i>Veillonella parvula</i> | MedD | 0,00264 | 0,08 | 0,35 | 0,0060 | 4w and 8w |
| msp_0930 | Firmicutes | <i>unclassified Lachnospiraceae</i> | MedD | 0,00294 | 0,08 | 0,34 | 0,0066 | 4w |
| msp_1219 | Firmicutes | <i>Veillonella rogosae</i> | MedD | 0,00302 | 0,08 | 0,32 | 0,0115 | 4w and 8w |
| msp_0189 | Firmicutes | <i>Blautia</i> sp. CAG:237 | MedD | 0,00366 | 0,09 | 0,29 | 0,0245 | baseline, 4w and 8w |
| msp_0265 | Firmicutes | <i>unclassified Faecalibacterium</i> | MedD | 0,00373 | 0,09 | 0,20 | 0,1173 | baseline, 4w and 8w |
| msp_0148c | Firmicutes | <i>Veillonella dispar</i> | MedD | 0,00581 | 0,10 | 0,31 | 0,0128 | 4w |
| msp_0457 | Firmicutes | <i>Faecalibacterium</i> sp. CAG:82 | MedD | 0,00581 | 0,10 | 0,30 | 0,0193 | 4w and 8w |
| msp_0296 | Firmicutes | <i>unclassified Lachnospiraceae</i> | MedD | 0,00665 | 0,10 | 0,32 | 0,0112 | 4w and 8w |
| msp_0898 | Firmicutes | <i>unclassified butyrate-producing Clostridiales</i> | MedD | 0,00670 | 0,10 | 0,27 | 0,0315 | 4w |
| msp_0468 | Firmicutes | <i>unclassified Clostridiales</i> | MedD | 0,00788 | 0,11 | 0,18 | 0,1566 | 4w |
| msp_0029 | Firmicutes | <i>Eubacterium eligens</i> | MedD | 0,00928 | 0,12 | 0,27 | 0,0317 | 4w and 8w |
| msp_0639 | Firmicutes | <i>Faecalibacterium prausnitzii</i> 6 | MedD | 0,00944 | 0,12 | 0,39 | 0,0015 | baseline, 4w and 8w |
| msp_1236 | Firmicutes | <i>unclassified Lachnoclostridium</i> | MedD | 0,01079 | 0,12 | 0,37 | 0,0027 | 4w |
| msp_0301 | Firmicutes | <i>Faecalibacterium prausnitzii</i> 1 (A2-165) | MedD | 0,01144 | 0,12 | 0,38 | 0,0022 | 4w |
| msp_0075 | Firmicutes | <i>Clostridium</i> sp. | MedD | 0,01145 | 0,12 | 0,28 | 0,0300 | 4w and 8w |
| msp_0820 | Firmicutes | <i>unclassified Clostridiales</i> | MedD | 0,01424 | 0,13 | 0,37 | 0,0031 | baseline, 4w and 8w |

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|-----------|----------------|---|------|---------|------|-------|--------|---------------------|
| msp_0473c | Firmicutes | <i>Clostridium sp.</i> | MedD | 0,02327 | 0,17 | 0,16 | 0,2225 | 4w and 8w |
| msp_0297 | Firmicutes | <i>unclassified Ruminococcaceae</i> | MedD | 0,02327 | 0,17 | -0,31 | 0,0136 | 4w |
| msp_0679 | Firmicutes | <i>unclassified Firmicutes</i> | MedD | 0,02439 | 0,17 | 0,25 | 0,0525 | baseline, 4w and 8w |
| msp_0572 | Firmicutes | <i>Lachnospira sp.</i> | MedD | 0,02460 | 0,17 | 0,33 | 0,0091 | 4w |
| msp_0015 | Firmicutes | <i>Roseburia faecis</i> | MedD | 0,02557 | 0,17 | 0,22 | 0,0888 | 4w |
| msp_0068 | Firmicutes | <i>Eubacterium rectale</i> | MedD | 0,02557 | 0,17 | 0,24 | 0,0658 | 4w |
| msp_0017 | Firmicutes | <i>Roseburia intestinalis</i> | MedD | 0,02610 | 0,17 | 0,31 | 0,0150 | 4w and 8w |
| msp_0563 | Firmicutes | <i>unclassified Clostridium</i> | MedD | 0,03159 | 0,19 | 0,34 | 0,0077 | 4w |
| msp_0125 | Firmicutes | <i>unclassified Clostridiales</i> | MedD | 0,03709 | 0,20 | 0,27 | 0,0373 | 4w |
| msp_1302 | Firmicutes | <i>unclassified Firmicutes</i> | MedD | 0,03912 | 0,20 | 0,24 | 0,0562 | 4w |
| msp_0986 | Firmicutes | <i>Coprococcus catus</i> | MedD | 0,03927 | 0,20 | 0,31 | 0,0137 | 4w |
| msp_0086 | Firmicutes | <i>Clostridium symbiosum</i> | MedD | 0,03984 | 0,20 | -0,41 | 0,0009 | 4w |
| msp_1143 | Firmicutes | <i>unclassified Oscillibacter</i> | MedD | 0,04124 | 0,20 | 0,23 | 0,0680 | 4w |
| msp_1339 | Actinobacteria | <i>Gordonibacter urolithinifaciens</i> | MedD | 0,04209 | 0,20 | 0,16 | 0,2228 | 4w |
| msp_0227 | Firmicutes | <i>Eubacterium sp. 36_13 & CAG:86</i> | MedD | 0,04285 | 0,20 | 0,37 | 0,0029 | 4w |
| msp_0133 | Firmicutes | <i>Coprococcus sp.</i> | MedD | 0,04861 | 0,22 | 0,28 | 0,0276 | baseline and 4w |

Total Number MSP species at 4w = 1051

| 8w | | | | | | | | |
|-----------|----------------|---|-------------|---------|---------|-------|----------|---------------------|
| MSP | Phylum | Species annotation | Enriched in | pvaluew | qvaluew | Rho | pvaluesp | Status VD |
| msp_0172 | Firmicutes | <i>Ruthenibacterium lactatiformans</i> | ConD | 0,002 | 0,12 | -0,27 | 0,033 | baseline, 4w and 8w |
| msp_0126 | Firmicutes | <i>Ruminococcus torques</i> | ConD | 0,002 | 0,12 | -0,33 | 0,009 | 4w and 8w |
| msp_0213 | Firmicutes | <i>Flavonifractor plautii</i> | ConD | 0,006 | 0,14 | -0,28 | 0,026 | 4w and 8w |
| msp_0058 | Firmicutes | <i>Ruminococcus gnavus</i> | ConD | 0,007 | 0,14 | -0,21 | 0,094 | 4w and 8w |
| msp_0132 | Firmicutes | <i>Coprobacillus cateniformis</i> | ConD | 0,007 | 0,14 | -0,22 | 0,082 | 4w and 8w |
| msp_0335 | Bacteroidetes | <i>unclassified Alistipes</i> | ConD | 0,007 | 0,14 | -0,37 | 0,003 | baseline, 4w and 8w |
| msp_0340 | Firmicutes | <i>Clostridium leptum</i> | ConD | 0,011 | 0,17 | -0,20 | 0,110 | 8w |
| msp_0263 | Actinobacteria | <i>Bifidobacterium adolescentis</i> | ConD | 0,012 | 0,17 | -0,28 | 0,029 | baseline and 8w |
| msp_0014 | Firmicutes | <i>Eisenbergiella tayi</i> | ConD | 0,012 | 0,17 | -0,27 | 0,034 | baseline, 4w and 8w |
| msp_0112 | Firmicutes | <i>Blautia hydrogenotrophica</i> | ConD | 0,014 | 0,18 | -0,27 | 0,037 | 8w |
| msp_0052 | Firmicutes | <i>Blautia</i> sp. CAG:257 | ConD | 0,016 | 0,19 | -0,34 | 0,007 | 4w and 8w |
| msp_0066 | Firmicutes | <i>Clostridium</i> sp. AT4 | ConD | 0,025 | 0,27 | -0,28 | 0,027 | baseline, 4w and 8w |
| msp_1724 | Firmicutes | <i>Phocea massiliensis</i> | ConD | 0,027 | 0,27 | -0,33 | 0,009 | 4w and 8w |
| msp_0005 | Proteobacteria | <i>Escherichia coli</i> | ConD | 0,028 | 0,27 | -0,24 | 0,058 | 8w |
| msp_0259 | Firmicutes | <i>Coprococcus comes</i> | ConD | 0,028 | 0,27 | -0,20 | 0,111 | 8w |
| msp_0056 | Firmicutes | <i>unclassified Clostridiales</i> | ConD | 0,035 | 0,32 | -0,23 | 0,070 | baseline, 4w and 8w |
| msp_0103 | Firmicutes | <i>Clostridium innocuum</i> | ConD | 0,036 | 0,32 | -0,22 | 0,090 | 4w and 8w |
| msp_0707 | Firmicutes | <i>unclassified Firmicutes</i> | ConD | 0,040 | 0,34 | -0,02 | 0,879 | 4w and 8w |
| msp_1244 | Actinobacteria | <i>Collinsella aerofaciens</i> | ConD | 0,040 | 0,34 | -0,19 | 0,138 | 8w |
| msp_0881 | Proteobacteria | <i>Haemophilus parainfluenzae</i> | MedD | 0,000 | 0,05 | 0,40 | 0,001 | 4w and 8w |
| msp_0906 | Firmicutes | <i>Clostridium</i> sp. | MedD | 0,000 | 0,07 | 0,36 | 0,004 | baseline, 4w and 8w |
| msp_0457 | Firmicutes | <i>Faecalibacterium</i> sp. CAG:82 | MedD | 0,002 | 0,12 | 0,33 | 0,008 | 4w and 8w |
| msp_0820 | Firmicutes | <i>unclassified Clostridiales</i> | MedD | 0,003 | 0,12 | 0,25 | 0,049 | baseline, 4w and 8w |
| msp_0388 | Firmicutes | <i>Faecalibacterium prausnitzii</i> 3 (L2-6) | MedD | 0,003 | 0,12 | 0,24 | 0,056 | 4w and 8w |
| msp_1643c | Firmicutes | <i>Ruminococcus</i> sp. JC304 | MedD | 0,003 | 0,12 | 0,30 | 0,017 | baseline, 4w and 8w |
| msp_0979 | NA | NA | MedD | 0,003 | 0,13 | 0,38 | 0,002 | baseline, 4w and 8w |
| msp_0164 | Firmicutes | <i>Ruminococcus</i> sp. | MedD | 0,004 | 0,13 | 0,23 | 0,074 | baseline, 4w and 8w |
| msp_0265 | Firmicutes | <i>unclassified Faecalibacterium</i> | MedD | 0,005 | 0,13 | 0,17 | 0,176 | baseline, 4w and 8w |
| msp_0029 | Firmicutes | <i>Eubacterium eligens</i> | MedD | 0,005 | 0,13 | 0,37 | 0,003 | 4w and 8w |

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|-----------|----------------|---|------|-------|------|------|-------|---------------------|
| msp_0075 | Firmicutes | <i>Clostridium</i> sp. | MedD | 0,006 | 0,14 | 0,27 | 0,031 | 4w and 8w |
| msp_0473c | Firmicutes | <i>Clostridium</i> sp. | MedD | 0,007 | 0,14 | 0,27 | 0,034 | 4w and 8w |
| msp_1641 | Firmicutes | <i>unclassified Lachnospiraceae</i> | MedD | 0,008 | 0,15 | 0,38 | 0,002 | 4w and 8w |
| msp_0285 | Firmicutes | <i>Clostridium</i> sp. CAG:217 | MedD | 0,011 | 0,17 | 0,05 | 0,717 | baseline, 4w and 8w |
| msp_0296 | Firmicutes | <i>unclassified Lachnospiraceae</i> | MedD | 0,012 | 0,17 | 0,26 | 0,040 | 4w and 8w |
| msp_1219 | Firmicutes | <i>Veillonella rogosae</i> | MedD | 0,012 | 0,17 | 0,20 | 0,121 | 4w and 8w |
| msp_0071 | Firmicutes | <i>Roseburia hominis</i> | MedD | 0,012 | 0,17 | 0,18 | 0,173 | 8w |
| msp_0017 | Firmicutes | <i>Roseburia intestinalis</i> | MedD | 0,014 | 0,18 | 0,24 | 0,065 | 4w and 8w |
| msp_0679 | Firmicutes | <i>unclassified Firmicutes</i> | MedD | 0,016 | 0,19 | 0,26 | 0,041 | baseline, 4w and 8w |
| msp_0639 | Firmicutes | <i>Faecalibacterium prausnitzii</i> 6 | MedD | 0,020 | 0,22 | 0,28 | 0,027 | baseline, 4w and 8w |
| msp_0189 | Firmicutes | <i>Blautia</i> sp. CAG:237 | MedD | 0,025 | 0,27 | 0,27 | 0,036 | baseline, 4w and 8w |
| msp_0313 | Firmicutes | <i>Veillonella parvula</i> | MedD | 0,031 | 0,29 | 0,21 | 0,099 | 4w and 8w |
| msp_0860 | Firmicutes | <i>unclassified Intestinibacter</i> | MedD | 0,042 | 0,35 | 0,25 | 0,052 | 8w |
| msp_0145 | Proteobacteria | <i>Parasutterella excrementihominis</i> | MedD | 0,044 | 0,36 | 0,01 | 0,927 | 8w |
| msp_0780 | Firmicutes | <i>unclassified Lachnospiraceae</i> | MedD | 0,047 | 0,38 | 0,22 | 0,081 | 8w |

Total Number MSP species at 8w = 1037