

**Supplementary Table 6** List of contrasted MSP within diets. List of contrasted MSP within ConD and MedD groups for the 4w-baseline and 8w-4w periods (after 20% occurrence filter) with their enrichment status and pvalues from paired Wilcoxon rank sum tests (pvaluew) and after adjustment for multiple comparisons using the Benjamini-Hochberg procedure (qvaluew).

ConD_baseline vs 4w					
MSP	phylum	species	pvaluew	qvaluew	Enriched at
msp_1349	Firmicutes	<i>unclassified Ruminococcaceae</i>	0,0046	0,79	baseline
msp_0215	Firmicutes	<i>Dialister</i> sp. CAG:357	0,0068	0,79	baseline
msp_1302	Firmicutes	<i>unclassified Firmicutes</i>	0,0113	0,80	baseline
msp_0554	Firmicutes	<i>Anaerostipes hadrus</i> 2	0,0147	0,86	baseline
msp_0324	Firmicutes	<i>Faecalibacterium prausnitzii</i> 7	0,0238	1,00	baseline
msp_0335	Bacteroidetes	<i>unclassified Alistipes</i>	0,0263	1,00	baseline
msp_1556	Firmicutes	<i>Holdemania filiformis</i>	0,0274	1,00	baseline
msp_1403	Firmicutes	<i>Blautia</i> sp.	0,0333	1,00	baseline
msp_0129	Firmicutes	<i>Clostridium</i> sp. CAG:58	0,0383	1,00	baseline
msp_0221	Firmicutes	<i>Acidaminococcus intestini</i>	0,0465	1,00	baseline
msp_0331	Firmicutes	<i>Oscillibacter</i> sp.	0,0475	1,00	baseline
msp_0440	Firmicutes	<i>unclassified Eubacterium</i>	0,0042	0,79	4w
msp_0893	Firmicutes	<i>Faecalibacterium prausnitzii</i> 2	0,0114	0,80	4w
msp_0035	Bacteroidetes	<i>Bacteroides dorei</i>	0,0349	1,00	4w

Total Number MSP species ConD baseline vs 4w = 975

## ConD\_4w vs 8w

MSP	phylum	species	pvaluew	qvaluew	Enriched at
msp_1362	Firmicutes	<i>Holdemania massiliensis</i>	0,014	0,701	4w
msp_0225	Bacteroidetes	<i>Alistipes obesi</i>	0,015	0,701	4w
msp_0432	unclassified	<i>unclassified</i>	0,017	0,701	4w
msp_0440	Firmicutes	<i>unclassified Eubacterium</i>	0,017	0,701	4w
msp_0046	Bacteroidetes	<i>Bacteroides uniformis</i>	0,018	0,701	4w
msp_0069	Bacteroidetes	<i>Bacteroides vulgatus</i>	0,034	0,793	4w
msp_0906	Firmicutes	<i>Clostridium sp.</i>	0,041	0,793	4w
msp_0259	Firmicutes	<i>Coprococcus comes</i>	0,008	0,701	8w
msp_1381	Firmicutes	<i>Butyricoccus sp.</i>	0,009	0,701	8w
msp_1244	Actinobacteria	<i>Collinsella aerofaciens</i>	0,009	0,701	8w
msp_1349	Firmicutes	<i>unclassified Ruminococcaceae</i>	0,015	0,701	8w
msp_1339	Actinobacteria	<i>Gordonibacter urolithinifaciens</i>	0,024	0,701	8w
msp_0126	Firmicutes	<i>Ruminococcus torques</i>	0,025	0,701	8w
msp_0215	Firmicutes	<i>Dialister sp. CAG:357</i>	0,025	0,701	8w
msp_0467	Firmicutes	<i>Firmicutes bacterium CAG:94</i>	0,026	0,701	8w
msp_0045	Firmicutes	<i>Ruminococcus bromii 2</i>	0,036	0,793	8w
msp_0385	Firmicutes	<i>Ruminococcaceae bacterium D16</i>	0,041	0,793	8w
msp_0419	Actinobacteria	<i>Bifidobacterium bifidum</i>	0,042	0,793	8w
msp_0874	Firmicutes	<i>unclassified Firmicutes</i>	0,045	0,793	8w

Total Number MSP species ConD 4w vs 8w = 960

## MedD\_baseline vs 4w

MSP	phylum	species	pvaluew	qvaluew	Enriched at
msp_0213	Firmicutes	<i>Flavonifractor plautii</i>	0,0001	0,0240	baseline
msp_0331	Firmicutes	<i>Oscillibacter</i> sp.	0,001	0,0815	baseline
msp_0342	Firmicutes	<i>Flavonifractor</i> sp.	0,001	0,0859	baseline
msp_0613	Firmicutes	unclassified Clostridiales	0,003	0,1030	baseline
msp_0565	Firmicutes	unclassified Ruminococcaceae	0,003	0,1030	baseline
msp_0024	Firmicutes	<i>Hungatella hathewayi</i> 2	0,005	0,1560	baseline
msp_0172	Firmicutes	<i>Ruthenibacterium lactatiformans</i>	0,006	0,1560	baseline
msp_1060c	Firmicutes	unclassified Flavonifractor	0,007	0,1560	baseline
msp_0781	Firmicutes	unclassified Clostridiales	0,008	0,1560	baseline
msp_0833	Firmicutes	<i>Streptococcus thermophilus</i>	0,009	0,1560	baseline
msp_0312	Firmicutes	<i>Firmicutes bacterium</i> CAG:110	0,012	0,1560	baseline
msp_0152	Firmicutes	<i>Ruminococcus faecis</i>	0,012	0,1560	baseline
msp_0467	Firmicutes	<i>Firmicutes bacterium</i> CAG:94	0,012	0,1560	baseline
msp_0500	Firmicutes	unclassified Firmicutes	0,012	0,1560	baseline
msp_0621	Firmicutes	<i>Intestinibacter bartlettii</i>	0,013	0,1560	baseline
msp_1349	Firmicutes	unclassified Ruminococcaceae	0,013	0,1560	baseline
msp_0364	Firmicutes	<i>Intestinimonas butyriciproducens</i>	0,013	0,1560	baseline
msp_0357	Firmicutes	<i>Clostridium</i> sp. CAG:169	0,013	0,1560	baseline
msp_0121	Firmicutes	unclassified <i>Oscillibacter</i>	0,014	0,1560	baseline
msp_0335	Bacteroidetes	unclassified <i>Alistipes</i>	0,014	0,1560	baseline
msp_1090	unclassified	unclassified	0,014	0,1560	baseline
msp_0308	Firmicutes	<i>Clostridium saccharolyticum</i> 2	0,014	0,1560	baseline
msp_0510	Firmicutes	<i>Clostridium glycyrrhizinilyticum</i>	0,017	0,1678	baseline
msp_0545	Firmicutes	<i>Pseudoflavonifractor</i> sp. An184	0,018	0,1678	baseline
msp_0314	Firmicutes	unclassified Clostridiales	0,019	0,1678	baseline
msp_0132	Firmicutes	<i>Coprobacillus cateniformis</i>	0,019	0,1678	baseline
msp_0462	Firmicutes	unclassified Clostridiales	0,020	0,1678	baseline
msp_0126	Firmicutes	<i>Ruminococcus torques</i>	0,020	0,1678	baseline
msp_0777	Firmicutes	<i>Firmicutes bacterium</i> CAG:129	0,021	0,1678	baseline
msp_0040	Bacteroidetes	<i>Bacteroides massiliensis</i>	0,022	0,1690	baseline
msp_0249	Firmicutes	unclassified Firmicutes	0,023	0,1717	baseline
msp_0592	Firmicutes	unclassified Clostridiales	0,024	0,1732	baseline
msp_0861	Firmicutes	unclassified <i>Oscillibacter</i>	0,025	0,1758	baseline
msp_1013	Firmicutes	unclassified Firmicutes	0,025	0,1771	baseline
msp_0027	Bacteroidetes	<i>Parabacteroides merdae</i>	0,027	0,1835	baseline
msp_0435	Firmicutes	unclassified <i>Oscillibacter</i>	0,029	0,1864	baseline
msp_1315	Firmicutes	unclassified Firmicutes	0,037	0,2189	baseline
msp_0205	Firmicutes	<i>Firmicutes bacterium</i> CAG:124	0,037	0,2189	baseline
msp_0317	Firmicutes	unclassified Clostridiales	0,038	0,2189	baseline
msp_1356	Firmicutes	<i>Anaeromassilibacillus</i> sp. An250	0,041	0,2291	baseline
msp_0144	Firmicutes	<i>Clostridium</i> sp. CAG:138	0,041	0,2291	baseline
msp_0471	Firmicutes	unclassified Clostridiales	0,044	0,2291	baseline
msp_0287	Bacteroidetes	<i>Alistipes ihumii</i>	0,044	0,2291	baseline
msp_1724	Firmicutes	<i>Phoceia massiliensis</i>	0,044	0,2291	baseline

msp_0046	Bacteroidetes	<i>Bacteroides uniformis</i>	0,047	0,2426	baseline
msp_0388	Firmicutes	<i>Faecalibacterium prausnitzii</i> 3 ( L2-6)	4,7E-08	0,00002	4w
msp_0906	Firmicutes	<i>Clostridium</i> sp.	0,001	0,0815	4w
msp_0756	Firmicutes	<i>unclassified Blautia</i>	0,002	0,0987	4w
msp_0296	Firmicutes	<i>unclassified Lachnospiraceae</i>	0,003	0,1030	4w
msp_0473c	Firmicutes	<i>Clostridium</i> sp.	0,007	0,1560	4w
msp_0015	Firmicutes	<i>Roseburia faecis</i>	0,008	0,1560	4w
msp_0881	Proteobacteria	<i>Haemophilus parainfluenzae</i>	0,008	0,1560	4w
msp_0047	Firmicutes	<i>Eubacterium</i> sp. CAG:115	0,008	0,1560	4w
msp_0572	Firmicutes	<i>Lachnospira</i> sp.	0,011	0,1560	4w
msp_1219	Firmicutes	<i>Veillonella rogosae</i>	0,012	0,1560	4w
msp_0071	Firmicutes	<i>Roseburia hominis</i>	0,015	0,1560	4w
msp_0075	Firmicutes	<i>Clostridium</i> sp.	0,017	0,1678	4w
msp_0772	Firmicutes	<i>Clostridiales</i> sp.	0,019	0,1678	4w
msp_0820	Firmicutes	<i>unclassified Clostridiales</i>	0,021	0,1678	4w
msp_0903	Firmicutes	<i>Oscilibacter</i> sp. 57_20	0,022	0,1690	4w
msp_1062	Firmicutes	<i>unclassified Oscilibacter</i>	0,022	0,1707	4w
msp_0654	Firmicutes	<i>Firmicutes bacterium</i> CAG:103	0,028	0,1864	4w
msp_1236	Firmicutes	<i>unclassified Lachnoclostridium</i>	0,029	0,1864	4w
msp_1533	Firmicutes	<i>unclassified Clostridiales</i>	0,029	0,1864	4w
msp_0175	Firmicutes	<i>unclassified Lachnospiraceae</i>	0,030	0,1887	4w
msp_0930	Firmicutes	<i>unclassified Lachnospiraceae</i>	0,036	0,2176	4w
msp_0139	Bacteroidetes	<i>Coprobacter fastidiosus</i>	0,041	0,2291	4w
msp_1492	Firmicutes	<i>unclassified Lachnospiraceae</i>	0,043	0,2291	4w
msp_0107	Firmicutes	<i>Anaerostipes hadrus</i> 1	0,049	0,2456	4w

Total Number MSP species MedD baseline vs 4w = 928

## MedD\_4w vs 8w

MSP	phylum	species	pvaluew	qvaluew	Enriched at
msp_0065	Firmicutes	<i>Blautia sp.</i>	0,0054	0,9540	4w
msp_0530	Firmicutes	<i>Dorea longicatena 2</i>	0,0111	0,9540	4w
msp_0930	Firmicutes	<i>unclassified Lachnospiraceae</i>	0,0129	0,9540	4w
msp_1622	Firmicutes	<i>Clostridium sp.</i>	0,0175	0,9540	4w
msp_0188	Firmicutes	<i>Coprobacillus sp.</i>	0,0179	0,9540	4w
msp_0005	Proteobacteria	<i>Escherichia coli</i>	0,0249	0,9540	4w
msp_0388	Firmicutes	<i>Faecalibacterium prausnitzii 3 (L2-6)</i>	0,0262	0,9540	4w
msp_0906	Firmicutes	<i>Clostridium sp.</i>	0,0314	0,9540	4w
msp_0018	Firmicutes	<i>Clostridium sp.</i>	0,0328	0,9540	4w
msp_0107	Firmicutes	<i>Anaerostipes hadrus 1</i>	0,0345	0,9540	4w
msp_0356	Firmicutes	<i>unclassified Clostridiales</i>	0,0352	0,9540	4w
msp_0572	Firmicutes	<i>Lachnospira sp.</i>	0,0355	0,9540	4w
msp_0340	Firmicutes	<i>Clostridium leptum</i>	0,0415	0,9580	4w
msp_0467	Firmicutes	<i>Firmicutes bacterium CAG:94</i>	0,0464	0,9580	4w
msp_0898	Firmicutes	<i>Clostridium sp.</i>	0,0467	0,9580	4w
msp_0342	Firmicutes	<i>Flavonifractor sp.</i>	0,0234	0,9540	8w
msp_0031	Bacteroidetes	<i>Bacteroides stercoris</i>	0,0422	0,9580	8w

Total Number MSP species MedD 4w vs 8w = 913