Figure S2

Image Image <th< th=""><th></th><th></th><th colspan="5">CON</th><th colspan="6">TSE</th><th></th><th></th></th<>			CON					TSE								
Bifidobacteriace Bifidobacteria 21.1 21.1 21.2			or 1	or 2			or 5	or 6	or 1		or 3	or 4	or 5	or 6		
Bifidobacteriace Bifidobacteria D11 Z <th>Family</th> <th>Genus</th> <th>Do</th> <th>Don</th> <th>Don</th> <th>Don</th> <th>Don</th> <th>Don</th> <th>۲ Do</th> <th>Don</th> <th>Don</th> <th>Don</th> <th>Don</th> <th>Don</th> <th></th> <th></th>	Family	Genus	Do	Don	Don	Don	Don	Don	۲ Do	Don	Don	Don	Don	Don		
Enterobacteriaceo Escherichia 1366 000 10.1 17.8 17.0 10.0 10.1 10.0 10.1 10.0 10	Bifidobacteriaceae	Bifidobacterium			24.01	19.27		23.03		51.61				46.93		
Bacteroidales unclassified Phocaeicala 75.3 1223 3.26 6.76 12.43 12.00 3.52 15.2 6.86 3.44 Tannereliceae Colisobet: 11 5.4 4.77 7.7 7.55 6.07 4.31 8.20 3.98 1.68 1.03 1.81 4.04 4.95 Coirobacterioree Collisobet 1.50 2.80 1.56 1.37 2.80 0.63 2.21 1.01 3.81 4.01 4.05 <	Bacteroidaceae	Bacteroides	12.26	17.68	23.88	10.90	27.10	11.08	5.43	6.10	15.02	11.36	20.57	4.39		
Tannerellaceae Parabacterioides Sead 1.7 2.71 2.55 6.07 3.15 2.91 1.68 0.76 0.05 0.83 2.94 0.05 0.83 Lachnospiraceae Euboteriaceae Euboteriaceae Euboteriaceae 2.22 1.60 1.03 1.03 1.03 1.03 1.03 1.03 1.03 1.03 1.03 1.03 1.04 1.04 1.04 1.03 1.04 1.03 1.04 1.03 1.04 1.03 1.04 1.03 1.04 1.03 1.04 1.04 1.03 1.04 1.03 1.04 1.03 1.04 1.03 1.04	Enterobacteriaceae	Escherichia	13.66	0.00	10.61	17.36	7.96	25.42	20.79	0.00	12.12	18.51	4.12	16.02		
Coriobacteriaceae Colimacity Colimacity <thc< td=""><td>Bacteroidales unclassified</td><td>Phocaeicola</td><td>7.53</td><td>12.31</td><td>3.26</td><td>5.75</td><td>3.62</td><td>6.94</td><td>12.43</td><td>10.02</td><td>3.52</td><td>1.52</td><td>6.08</td><td>3.84</td><td></td><td></td></thc<>	Bacteroidales unclassified	Phocaeicola	7.53	12.31	3.26	5.75	3.62	6.94	12.43	10.02	3.52	1.52	6.08	3.84		
Lachnospiraceae Enteroclostr 100 <td>Tannerellaceae</td> <td>Parabacteroides</td> <td>5.64</td> <td>4.17</td> <td>2.71</td> <td>2.55</td> <td>6.07</td> <td>4.31</td> <td>8.20</td> <td>3.98</td> <td>7.49</td> <td>1.16</td> <td>4.10</td> <td>4.95</td> <td></td> <td></td>	Tannerellaceae	Parabacteroides	5.64	4.17	2.71	2.55	6.07	4.31	8.20	3.98	7.49	1.16	4.10	4.95		
EubacteriaceeeEubacteriaceeInpa10,010,011,112,012,010,0	Coriobacteriaceae	Collinsella	2.11	5.34	1.89	0.99	0.00	1.56	3.15	2.91	1.68	0.78	0.05	0.38		
LachnospiraceeDore2.336.306.006.006.106.106.106.00<	Lachnospiraceae	Enterocloster	1.50	2.80	1.56	1.37	2.80	0.63	2.82	2.19	1.12	1.03	1.81	2.01		
RikenellaceaeAlisis besoInstantInst	Eubacteriaceae	Eubacterium	1.93	0.00	0.00	0.00	1.32	0.21	2.07	0.00	0.00	0.00	0.04	0.00		
Ruminococcacee Ruminococcace Ruminoc	Lachnospiraceae	Dorea	2.35	1.77	3.47	3.22	0.88	1.96	1.70	0.38	2.57	0.75	0.42	1.64		
International Interna International International<	Rikenellaceae	Alistipes	2.27	1.66	4.33	4.51	1.40	1.27	1.59	1.56	1.95	3.75	1.73	0.97		
Index Index< Index Index< Index <	Ruminococcaceae	Ruminococcus	5.28	0.80	1.03	1.15	0.00	0.03	1.29	0.29	0.54	0.36	0.00	0.02		
InstructureInstructur	Clostridiaceae	Clostridium	1.74	5.35	0.49	1.30	0.46	0.39	1.00	4.50	0.26	1.02	0.53	0.33	e	
Individual and any and any	Lachnospiraceae	Blautia	0.95	1.20	0.03	1.76	0.51	0.24	0.99	0.11	0.00	0.80	0.86	0.05	an	
Individual and any and any	Ruminococcaceae	Gemmiger	2.49	0.34	1.99	4.37	3.70	0.19	0.80	0.17	0.13	6.95	2.88	0.08	pur	
Individual and any and any	Lachnospiraceae	Roseburia	1.46	0.03	0.00	0.12	0.00	0.02	0.41	0.00	0.00	0.01	0.00	0.05	abı	
Individual and any and any	Veillonellaceae	Veillonella	0.80	0.00	0.84	0.00	0.00	2.06	0.29	0.25	2.40	0.00	0.08	3.28	ve	
Individual and any and any	Enterobacteriaceae	Citrobacter	0.00	5.40	3.88	0.00	0.00	0.00	0.28	5.41	5.90	0.00	0.00	0.00	lati	
InstructureInstructur	Lachnospiraceae	Lacrimispora	1.12	0.08	0.51	0.48	0.88	3.54	0.25	0.17	0.04	0.19	0.49	1.18	re	
Ruminococcacea GGB9633 0.2 1.45 0.00	Prevotellaceae	Paraprevotella	1.61	0.00	0.00	0.00	0.00	0.00	0.21	0.00	0.00	0.00	0.00	0.00	%	
Acidaminococcacaea Phascolarctobacterium 0.00	Lachnospiraceae	Mediterraneibacter	0.26	0.36	0.00	0.00	1.40	0.57	0.10	0.28	0.00	0.00	0.52	0.23		
Bacteroidacea BacteroidaceaOnd <t< td=""><td>Ruminococcaceae</td><td>GGB9633</td><td>0.22</td><td>1.45</td><td>0.00</td><td>1.70</td><td>0.00</td><td>0.00</td><td>0.10</td><td>0.19</td><td>0.00</td><td>0.66</td><td>0.00</td><td>0.00</td><td></td><td></td></t<>	Ruminococcaceae	GGB9633	0.22	1.45	0.00	1.70	0.00	0.00	0.10	0.19	0.00	0.66	0.00	0.00		
Prevotellacea Grad Grad <thgrad< th=""> Grad Grad</thgrad<>	Acidaminococcaceae	Phascolarctobacterium	0.10	0.09	0.90	0.00	2.61	0.00	0.00	0.12	1.08	0.00	2.19	0.00		
Sutterella ClostridiaSutterella (ClostridiaS	Bacteroidaceae	unclassified	0.00	0.00	0.00	0.00	0.00	3.72	0.00	0.00	0.00	0.00	0.00	1.48		
Clostridia_unclassified ClostridiaceaClostridia_unclassified GGB38170.000.020.00 <th< td=""><td>Prevotellaceae</td><td>GGB1270</td><td>0.00</td><td>1.29</td><td>0.00</td><td>0.00</td><td>2.60</td><td>0.00</td><td>0.00</td><td>2.89</td><td>0.00</td><td>0.00</td><td>0.16</td><td>0.00</td><td></td><td></td></th<>	Prevotellaceae	GGB1270	0.00	1.29	0.00	0.00	2.60	0.00	0.00	2.89	0.00	0.00	0.16	0.00		
Clostridia_unclassified GGB3817 0.00 1.04 0.00	Sutterellaceae	Sutterella	0.00	1.22	1.70	0.38	0.00	1.95	0.00	0.95	1.35	0.55	0.00	2.70		
Lost Clostridiacea Clostridiacea Clostridiacea Clostridiacea UnclossifiedClostridiacea Clostridiacea EvtepiaLost Clostridiacea LachnospiraceaClostridiacea EvtepiaLost LaLost LostLost Los	Clostridia_unclassified	Clostridia unclassified	0.11	0.00	0.20	0.95	0.40	1.13	0.00	0.00	0.00	0.54	0.26	0.00		
Clostridiales unclassified LachnospiraceaeEnd <td>Clostridia_unclassified</td> <td>GGB3817</td> <td>0.00</td> <td>1.04</td> <td>0.00</td> <td></td> <td></td>	Clostridia_unclassified	GGB3817	0.00	1.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00		
LachnospiraceaeFusicatenibacter0.000.140.001.734.130.140.000.001.961.6.920.00OscillospiraceaeDysosmobacter1.571.771.101.591.140.110.000.000.001.280.970.00OscillospiraceaeOscillibacter0.320.370.982.141.190.380.000.000.001.280.000.00RuminococcaceaeFaecalibacterium0.640.170.722.220.430.650.000.000.000.060.000.	Clostridiaceae	Clostridiaceae unclassified	1.93	2.22	1.94	1.74	2.84	0.37	0.00	0.00	0.00	0.34	0.19	0.01		
Oscillospiraceae Dysosmobacter 1.57 1.77 1.10 1.59 1.14 0.11 0.00 0.00 1.28 0.97 0.00 Oscillospiraceae Dysosmobacter 0.32 0.37 0.98 2.14 1.19 0.38 0.00 0.00 0.00 0.88 0.48 0.00 Ruminococcaceae Faecalibacterium 0.64 0.17 0.72 2.22 0.43 0.65 0.00 0.00 0.08 0.48 0.48 0.00 Ruminococcaceae Flavonifractor 0.60 0.99 0.26 1.48 0.00	Clostridiales unclassified	Evtepia	1.13	1.05	0.00	0.00	0.27	0.00	0.00	0.00	0.00	0.00	0.29	0.00		
Oscillospiraceae Oscillibacter 0.32 0.37 0.98 2.14 1.19 0.38 0.00 0.00 0.88 0.48 0.00 Ruminococcaceae Faecalibacterium 0.64 0.17 0.72 2.22 0.43 0.65 0.00 0.00 0.88 0.48 0.00 Ruminococcaceae Flavonifractor 0.66 0.09 0.26 1.48 0.07 0.08 0.00	Lachnospiraceae	Fusicatenibacter	0.00	0.14	0.20	1.73	4.13	0.14	0.00	0.00	0.00	1.96	16.92	0.04		
RuminococcaceaeFaecalibacterium6.016.036.036.177.177.136.006.006.006.006.006.00RuminococcaceaeFlavonifractor0.600.090.261.480.070.080.000	Oscillospiraceae	Dysosmobacter	1.57	1.77	1.10	1.59	1.14	0.11	0.00	0.00	0.00	1.28	0.97	0.00		
Ruminococcaceae Flavonifractor 0.00	Oscillospiraceae	Oscillibacter	0.32	0.37	0.98	2.14	1.19	0.38	0.00	0.00	0.00	0.88	0.48	0.00		
Ruminococcaceae GGB9621 0.00 1.33 0.00 0	Ruminococcaceae	Faecalibacterium	0.64	0.17	0.72	2.22	0.43	0.65	0.00	0.00	0.04	1.04	0.26	0.00		
Ruminococcaceae GGB9632 0.28 0.00 2.67 0.35 0.00 0.05 0.00 0.10 0.33 0.00 0.00 Ruminococcaceae GGB9634 0.00 0.10 0.00 0.00 1.10 0.00 <td>Ruminococcaceae</td> <td>Flavonifractor</td> <td>0.60</td> <td>0.09</td> <td>0.26</td> <td>1.48</td> <td>0.07</td> <td>0.08</td> <td>0.00</td> <td>0.00</td> <td>0.00</td> <td>0.66</td> <td>0.21</td> <td>0.02</td> <td></td> <td></td>	Ruminococcaceae	Flavonifractor	0.60	0.09	0.26	1.48	0.07	0.08	0.00	0.00	0.00	0.66	0.21	0.02		
Ruminococcaceae GGB9634 0.00 0.10 0.00 1.60 0.00 0	Ruminococcaceae	GGB9621	0.00	1.33	0.00	0.00	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.00		
Ruminococcaceae GGB9644 0.00 0.00 0.81 1.21 0.00 0	Ruminococcaceae	GGB9632	0.28	0.00	2.67	0.35	0.00	0.05	0.00	0.00	0.10	0.33	0.00	0.00		
Coriobacteriaceae Senegalimassilia 0.00 0.30 0.00 1.11 0.00 0.31 0.00 0.30 0.00 1.28 0.14 0.00 0.37 0.00 0.00 0.20 0.20 Eggerthellaceae Eggerthella 0.00 0.00 0.15 0.00 1.19 0.00	Ruminococcaceae	GGB9634	0.00	0.10	0.00	0.00	1.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00		
Eggerthellaceae Eggerthella 0.00 0.00 0.01 0.00 0.01 0.00 0.00 0.00 0.01 0.00 0.00 0.01 0.00 <	Ruminococcaceae	GGB9644	0.00	0.00	0.81	1.21	0.00	0.00	0.00	0.00	0.19	0.62	0.00	0.00		
Enterococcaceae Enterococcus 0.00 0.93 0.00 0.00 0.00 4.73 0.00 1.31 0.00 0.00 4.68 Akkermansiaceae Akkermansia 0.00 0.00 0.11 1.86 0.14 0.05 0.00 0.00 1.31 0.00 0.00 4.68	Coriobacteriaceae	Senegalimassilia	0.00	0.30	0.00	0.00	1.28	0.14	0.00	0.37	0.00	0.00	0.72	0.20		
Enterococcaceae Enterococcus 0.00 0.93 0.00 0.00 0.00 4.73 0.00 1.31 0.00 0.00 4.68 Akkermansiaceae Akkermansiaceae 0.00 0.00 0.11 1.86 0.14 0.05 0.00 0.00 1.18 0.14 0.05 0.00 0.00 1.18 0.14 0.05 0.00 1.08 0.13 0.00 1.08 0.14 0.05 0.00 1.00 1.08 0.14 0.05 0.00 1.08 0.13 0.05 0.00 1.08 0.14 0.05 0.00 0.00 1.18 0.14 0.05 0.00 0.00 1.08 0.14 0.05 0.00 0.00 1.08 0.06 0.00 0.00 1.08 0.05 0.00	Eggerthellaceae	Eggerthella														
Akkermansiaceae Akkermansia 0.00 0.00 0.11 1.86 0.14 0.05 0.00 0.00 1.18 0.13 0.06	Enterococcaceae	Enterococcus														
	Akkermansiaceae	Akkermansia														
		other														