:: Supplementary Table 1 ::

	TNFi (n=15)	IL-17i (n=14)	p-value
Age in years, mean ± SD (range)	38.9 ± 9.5 (22-53)	47.6 ± 16.2 (22-78)	0.084
Female, n (%)	4 (26.7)	9 (64.3)	0.066
Race/Ethnicity, n (%)			0.651
Caucasian Non-Hispanic	11 (73.3)	12 (85.7)	
Caucasian Hispanic	4 (26.7)	2 (14.3)	
Body mass index in kg/m^2, mean ± SD (range)	26.8 (6.0)	27.6 (6.1)	0.722
HLA-B27 positive, n (%)	2 (13.3)	1 (7.14)*	0.512
Disease Phenotype, n (%)			
Peripheral PsA	8 (53.3)	5 (35.7)	0.462
Axial PsA	0 (0)	1 (7.1)	0.483
Peripheral/axial PsA	7 (46.7)	4 (28.6)	0.450
Axial SpA	0 (0)	3 (21.4)	0.100
Psoriasis	15 (100)	9 (64.3)	**0.017**
Elevated CRP, n (%)			
Elevated above ULN	5 (33.3)	4 (28.6)	0.316
Elevated 2x above ULN	3 (20.0)	1 (7.1)	0.222
Psoriasis severity, mean ± SD %[#]	2.1 ± 2.3	N/A	N/A
<3% BSA, n (%)	12 (80.0%)		
3-10% BSA, n (%)	3 (20.0%)		
>10% BSA, n (%)	0 (0%)		
Tender joint count, mean ± SD (range)[#]	5.5 ± 6.6 (0-22)	N/A	N/A
Swollen joint count, mean ± SD (range)[#]	3.6 ± 2.9 (0-11)	N/A	N/A

:: Supplementary Table 2 ::

Taxa	Taxonomic level	p-value relative abundance TNFi pre vs maintenance	p-value relative abundance IL-17i pre vs loading	p-value relative abundance IL-17i pre vs maintenance	p-value magnitude of relative abundance change TNFi pre-maintenance vs IL-17i pre-loading	p-value magnitude of relative abundance change TNFi pre-maintenance vs IL-17i pre-maintenance
p__Bacteroidetes	Phylum	0.064	0.296	0.432	0.591	1.000
p__Firmicutes	**Phylum**	0.064	0.358	0.432	0.051	**0.016**
p__Proteobacteria	Phylum	0.978	0.173	0.322	0.747	0.238
p__Verrucomicrobia	Phylum	0.052	0.173	0.726	0.400	0.488
c__Actinobacteria	Class	0.359	0.463	0.557	0.477	0.807
c__Bacteroidia	Class	0.064	0.358	0.432	0.591	1.000
c__Clostridia	**Class**	**0.048**	0.426	0.695	**0.004**	**0.016**
c__Epsilonproteobacteria	Class	0.789	0.100	0.100	0.581	0.151
c__Verrucomicrobiae	Class	0.052	0.173	0.726	0.377	0.488
o__Bacteroidales	Order	0.064	0.358	0.432	0.591	1.000
o__Campylobacterales	Order	0.789	0.100	0.100	0.581	0.151
o__Clostridiales	**Order**	**0.048**	0.426	0.695	**0.004**	**0.016**
o__Turicibacterales	Order	0.181	1.000	1.000	0.765	0.968
f__Bacillaceae	**Family**	n.a.	0.441	0.181	**0.001**	**0.031**
f__Bacteroidaceae	Family	0.107	0.326	0.557	0.715	0.567
f__Christensenellaceae	Family	0.683	0.760	0.363	0.877	0.933
f__Clostridiaceae	Family	0.303	0.173	0.770	0.652	0.367
f__Enterococcaceae	**Family**	0.590	0.726	**0.006**	0.099	**0.002**
f__Erysipelotrichaceae	Family	0.421	0.670	0.275	0.102	0.935
f__Eubacteriaceae	Family	0.363	0.624	0.529	0.697	0.106
f__Lachnospiraceae	Family	0.083	0.903	0.232	0.847	0.115
f__Peptococcaceae	Family	0.407	0.208	0.295	0.763	0.667
f__Peptostreptococcaceae	Family	1.000	0.952	0.770	0.217	0.683
f__Porphyromonadaceae	Family	0.706	0.426	0.813	0.290	0.292
f__Prevotellaceae	Family	0.890	0.402	0.695	0.451	0.765
f__Ruminococcaceae	Family	0.639	0.358	0.375	0.780	0.935
f__Turicibacteraceae	Family	0.181	1.000	1.000	0.765	0.968
f__Veillonellaceae	Family	0.208	0.241	0.193	0.715	0.062
g__Akkermansia	Genus	0.052	0.173	0.726	0.377	0.488
g__Bacteroides	Genus	0.107	0.326	0.557	0.715	0.567
g__Bifidobacterium	Genus	0.346	0.367	0.080	0.879	0.255
g__Blautia	Genus	0.934	0.670	0.160	0.505	0.643
g__Catenibacterium	Genus	0.363	0.201	0.423	0.150	0.329
g__Clostridium	**Genus**	0.151	**0.009**	0.322	0.561	0.723
g__Coprobacillus	Genus	0.272	0.838	0.554	0.129	0.339
g__Coprococcus	Genus	0.804	0.426	0.105	0.400	0.892
g__Dialister	Genus	0.727	0.327	0.108	0.132	0.358
g__Enterococcus	**Genus**	0.590	0.726	**0.010**	0.099	**0.002**
g__Erwinia	Genus	0.722	0.120	0.933	0.163	0.268
g__[Eubacterium]	Genus	0.616	0.184	0.322	0.295	0.196
g__Faecalibacterium	Genus	0.847	0.485	0.232	0.234	1.000
g__Haemophilus	Genus	0.255	0.359	1.000	0.947	0.801
g__Lachnospira	Genus	0.083	0.364	0.846	0.715	0.892
g__Oribacterium	**Genus**	0.855	n.a.	0.181	**0.045**	0.779
g__Parabacteroides	Genus	0.706	0.426	0.813	0.290	0.292
g__Paraprevotella	Genus	0.441	0.447	0.675	0.578	0.310
g__Prevotella	Genus	0.890	0.402	0.695	0.451	0.765
g__Proteus	Genus	0.371	n.a.	n.a.	0.180	0.263
g__Pseudobutyrivibrio	Genus	1.000	n.a.	n.a.	0.370	0.462
g__Ruminococcus	Genus	0.950	0.903	0.846	0.451	0.397
g__Turicibacter	Genus	0.181	1.000	1.000	0.765	0.968
g__Veillonella	Genus	0.060	0.224	0.193	0.585	0.076

:: Supplementary Table 3A ::

TNFi pre

Treatment phase	Node ID	Taxon	Taxonomic rank
TNFi pre	1	[Barnesiellaceae]	family
TNFi pre	2	[Eubacterium]	genus
TNFi pre	3	[Paraprevotellaceae]	family
TNFi pre	4	[Prevotella]	genus
TNFi pre	5	[Ruminococcus]	genus
TNFi pre	6	Akkermansia	genus
TNFi pre	7	Bifidobacterium	genus
TNFi pre	8	Catenibacterium	genus
TNFi pre	9	Christensenellaceae	family
TNFi pre	10	Clostridiaceae	family
TNFi pre	11	Clostridium	genus
TNFi pre	12	Collinsella	genus
TNFi pre	13	Coriobacteriaceae	family
TNFi pre	14	Desulfovibrio	genus
TNFi pre	15	Dialister	genus
TNFi pre	16	Dorea	genus
TNFi pre	17	Enterobacteriaceae	family
TNFi pre	18	Erysipelotrichaceae	family
TNFi pre	19	Fusobacterium	genus
TNFi pre	20	Haemophilus	genus
TNFi pre	21	Lachnospira	genus
TNFi pre	22	Methanobrevibacter	genus
TNFi pre	23	Oscillospira	genus
TNFi pre	24	Pasteurellaceae	family
TNFi pre	25	Peptostreptococcaceae	family
TNFi pre	26	Phascolarctobacterium	genus
TNFi pre	27	Prevotella	genus
TNFi pre	28	RF39	order
TNFi pre	29	Roseburia	genus
TNFi pre	30	Ruminococcus	genus
TNFi pre	31	S24-7	family
TNFi pre	32	SMB53	genus
TNFi pre	33	Streptococcus	genus
TNFi pre	32	Sutterella	genus
TNFi pre	35	Veillonella	genus

TNFi maintenance

Treatment phase	Node ID	Taxon	Taxonomic rank
TNFi maintenance	1	[Barnesiellaceae]	family
TNFi maintenance	2	[Eubacterium]	genus
TNFi maintenance	3	[Paraprevotellaceae]	family
TNFi maintenance	4	[Prevotella]	genus
TNFi maintenance	5	[Ruminococcus]	genus
TNFi maintenance	6	Akkermansia	genus
TNFi maintenance	7	Bifidobacterium	genus
TNFi maintenance	8	Catenibacterium	genus
TNFi maintenance	9	Christensenellaceae	family
TNFi maintenance	10	Clostridiaceae	family
TNFi maintenance	11	Clostridium	genus
TNFi maintenance	12	Collinsella	genus
TNFi maintenance	13	Coriobacteriaceae	family
TNFi maintenance	14	Desulfovibrio	genus
TNFi maintenance	15	Dorea	genus
TNFi maintenance	16	Enterobacteriaceae	family
TNFi maintenance	17	Erysipelotrichaceae	family
TNFi maintenance	18	Fusobacterium	genus
TNFi maintenance	19	Haemophilus	genus
TNFi maintenance	20	Lachnospira	genus
TNFi maintenance	21	Methanobrevibacter	genus
TNFi maintenance	22	Oscillospira	genus
TNFi maintenance	23	Paraprevotella	genus
TNFi maintenance	24	Pasteurellaceae	family
TNFi maintenance	25	Peptostreptococcaceae	family
TNFi maintenance	26	Phascolarctobacterium	genus
TNFi maintenance	27	Prevotella	genus
TNFi maintenance	28	RF39	order
TNFi maintenance	29	Roseburia	genus
TNFi maintenance	30	Ruminococcus	genus
TNFi maintenance	31	S24-7	family
TNFi maintenance	32	SMB53	genus
TNFi maintenance	33	Streptococcus	genus
TNFi maintenance	34	Sutterella	genus
TNFi maintenance	35	Veillonella	genus

:: Supplementary Table 3B ::

IL-17i pre

Treatment phase	Node ID	Taxon	Taxonomic rank
IL-17i pre	1	[Barnesiellaceae]	family
IL-17i pre	2	[Eubacterium]	genus
IL-17i pre	3	[Prevotella]	genus
IL-17i pre	4	[Ruminococcus]	genus
IL-17i pre	5	Akkermansia	genus
IL-17i pre	6	Bifidobacterium	genus
IL-17i pre	7	Bilophila	genus
IL-17i pre	8	Butyricimonas	genus
IL-17i pre	9	Catenibacterium	genus
IL-17i pre	10	Christensenellaceae	family
IL-17i pre	11	Clostridiaceae	family
IL-17i pre	12	Clostridium	genus
IL-17i pre	13	Collinsella	genus
IL-17i pre	14	Coriobacteriaceae	family
IL-17i pre	15	Dialister	genus
IL-17i pre	16	Dorea	genus
IL-17i pre	17	Enterobacteriaceae	family
IL-17i pre	18	Erwinia	genus
IL-17i pre	19	Erysipelotrichaceae	family
IL-17i pre	20	Haemophilus	genus
IL-17i pre	21	Lachnobacterium	genus
IL-17i pre	22	Lachnospira	genus
IL-17i pre	23	Lactobacillus	genus
IL-17i pre	24	Oscillospira	genus
IL-17i pre	25	Paraprevotella	genus
IL-17i pre	26	Peptostreptococcaceae	family
IL-17i pre	27	Phascolarctobacterium	genus
IL-17i pre	28	Prevotella	genus
IL-17i pre	29	RF32	order
IL-17i pre	30	RF39	order
IL-17i pre	31	Roseburia	genus
IL-17i pre	32	Ruminococcus	genus
IL-17i pre	33	SMB53	genus
IL-17i pre	32	Streptococcus	genus
IL-17i pre	35	Succinivibrio	genus
IL-17i pre	36	Sutterella	genus
IL-17i pre	37	Veillonella	genus

IL-17i maintenance

Treatment phase	Node ID	Taxon	Taxonomic rank
IL-17i maintenance	1	[Barnesiellaceae]	family
IL-17i maintenance	2	[Prevotella]	genus
IL-17i maintenance	3	[Ruminococcus]	genus
IL-17i maintenance	4	Catenibacterium	genus
IL-17i maintenance	5	Christensenellaceae	family
IL-17i maintenance	6	Clostridiaceae	family
IL-17i maintenance	7	Clostridium	genus
IL-17i maintenance	8	Collinsella	genus
IL-17i maintenance	9	Coriobacteriaceae	family
IL-17i maintenance	10	Dialister	genus
IL-17i maintenance	11	Dorea	genus
IL-17i maintenance	12	Enterobacteriaceae	family
IL-17i maintenance	13	Erwinia	genus
IL-17i maintenance	14	Erysipelotrichaceae	family
IL-17i maintenance	15	Haemophilus	genus
IL-17i maintenance	16	Lachnobacterium	genus
IL-17i maintenance	17	Lachnospira	genus
IL-17i maintenance	18	Lactobacillus	genus
IL-17i maintenance	19	Oscillospira	genus
IL-17i maintenance	20	Paraprevotella	genus
IL-17i maintenance	21	Peptostreptococcaceae	family
IL-17i maintenance	22	Phascolarctobacterium	genus
IL-17i maintenance	23	Prevotella	genus
IL-17i maintenance	24	RF39	order
IL-17i maintenance	25	Roseburia	genus
IL-17i maintenance	26	Ruminococcus	genus
IL-17i maintenance	27	SMB53	genus
IL-17i maintenance	28	Streptococcus	genus
IL-17i maintenance	29	Succinivibrio	genus
IL-17i maintenance	30	Sutterella	genus
IL-17i maintenance	31	Veillonella	genus

:: Supplementary Table 4 ::

Taxa	Taxonomic level	p-value relative abundance TNFi pre vs maintenance	p-value relative abundance IL-17i pre vs loading	p-value relative abundance IL-17i pre vs maintenance	p-value magnitude of relative abundance change TNFi pre-maintenance vs IL-17i pre-loading	p-value magnitude of relative abundance change TNFi pre-maintenance vs IL-17i pre-maintenance
p__Ascomycota	Phylum	0.847	0.670	0.232	0.747	0.807
c__Saccharomycetes	Class	0.135	0.173	0.084	0.172	0.196
c__Tremellomycetes	**Class**	0.423	0.059	0.673	0.455	**0.031**
o__Saccharomycetales	Order	0.135	0.173	0.084	0.172	0.196
o__Tremellales	**Order**	n.a.	0.181	0.181	0.069	**0.031**
f__Glomerellaceae	Family	0.371	n.a.	n.a.	0.180	0.263
f__Incertae sedis	Family	0.720	0.808	0.160	0.400	0.338
f__Mucoraceae	Family	0.371	0.371	0.100	0.971	0.251
f__Mycosphaerellaceae	Family	0.802	0.919	0.675	0.913	0.358
f__Plectosphaerellaceae	Family	0.371	1.000	1.000	0.563	0.922
f__Saccharomycetaceae	Family	0.303	0.358	0.275	0.683	0.338
f__Sclerotiniaceae	Family	0.371	n.a.	n.a.	0.180	0.263
g__Aspergillus	Genus	0.188	0.058	0.375	0.290	0.196
g__Candida	Genus	0.720	0.808	0.160	0.400	0.338
g__Debaryomyces	Genus	0.092	0.845	0.183	0.555	0.597
g__Glomerella	Genus	0.371	n.a.	n.a.	0.180	0.263
g__Penicillium	Genus	0.754	0.391	0.084	0.561	0.196
g__Plectosphaerella	Genus	1.000	1.000	1.000	1.000	0.768
g__Saccharomyces	**Genus**	0.421	0.903	0.846	0.451	**0.041**
s__Aspergillus niger	**Species**	0.255	**0.021**	0.432	0.646	0.890
s__Candida albicans	**Species**	0.169	0.426	0.492	0.270	**0.041**
s__Candida dubliniensis	Species	0.590	0.584	1.000	0.811	0.973
s__Candida fermenticarens	**Species**	0.208	n.a.	n.a.	**0.011**	**0.029**
s__Candida parapsilosis	Species	1.000	0.505	0.106	0.930	0.456
s__Candida tropicalis	**Species**	0.576	0.363	0.106	0.165	**0.023**
s__Fusarium sp 4 TMS 2011	Species	0.371	1.000	n.a.	0.563	0.263
s__Hypocrea pseudokoningii	Species	0.181	n.a.	n.a.	0.091	0.154
s__Penicillium charlesii	Species	0.371	1.000	n.a.	0.563	0.263
s__Pichia sp 1 TMS 2011	Species	0.371	1.000	1.000	0.856	0.696
s__Rhodotorula sp RhSoW01	**Species**	0.584	n.a.	0.059	**0.045**	0.333
s__Saccharomyces cerevisiae	**Species**	0.421	0.903	0.846	0.451	**0.041**
s__Trichoderma longibrachiatum	Species	0.181	n.a.	n.a.	0.091	0.154

:: Supplementary Table 5 ::

Pathway	Mean pre	Mean maintenance	Kruskal-Wallis p-value	Wilcoxon p-value
PWY-6121: 5-aminoimidazole ribonucleotide biosynthesis I | Streptococcus (g); Streptococcus salivarius (s)	1.290E-06	0.000E+00	**0.017**	0.059
PWY0-166: superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis (E. coli)	1.820E-04	1.263E-04	**0.017**	**0.008**
PWY-7184: pyrimidine deoxyribonucleotides de novo biosynthesis I	1.508E-04	1.007E-04	**0.026**	**0.003**
1CMET2-PWY: N10-formyl-tetrahydrofolate biosynthesis | Bacteroides (g); Bacteroides xylanisolvens (s)	4.380E-06	6.880E-07	**0.029**	**0.009**
FUCCAT-PWY: fucose degradation	1.310E-05	3.600E-05	**0.033**	**0.005**
PWY-7197: pyrimidine deoxyribonucleotide phosphorylation	1.146E-04	7.600E-05	**0.033**	**0.007**
PWY-7221: guanosine ribonucleotides de novo biosynthesis | Bacteroides (g); Bacteroides xylanisolvens (s)	6.780E-06	1.220E-06	**0.034**	**0.014**
PWY-7111: pyruvate fermentation to isobutanol (engineered) | Clostridium (g); Clostridium nexile (s)	0.000E+00	3.060E-06	**0.035**	0.100
PWY0-1296: purine ribonucleosides degradation | Clostridium (g); Clostridium nexile (s)	0.000E+00	3.720E-06	**0.035**	0.100
UNINTEGRATED | Clostridium (g); Clostridium nexile (s)	0.000E+00	3.822E-03	**0.035**	0.100
VALSYN-PWY: L-valine biosynthesis | Clostridium (g); Clostridium nexile (s)	0.000E+00	2.830E-06	**0.035**	0.100
GLYCOGENSYNTH-PWY: glycogen biosynthesis I (from ADP-D-Glucose)	1.194E-04	1.717E-04	**0.036**	0.083
PPGPPMET-PWY: ppGpp biosynthesis | unclassified	3.250E-06	9.510E-07	**0.041**	**0.009**
PWY-7282: 4-amino-2-methyl-5-phosphomethylpyrimidine biosynthesis (yeast) | Bacteroides (g); Bacteroides xylanisolvens (s)	4.640E-06	8.820E-07	**0.047**	0.058
PWY0-845: superpathway of pyridoxal 5’-phosphate biosynthesis and salvage | Bacteroides (g); Bacteroides xylanisolvens (s)	4.700E-06	7.250E-07	**0.047**	**0.044**

:: Supplementary Table 6 ::

Pathway	Mean pre	Mean loading	Mean maintenance	Kruskal-Wallis p-value	Wilcoxon pre-loading p-value	Wilcoxon pre-maintenance p-value
PWY-6595: superpathway of guanosine nucleotides degradation (plants)	7.260E-06	1.010E-05	2.750E-06	**0.012**	0.153	**0.037**
TRPSYN-PWY: L-tryptophan biosynthesis | unclassified	7.040E-06	1.820E-05	7.690E-06	**0.015**	**0.005**	0.286
PWY-621: sucrose degradation III (sucrose invertase) | unclassified	7.900E-06	1.310E-05	1.950E-06	**0.017**	0.078	**0.030**
DTDPRHAMSYN-PWY: dTDP-L-rhamnose biosynthesis I Eggerthella (g); Eggerthella lenta (s)	0.000E+00	4.270E-07	0.000E+00	**0.024**	0.100	NaN
PWY-6263: superpathway of menaquinol-8 biosynthesis II	0.000E+00	1.040E-06	1.160E-07	**0.029**	0.059	1
PWY-6386: UDP-N-acetylmuramoyl-pentapeptide biosynthesis II (lysine-containing) | Flavonifractor (g); Flavonifractor plautii (s)	6.830E-07	5.900E-08	0.000E+00	**0.031**	0.059	0.100
PWY-6387: UDP-N-acetylmuramoyl-pentapeptide biosynthesis I (meso-diaminopimelate containing) | Flavonifractor (g); Flavonifractor plautii (s)	6.140E-07	5.550E-08	0.000E+00	**0.035**	0.178	0.100
COBALSYN-PWY: adenosylcobalamin salvage from cobinamide I|unclassified	2.870E-06	4.080E-06	0.000E+00	**0.039**	0.286	0.059

:: Supplementary Table 7 ::

Cytokine or protein	Specimen	Wilcoxon TNFi pre-maintenance p-value	Wilcoxon IL-17i pre-loading p-value	Wilcoxon IL-17i pre-maintenance p-value
Calprotectin	fecal	0.847	0.685	0.820
CCL20	fecal	0.447	0.208	0.418
S100	fecal	0.706	0.784	0.250
sIgA	fecal	0.389	0.685	0.734
IL-12p70	fecal	0.208	0.305	0.496
IL-23	fecal	0.364	0.965	0.675
IL-21	fecal	0.490	0.100	0.944
IL-17A	fecal	0.126	1.000	0.361
IL-17E (IL-25)	fecal	0.187	0.255	0.407
IL-17F	fecal	0.141	0.181	0.423
IL-33	fecal	0.418	1.000	1.000

:: Supplementary Table 8 ::

Metabolite	Specimen	Wilcoxon TNFi pre-maintenance p-value	Wilcoxon IL-17i pre-loading p-value	Wilcoxon IL-17i pre-maintenance p-value
Acetic acid (C=2)	fecal	0.281	0.361	1.000
Propionic acid (C=3)	fecal	0.505	0.784	0.441
Butyric acid (C=4)	fecal	0.889	0.894	0.575
Isovaleric acid (C=5)	fecal	n.a.	0.346	n.a.
Valeric acid (C=5)	fecal	1.000	0.556	0.726
Hexanoic acid (C=6)	fecal	0.851	0.726	0.675
Heptanoic acid (C=7)	fecal	0.683	0.091	0.441
Octanoic acid (C=8)	fecal	0.379	0.402	0.232
Nonanoic acid (C=9)	fecal	0.135	1.000	**0.014**
Decanoic acid (C=10)	fecal	0.890	0.808	0.846
Dodecanoic acid (C=12)	fecal	0.414	0.715	0.813
Myristic acid (C=14)	fecal	0.802	0.358	0.846
Palmitoleic acid (C=16)	fecal	0.454	0.153	0.625
Palmitic acid (C=16)	fecal	0.890	0.153	0.492
Oleic acid (C=18)	fecal	0.720	0.358	0.846
Stearic acid (C=18)	fecal	0.359	0.078	0.695
Arachidic acid (C=20)	fecal	1.000	0.135	0.846
Nervonic acid (C=24)	fecal	0.754	0.670	1.000
Lignoceric acid (C=24)	fecal	0.572	0.670	0.922