


A

ALPHA DIVERSITY							
Shanon-Kluskal-Wallis test PHYLUM				Shanon-Kluskal-Wallis test GENUS			
Pair	Statistic	P-value	FDR	Pair	Statistic	P-value	FDR
TG vs WT	100.0	0.2039	0.2039	TG vs WT	133.0	0.92923	0.92923

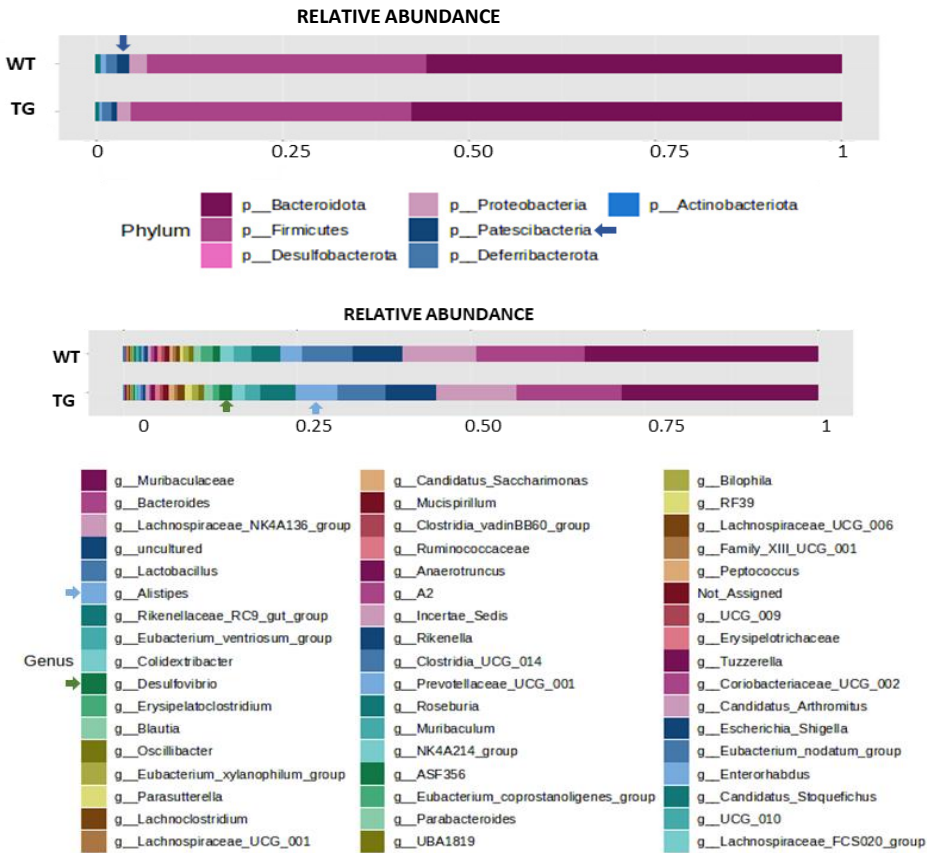
B

BETA DIVERSITY-BRAY-CURTIS (Phylum)					BETA DIVERSITY-BRAY-CURTIS (Genus)				
Pair	F-value	R-squared	P-value	FDR	Pair	F-value	R-squared	P-value	FDR
TG vs WT	0.16072	0.0051578	0.787	0.787	TG vs WT	0.82031	0.025779	0.494	0.494

C

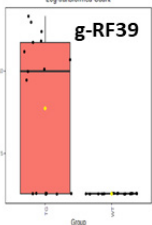
Linear Discriminant Analysis Effect Size (LEfSe)					
					
Name	Pvalues	FDR	TG	WT	LDAScore
g__RF39	3.9641E-4	0.020614	2210.8	0.0	3.04

D



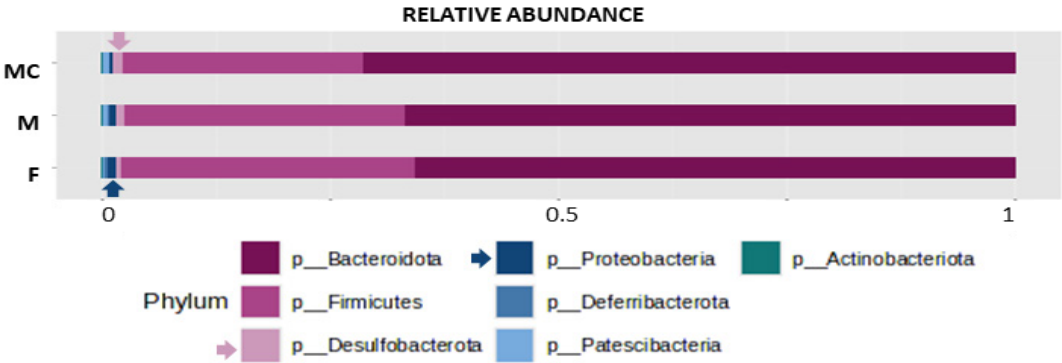
E

Single-factor Statistical Comparisons (Mann-Whitney/Kruskal-Wallis)					
Name	log2FC	Pvalues	FDR	Statistics	logCPM
g__RF39	-10.4115	4.3103E-4	0.022413	216.0	9.70261

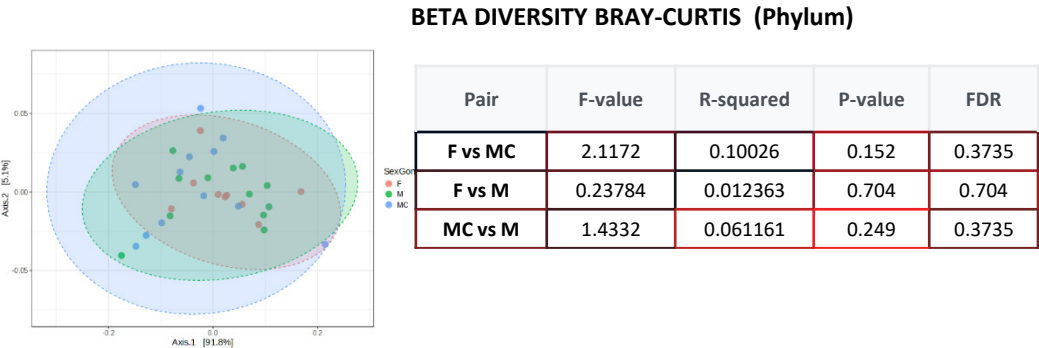


Supplementary Figure 1

A



B



C

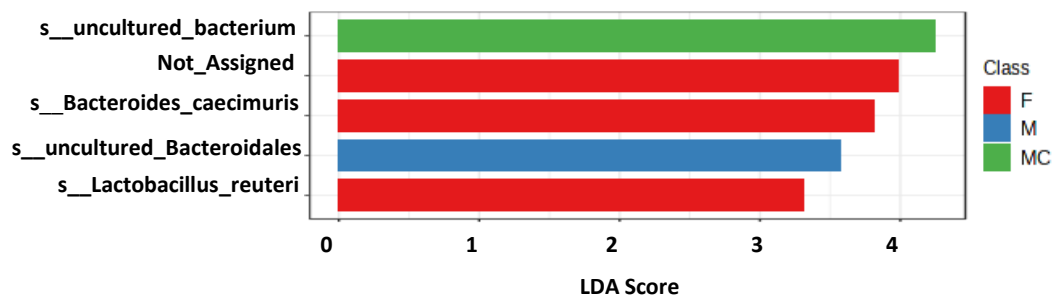
Linear Discriminant Analysis Effect Size (LEfSe)

Name	Pvalues	FDR	F	M	MC	LDAScore
g__Eubacterium_ventriosum_group	9.9473E-5	0.0050731	23612.0	3106.1	30288.0	4.13
g__Lachnospiraceae_FCS020_group	2.7031E-4	0.0054165	725.15	130.88	0.0	2.56
g__Prevotellaceae_UCG_001	5.0945E-4	0.0054165	1124.6	3158.5	1186.6	3.01
g__Parasutterella	5.1475E-4	0.0054165	7600.5	5098.4	823.07	3.53
g__Alistipes	5.3103E-4	0.0054165	25516.0	69056.0	19611.0	4.39
g__Peptococcus	9.5509E-4	0.0081183	178.38	1890.4	442.07	2.93
g__Lactobacillus	0.0020136	0.014671	81077.0	15278.0	35380.0	4.52
g__Bacteroides	0.0030795	0.019279	194590.0	58513.0	97026.0	4.83
g__Rikenella	0.0036983	0.019279	744.54	3318.4	3603.5	3.16
g__Candidatus_Saccharimonas	0.0038701	0.019279	674.74	4496.3	5214.7	3.36
g__ASF356	0.0041583	0.019279	3342.7	657.29	540.96	3.15
g__uncultured	0.0045474	0.019327	55856.0	81591.0	40929.0	4.31
g__UCG_009	0.0049525	0.019429	473.09	1268.0	279.2	2.69
g__Colidextribacter	0.0056335	0.020522	7329.1	15659.0	11508.0	3.62
g__Eubacterium_nodatum_group	0.0064798	0.022031	391.66	994.66	197.77	2.6
g__Oscillibacter	0.0097924	0.031213	3311.7	7212.7	3405.7	3.29
g__Blautia	0.01271	0.038131	1931.2	9597.6	2352.9	3.58
g__Clostridia_UCG_014	0.021093	0.059763	50.412	3801.2	1695.6	3.27
Not_Assigned	0.025938	0.069623	1531.7	2533.2	590.4	2.99
g__Muribaculaceae	0.030287	0.077232	397840.0	506120.0	554100.0	4.89

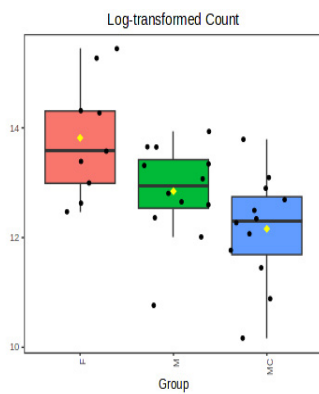
Supplementary Figure 2

Linear Discriminant Analysis Effect Size (LEfSe)

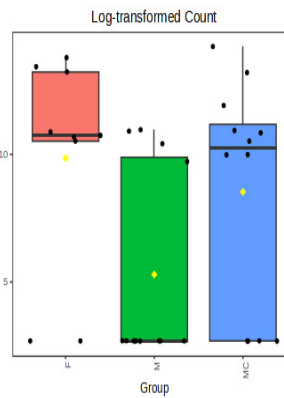
Name	Pvalues	FDR	F	M	MC	LDAScore
s__uncultured_bacterium	0.0013222	0.0092551	928930.0	953780.0	964730.0	4.25
Not_Assigned	0.0054842	0.017112	36921.0	19460.0	17936.0	3.98
s__Bacteroides_caecimuris	0.0073338	0.017112	18590.0	8445.9	5555.0	3.81
s__Lactobacillus_reuteri	0.05312	0.09296	4610.7	508.96	3306.8	3.31
s__uncultured_Bacteroidales	0.070293	0.098411	9380.4	15121.0	7634.5	3.57



s\_\_Bacteroides\_caecimuris



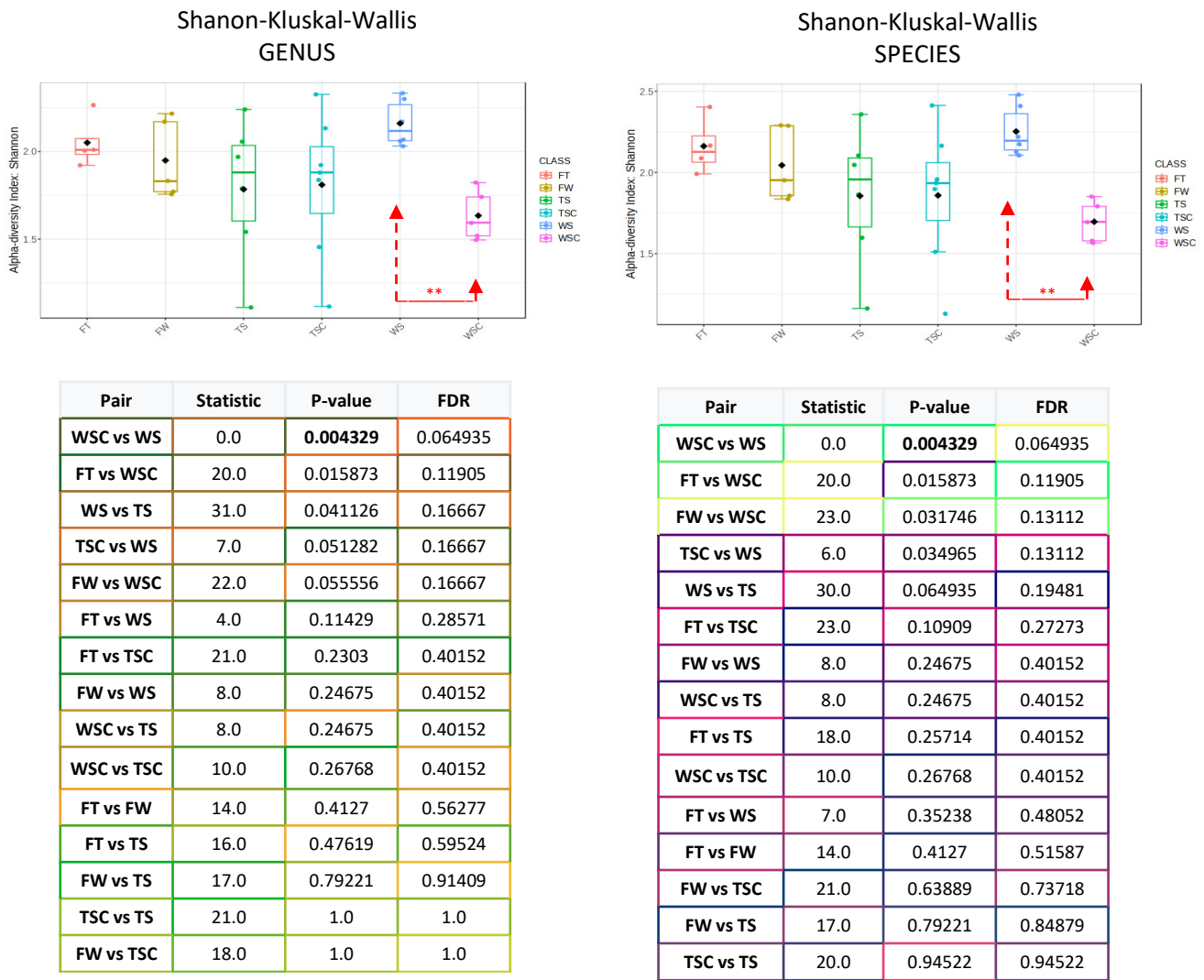
s\_\_Lactobacillus\_reuteri



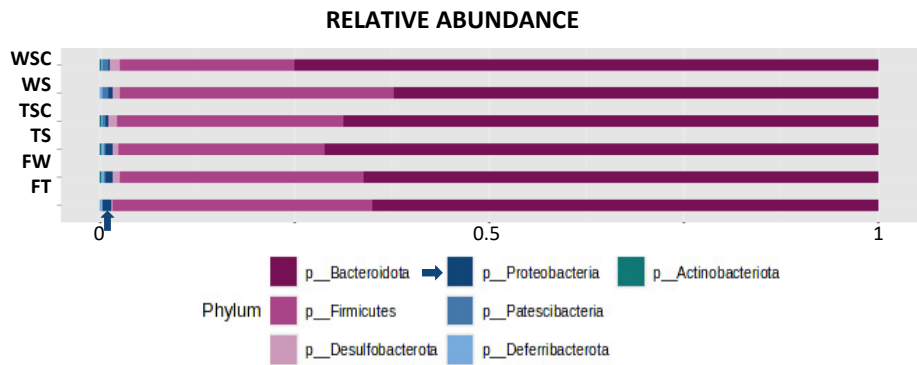
Supplementary Figure 3

ALPHA DIVERSITY - GROUPS

A



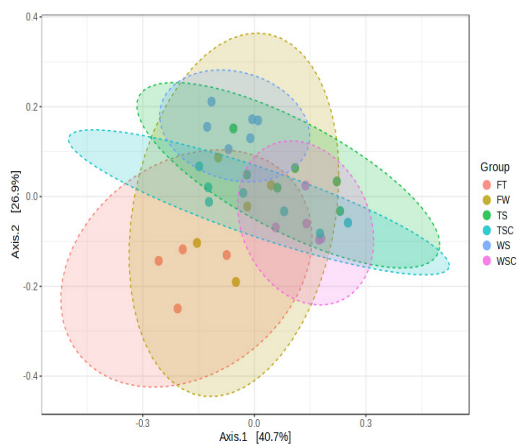
B



Supplementary Figure 4

A

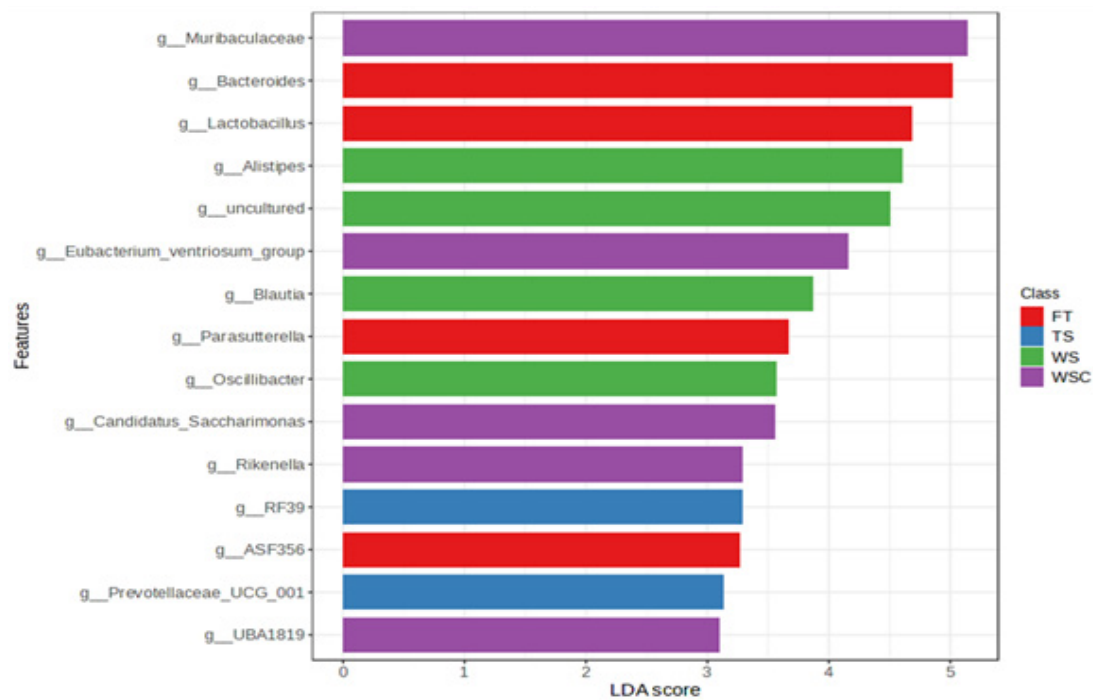
BETA DIVERSITY-BRAY-CURTIS  
(Genus Level)



Pair	F-value	R-squared	P-value	FDR
TSC vs WS	4.149	0.27388	0.003	0.015
FW vs WS	4.7624	0.34605	0.005	0.015
FT vs WSC	11.638	0.62442	0.006	0.015
FT vs WS	12.856	0.61642	0.006	0.015
FT vs TS	9.1059	0.53232	0.006	0.015
WSC vs WS	15.373	0.63073	0.006	0.015
FW vs WSC	4.2859	0.34885	0.01	0.021429
FW vs TS	3.0789	0.2549	0.019	0.033333
FT vs TSC	4.2111	0.31876	0.02	0.033333
WS vs TS	4.2566	0.29857	0.025	0.0375
WSC vs TS	2.263	0.20092	0.064	0.087273
FT vs FW	2.2545	0.24361	0.106	0.12808
WSC vs TSC	2.2566	0.18412	0.111	0.12808
TSC vs TS	1.6672	0.13162	0.138	0.14786
FW vs TSC	0.80278	0.074312	0.546	0.546

B

Linear Discriminant Analysis (LDA)



Supplementary Figure 5

Linear Discriminant Analysis Effect Size (LEfSe)

Phylum	Name	P-values	FDR	FT	FW	TS	TSC	WS	WSC
	p__Patescibacteria	0.0023135	0.011406	462.43	844.59	2326.7	3564.8	6666.0	3.55
	p__Proteobacteria	0.0032588	0.011406	9684.8	7573.4	6846.3	1710.1	4374.2	3.68

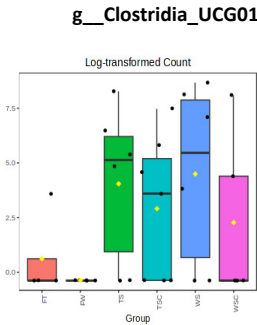
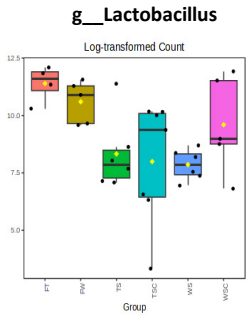
Genus	Name	P-values	FDR	FT	FW	TS	TSC	WS	WSC
	g__RF39	2.8838E-4	0.014708	0.0	0.0	3821.6	1999.3	0.0	3.28
	g__Lachnospiraceae_FCS020_group	0.0018574	0.019665	427.53	963.25	69.801	0.0	191.95	2.68
	g__Alistipes	0.0020243	0.019665	21734.0	28542.0	42195.0	16952.0	95918.0	4.6
	g__Eubacterium_ventriosum_group	0.0020378	0.019665	26891.0	20989.0	3612.2	29411.0	2600.1	4.16
	g__Peptococcus	0.0020876	0.019665	104.7	237.32	1372.7	732.91	2408.1	3.07
	g__Candidatus_Saccharimonas	0.0023135	0.019665	462.43	844.59	2326.7	3564.8	6666.0	3.55
	g__Parasutterella	0.0048378	0.032568	9248.6	6282.1	6747.4	1301.3	3449.3	3.66
	g__Prevotellaceae_UCG_001	0.0051087	0.032568	1378.6	921.37	3588.9	997.15	2728.0	3.13
	g__Muribaculaceae	0.0071891	0.034466	333760.0	449100.0	581180.0	515150.0	431060.0	5.14
	g__UCG_009	0.0073794	0.034466	732.91	265.24	1122.6	478.63	1413.5	2.85
	g__Blautia	0.0075002	0.034466	1919.5	1940.5	2908.4	3041.3	16287.0	3.87
	g__NK4A214_group	0.0081095	0.034466	261.75	1389.0	1931.2	299.15	1948.6	2.99
	g__uncultured	0.011283	0.041897	57952.0	54179.0	73942.0	51383.0	89240.0	4.5
	g__Bacteroides	0.011814	0.041897	257280.0	144450.0	53136.0	112730.0	63891.0	5.01
	g__Lactobacillus	0.012323	0.041897	104050.0	62702.0	22016.0	21324.0	8539.0	4.68
	g__Oscillibacter	0.013898	0.044299	2268.5	4146.2	5851.6	4886.1	8573.9	3.56
	g__ASF356	0.01803	0.054089	3847.8	2938.6	738.72	802.71	575.86	3.26
	WSC	0.023793	0.066208	0.0	1061.0	744.54	563.39	1128.4	3.1
	g__Rikenella	0.024666	0.066208	1003.4	537.47	3466.8	3101.1	3170.1	3.28
	g__Eubacterium_nodatum_group	0.027013	0.068884	689.28	153.56	785.26	279.2	1204.1	2.75

Supplementary Figure 6

Single-factor Statistical Comparisons (DESeq2)

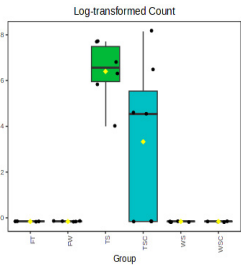
WS/FW

Name	log2FC	lfcSE	P-values	FDR
g__Clostridia_UCG_014	-24.137	2.4239	2.3276E-23	1.1638E-21
g__Lactobacillus	3.5763	0.87531	4.3925E-5	0.0010981
g__Bacteroides	1.7581	0.57489	0.0022268	0.037114



WS/TS

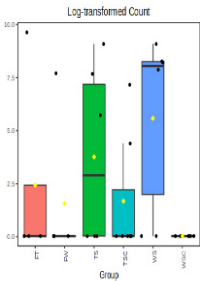
Name	log2FC	lfcSE	P-values	FDR
g__RF39	9.2224	2.0958	1.0799E-5	5.3997E-4



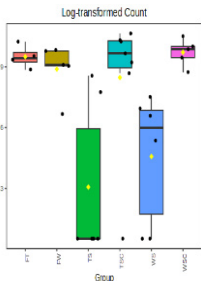
WS/WSC

Name	log2FC	lfcSE	P-values	FDR
g__Lachnospiraceae_UCG_001	-24.432	3.7926	1.1784E-10	5.8922E-9
g__UCG_009	-6.8705	1.5018	4.7682E-6	1.1921E-4
g__Lactobacillus	3.5178	0.87533	5.8484E-5	8.4505E-4
g__Peptococcus	-6.3845	1.6023	6.7604E-5	8.4505E-4
g__uncultured	-1.1266	0.33636	8.0982E-4	0.0067644
Not_Assigned	-7.0464	2.1042	8.1173E-4	0.0067644
g__Eubacterium_ventriosum_group	4.2241	1.4181	0.0028956	0.020683
g__Blautia	-2.6008	0.96637	0.0071176	0.037649
g__Alistipes	-1.2945	0.48297	0.007356	0.037649
g__Muribaculaceae	1.2287	0.45977	0.0075299	0.037649

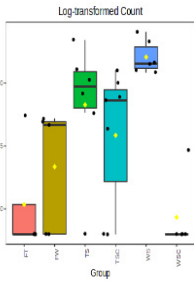
g\_\_Lachnospiraceae\_UCG\_001



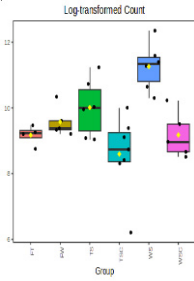
g-Eubacterium-ventriosum group



g-Peptococcus

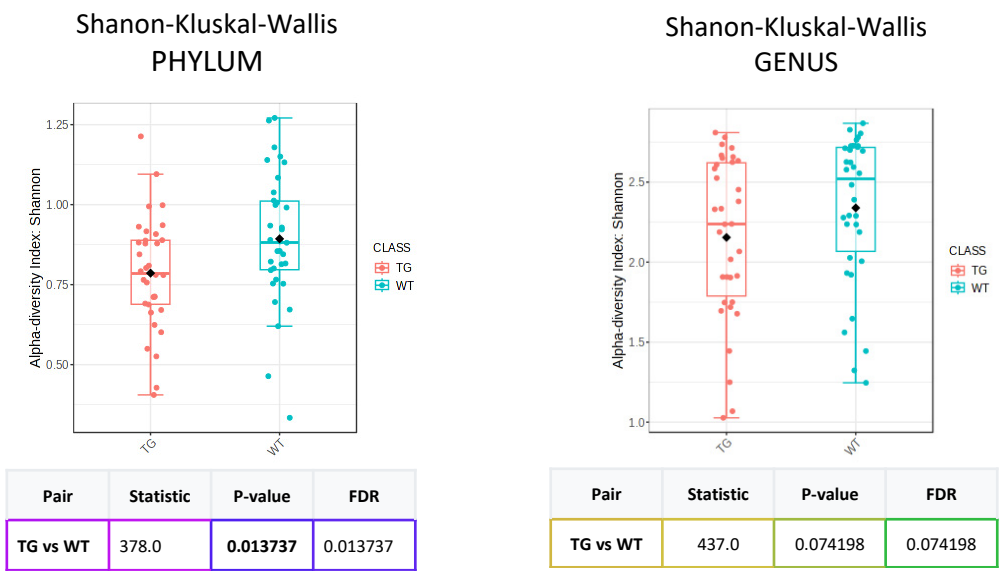


g-Alistipes

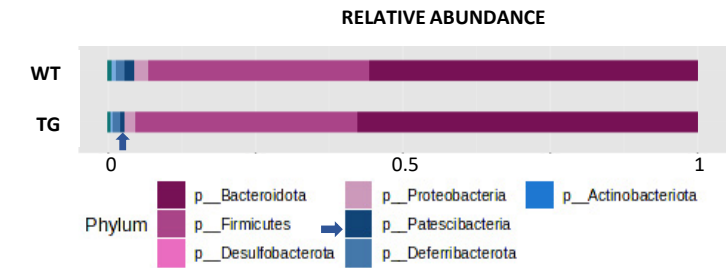


Supplementary Figure 7

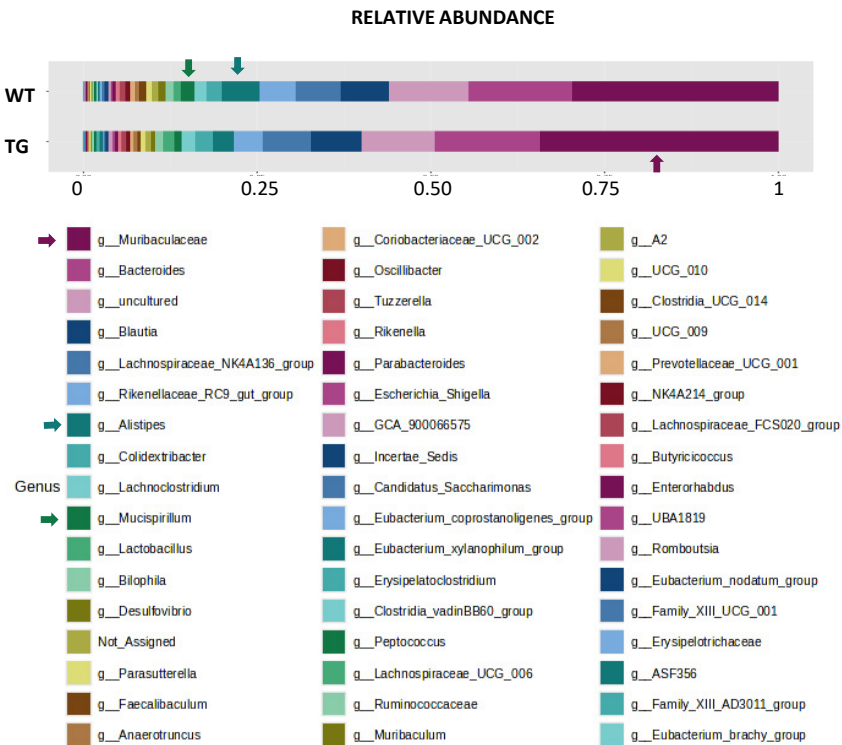
A



B



C

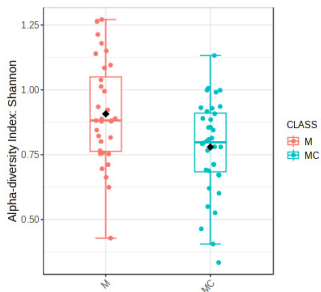


Supplementary Figure 8



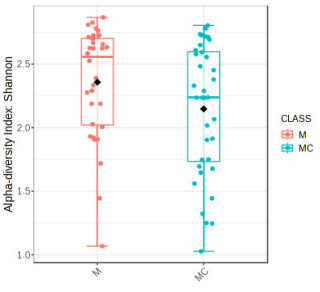
A

Shanon-Kluskal-Wallis  
PHYLUM



Pair	Statistic	P-value	FDR
M vs MC	779.0	0.012184	0.012184

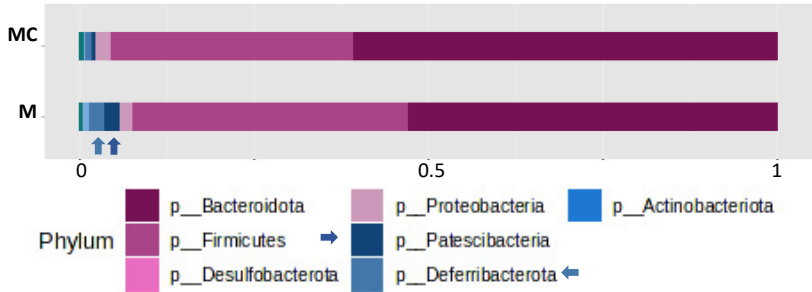
Shanon-Kluskal-Wallis  
GENUS



Pair	Statistic	P-value	FDR
M vs MC	742.0	0.04147	0.04147

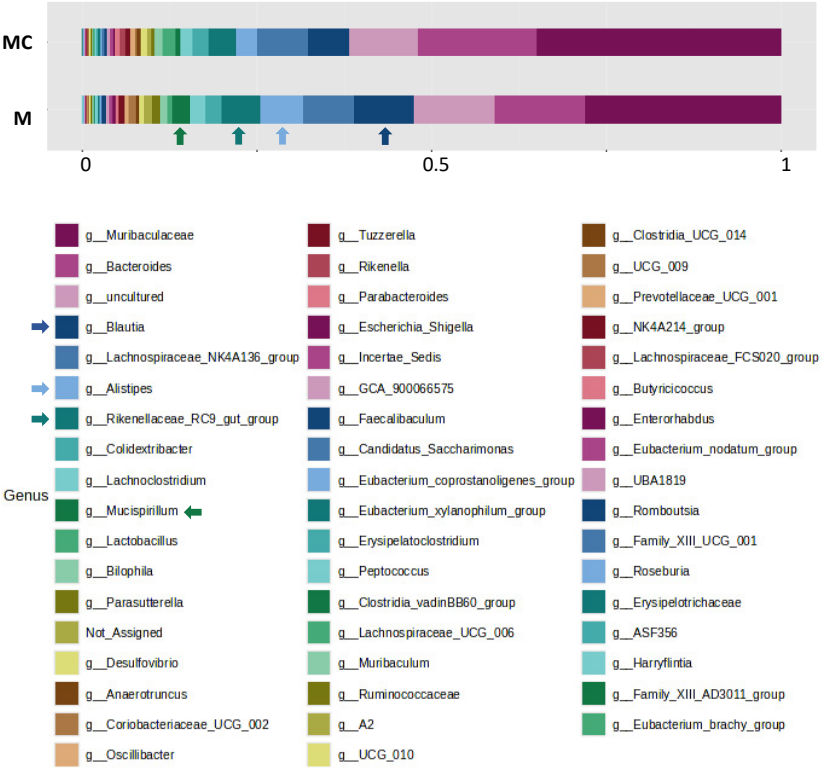
B

RELATIVE ABUNDANCE



C

RELATIVE ABUNDANCE



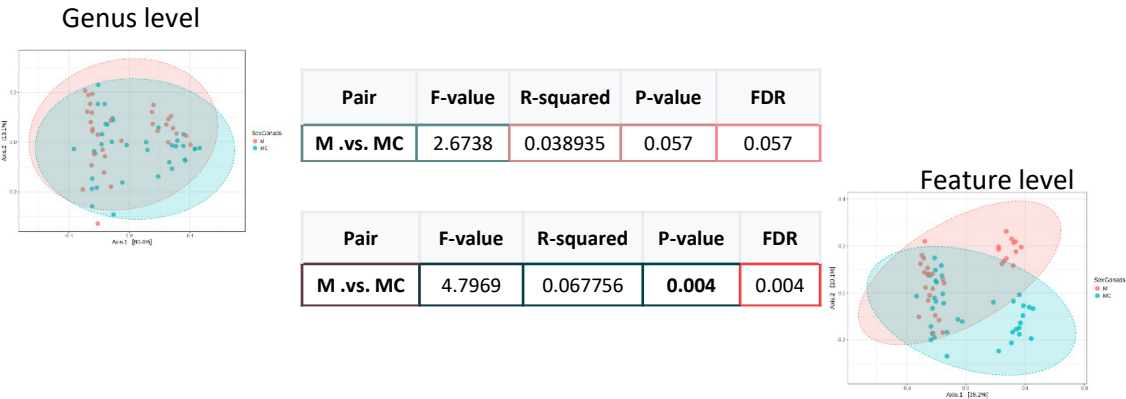
Supplementary Figure 9

BETA DIVERSITY BRAY-CURTIS

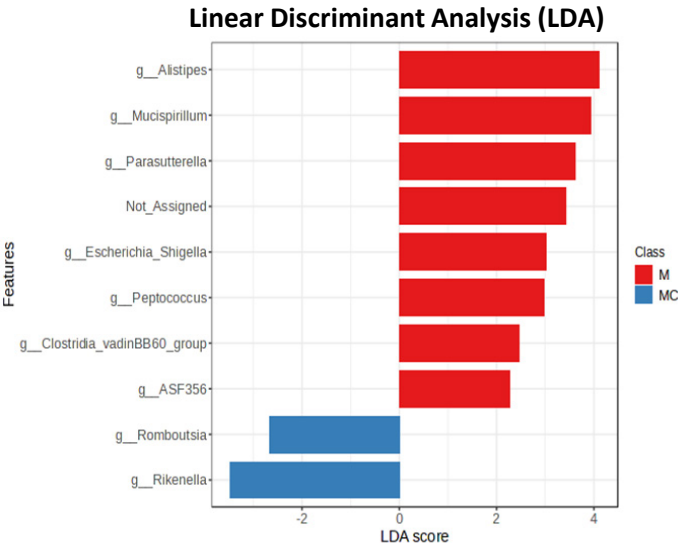
A

Pair	F-value	R-squared	P-value	FDR
TG .vs. WT	1.0368	0.015466	0.344	0.344

B



C



Linear Discriminant Analysis Effect Size (LEfSe)

Name	P-values	FDR	M	MC	LDAScore
p__Deferribacterota	0.0016482	0.0062726	23311.0	5726.6	3.94
p__Proteobacteria	0.0017922	0.0062726	19030.0	8816.2	3.71

Name	P-values	FDR	M	MC	LDAScore
g__Rikenella	1.4462E-6	7.5204E-5	1939.5	8019.7	-3.48
g__Peptococcus	1.5248E-5	3.9644E-4	2825.6	900.82	2.98
g__Alistipes	4.3992E-5	7.6252E-4	57206.0	31176.0	4.11
g__Romboutsia	7.3245E-4	0.0089357	113.57	1028.4	-2.66
Not_Assigned	8.592E-4	0.0089357	10444.0	5203.0	3.42
g__Mucispirillum	0.0016482	0.014285	23311.0	5726.6	3.94
g__ASF356	0.0039815	0.029577	595.32	224.09	2.27
g__Clostridia_vadinBB60_group	0.0073736	0.047929	1943.2	1372.3	2.46
g__Escherichia_Shigella	0.0091504	0.052869	5706.1	3614.4	3.02
g__Parasutterella	0.01262	0.065623	13324.0	5201.9	3.61

## Linear Discriminant Analysis Effect Size (LEfSe)

Name	P-values	FDR	H	L	S	LDAScore
g__Prevotellaceae_UCG_001	1.7864E-11	9.2895E-10	0.0	192.34	2265.0	3.05
g__Bilophila	6.2674E-11	1.6295E-9	22460.0	15992.0	872.17	4.03
g__Tuzzerella	1.6502E-9	1.9557E-8	10639.0	7687.0	658.27	3.7
g__Blautia	1.8142E-9	1.9557E-8	96303.0	117820.0	6718.7	4.74
g__Muribaculaceae	1.8804E-9	1.9557E-8	165920.0	204910.0	563890.0	5.3
g__Lachnoclostridium	3.1937E-9	2.7679E-8	29661.0	22849.0	4566.4	4.1
g__Ruminococcaceae	4.6158E-9	3.4289E-8	0.0	275.25	3593.1	3.25
g__Lactobacillus	4.3383E-8	2.8199E-7	797.88	11758.0	25779.0	4.1
g__uncultured	8.2345E-8	4.7577E-7	151070.0	121780.0	51265.0	4.7
g__GCA_900066575	1.3962E-7	7.2605E-7	7005.8	5689.0	606.87	3.51
g__Butyricicoccus	1.6436E-7	7.7696E-7	1603.7	744.49	76.273	2.88
g__Eubacterium_xylanophilum_group	7.009E-7	3.0372E-6	783.95	711.33	5025.7	3.33
Not_Assigned	1.3458E-6	5.3832E-6	12812.0	9370.0	1674.7	3.75
g__Family_XIII_UCG_001	4.9388E-6	1.8108E-5	47.754	197.32	1135.8	2.74
g__Escherichia_Shigella	5.3925E-6	1.8108E-5	9735.8	4591.3	397.95	3.67
g__Lachnospiraceae_FCS020_group	5.5718E-6	1.8108E-5	1251.5	1223.7	71.299	2.77
g__Parabacteroides	1.2864E-5	3.9349E-5	4998.2	8099.9	1200.5	3.54
g__Mucispirillum	2.2433E-5	6.4806E-5	15800.0	23267.0	3420.7	4.0
g__Faecalibaculum	3.0877E-5	8.4505E-5	4723.6	7239.3	164.15	3.55
g__Erysipelatoclostridium	4.1613E-5	1.0819E-4	0.0	3465.5	3041.0	3.24
g__Incertae_Sedis	7.9447E-5	1.9673E-4	6215.9	4259.7	2832.1	3.23
g__Bacteroides	9.151E-5	2.163E-4	182820.0	192260.0	84555.0	4.73
g__Colidextribacter	1.5248E-4	3.4474E-4	37586.0	25105.0	14838.0	4.06
g__Desulfovibrio	3.8539E-4	8.3501E-4	7998.7	3211.8	12154.0	3.65
g__Anaerotruncus	5.5784E-4	0.0011603	9556.7	7381.9	3669.4	3.47
g__UBA1819	8.386E-4	0.0016772	171.12	316.7	1416.0	2.79
g__Coriobacteriaceae_UCG_002	0.0017691	0.0034072	8496.2	10302.0	593.6	3.69
g__Parasutterella	0.0022185	0.0041201	7304.3	16014.0	3518.5	3.8
g__Romboutsia	0.0026538	0.0047585	1142.1	759.41	0.0	2.76
g__A2	0.0035236	0.0059157	286.52	582.0	2379.4	3.02
g__Lachnospiraceae_UCG_006	0.0035267	0.0059157	3796.4	379.71	1318.2	3.23
g__Enterococcus	0.0045995	0.0074742	525.29	114.41	49.743	2.38
g__Roseburia	0.009483	0.014943	961.04	523.96	0.0	2.68
g__Muribaculum	0.013648	0.020873	690.44	1653.1	1503.9	2.68
g__Eubacterium_nodatum_group	0.017924	0.02663	206.93	915.28	616.82	2.55
g__NK4A214_group	0.019417	0.028047	551.16	606.87	1369.6	2.61

# Single-factor Statistical Comparisons (DESeq2)

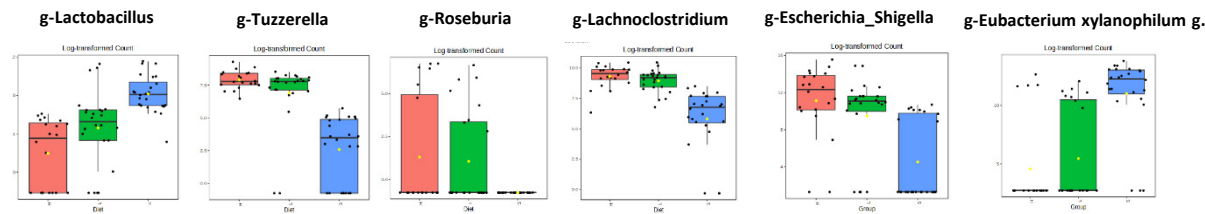
(FDR<0.04)

S vs H

Name	log2FC	lfcSE	P-values	FDR
g__Erysipelatoclostridium	-24.398	1.6009	1.9212999999999995E-52	9.798399999999999E-51
g__Bilophila	3.7851	0.38321	5.2186000000000004E-23	1.3308E-21
g__Blautia	3.3518	0.3633	2.8122999999999996E-20	4.7809000000000005E-19
g__Muribaculaceae	-2.666	0.29107	5.2310999999999995E-20	6.6696E-19
g__Prevotellaceae_UCG_001	-8.8569	1.0936	5.5494E-16	5.6604E-15
g__Tuzzerella	3.4179	0.43656	4.9102E-15	4.1737E-14
g__Lactobacillus	-5.7487	0.78275	2.0696E-13	1.5079E-12
g__Ruminococcaceae	-9.6815	1.3398	4.9653E-13	3.1654E-12
g__Lachnoclostridium	2.2343	0.32992	1.2682E-11	7.1863E-11
g__Butyrivococcus	4.6415	0.74634	5.001E-10	2.3555E-9
g__Clostridia_UCG_014	-9.1181	1.4667	5.0805E-10	2.3555E-9
g__Escherichia_Shigella	4.3526	0.81859	1.0539E-7	4.4793E-7
g__uncultured	0.92617	0.1839	4.7434E-7	1.8609E-6
g__GCA_900066575	3.1715	0.68987	4.2817E-6	1.5597E-5
g__Lachnospiraceae_FCS020_group	3.8051	0.92064	3.5783E-5	1.2166E-4
g__Family_XIII_UCG_001	-5.1829	1.3149	8.0908E-5	2.5347E-4
g__Faecalibaculum	4.5939	1.1686	8.4489E-5	2.5347E-4
g__Romboutsia	6.3343	1.6374	1.0951E-4	3.1029E-4
Not_Assigned	2.211	0.61096	2.958E-4	7.94E-4
g__Lachnospiraceae_NK4A136_group	-0.91394	0.25566	3.5048E-4	8.9372E-4
g__UBA1819	-3.6582	1.0909	7.988E-4	0.0019399
g__Mucispirillum	1.9199	0.58289	9.8878E-4	0.0022922
g__Parabacteroides	1.4956	0.47007	0.0014639	0.0032461
g__Eubacterium_xylanophilum_group	-3.557	1.1329	0.0016906	0.0035925
g__Coriobacteriaceae_UCG_002	3.2381	1.0479	0.002001	0.004082
g__A2	-3.7078	1.4647	0.01136	0.022283
g__Candidatus_Saccharimonas	-1.532	0.61465	0.012685	0.02396
g__Muribaculum	-1.9525	0.82776	0.018333	0.033391
g__Erysipelotrichaceae	-2.3434	1.0212	0.02174	0.038232

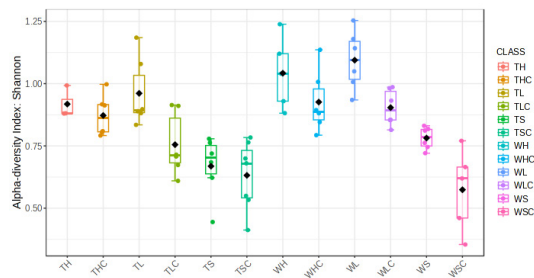
L vs H

Name	log2FC	lfcSE	P-values	FDR
g__Erysipelatoclostridium	-24.486	1.5883	1.2679999999999998E-53	6.5934999999999984E-52
g__Lactobacillus	-4.3587	0.78467	2.7801E-8	7.2283E-7
g__Prevotellaceae_UCG_001	-5.2694	1.0953	1.5035E-6	2.6061E-5
g__Ruminococcaceae	-5.9152	1.3338	9.2134E-6	1.1977E-4



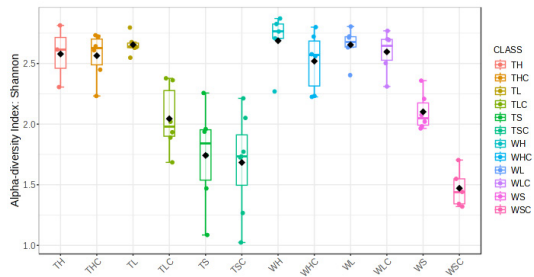
Supplementary Figure 12

Shanon-Kluskal-Wallis test  
PHYLUM



Pair	Statistic	P-value	FDR
WLC vs TSC	42.0	0.0011655	0.010989
WLC vs TS	36.0	0.0021645	0.010989
THC vs TS	36.0	0.0021645	0.010989
WHC vs TS	36.0	0.0021645	0.010989
TL vs WS	36.0	0.0021645	0.010989
TL vs TS	36.0	0.0021645	0.010989
WL vs WS	36.0	0.0021645	0.010989
WL vs TS	36.0	0.0021645	0.010989
WLC vs WS	34.0	0.008658	0.022857
WHC vs WS	33.0	0.015152	0.038462
WLC vs TLC	30.0	0.064935	0.11278
WLC vs WSC	30.0	0.004329	0.012987
TLC vs TSC	30.0	0.23427	0.32212
WH vs WS	30.0	0.004329	0.012987
WH vs TS	30.0	0.004329	0.012987
WS vs TS	30.0	0.064935	0.11278
THC vs WS	27.0	0.17965	0.25228
WLC vs THC	24.0	0.39394	0.48148
TLC vs WSC	24.0	0.12554	0.19805
TLC vs TS	21.0	0.69913	0.74424

Shanon-Kluskal-Wallis test  
GENUS



Pair	Statistic	P-value	FDR
WLC vs TSC	42.0	0.0011655	0.011905
WLC vs TS	36.0	0.0021645	0.011905
TL vs WS	36.0	0.0021645	0.011905
TL vs TS	36.0	0.0021645	0.011905
WL vs WS	36.0	0.0021645	0.011905
WL vs TS	36.0	0.0021645	0.011905
WLC vs WS	35.0	0.004329	0.012422
THC vs WS	35.0	0.004329	0.012422
THC vs TS	35.0	0.004329	0.012422
WLC vs TLC	34.0	0.008658	0.019048
WHC vs WS	34.0	0.008658	0.019048
WHC vs TS	34.0	0.008658	0.019048
TLC vs TSC	31.0	0.18065	0.27728
WS vs TS	31.0	0.041126	0.075397
WLC vs WSC	30.0	0.004329	0.012422
WH vs TS	30.0	0.004329	0.012422
TLC vs WSC	29.0	0.008658	0.019048
WH vs WS	29.0	0.008658	0.019048
TLC vs TS	25.0	0.30952	0.4256
WLC vs WHC	21.0	0.69913	0.78571

Supplementary Figure 13

**BETA DIVERSITY GROUPS  
GENUS**

Pair	F-value	R-squared	P-value	FDR
TSC vs THC	15.019	0.57723	<b>0.001</b>	0.012375
TSC vs WHC	9.8025	0.47122	<b>0.001</b>	0.012375
TSC vs TL	20.31	0.64867	<b>0.001</b>	0.012375
TL vs TS	25.404	0.71755	<b>0.001</b>	0.012375
WLC vs WSC	36.68	0.80298	<b>0.002</b>	0.012375
WSC vs TL	31.694	0.77884	<b>0.002</b>	0.012375
TSC vs WL	15.327	0.58218	<b>0.002</b>	0.012375
THC vs WS	18.354	0.64731	<b>0.002</b>	0.012375
WHC vs TS	13.444	0.57346	<b>0.002</b>	0.012375
WL vs WS	18.781	0.65255	<b>0.002</b>	0.012375
WLC vs TSC	19.222	0.63603	<b>0.003</b>	0.012375
WSC vs WL	24.816	0.73385	<b>0.003</b>	0.012375
WSC vs WS	15.606	0.63424	<b>0.003</b>	0.012375
TSC vs WS	3.9571	0.26456	<b>0.003</b>	0.012375
THC vs WH	3.2835	0.26731	<b>0.003</b>	0.012375
WH vs WS	20.442	0.69432	<b>0.003</b>	0.012375
TSC vs WH	16.925	0.62859	<b>0.004</b>	0.013895
THC vs TS	20.0	0.66667	<b>0.004</b>	0.013895
WL vs TS	19.463	0.66059	<b>0.004</b>	0.013895
WLC vs WS	26.371	0.72506	<b>0.005</b>	0.014348

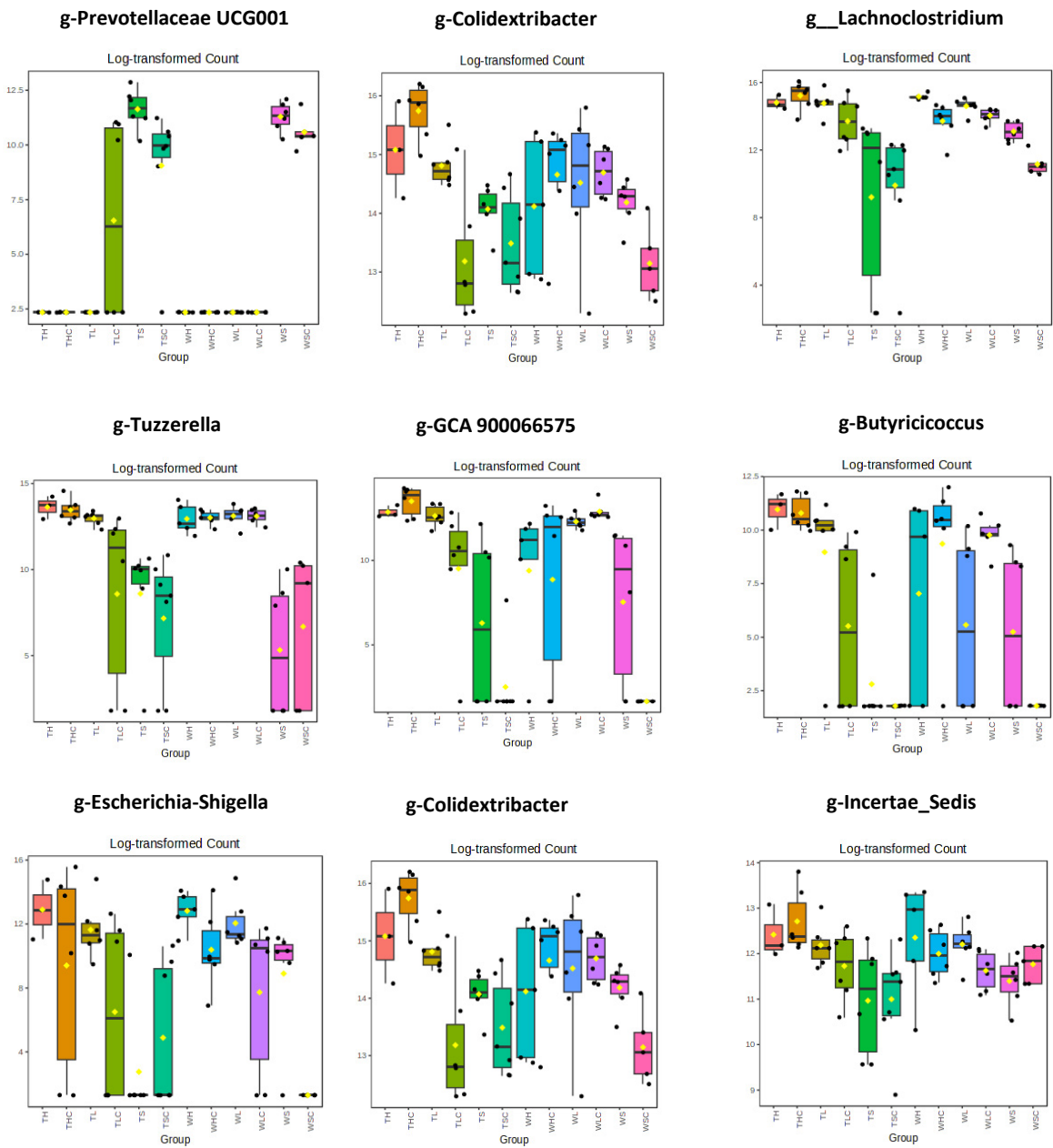
**Supplementary Figure 14**

## Linear Discriminant Analysis Effect Size (LEfSe)

Name	P-values	FDR	TH	THC	TL	TLC	TS	TSC
g__Prevotellaceae_UCG_001	3.8255E-8	2.0275E-6	0.0	0.0	0.0	736.2	3734.1	3.27
g__Bilophila	7.9649E-8	2.1107E-6	18279.0	31391.0	22066.0	4788.6	1074.5	4.19
g__Lachnoclostridium	4.0876E-7	5.3301E-6	28254.0	38501.0	29859.0	19055.0	4483.5	4.25
g__Blautia	4.2081E-7	5.3301E-6	115230.0	100280.0	200050.0	55958.0	3190.2	5.0
g__Tuzzerella	5.0284E-7	5.3301E-6	13994.0	12370.0	8608.9	3210.1	848.95	3.84
g__Muribaculaceae	6.1749E-7	5.3384E-6	67611.0	186700.0	121780.0	347190.0	608370.0	5.47
g__Ruminococcaceae	7.0507E-7	5.3384E-6	0.0	0.0	0.0	1160.7	1233.6	3.37
g__GCA_900066575	1.5088E-6	9.9956E-6	7388.5	13444.0	7216.1	2427.5	1021.4	3.83
g__uncultured	2.967E-6	1.7472E-5	131850.0	178860.0	153170.0	56946.0	60030.0	4.88
g__Rikenella	6.2027E-6	3.2874E-5	0.0	10201.0	3329.5	3860.1	3826.9	3.87
Not_Assigned	7.7015E-6	3.7107E-5	15626.0	12661.0	12741.0	2739.2	3860.1	3.92
g__Butyricicoccus	1.5521E-5	6.8549E-5	2188.7	1896.9	1101.0	391.31	39.795	3.04
g__Erysipelatoclostridium	2.3424E-5	9.5497E-5	0.0	0.0	0.0	13862.0	4609.5	3.84
g__Lactobacillus	3.6947E-5	1.3987E-4	955.07	610.18	2235.1	41466.0	23592.0	4.42
g__Romboutsia	6.2724E-5	2.2162E-4	0.0	1591.8	557.13	126.02	0.0	3.07
g__Eubacterium_xylanophilum_group	8.565E-5	2.8372E-4	0.0	2692.8	577.02	1585.2	5259.5	3.53
g__Escherichia_Shigella	1.2726E-4	3.9677E-4	12350.0	14174.0	7163.0	1870.3	179.08	3.85
g__Mucispirillum	1.4253E-4	4.1967E-4	29700.0	5511.6	19785.0	5717.2	3641.2	4.46
g__Peptococcus	5.2458E-4	0.0014633	4337.6	1253.5	3840.2	510.7	1492.3	3.33
g__Colidextribacter	6.1405E-4	0.0016272	38866.0	56800.0	29614.0	13106.0	17788.0	4.36
g__Family_XIII_UCG_001	6.6204E-4	0.0016709	0.0	0.0	0.0	683.14	1764.2	2.95
g__Candidatus_Saccharimonas	8.1548E-4	0.0019646	1034.7	1180.6	4510.1	2228.5	2460.6	3.55
g__Parabacteroides	8.8454E-4	0.0020383	3382.5	2739.2	1910.1	17404.0	902.01	3.92
g__Alistipes	9.7947E-4	0.002163	65038.0	10725.0	44563.0	24573.0	41221.0	4.55
g__Faecalibaculum	0.0013205	0.0027994	1870.3	1552.0	10479.0	2666.2	106.12	3.72
g__Lachnospiraceae_FCS020_group	0.001891	0.0038546	981.6	1545.4	1883.6	391.31	86.222	2.97
g__Oscillibacter	0.0021464	0.0042133	4191.7	9199.2	7275.8	3959.6	7123.2	3.72
g__UCG_009	0.0022765	0.0043091	172.44	1246.9	974.97	397.95	1346.4	3.13
g__Harryflintia	0.0030904	0.0055501	941.81	636.71	53.06	59.692	0.0	2.67
g__Coriobacteriaceae_UCG_002	0.0031416	0.0055501	915.28	2745.8	20886.0	2639.7	855.59	4.11
g__UBA1819	0.0045984	0.0076733	0.0	33.162	145.91	676.51	875.48	3.21
g__Desulfovibrio	0.0046329	0.0076733	3488.7	0.0	1227.0	3820.3	10121.0	4.0
g__Lachnospiraceae_NK4A136_group	0.007086	0.011352	74575.0	83483.0	48967.0	35643.0	71140.0	4.73
g__Incertae_Sedis	0.0072823	0.011352	6579.4	7448.2	4801.9	3873.3	2692.8	3.4
g__Bacteroides	0.0082883	0.012551	250390.0	152170.0	139550.0	247090.0	57828.0	4.98
g__Eubacterium_nodatum_group	0.0087091	0.012822	344.89	318.36	988.23	1525.5	696.41	2.86
g__Parasutterella	0.016835	0.024114	0.0	590.29	13928.0	12854.0	7269.2	4.03
g__Anaerotruncus	0.018275	0.025489	6857.9	11925.0	7103.3	7136.5	2891.7	3.71
g__NK4A214_group	0.018879	0.025656	0.0	391.31	517.33	1671.4	1804.0	3.05
g__ASF356	0.022563	0.029718	198.97	0.0	523.96	809.16	809.16	2.62
g__Clostridia_vadinBB60_group	0.023195	0.029718	570.39	1140.8	2891.7	238.77	537.23	3.42
g__A2	0.02355	0.029718	411.21	252.03	0.0	1883.6	2473.9	3.28

**Supplementary Figure 15**

Linear Discriminant Analysis Effect Size (LEfSe)



Supplementary Figure 16



## SUPPLEMENTARY FIGURES

### Supplementary Figure 1

- A-The Plots show alpha diversity analysis from WT and TG (APP/PS1) groups, the corresponding Kluskal-Walllis statistical analysis was indicated below.
- B-The beta diversity data from WT vs TG , at phylum and Genus level were indicated, using Bray Curtis analysis.
- C- The differences WT vs TG were additionally analysed using Linear Discrimination Test (LEfSe), showing only a genus (g-RF39) statistically significantly different in TG
- D- The stacked bar plots represent relative abundance profile TG and WT mice groups, at phylum taxonomic rank (top graph); and at genus taxonomic rank (lower graph). In both cases some obvious differences were marked with colour arrows.
- E- In addition of the Linear Discrimination Test (LEfSe) presented in Figure 1 we did a Single-factor Statistical Comparison. The data at genus taxonomic rank, confirmed g-RF39 statistically significantly different in TG as indicated the p value.

### Supplementary Figure 2

- A-** The stacked bar plots represent relative abundance profile from sexual mice groups (F, M and MC), at phylum taxonomic rank. Some obvious differences were marked with colour arrows.
- B-**Plots show beta diversity analysis from sexual mice groups considered (F, M and MC), using Bray Curtis, at phylum level. The corresponding statistical analysis was indicated on the right table, showing p and DFR values.
- C-**The data from sexual mice groups considered (F, M and MC), were additionally analysed using Linear Discrimination Test (LEfSe), at genus taxonomic rank showing significantly differences in p and FDR values (Note that p values were represented in bold only when with FDR below 0.04.)

### Supplementary Figure 3

- We additionally analysed F, M and MC sexual groups, using Linear Discrimination Test (LEfSe). At specie taxonomic rank, we found significantly differences in four species as indicated in the table (Note that p values were represented in bold only when with FDR below 0.04.)
- In addition, LDA plots from F, M and MC mice shown more abundant species in each group, when considering LDA >2. The graphics below, represent the log-transformed values from most significantly altered species among groups (*Bacteroides caecimuris* and *Lactobacillus reuteri*).

#### **Supplementary Figure 4**

**A-**Plots show the alpha analysis from the three sexual groups and the two genotypes considered (FW, FT, WS, WSC and TS, TSC), at genus (left) and specie (right) taxonomic rank using Shannon test, using a Kluskal-Wallis. The asterisks (\*\*-  $p < 0.001$ ) represent p value when WS and WSC was statistical analysis.

The tables below represent the represent p value and FDR value from Kluskal-Wallis statistical analysis, from each group, in pairs.

**B-** The stacked bar plots represent the relative abundance profile in FW, FT, WS, WSC and TS, TSC mice groups, at phylum taxonomic rank. Some obvious difference was marked with colour arrow.

#### **Supplementary Figure 5**

**A-**Plots show beta diversity analysis from mice groups feed with each diet, when we additionally considered genotype and sexual groups. Considering genotypes, we represented WS, WH, WL; WSC, WHC, WLC (wild-type); and TS, TH, TL, TSC, THC, TLC (APP/PS1), using Bray Curtis test, at genus taxonomic rank. The corresponding statistical analysis was represented on the right table, representing p and DFR values. (Note that p values were represented in bold only when with FDR below 0.04.)

**B.** Plots show Linear Discrimination Analysis (LDA) from above mice groups, at genus taxonomic rank, show some genera more abundant in the groups previously considered (Represented only when considering  $LDA > 2$ ).

#### **Supplementary Figure 6**

The data from considering groups (WS, WH, WL; WSC, WHC, WLC; and TS, TH, TL, TSC, THC, TLC) were additionally analysed using Linear Discrimination Test (LEfSe). The tables represent the data from phylum and genus taxonomic ranks where p values were represented in bold only when with  $FDR \leq 0.04$ .

#### **Supplementary Figure 7**

Additionally, to the Linear Discrimination Test we performed a Single Factor statistical analysis (DESeq2) to reinforce the differences between: male versus female in wild type groups (WS /FW), wild-type versus transgenic (WS/TS), and castrated-males versus males (WS/WSC), all groups in standard food diet (S).

The corresponding statistical analysis were represented in each table, representing p and DFR values. (Note that p values were represented in bold only when with FDR below 0.04.). The graphics below, represent the log-transformed values from most significantly altered genera between groups.

#### **Supplementary Figure 8**

**A-**Plots show the alpha analysis at phylum and genus level, from TG and WT mice groups, using Shannon test, when all diets were considered. The table represent the represent p value and FDR value from Kluskal-Wallis statistical analysis. (Note that p values were represented in bold only when with FDR below 0.03.)

**B-C-** The stacked bar plots represent relative abundance profile TG and WT mice groups (all diets considered), at phylum taxonomic rank (**B**); and at genus taxonomic rank (**C**). In both cases some obvious differences were marked with colour arrows.

#### **Supplementary Figure 9**

**A-**Plots show the alpha analysis at phylum and genus level, from M and MC mice groups, using Shannon test, when all diets were considered. The table represent the represent p value and FDR value from Kluskal-Wallis statistical analysis. (Note that p values were represented in bold only when with FDR below 0.03.)

**B-C-** The stacked bar plots represent relative abundance profile M and MC mice groups (all diets considered), at phylum taxonomic rank (**B**); and at genus taxonomic rank (**C**). In both cases some obvious differences were marked with colour arrows.

#### **Supplementary Figure 10**

**A-**Plots show beta diversity analysis from TG and WT mice groups (all diets considered), using Bray Curtis test, at genus taxonomic rank. The corresponding statistical analysis was represented on the right table, representing p and DFR values.

**B-**Plots show beta diversity analysis from M and MC mice groups, using Shannon test, when all diets were considered, using Bray Curtis test, at genus and featured-level taxonomic rank. The corresponding statistical analysis was represented on the right table, representing p and DFR values. (Note that p values were represented in bold only when with FDR below 0.04.)

**C-** Plots show Linear Discrimination Analysis (LDA) from M and MC mice groups, at genus taxonomic rank, show some genera more abundant in these groups (Represented only when considering LDA >, or < 2).

The table below represent the additional analysed using Linear Discrimination Test (LEfSe) test, from M and MC. The tables represent the data from phylum and genus taxonomic ranks. The p values were denoted in bold only when with  $FDR \leq 0.04$ .

#### **Supplementary Figure 11**

The table represent the additional analysed using Linear Discrimination Test (LEfSe) test, from the mice groups fed with each diet (S, L and H), at genus taxonomic rank. The p values were denoted in bold only when with  $FDR \leq 0.04$ .

#### **Supplementary Figure 12**

In addition of the previous Linear Discrimination Test (LEfSe) presented in Supl. Figure 11 we did a Single-factor Statistical Comparison (DESeq2). The data at genus taxonomic rank, was performed between S and H diet, and between L and S diets.

The statistically significant p values were represented in bold only when with  $FDR \leq 0.04$ .

The graphical below represent the log-transformed values from most significantly altered genera when compared with H diet

#### **Supplementary Figure 13**

Plots show the alpha analysis at phylum and genus level, from all groups and the different diets considered [WS, WH, WL; WSC, WHC, WLC (wild-type); and TS, TH, TL, TSC, THC, TLC (APP/PS1)], using Shannon test.

The tables represent the represent p value and FDR value from Kluskal-Wallis statistical analysis. (Note that p values were represented in bold only when with FDR below 0.03.)

#### **Supplementary Figure 14**

Table show beta diversity analysis from (WS, WH, WL; WSC, WHC, WLC; and TS, TH, TL, TSC, THC, TLC), mice groups, when all diets were considered, using Bray Curtis test, at genus taxonomic rank. The statistical analysis represented in the table, represent p and DFR values. (Note that p values were represented in bold only when with FDR below 0.04.)

#### **Supplementary Figure 15**

Table of the Linear Discrimination Test (LEfSe) from (WS, WH, WL; WSC, WHC, WLC; and TS, TH, TL, TSC, THC, TLC), mice groups, at genus taxonomic rank. The statistical analysis represented in the table, represent p and DFR values. (Note that p values were represented in bold only when with FDR below 0.03.)

### **Supplementary Figure 16**

The figures represent the log-transformed values from most significantly altered genera when compared all diets from (WS, WH, WL; WSC, WHC, WLC; and TS, TH, TL, TSC, THC, TLC) mice groups: In this case we represent those in which H diet in transgenic mice (TH or THC) was significantly different from L or S diet in transgenic mice (TS, TSC, TL, TLC).