

Supplementary Table 4. Linear discriminant analysis (LDA) scores were computed for bacterial differentially abundant (order, family, and genus).

Bacteria	LDA	p- value	q-value
F0 3xTg-Ctrl			
f_S24-7	5.5629	0.0005	0.0051
g_Lactobacillus	3.3776	0.0043	0.0282
g_Odoribacter	3.8558	0.0011	0.0084
g_Clostridium	3.9208	0.0011	0.0084
g_Bacteroides	4.9983	0.0003	0.0034
o_Clostridiales	4.9646	0.0003	0.0034
f_Lachnospiraceae	4.7685	0.0003	0.0034
g_Paraprevotella	4.3644	0.0003	0.0034
f_Rikenellaceae	4.2801	0.0003	0.0034
f_Paraprevotellaceae_g_Prevotella	4.7645	0.0003	0.0034
f_Ruminococcaceae	4.1134	0.0003	0.0034
f_Prevotellaceae_g_Prevotella	4.7275	0.0003	0.0034
g_Oscillospira	4.0017	0.0037	0.0261
g_Dehalobacterium	2.6281	0.0272	0.1668
o_Bacteroidales	4.4661	0.0011	0.0084
F0 3xTg-Abx at PD30			
f_Enterobacteriaceae	3.6351	0.0272	0.6256
g_Klebsiella	4.9506	0.0006	0.0322
g_Sutterella	4.6674	0.0100	0.3066
g_Enterobacter	5.8677	0.0007	0.0322
F1 3xTg-Ctrl at PD30			
f_S24 7	5.5646	0.0002	0.0046
f_Rikenellaceae_g_AF12	3.4837	0.0110	0.0532
g_Lactobacillus	4.9443	0.0002	0.0046
g_Parabacteroides	3.3236	0.0245	0.0980
g_Streptococcus	3.6290	0.0245	0.0980
g_Bacteroides	5.0075	0.0002	0.0046
o_Clostridiales	4.7971	0.0009	0.0111
g_Prevotella	4.5567	0.0017	0.0111
f_Ruminococcaceae_g_Ruminococcus	3.3869	0.0017	0.0111
f_Lachnospiraceae_g_Ruminococcus	3.6134	0.0017	0.0111
f_Desulfovibrionaceae	3.3822	0.0017	0.0111
f_Rikenellaceae	4.4614	0.0002	0.0046
f_Lachnospiraceae	4.5938	0.0009	0.0110
f_Ruminococcaceae	3.9310	0.0046	0.0248
g_Odoribacter	3.8225	0.0046	0.0248
g_Prevotella	4.5770	0.0006	0.0110
f_Clostridiaceae_g_CandidatusArthromitus	3.8482	0.0110	0.0532
f_Erysipelotrichaceae	3.1710	0.0017	0.0111
g_Oscillospira	4.1941	0.0017	0.0111
o_Bacteroidales	3.3253	0.0017	0.0111
g_Flexispira	3.5329	0.0245	0.0980
f_Helicobacteraceae	3.3771	0.0046	0.2948
g_Coprobacillus	2.8083	0.0245	0.0980
f_Rikenellaceae_g_AF12	3.4837	0.0110	0.0532

F1 3xTg-Abx at PD30			
<i>g_Mycoplasma</i>	3.1694	0.0128	0.2940
<i>g_Klebsiella</i>	5.0103	0.0029	0.0889
<i>g_Sutterella</i>	4.8105	0.0005	0.0230
<i>g_Enterobacter</i>	5.8821	0.0002	0.0184
F1 NoTg-Ctrl at PD30			
<i>o_Bacteroidales_f_S24_7</i>	5.5400	0.0000	0.0000
<i>g_Lactobacillus</i>	3.8395	0.0001	0.0010
<i>g_Parabacteroides</i>	3.5146	0.0305	0.1476
<i>g_Bacteroides</i>	4.7280	0.0000	0.0000
<i>o_Clostridiales</i>	5.0571	0.0000	0.0000
<i>g_Prevotella</i>	4.2382	0.0051	0.0335
<i>f_Lachnospiraceae_g_Ruminococcus</i>	3.6263	0.0006	0.0050
<i>f_Ruminococcaceae_g_Ruminococcus</i>	3.6501	0.0130	0.0747
<i>f_Rikenellaceae</i>	5.0976	0.0000	0.0000
<i>f_Lachnospiraceae</i>	4.3621	0.0000	0.0000
<i>g_Edwardsiella</i>	4.1715	0.0130	0.0747
<i>f_Ruminococcaceae</i>	4.1587	0.0001	0.0010
<i>g_Prevotella</i>	4.6131	0.0000	0.0000
<i>c_Alphaproteobacteria</i>	3.4730	0.0051	0.0335
<i>f_Clostridiaceae_g_CandidatusArthromitus</i>	3.8461	0.0019	0.0145
<i>f_Erysipelotrichaceae</i>	2.9173	0.0305	0.1476
<i>g_Oscillospira</i>	4.2932	0.0000	0.0000
<i>g_Dehalobacterium</i>	2.542	0.0305	1.0000
<i>o_Bacteroidales</i>	4.0835	0.0006	0.0050
<i>g_Flexispira</i>	2.9978	0.0305	0.0145
F1 3xTg-Ctrl at PD150			
<i>o_Bacteroidales_f_S24_7</i>	5.5248	0.0468	0.2443
<i>f_Rikenellaceae_g_AF12</i>	3.4295	0.0150	0.1533
<i>g_Lactobacillus</i>	4.4110	0.0276	0.2116
<i>g_Odoribacter</i>	3.6578	0.0234	0.2032
<i>g_Dorea</i>	4.3169	0.0106	0.1393
<i>g_Clostridium</i>	3.8163	0.0023	0.0705
<i>g_Allobaculum</i>	4.7245	0.0364	0.2232
<i>o_Clostridiales</i>	5.0991	0.0090	0.1393
<i>f_Lachnospiraceae</i>	4.5570	0.0023	0.0703
<i>g_Paraprevotella</i>	3.5331	0.0243	0.2032
<i>f_Desulfovibrionaceae</i>	3.9334	0.0034	0.0782
<i>f_Rikenellaceae</i>	4.4931	0.0015	0.0705
<i>g_Ruminococcus</i>	3.4270	0.0106	0.1393
<i>f_Ruminococcaceae</i>	3.9809	0.0361	0.2232
<i>g_Bifidobacterium</i>	4.3100	0.0309	0.2186
<i>g_Prevotella</i>	4.8369	0.0468	0.2443
<i>g_Oscillospira</i>	4.0087	0.0124	0.1426
<i>f_Helicobacteraceae</i>	3.9994	0.0478	0.2443
F1 3xTg-Abx at PD150			
<i>g_Mycoplasma</i>	3.5450	0.0123	0.2829
<i>f_Enterobacteriaceae</i>	3.9462	0.0412	0.7580
<i>g_Klebsiella</i>	4.7940	0.0089	0.2760
<i>g_Sutterella</i>	4.7879	0.0035	0.2760
<i>g_Enterobacter</i>	5.7191	0.0090	0.2760

F1 NoTg-Ctrl at PD150			
o__Bacteroidales_f__S24_7	5.5223	0.0000	0.0000
g__Coprococcus	2.9091	0.0305	0.1753
f__Rikenellaceae_g__AF12	3.3451	0.0359	0.1942
g__Lactobacillus	4.7896	0.0000	0.0000
g__Clostridium	3.8841	0.0305	0.1753
g__Bacteroides	3.8112	0.0016	0.0184
o__Clostridiales	5.1807	0.0003	0.0046
g__Prevotella	4.5118	0.0001	0.0023
g__Ruminococcus	3.4279	0.0450	0.2300
g__Ruminococcus_	3.7308	0.0118	0.0904
f__Rikenellaceae	4.5612	0.0003	0.0046
f__Lachnospiraceae	4.7433	0.0011	0.0144
f__Ruminococcaceae	3.9085	0.0037	0.0377
g__Odoribacter	3.8747	0.0081	0.6774
g__Prevotella	4.5482	0.0000	0.0000
f__Erysipelotrichaceae	2.8093	0.0305	0.1753
g__Oscillospira	3.9837	0.0041	0.0372
g__Mycoplasma	2.6120	0.0130	0.0920
F1 NoTg-Abx at PD150			
f__Enterobacteriaceae	4.4381	0.0000	0.0000
g__Klebsiella	4.7965	0.0000	0.0000
g__Sutterella	5.0282	0.0001	0.0030
g__Enterobacter	5.8133	0.0001	0.0023

The threshold on the logarithmic LDA score was set to 2.5. p and q values < 0.05 were considered statistically significant. * p -value was adjusted with Benjamini-Hochberg method and generated FDR value (q -value). The name of each taxon level appears in abbreviation before its taxon. “f”, family; “g”, genus. “LDA” Linear discriminant analysis.