

## Nutrients

### Supplementing Ryegrass Ameliorates Commercial Diet-Induced Gut Microbial Dysbiosis-Associated Spleen Dysfunctions by Gut–Microbiota–Spleen Axis

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**Table S1: The nutrients and chemical composition of the diet (two stages) offered to geese.**

Ingredients, %	Diets	
	Grower	Finisher
Wheat	57.3	59
Rice bran	5	4
Corn germ cake (exp.)	4	3.2
Corn oil	5	7
Dumpling powder	3	2
Corn distiller's grains (DDGS)	6.5	7
Spouting germ meal	3	2
Soybean meal (sol.)	7	6
Peanut meal (sol.)	1.5	1

Albumen powder	2	1.5
Stone powder	1.1	1
Liquid methionine	0.25	0.3
MuLaoDa-2	1.25	2
201/202 gunk	2.5	3
Calcium hydrogen phosphate	0.6	1
<i>Chemical composition (%)</i>		
Crude protein	20.12	15.54
Ash	12.89	12.86
Neutral detergent fiber	13.25	30.55
Acid detergent fiber	5.5	27.02
Calcium	1.15	1.07
Phosphorous	0.47	0.32

**Table S2. Primer sequences used for quantitative real-time PCR**

Gene	Forward primer (Sequence 5'- 3')	Reverse primer (Sequence 5'- 3')
Srck	CTGCCGAATCCAAGCTCTTC	TAGTGAGGGAATGAGCCAGC
PI3K	TTCTTGAGACTGGGAGCAG	GCCTGTTCTCGTTGCTATG
P47 <sup>Phox</sup>	CCAAAGGATGCCAAGAAAAA	CAGCCCCGTTTATTCTTCAA
NADPH	ATGTCCAGCCACCCATGTTA	CAACCCTCCGACGTGATTTTC
TLR2	CCTGGTGGTGTCTTTGATCT	GTAGCAGATGTCTTTTGCG
TLR4	AGGGCTACAGGTCAACAGAC	GACGTTCAACAGCCGAATAC
MyD88	CTGCGTCTTTGATCGGGATG	GGCTTTGCACTTCACTGGAA
NIK	CAACCCTCCGACGTGATTTTC	TTTGCTGCTCGATACGCTTC
IKK $\alpha$	GCATGTACCTACCCGCTAT	ACACCGACAGGCTTACCATC
NF- $\kappa$ B	GGCAGAGATGGTGGAAAGACT	GTTTGCCATCACCACCATGT
IRAK	ACTGCTGAGCTCATGACCTT	TGGGAGAGCACAGTAAGCAC
TRAF6	AGAGGAATGAACTGGCACGA	TTGTCTTACCAGGCGACCTT
TAK1	CGGGATTCAGATGGGCATTG	GCAGTGTCTCAATCGCCATT
IKB- $\alpha$	AAAGCTGGATGTGACCTGGA	GTTGTAGTTGGTTGCCTGCA
NLRP3	AAACAAACCCGATGCCAAGG	CAGGTTGCTGTGGTTGTTCA
Caspase-1	ATACACTTGCCACGGGAGAC	TGCAAAATCCTTCATGACCA
IL-1 $\beta$	CACATCACAACCCACAGCAA	CTGCCCCCTCCGTCTTCTTA
IL-18	AAAGAAGGAAGGTGGAGGGG	TCTGTCTCTCTAACGCTGCC
GPR109A	AGCCAGGGGACATATACGTG	TCCCTCGGATCATGAAGCTC
FFAR2	GCACCAGAGATCCTAAGGGG	ATGGGAGGCCTTGACAGAAA
FFAR3	AGCAAGGATCTGGAAGTCT	TCCAAGTACTCAGCAAGGGG
AMPK	TCTCGCCCTCATCCTGAAAG	CTCGACACACTTCAGCCATG
HDAC	GAACAACCTCTGCCACGGTT	CCTCCGACTTCACATCCACT
Keap1	CTGAACGAGGCCCTCAAGTA	CAAACCTCGTAGCGGGGAATG
NFE2L2	CGCCTTGAAGCTCATCTCAC	CCTCTCCTGCGTATATCCCG

NRF2	CGCCTTGAAGCTCATCTCAC	CCTCTCCTGCGTATATCCCG
NQ01	GACCCCAAGCACTTCGTCTA	CGAAGCCTTGGATGATGACG
GCLC	GGAGAGTGGAATTCAGGCCT	AGAGCCACATCCATCCACAA
GCLM	TGCCCCACCTCCTATTGAAG	TGTGAGATCAGGTGGCATCA
GSTA4	GCACCTCTGTTCCAAAGCAA	AATCCAGGACACAGCCATCA
HMOX1	AGGGCTGGCTTTCTTTACCT	GTGACCGTTTTCTGGCTTT
SOD	GGAAGAATCAGCGGCTTGTC	CCAATGATGCAGTGTGGTCC
GPx	GCTTCCCCCTCCAACCAATTC	TAGACCTTCTGCTCCTTGGC
CAT	CCGAGTCTTTGCATCAGGTG	GCCTTCCTGCTTCCTCTACA
IL-4	TGACAGGGTATTGGTCCACC	ACGGAAGAAGCAGAAGGTGA
IL-10	CATCAAGAACAGCGAGCACC	GCACCCACCTTTTCAAACGT
iNOS	CTCATTCTCCAAGCGAACGG	GCACTCCTATCTCTGTCCCC
COX2	GGTTCTACAATGGAGAGCGC	TGTTCTTGCCACTTGAGCTG
TNF- $\alpha$	GGTCCACAACGAGTTCATCC	AGGAGGAGGAGGAGATGGAG
IL-6	GGAAGACCCTTGCTCTCCTT	TGGAGCCAGAAGATGAGTGG
CD4	AGCAAGACAGAGCTGGTGGT	TCCATCAGGTGACAGTTCCA
B220	GGCCATACTACCCAAAGCAA	ATGCCTCCTGCTTGTTTTT
CD19	GGAGGAGAATTGGATGCTGA	CTCGTTCTCCACTCGTAGCC
IgD	TTTCTAACAGCACCGCCTCT	GGTCGCTCTTCGTCTTCATC
CD3	TTGGGTGCAATTTATGACGA	ACAGCAACCATCAGGAGGAC
CD8	GTGAAGTTGCCACAGCAAAA	GCAGCTTTTTTGAGAGGATG
IL-2	AGAAAAGCTGGGAACAAGCA	ACAGATCTTGCATCCCGTTC
TGF-B	AGCTAGCGGTCTTGACATT	GATTGTTCCCCACATCCAAC
IL-17	CTGCCTACGGGAAGGTGATA	GGTCCTCGTCGATCCTGTAA
$\beta$ -actin	CAACGAGCGGTTCAAGTGT	TGGAGTTGAAGGTGGTCTCG

Species	Relative abundance in IHF group (45 Days)	Relative abundance in AGF group (45 Days)	Log2FC	P-Value	FDR
<i>Clostridia</i>	55.766667	32.550000	-0.7767455	1.06E-06	1.32E-06
<i>Bacteroidia</i>	43.556667	20.576667	-1.0818843	9.47E-08	1.70E-07
<i>Bacilli</i>	11.570000	12.543333	0.1165319	5.86E-06	6.21E-06
<i>Coriobacteriia</i>	3.407667	3.598667	0.0786783	1.37E-05	1.37E-05
<i>Actinobacteria</i>	2.777000	5.294667	0.9310127	3.51E-08	9.46E-08
<i>Vampirivibrionia</i>	1.217333	4.904333	2.0103328	1.47E-07	2.52E-07

<i>Gammaproteobacteria</i>	0.3723333	0.1938667	-0.9415300	6.98E-08	1.40E-07
<i>Desulfovibrionia</i>	0.3084333	0.2547667	-0.2757822	4.82E-06	5.26E-06
<i>Verrucomicrobiae</i>	0.0062670	0.2127667	5.0853533	5.06E-08	1.07E-07
<i>Alphaproteobacteria</i>	0.0092160	0.4268333	5.5333883	3.00E-09	1.08E-08
<i>Negativicutes</i>	0.1705000	0.0766767	-1.1529122	2.12E-06	2.39E-06
Species	Relative abundance in IHF group (60 Days)	Relative abundance in AGF group (60 Days)	Log2FC	P-Value	FDR
<i>Clostridia</i>	58.7833333	47.9333333	-0.2943779	3.82E-06	3.82E-06
<i>Bacteroidia</i>	17.6533333	16.0700000	-0.1355707	2.22E-06	2.28E-06
<i>Bacilli</i>	9.1833333	25.5633333	1.4769862	1.86E-07	3.53E-07
<i>Coriobacteriia</i>	8.3870000	6.4136667	-0.3870055	3.57E-07	5.35E-07
<i>Actinobacteria</i>	0.1537333	1.5070000	3.2931775	2.55E-07	4.59E-07
<i>Vampirivibrionia</i>	0.4473667	2.2076667	2.3029927	2.58E-08	7.15E-08
<i>Gammaproteobacteria</i>	2.9070000	1.0683333	-1.4441692	6.57E-08	1.48E-07
<i>Desulfovibrionia</i>	0.5774333	0.1263667	-2.1920384	2.73E-09	1.09E-08
<i>Verrucomicrobiae</i>	0.1465000	0.2055000	0.4882377	3.17E-09	1.74E-08
<i>Alphaproteobacteria</i>	0.0309700	0.0390767	0.3354360	8.45E-08	1.69E-07
<i>Negativicutes</i>	0.0313500	0.0140367	-1.1592651	7.41E-08	1.57E-07
Species	Relative abundance in IHF group (90 Days)	Relative abundance in AGF group (90 Days)	Log2FC	P-Value	FDR
<i>Clostridia</i>	61.4633333	46.6433333	-0.3980551	9.11E-07	1.21E-06
<i>Bacteroidia</i>	32.6400000	14.6600000	-1.1547560	1.55E-07	2.78E-07
<i>Bacilli</i>	10.2233333	14.4833333	0.5025280	2.48E-05	2.63E-05
<i>Coriobacteriia</i>	5.2470000	6.3533333	0.2760209	7.26E-07	1.03E-06
<i>Actinobacteria</i>	0.2707000	1.2470000	2.2036947	4.25E-07	6.95E-07
<i>Vampirivibrionia</i>	0.3247000	0.9645000	1.5706739	9.18E-02	5.21E-08
<i>Gammaproteobacteria</i>	0.1896333	0.0733633	-1.3700815	5.33E-07	8.34E-07
<i>Desulfovibrionia</i>	1.8086667	1.7050000	-0.0851548	2.53E-04	2.60E-04
<i>Verrucomicrobiae</i>	0.0910533	0.1166333	0.3571964	1.10E-05	1.24E-05
<i>Alphaproteobacteria</i>	0.0427700	0.1185000	1.4702159	3.15E-06	3.78E-06
<i>Negativicutes</i>	0.1457000	0.0785367	-0.8915626	5.96E-07	8.94E-07

**Table S3. Effect of ryegrass on gut microbial richness of geese at class level**

Table S4. Effect of ryegrass on the gut microbial richness of geese at a family level

Species	Relative abundance in IHF group (45 Days)	Relative abundance in AGF group (45 Days)	Log2FC	P-Value	FDR
<i>Ruminococcaceae</i>	22.133333	8.607	-1.362638	4.16E-07	5.71E-07
<i>Bacteroidaceae</i>	8.884333	23.143333	1.381261	1.19E-06	1.44E-06
<i>Lachnospiraceae</i>	9.985333	8.288333	-0.268729	6.94E-07	8.96E-07
<i>norank_o__Clostridia_UCG-014</i>	8.146	0.989767	-3.040931	8.51E-09	5.67E-08
<i>Oscillospiraceae</i>	4.448333	6.825667	0.617705	1.57E-07	3.31E-07
<i>Rikenellaceae</i>	3.736667	8.908333	1.253404	8.31E-09	5.67E-08
<i>norank_o__RF39</i>	3.033667	0.1326	-4.51591	1.38E-07	3.06E-07
<i>Prevotellaceae</i>	5.265667	3.224333	-0.707615	3.33E-07	4.94E-07
<i>Eubacterium_coprostanoligenes_group</i>	3.375	0.062727	-5.749665	3.97E-08	1.36E-07
<i>Erysipelatoclostridiaceae</i>	4.366667	1.179	-1.888969	2.19E-06	2.57E-06
<i>Enterococcaceae</i>	3.155	0.153766667	-4.358825	2.07E-07	3.95E-07
<i>Eggerthellaceae</i>	1.498333	2.818667	0.911654	3.19E-08	1.36E-07
<i>Peptococcaceae</i>	2.227333	1.647667	-0.434893	2.65E-06	3.02E-06
<i>Christensenellaceae</i>	1.448333	0.6197	-1.224752	4.28E-07	5.71E-07
<i>Lactobacillaceae</i>	0.697533	6.156667	3.141815	4.59E-06	4.96E-06
<i>Peptostreptococcaceae</i>	1.457667	0.02545	-5.839851	1.02E-07	2.62E-07
<i>norank_o__Gastranaerophilales</i>	1.216667	4.904333	2.011123	2.61E-07	4.36E-07
<i>Erysipelotrichaceae</i>	4.4	0.254767	-4.110255	1.16E-03	1.16E-03
<i>Bifidobacteriaceae</i>	1.834667	5.258333	1.519088	2.32E-07	4.06E-07
<i>Butyricicoccaceae</i>	1.083333	2.337667	1.109592	8.83E-07	1.10E-06
<i>Coriobacteriaceae</i>	0.969533	0.126833	-2.934357	7.04E-09	5.67E-08
<i>Tannerellaceae</i>	0.6593	3.343667	2.342424	4.22E-07	5.71E-07
<i>Muribaculaceae</i>	0.795333	2.786667	1.808909	2.75E-06	3.05E-06
<i>Atopobiaceae</i>	1.133333	0.001856	-9.253901	2.12E-04	2.18E-04
<i>Anaerovoracaceae</i>	0.553667	0.189333	-1.548089	1.05E-07	2.62E-07
<i>Desulfovibrionaceae</i>	0.254667	0.3084	0.276193	9.43E-06	9.92E-06
<i>norank_o__Bacteroidales</i>	0.038767	0.8877	4.517184	7.71E-10	2.67E-08
<i>Barnesiellaceae</i>	1.838667	0.3237	-2.505931	4.09E-08	1.36E-07
<i>Streptococcaceae</i>	0.063767	0.339567	2.41282	3.22E-08	1.36E-07
<i>Enterobacteriaceae</i>	0.3676	0.099543	-1.88474	4.09E-08	1.36E-07
<i>norank_o__Clostridia_vadinBB60_group</i>	0.049383	2.185667	5.467905	3.07E-07	4.91E-07
<i>Coriobacteriales_Incertae_Sedis</i>	0.020273	0.459467	4.502305	6.92E-08	1.98E-07
<i>Monoglobaceae</i>	0.085883	0.220733	1.361854	1.35E-07	3.06E-07
<i>UCG-010</i>	0.2047	0.399867	0.966008	2.33E-07	4.06E-07
<i>Succinivibrionaceae</i>	0.022477	0.001107	-4.343701	2.06E-08	1.17E-07
<i>Planococcaceae</i>	0.000369	0.003318	3.168737	6.39E-09	5.67E-08
<i>Akkermansiaceae</i>	0.006267	0.212767	5.085353	5.06E-08	1.56E-07
<i>Marinifilaceae</i>	0.134833	0.019177	-2.813753	2.01E-07	3.95E-07

<i>Anaerofustaceae</i>	0.2925	0.050877	-2.523361	3.20E-07	4.92E-07
<i>unclassified_c__Clostridia</i>	0.026177	0.090683	1.792556	1.34E-09	2.67E-08
Species	Relative abundance in IHF group (60 Days)	Relative abundance in AGF group (60 Days)	Log2FC	P-Value	FDR
<i>Ruminococcaceae</i>	21.606667	10.543333	-1.035145	1.82E-07	4.84E-07
<i>Bacteroidaceae</i>	6.536	8.072	0.304518	2.12E-07	5.02E-07
<i>Lachnospiraceae</i>	3.97	14.536667	1.872486	1.24E-06	1.99E-06
<i>norank_o__Clostridia_UCG-014</i>	11.846667	4.994667	-1.246021	3.83E-07	8.52E-07
<i>Oscillospiraceae</i>	3.095333	4.543667	0.553762	1.30E-06	2.00E-06
<i>Rikenellaceae</i>	3.9733333	4.427	0.155980	0.022095	0.022095
<i>norank_o__RF39</i>	6.394667	3.058	-1.064281	1.25E-07	4.49E-07
<i>Prevotellaceae</i>	4.373	0.9485	-2.204904	1.54E-07	4.49E-07
<i>Eubacterium_coprostanoligenes_group</i>	7.504	2.85	-1.396698	1.87E-06	2.58E-06
<i>Erysipelatoclostridiaceae</i>	2.615667	2.35	-0.154518	6.16E-04	6.32E-04
<i>Enterococcaceae</i>	9.964333	1.706	-2.546156	3.26E-09	3.26E-08
<i>Eggerthellaceae</i>	2.533333	4.263333	0.750945	1.67E-05	1.86E-05
<i>Peptococcaceae</i>	5.593667	0.477433	-3.550423	4.49E-08	2.00E-07
<i>Christensenellaceae</i>	2.386333	1.484333	-0.68498	2.46E-06	3.17E-06
<i>Lactobacillaceae</i>	0.135667	3.667	4.756462	1.78E-10	3.56E-09
<i>Peptostreptococcaceae</i>	2.004333	4.556	1.184645	2.13E-07	5.02E-07
<i>norank_o__Gastranaerophilales</i>	0.4473	2.206333	2.302336	1.21E-07	4.49E-07
<i>Erysipelotrichaceae</i>	1.294667	1.924333	0.571778	5.60E-07	1.13E-06
<i>Bifidobacteriaceae</i>	0.04348	1.463333	5.072763	2.77E-06	3.47E-06
<i>Butyricicoccaceae</i>	0.434833	0.864633	0.991626	2.99E-24	1.19E-22
<i>Coriobacteriaceae</i>	4.105	0.1717	-4.57942	3.91E-08	1.96E-07
<i>Tannerellaceae</i>	0.584633	0.498433	-0.230132	6.73E-07	1.24E-06
<i>Muribaculaceae</i>	0.407333	0.5825	0.516048	9.58E-06	1.09E-05
<i>Atopobiaceae</i>	1.493667	0.548733	-1.444681	1.68E-06	2.40E-06
<i>Anaerovoracaceae</i>	1.087333	0.611567	-0.830213	1.57E-07	4.49E-07
<i>Desulfovibrionaceae</i>	0.126267	0.577333	2.192931	2.73E-09	3.26E-08
<i>norank_o__Bacteroidales</i>	0.714633	1.056667	0.564245	2.30E-06	3.06E-06
<i>Barnesiellaceae</i>	0.711767	0.556367	-0.355368	8.28E-07	1.44E-06
<i>Streptococcaceae</i>	0.290733	0.364333	0.325563	3.69E-06	4.48E-06
<i>Enterobacteriaceae</i>	2.786333	0.085873	-5.020014	7.93E-09	5.69E-08
<i>norank_o__Clostridia_vadinBB60_group</i>	0.126533	0.222567	0.81472	1.51E-06	2.23E-06
<i>Coriobacteriales_Incertae_Sedis</i>	0.212667	1.185	2.478221	5.65E-07	1.13E-06
<i>Monoglobaceae</i>	0.173	0.295567	0.772712	1.38E-04	1.45E-04
<i>UCG-010</i>	0.096567	0.225367	1.222677	8.71E-07	1.45E-06
<i>Succinivibrionaceae</i>	0.9567	0.037667	-4.666706	1.05E-08	6.01E-08
<i>Planococcaceae</i>	0.003676	0.590567	7.327819	8.53E-09	5.69E-08
<i>Akkermansiaceae</i>	0.145367	0.205433	0.498974	1.54E-07	4.49E-07
<i>Marinifilaceae</i>	0.226667	0.102267	-1.148236	8.08E-06	9.50E-06

<i>Anaerofustaceae</i>	0.06708	0.056533	-0.246781	9.23E-05	9.98E-05
<i>unclassified_c__Clostridia</i>	0.05346	0.064867	0.279017	6.83E-07	1.24E-06
Species	Relative abundance in IHF group (90 Days)	Relative abundance in AGF group (90 Days)	Log2FC	P-Value	FDR
<i>Ruminococcaceae</i>	12.583333	18.356667	0.54479	1.67E-07	5.77E-07
<i>Bacteroidaceae</i>	6.726333	14.38	1.096171	9.11E-07	1.92E-06
<i>Lachnospiraceae</i>	9.352667	9.525667	0.026442	1.67E-05	1.91E-05
<i>norank_o__Clostridia_UCG-014</i>	10.746667	9.762333	-0.138591	1.12E-05	1.36E-05
<i>Oscillospiraceae</i>	5.114	10.18	0.993213	2.36E-06	3.49E-06
<i>Rikenellaceae</i>	3.644667	8.455	1.2140179	9.6E-09	1.28E-07
<i>norank_o__RF39</i>	5.885	4.733333	-0.314186	0.000394	0.000404
<i>Prevotellaceae</i>	5.132667	1.594333	-1.686755	4.44E-09	1.28E-07
<i>Eubacterium_coprostanoligenes_group</i>	2.935333	1.236333	-1.247457	1.73E-07	5.77E-07
<i>Erysipelatoclostridiaceae</i>	4.263	2.213667	-0.945431	1.32E-08	1.32E-07
<i>Enterococcaceae</i>	1.398333	0.133333	-3.390599	1.25E-06	2.3E-06
<i>Eggerthellaceae</i>	1.002667	3.946667	1.976793	0.000013	1.53E-05
<i>Peptococcaceae</i>	0.861733	0.648767	-0.409542	1.96E-07	5.81E-07
<i>Christensenellaceae</i>	3.198333	1.894333	-0.75563	1.18E-06	2.3E-06
<i>Lactobacillaceae</i>	0.1267	0.155533	0.295807	1.07E-05	1.34E-05
<i>Peptostreptococcaceae</i>	1.406667	0.683733	-1.040775	6.8E-08	3.02E-07
<i>norank_o__Gastranaerophilales</i>	0.964433	0.324633	-1.57087	4.89E-08	2.44E-07
<i>Erysipelotrichaceae</i>	1.445333	0.907267	-0.671804	2.35E-06	3.49E-06
<i>Bifidobacteriaceae</i>	0.098057	1.237333	3.657475	4.11E-08	2.35E-07
<i>Butyricicoccaceae</i>	1.074	2.835667	1.400694	2.86E-07	7.64E-07
<i>Coriobacteriaceae</i>	1.785	0.817667	-1.126339	4.65E-07	1.1E-06
<i>Tannerellaceae</i>	1.267667	0.4507	-1.491936	4.08E-08	2.35E-07
<i>Muribaculaceae</i>	0.660567	1.287667	0.962983	2.03E-07	5.81E-07
<i>Atopobiaceae</i>	2.124333	1.193	-0.832416	1.6E-06	2.67E-06
<i>Anaerovoracaceae</i>	1.846667	1.125	-0.714998	1.71E-06	2.73E-06
<i>Desulfovibrionaceae</i>	1.704333	1.808	0.085187	0.000253	0.000266
<i>norank_o__Bacteroidales</i>	0.9415	0.949467	0.012156	0.00014	0.000151
<i>Barnesiellaceae</i>	0.439633	0.3577	-0.297551	1.32E-06	2.3E-06
<i>Streptococcaceae</i>	0.8545	1.828	1.097114	6.38E-07	1.42E-06
<i>Enterobacteriaceae</i>	0.065623	0.005528	-3.569379	2.84E-08	2.28E-07
<i>norank_o__Clostridia_vadinBB60_group</i>	0.151833	0.3928	1.371306	9.57E-09	1.28E-07
<i>Coriobacteriales_Incertae_Sedis</i>	0.254433	0.283333	0.155213	5.99E-06	7.98E-06
<i>Monoglobaceae</i>	0.3748	0.4634	0.306137	2.55E-06	3.64E-06
<i>UCG-010</i>	0.183833	0.204567	0.154173	1.29E-06	2.3E-06
<i>Succinivibrionaceae</i>	0.03983	0.024667	-0.691293	6.19E-06	7.98E-06
<i>Planococcaceae</i>	0.004056	0.257333	5.987437	3.47E-06	4.79E-06
<i>Akkermansiaceae</i>	0.09105	0.1165	0.355599	7.72E-08	3.09E-07
<i>Marinifilaceae</i>	0.125667	0.07115	-0.820666	3.16E-07	7.9E-07

<i>Anaerofustaceae</i>	0.04903	0.038633	-0.343819	2.72E-05	3.02E-05
<i>unclassified_c__Clostridia</i>	0.1464	0.148467	0.020224	0.00207	0.00207

**Table S5. Gut microbiota and KEGG orthologues involved in LPS production**

Family	KEGG strains regarding LPS biosynthesis	Correlation	P-value	Adj P-value	Significance
<i>Ruminococcaceae</i>	Bacterial invasion of epithelial cells	0.7812	0.0001	0.0005	***
<i>Ruminococcaceae</i>	Legionellosis	0.4550	0.0578	0.1386	
<i>Ruminococcaceae</i>	Epithelial cell signaling in Helicobacter pylori infection	0.2321	0.3541	0.6912	
<i>Ruminococcaceae</i>	Salmonella infection	0.2922	0.2393	0.4102	
<i>Ruminococcaceae</i>	Pertussis	0.6236	0.0057	0.0091	**
<i>Ruminococcaceae</i>	Vibrio cholerae infection	0.1813	0.4715	0.6708	
<i>Bacteroidaceae</i>	Bacterial invasion of epithelial cells	-0.6212	0.0059	0.0071	**
<i>Bacteroidaceae</i>	Legionellosis	-0.2588	0.2998	0.4498	
<i>Bacteroidaceae</i>	Epithelial cell signaling in Helicobacter pylori infection	-0.4810	0.0433	0.1299	*
<i>Bacteroidaceae</i>	Salmonella infection	-0.3650	0.1364	0.3274	
<i>Bacteroidaceae</i>	Pertussis	-0.8782	0.0000	0.0000	***
<i>Bacteroidaceae</i>	Vibrio cholerae infection	-0.5081	0.0313	0.0752	*
<i>Lachnospiraceae</i>	Bacterial invasion of epithelial cells	-0.5630	0.0150	0.0163	*
<i>Lachnospiraceae</i>	Legionellosis	-0.1201	0.6349	0.7619	
<i>Lachnospiraceae</i>	Epithelial cell signaling in Helicobacter pylori infection	0.0865	0.7328	0.8564	
<i>Lachnospiraceae</i>	Salmonella infection	-0.2964	0.2324	0.4102	
<i>Lachnospiraceae</i>	Pertussis	-0.2175	0.3859	0.3859	
<i>Lachnospiraceae</i>	Vibrio cholerae infection	-0.0442	0.8618	0.8618	
<i>norank_o__Clostridia_UCG-014</i>	Bacterial invasion of epithelial cells	0.6676	0.0025	0.0037	**
<i>norank_o__Clostridia_UCG-014</i>	Legionellosis	0.4894	0.0393	0.1178	*
<i>norank_o__Clostridia_UCG-014</i>	Epithelial cell signaling in Helicobacter pylori infection	0.7280	0.0006	0.0037	***
<i>norank_o__Clostridia_UCG-014</i>	Salmonella infection	0.0239	0.9251	0.9251	
<i>norank_o__Clostridia_UCG-014</i>	Pertussis	0.6260	0.0054	0.0091	**
<i>norank_o__Clostridia_UCG-014</i>	Vibrio cholerae infection	0.1205	0.6338	0.7481	
<i>Oscillospiraceae</i>	Bacterial invasion of epithelial cells	-0.6302	0.0051	0.0067	**
<i>Oscillospiraceae</i>	Legionellosis	0.0890	0.7253	0.7913	
<i>Oscillospiraceae</i>	Epithelial cell signaling in Helicobacter pylori infection	0.3306	0.1803	0.4327	
<i>Oscillospiraceae</i>	Salmonella infection	-0.8666	0.0000	0.0000	***
<i>Oscillospiraceae</i>	Pertussis	-0.8019	0.0001	0.0002	***
<i>Oscillospiraceae</i>	Vibrio cholerae infection	-0.7021	0.0012	0.0046	**
<i>Rikenellaceae</i>	Bacterial invasion of epithelial cells	-0.7054	0.0011	0.0023	**



<i>Rikenellaceae</i>	Legionellosis	-0.2827	0.2556	0.4382	
<i>Rikenellaceae</i>	Epithelial cell signaling in Helicobacter pylori infection	-0.2038	0.4173	0.6912	
<i>Rikenellaceae</i>	Salmonella infection	-0.5458	0.0191	0.0573	*
<i>Rikenellaceae</i>	Pertussis	-0.8866	0.0000	0.0000	***
<i>Rikenellaceae</i>	Vibrio cholerae infection	-0.5117	0.0299	0.0752	*
<i>norank_o_RF39</i>	Bacterial invasion of epithelial cells	0.5459	0.0191	0.0191	*
<i>norank_o_RF39</i>	Legionellosis	0.3057	0.2173	0.4347	
<i>norank_o_RF39</i>	Epithelial cell signaling in Helicobacter pylori infection	0.7277	0.0006	0.0037	***
<i>norank_o_RF39</i>	Salmonella infection	0.0469	0.8534	0.9251	
<i>norank_o_RF39</i>	Pertussis	0.6198	0.0061	0.0091	**
<i>norank_o_RF39</i>	Vibrio cholerae infection	0.2324	0.3533	0.6057	
<i>Prevotellaceae</i>	Bacterial invasion of epithelial cells	0.8187	0.0000	0.0004	***
<i>Prevotellaceae</i>	Legionellosis	0.6896	0.0015	0.0062	**
<i>Prevotellaceae</i>	Epithelial cell signaling in Helicobacter pylori infection	0.0488	0.8474	0.8564	
<i>Prevotellaceae</i>	Salmonella infection	0.2666	0.2849	0.4274	
<i>Prevotellaceae</i>	Pertussis	0.3968	0.1030	0.1236	
<i>Prevotellaceae</i>	Vibrio cholerae infection	-0.1688	0.5031	0.6708	
<i>Eubacterium_coprostanoligenes_group</i>	Bacterial invasion of epithelial cells	0.7803	0.0001	0.0005	***
<i>Eubacterium_coprostanoligenes_group</i>	Legionellosis	-0.0268	0.9160	0.9160	
<i>Eubacterium_coprostanoligenes_group</i>	Epithelial cell signaling in Helicobacter pylori infection	0.0459	0.8564	0.8564	
<i>Eubacterium_coprostanoligenes_group</i>	Salmonella infection	0.7393	0.0005	0.0018	***
<i>Eubacterium_coprostanoligenes_group</i>	Pertussis	0.9282	0.0000	0.0000	***
<i>Eubacterium_coprostanoligenes_group</i>	Vibrio cholerae infection	0.7297	0.0006	0.0045	***
<i>Erysipelatoclostridiaceae</i>	Bacterial invasion of epithelial cells	0.6954	0.0014	0.0023	**
<i>Erysipelatoclostridiaceae</i>	Legionellosis	0.8117	0.0000	0.0005	***
<i>Erysipelatoclostridiaceae</i>	Epithelial cell signaling in Helicobacter pylori infection	0.5156	0.0285	0.1141	*
<i>Erysipelatoclostridiaceae</i>	Salmonella infection	0.0375	0.8826	0.9251	
<i>Erysipelatoclostridiaceae</i>	Pertussis	0.5640	0.0148	0.0197	*
<i>Erysipelatoclostridiaceae</i>	Vibrio cholerae infection	-0.1025	0.6858	0.7481	
<i>Enterococcaceae</i>	Bacterial invasion of epithelial cells	0.7481	0.0004	0.0011	***
<i>Enterococcaceae</i>	Legionellosis	-0.1335	0.5976	0.7619	
<i>Enterococcaceae</i>	Epithelial cell signaling in Helicobacter pylori infection	-0.1629	0.5184	0.6912	
<i>Enterococcaceae</i>	Salmonella infection	0.8053	0.0001	0.0003	***
<i>Enterococcaceae</i>	Pertussis	0.8240	0.0000	0.0001	***
<i>Enterococcaceae</i>	Vibrio cholerae infection	0.7205	0.0007	0.0045	***
<i>Eggerthellaceae</i>	Bacterial invasion of epithelial cells	-0.6965	0.0013	0.0023	**
<i>Eggerthellaceae</i>	Legionellosis	-0.7564	0.0003	0.0017	***

<i>Eggerthellaceae</i>	Epithelial cell signaling in Helicobacter pylori infection	-0.1672	0.5072	0.6912	
<i>Eggerthellaceae</i>	Salmonella infection	-0.0952	0.7071	0.9251	
<i>Eggerthellaceae</i>	Pertussis	-0.2843	0.2528	0.2758	
<i>Eggerthellaceae</i>	Vibrio cholerae infection	0.3031	0.2215	0.4430	

**Table S6. Effect of ryegrass on the relationship of gut microbiota at class level and SCFAs**

<b>Class</b>	<b>SCFAs</b>	<b>Correlation</b>	<b>P-value</b>	<b>Adj P-value</b>	<b>Significance</b>
<i>Clostridia</i>	Acetic acid	-0.760860651	0.000245813	0.000807587	***
<i>Clostridia</i>	Propionic acid	-0.596365112	0.008993928	0.019588471	**
<i>Clostridia</i>	Butyric acid	-0.275107922	0.269210243	0.423044667	
<i>Clostridia</i>	Isovaleric acid	-0.616862556	0.006393533	0.011721477	**
<i>Clostridia</i>	Valeric acid	-0.743142063	0.000409572	0.001501762	***
<i>Bacteroidia</i>	Acetic acid	0.747065026	0.000367085	0.000807587	***
<i>Bacteroidia</i>	Propionic acid	0.585489825	0.010684621	0.019588471	*
<i>Bacteroidia</i>	Butyric acid	0.382701362	0.117006009	0.214511016	
<i>Bacteroidia</i>	Isovaleric acid	0.660509643	0.002847679	0.006264895	**
<i>Bacteroidia</i>	Valeric acid	0.690451586	0.001514367	0.004164508	**
<i>Bacilli</i>	Acetic acid	-0.059546753	0.81443691	0.81443691	
<i>Bacilli</i>	Propionic acid	-0.042888517	0.865816902	0.865816902	
<i>Bacilli</i>	Butyric acid	-0.137166979	0.587303383	0.646033722	
<i>Bacilli</i>	Isovaleric acid	-0.225329295	0.368652895	0.368652895	
<i>Bacilli</i>	Valeric acid	-0.027773637	0.91288959	0.91288959	
<i>Coriobacteriia</i>	Acetic acid	-0.750289603	0.000334995	0.000807587	***
<i>Coriobacteriia</i>	Propionic acid	-0.615231128	0.006575051	0.018081389	**
<i>Coriobacteriia</i>	Butyric acid	-0.535070837	0.022130606	0.060859168	*
<i>Coriobacteriia</i>	Isovaleric acid	-0.804710516	5.65E-05	0.000621147	***
<i>Coriobacteriia</i>	Valeric acid	-0.547085879	0.018787949	0.034444574	*
<i>Actinobacteria</i>	Acetic acid	0.282118009	0.256699181	0.352961374	
<i>Actinobacteria</i>	Propionic acid	0.205654663	0.412965663	0.567827787	
<i>Actinobacteria</i>	Butyric acid	0.105539165	0.676834527	0.676834527	
<i>Actinobacteria</i>	Isovaleric acid	0.675201286	0.002107151	0.005794665	**
<i>Actinobacteria</i>	Valeric acid	0.141273895	0.5760514	0.704062822	
<i>Vampirivibrionia</i>	Acetic acid	0.858516074	5.13E-06	2.82E-05	***
<i>Vampirivibrionia</i>	Propionic acid	0.752317227	0.000316052	0.001738285	***
<i>Vampirivibrionia</i>	Butyric acid	0.39450113	0.105217636	0.214511016	
<i>Vampirivibrionia</i>	Isovaleric acid	0.775033003	0.000158301	0.000870656	***
<i>Vampirivibrionia</i>	Valeric acid	0.848006077	8.79E-06	4.83E-05	***
<i>Gammaproteobacteria</i>	Acetic acid	-0.584250244	0.010892466	0.017116733	*
<i>Gammaproteobacteria</i>	Propionic acid	-0.495291065	0.036618501	0.057543358	*
<i>Gammaproteobacteria</i>	Butyric acid	-0.649178796	0.003554555	0.01955005	**

<i>Gammaproteobacteria</i>	Isovaleric acid	-0.38964613	0.109960148	0.134395736	
<i>Gammaproteobacteria</i>	Valeric acid	-0.367365434	0.133685619	0.210077401	
<i>Desulfovibrionia</i>	Acetic acid	-0.204855733	0.414822928	0.507005801	
<i>Desulfovibrionia</i>	Propionic acid	-0.178886422	0.477564086	0.583689439	
<i>Desulfovibrionia</i>	Butyric acid	0.218446909	0.383839731	0.469137449	
<i>Desulfovibrionia</i>	Isovaleric acid	-0.463484786	0.052716169	0.082839694	
<i>Desulfovibrionia</i>	Valeric acid	-0.262926382	0.291832761	0.401270046	
<i>Verrucomicrobiae</i>	Acetic acid	-0.674859318	0.002122366	0.003891004	**
<i>Verrucomicrobiae</i>	Propionic acid	-0.625309366	0.005517479	0.018081389	**
<i>Verrucomicrobiae</i>	Butyric acid	-0.56139749	0.015340034	0.05624679	*
<i>Verrucomicrobiae</i>	Isovaleric acid	-0.442374823	0.066021251	0.09077922	
<i>Verrucomicrobiae</i>	Valeric acid	-0.675302275	0.002102675	0.004625885	**
<i>Alphaproteobacteria</i>	Acetic acid	0.895861132	0	5.49E-06	***
<i>Alphaproteobacteria</i>	Propionic acid	0.866090727	3.39E-06	3.73E-05	***
<i>Alphaproteobacteria</i>	Butyric acid	0.661119518	0.002813183	0.01955005	**
<i>Alphaproteobacteria</i>	Isovaleric acid	0.743842552	0.000401696	0.001472886	***
<i>Alphaproteobacteria</i>	Valeric acid	0.888353753	8.51E-07	9.36E-06	***
<i>Negativicutes</i>	Acetic acid	0.177021289	0.482242506	0.530466756	
<i>Negativicutes</i>	Propionic acid	0.05958413	0.814322352	0.865816902	
<i>Negativicutes</i>	Butyric acid	0.245332174	0.326475723	0.448904119	
<i>Negativicutes</i>	Isovaleric acid	0.298804715	0.228408411	0.251249252	
<i>Negativicutes</i>	Valeric acid	-0.058013169	0.81914022	0.901054242	

**Table S7. Effect of ryegrass on the relationship of gut microbiota at a family level and SCFAs**

Family	SCFAs	Correlation	P-value	Adj P-value	Significance
<i>Ruminococcaceae</i>	Acetic acid	-0.5828454	0.0111319	0.0190833	*
<i>Ruminococcaceae</i>	Propionic acid	-0.4575359	0.0562406	0.0749875	
<i>Ruminococcaceae</i>	Butyric acid	-0.2415943	0.3341332	0.445511	
<i>Ruminococcaceae</i>	Isovaleric acid	-0.2423201	0.3326381	0.4989571	
<i>Ruminococcaceae</i>	Valeric acid	-0.5956671	0.0090955	0.0155923	**
<i>Bacteroidaceae</i>	Acetic acid	0.91292962	1.26E-07	1.51E-06	***
<i>Bacteroidaceae</i>	Propionic acid	0.92041418	6.29E-08	7.55E-07	***
<i>Bacteroidaceae</i>	Butyric acid	0.79392723	8.37E-05	0.0003418	***
<i>Bacteroidaceae</i>	Isovaleric acid	0.76442845	0.0002207	0.0013239	***
<i>Bacteroidaceae</i>	Valeric acid	0.86549546	3.50E-06	4.20E-05	***
<i>Lachnospiraceae</i>	Acetic acid	0.12276315	0.6274701	0.6845128	
<i>Lachnospiraceae</i>	Propionic acid	0.06583131	0.7952275	0.7952275	
<i>Lachnospiraceae</i>	Butyric acid	0.05964273	0.8141428	0.8141428	
<i>Lachnospiraceae</i>	Isovaleric acid	-0.0583754	0.8180288	0.8180288	
<i>Lachnospiraceae</i>	Valeric acid	0.0345728	0.8916715	0.8916715	

<i>norank_o__Clostridia_UCG-014</i>	Acetic acid	-0.8330951	1.77E-05	7.07E-05	***
<i>norank_o__Clostridia_UCG-014</i>	Propionic acid	-0.7583392	0.000265	0.0007274	***
<i>norank_o__Clostridia_UCG-014</i>	Butyric acid	-0.4358307	0.0706124	0.1210499	
<i>norank_o__Clostridia_UCG-014</i>	Isovaleric acid	-0.7341886	0.0005222	0.0020889	***
<i>norank_o__Clostridia_UCG-014</i>	Valeric acid	-0.8034709	5.92E-05	0.0003549	***
<i>Oscillospiraceae</i>	Acetic acid	0.43131856	0.0739127	0.0985503	
<i>Oscillospiraceae</i>	Propionic acid	0.53125422	0.0232846	0.0349269	*
<i>Oscillospiraceae</i>	Butyric acid	0.7933386	8.55E-05	0.0003418	***
<i>Oscillospiraceae</i>	Isovaleric acid	0.13405773	0.5958825	0.6500536	
<i>Oscillospiraceae</i>	Valeric acid	0.33763408	0.1706049	0.2274731	
<i>Rikenellaceae</i>	Acetic acid	0.72096771	0.0007352	0.0017645	***
<i>Rikenellaceae</i>	Propionic acid	0.80096213	6.49E-05	0.0002597	***
<i>Rikenellaceae</i>	Butyric acid	0.81743235	3.44E-05	0.0003418	***
<i>Rikenellaceae</i>	Isovaleric acid	0.47868561	0.0444666	0.1067198	*
<i>Rikenellaceae</i>	Valeric acid	0.69710176	0.0013032	0.0039097	**
<i>norank_o__RF39</i>	Acetic acid	-0.8660976	3.39E-06	2.03E-05	***
<i>norank_o__RF39</i>	Propionic acid	-0.8011408	6.45E-05	0.0002597	***
<i>norank_o__RF39</i>	Butyric acid	-0.5274954	0.0244666	0.0489331	*
<i>norank_o__RF39</i>	Isovaleric acid	-0.8504904	7.77E-06	9.32E-05	***
<i>norank_o__RF39</i>	Valeric acid	-0.7900829	9.58E-05	0.0003831	***
<i>Prevotellaceae</i>	Acetic acid	-0.1293386	0.6090011	0.6845128	
<i>Prevotellaceae</i>	Propionic acid	-0.2398059	0.3378335	0.4054002	
<i>Prevotellaceae</i>	Butyric acid	-0.2229378	0.3738913	0.4486696	
<i>Prevotellaceae</i>	Isovaleric acid	0.17956409	0.4758698	0.6344931	
<i>Prevotellaceae</i>	Valeric acid	-0.2038791	0.4170993	0.5005192	
<i>Eubacterium_coprostanoligenes_group</i>	Acetic acid	-0.7999961	6.73E-05	0.0002018	***
<i>Eubacterium_coprostanoligenes_group</i>	Propionic acid	-0.7537672	0.0003031	0.0007274	***
<i>Eubacterium_coprostanoligenes_group</i>	Butyric acid	-0.7827986	0.0001227	0.0003682	***
<i>Eubacterium_coprostanoligenes_group</i>	Isovaleric acid	-0.5255044	0.0251114	0.0753341	*
<i>Eubacterium_coprostanoligenes_group</i>	Valeric acid	-0.6525184	0.0033327	0.0079986	**
<i>Erysipelatoclostridiaceae</i>	Acetic acid	-0.5100922	0.0305622	0.0458432	*
<i>Erysipelatoclostridiaceae</i>	Propionic acid	-0.598447	0.0086963	0.0173926	**
<i>Erysipelatoclostridiaceae</i>	Butyric acid	-0.3963547	0.1034463	0.1551694	
<i>Erysipelatoclostridiaceae</i>	Isovaleric acid	-0.2963813	0.2323871	0.3983778	
<i>Erysipelatoclostridiaceae</i>	Valeric acid	-0.6332507	0.0047854	0.0095707	**
<i>Enterococcaceae</i>	Acetic acid	-0.6304261	0.0050361	0.0100722	**
<i>Enterococcaceae</i>	Propionic acid	-0.5686779	0.0137901	0.0236402	*
<i>Enterococcaceae</i>	Butyric acid	-0.6642466	0.0026417	0.00634	**
<i>Enterococcaceae</i>	Isovaleric acid	-0.3278104	0.1841826	0.3683652	
<i>Enterococcaceae</i>	Valeric acid	-0.4672694	0.0505622	0.0758434	
<i>Eggerthellaceae</i>	Acetic acid	0.07446043	0.7690354	0.7690354	
<i>Eggerthellaceae</i>	Propionic acid	0.21938272	0.3817547	0.4164597	

<i>Eggerthellaceae</i>	Butyric acid	0.17075289	0.498129	0.5434135	
<i>Eggerthellaceae</i>	Isovaleric acid	-0.1544552	0.5405751	0.6486901	
<i>Eggerthellaceae</i>	Valeric acid	0.17964852	0.4756589	0.5189007	

**Table S8: Effect of ryegrass on the relationship of gut microbiota and host markers**

Family	Host markers	Correlation	P-value
<i>Ruminococcaceae</i>	NLRP3	0.822088731	2.84E-05
<i>norank_o_Clostridia_UCG-014</i>	T-AOC	-0.87738917	1.74E-06
<i>norank_o_Clostridia_UCG-014</i>	CAT	-0.816130055	3.62E-05
<i>Oscillospiraceae</i>	IgM	0.921699728	5.55E-08
<i>Oscillospiraceae</i>	IgD	0.828379199	2.18E-05
<i>Oscillospiraceae</i>	MDA	-0.824228115	2.60E-05
<i>Oscillospiraceae</i>	NFE2L2	0.93727161	9.89E-09
<i>Oscillospiraceae</i>	B220	0.855771889	5.93E-06
<i>Oscillospiraceae</i>	CD8	0.933653344	1.53E-08
<i>Oscillospiraceae</i>	CD3	0.964208136	1.21E-10
<i>Rikenellaceae</i>	GSR	0.828623167	2.15E-05
<i>Rikenellaceae</i>	NFE2L2	0.865444978	3.51E-06
<i>Rikenellaceae</i>	CD3	0.879847477	1.49E-06
<i>norank_o_RF39</i>	T-AOC	-0.822880024	2.75E-05
<i>norank_o_RF39</i>	HDAC	0.800443762	6.62E-05
<i>Prevotellaceae</i>	IgG	-0.897932876	4.28E-07
<i>Prevotellaceae</i>	GSH-Px	-0.87194576	2.41E-06
<i>Prevotellaceae</i>	IgA	-0.807517949	5.08E-05
<i>Prevotellaceae</i>	T-SOD	-0.953818377	9.00E-10
<i>Prevotellaceae</i>	ROS	0.953977261	8.76E-10
<i>Prevotellaceae</i>	AA	-0.810389247	4.55E-05
<i>Prevotellaceae</i>	PA	-0.907072702	2.08E-07
<i>Prevotellaceae</i>	BA	-0.866175564	3.37E-06
<i>Prevotellaceae</i>	Nrf2	-0.926249343	3.49E-08
<i>Prevotellaceae</i>	HO-1	-0.944498827	3.80E-09
<i>Prevotellaceae</i>	CD19	-0.833654984	1.72E-05
<i>Prevotellaceae</i>	IL-10	-0.91581898	9.71E-08
<i>Prevotellaceae</i>	AMPK	-0.832031217	1.85E-05
<i>Prevotellaceae</i>	IL-4	-0.900934841	3.40E-07
<i>Prevotellaceae</i>	TGF-B	0.876003461	1.89E-06
<i>Prevotellaceae</i>	Inos	0.858188024	5.22E-06
<i>Eubacterium_coprostanoligenes_group</i>	IgM	-0.840840735	1.24E-05
<i>Eubacterium_coprostanoligenes_group</i>	GSR	-0.810477604	4.53E-05
<i>Eubacterium_coprostanoligenes_group</i>	MDA	0.813679292	4.00E-05
<i>Eubacterium_coprostanoligenes_group</i>	Keap1	0.974434551	8.47E-12
<i>Erysipelatoclostridiaceae</i>	Nrf2	-0.819918375	3.11E-05
<i>Erysipelatoclostridiaceae</i>	TGF-B	0.856131446	5.82E-06
<i>Erysipelatoclostridiaceae</i>	iNOS	0.889662623	7.77E-07
<i>Enterococcaceae</i>	IgM	-0.844572326	1.04E-05
<i>Enterococcaceae</i>	Keap1	0.987353424	3.16E-14
<i>Eggerthellaceae</i>	GSH-Px	0.891038582	7.06E-07
<i>Eggerthellaceae</i>	T-SOD	0.851112813	7.53E-06
<i>Eggerthellaceae</i>	ROS	-0.94904994	1.95E-09
<i>Eggerthellaceae</i>	PA	0.878140621	1.66E-06

<i>Eggerthellaceae</i>	BA	0.816194259	3.61E-05
<i>Eggerthellaceae</i>	Nrf2	0.923655303	4.56E-08
<i>Eggerthellaceae</i>	HO-1	0.86318937	3.98E-06
<i>Eggerthellaceae</i>	IL-10	0.85147303	7.39E-06
<i>Eggerthellaceae</i>	IL-4	0.858606369	5.10E-06
<i>Eggerthellaceae</i>	TGF-B	-0.821636212	2.89E-05
<i>Eggerthellaceae</i>	iNOS	-0.829187199	2.10E-05