Table S1. Microbial identification by 16s ribosomal RNA sequencing

Sample name: BS211229

Number of bases: 1492 bps   GC: 50.8%   AT: 49.2%

Primer: 27F and 1429R

GCTTGCTCCCTGATGTTAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCCGGGAAACCGGGGCTAATACCGGATGGTTGTTTGAACCGCATGGT
TCAGACATAAAAGGTGGCTTCGGCTACCACTTACAGATGGACCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGATC
GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGTTTTCG
GATCGTAAAGCTCTGTTGTTAGGGAAGAACAAGTGCCGTTCAAATAGGGCGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTA
GGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGGGCTCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAAACTGGGGAACTTGAG
TGCAGAAGAGGAGAGTGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAACACCAGTGGCGAAGGCGACTCTCTGGTCTGTAACTGACGCTGAGGAGCGAAAGCG
TGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGG
AGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCTCTGA
CAATCCTAGAGATAGGACGTCCCCTTCGGGGGCAGAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGATCTT
AGTTGCCAGCATTCAGTTGGGCACTCTAAGGTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTGCTACAAT
GGACAGAACAAAGGGCAGCGAAACCGCGAGGTTAAGCCAATCCCACAAATCTGTTCTCAGTTCGGATCGCAGTCTGCAACTCGACTGCGTGAAGCTGGAATCGCTAGTAATCGCGG
ATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTT

BLASTN 2.2.30+ Database: Nucleotide collection (nt)   57,030,965 sequences;   257,768,224,489 total letters
Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

Description	Scientific Name	Max Score	Total Score	Query Cover	Percent Identity	Accession Length	Accession
Bacillus subtilis strain JCM 1465 16S ribosomal RNA, partial sequence	Bacillus subtilis	2466	2466	100%	99.63	1472	NR_113265.1
Bacillus subtilis strain NBRC 13719 16S ribosomal RNA, partial sequence	Bacillus subtilis	2466	2466	100%	99.63	1475	NR_112629.1
Bacillus subtilis strain DSM 10 16S ribosomal RNA, partial sequence	Bacillus subtilis	2466	2466	100%	99.63	1517	NR_027552.1
Bacillus subtilis strain IAM 12118 16S ribosomal RNA, complete sequence	Bacillus subtilis	2460	2460	100%	99.56	1550	NR_112116.2
Bacillus subtilis strain BCRC 10255 16S ribosomal RNA, partial sequence	Bacillus subtilis	2460	2460	100%	99.56	1468	NR_116017.1
Bacillus subtilis strain NCDO 1769 16S ribosomal RNA, partial sequence	Bacillus subtilis	2416	2416	100%	98.96	1427	NR_118972.1
Bacillus subtilis strain SBMP4 16S ribosomal RNA, partial sequence	Bacillus subtilis	2399	2399	100%	98.74	1463	NR_118383.1
Bacillus subtilis strain NRRL NRS-744 16S ribosomal RNA, partial sequence	Bacillus subtilis	2130	2130	86%	99.57	1168	NR_116192.1
Bacillus subtilis strain NRRL B-4219 16S ribosomal RNA, partial sequence	Bacillus subtilis	2130	2130	86%	99.57	1168	NR_116183.1

Company: Cosmogenetech co, Ltd.

Website: www.cosmogenetech.com

Table S2. Western blot antibodies information

Peptide/Protein target	Manufacturer	Catalog	Dilution ratio
Actin	Thermo Fisher scientific	MA 5-11869	1:1,000
GPAM	abcam	ab69990	1:1,000
SREBP-1	abcam	ab28481	1:1,000
Total AMPK-α	Cell signaling technology	#5831	1:1,000
Phospho AMPK-α	Cell signaling technology	#2535	1:1,000
PPAR-α	abcam	ab24509	1:1,000
Nrf2	Cell signaling technology	#12721	1:1,000
Lamin B1	abcam	ab16048	1:1,000
HO-1	Thermo Fisher scientific	MA1-112	1:1,000
Goat Anti-Rabbit IgG (HRP)	GeneTex	GTX213110-01	1:5,000
Goat Anti-Mouse IgG (HRP)	GeneTex	GTX213111-01	1:5,000

Abbreviations: GAMP, Glycerol-3-Phosphate Acyltransferase, Mitochondrial; PPAR- α, Peroxisome proliferator-activated receptor; AMPK, AMP-activated protein kinase; FAS, fatty acid synthase; SREBP-1, Sterol regulatory element-binding protein 1; Nrf2, Nuclear factor E2-related factor; HO-1, Heme oxygenase-1; HRP, horseradish peroxidase; IgG, Immunoglobulin G.
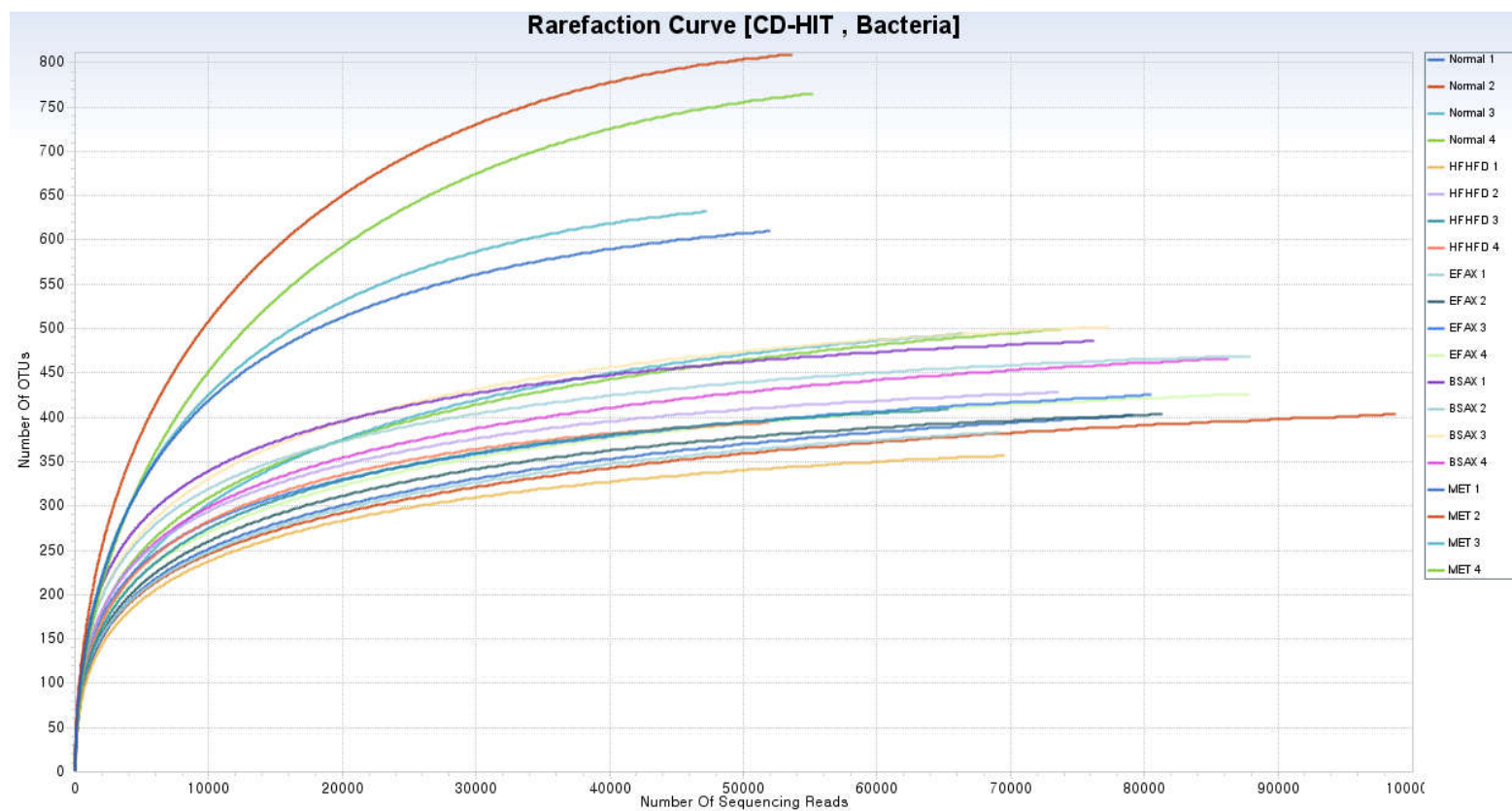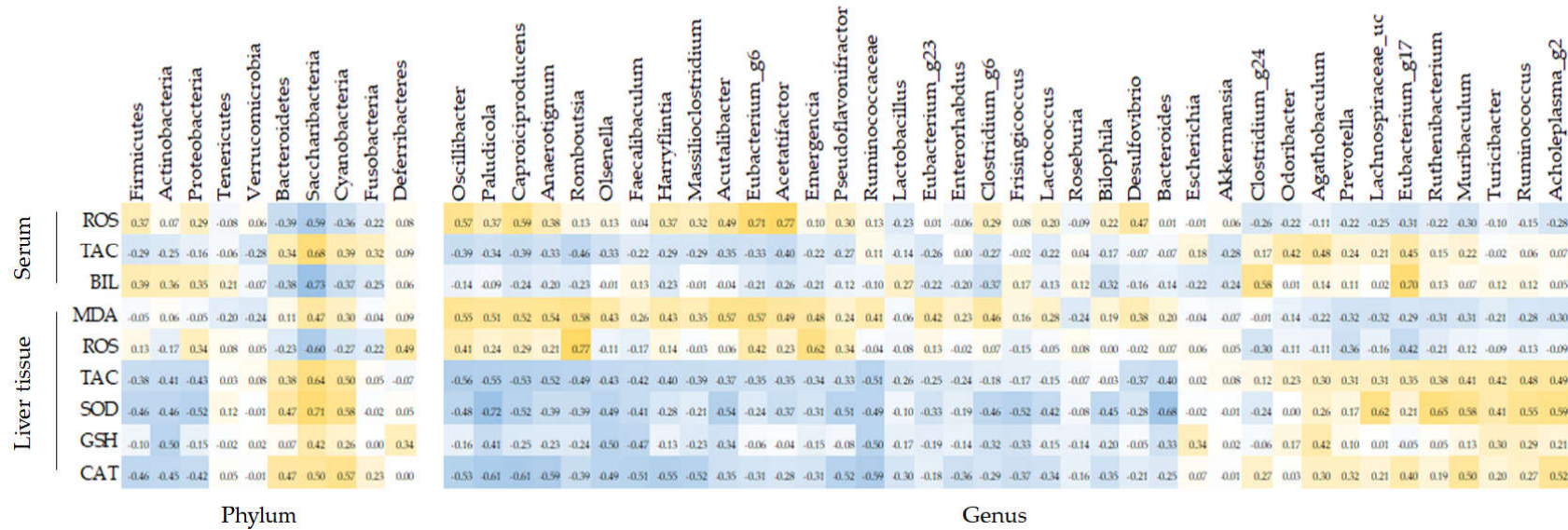
Figure S1. Data of rarefaction curve

Figure S2. Correlation between gut microbiota and oxidative stress-related parameters

Phylum

	Firmicutes	Actinobacteria	Proteobacteria	Tenericutes	Verrucomicrobia	Bacteroidetes	Saccharibacteria	Cyanobacteria	Fusobacteria	Deferribacteres
Serum ROS	0.37	0.07	0.29	-0.08	0.06	-0.39	-0.59	-0.36	-0.22	0.08
Serum TAC	-0.29	-0.25	-0.16	-0.06	-0.28	0.34	0.68	0.39	0.32	0.09
Serum BIL	0.39	0.36	0.35	0.21	-0.07	-0.38	-0.73	-0.37	-0.25	0.06
Liver MDA	-0.05	0.06	-0.05	-0.20	-0.24	0.11	0.47	0.30	-0.04	0.09
Liver ROS	0.13	0.17	0.34	0.08	0.05	-0.23	-0.60	-0.27	-0.22	0.49
Liver TAC	-0.38	-0.41	-0.43	0.03	0.08	0.38	0.64	0.50	0.05	-0.07
Liver SOD	-0.46	-0.46	-0.52	0.12	-0.01	0.47	0.71	0.58	0.02	0.05
Liver GSH	-0.10	-0.50	-0.15	-0.02	0.02	0.07	0.42	0.26	0.00	0.34
Liver CAT	-0.46	-0.45	-0.42	0.05	-0.01	0.47	0.50	0.57	0.23	0.00

Genus

	Oscillibacter	Paludicola	Caproiciproducens	Anaerotignum	Romboutsia	Olsenella	Faecalibaculum	Harryflintia	Massilioclostridium	Acutalibacter	Eubacterium_g6	Acetatifactor	Emergencia	Pseudoflavonifractor	Ruminococcaceae	Lactobacillus	Eubacterium_g23	Enterorhabdus	Clostridium_g6	Frisingicoccus	Lactococcus	Roseburia	Bilophila	Desulfovibrio	Bacteroides	Escherichia	Akkermansia	Clostridium_g24	Odoribacter	Agathobaculum	Prevotella	Lachnospiraceae_uc	Eubacterium_g17	Ruthenibacterium	Muribaculum	Turicibacter	Ruminococcus	Acholeplasma_g2
Serum ROS	0.57	0.37	0.59	0.38	0.13	0.13	0.04	0.37	0.32	0.49	0.71	0.77	0.10	0.30	0.13	-0.23	0.01	-0.06	0.29	0.08	0.20	-0.09	0.22	0.47	0.01	-0.01	0.06	-0.26	-0.22	-0.11	-0.22	-0.25	-0.31	-0.22	-0.30	-0.10	-0.15	-0.28
Serum TAC	-0.39	-0.34	-0.39	-0.33	-0.46	-0.33	-0.22	-0.29	-0.29	-0.35	-0.33	-0.40	-0.22	-0.27	0.11	0.14	-0.26	0.00	-0.27	-0.02	-0.22	0.04	0.17	-0.07	-0.07	0.18	0.28	0.17	0.42	0.48	0.24	0.21	0.45	0.15	0.22	-0.02	0.06	0.07
Serum BIL	-0.14	-0.09	-0.24	0.20	-0.23	0.01	0.13	0.23	-0.01	0.04	-0.21	-0.26	-0.21	0.12	-0.10	0.27	-0.22	-0.20	-0.37	0.17	0.13	0.12	0.32	-0.16	0.14	-0.22	0.24	0.58	0.01	0.14	0.11	0.02	0.70	0.13	0.07	0.12	0.12	0.05
Liver MDA	0.55	0.51	0.52	0.54	0.58	0.43	0.26	0.43	0.35	0.57	0.57	0.49	0.48	0.24	0.41	-0.06	0.42	0.23	0.46	0.16	0.28	-0.24	0.19	0.38	0.20	-0.04	0.07	-0.01	-0.14	-0.22	-0.32	-0.32	0.29	-0.31	-0.31	-0.21	-0.28	-0.30
Liver ROS	0.41	0.24	0.29	0.21	0.77	0.11	-0.17	0.14	-0.03	0.06	0.42	0.23	0.62	0.34	-0.04	-0.08	0.13	-0.02	0.07	-0.15	-0.05	0.08	0.00	-0.02	0.07	0.06	0.05	-0.30	-0.11	-0.11	-0.36	-0.16	-0.42	-0.21	0.12	-0.09	0.13	-0.09
Liver TAC	-0.56	-0.55	-0.53	-0.52	-0.49	-0.43	-0.42	-0.40	-0.39	-0.37	-0.35	-0.35	-0.34	-0.33	-0.51	0.26	-0.25	-0.24	-0.18	-0.17	-0.15	-0.07	-0.03	-0.37	0.40	0.02	0.08	0.12	0.23	0.30	0.31	0.31	0.35	0.38	0.41	0.42	0.48	0.49
Liver SOD	-0.48	-0.72	-0.52	-0.39	-0.39	-0.49	-0.41	-0.28	-0.21	0.54	-0.24	-0.37	-0.31	-0.51	-0.49	-0.10	-0.33	-0.19	-0.46	-0.52	0.42	-0.08	0.45	-0.28	0.68	-0.02	-0.01	-0.24	0.00	0.26	0.17	0.62	0.21	0.65	0.58	0.41	0.55	0.59
Liver GSH	-0.16	-0.41	-0.25	0.23	-0.24	-0.50	-0.47	0.13	-0.23	0.34	-0.06	-0.04	-0.15	-0.08	-0.50	0.17	-0.19	-0.14	-0.32	-0.33	0.15	-0.14	0.20	-0.05	0.33	0.34	0.02	-0.06	0.17	0.42	0.10	0.01	-0.05	0.05	0.13	0.30	0.29	0.21
Liver CAT	-0.53	-0.61	-0.61	-0.59	-0.39	-0.49	-0.51	-0.55	-0.52	0.35	-0.31	-0.28	-0.31	-0.52	-0.59	0.30	-0.18	-0.36	-0.29	-0.37	-0.34	-0.16	-0.35	-0.21	0.25	0.07	-0.01	0.27	0.03	0.30	0.32	0.21	0.40	0.19	0.50	0.20	0.27	0.52

Row groups: Serum (ROS, TAC, BIL); Liver tissue (MDA, ROS, TAC, SOD, GSH, CAT).

The two-tailed Pearson's correlation test was performed by SPSS 17.0. As the colors scale shows, the Pearson correlation coefficient (r) presents inside the grid, the yellow color indicates a positive correlation, and the blue color displays a negative correlation. r value (Pearson correlation coefficient) more than 0.4 or less than -0.4 were considered as a strong correlation with positive and negative, respectively.