

Supplementary tables

Table 1 Comparison of the nutritional ingredient of germinated brown rice and refined rice

Nutrients	Refined rice	Germinated brown rice
Protein (g/100 g)	6.80 ± 0.05 ^a	7.30 ± 0.29 ^a
Fat (g/100 g)	1.30 ± 0.03 ^b	2.90 ± 0.14 ^a
Carbohydrate (g/100 g)	78.0 ± 1.18 ^a	76.2 ± 1.59 ^a
Dietary fiber (g/100 g)	0.74 ± 0.35 ^b	2.80 ± 0.56 ^a
Insoluble dietary fiber (g/100 g)	0.63 ± 0.21 ^b	2.21 ± 0.17 ^a
Soluble dietary fiber (g/100 g)	0.11 ± 0.08 ^b	0.59 ± 0.06 ^a
VB ₁ (mg/100 g)	0.12 ± 0.02 ^b	0.30 ± 0.09 ^a
VE (mg/100 g)	0.40 ± 0.06 ^b	1.70 ± 0.06 ^a
γ-aminobutyric acid (mg/100 g)	1.50 ± 0.11 ^b	16.5 ± 0.61 ^a
Inositol hexaphosphate (mg/100 g)	0.03 ± 0.02 ^b	0.11 ± 0.04 ^a
Mg (mg/100 g)	33.0 ± 0.98 ^b	74.0 ± 1.35 ^a
Fe (mg/100 g)	0.50 ± 0.23 ^b	1.10 ± 0.08 ^a
Ca (mg/100 g)	6.00 ± 0.28 ^a	8.10 ± 0.24 ^a

The results are presented as mean ± standard deviation (n=3), and the values in each line with different letters are significantly different ($p < 0.05$).

Table 2 Composition of experimental diets

Ingredient (%)	Experimental group ^a					
	Con		HFD		HFD+GBR	
Soybean meal	18.0		18.0		18.0	
Fish meal	10.0		10.0		10.0	
Soybean oil	3.0		3.0		3.0	
Wheat bran	5.0		3.0		3.0	
Maltodextrin	2.0		2.0		2.0	
Alfalfa Powder	2.0		2.0		2.0	
Beer yeast powder	1.0		1.0		1.0	
Minerals, vitamins, etc	1.0		1.0		1.0	
Wheat	10.0		-		-	
Corn	2.0		-		-	
Lard oil	-		10		10	
Yolk powder	-		5		5	
Whole milk powder	-		4		4	
Cholesterol	-		1		1	
Sodium cholate	-		0.2		0.2	
Refined rice	40		40		-	
Germinated brown rice	-		-		40	
	gm%	kcal%	gm%	kcal%	gm%	kcal%
Protein	20	17.9	20.5	15.7	20.5	15.7
Carbohydrate	69	61.9	53.5	41.1	53.5	41.1
Fat	10	20.2	25	43.2	25	43.2
Total calories (kcal/gm)	4.46		5.21		5.21	

^aThe Con group: a normal chow diet based on 40.0 % (w/w) refined rice; the HFD group: a high-fat diet based on 40.0% (w/w) refined rice; the HFD+GBR group: a high-fat diet based on 40.0% (w/w) germinated brown rice.

Table 3 List of PCR primer sequences for RT-qPCR

Gene name	Forward primer (5' to 3')	Reverse primer (5' to 3')
<i>β-actin</i>	ATC ATG TTT GAG ACC TTC AAC ACC	AGA GCA ACA TAG CAC AGC TTC TCT T
<i>Pcsk9</i>	CAT TGT GGT GCT GAT GGA GGA GAC	CCA ACA GGT CAC TGC TCA TCT TCA C
<i>Hmgcr</i>	TTG GTC CTT GTT CAC GCT CAT AGT C	TCA CTT GCT CAA TGT CCA TGC TGA T
<i>Srebp-2</i>	AGC GGT GGA GTC CTT GGT GAA	CGG AAC TGC TGG AGA ATG GTG AG
<i>Apob</i>	ATC AAG GCT GGT GTA AGA CTG GAA T	TGA CTC GTG GAA GAA GTT GGT GTT
<i>Abca1</i>	AGT CCT ATG TGT CCT CTA CCA ACC T	ACT GCC ATT GAT GCC GAT GAA GA
<i>Ldlr</i>	GTC TGT CAC CTG TCA GTC CAA TCA A	CCA TCC TGG CAT CGG AAG TCA TC
<i>Cyp7a1</i>	GCT GTG GTA GTG AGC TGT TG	GTT GTC CAA AGG AGG TTC ACC
<i>Lxra</i>	TCT TCC GCC GCA GTG TCA TCA	GTT CCT CTT CTT GCC GCT TCA GTT
<i>Zo-1</i>	GCC GCT AAG AGC ACA GCA A	TCC CCA CTC TGA AAA TGA GGA
<i>Claudin-1</i>	GGG GAC AAC ATC GTG ACC G	AGG AGT CGA AGA CTT TGC ACT
<i>Il-6</i>	GAG CCC ACC AAG AAC GAT A	TTG TCA CCA GCA TCA GTC C
<i>Il-1β</i>	CCT TCC AGG ATG AGG ACA TGA	TGA GTC ACA GAG GAT GGG CTC
<i>Leptin</i>	ATG TTC AAG CAG TGC CTA TCC AGA A	CAG GAA TGA AGT CCA AGC CAG TGA
<i>Adiponectin</i>	CGG CAG CAC TGG CAA GTT CTA	TCC TGA TAC TGG TCG TAG GTG AAG A
<i>Resistin</i>	ACT TCA ACT CCC TGT TTC CAA ATG C	GCT CAA GAC TGC TGT GCC TTC T
<i>Tnfa</i>	CGGTGCCTATGTCTCAGCCTCTTCT	TGGTGGTTTGTGAGTGTGAGGGTCT
<i>Inos</i>	GACGAGACGGATAGGCAGAGATTG	GAACTCTTCAAGCACCTCCAGGAA

<i>Cox2</i>	<i>CAATGGGCTGGAAGACATATCA</i>	<i>GCCAGGGCTGAACTTCGAA</i>
<i>Cat</i>	<i>AGGTGTTGAACGAGGAGGAGAGG</i>	<i>TCAGCGTTGTACTIONTGTCCAGAAGAG</i>
<i>Sod1</i>	<i>AGCGGTGAACCAGTTGTGTTGTC</i>	<i>AGTCACATTGCCAGGTCTCCAA</i>
<i>Ucp2</i>	<i>CGAAGCCTACAAGACCAT</i>	<i>CTCAGCACAGTTGACAATG</i>
<i>Acc1</i>	<i>AATGTGGTTGTTCTGAATGGCTGTG</i>	<i>TGCTGAGTGATGGCTCCGTAGT</i>
<i>Fasn</i>	<i>CCGTGTGACCGCCATCTATATCG</i>	<i>CGTGAGGTTGCTGTCTGTCTGTAG</i>
<i>Dgat1</i>	<i>GCTATCCAGACAACCTGACCTACC</i>	<i>AAGAGCATCTCAAGAACTCGTCGTA</i>
<i>Srebplc</i>	<i>GCCATCGACTACATCCGCTTCTT</i>	<i>TGCCTCCTCCACTGCCACAA</i>
<i>Cd36</i>	<i>TTGCGACATGATTAATGGCACAGAC</i>	<i>TCCGAACACAGCGTAGATAGACCT</i>
<i>Ppara</i>	<i>AGAATCCACGAAGCCTACCTGAAGA</i>	<i>GGAAGAATCGGACCTCTGCCTCT</i>
<i>Pparγ</i>	<i>CTGTTCCCAAGGTGCTCCA</i>	<i>GGCTCATGTCTGTCTCTGTCTTCTT</i>
<i>Atgl</i>	<i>CCTTCGCAATCTCTACCGCCTCT</i>	<i>CTCCACCACAGCAGCTTCCTCT</i>
<i>Hsl</i>	<i>CACGGCGGCTGTCTAATGTCTT</i>	<i>TGGTGTCTCTGTGTCCAGGTCAA</i>
<i>Cpt1</i>	<i>CACAACAACGGCAGAGCAGAG</i>	<i>GGACACCACATAGAGGCAGAAGA</i>
<i>Acox1</i>	<i>CCACCGCCTATGCCTTCCACTT</i>	<i>CACCGCAAGCCATCCGACATTC</i>
<i>Pdk4</i>	<i>CCTGCCTGACCGCTTAGTGAAC</i>	<i>CCAGGATGCCTTGAGCCATTGTAG</i>
<i>Nrf1</i>	<i>GATGGCACCGTGTCGCTCAT</i>	<i>ATGCTTGCGTCGTCTGGATGG</i>
<i>Tfam</i>	<i>CTTCCAGGAGGCAAAGGATGATTCG</i>	<i>ATCACTTCGTCCAACCTCAGCCATC</i>
<i>Sirt1</i>	<i>GAGACGGTATCTATGCTCGCCTTG</i>	<i>TGACACAGAGACGGCTGGAACCT</i>
<i>Pgc1α</i>	<i>GAGTGTGCTGCTCTGGTTGGT</i>	<i>AGGCTCATTGTTGTACTIONTGGTTGGAT</i>

Table 4 The table of the number of reads for each sample analyzed for sequencing

Sample\Info	Seq_num	Base_num	Mean_length	Min_length	Max_length
Con1	55131	22999277	417.175038	245	431
Con2	56553	23943074	423.374074	252	510
Con3	69226	28940246	418.054575	265	432
Con4	51556	21792217	422.69022	259	500
Con5	52728	22083119	418.811997	325	432
Con6	52464	21956259	418.50143	259	489
HFD1	48439	20679607	426.920601	325	482
HFD2	53239	22484973	422.340258	315	505
HFD3	42287	17937442	424.183366	298	431
HFD4	57241	24053886	420.221275	283	498
HFD5	40343	17099506	423.85311	325	478
HFD6	54916	23232530	423.055758	280	467
HFD+GBR1	49906	20990046	420.591632	258	457
HFD+GBR2	46417	19360408	417.097357	216	432
HFD+GBR3	50144	21036909	419.529934	330	464
HFD+GBR4	35127	14927751	424.965155	311	431
HFD+GBR5	46547	19727072	423.809741	298	509
HFD+GBR6	49366	20756307	420.457542	282	499

Supplementary figures

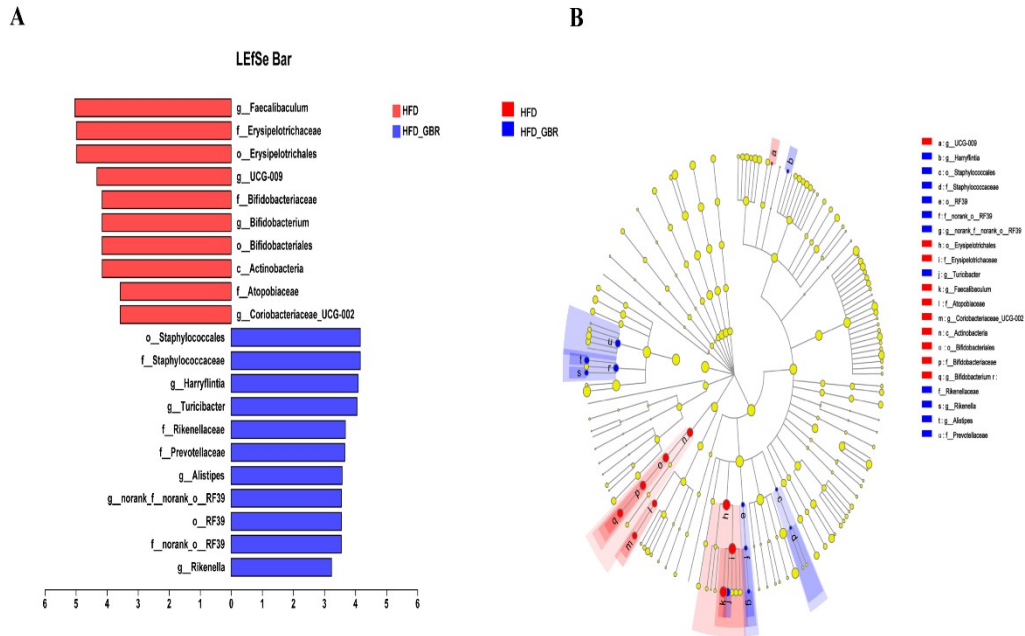


Fig.S1 LEfSe multi-level species difference discriminant analysis was applied to discriminate the gut microbiota between the HFD group and the HFD+GBR group (Log LDA > 2.0)

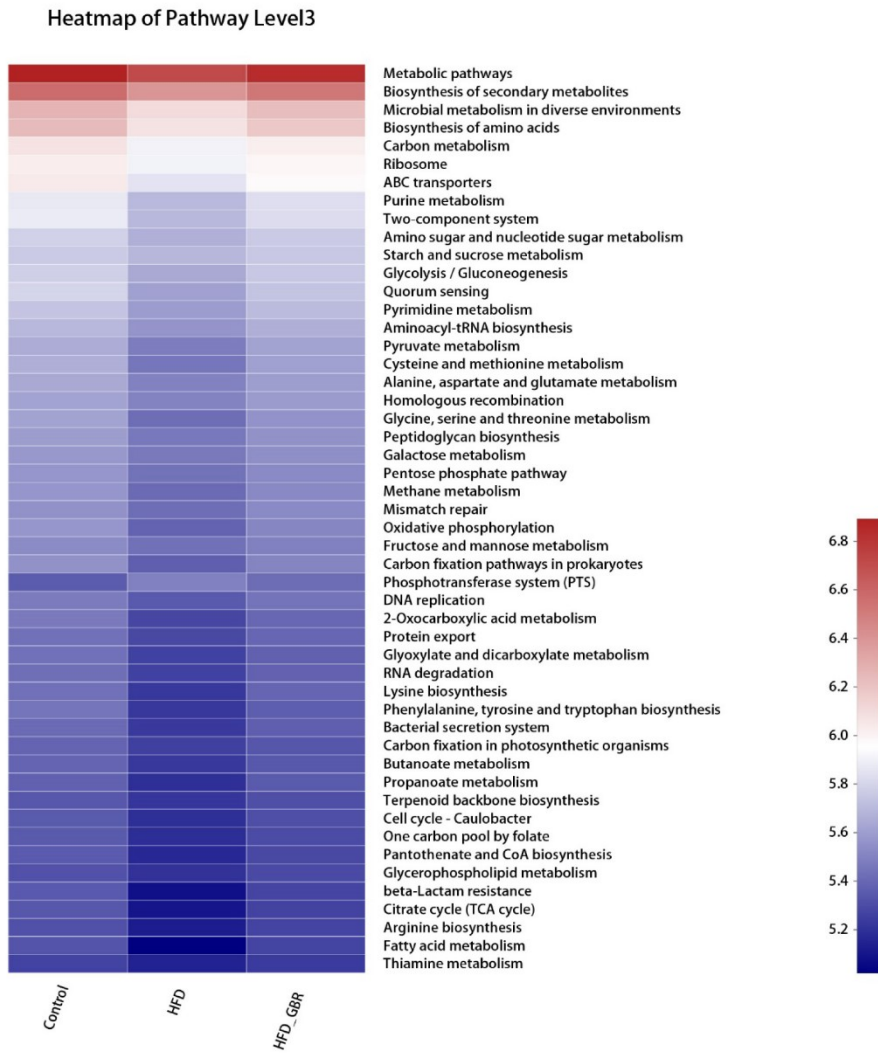


Fig.S2 The KEGG pathway in level-3 functional prediction by PICRUSt2 (n=10)

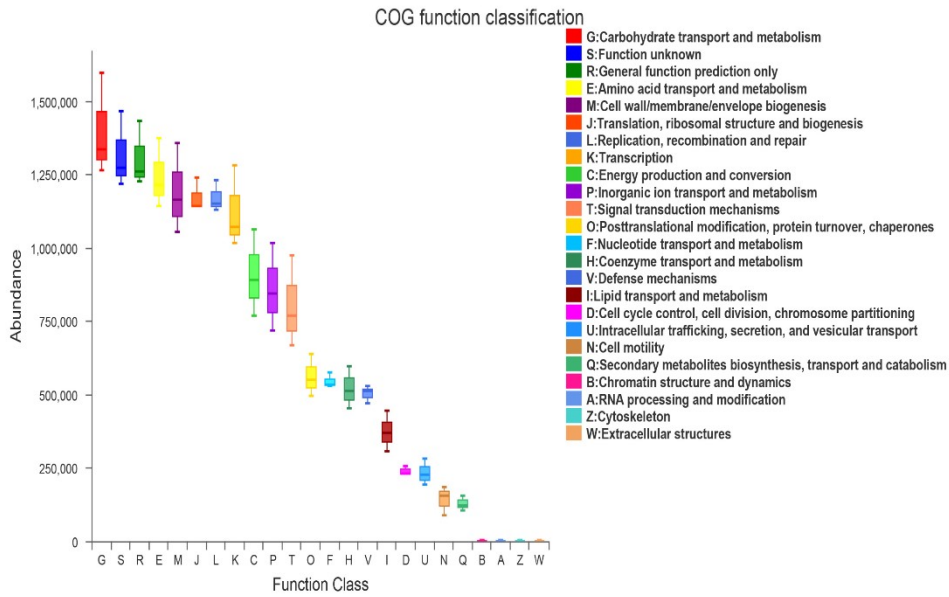


Fig.S3 PICRUST function Prediction. The OTU abundance table was standardized by PICRUST to remove the influence of 16S marker gene copy number in the genome of the species. Then, COG and KEGG functional annotation of OTU were performed through the corresponding greengene id of each OTU, and the annotation information of OTU at each COG and KEGG functional level and the abundance information of each function in different samples were obtained.

