

Supplementary

Table 1: Nutritional information of the modified cereal bran mixed in the HFD diet.

Nutrients	mFMB (%)	mKMB (%)	mRB (%)
Protein	15.85	3.15	10.44
Carbohydrate	62.85	89.69	74.24
Fat	0.8	0.47	3.59
Total dietary fibers	49.45	65.80	54.03
Ash	5.38	3.50	5.84

Table 2: Experimental diets used in the study (w/w) %.

Ingredients (g)	HFD	HFD+mFMB	HFD+mKMB	HFD+mRB	HFD+mCB
NPD	36.5	32.85	32.85	32.85	32.85
Milk casein	25	22.5	22.5	22.5	22.5
Vitamin & mineral mix	6.0	5.4	5.4	5.4	5.4
DL-methionine	0.3	0.27	0.27	0.27	0.27
Sodium chloride	0.1	0.09	0.09	0.09	0.09
Lard	32	28.8	28.8	28.8	28.8
mFMB	0	10	0	0	3.3
mKMB	0	0	10	0	3.3
mRB	0	0	0	10	3.3
Energy (kcal/g)	5.26	4.95	4.98	4.99	4.97

Table 3: Effect of high-fat diet and bran supplementation diets on the average weight of different organs.

Treatments	WAT	Liver	Kidney	BAT	Spleen	Pancreas	Colon
Control	0.35±0.04	1.06±0.03	0.30±0.01	0.09±0.006	0.09±0.01	0.09±0.01	0.76±0.03
HFD	1.27±0.24**	1.27±0.10*	0.42±0.02***	0.17±0.03***	0.13±0.02*	0.16±0.006***	0.46±0.04
mFMB	0.71±0.12	0.96±0.06##	0.33±0.02##	0.09±0.01	0.10±0.02#	0.12±0.07	0.49±0.06
mKMB	0.86±0.20	0.99±0.13#	0.33±0.02##	0.15±0.01	0.09±0.02##	0.13±0.01	0.54±0.04
mRB	0.88±0.16	0.81±0.04###	0.28±0.01###	0.08±0.01	0.07±0.01#	0.08±0.01	0.38±0.03
mCB	0.58±0.16	0.97±0.05##	0.34±0.02#	0.11±0.01	0.09±0.01#	0.10±0.01	0.43±0.03

All data were represented as mean ± SEM and were analyzed by one-way ANOVA followed by Tukey's multiple comparisons. *p≤0.05, **p≤0.01, ***p≤0.001 is significant to control. #p≤0.05, ##p≤0.01, ###p≤0.001 is significant to HFD.

Table 4. List of primers used for qPCR

No.	Primer ID	Forward primer 5'-3'	Reverse primer 5'-3'
1	<i>β-act</i>	TGTTACCAACTGGGACGACA	GGGGTGTGAAGGTCTCAAA
2	<i>Occ</i>	GGCAAGCGATCATACCCAGA	TCATAGTGGTCAGGGTCCGT
3	<i>ZO1</i>	TAAGTTGGGGAGGGAGGGTC	GGTAAGGCATTCTGCTGGT
4	<i>Cldn-2</i>	TCACACTTGAGTCATCGCCC	TCCCACCTCAAGCACAATCC
5	<i>Cldn-4</i>	GACCTAGAAGCAGCCCAGTG	CTCAGAGGGGCCAACTCAAG
6	<i>Muc1</i>	GCCGAAAGAGCTATGGGCA	CTGCCATTACCTGCCGAAAC
7	<i>Muc2</i>	GGCCTCACCACCAAGCGTCC	TGGGCTGGCAGGTGGGTTCT
8	<i>Muc3</i>	AGTGCTGTTGGTGATCCTCG	AGAGTCCAGGGGCATGTAGT
9	<i>Muc4</i>	TTGCACCTGTCCCCCTGCCT	GTTCCGCCACCGAGGCGTTGA
10	<i>GCK</i>	GTCGTTGACTCTGGTAGAGC	CCAACTTCTGAGCCTTCTGG
11	<i>GSK3</i>	GCGGGACCCAAATGTCAAAC	GTCCACGGTCTCCAGCATTA

12	<i>G6PC</i>	CACATCCGGGGCATCTACAA	GCTGGCAAAGGGTGTAGTGT
13	<i>PCK1</i>	TGGAAGGTCTGAATGTGTGGG	CAGTAAACACCCCCATCGCT
14	<i>ATGL</i>	TGGAGAGGAGGATCAATTGCA	CAAGCGGATGGTGAAGGACA
15	<i>HSL</i>	GACCATCAACCGACCAGGA	GTTGCGTTTGTAGTGCTCCC
16	<i>LPL</i>	CTCGCTCTCAGATGCCCTA	AGCAGTTCTCCGATGTCCAC
17	<i>IR</i>	TTTTTGTCCCCAGGCCATCC	ATGCGGTACCCAGTGAAGTG
18	<i>IRS2</i>	CACAACCTATCGTGGCACCT	AAGGTCTCTGAACTGTGGCG
19	<i>GLUT4</i>	CTATGCTGGCCAACAATGTCT	GACGATGGCCAGTTGGTTG
20	<i>CREB</i>	CAGCACCCACTAGCACCATT	AGCACTGCCACTCTGTTCTC
21	<i>ADIPOQ</i>	ATCGCTCAGGCTTCAGTGTG	AACGGCCTTGTCCTTCTTGA
22	<i>CRTC1</i>	TGCCAACGTGAACCAGATT	GTCGCCCATGCTTGTCTACT
23	<i>CRTC2</i>	GGTTGGTGGAAACGGGTACAA	TCCTGTTAAGTGCAGACGGC
24	<i>SREBP</i>	GTACCTGCGGGACAGCTTA	GGTCATGTTGGAAACCAC
25	<i>MGL L</i>	CGGAACAAGTCGGAGGTTGA	TGTCCTGACTCCGGGATGAT
26	<i>SCD-1</i>	ATCGCCCCTACGACAAGAAC	GTTGATGTGCCAGCGGTACT
27	<i>DGPAT-2</i>	CTGCATCTTCCATGGCCGAG	TTTCTGGGTCTGGGTGCTC
25	<i>FOXO1</i>	AATTCGGTCATGCCAGCGTA	TAAAGGTGTCTTCACGGGGG

Table 5. List of primers used for qPCR in bacterial abundance estimation.

No.	Primer ID	Forward primer 5'-3'	Reverse primer 5'-3'
1	<i>Total Bacteria_d</i>	GCAGGCCTAACACATGCAAGTC	CTGCTGCCTCCCGTAGGAGT
2	<i>Bacteroidetes_p</i>	ACGCTAGCTACAGGCTTAACA	ACGCTACTTGGCTGGTTCA
3	<i>Firmicutes_p</i>	GCGTGAGTGAAGAAGT	CTACGCTCCCTTTACAC
4	<i>Akkermansia_g</i>	AACGAACGCTGGCGGCGTGGAT AAGACAT	CATCCCAGTTACCAGTCTCAC CTTAGGACCCT
5	<i>Bacteroides_g</i>	GAGAGGAAGGTCCCCCAC	CGCKACTTGGCTGGTTCAG
6	<i>Bifidobacterium_g</i>	GATTCTGGCTCAGGATGA	CTGATAGGACGCGACCCC
7	<i>Clostridium_g</i>	CGGGTGAGTAACGCGTGAGT	AACCTCTCAGTCCGGCTACC

8	<i>Fecalibacterium_g</i>	GAGGAAGATAATGACGGTAC	ACCTCTGCACTACTCAAGA
9	<i>Roseburia_g</i>	GCGGTRCGGCAAGTCTGA	CCTCCGACACTCTAGTMCGA
10	<i>Lactobacillus_g</i>	CACCGCTACACATGGAG	AGCAGTAGGGAATCTTCCA
11	<i>Prevotella_g</i>	GGTGTCGGCTTAAGTGCCAT	CGGAYGTAAGGGCCGTGC
12	<i>Eubacterium-g</i>	GCTGTGAAGCCGAGCAAATC	GGTTAGGTCACTGGCTTCGG
13	<i>Ruminococci-g</i>	GGCGGCYTRCTGGGCTTT	CCAGGTGGATWACTTATTGTG TTAA
14	<i>Lachnospiraceae-g</i>	CGGTACCTGACTAAGAAGC	AGTTTYATTCTTGCGAACG

_d = domain, _p = phylum, _g = genus