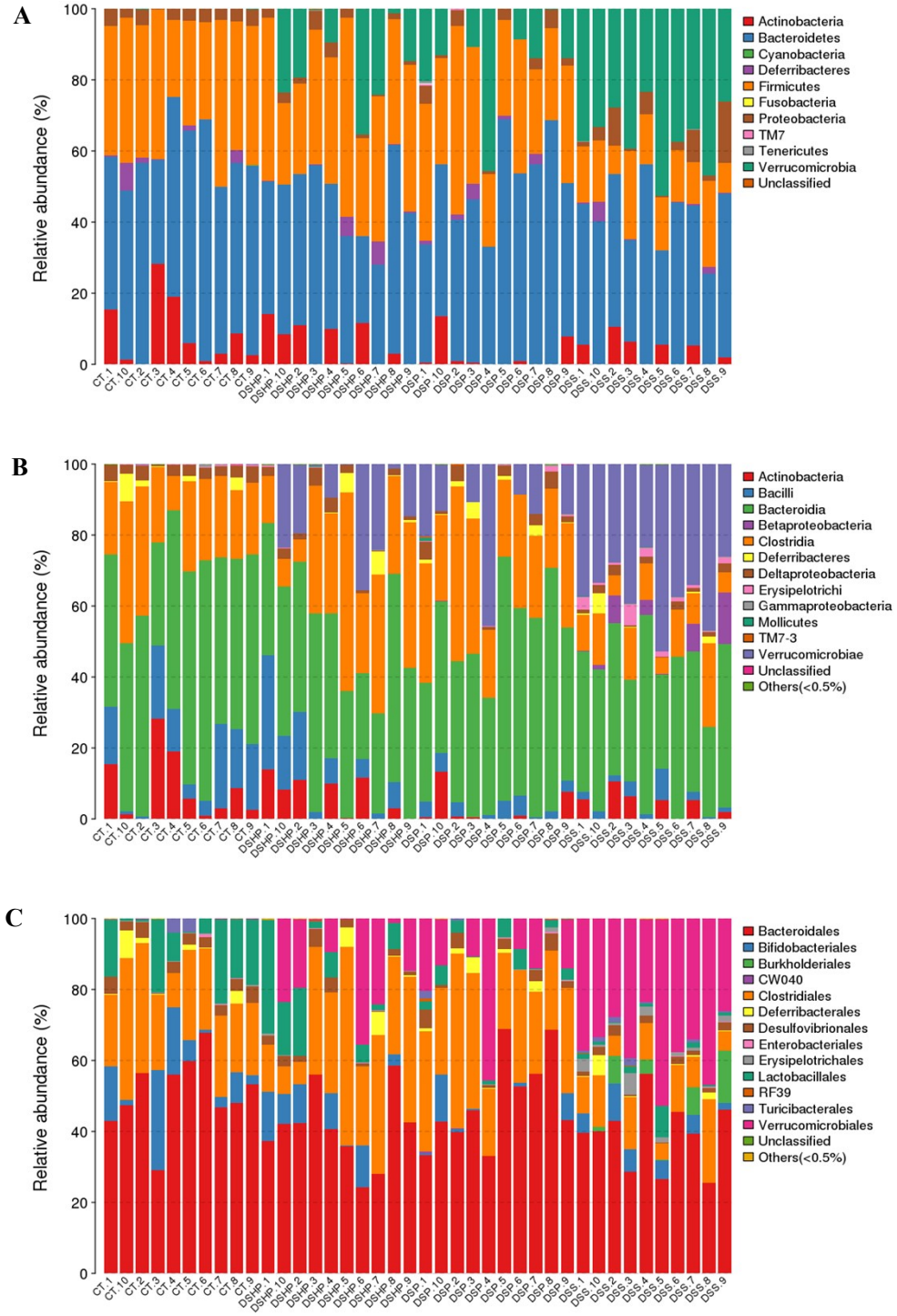
1. Supplemental Methods

1.1 Preparation of WPEP

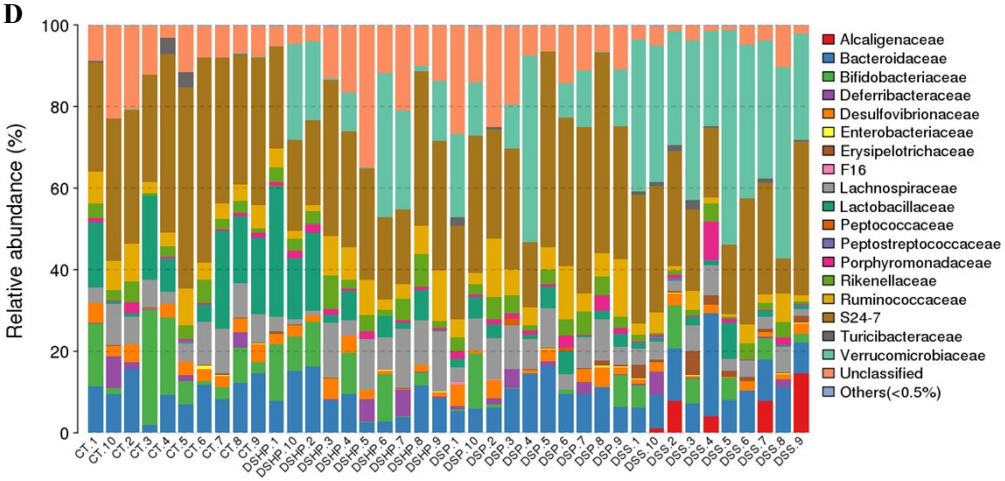
Briefly, fresh P. eryngii was dried (60 °C), powdered and sieved through 300 mesh. The powder was firstly refluxed with 85% ethanol at room temperature overnight to remove lipophilic compounds and collect the precipitates. After the precipitate was extracted with distilled water under an optimized condition (ratio of water to material of 25 mL/g, leaching temperature of 70 °C, leaching time of 2 h). After the supernatant was deproteinized with Sevag reagent (chloroform: butanol, 4:1), 4-fold volume anhydrous ethanol was added to obtain the crude polysaccharide (PEP) for 12 h at 4 °C. After the preparation of PEP, 200 mg PEP was dissolved in 400 mL distilled water to get a PEP solution with a concentration of 0.5 mg/mL. The solution was pre-purified through a 0.45 μm membrane to get the permeation solution following an ultra-filtration machine (Millipore Co., Ltd.) equipped with membrane with molecular weight cut off 100 kDa (Millipore Co., Ltd.) to collect the retentate solution. Then the retentate solution was subjected to a DEAE-52 cellulose column (2.6 cm × 30 cm) with a stepwise elution of 0 - 0.5 M NaCl solubilized in deionized water at a flow rate of 4 mL/min to collect the different fractions (10 mL/tube) according to the total carbohydrate content quantified by phenol-sulfuric acid method using an automatic fraction collector [30] which were named PEP-1 and PEP-2 on the basis of different elution. Consequently, PEP-1 was further purified with a Sephadex G-200 column (2.6 cm × 60 cm) eluted with distilled water at the flow rate of 0.2 mL/min to yield two final elution products named WPEP.

2. Supplemental Figures

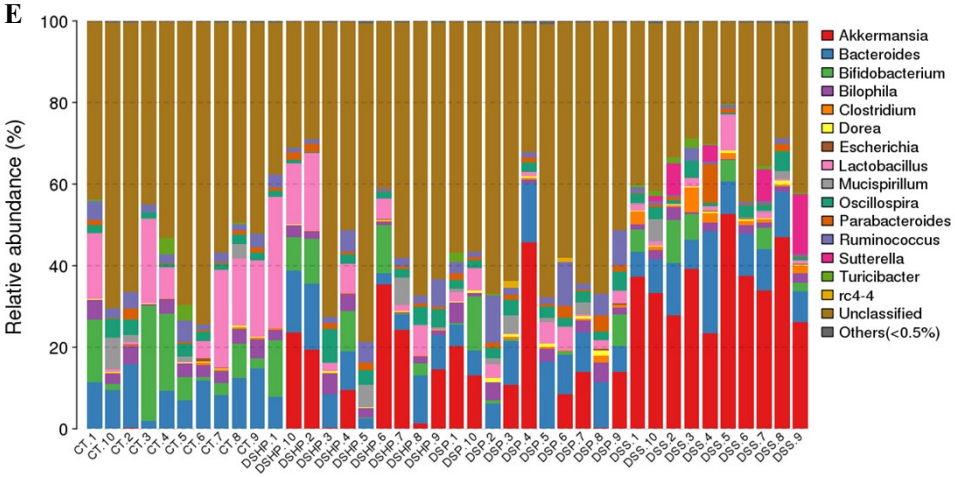
Supplemental Figure. 1. Bacterial taxonomic profiling in the phylum (A), class (B), order (C), family (D), Genus (E), and Species (F) level of fecal microbiota from different treatments.



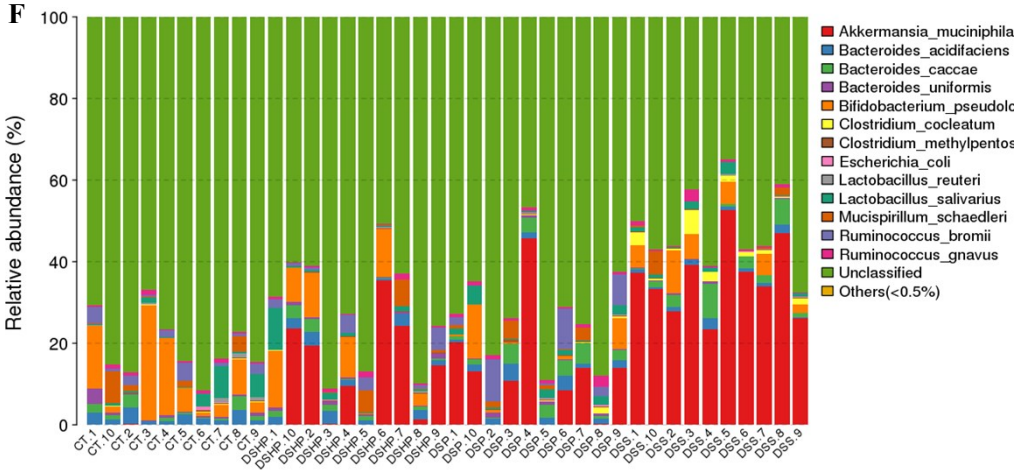
D


Relative abundance (%)
0
20
40
60
80
100
CT.1
CT.10
CT.2
CT.3
CT.4
CT.5
CT.6
CT.7
CT.8
CT.9
DSHP.1
DSHP.10
DSHP.2
DSHP.3
DSHP.4
DSHP.5
DSHP.6
DSHP.7
DSHP.8
DSHP.9
DSP.1
DSP.10
DSP.2
DSP.3
DSP.4
DSP.5
DSP.6
DSP.7
DSP.8
DSP.9
DSS.1
DSS.10
DSS.2
DSS.3
DSS.4
DSS.5
DSS.6
DSS.7
DSS.8
DSS.9
Alcaligenaceae
Bacteroidaceae
Bifidobacteriaceae
Deferribacteraceae
Desulfovibrionaceae
Enterobacteriaceae
Erysipelotrichaceae
F16
Lachnospiraceae
Lactobacillaceae
Peptococcaceae
Peptostreptococcaceae
Porphyromonadaceae
Rikenellaceae
Ruminococcaceae
S24-7
Turicibacteraceae
Verrucomicrobiaceae
Unclassified
Others(<0.5%)

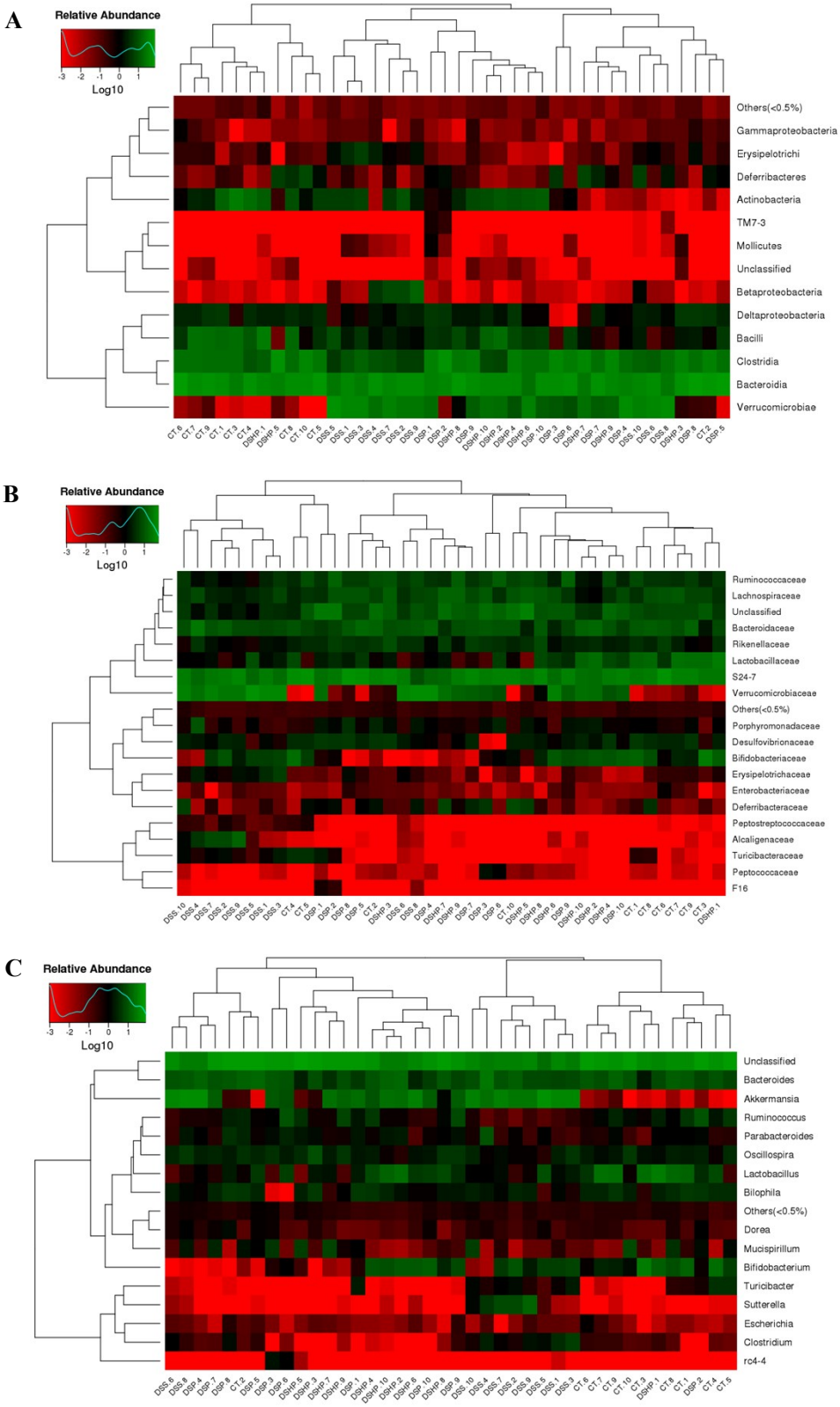
E

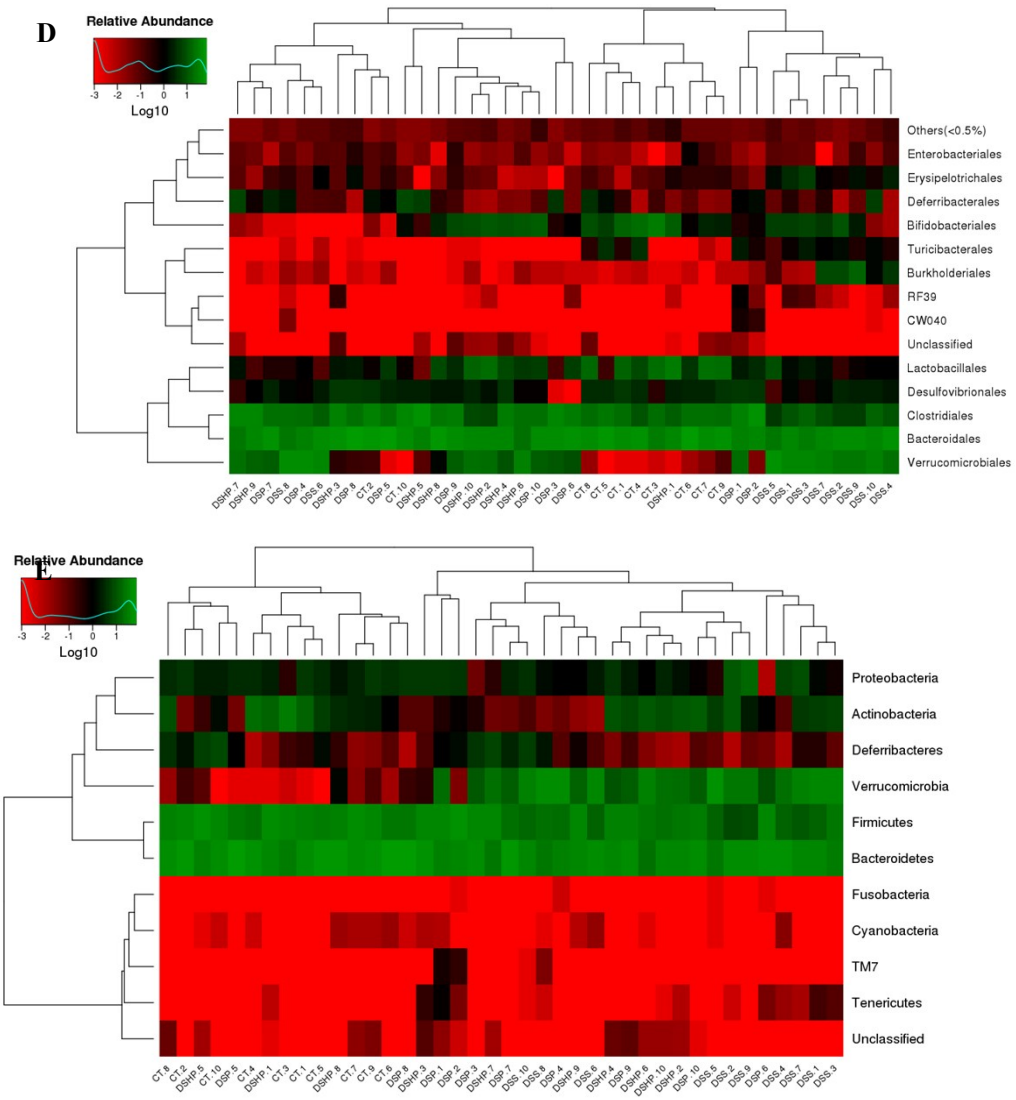

Relative abundance (%)
0
20
40
60
80
100
CT.1
CT.10
CT.2
CT.3
CT.4
CT.5
CT.6
CT.7
CT.8
CT.9
DSHP.1
DSHP.10
DSHP.2
DSHP.3
DSHP.4
DSHP.5
DSHP.6
DSHP.7
DSHP.8
DSHP.9
DSP.1
DSP.10
DSP.2
DSP.3
DSP.4
DSP.5
DSP.6
DSP.7
DSP.8
DSP.9
DSS.1
DSS.10
DSS.2
DSS.3
DSS.4
DSS.5
DSS.6
DSS.7
DSS.8
DSS.9
Akkermansia
Bacteroides
Bifidobacterium
Bilophila
Clostridium
Dorea
Escherichia
Lactobacillus
Mucispirillum
Oscillospira
Parabacteroides
Ruminococcus
Sutterella
Turicibacter
rc4-4
Unclassified
Others(<0.5%)

F


Relative abundance (%)
0
20
40
60
80
100
CT.1
CT.10
CT.2
CT.3
CT.4
CT.5
CT.6
CT.7
CT.8
CT.9
DSHP.1
DSHP.10
DSHP.2
DSHP.3
DSHP.4
DSHP.5
DSHP.6
DSHP.7
DSHP.8
DSHP.9
DSP.1
DSP.10
DSP.2
DSP.3
DSP.4
DSP.5
DSP.6
DSP.7
DSP.8
DSP.9
DSS.1
DSS.10
DSS.2
DSS.3
DSS.4
DSS.5
DSS.6
DSS.7
DSS.8
DSS.9
Akkermansia_muciniphila
Bacteroides_acidifaciens
Bacteroides_caccae
Bacteroides_uniformis
Bifidobacterium_pseudolo
Clostridium_cocleatum
Clostridium_methylpentos
Escherichia_coli
Lactobacillus_reuteri
Lactobacillus_salivarius
Mucispirillum_schaedleri
Ruminococcus_bromii
Ruminococcus_gnavus
Unclassified
Others(<0.5%)

Supplemental Figure. 2. Heatmaps of bacterial taxonomic profiling in the phylum (A), class (B), order (C), family (D), and Genus (E) level of fecal microbiota from different treatments.




D
Relative Abundance
-3 -2 -1 0 1
Log10
Others(<0.5%)
Enterobacteriales
Erysipelotrichales
Deferribacterales
Bifidobacteriales
Turicibacterales
Burkholderiales
RF39
CW040
Unclassified
Lactobacillales
Desulfovibrionales
Clostridiales
Bacteroidales
Verrucomicrobiales
DSHP.7 DSHP.9 DSP.7 DSS.8 DSP.4 DSS.6 DSHP.3 DSP.8 CT.2 DSP.5 CT.10 DSHP.5 DSP.9 DSHP.10 DSHP.2 DSHP.4 DSHP.6 DSP.10 DSP.3 DSP.6 CT.8 CT.5 CT.1 CT.4 CT.3 DSHP.1 CT.6 CT.7 CT.9 DSP.1 DSP.2 DSS.5 DSS.1 DSS.3 DSS.7 DSS.2 DSS.9 DSS.10 DSS.4

E
Relative Abundance
-3 -2 -1 0 1
Log10
Proteobacteria
Actinobacteria
Deferribacteres
Verrucomicrobia
Firmicutes
Bacteroidetes
Fusobacteria
Cyanobacteria
TM7
Tenericutes
Unclassified
CT.8 CT.2 DSHP.5 CT.10 DSP.5 CT.4 DSHP.1 CT.3 CT.1 CT.5 DSHP.8 CT.7 CT.9 CT.6 DSP.8 DSHP.3 DSP.1 DSP.2 DSP.3 DSHP.7 DSP.7 DSS.10 DSS.8 DSP.4 DSHP.9 DSS.6 DSHP.4 DSP.9 DSHP.6 DSHP.10 DSHP.2 DSP.10 DSS.5 DSS.2 DSS.9 DSP.6 DSS.4 DSS.7 DSS.1 DSS.3

Supplemental Table. 1. Preliminary characteristics of WPEP.

	Purity	Molecular weight	Monosaccharide composition (%)[a]					
	(%)	(kDa)	Sulfate	Uronic acid	Xylose	Mannose	Glucose	Galactose
WPEP	99.97	167	-[b]	-[b]	21.35	3.28	73.22	1.63

[a] Data are presented as mol% for each sugar.

[b] Not detected.

Supplemental Table. 2. Nutrition ingredients of standard AIN-93G diet.

Ingredient	kcal./gm	grams/kg	kcal./kg
Casein	3.58	200	716.00
L-Cystine	4	3	12.00
Sucrose	4	350	1400.00
Cornstarch	3.6	315	1134.00
Dyetrose	3.8	35	133.00
Soybean Oil	9	25	225.00
t-Butylhydroquinone	0	0.005	0.00
Lard	9	20	180.00
Cellulose	0	50	0.00
Mineral Mix #210088	1.6	10	16.00
Dicalcium Phosphate	0	13	0.00
Calcium Carbonate	0	5.5	0.00
Potassium Citrate H_2O	0	16.5	0.00
Vitamin Mix # 300050	3.92	10	39.20
Choline Bitartrate	0	2	0.00