

Supplementary Table 1. Detailed Dietary Ingredients for All Diets

Ingredient (g/kg)	ISP	DWMP	MPC	MFGM
Isolated Soy Protein	210			
Dried Whole Milk Powder		390		
Milk Protein Concentrate			230	
Milk Fat Globule Membrane Protein				325
Casein		95		
DL-Methionine	2.5			3
L-Cystine	1.05	2.2	2.3	1.05
Sucrose	190	40	190	190
Corn Starch	188.13	175.58	189.28	178.68
Maltodextrin	100	100	100	100
Cellulose	140	140	140	110
Soybean Oil	20	20	20	20
Anhydrous Milkfat				27
Lard	100		95	
Mineral Mix, w/o Ca & P (98057)	17	17	17	17
Vitamin Mix, AIN-93-VX (94047)	12.7	12.7	12.7	12.7
Calcium Phosphate, dibasic	10.9		0.5	9.2
Calcium Carbonate	4.5	4.3		3.15
Choline Bitartrate	3.2	3.2	3.2	3.2
TBHQ, antioxidant	0.02	0.02	0.02	0.02

Supplementary Table 2. Composed Diet Analyses: Amino Acids* (% w/w)

	<i>ISP</i>	<i>DWMP</i>	<i>MPC</i>	<i>MFGM</i>	<i>CHOW</i>
<i>Taurine</i>	0.15	0.15	0.22	0.22	0.16
<i>Hydroxyproline</i>	0.00	0.00	0.14	0.00	0.01
<i>Aspartic Acid</i>	2.08	1.31	1.78	1.41	2.26
<i>Threonine</i>	0.68	0.74	1.13	0.81	0.89
<i>Serine</i>	0.82	0.80	0.82	0.92	0.98
<i>Glutamic Acid</i>	3.64	3.87	2.87	3.96	4.17
<i>Proline</i>	0.92	1.72	0.87	1.76	1.34
<i>Lanthionine</i>	0.00	0.00	0.00	0.00	0.00
<i>Glycine</i>	0.79	0.36	0.43	0.35	1.23
<i>Alanine</i>	0.81	0.58	0.87	0.62	1.21
<i>Cysteine</i>	0.32	0.26	0.46	0.31	0.38
<i>Valine</i>	0.95	1.17	1.01	1.21	1.23
<i>Methionine</i>	0.48	0.44	0.62	0.52	0.38
<i>Isoleucine</i>	0.92	0.96	1.03	0.99	1.05
<i>Leucine</i>	1.52	1.72	1.81	1.84	1.91
<i>Tyrosine</i>	0.58	0.78	0.42	0.77	0.72
<i>Phenylalanine</i>	1.01	0.90	0.64	0.91	1.15
<i>Hydroxylysine</i>	0.02	0.03	0.02	0.02	0.05
<i>Ornithine</i>	0.01	0.00	0.00	0.00	0.02
<i>Lysine</i>	1.18	1.42	1.62	1.52	1.40
<i>Histidine</i>	0.47	0.50	0.36	0.52	0.59
<i>Arginine</i>	1.34	0.62	0.54	0.64	1.55
<i>Tryptophan</i>	0.28	0.28	0.34	0.26	0.31
<i>TOTAL</i>	18.97	18.61	18.00	19.56	22.99
<i>Branched Chain Amino Acids</i>	3.39	3.85	3.85	4.04	4.19

*Dietary amino acid analysis was conducted by the Agricultural Experiment Station Chemical Laboratories at the University of Missouri-Columbia.

Supplementary Table 3. Composed Diet Analyses: Fatty Acid Profiles* (% AUC)

	<i>ISP</i>	<i>DWMP</i>	<i>MPC</i>	<i>MFGM</i>	<i>CHOW</i>
<i>C6:0</i>	0.00	0.06	0.00	0.15	0.00
<i>C8:0</i>	0.00	0.61	0.00	0.60	0.00
<i>C10:0</i>	0.07	1.28	0.12	2.26	0.04
<i>C11:0</i>	0.00	0.03	0.00	0.00	0.00
<i>C12:0</i>	0.08	2.94	0.14	2.85	0.06
<i>C13:0</i>	0.00	0.11	0.00	0.11	0.00
<i>C14:0</i>	1.21	9.86	1.54	9.25	0.83
<i>C14:1</i>	0.03	1.03	0.09	0.87	0.04
<i>C16:0</i>	21.5	29.9	22.2	27.7	15.2
<i>C16:1</i>	1.65	1.21	1.79	1.10	1.47
<i>C18:0</i>	10.6	11.3	11.3	12.4	3.7
<i>c18:1t9</i>	0.28	1.34	0.49	0.00	0.00
<i>C18:1c9</i>	31.9	22.2	32.0	25.5	20.4
<i>C18:1c11</i>	4.85	3.00	5.65	3.96	3.51
<i>C18:2</i>	24.3	12.8	21.6	11.3	46.9
<i>C18:3</i>	2.00	1.76	1.69	1.36	5.31
<i>C20:0</i>	0.19	0.22	0.20	0.20	0.17
<i>C20:1</i>	0.04	0.02	0.03	0.07	0.10
<i>C20:2</i>	0.57	0.08	0.55	0.10	0.34
<i>C20:3</i>	0.20	0.15	0.24	0.17	0.20
<i>C20:4</i>	0.51	0.00	0.46	0.00	0.00
<i>C22:0</i>	0.04	0.00	0.00	0.00	0.00
<i>C22:1</i>	0.00	0.00	0.00	0.00	0.85
<i>C22:6</i>	0.00	0.00	0.00	0.00	0.68
<i>C24:0</i>	0.00	0.02	0.00	0.00	0.10
<i>C24:1</i>	0.00	0.00	0.00	0.00	0.12
<i>SFA</i>	33.7	56.4	35.5	55.5	20.0
<i>SC SFA</i>	1.36	14.89	1.8	15.22	0.93
<i>MUFA</i>	39.7	26.5	40.1	31.5	26.5
<i>PUFA</i>	26.5	14.9	24.5	12.9	53.4

*Lipids were extracted from composed diet pellets and fatty acids analyzed by gas chromatography as previously described (Meat Science. 2006;73:432-441).

Supplementary Table 4. Analyzed Gene Targets and qPCR Primer Sequences

Gene Name	Gene Shortcode	Classification	FWD Primer Sequence
B-Actin	<i>ACTB</i>	PCR Reference Gene	GGC TGT ATT CCC CTC CAT CG
Apolipoprotein A1	<i>APOA1</i>	Inflammation	GCA CGT ATG GCA GCA AGA TG
Toll-like receptor 4	<i>TLR4</i>	Inflammation	AGG AAG TTT CTC TGG ACT AAC AAG TTT AG
Toll-like receptor 5	<i>TLR5</i>	Inflammation	GCC ACA TCA TTT CCA CTC CT
Myeloid differentiation primary response protein 88	<i>MYD88</i>	Inflammation	CTA GGA CAA ACG CCG GAA CT
Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	<i>NFκβ1</i>	Inflammation	ACA CGA GGC TAC AAC TCT GC
Tumor necrosis factor - alpha	<i>TNFα</i>	Inflammation	CCA CCA CGC TCT TCT GTC TAC
Zona occludens protein 1 (aka Tight junction protein 1: TJP1)	<i>ZO1</i>	Gut permeability	TTT TTG ACA GGG GGA GTG G
Fatty acid amide hydrolase	<i>FAAH</i>	eCB-Metabolism	ACA GGC AGG CCT ATA CCC TT
Monoacylglycerol lipase	<i>MGL</i>	eCB-Metabolism	CAG AGA GGC CAA CCT ACT TTT C
N-acylphosphatidylethanolamine phospholipase D	<i>NAPE-PLD</i>	eCB-Metabolism	GGG CGG CTC TCA CTT TCT A
Cannabinoid receptor type 1	<i>CB1</i>	eCB-Signaling	CTG ATG TTC TGG ATC GGA GTC
Cannabinoid receptor type 2	<i>CB2</i>	eCB-Signaling	TGA CAA ATG ACA CCC AGT CTT CT
Transient receptor potential cation channel, subfamily V, member 1	<i>TRPV1</i>	eCB-Signaling	CCT GCA TTG ACA CCT GTG
G protein-coupled receptor 119	<i>GPR119</i>	eCB-Signaling	GCC TTC GGA TGG CAT TTG TC
G protein-coupled receptor 41	<i>GPR41</i>	eCB-Signaling	TTT CTG AGC GTG GCC TAT CC
G protein-coupled Receptor 55	<i>GPR55</i>	eCB-Signaling	CTA TCT ACA TGA TCA ACT TGG CTG TTT

Supplementary Table 5 (cont.) Analyzed Gene Targets and qPCR Primer Sequences

Acetyl-CoA carboxylase	<i>ACC</i>	Lipogenesis	TGT TGA GAC GCT GGT TTG TAG AA
Fatty acid synthase	<i>FASN</i>	Lipogenesis	TTC CAA GAC GAA AAT GAT GC
Sterol regulatory element-binding protein 1c	<i>SREBP-1c</i>	Lipogenesis	GAT CAA AGA GGA GCC AGT GC
Adipocyte protein 2 (aka fatty acid binding protein 4: FABP4)	<i>AP2</i>	Adipocyte Differentiation	GAT GCC TTT GTG GGA ACC TG
CCAAT/Enhancer Binding Protein	<i>C/EBP</i>	Adipocyte Differentiation	GAG CCG AGA TAA AGC CAA ACA
Peroxisome proliferator-activated receptor gamma	<i>PPARγ</i>	Adipocyte Differentiation	CTG CTC AAG TAT GGT GTC CAT GA
Peroxisome proliferator-activated receptor alpha	<i>PPARα</i>	Adipocyte Differentiation	TCG GCG AAC TAT TCG GCT G

Supplementary Table 5. Organ Weights as Percent of Body Weight

	<i>ISP</i>	<i>DWMP</i>	<i>MPC</i>	<i>MFGM</i>	<i>p-value</i>
<i>Liver</i>	3.99 ± 0.07 ^{a,b}	3.67 ± 0.14 ^b	3.62 ± 0.10 ^b	4.13 ± 0.11 ^a	0.003
<i>Cecum</i>	1.09 ± 0.08 ^{a,b}	1.28 ± 0.11 ^a	1.11 ± 0.04 ^{a,b}	0.87 ± 0.05 ^b	0.001
<i>Retroperitoneal Fat Pad</i>	1.06 ± 0.07 ^{a,b}	0.90 ± 0.07 ^b	0.93 ± 0.04 ^{a,b}	1.14 ± 0.06 ^a	0.024
<i>Gastrocnemius Muscle</i>	0.50 ± 0.05	0.53 ± 0.02	0.54 ± 0.01	0.51 ± 0.02	0.701
<i>Spleen</i>	0.35 ± 0.07	0.24 ± 0.02	0.25 ± 0.01	0.27 ± 0.03	0.226
<i>Thymus</i>	0.11 ± 0.01	0.10 ± 0.01	0.11 ± 0.01	0.11 ± 0.01	0.817

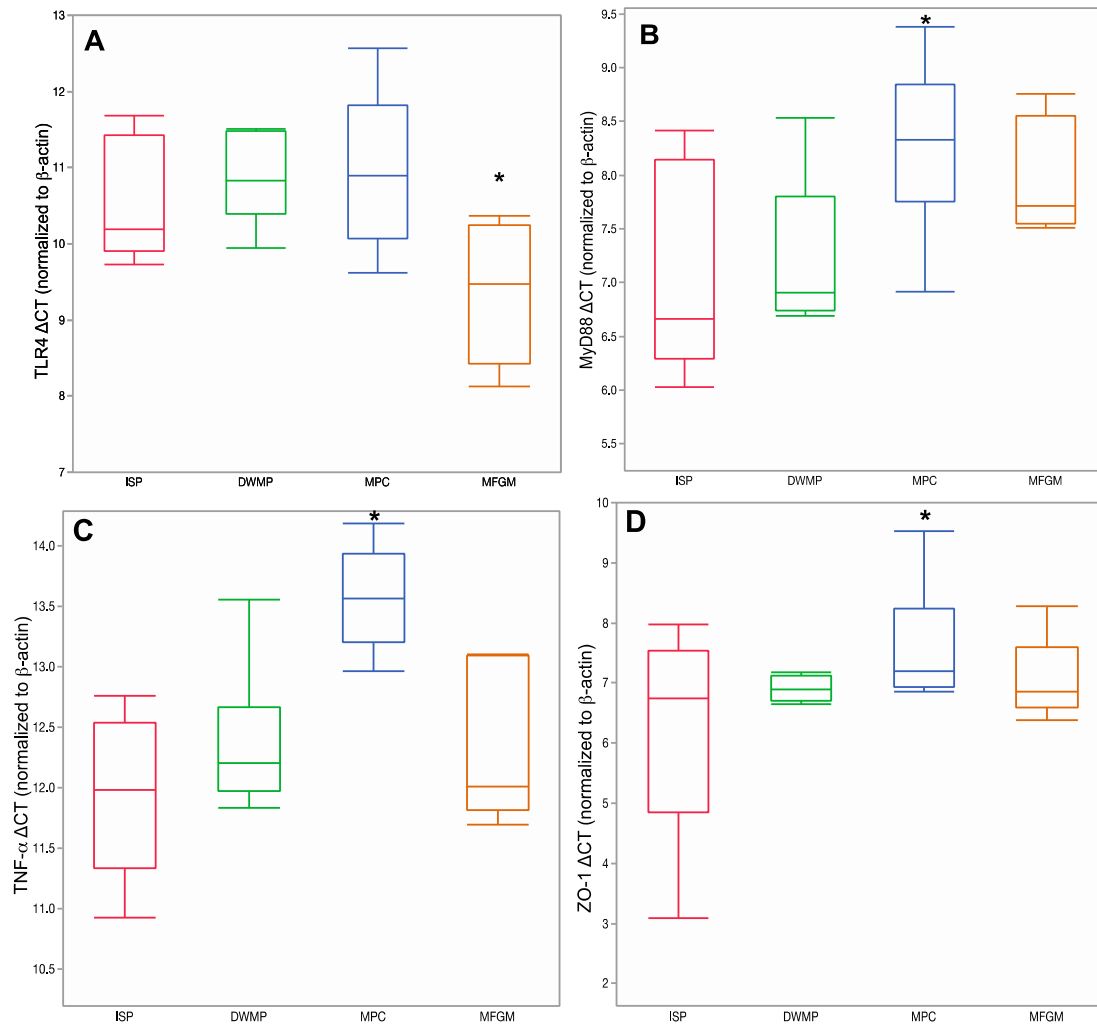
Values are means (%BW) ± standard errors; different letters signify differences between groups (p<0.05).

Supplementary Table 6. Plasma Cytokine Concentrations of Chow-fed vs Purified Diet-fed Mice

	ISP	DWMP	MPC	MFGM	Chow
IFN-γ	<LOD	<LOD	0.04 $\pm$ 0.04	<LOD	<LOD
IL-1β	0.55 $\pm$ 0.55	3.59 $\pm$ 3.59	5.08 $\pm$ 1.75	3.18 $\pm$ 1.52	5.12 $\pm$ 1.97
IL-6	100 $\pm$ 52.9	41.9 $\pm$ 24.3	57.6 $\pm$ 18.9	35.4 $\pm$ 14.7	36.3 $\pm$ 26.8
IL-12p70	8.81 $\pm$ 3.66	7.11 $\pm$ 3.67	4.42 $\pm$ 1.52	1.84 $\pm$ 1.23	12.4 $\pm$ 2.29
MIP-2	112 $\pm$ 43.0	90.8 $\pm$ 39.1	94.6 $\pm$ 25.8	96.9 $\pm$ 25.2	166 $\pm$ 23.2
TNF-α	0.43 $\pm$ 0.33	1.84 $\pm$ 1.84	18.2 $\pm$ 7.14	4.84 $\pm$ 1.67	0.29 $\pm$ 0.29
IL-10	0.21 $\pm$ 0.21	<LOD	<LOD	0.35 $\pm$ 0.28	7.24 $\pm$ 2.46

Values are means (pg/mL) $\pm$ standard errors; chow-fed mice data are provided for reference purposes only and were not included in any statistical analyses.

Supplementary Figure 1. Normalized C_T (ΔC_T) values for small intestine inflammatory gene expression



Normalized gene expression values (ΔC_T) are shown for those genes that reached significance of p-value <0.05 ANOVA and Tukey's HSD post-hoc analysis.

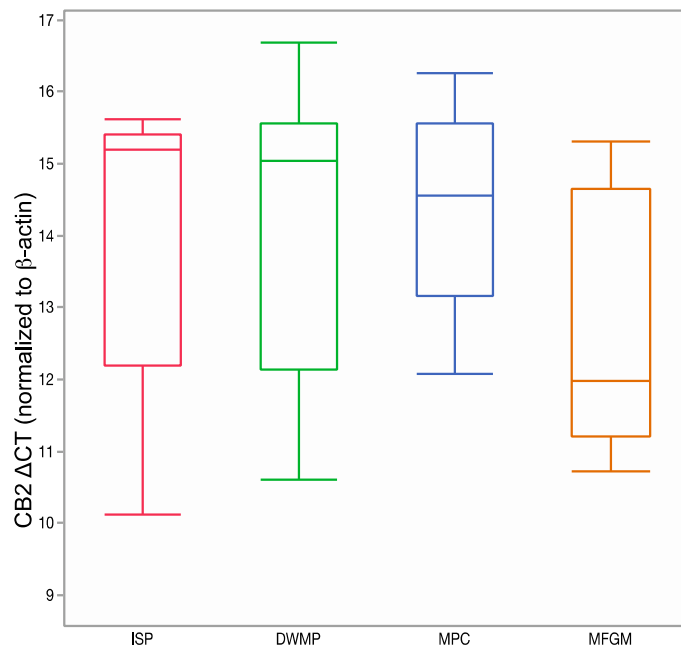
Panel A: *TLR4* ΔC_T was significantly reduced in MFGM compared the other diets (p = 0.0285).

Panel B: *MyD88* ΔC_T was highest in MPC and MFGM, nearing statistical significance (p = 0.0591).

Panel C: *TNF α* ΔC_T was highest in MPC (p = 0.0017).

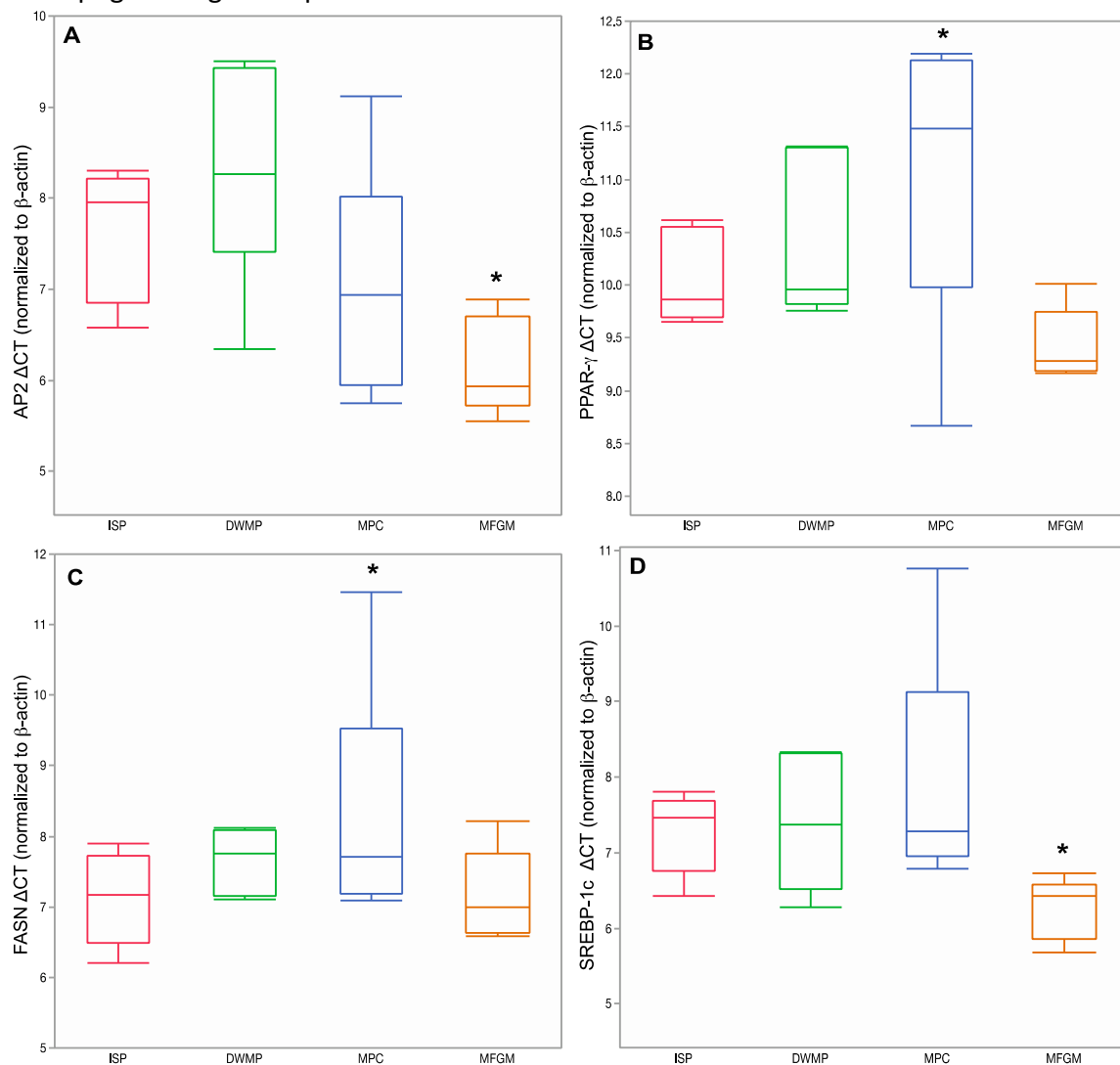
Panel D: *ZO-1* did not show a difference statistically in ΔC_T (p = 0.308).

Supplementary Figure 2. Normalized C_T (ΔC_T) values for small intestine cannabinoid gene expression



Normalized gene expression values (ΔC_T) are shown for those genes that reached significance by fold-change of greater than 2.0 or less than 0.5 as defined in methods. *CB2* did not show statistical differences for ΔC_T values ($p = 0.527$), but fold change of MFGM relative to ISP were greater than 2-fold.

Supplementary Figure 3. Normalized C_T (ΔC_T) values for small intestine adipocyte differentiation and lipogenesis gene expression



Normalized gene expression values (ΔC_T) are shown for those genes that reached significance by fold-change of greater than 2.0 or less than 0.5 as defined in methods. P-values from ANOVA and Tukey's HSD post-hoc analysis are provided.

Panel A: *AP2* was reduced in MFGM compared the other diets ($p = 0.0208$). Panel B: *PPAR- γ* was reduced in MFGM compared to DWMP ($p = 0.039$). Panel C: *FASN* did not show a difference statistically in ΔC_T ($p = 0.179$). Panel D: *SREBP-1c* did not show a difference statistically in ΔC_T ($p = 0.076$).