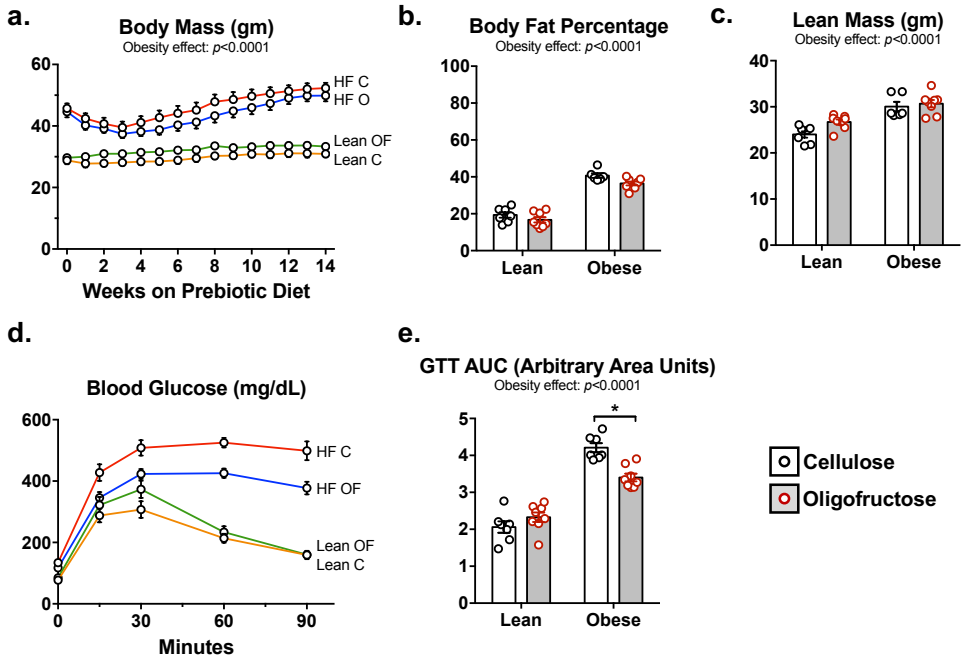
Supplemental Materials

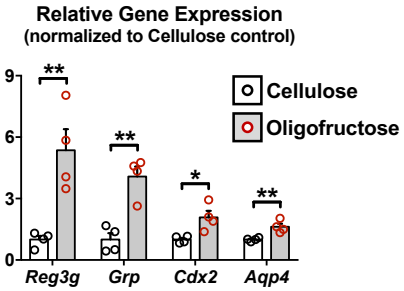
Methods

NGS data processing and alignment: Raw reads generated from the Illumina HiSeq2500 sequencer were demultiplexed using configurebcl2fastq.pl version 1.8.4. Quality filtering and adapter removal were performed using Trimmomatic version 0.32 with the following parameters: "SLIDINGWINDOW:4:20TRAILING:13LEADING:13ILLUMINACLIP:adapters.fasta:2:30:10 MINLEN:15". Processed/cleaned reads were then mapped to the GENOME OF INTEREST with STAR_2.4.2a with the following parameters: "--twopassMode Basic --runThreadN ${CPUS} --runMode alignReads --genomeDir ${STARREF}--readFilesInclt_${SAMPLE}_R1.fastq--outSAMtypeBAM SortedByCoordinate--outSAMstrandFieldintronMotif--outFileNamePrefix clt_${SAMPLE}_--outTmpDir/local_scratch/$SLURM_JOB_ID/tmp--outFilterIntronMotifs RemoveNoncanonical --outReadsUnmapped Fastx". Initial differential expression analysis was performed using Cufflinks version 2.0.2; specifically, cuffdiff2 and usage of the general transfer format (GTF) annotation file for the given reference genome with the following parameters: "--library-type fr-firststrand --FDR 0.05 -u -b GENOME". Additionally, DESeq2-1.10.1 was also used to perform data normalization and differential expression analysis with an adjusted p-value threshold of 0.05.

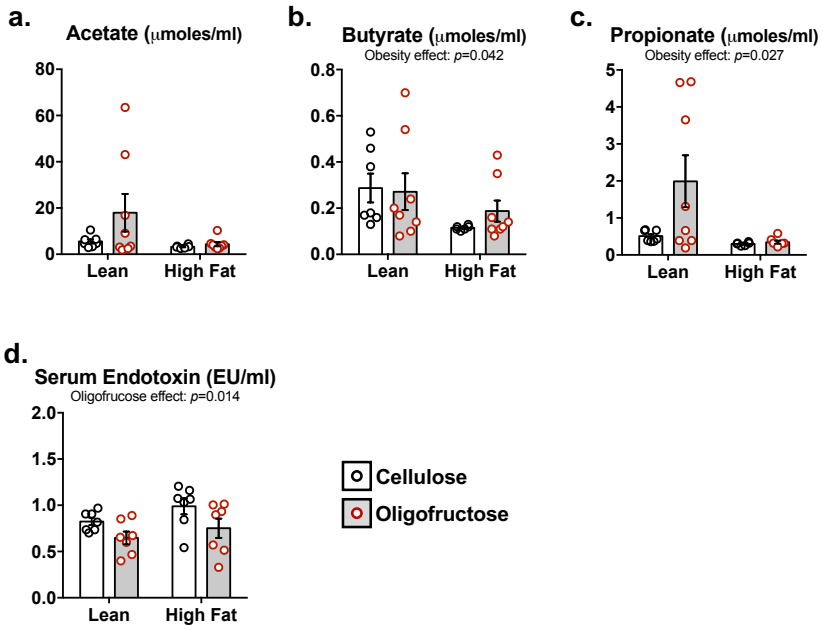
Supplemental Data



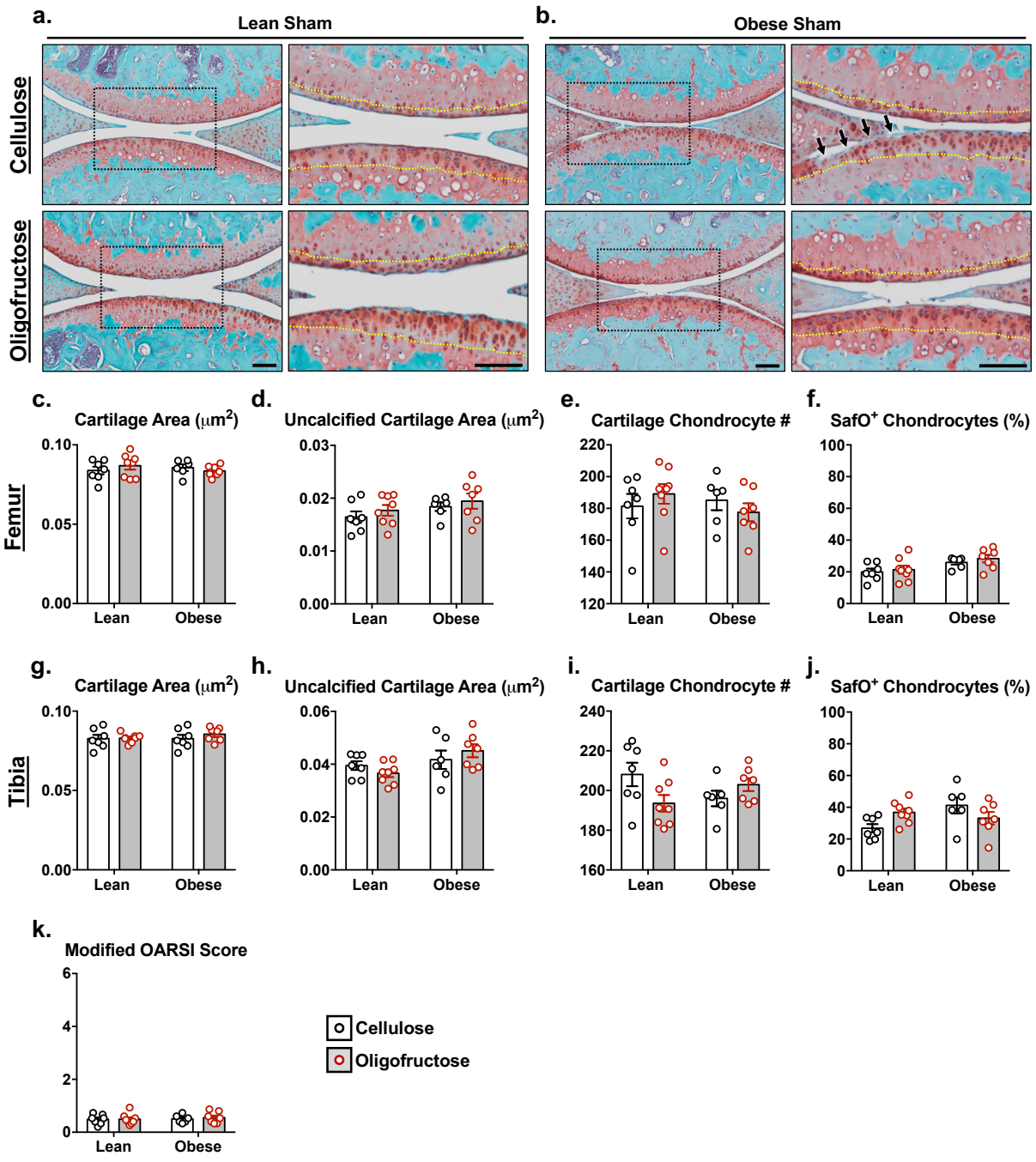
Supplemental Fig. 1: Oligofructose does not impact body composition parameters in high fat diet-induced obesity. Mice were fed lean or high fat experimental diet for 12 weeks to induce obesity. At 12 weeks, the lean and high fat diets were supplemented with cellulose (C) or oligofructose (OF). (**a**) Following addition of the prebiotics to the respective diets in lean and obese mice, body mass was measured, starting immediately after initiation of supplementation and every 2 weeks for 14 weeks. After 14 weeks of prebiotic supplementation, DEXA scanning was performed to quantify body fat percentage (**b**) and lean mass (**c**). At this point, mice were challenged with a glucose tolerance test (GTT) to evaluate the development of type 2 diabetes. Blood glucose levels were measured at 15, 30 60 and 90 minutes post-challenge (**d**), and area under each curve (AUC) was determined for further statistical analysis (**e**). The symbols in (**d**) represent the mean blood glucose level (+/-SEM, N=6-8). The bars in (**e**) represent the average AUC (+/-SEM), and each symbol represents the AUC measurement from the GTT test in an individual mouse. Significance testing in (**a**), (**b**), (**c**) and (**e**) involved 2-way ANOVA with a Tukey multiple comparison post-test (*p*-values for the obesity effect are reported; *$p<0.05$).



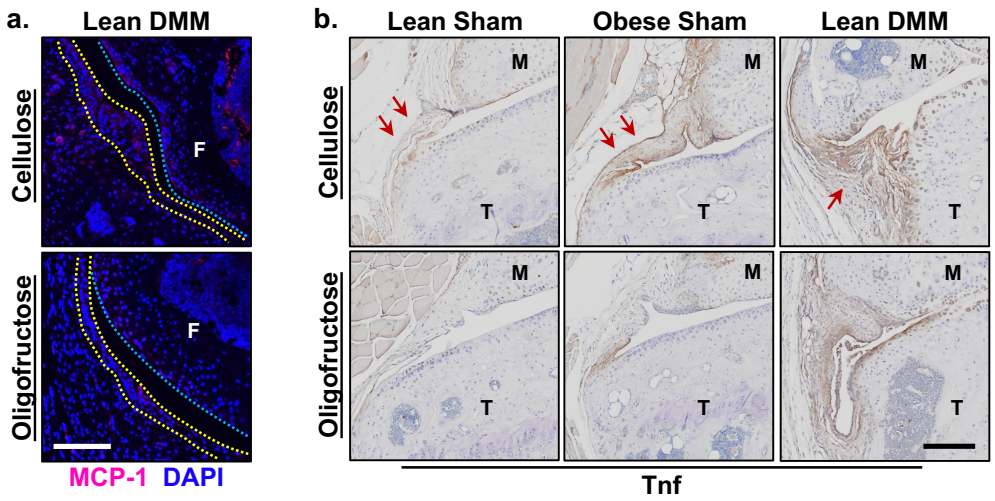
Supplemental Fig. 2: qRTPCR validation of several genes related to intestinal function initially identified via RNAseq. RNA samples from the RNAseq experiment depicted in Fig. 3c were further analyzed via qRTPCR to confirm upregulation of four genes involved in intestinal function. cDNAs generated from RNA isolated from colonic tissue of obese mice supplemented with or without oligofructose were analyzed to quantify the expression of *Reg3g*, *Grp*, *Cdx2*, and *Aqp4*. *GAPDH* levels were also assessed to provide an input control for each gene, and relative expression level was determined by normalizing to the Cellulose control. Significant differences were identified via unpaired two-tailed t tests (*p<0.05, **p<0.01, N=4).



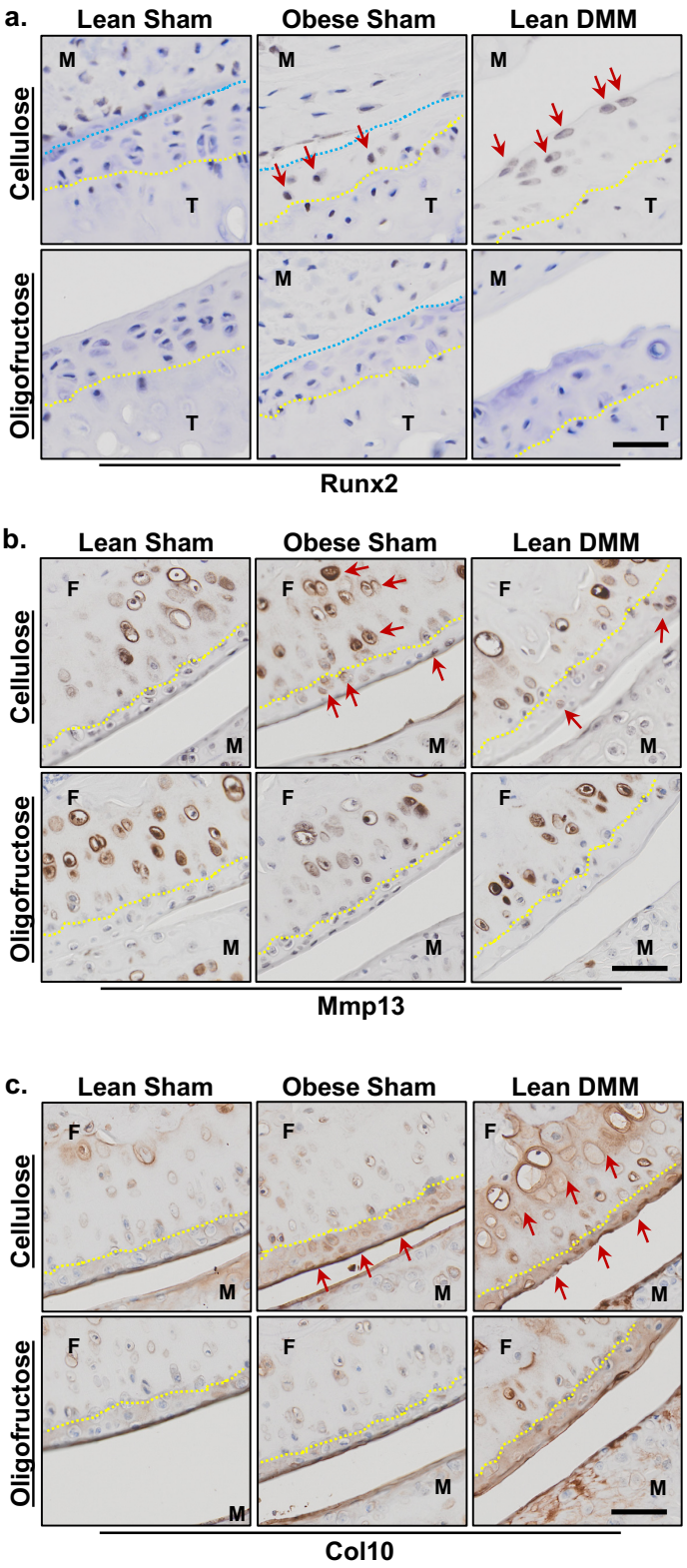
Supplemental Fig. 3: Obesity and oligofructose had minor mixed effects on short chain fatty acids and endotoxin levels in serum. After completion of GTT testing in Supplemental Fig. 1D, additional serum was collected for analysis of acetate (**a**), butyrate (**b**), proprionate (**c**) and endotoxin (**d**) levels via a commercial service. The bars in each panel represent the mean serum level (+/-SEM), and each symbol represents the serum level in an individual mouse (N=7-8). Significance testing involved 2-way ANOVA with a Tukey multiple comparison post-test (*p*-values for the obesity or oligofructose group effects are reported).



Supplemental Fig. 4: Examination of joint structure in lean and obese mice supplemented with prebiotic. Findings presented in this figure encompass Sham-operated control groups for the dataset presented in Fig. 5 where joints were induced to undergo PTOA via DMM surgery. Representative Safranin O/Fast Green stained sagittal sections in lean (**a**) and obese (**b**) mice are presented for the Sham-operated control joints, with black dotted boxes denoting areas that are shown at higher magnification to the immediate right (black scale bars = 100μm) and yellow dotted lines demarcating the tide marks. Black arrows denote surface changes consistent with early OA change. Sections like those shown in (**a**) and (**b**) were used to perform histomorphometry on femur (**c**-**f**) and tibia (**g**-**j**) articular cartilage, as well as OARSI scoring (**k**). Bars represent the group mean (+/-SEM) for each parameter, and individual symbols depict the average of measurements made in 3 histologic levels from 6-8 individual joints. Significance testing was performed using 2-way ANOVA with a Tukey multiple comparison post-test (no significance was detected for any group effect or tested comparison in Sham-operated joints).



Supplemental Fig. 5: Oligofructose mitigates obesity-induced synovial inflammation. Findings presented in this figure encompass various control groups for the datasets presented in Fig. 6a. Two weeks after lean and obese mice were initiated on cellulose or oligofructose, DMM or sham surgery was performed. Knee joints were collected 12 weeks later and sagittal sections were subjected to immunohistochemistry-based evaluation of MCP-1 and Tnf. (**a**) Representative MCP-1 immunofluorescence staining is presented, with nuclei stained blue with DAPI, yellow dotted lines demarcating the synovial membrane, blue dotted lines identifying the femoral condyle articular cartilage surface, and the white scale bar represents 50μm (F = femur). (**b**) Representative Tnf immunohistochemistry is presented, with red arrows pointing to synovial areas with positive staining, and the black scale representing 200μm (M = meniscus, T = tibia).



Supplemental Fig. 6: Oligofructose mitigates obesity-induced articular chondrocyte hypertrophy. Findings presented in this figure encompass various control groups for the datasets presented in Fig. 6b. Two weeks after lean and obese mice were initiated on cellulose or oligofructose, DMM or sham surgery was performed. Knee joints were collected 12 weeks later and sagittal sections were subjected to immunohistochemistry-based evaluation of chondrocyte hypertrophy-associated proteins. (**a**) Runx2 immunohistochemistry was performed, with positive chondrocytes identified with

red arrows, yellow dotted lines denoting tidemarks, and blue dotted lines demarcating the location where the meniscus is touching the tibial articular cartilage surface. Mmp13 (**b**) and Col10 (**c**) immunohistochemistry was also performed, with yellow dotted lines demarcating the tidemarks and red arrows pointing to cells or areas in the uncalcified cartilage with positive staining. In all panels, black scale bars represent 50μm (M = meniscus, T = tibia, F = femur).

Supplemental Table 1

Genes Upregulated in Obese v Lean			
Gene Name	**Log2 Fold Change**	***p* Value**	**Adjusted *p* Value**
Creb3l3	1.16	1.23E-10	6.78E-07
Arg2	1.05	1.11E-09	4.62E-06
Anxa8	0.98	5.11E-09	1.69E-05
Lama3	0.93	2.26E-11	3.75E-07
Naip3	0.9	1.47E-08	3.47E-05
Slurp1	0.89	1.08E-06	8.93E-04
Steap4	0.87	2.21E-07	2.32E-04
Ighv2-9	0.8	2.24E-07	2.32E-04
Ubd	0.79	6.29E-06	3.06E-03
Gm15895	0.79	1.28E-05	5.43E-03
Pla2g2c	0.77	1.37E-05	5.67E-03
Msln	0.77	2.12E-05	7.79E-03
Gp2	0.77	2.44E-05	8.61E-03
Edn1	0.76	8.66E-06	4.10E-03
Gm26514	0.75	2.25E-05	8.10E-03
Gm38357	0.74	9.71E-06	4.35E-03
Hmox1	0.72	2.94E-05	9.55E-03
Ahnak2	0.71	9.63E-09	2.66E-05
Gm9581	0.71	3.57E-05	1.11E-02
Lamb3	0.7	5.92E-11	4.90E-07
C3	0.7	4.85E-05	1.29E-02
Fbxo32	0.69	2.20E-07	2.32E-04
Tef	0.67	1.55E-04	2.70E-02
Slc17a4	0.66	2.92E-07	2.81E-04
Hspa12a	0.66	3.41E-06	2.02E-03
2010016I18Rik	0.66	3.77E-05	1.11E-02
Gpr137b-ps	0.66	7.91E-05	1.77E-02
Gm28719	0.65	2.68E-04	3.86E-02
Sell	0.65	3.71E-04	4.65E-02
A330023F24Rik	0.64	4.19E-05	1.20E-02
Ms4a4b	0.64	4.26E-04	4.92E-02
Chst15	0.63	1.44E-06	1.08E-03
Slpi	0.63	1.23E-04	2.40E-02
Cxcl1	0.63	3.30E-04	4.42E-02
Adgb	0.62	2.27E-04	3.35E-02
Sh3d21	0.61	1.16E-06	9.13E-04
Egln3	0.61	1.46E-05	5.78E-03
Gpr137b	0.61	1.63E-05	6.14E-03
Nr1d2	0.61	1.39E-04	2.53E-02
Cd200r1	0.61	2.18E-04	3.35E-02
Abtb2	0.6	1.43E-05	5.78E-03
Mmp12	0.6	2.92E-05	9.55E-03
Ccbl1	0.6	1.34E-04	2.49E-02
Ankrd12	0.59	3.07E-06	2.01E-03
B3gnt8	0.59	3.74E-04	4.66E-02
Stxbp1	0.58	5.99E-05	1.47E-02
Zfp953	0.58	2.83E-04	3.98E-02

Genes Downregulated in Obese v Lean			
Gene Name	**Log2 Fold Change**	***p* Value**	**Adjusted *p* Value**
Pcsk9	-1.01	2.06E-08	4.26E-05
Gm10499	-0.84	3.08E-06	2.01E-03
Igkv4-61	-0.82	1.16E-07	1.60E-04
Cav3	-0.71	9.30E-05	1.97E-02
Gm11946	-0.7	3.14E-08	5.78E-05
Fgfbp1	-0.69	7.02E-08	1.06E-04
Fads1	-0.69	2.57E-06	1.85E-03
Col8a1	-0.69	1.47E-04	2.65E-02
Nkd2	-0.68	4.35E-06	2.25E-03
Ighv1-81	-0.68	2.86E-05	9.55E-03
Fos	-0.68	5.94E-05	1.47E-02
A930011G23Rik	-0.67	2.18E-04	3.35E-02
Igkv4-74	-0.66	4.01E-06	2.14E-03
Slc34a2	-0.66	1.03E-04	2.15E-02
Igf2	-0.65	6.96E-05	1.62E-02
Cdkl1	-0.65	3.55E-04	4.52E-02
Fbxl22	-0.63	3.74E-05	1.11E-02
Nrarp	-0.62	3.96E-06	2.14E-03
Fzd2	-0.62	7.15E-05	1.62E-02
E2f2	-0.62	2.75E-04	3.92E-02
Wscd2	-0.62	2.90E-04	4.03E-02
Tenm2	-0.62	3.92E-04	4.81E-02
Bmp4	-0.61	1.57E-05	6.04E-03
Gm15912	-0.61	2.15E-04	3.35E-02
Fgf11	-0.6	7.10E-05	1.62E-02
Ifitm1	-0.58	5.79E-05	1.47E-02
Lrfn3	-0.57	2.92E-04	4.04E-02
Syde2	-0.56	8.53E-05	1.86E-02
Pla2g3	-0.55	2.83E-04	3.98E-02
Nol4l	-0.54	4.85E-06	2.43E-03
1810041L15Rik	-0.54	1.32E-04	2.48E-02
Greb1	-0.54	2.17E-04	3.35E-02
Tob1	-0.51	9.50E-06	4.35E-03
Phf23	-0.5	3.15E-06	2.01E-03
Sult1c2	-0.5	3.33E-06	2.02E-03
Kdm6b	-0.5	1.07E-04	2.20E-02
Gsta4	-0.5	2.24E-04	3.35E-02
Lmod1	-0.5	3.49E-04	4.49E-02
Mid1ip1	-0.48	4.55E-05	1.25E-02
Arhgef19	-0.48	2.27E-04	3.35E-02
Mov10	-0.48	3.37E-04	4.43E-02
Hmga1	-0.47	1.12E-04	2.20E-02
Sema3a	-0.47	2.98E-04	4.07E-02
Gcat	-0.46	5.92E-05	1.47E-02
Enc1	-0.45	4.07E-05	1.18E-02
Axin2	-0.44	3.97E-04	4.81E-02
Osbpl7	-0.42	2.16E-04	3.35E-02

Genes Upregulated in Obese v Lean			
Gene Name	**Log2 Fold Change**	***p* Value**	**Adjusted *p* Value**
Gch1	0.54	1.09E-05	4.75E-03
Sptbn2	0.54	5.70E-05	1.47E-02
Card6	0.53	3.68E-05	1.11E-02
Gm37261	0.53	1.36E-04	2.51E-02
Ulk3	0.5	4.03E-07	3.51E-04
Gm21781	0.5	2.81E-05	9.55E-03
Kmt2c	0.5	4.22E-04	4.92E-02
Fancm	0.49	2.11E-04	3.35E-02
Mbip	0.49	3.48E-04	4.49E-02
Dgkh	0.48	6.32E-05	1.52E-02
Apob	0.48	1.53E-04	2.70E-02
Rdh16	0.48	1.82E-04	3.12E-02
Gm27149	0.47	3.69E-04	4.65E-02
Phip	0.46	4.28E-04	4.92E-02
Narf	0.45	3.05E-07	2.81E-04
Ing3	0.45	1.11E-04	2.20E-02
Ssh2	0.45	2.54E-04	3.69E-02
Nt5e	0.45	3.99E-04	4.81E-02
Lipa	0.44	1.71E-07	2.18E-04
Hook3	0.44	6.61E-05	1.56E-02
Cgnl1	0.44	2.18E-04	3.35E-02
Epb4.1l4a	0.42	1.54E-04	2.70E-02
Rdh10	0.42	1.87E-04	3.17E-02
Fosl2	0.4	6.59E-08	1.06E-04
Atg14	0.4	4.37E-05	1.23E-02
Ttc14	0.4	1.82E-04	3.12E-02
Adgrl2	0.39	1.10E-04	2.20E-02
Acadl	0.37	4.73E-05	1.29E-02
Camk2n1	0.37	2.21E-04	3.35E-02
Cenpc1	0.36	2.25E-04	3.35E-02
Bcar3	0.36	4.00E-04	4.81E-02
Mycbp2	0.34	6.03E-05	1.47E-02
Mon1b	0.34	8.05E-05	1.78E-02
Hadha	0.3	3.63E-06	2.07E-03
Pglyrp1	0.29	3.36E-05	1.07E-02
Sptan1	0.29	2.99E-04	4.07E-02
Rbm5	0.23	4.25E-04	4.92E-02

Genes Downregulated in Obese v Lean			
Gene Name	**Log2 Fold Change**	***p* Value**	**Adjusted *p* Value**
Spire2	-0.4	1.09E-04	2.20E-02
Zfp462	-0.4	1.29E-04	2.45E-02
Pelo	-0.39	3.23E-04	4.35E-02
Hyal2	-0.38	2.13E-04	3.35E-02
Ahdc1	-0.38	3.80E-04	4.70E-02
Cdc25a	-0.35	4.22E-04	4.92E-02
Igkv8-18	-0.34	9.01E-05	1.94E-02
Rgmb	-0.33	1.26E-04	2.43E-02
Tusc2	-0.32	4.15E-04	4.92E-02
Ciapin1	-0.31	3.40E-04	4.43E-02
Slc29a1	-0.28	3.36E-04	4.43E-02
Ptbp1	-0.27	2.49E-04	3.66E-02
Llgl2	-0.23	4.37E-04	4.99E-02
Cdk16	-0.19	2.10E-04	3.35E-02

Supplemental Table 1: Genes differentially expressed in the colon of obese compared to lean mice. All significantly differentially expressed genes in the colon RNAseq experiment depicted in the heat map shown in Fig. 3a are listed in rank order from the most upregulated (left column) and most downregulated (right column). Log2 fold changes, *p*-values and adjusted *p*-values are reported for each gene.

Supplemental Table 2

Genes Upregulated in Obese-OF v Obese-C			
Gene Name	**Log2 Fold Change**	***p* Value**	**Adjusted *p* Value**
Nos2	1.66	1.09E-23	1.88E-19
Ces1f	1.23	5.96E-19	5.15E-15
Cd177	1.09	6.18E-13	2.67E-09
Tnf	0.92	2.87E-07	3.54E-04
Aqp4	0.9	9.37E-08	1.47E-04
Bhlha15	0.89	1.62E-06	1.27E-03
Zc3h12a	0.88	6.95E-10	2.40E-06
Sgk2	0.87	5.82E-08	1.10E-04
2210407C18Rik	0.86	1.12E-06	1.02E-03
Apol9a	0.85	9.13E-06	4.38E-03
Ceacam2	0.83	2.03E-07	2.70E-04
Hmgcs2	0.82	3.82E-06	2.28E-03
Igkv4-61	0.82	5.87E-06	3.17E-03
Muc3a	0.81	7.10E-06	3.62E-03
Rdh9	0.81	7.11E-06	3.62E-03
Slc51b	0.81	1.24E-05	5.26E-03
Mfsd2a	0.81	2.14E-05	7.87E-03
Mptx1	0.8	3.54E-06	2.27E-03
Tmem181c-ps	0.78	1.44E-05	5.65E-03
Gm15998	0.78	2.40E-05	8.30E-03
Padi2	0.77	5.43E-05	1.47E-02
Cyp2c69	0.76	3.45E-07	3.98E-04
Fkbp11	0.76	5.16E-05	1.42E-02
Slc13a2	0.74	2.58E-06	1.79E-03
2010109I03Rik	0.74	4.43E-05	1.34E-02
Gm10499	0.74	8.32E-05	2.00E-02
Cyp2d9	0.73	4.57E-06	2.63E-03
Duoxa2	0.73	4.59E-05	1.34E-02
Zbp1	0.73	7.59E-05	1.86E-02
Igf2bp1	0.73	9.27E-05	2.12E-02
Btnl7-ps	0.72	1.01E-04	2.21E-02
Reg3g	0.72	1.03E-04	2.22E-02
Chn2	0.72	1.70E-04	2.96E-02
Duox2	0.71	1.04E-05	4.70E-03
Igkv14-100	0.71	2.90E-05	9.63E-03
Angptl7	0.71	8.73E-05	2.07E-02
Alox5	0.71	1.69E-04	2.96E-02
Ighv1-39	0.71	1.72E-04	2.97E-02
Igha	0.7	7.01E-05	1.78E-02
Rtn4r	0.7	1.92E-04	3.26E-02
Nags	0.7	2.33E-04	3.66E-02
Clca1	0.69	5.86E-05	1.56E-02
Fzd9	0.69	1.06E-04	2.22E-02
Cd300lf	0.69	1.50E-04	2.81E-02
Gm14137	0.69	2.02E-04	3.28E-02
Hsd17b13	0.69	3.06E-04	4.31E-02
Krt20	0.68	3.64E-05	1.19E-02

Genes Downregulated in Obese-OF v Obese-C			
Gene Name	**Log2 Fold Change**	***p* Value**	**Adjusted *p* Value**
Ahnak2	-0.87	3.49E-17	2.01E-13
5033404E19Rik	-0.77	1.81E-05	6.82E-03
4930432K21Rik	-0.77	5.01E-05	1.42E-02
Pappa2	-0.72	4.65E-05	1.34E-02
Dll1	-0.67	2.53E-06	1.79E-03
Slc16a12	-0.67	2.54E-05	8.60E-03
Slc30a10	-0.67	2.27E-04	3.60E-02
Abo	-0.67	3.23E-04	4.32E-02
Sptbn2	-0.63	1.25E-05	5.26E-03
AI854703	-0.6	4.85E-06	2.70E-03
Slc17a4	-0.56	4.30E-05	1.33E-02
Shisa2	-0.48	4.09E-08	1.01E-04
Arid5b	-0.43	1.55E-04	2.88E-02
Lrrc26	-0.41	9.51E-05	2.13E-02
Foxa2	-0.41	1.12E-04	2.31E-02
Krt7	-0.41	1.97E-04	3.28E-02
Nek8	-0.36	2.71E-04	3.96E-02

Genes Upregulated in Obese-OF v Obese-C			
Gene Name	**Log2 Fold Change**	***p* Value**	**Adjusted *p* Value**
Slc1a4	0.68	9.24E-05	2.12E-02
Sectm1a	0.68	9.63E-05	2.13E-02
Igkv6-17	0.68	3.14E-04	4.32E-02
Fa2h	0.67	1.40E-05	5.63E-03
Grp	0.67	2.72E-04	3.96E-02
Dync1i1	0.67	3.12E-04	4.32E-02
Aqp8	0.66	5.06E-07	5.47E-04
Higd1a	0.66	2.41E-04	3.71E-02
Slc15a2	0.66	2.52E-04	3.82E-02
Ighv1-81	0.66	2.61E-04	3.89E-02
Hsd3b3	0.66	2.93E-04	4.19E-02
Cdx2	0.66	3.36E-04	4.43E-02
Gm15635	0.66	3.49E-04	4.54E-02
Agpat9	0.66	4.01E-04	4.97E-02
Casp4	0.64	2.01E-04	3.28E-02
Dpep1	0.64	2.44E-04	3.73E-02
Lhfpl2	0.63	6.36E-08	1.10E-04
Rsad2	0.63	2.72E-04	3.96E-02
Hist1h4i	0.62	1.33E-04	2.62E-02
Zbtb7c	0.61	2.31E-05	8.23E-03
Ceacam10	0.61	1.61E-04	2.93E-02
Cxcl13	0.6	3.78E-04	4.81E-02
Epha2	0.59	4.02E-05	1.26E-02
4833407H14Rik	0.59	1.37E-04	2.62E-02
Fos	0.59	2.03E-04	3.28E-02
Abhd6	0.58	1.27E-07	1.83E-04
Sult2b1	0.57	1.53E-06	1.26E-03
Ang4	0.57	9.31E-05	2.12E-02
St3gal4	0.56	1.28E-04	2.55E-02
Ethe1	0.56	2.93E-04	4.19E-02
Mep1b	0.56	3.19E-04	4.32E-02
Hk2	0.55	5.74E-07	5.84E-04
Sectm1b	0.55	3.79E-06	2.28E-03
Cldn23	0.55	4.00E-04	4.97E-02
Pde9a	0.54	3.72E-08	1.01E-04
Slc26a3	0.54	6.34E-07	6.09E-04
Socs3	0.54	2.03E-04	3.28E-02
Gda	0.54	2.10E-04	3.36E-02
Ly6a	0.53	3.73E-05	1.19E-02
Ier3	0.53	1.56E-04	2.88E-02
Cks1b	0.53	1.66E-04	2.96E-02
Ptp4a1	0.52	1.06E-05	4.70E-03
Tmem189	0.51	3.18E-06	2.11E-03
Gpr160	0.51	7.42E-05	1.86E-02
Gramd3	0.51	3.39E-04	4.44E-02
Tnip3	0.51	3.96E-04	4.97E-02
Gcnt2	0.5	1.70E-06	1.27E-03
Gpx2	0.5	8.85E-06	4.37E-03
Nr1h4	0.5	1.06E-05	4.70E-03

Genes Upregulated in Obese-OF v Obese-C			
Gene Name	**Log2 Fold Change**	***p* Value**	**Adjusted *p* Value**
Trpm6	0.5	4.50E-05	1.34E-02
Ptk6	0.5	1.15E-04	2.33E-02
Metrnl	0.49	5.18E-05	1.42E-02
Ptgs1	0.49	6.80E-05	1.76E-02
Sfn	0.49	6.82E-05	1.76E-02
Gprc5a	0.49	3.25E-04	4.32E-02
Slc16a5	0.48	6.29E-08	1.10E-04
Mxd1	0.48	2.33E-05	8.23E-03
Cbr3	0.48	1.04E-04	2.22E-02
Slc35d1	0.48	1.07E-04	2.22E-02
Fkbp5	0.48	1.65E-04	2.96E-02
Ahcyl2	0.47	1.35E-04	2.62E-02
Egln3	0.47	1.45E-04	2.75E-02
Cpne2	0.46	1.28E-05	5.26E-03
Btnl6	0.46	4.02E-04	4.97E-02
Slc9a2	0.45	1.28E-04	2.55E-02
Ppp1r14d	0.43	2.60E-04	3.89E-02
Car9	0.42	1.76E-04	3.01E-02
Actb	0.4	3.20E-04	4.32E-02
Cdhr2	0.38	7.66E-05	1.86E-02
Vegfa	0.38	3.70E-04	4.74E-02
Sema4b	0.37	3.07E-04	4.31E-02
Misp	0.35	1.35E-06	1.17E-03
Osbpl3	0.35	2.36E-04	3.68E-02
Neu1	0.35	3.19E-04	4.32E-02
Wsb1	0.35	3.63E-04	4.69E-02
Ildr1	0.34	1.59E-05	6.12E-03

Supplemental Table 2: Genes differentially expressed in the colon of obese mice compared to obese mice supplemented with oligofructose. All significantly differentially expressed genes in the colon RNAseq experiment depicted in the heat map shown in Fig. 3b are listed in rank order from the most upregulated (left column) and most downregulated (right column). Log2 fold changes, *p*-values and adjusted *p*-values are reported for each gene.

Supplemental Table 3

Transcript	Forward Primer	Reverse Primer
Reg3g	GCCTGATGCTCCTTTCTCAGG	CAATAGGAGCCATAGGCACGG
Grp	CGAGGACGGCAGCTACTTTA	GTTTTGCTCCTTGGAAGCCG
Cdx2	CTGGACAAGGACGTGAGCAT	ACTGCGGAGGACTGACAAAG
Aqp4	CAGCATCGCTAAGTCCGTCT	GGTGATTTGGGTGAGCGTTTGGTA
Gapdh	CCAGGAGCGAGACCCCACTAAC	GGCGGAGATGATGACCCTTTTG

Supplemental Table 3: Forward and reverse primer sets used for qRTPCR-based validation of specific genes uncovered in the RNAseq study of the colon transcriptome. Primers for Reg3g, Grp, Cdx2, Aqp4 and Gapdh were designed using PrimerBlast, an online utility made available from the NCBI. Forward and reverse primer sequences are presented in the 5' to 3' direction.