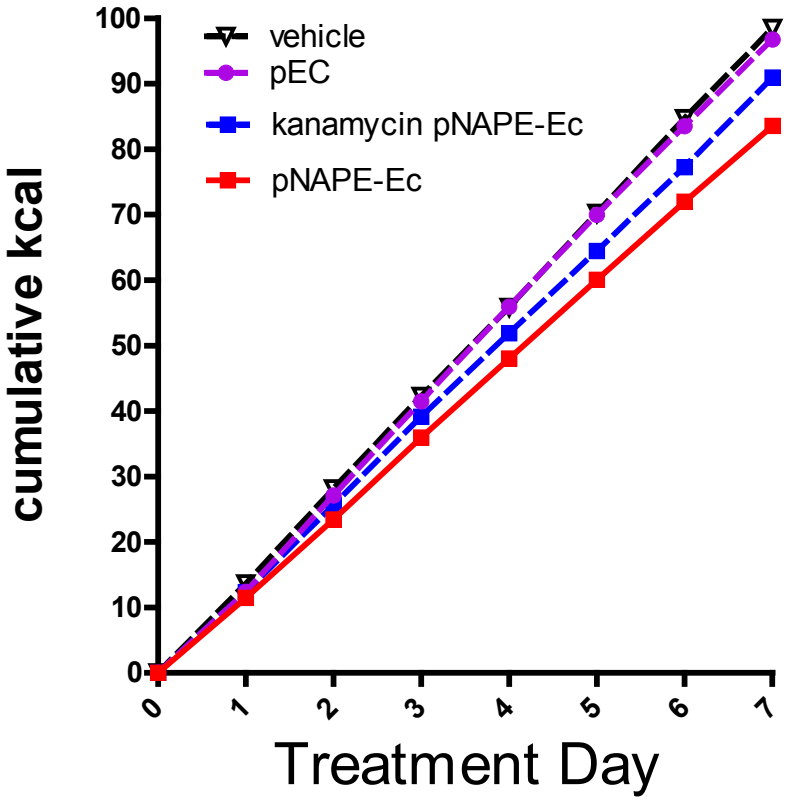
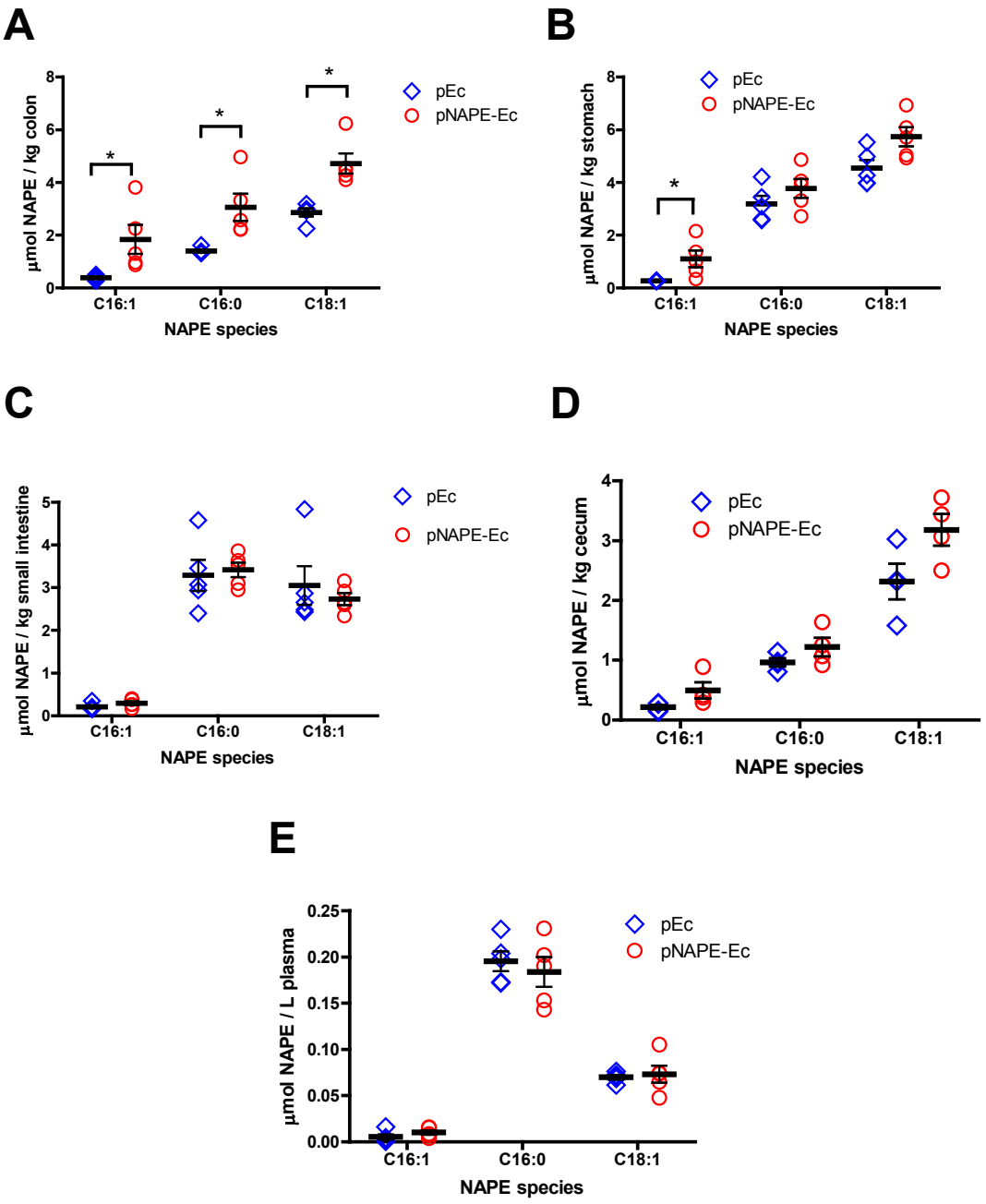
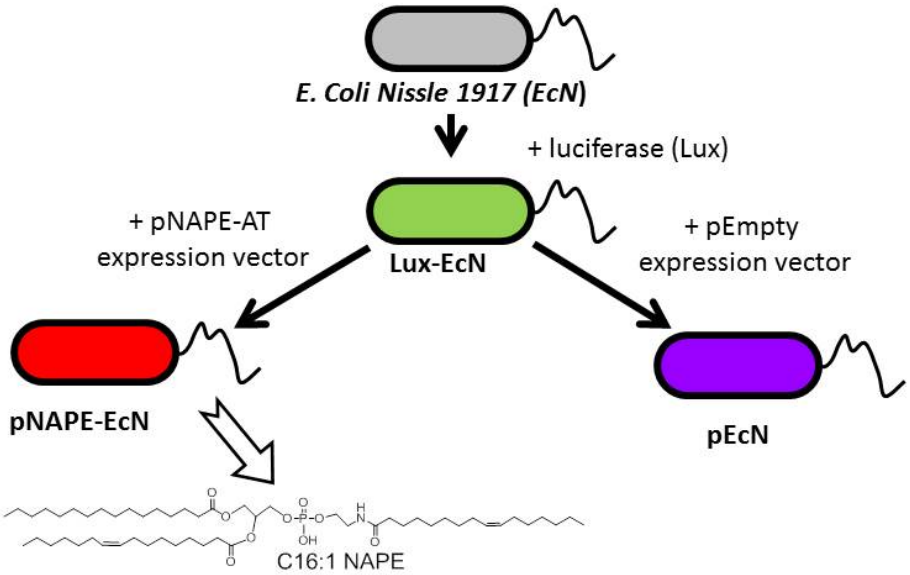


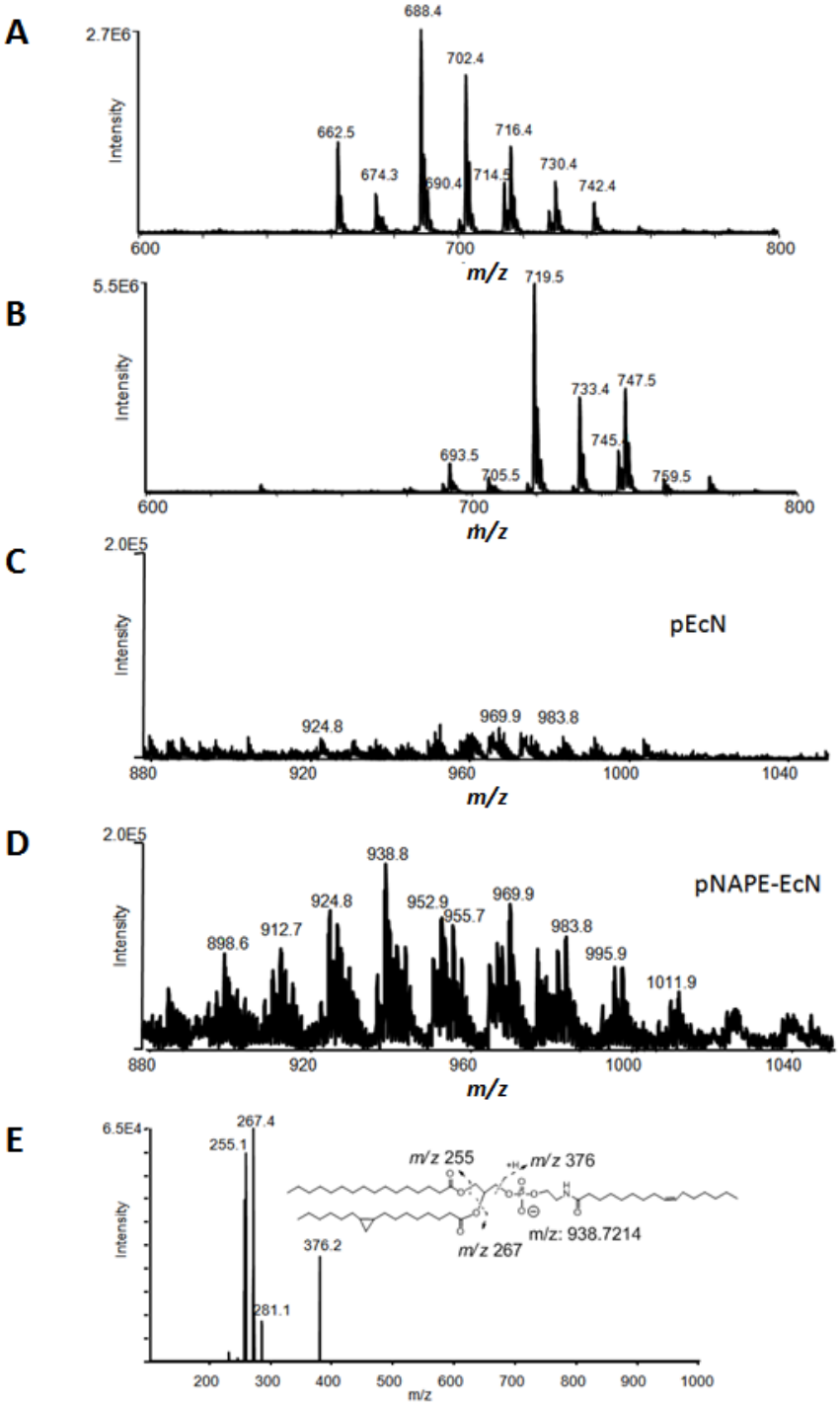

**Supplemental Figure 1.** Administration of living NAPE secreting bacteria reduces cumulative food intake in lean mice. Groups of lean C57BL6 mice (n=5 mice per group) were administered a daily bolus of $10^{11}$ cfu of pEc, pNAPE-Ec bacteria, or kanamycin-killed pNAPE-Ec bacteria by oral gavage for seven days. All mice received chow diets. Vehicle was LB broth without bacteria. 2-way RM ANOVA $p<0.0001$ for interaction of time and treatment. pNAPE-Ec differed from vehicle by Bonferroni post-hoc multiple comparison at day 6 and 7 ($p<0.01$).



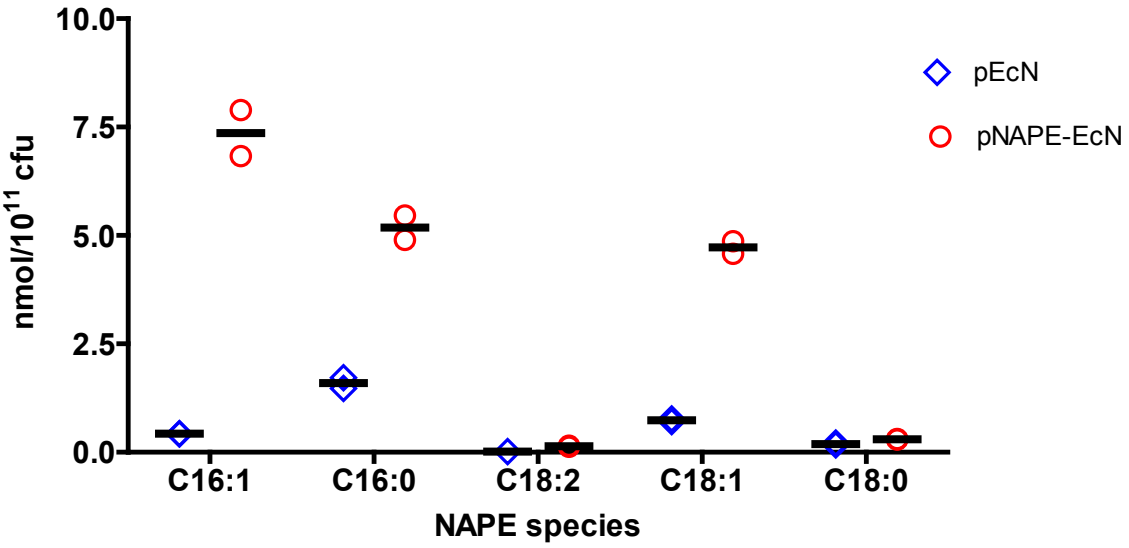

**Supplemental Figure 2**. NAPE expressed by bacteria is absorbed by the colon but not other tissue. NAPE levels in colon of mice (n=5 mice per group) administered a daily bolus of $10^{11}$ cfu for seven days of either pEc bacteria or pNAPE-Ec bacteria by oral gavage. Four hour after final gavage, mice were euthanized, the GI tract harvested and flushed with phosphate buffered saline solution to remove intraluminal content. NAPE levels were measured by LC/MS/MS after methylamine hydrolysis. *$p<0.05$ Student's t-test. All results are mean±SEM. A. Colon. B. Stomach. C. Small intestine. D. Cecum. E. Plasma.



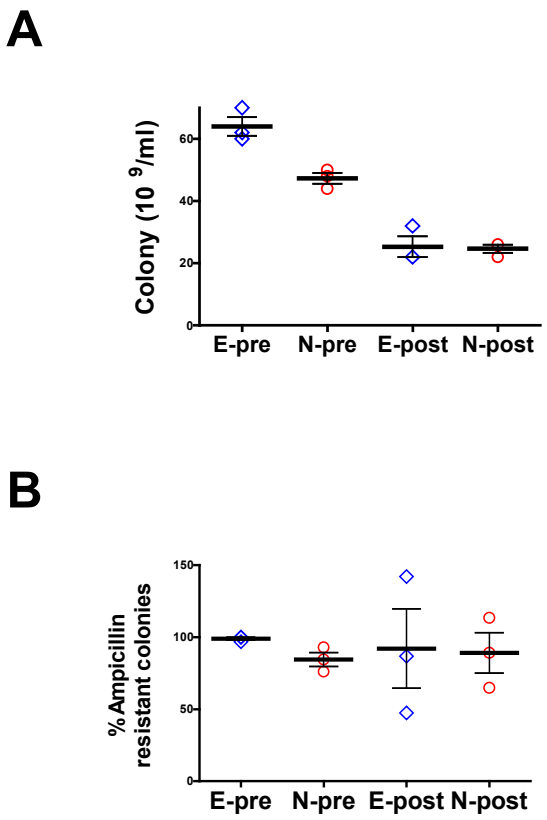

**Supplemental Figure 3.** Construction of therapeutically modified bacteria. The probiotic bacterium *E. coli Nissle 1917* (EcN) was modified to secrete *N*-acyl-phosphatidylethanolamines (NAPEs) by transformation with an expression plasmid for the *A. thaliana* NAPE acyltransferase (At1g78690p). To enable tracking of EcN by bioluminescence, the *P. luminescens* luciferase operon was inserted into the RecA gene of EcN prior to transformation with either empty expression plasmid (pEcN) or the NAPE acyltransferase expression plasmid (pNAPE-EcN).



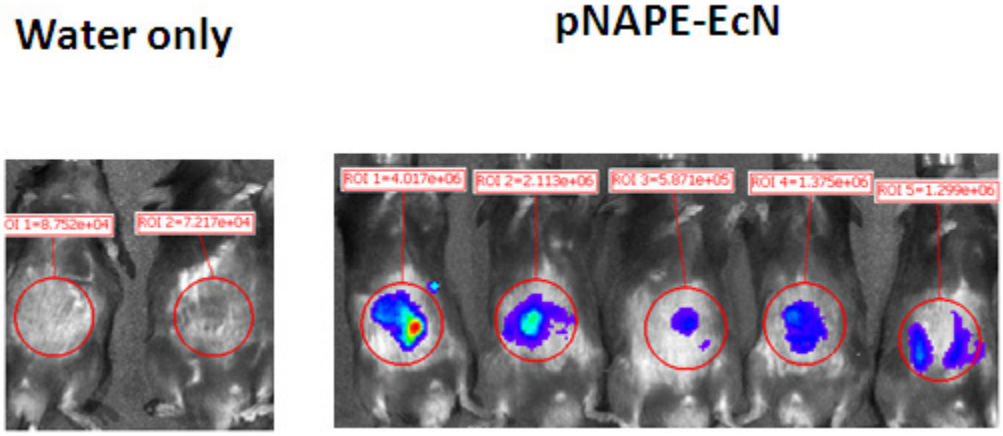

**Supplemental Figure 4.** Identification of major *N*-acyl phosphatidylethanolamines (NAPE) in pNAPE-EcN by mass spectral analysis. **A.** Mass spectrum (m/z 600 to 800) from phosphatidylethanolamine (PE) region (Rt 4.5-5.0 min.) of HPLC chromatograph from EcN transformed with vector lacking the At1g78690 gene (pEcN). Identity of each major PE species is given in Table S1. **B.** Mass spectrum (*m/z* 600 to 800) from phosphatidylglycerol (PG) region (Rt 3.0-3.3 min) of HPLC chromatograph from pEcN. Identity of each major PG species given in Table S2. **C**.Mass spectrum (m/z 880 to 1050) from triacyl anionic phospholipid region of HPLC chromatograph from pEcN. Identifications of individual NAPE and acyl-PG species given in Table S1 and S2, respectively. **D.** Same mass spectrum range for pNAPE-EcN. **E**. Collision Induced Disassociation (CID) spectrum of *m/z* ion 938.8. Interpretation of product ions are shown in inset.



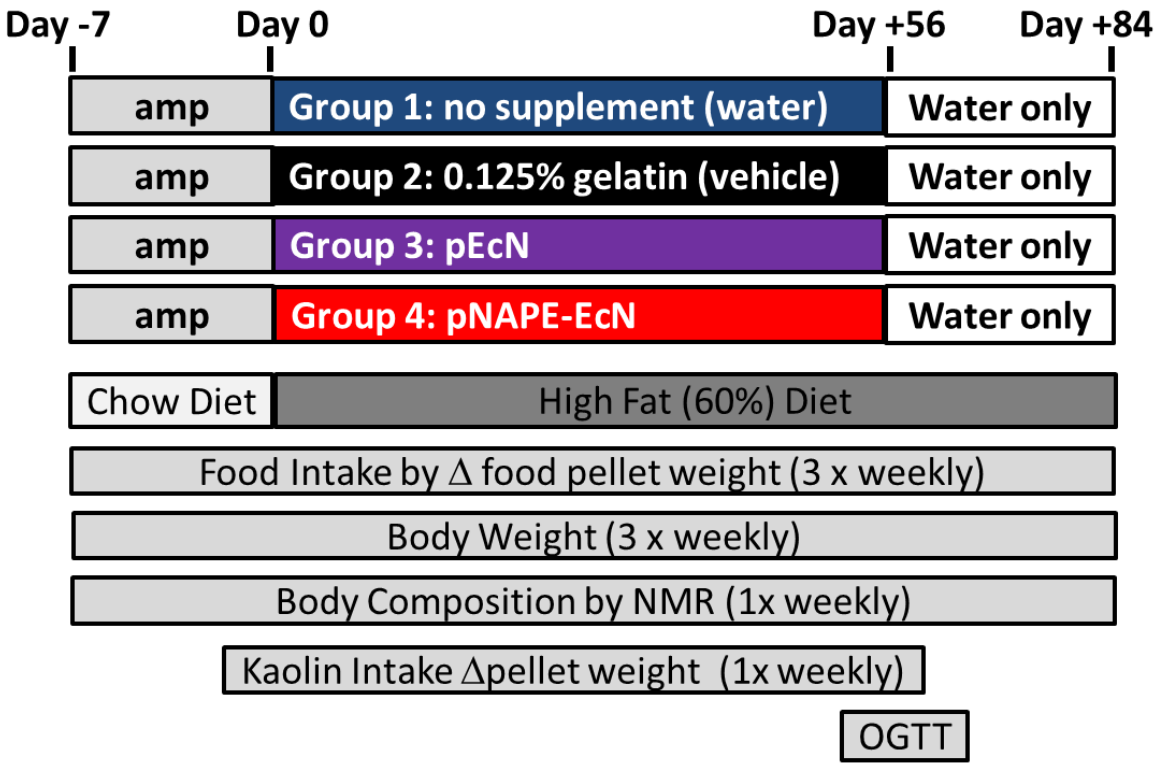

**Supplemental Figure 5**. Transformation of EcN with At1g78690 (pNAPE-EcN) markedly increases levels of saturated and monounsaturated NAPE species compared to EcN transformed with empty vector (pEcN). Horizontal bar represents mean of duplicate samples.



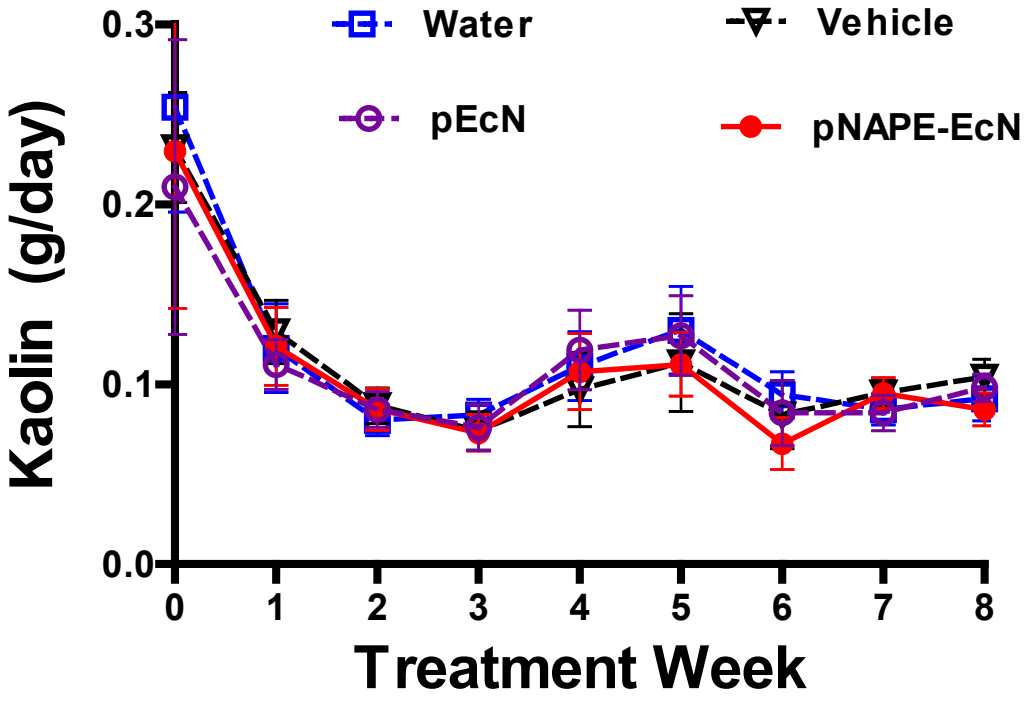

**Supplemental Figure 6.** Viability and retention of NAPE expression plasmid during incubation of pNAPE-EcN in drinking water for 48 h. **A**. The number of viable bacteria present in drinking water supplemented with $5x10^9$ cfu/ml pEcN (E) or pNAPE-EcN (N) prior to (pre) and following (post) 48 incubation at room temperature. (n = 3 per group). **B**. Percent of viable colonies that maintained subsequent ampicillin resistance (i.e. NAPE expression plasmid) despite incubation without selection for 48 h.



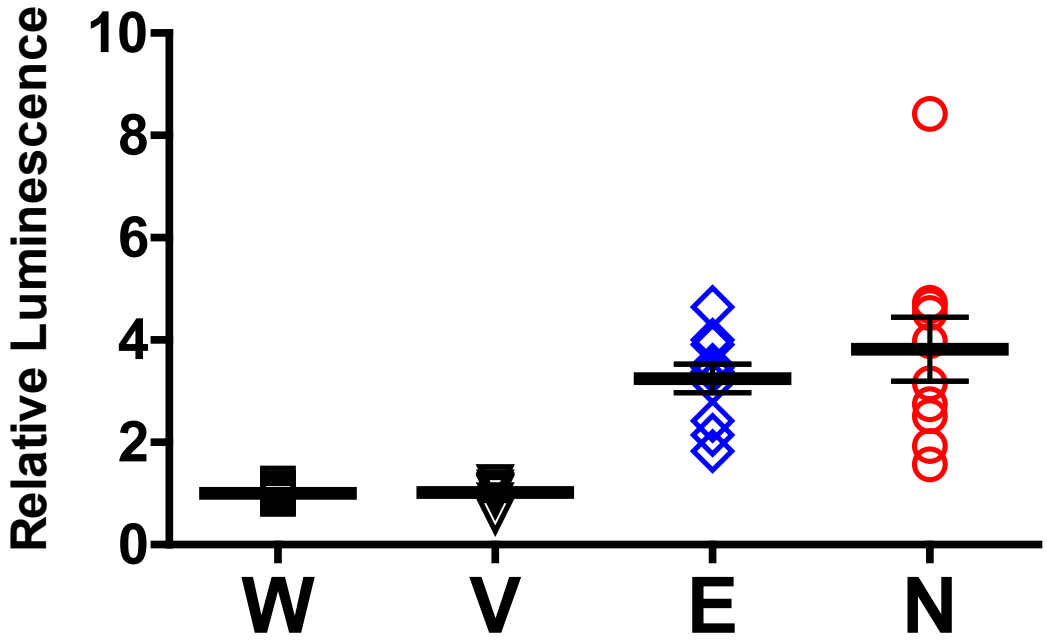

**Supplemental Figure 7** pNAPE-EcN supplemented in drinking water accumulates in the gut. Mice were given either standard drinking water (water only) or water supplemented with $5x10^9$cfu of pNAPE-EcN (which are bioluminescent due to insertion of luciferase operon) for four days. The underbellies of the mice were shaved to reduce light absorbance during emission from the gut. Emitted luminescence was measured by IVIS imaging system. Luminescent intensity is shown as false color overlaid on black and white image of mice, with the quantified intensity within the region of interest (ROI) shown above each animal.



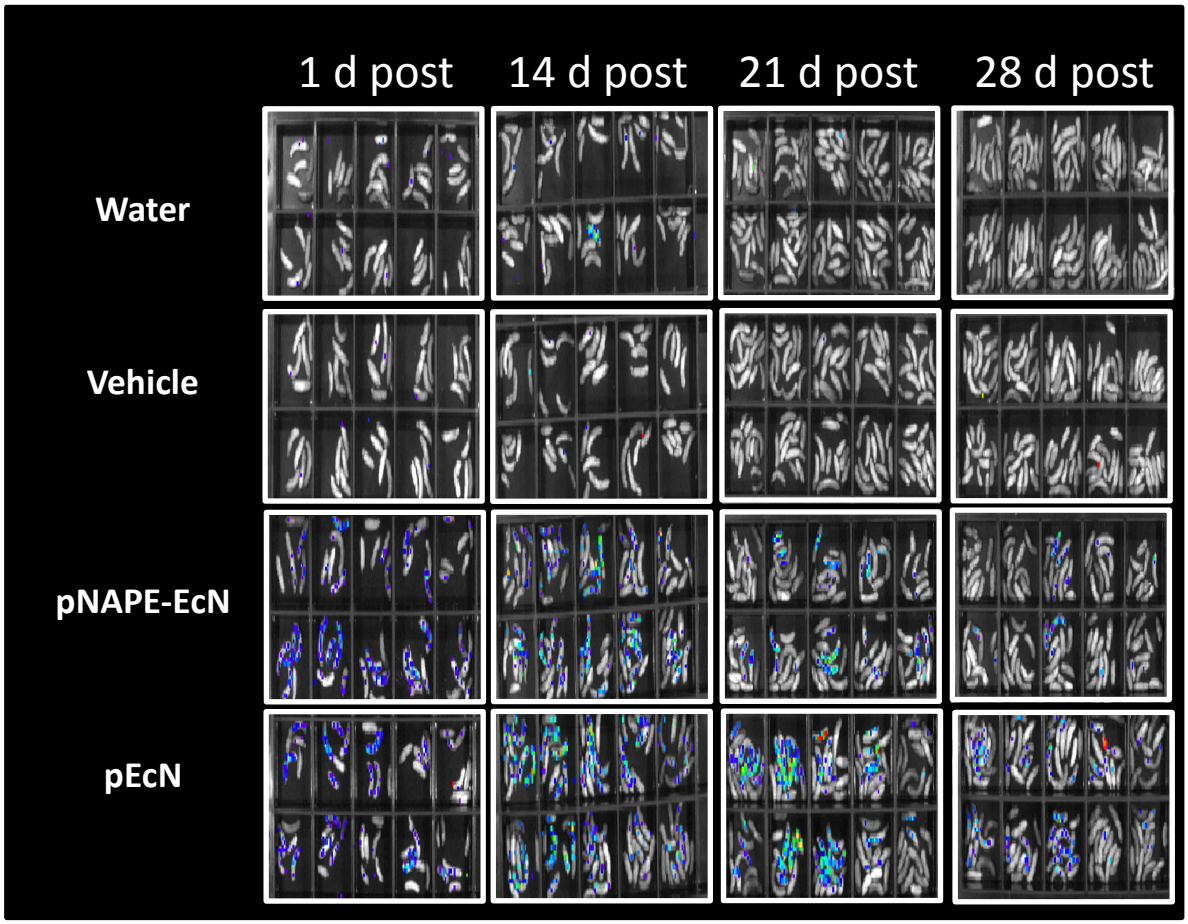

**Supplemental Figure 8.** Experimental Design. Male C57BL6 mice (n=10 mice per group) were given ampicillin for the 7 days prior to starting treatment with bacteria. At start of treatment, all mice began a high fat diet. Mice were treated using drinking water supplemented with $5x10^9$ cfu/ml pNAPE-EcN, $5x10^9$ cfu/ml pEcN, 0.125% gelatin (vehicle), or no treatment (water). Food intake and body weight were measured three times per week and body fat composition and kaolin intake were measured once a week. An oral glucose tolerance test (OGTT) was performed after the last treatment day. After cessation of bacterial treatment, food intake and body parameters were followed for another 4 weeks.




**Supplementa1 Figure 9.** Supplementation of drinking water with bacteria did not induce gastrointestinal distress. Distress was monitored by consumption of kaolin clay pellets (pica), with pre-weighed pellets added to the cages and change in pellet weight measured once a week and then averaged per day. Results are shown as mean±SEM (n=10 mice per group). There was no significant difference between groups.

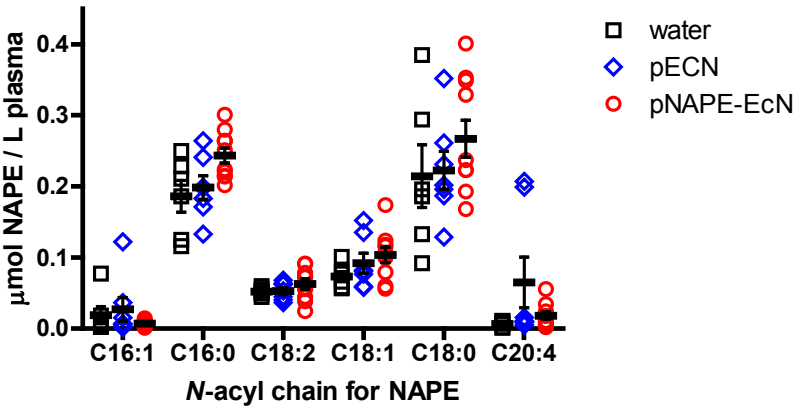



**Supplemental Figure 10.** Secretion of NAPE does not cause overgrowth of EcN. Intestinal levels of pEcN (E) and pNAPE-EcN (N) were measured by in vivo imaging in comparison to mice receiving standard drinking water (W) or vehicle (V) (n=10 per group, mean ± SEM). Bioluminescence levels were not significantly different between pEcN and pNAPE-EcN, indicating that differences in food intake and adiposity are not the result of increased bacterial load**.**

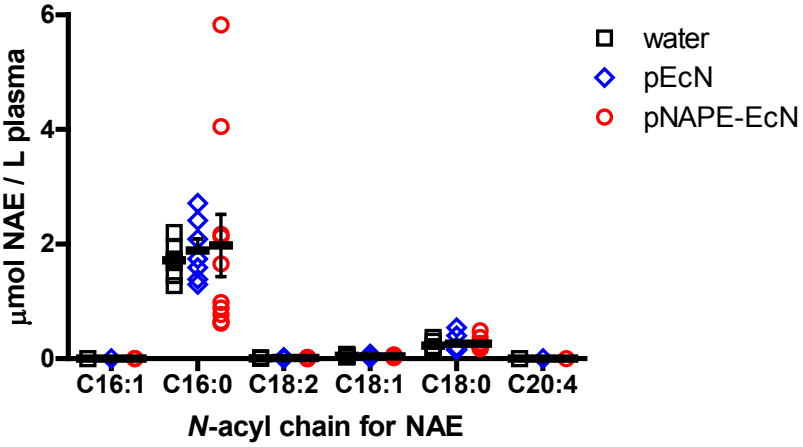



**Supplemental Figure 11.** Bioluminescent bacteria continue to be excreted in feces for at least 4 weeks after cessation of bacterial administration. Feces from each mouse cage (n=10 mice per group) were collected 1 day, 14 days, 21 days, and 28 days post-treatment and placed in 24-well plates (1 well per mouse). Luminescence of all feces collected on the same day were measured simultaneously using an IVIS instrument. Images from separate collection days have been placed side by side above. Intensity is displayed using false-color.

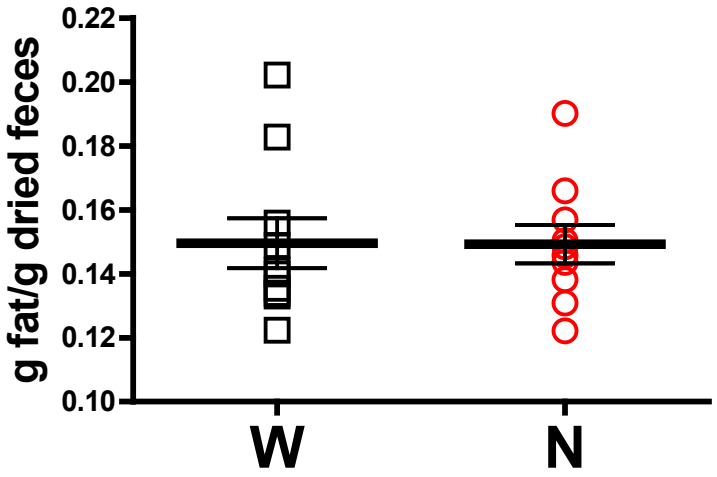
A



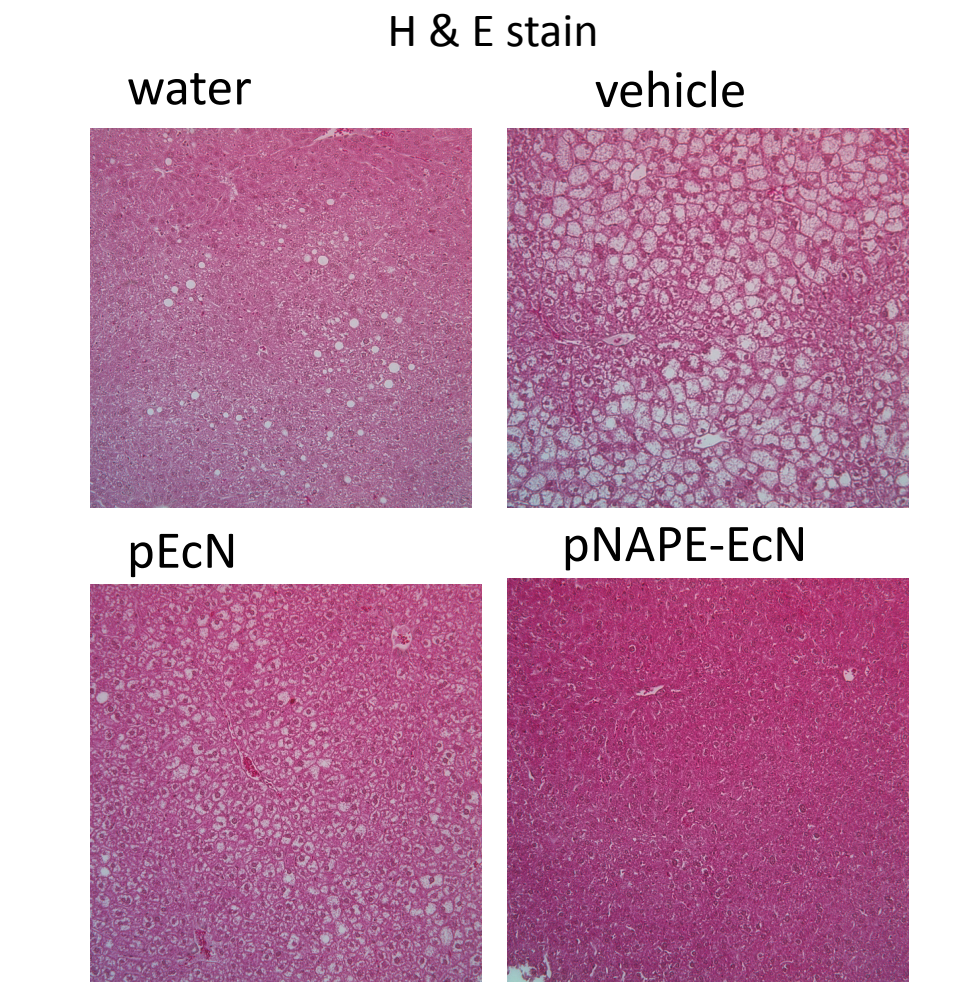

B

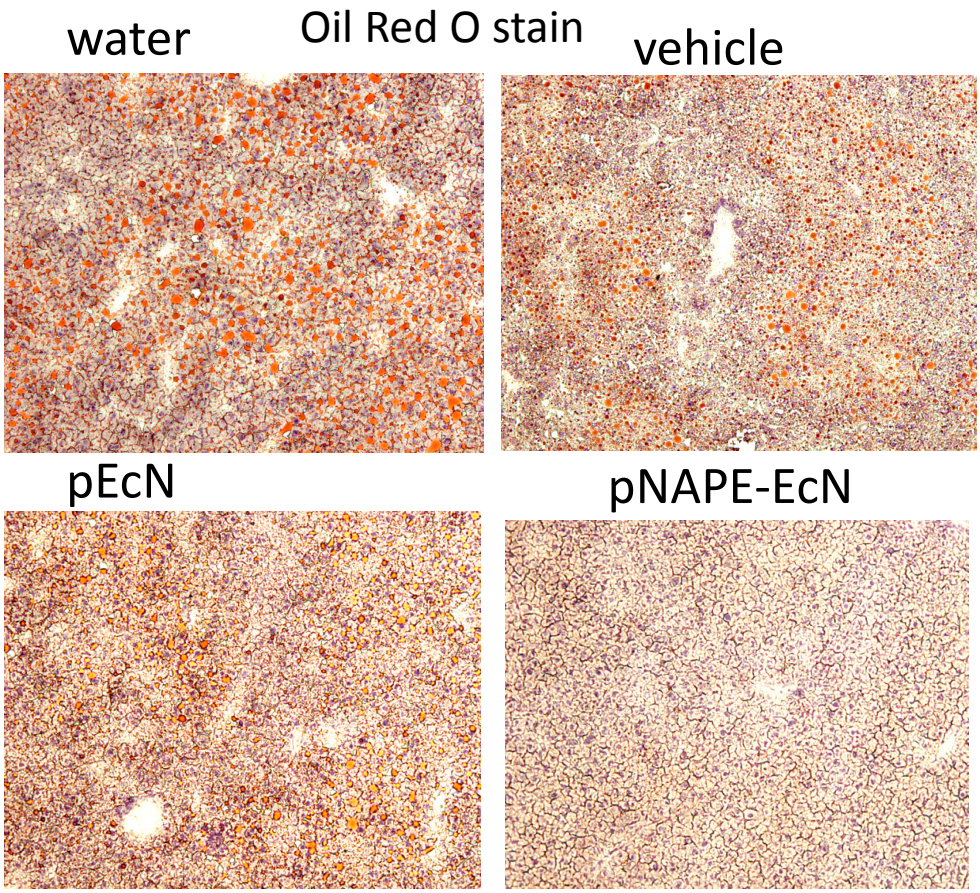



**Supplemental Figure 12.** Treatment with pNAPE-EcN does not increase plasma NAPE or NAE levels. Mice were treated for five weeks and fasted for 4 h prior to blood collection. NAPE and NAE were measured by LC/MS in all samples where sufficient plasma was obtained for measurement. (All values represent mean ± SEM; n=6 mice, standard water treatment; n=7 mice, pEcN; and n=10, pNAPE-EcN) A. Plasma NAPE levels. There were no significant differences between groups for individual NAPE species or for the summed total NAPE (0.55±0.06 µM, water, 0.66±0.06 µM, pEcN, or 0.70±0.06 µM, pNAPE-EcN; 1wayANOVA p=0.134) B. Plasma NAE levels. There were no significant differences between groups for individual NAE species or for the summed total NAE (2.01±0.14 µM, water, 2.21±0.26 µM, pEcN, or 2.30±0.57 µM, pNAPE-EcN; 1wayANOVA p=0.910).

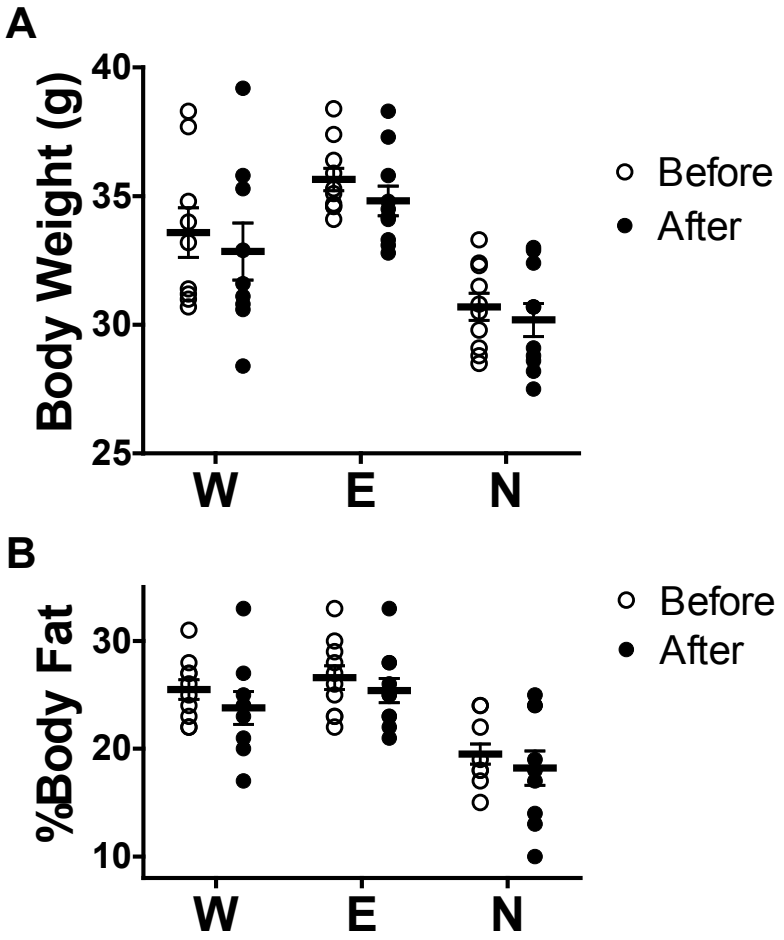



**Supplemental Figure 13** Treatment with pNAPE-EcN does not significantly change fecal lipid content. Feces were collected from mice fed high fat diet with standard drinking water (W) or HFD with water supplemented with $5x10^9$ cfu pNAPE-EcN (N) for 8 weeks, and the dried feces analyzed for total lipid by extraction in hexane/isoproponal. (Bars represent mean ± SEM, n=10 mice per group).

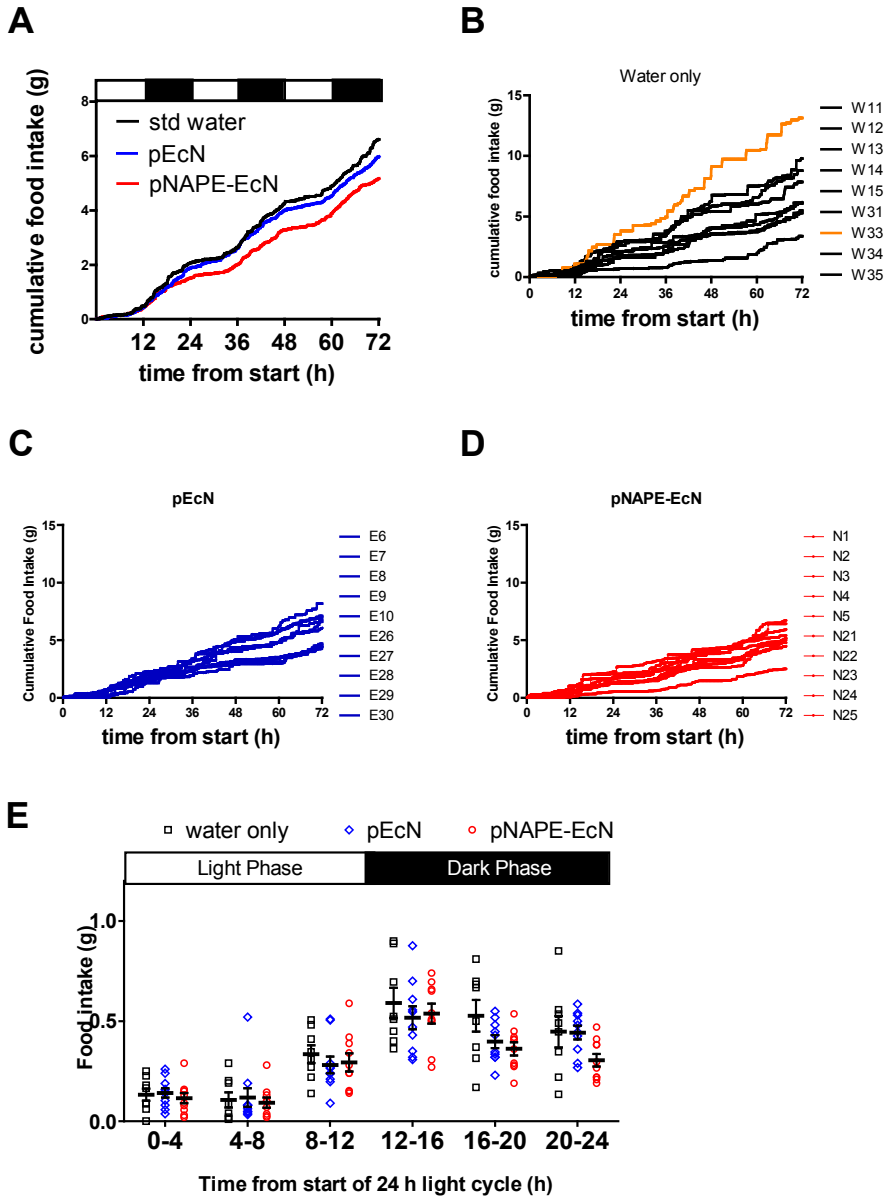


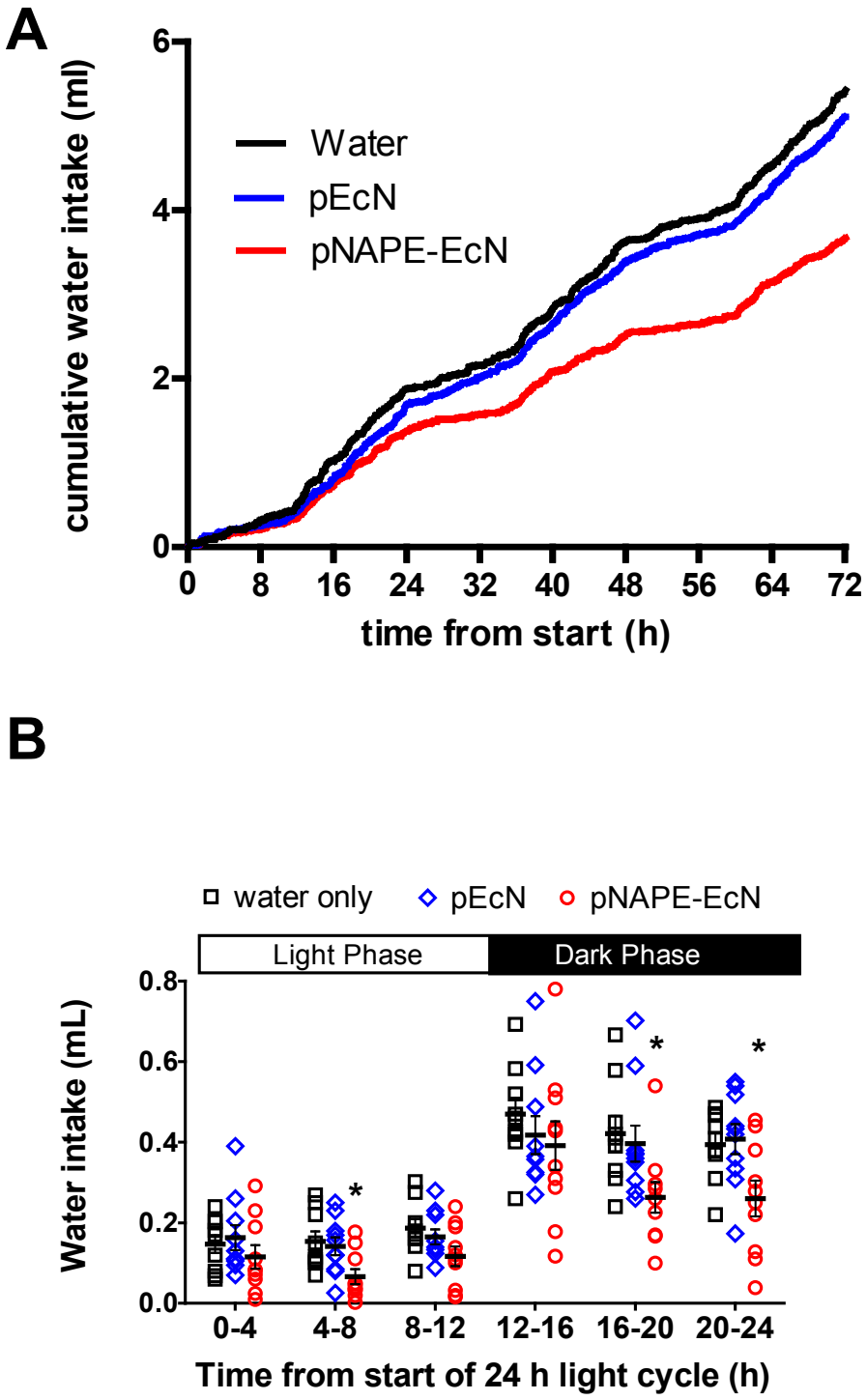

**Supplemental Figure 14**
Treatment with pNAPE-EcN reduces triglyceride accumulation in liver. Top panels: hemotoxylin and eosin (H&E) stain of liver sections. Lower panels: Oil Red O stain of liver sections. Magnification of each panel is 40 x magnification.



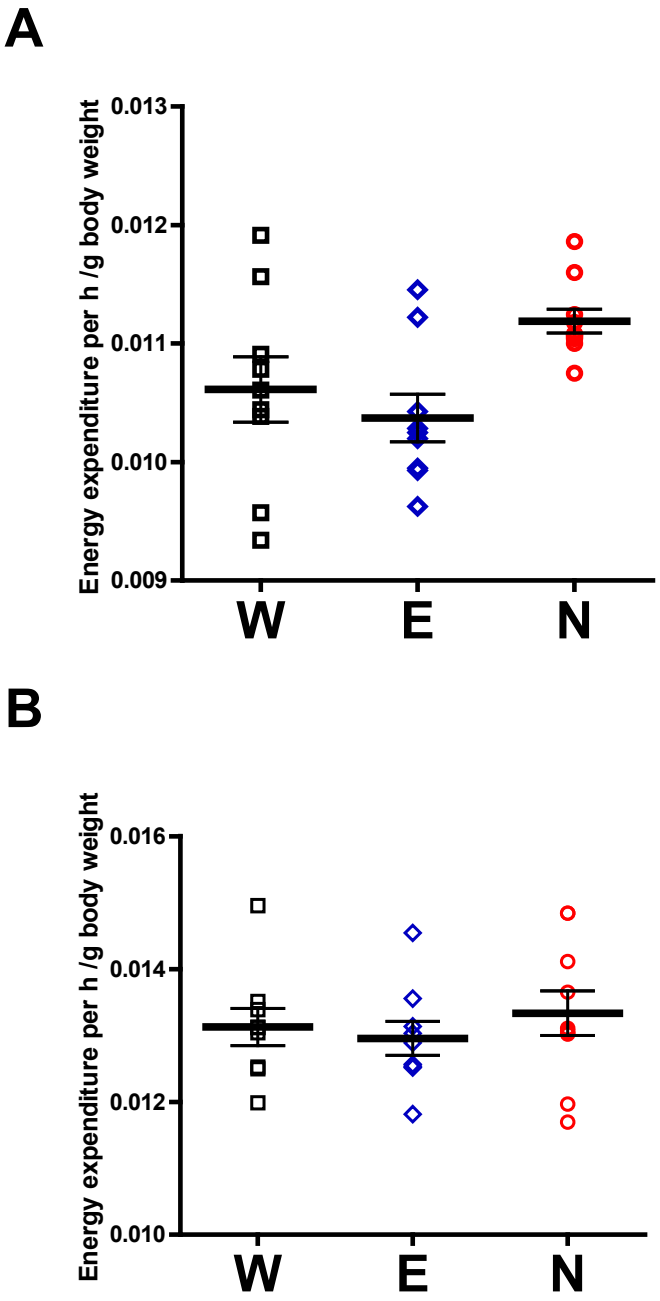

**Supplemental Figure 15.** Effect of 7 day stay in Promethion metabolic monitoring system on body weight and body fat. Mice treated with standard drinking water (W, n=9 mice), pEcN (E, n=10 mice), or pNAPE-EcN (N, n=10 mice) were weighed just prior to transfer to metabolic cages and then immediately following transfer 7 days later. (Bars represent mean± SEM)



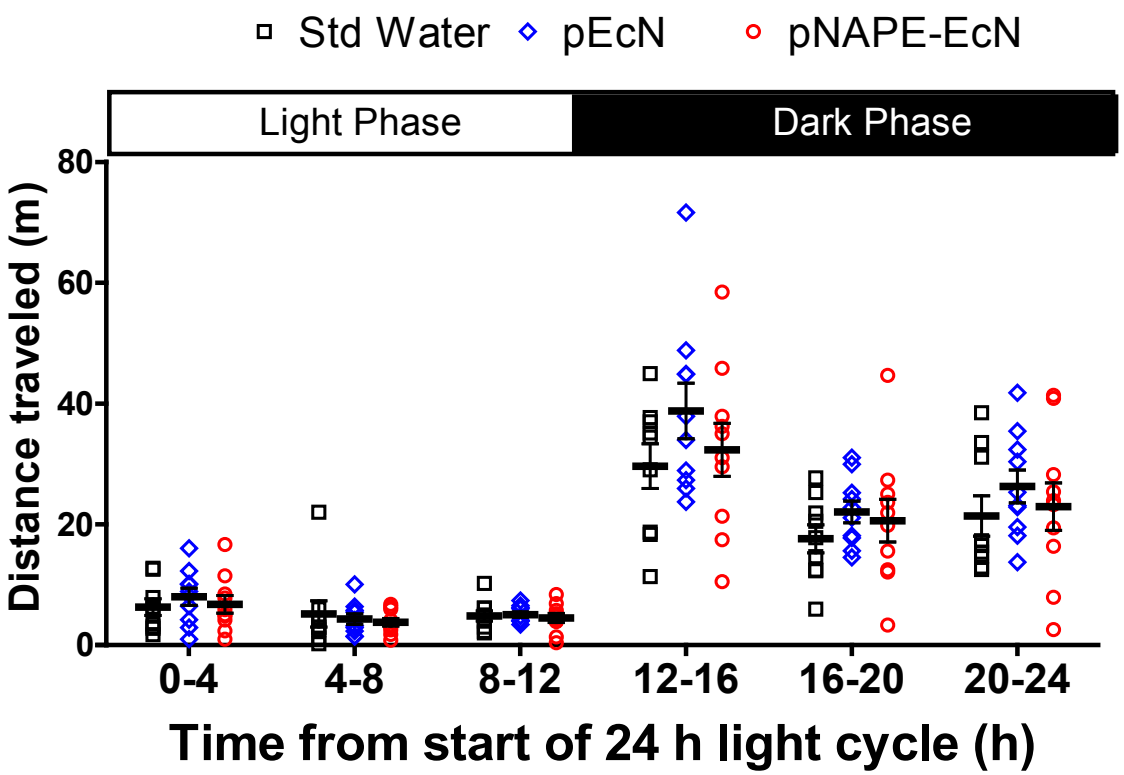

**Supplemental Figure 16**. Effect of pNAPE-EcN treatment on food intake as measured by Sable Promethion system. **A.** Effect of treatment on cumulative food intake during 72 h of continuous monitoring. Average for each group is shown. For standard drinking water group, mouse W33 was not included for group average. **B.** Water only treated mice. The orange colored food intake trace for mouse W33 was excluded from the averaged food intake trace in the analysis shown in A and E of this figure and in Figure 9A and D. This exclusion was based on outlier analysis which showed that the Promethion system recorded an unusually high number of extremely large meal events (category X) for mouse W33 (meal size >3 SD above the grand mean meal size). These large meal events may be the result of the mouse removing a food pellet from the hopper rather than eating the food in the hopper as is typical. Mouse W33 had 17 category X meal events. In contrast, the second largest number of category X meals per mouse was 7 and median number of such meal events was 2. **C.** pEcN treated mice cumulative food intake traces. **D.** pNAPE-EcN treated mice cumulative food intake traces. **E.** Average food intake during each 4 h time block of the 24 light-dark cycle. Each point is average for that 4h time block from the 3 days of monitoring for each individual mouse.



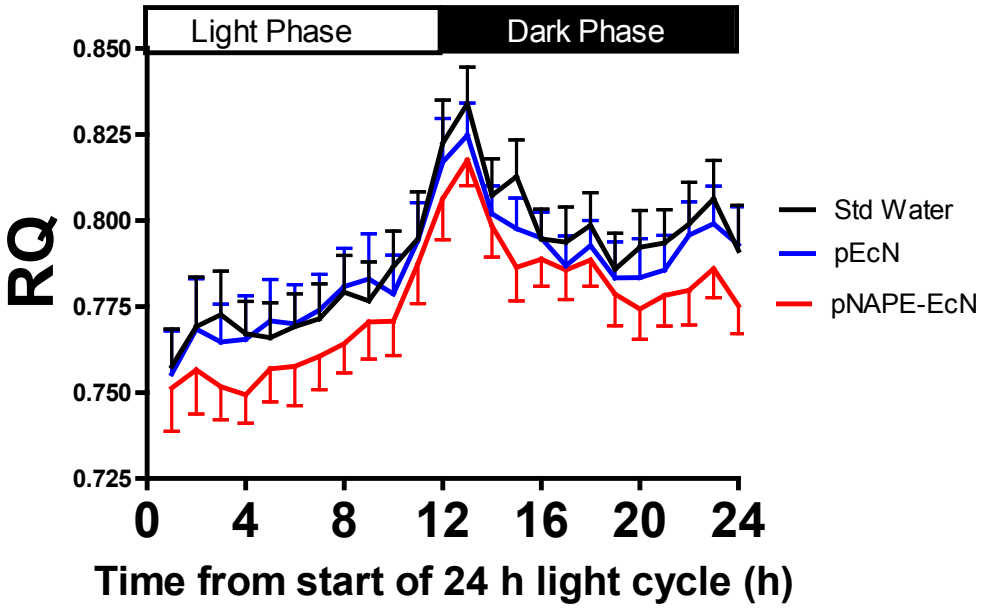

**Supplemental Figure 17**. Effect of pNAPE-EcN on water intake. A. Effect of treatment on cumulative food intake during 72 h of continuous monitoring. Average for each group is shown. B. Average water intake during each 4 h time block of the 24 h light cycle. Each point is average for that 4h block from 3 days of monitoring for each individual mouse. *1wayANOVA $p<0.05$ and Dunnett's Multiple Comparison test $p<0.05$ vs water. (Bars represent mean ± SEM, n=9-10 mice per group).



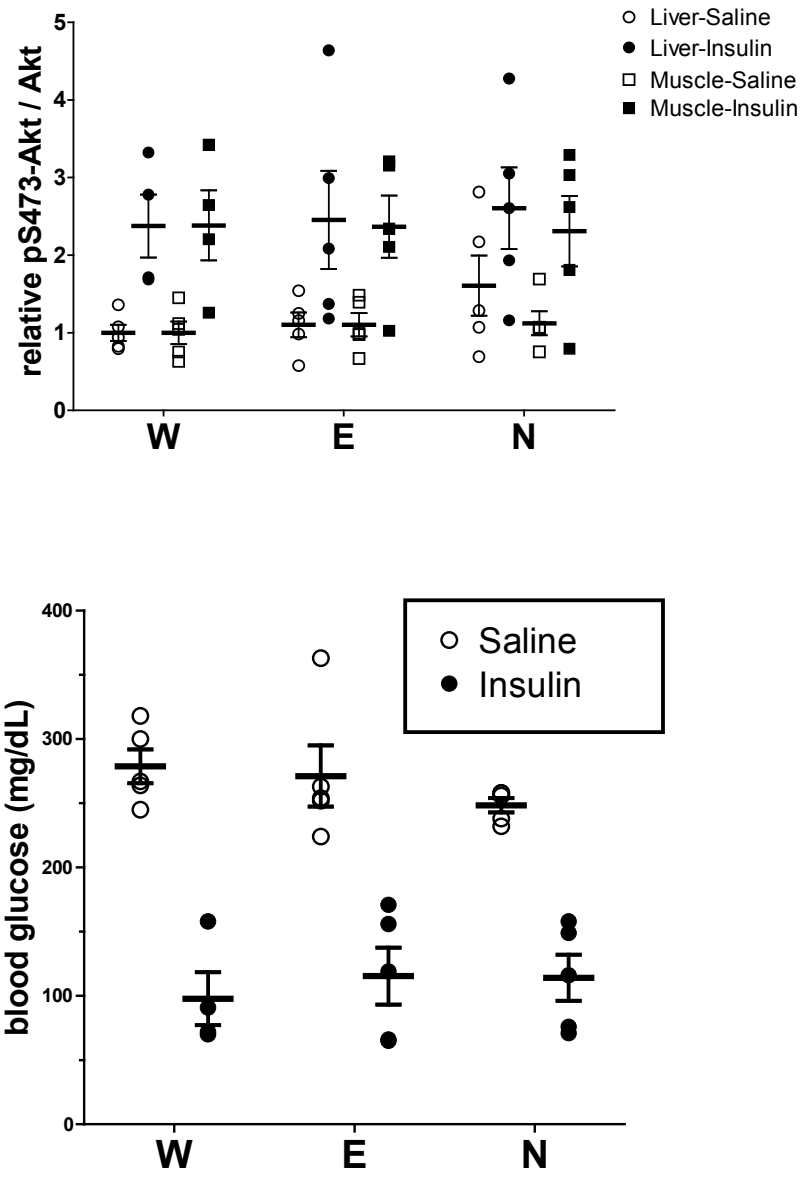

**Supplemental Figure 18**. Effect of pNAPE-EcN treatment on energy expenditure per g body weight. Energy expenditure of mice treated with standard drinking water (W), or with water containing pEcN (E) or pNAPE-EcN (N) was measured by indirect calorimetry using Promethion monitoring system. A. Light phase. 1wayANOVA p=0.0206. B. Dark phase. 1wayANOVA p=0.6612. (All values mean ± SEM, n=9-10 mice per group).



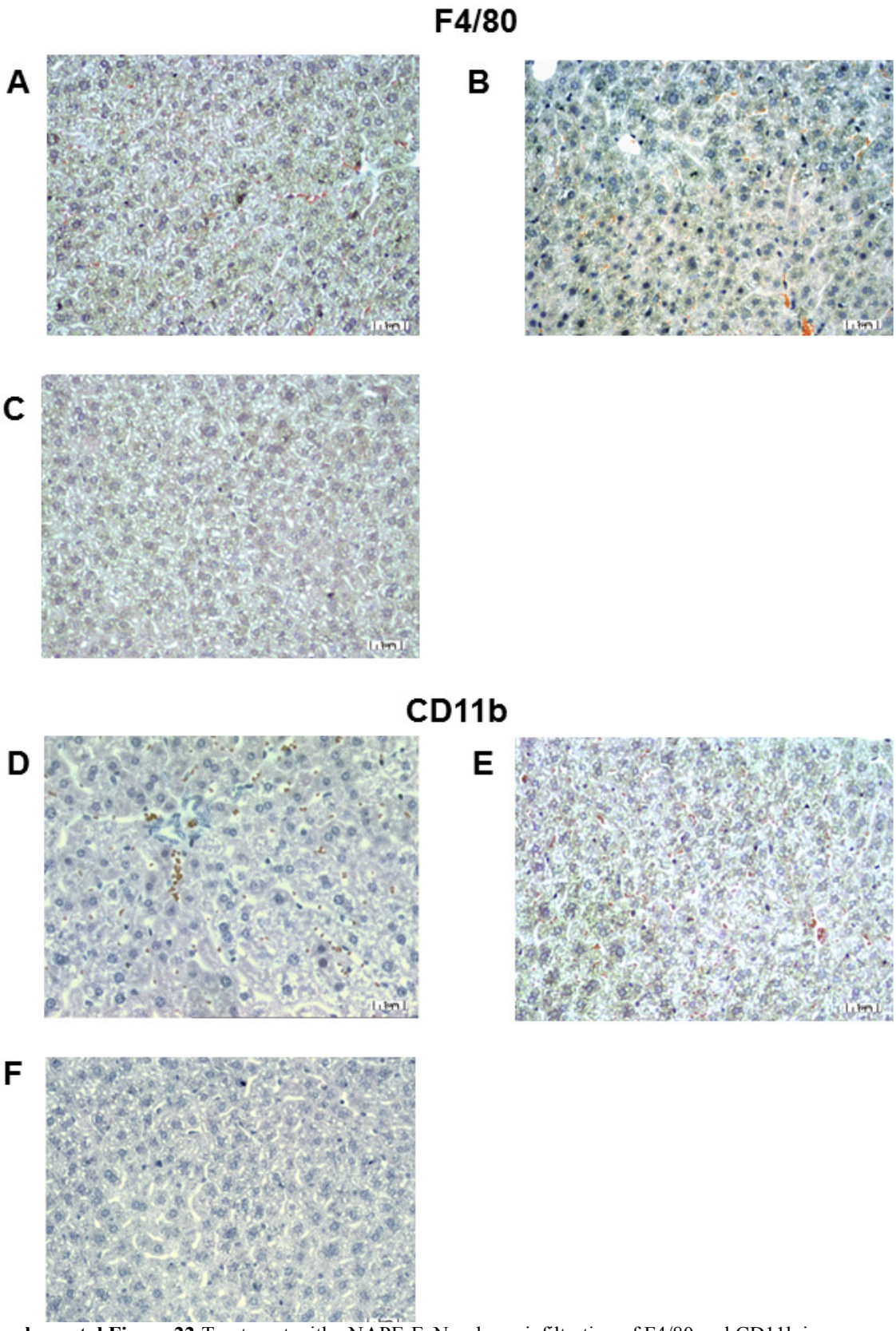

**Supplemental Figure 19**. Effect of treatment on physical activity. Distance traveled was estimated from x y position of beam breaks. There were no statistically significant differences between treatment groups in any of the time blocks. (All values mean ± SEM, n=9-10 mice per group.)




**Supplemental Figure 20.** Effect of pNAPE-EcN treatment on respiratory quotient (RQ). Average hourly RQ for each treatment group (Mean ±SEM, n=9-10 mice per group). There were no statistically significant differences between treatment groups at any time point.




**Supplemental Figure 21.** Treatment with pNAPE-EcN preserves sensitivity to endogenous insulin, but does not increase response to pharmacological dose of insulin. Mice treated with standard water only (W), with pEcN (E), or with pNAPE-EcN (N) for six weeks were fasted for 4 h and then injected i.p. with either saline (to determine response to endogenous levels of insulin, n=5 per group) or 0.75 IU/kg insulin (to determine response to exogenous, pharmacological levels of insulin, n=4-5 per group). 15 min after injection, mice were euthanized and tissue collected. A. Extent of activating phosphorylation of serine 473 of Akt (pAKT) in liver of saline injected mice. All values were normalized to overall Akt levels and expressed relative to average for saline injected, water only treated mice. While insulin injection significantly increased pAkt levels in each treatment group, there were no difference in the insulin-stimulated pAkt levels between the treatment groups. B. Effect of insulin injection on plasma glucose levels. Insulin injection significantly reduced glucose levels in each group compared to saline injection, but there were no significant differences in insulin-stimulated glucose levels between groups.




**Supplemental Figure 22** Treatment with pNAPE-EcN reduces infiltration of F4/80 and CD11b immunopositive leukocytes into liver of TallyHo mice fed standard chow diet. Slides were immunostained with either anti-F4/80 (A-

C) or anti-CD11b (D-F) antibodies (bright red stain) and counter stained with hemotoxylin and eosin. Representative photomicrographs are shown. Bar = 5 μm. A and D. Standard drinking water only. B and E. Treated with pEcN. C and F. Treated with pNAPE-EcN.

**Supplemental Tables**

**Supplemental Table 1.** Expected masses for major phosphatidylethanolamine (PE) and *N*-acyl-PE (NAPE) species in *E. coli Nissle 1917* transformed with At1g78690p.

| **PE species** | | **Resulting NAPE species** | | | |
|---|---|---|---|---|---|
| ***O*-acyl chains** | | ***N*-acyl chain added** | | | |
| | unmodified PE | ***N*-C16:1** | ***N*-C16:0** | ***N*-C17c** | ***N*-C18:1** |
| **C17cy+C16:0** | 702.5 | 938.7 | 940.7 | 952.7 | 966.7 |
| **C16:0+C16:1** | 688.5 | 924.7 | 926.7 | 938.7 | 952.7 |
| **C14:0+C18:1** | 688.5 | 924.7 | 926.7 | 938.7 | 952.7 |
| **C16:0+C16:0** | 690.5 | 926.7 | 928.7 | 940.7 | 954.8 |
| **C14:0+C16:0** | 662.5 | 898.7 | 900.7 | 912.7 | 926.7 |
| **C17cy+C18:0** | 730.5 | 966.7 | 968.7 | 980.7 | 994.8 |
| **C18:1+C16:0** | 716.5 | 952.7 | 954.7 | 966.7 | 980.8 |
| **C18:0+C16:1** | 716.5 | 952.7 | 954.7 | 966.7 | 980.8 |
| **C18:1+C16:1** | 714.5 | 950.7 | 952.7 | 964.7 | 978.8 |

**Supplemental Table 2.** Expected masses for major phosphatidylglycerol (PG) and O-acyl PG (acyl-PG) species in *E.coli Nissle 1917* transformed with At1g78690p.

| **PG species** | | **Resulting Acyl-PG species** | | | |
|---|---|---|---|---|---|
| **O-acyl chains** | | ***O*-acyl chain added** | | | |
| | **Unmodified PG** | **O-C16:1** | **O-C16:0** | **O-C17cy** | **O-C18:1** |
| **C17c+C16:0** | 733.5 | 969.7 | 971.7 | 983.7 | 997.7 |
| **C16:0+C16:1** | 719.5 | 955.7 | 957.7 | 969.7 | 983.7 |
| **C14:0+C18:1** | 719.5 | 955.7 | 957.7 | 969.7 | 983.7 |
| **C16:0+C16:0** | 721.5 | 957.7 | 959.7 | 971.7 | 985.7 |
| **C14:0+C16:0** | 693.5 | 929.7 | 931.7 | 943.7 | 957.7 |
| **C17c+C18:0** | 761.5 | 997.7 | 999.7 | 1011.7 | 1025.7 |
| **C18:1+C16:0** | 747.5 | 983.7 | 985.7 | 997.7 | 1011.7 |
| **C18:0+C16:1** | 747.5 | 983.7 | 985.7 | 997.7 | 1011.7 |
| **C18:1+C16:1** | 745.5 | 981.7 | 983.7 | 995.7 | 1009.7 |

**Supplementa1 Table 3.** Effect of pNAPE-EcN administration on muscle strength, speed, and coordination.

| | **Water** | **Vehicle** | **pEcN** | **pNAPE-EcN** | **ANOVA** |
|---|---|---|---|---|---|
| Inverted screen latency to fall (secs)† | 50.7±18.8 | 50.6±13.3 | 57.6±7.6 | 53.0±14.82 | 0.6637 |
| Wire hang latency to fall (secs)† | 32.2±21.2 | 43.7±18.9 | 52.5±12.8 | 53.8±12.7 | 0.0249 |
| Pole descent latency (secs) | 15.7±5.7 | 12.6±2.1 | 17.0±6.7 | 12.8±5.7 | 0.1920 |
| †Maximum latency to fall allowed was 60 secs. | | | | | |

# Supplementary Table 4

| | Week 8 %total bacteria | | | | | | Week 12 %total bacteria | | | | | | Week 8 t-test | | | Week 12 t-test | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | vehicle | | pEcN | | pNAPE-EcN | | vehicle | | pEcN | | pNAPE-EcN | | pEcN | pNAPE-EcN | pNAPE-EcN | pEcN | pNAPE-EcN | pNAPE-EcN |
| **Species** | **mean** | SD | **mean** | SD | **mean** | SD | **mean** | SD | **mean** | SD | **mean** | SD | vs veh | vs veh | vs pEcN | vs veh | vs veh | vs pEcN |
| **Bacteroidetes** | | | | | | | | | | | | | | | | | | |
| algoriphagus hongiella aquaeductus | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.03 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | |
| alistipes finegoldii | **4.14** | 3.26 | **2.94** | 3.07 | **2.69** | 2.43 | **11.26** | 4.90 | **6.97** | 4.75 | **4.47** | 2.65 | | | | 0.07 | 0.00 | |
| alistipes massiliensis | **0.71** | 0.50 | **0.64** | 0.71 | **0.61** | 0.60 | **3.91** | 1.97 | **3.06** | 2.22 | **1.76** | 0.97 | | | | | 0.01 | |
| alistipes putredinis | **0.71** | 0.55 | **0.49** | 0.46 | **0.43** | 0.38 | **2.43** | 1.31 | **1.69** | 1.19 | **0.97** | 0.61 | | | | | 0.01 | |
| bacteroides acidifaciens | **15.97** | 7.46 | **27.80** | 8.59 | **26.60** | 5.83 | **12.82** | 4.01 | **13.32** | 3.94 | **14.56** | 3.99 | 0.01 | 0.00 | | | | |
| bacteroides capillosus | **0.60** | 0.25 | **0.86** | 1.22 | **0.51** | 0.47 | **1.13** | 0.65 | **2.10** | 1.28 | **1.88** | 0.53 | | | | 0.06 | 0.01 | |
| bacteroides coprophilus | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.11** | 0.12 | **0.15** | 0.15 | | | | 0.01 | 0.01 | |
| bacteroides massiliensis | **3.71** | 6.02 | **5.08** | 3.31 | **4.42** | 2.82 | **2.55** | 2.41 | **5.22** | 3.69 | **3.59** | 2.38 | | | | 0.08 | | |
| bacteroides ovatus | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | |
| bacteroides pectinophilus | **6.91** | 3.04 | **0.07** | 0.10 | **0.16** | 0.11 | **7.14** | 2.87 | **6.43** | 3.64 | **10.99** | 4.16 | 0.00 | 0.00 | 0.08 | | 0.03 | 0.02 |
| bacteroides uniformis | **2.56** | 1.57 | **7.89** | 2.66 | **5.51** | 2.17 | **4.72** | 3.82 | **9.93** | 2.97 | **9.59** | 6.22 | 0.00 | 0.00 | 0.05 | 0.00 | 0.06 | |
| bacteroides xylanisolvens | **2.14** | 1.49 | **5.18** | 1.55 | **4.98** | 1.13 | **2.44** | 0.67 | **2.00** | 0.68 | **2.90** | 1.56 | 0.00 | 0.00 | | | | |
| chitinophaga arvensicola | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.02 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | |
| cytophaga hutchinsonii | **0.00** | 0.00 | **0.00** | 0.00 | **0.03** | 0.07 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | |
| flavobacterium columnare | **0.00** | 0.00 | **0.00** | 0.00 | **0.02** | 0.05 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | |
| flavobacterium flevense | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.03 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | |
| flavobacterium succinicans | **0.00** | 0.00 | **0.00** | 0.00 | **0.06** | 0.08 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | 0.04 | 0.05 | | | |
| parabacteroides distasonis | **0.60** | 1.13 | **0.69** | 0.89 | **0.03** | 0.08 | **2.50** | 1.83 | **2.48** | 1.90 | **2.64** | 1.90 | | | 0.03 | | | |
| parabacteroides goldsteinii | **19.35** | 12.09 | **27.10** | 7.26 | **22.48** | 4.75 | **10.86** | 4.03 | **6.88** | 2.82 | **7.85** | 4.30 | | | | 0.02 | | |
| parabacteroides merdae | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | |
| pedobacter cryoconitis | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.02 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | |
| pontibacter korlensis | **0.08** | 0.13 | **0.10** | 0.18 | **0.00** | 0.00 | **0.47** | 0.35 | **0.16** | 0.17 | **0.32** | 0.37 | | 0.09 | 0.09 | 0.02 | | |
| porphyromonas cangingivalis | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.02 | **0.01** | 0.02 | | | | | | |
| prevotella oralis | **0.00** | 0.00 | **0.01** | 0.04 | **0.00** | 0.00 | **0.00** | 0.00 | **0.38** | 0.87 | **0.00** | 0.00 | | | | | | |
| | | | | | | | | | | | | | | | | | | |
| **Firmicutes** | | | | | | | | | | | | | | | | | | |
| anaeroplasma bactoclasticum | **0.02** | 0.04 | **0.00** | 0.00 | **0.00** | 0.00 | **0.07** | 0.13 | **0.01** | 0.03 | **0.00** | 0.02 | | | | | | |
| anaerostipes caccae | **0.11** | 0.09 | **0.06** | 0.11 | **0.04** | 0.04 | **0.08** | 0.07 | **0.02** | 0.03 | **0.03** | 0.03 | | 0.03 | | 0.03 | 0.03 | |
| anaerostipes clostridium fimetarium | **0.01** | 0.02 | **0.00** | 0.00 | **0.01** | 0.01 | **0.01** | 0.01 | **0.01** | 0.02 | **0.01** | 0.01 | | | | | | |
| anaerotruncus colihominis | **0.31** | 0.23 | **0.02** | 0.01 | **0.08** | 0.05 | **0.17** | 0.13 | **0.31** | 0.26 | **0.27** | 0.20 | 0.00 | 0.01 | 0.01 | | | |
| blautia hydrogenotrophica | **0.13** | 0.16 | **0.02** | 0.05 | **0.06** | 0.11 | **0.02** | 0.03 | **0.16** | 0.16 | **0.16** | 0.15 | 0.08 | | | 0.02 | 0.01 | |
| blautia producta | **0.40** | 0.42 | **0.54** | 0.75 | **0.70** | 0.48 | **0.42** | 0.36 | **0.57** | 0.45 | **0.67** | 0.47 | | | | | | |
| blautia ruminococcus obeum | **0.03** | 0.03 | **0.00** | 0.00 | **0.01** | 0.02 | **0.09** | 0.13 | **0.03** | 0.04 | **0.05** | 0.06 | 0.03 | | 0.05 | | | |
| bryantella formatexigens | **0.04** | 0.04 | **0.06** | 0.06 | **0.07** | 0.04 | **0.05** | 0.06 | **0.05** | 0.05 | **0.06** | 0.10 | | 0.09 | | | | |
| clostridium acetireducens | **0.08** | 0.13 | **0.01** | 0.02 | **0.00** | 0.00 | **0.08** | 0.09 | **0.05** | 0.05 | **0.03** | 0.02 | | 0.08 | 0.10 | | 0.10 | |
| clostridium aerotolerans | **0.04** | 0.08 | **0.02** | 0.02 | **0.02** | 0.03 | **0.02** | 0.03 | **0.02** | 0.03 | **0.03** | 0.03 | | | | | | |
| clostridium aldenense | **1.66** | 2.10 | **0.41** | 0.31 | **0.89** | 0.57 | **0.04** | 0.04 | **0.22** | 0.21 | **0.09** | 0.05 | 0.10 | | 0.04 | 0.02 | 0.02 | 0.08 |
| clostridium algidixylanolyticum | **0.00** | 0.01 | **0.00** | 0.00 | **0.00** | 0.00 | **0.02** | 0.03 | **0.01** | 0.01 | **0.02** | 0.04 | | | | | | |
| clostridium asparagiforme | **0.06** | 0.12 | **0.00** | 0.00 | **0.00** | 0.00 | **0.03** | 0.07 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | |
| clostridium bartlettii | **0.41** | 0.40 | **0.01** | 0.04 | **0.01** | 0.01 | **1.01** | 0.71 | **0.42** | 0.25 | **0.35** | 0.14 | 0.01 | 0.01 | | 0.02 | 0.01 | |
| clostridium bifermentans | **0.60** | 0.49 | **0.00** | 0.00 | **0.00** | 0.00 | **0.85** | 0.62 | **0.36** | 0.22 | **0.38** | 0.12 | 0.00 | 0.00 | | 0.03 | 0.03 | |
| clostridium bolteae | **0.00** | 0.01 | **0.01** | 0.02 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.01 | **0.00** | 0.01 | | | | | | |
| clostridium celerecrescens | **0.00** | 0.00 | **0.01** | 0.01 | **0.01** | 0.01 | **0.00** | 0.00 | **0.00** | 0.01 | **0.00** | 0.00 | 0.06 | 0.03 | | 0.09 | | |
| clostridium cocleatum | **3.98** | 4.66 | **0.58** | 1.14 | **0.38** | 0.26 | **0.79** | 0.43 | **0.55** | 0.24 | **0.42** | 0.22 | 0.05 | 0.03 | | | 0.03 | |
| clostridium difficile | **0.26** | 0.43 | **0.36** | 0.19 | **0.27** | 0.10 | **0.00** | 0.00 | **0.28** | 0.23 | **0.22** | 0.22 | | | | 0.00 | 0.01 | |
| clostridium disporicum | **0.18** | 0.23 | **0.00** | 0.00 | **0.00** | 0.00 | **0.09** | 0.14 | **0.02** | 0.04 | **0.03** | 0.03 | 0.03 | 0.02 | | | | |
| clostridium fusiformis cm973 | **1.22** | 0.82 | **0.34** | 0.27 | **0.43** | 0.16 | **0.76** | 0.40 | **0.97** | 0.35 | **0.99** | 0.37 | 0.01 | 0.01 | | | | |
| clostridium hathewayi | **0.40** | 0.26 | **0.35** | 0.56 | **0.55** | 0.41 | **0.23** | 0.23 | **0.55** | 0.32 | **0.46** | 0.18 | | | | 0.02 | 0.03 | |
| clostridium hylemonae | **0.29** | 0.21 | **0.03** | 0.05 | **0.08** | 0.12 | **0.17** | 0.20 | **0.23** | 0.16 | **0.30** | 0.13 | 0.00 | 0.01 | | | 0.10 | |
| clostridium indolis | **0.09** | 0.13 | **0.08** | 0.17 | **0.06** | 0.13 | **0.09** | 0.13 | **0.06** | 0.07 | **0.08** | 0.11 | | | | | | |
| clostridium innocuum | **0.55** | 0.78 | **0.69** | 0.61 | **0.54** | 0.49 | **0.04** | 0.04 | **0.17** | 0.24 | **0.04** | 0.05 | | | | | | |
| clostridium lactatifermentans | **0.50** | 0.55 | **0.05** | 0.06 | **0.04** | 0.06 | **0.29** | 0.18 | **0.50** | 0.30 | **0.24** | 0.17 | 0.03 | 0.02 | | 0.09 | | 0.03 |
| clostridium lavalense | **2.45** | 2.19 | **1.87** | 1.70 | **1.84** | 2.39 | **3.82** | 2.53 | **3.84** | 1.65 | **3.95** | 1.66 | | | | | | |
| clostridium leptum | **1.26** | 1.92 | **0.15** | 0.21 | **0.35** | 0.48 | **1.17** | 0.61 | **1.56** | 2.68 | **0.73** | 1.07 | 0.10 | | | | | |
| clostridium metallolevans | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.01 | **0.01** | 0.01 | **0.00** | 0.01 | | | | | | |
| clostridium methoxybenzovorans | **0.03** | 0.03 | **0.00** | 0.01 | **0.00** | 0.01 | **0.03** | 0.07 | **0.02** | 0.03 | **0.02** | 0.02 | 0.02 | 0.02 | | | | |
| clostridium methylpentosum | **0.66** | 0.44 | **0.01** | 0.02 | **0.02** | 0.05 | **0.74** | 0.46 | **0.53** | 0.41 | **0.63** | 0.35 | 0.00 | 0.00 | | | | |
| clostridium orbiscindens | **0.32** | 0.28 | **0.00** | 0.00 | **0.00** | 0.01 | **0.41** | 0.30 | **0.11** | 0.12 | **0.13** | 0.16 | 0.00 | 0.00 | | 0.01 | 0.02 | |
| clostridium papyrosolvens | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.02** | 0.05 | **0.00** | 0.01 | **0.04** | 0.12 | | | | | | |
| clostridium propionicum | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.02 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | |
| clostridium saccharolyticum | **3.15** | 3.55 | **2.59** | 3.69 | **7.25** | 8.31 | **0.82** | 0.51 | **3.69** | 3.69 | **4.30** | 6.20 | | | | 0.03 | | |
| clostridium scindens | **6.20** | 2.51 | **1.73** | 1.21 | **2.81** | 1.39 | **7.98** | 3.65 | **8.01** | 3.47 | **9.68** | 4.90 | 0.00 | 0.00 | 0.09 | | | |
| clostridium sphenoides | **0.01** | 0.02 | **0.04** | 0.03 | **0.04** | 0.04 | **0.14** | 0.07 | **0.09** | 0.06 | **0.12** | 0.11 | 0.02 | 0.04 | | 0.10 | | |
| clostridium subterminale | **0.00** | 0.01 | **0.02** | 0.03 | **0.01** | 0.01 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | 0.07 | | | | | |
| clostridium sulfatireducens | **0.49** | 0.36 | **0.06** | 0.06 | **0.10** | 0.20 | **0.26** | 0.24 | **0.32** | 0.19 | **0.35** | 0.18 | 0.00 | 0.01 | | | | |
| clostridium symbiosum | **0.09** | 0.13 | **0.19** | 0.15 | **0.12** | 0.17 | **0.06** | 0.09 | **0.04** | 0.04 | **0.27** | 0.24 | | | | | 0.02 | 0.01 |
| clostridium thermocellum | **0.02** | 0.08 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.02 | | | | | | |
| clostridium thiosulfatireducens | **0.85** | 1.07 | **0.81** | 0.70 | **2.20** | 1.29 | **0.17** | 0.29 | **0.80** | 1.36 | **0.47** | 0.81 | | 0.02 | 0.01 | | | |
| clostridium xylanolyticum | **0.64** | 0.35 | **0.64** | 0.35 | **0.69** | 0.46 | **0.90** | 0.72 | **0.74** | 0.61 | **0.90** | 0.77 | | | | | | |
| coprobacillus cateniformis | **0.01** | 0.03 | **0.00** | 0.00 | **0.03** | 0.07 | **0.01** | 0.03 | **0.00** | 0.01 | **0.00** | 0.00 | | | | | | |
| coprococcus catus | **0.02** | 0.02 | **0.00** | 0.00 | **0.00** | 0.00 | **0.09** | 0.10 | **0.01** | 0.01 | **0.04** | 0.05 | 0.04 | 0.03 | | 0.02 | | 0.09 |
| coprococcus clostridium phytofermentans | **0.02** | 0.02 | **0.00** | 0.01 | **0.00** | 0.00 | **0.01** | 0.02 | **0.02** | 0.03 | **0.01** | 0.01 | 0.10 | 0.02 | | | | |
| coprococcus clostridium sp. ss2/1 | **0.02** | 0.05 | **0.02** | 0.05 | **0.00** | 0.01 | **0.12** | 0.14 | **0.06** | 0.06 | **0.03** | 0.03 | | | | | 0.08 | |
| dorea formicigenerans | **0.47** | 0.49 | **0.12** | 0.16 | **0.22** | 0.18 | **0.17** | 0.15 | **0.89** | 0.73 | **0.55** | 0.23 | 0.06 | | | 0.01 | 0.00 | |
| enterococcus faecium | **0.01** | 0.02 | **0.00** | 0.00 | **0.00** | 0.01 | **0.01** | 0.03 | **0.00** | 0.00 | **0.01** | 0.02 | | | | | | |
| enterococcus hirae | **0.03** | 0.05 | **0.01** | 0.02 | **0.01** | 0.02 | **0.03** | 0.09 | **0.03** | 0.06 | **0.03** | 0.05 | | | | | | |
| enterococcus mundtii | **0.05** | 0.08 | **0.03** | 0.05 | **0.04** | 0.06 | **0.02** | 0.04 | **0.01** | 0.03 | **0.07** | 0.17 | | | | | | |
| eubacterium cylindroides | **0.04** | 0.10 | **0.00** | 0.01 | **0.03** | 0.05 | **0.05** | 0.05 | **0.05** | 0.06 | **0.03** | 0.04 | | | | | | |
| eubacterium dolichum | **0.13** | 0.18 | **0.02** | 0.05 | **0.03** | 0.05 | **0.14** | 0.21 | **0.09** | 0.09 | **0.05** | 0.07 | 0.09 | | | | | |
| eubacterium sulci | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.01 | **0.00** | 0.01 | **0.01** | 0.01 | | | | | | |
| faecalibacterium prausnitzii | **0.00** | 0.00 | **0.06** | 0.08 | **0.00** | 0.01 | **0.04** | 0.05 | **0.01** | 0.02 | **0.01** | 0.01 | 0.02 | | 0.02 | 0.06 | 0.09 | |
| lactobacillus johnsonii | **0.00** | 0.00 | **0.00** | 0.00 | **0.02** | 0.05 | **0.00** | 0.00 | **0.00** | 0.00 | **0.12** | 0.38 | | | | | | |
| lactococcus lactis | **1.49** | 1.38 | **0.19** | 0.22 | **0.16** | 0.09 | **0.60** | 0.29 | **0.30** | 0.14 | **0.44** | 0.22 | 0.01 | 0.01 | | 0.01 | | |
| moryella spp. | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.01 | | | | | | |
| oscillospira spp. | **2.27** | 1.14 | **0.40** | 0.19 | **0.55** | 0.30 | **2.22** | 0.58 | **1.92** | 0.63 | **2.44** | 0.66 | 0.00 | 0.00 | | | | 0.09 |
| paenibacillus taiwanensis | **0.11** | 0.34 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | |
| pseudobutyrivibrio fibrisolvens | **0.02** | 0.02 | **0.00** | 0.00 | **0.00** | 0.00 | **0.04** | 0.04 | **0.01** | 0.01 | **0.03** | 0.04 | 0.04 | 0.03 | | 0.09 | | |
| pseudobutyrivibrio ruminis | **0.05** | 0.04 | **0.00** | 0.00 | **0.00** | 0.00 | **0.08** | 0.04 | **0.02** | 0.03 | **0.03** | 0.04 | 0.00 | 0.00 | | 0.00 | 0.01 | |
| roseburia eubacterium rectale | **2.80** | 2.26 | **1.79** | 1.29 | **2.36** | 1.05 | **1.74** | 0.63 | **3.35** | 1.71 | **3.99** | 1.87 | | | | 0.02 | 0.00 | |
| roseburia faecis | **0.00** | 0.00 | **0.01** | 0.02 | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.03 | **0.00** | 0.01 | | | | | | |
| roseburia intestinalis | **1.38** | 0.81 | **1.26** | 0.60 | **2.51** | 1.70 | **1.14** | 0.49 | **1.24** | 1.14 | **0.87** | 0.85 | | 0.07 | 0.05 | | | |
| ruminococcus bromii | **0.05** | 0.07 | **0.01** | 0.02 | **0.00** | 0.00 | **0.04** | 0.06 | **0.00** | 0.01 | **0.03** | 0.04 | | 0.04 | | | | 0.03 |
| ruminococcus flavefaciens | **1.11** | 2.41 | **0.00** | 0.01 | **0.00** | 0.01 | **1.74** | 1.56 | **0.24** | 0.45 | **0.20** | 0.35 | | | | 0.01 | 0.01 | |
| ruminococcus gnavus | **0.40** | 0.29 | **0.05** | 0.05 | **0.14** | 0.10 | **0.38** | 0.20 | **0.38** | 0.20 | **0.28** | 0.14 | 0.00 | 0.02 | 0.03 | | | |
| shuttleworthia satelles | **0.00** | 0.01 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.01 | **0.02** | 0.03 | | | | | | |
| spiroplasma culicicola | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | |
| turicibacter sanguinis | **0.12** | 0.10 | **0.00** | 0.00 | **0.00** | 0.00 | **0.16** | 0.17 | **0.09** | 0.09 | **0.08** | 0.09 | 0.00 | 0.00 | | | | |
| **Continued** | | | | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Other** | | | | | | | | | | | | | | | | | | | |
| adlercreutzia equolifaciens | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.03** | 0.10 | **0.18** | 0.12 | **0.15** | 0.11 | | | | 0.01 | 0.02 | | |
| geitlerinema spp. | **0.00** | 0.00 | **0.01** | 0.02 | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.05 | **0.00** | 0.00 | | | | | | | |
| gemmata obscuriglobus | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.02 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | | |
| geodermatophilus obscurus | **0.00** | 0.00 | **0.00** | 0.00 | **0.02** | 0.03 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | 0.08 | 0.10 | | | | |
| geodermatophilus obscurus g16 dolomite ma | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.03 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | | |
| microbacterium shrimpcida | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.02 | | | | | | | |
| mucispirillum schaedleri | **2.33** | 3.84 | **0.04** | 0.07 | **0.00** | 0.00 | **5.58** | 7.28 | **3.48** | 3.28 | **0.89** | 1.58 | 0.09 | 0.07 | | | 0.06 | 0.04 | |
| streptomyces specialis | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.03 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | | |
| | | | | | | | | | | | | | | | | | | | |
| **Proteobacteria** | | | | | | | | | | | | | | | | | | | |
| aromatoleum azoarcus buckelii | **0.25** | 0.33 | **0.02** | 0.05 | **0.00** | 0.01 | **0.12** | 0.12 | **0.10** | 0.12 | **0.08** | 0.06 | 0.06 | 0.03 | | | | | |
| azoarcus tolulyticus | **0.01** | 0.02 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.01 | **0.00** | 0.01 | **0.01** | 0.02 | 0.06 | 0.04 | | | | | |
| candidatus pelagibacter ubique | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.03 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | | |
| crenothrix polyspora | **0.00** | 0.00 | **0.00** | 0.00 | **0.02** | 0.06 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | | |
| cupriavidus gilardii | **0.33** | 0.39 | **0.03** | 0.06 | **0.02** | 0.06 | **0.14** | 0.09 | **0.12** | 0.12 | **0.11** | 0.11 | 0.04 | 0.02 | | | | | |
| desulfovibrio desulfuricans | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.03 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | | |
| escherichia coli | **0.00** | 0.00 | **0.28** | 0.12 | **0.27** | 0.21 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | 0.00 | 0.00 | | | | | |
| methyloversatilis spp. | **0.02** | 0.02 | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.02 | **0.00** | 0.01 | **0.01** | 0.01 | 0.05 | 0.04 | | | | | |
| ochrobactrum spp. | **0.00** | 0.00 | **0.04** | 0.12 | **0.02** | 0.03 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | 0.04 | | | | | |
| oxalobacter spp. | **0.03** | 0.05 | **0.00** | 0.01 | **0.00** | 0.01 | **0.01** | 0.02 | **0.00** | 0.01 | **0.01** | 0.02 | | | | | | | |
| pseudomonas thermaerum | **0.00** | 0.00 | **0.07** | 0.08 | **0.00** | 0.01 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | 0.01 | | 0.02 | | | | |
| rhodoferax ferrireducens | **0.00** | 0.00 | **0.00** | 0.00 | **0.01** | 0.02 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | | | | | | |
| rhodospirillum rubrum | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.06** | 0.14 | **0.16** | 0.22 | **0.12** | 0.13 | | | | | | | |
| salmonella enterica | **0.14** | 0.30 | **0.12** | 0.14 | **0.22** | 0.15 | **0.00** | 0.00 | **0.00** | 0.01 | **0.03** | 0.08 | | | | | | | |
| serratia marcescens | **0.00** | 0.00 | **0.16** | 0.09 | **0.16** | 0.11 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | 0.00 | 0.00 | | | | | |
| shigella dysenteriae | **0.00** | 0.00 | **0.12** | 0.08 | **0.11** | 0.08 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | 0.00 | 0.00 | | | | | |
| shigella sonnei | **0.00** | 0.00 | **4.01** | 1.33 | **3.78** | 2.15 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.01 | 0.00 | 0.00 | | | | | |
| stenotrophomonas maltophilia | **0.00** | 0.00 | **0.04** | 0.08 | **0.10** | 0.09 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | 0.09 | 0.00 | | | | | |
| stenotrophomonas maltophilia vun10003 | **0.00** | 0.01 | **0.03** | 0.06 | **0.25** | 0.15 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | 0.00 | 0.00 | | | | |
| syntrophus sp. | **0.00** | 0.00 | **0.03** | 0.06 | **0.00** | 0.00 | **0.00** | 0.00 | **0.48** | 0.73 | **0.00** | 0.00 | | | | 0.06 | | 0.05 | |
| | | | | | | | | | | | | | | | | | | | |
| **Tenericutes** | | | | | | | | | | | | | | | | | | | |
| allobaculum sp id4 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | **0.12** | 0.34 | **0.16** | 0.22 | **0.48** | 0.70 | | | | | | | |
| mycoplasma microti | **0.07** | 0.07 | **0.06** | 0.11 | **0.06** | 0.09 | **0.13** | 0.09 | **0.04** | 0.05 | **0.09** | 0.05 | | | | 0.01 | | 0.05 | |
| ureaplasma urealyticum | **0.61** | 0.44 | **0.19** | 0.19 | **0.37** | 0.53 | **0.81** | 0.30 | **0.40** | 0.54 | **0.41** | 0.21 | 0.02 | | | 0.06 | 0.00 | | |
| | | | | | | | | | | | | | | | | | | | |
| **Verrucomicrobia** | | | | | | | | | | | | | | | | | | | |
| akkermansia muciniphila | **0.58** | 1.68 | **0.16** | 0.39 | **0.20** | 0.58 | **0.00** | 0.00 | **0.02** | 0.05 | **0.00** | 0.01 | | | | | | | |
| opitutus terrae | **0.00** | 0.00 | **0.00** | 0.00 | **0.02** | 0.02 | **0.00** | 0.00 | **0.00** | 0.00 | **0.00** | 0.00 | | 0.01 | 0.02 | | | | |

**Supplementary Table 4.** 128 species whose abundance represented at least 0.01% of total bacteria were detected in feces collected during the 8th treatment week (study week 8) or the 4th week of follow-up (study week 12). At week 8, 38 of these 128 species were significantly altered by both types of EcN treatments compared to vehicle, with the direction of change compared to vehicle being identical for both EcN treatments. Of the 38 species changed at week 8, 5 species (*Bacteroides uniformis ,Clostridium bartlettii, Clostridium bifermentans, Clostridium orbiscindens* ,and *Pseudobutyrivibrio ruminis*) still remained significantly altered compared to vehicle for both EcN treated groups at week 12. T-tests were not corrected for multiple comparisons. An additional 9 species were altered in both EcN treatments only at week 12.

**Supplemental Table 5 Effects of NAPE secreting bacteria on TallyHo mice.**

| | vehicle (n=5) | pEcN (n=5) | pNAPE-EcN (n=5) | 1way-ANOVA |
|---|---|---|---|---|
| **Lipid Accumulatin** | | | | |
| Week 3 Body Fat (g) | 4.6±0.8 | 5.2±1.5 | 4.5±0.5 | p=0.4700 |
| Week 12 Body Fat (g) | 6.2±1.0 | 6.2±1.5 | 5.3±0.7 | p=0.3426 |
| Liver Triglyceride (mg/g tissue) | 5.7±3.1 | 8.0±2.1 | 4.9±2.1 | p=0.1701 |
| **Plasma hormones** | | | | |
| Insulin (ng $mL^{-1}$) | 0.7±0.4 | 1.3±0.6 | 0.6±0.4 | p=0.0883 |
| Leptin (ng $mL^{-1}$) | 3.6±1.6 | 4.2±1.8 | 2.3±1.5 | p=0.2302 |
| **Liver mRNA (fold vehicle)** | | | | |
| Ppara | 1.00±0.12 | 0.94±0.16 | 1.32±0.25[a] | p=0.0030 |
| Cpt1a | 1.00±0.19 | 1.13±0.21 | 1.36±0.12[a] | p=0.0096 |
| AOX | 1.00±0.06 | 1.11±0.28 | 1.42±0.58 | p=0.1235 |
| Ccl2 | 1.00±0.18 | 1.18±0.55 | 0.88±0.08 | p=0.3271 |
| Cd68 | 1.00±0.28 | 0.99±0.28 | 0.81±0.11 | p=0.2598 |
| Cd36 | 1.00±0.19 | 1.04±0.36 | 0.84±0.10 | p=0.2805 |

**[a]p<0.05 vs vehicle, Dunnett's Multiple Comparison's test Mean±SD**

**Livers and plasma collected after euthanasia at treatment week 15.**