Supplemental Table 1. Adipogenesis gene array results

Name	**Symbol**	**Fold Change**
Acetyl-Coenzyme A carboxylase beta	Acacb	1.209
Adipogenin	Adig	0.976
Adiponectin, CIQ and collagen domain binding	Adipoq	0.916
Adrenergic receptor beta 2	Adrb2	1.180
Angiotensinogen	Agt	0.734
Angiopoietin 2	Angpt2	0.699
Axin 1	Axin1	0.569
Bone morphogenetic protein 2	Bmp2	0.991
Bone morphogenetic protein 4	Bmp4	1.103
Bone morphogenetic protein 7	Bmp7	0.172
Cyclin D1	Ccnd1	1.179
Cyclin-dependent kinase 4	Cdk4	0.721
Cyclin-dependent kinase inhibitor 1A (P21)	Cdkn1a	0.669
Cyclin-dependent dependent kinase inhibitor 1B	Cdkn1b	0.491
CCAAT/enhancer binding protein (C/EBP), alpha	Cebpa	1.339
CCAAT/enhancer binding protein (C/EBP), beta	Cebpb	1.035
CCAAT/enhancer binding protein (C/EBP), delta	Cebpd	0.897
Complement factor D	Cfd	1.077
CAMP responsive binding protein 1	Creb1	0.554
DNA-damage inducible transcript 3	Ddit3	0.844
Deiodinase, iodothyronine type II	Dio2	0.873
Dickkopf homolog 1	Dkk1	4.234
Delta-like 1 homolog	Dlk1	1.332
E2F transcription factor 1	E2f1	0.413
Early growth response 2	Egr2	0.560
Fatty acid binding protein 4, adipocyte	Fabp4	1.212
Fatty acid synthase	Fasn	1.347
Fibroblast growth factor 1	Fgf1	0.972
Fibroblast growth factor 10	Fgf10	1.043
Fibroblast growth factor 2	Fgf2	1.284
Forkhead box C2	Foxc2	1.084
Forkhead box O1	Foxo1	0.896
GATA binding protein 2	Gata2	1.023
GATA binding protein 3	Gata3	0.051
Hairy and enhancer of split 1	Hes1	1.066
Insulin receptor	Insr	0.947
Insulin receptor substrate 1	Irs1	1.326
Insulin receptor substrate 2	Irs2	1.825
Jun oncogene	Jun	1.566
Kruppel-like factor 15	Klf15	0.702
Kruppel-like factor 2	Klf2	1.766
Kruppel-like factor 3	Klf3	0.672
Kruppel-like factor 4	Klf4	1.445
Leptin	Lep	1.148
Lipase, hormone sensitive	Lipe	1.191
Lamin A	Lmna	0.949
Lipoprotein lipase	Lpl	1.072

Low density lipoprotein receptor-related protein 5	Lrp5	0.728
Mitogen-activated protein kinase 14	Mapk14	0.795
Nuclear receptor coactivator 2	Ncoa2	0.760
Nuclear receptor co-repressor 2	Ncor2	0.750
Nuclear receptor subfamily 0, group B, member 2	Nr0b2	0.425
Nuclear receptor subfamily 1, group H, member 3	Nr1h3	1.024
Nuclear respiratory factor 1	Nrf1	0.511
Peroxisome proliferator activated receptor alpha	Ppara	1.116
Peroxisome proliferator activated receptor delta	Ppard	0.822
Peroxisome proliferator activated receptor gamma	Pparg	1.162
Peroxisome proliferative activated receptor gamma, coactivator 1 alpha	Ppargc1a	0.733
Peroxisome proliferative activated receptor gamma, coactivator 1 beta	Ppargc1b	1.189
PR domain containing 16	Prdm16	1.315
Retinoblastoma 1	Rb1	1.000
Resistin	Retn	0.775
Runt-related transcription factor 1	Runx1t1	0.647
Retinoid X receptor alpha	Rxra	0.774
Secreted frizzled-related protein 1	Sfrp1	0.852
Secreted frizzled-related sequence protein 5	Sfrp5	0.973
Sonic hedgehog	Shh	ND
Sirtuin 1	Sirt1	0.817
Sirtuin 2	Sirt2	0.907
Sirtuin 3	Sirt3	1.074
Solute carrier family 2, member 4	Slc2a4	1.169
Rous sarcoma oncogene	Src	0.480
Sterol regulatory element binding transcription factor 1	Srebf1	0.996
Tafazzin	Taz	1.026
Transcription factor 7-like 2, T-cell specific, HMG-box	Tcf7l2	1.175
TSC22 domain family, member 3	Tsc22d3	0.641
Twist homolog 1	Twist1	1.027
Uncoupling protein 1	Ucp1	1.114
Vitamin D receptor	Vdr	1.656
Wingless-related MMTV integration site 1	Wnt1	0.407
Wingless-related MMTV integration site 10b	Wnt10b	1.007
Wingless-related MMTV integration site 3A	Wnt3a	ND
Wingless-related MMTV integration site 5A	Wnt5a	1.187
Wingless-related MMTV integration site 5B	Wnt5b	0.596

Listed are the gene names, symbols and fold changes versus control as determined in samples obtained from mice consuming the 0.5μm beads at a dose of 1μg/ml. ND: not determined

Supplemental Table 2. Raw and Trimmed Read Count per Sample

Raw File Name	Total Raw Reads	Trimmed File Name	Total Trimmed Reads
barcode01_17_Blue_all.fastq	16,523	barcode01_17_Blue_all_chop.q9.fastq	11,821
barcode02_18_Blue_all.fastq	14,695	barcode02_18_Blue_all_chop.q9.fastq	10,234
barcode04_19_Blue_all.fastq	32,622	barcode04_19_Blue_all_chop.q9.fastq	23,140
barcode05_20_Blue_all.fastq	13,821	barcode05_20_Blue_all_chop.q9.fastq	9,918
barcode07_21_Blue_all.fastq	13,749	barcode07_21_Blue_all_chop.q9.fastq	9,851
barcode08_22_Blue_all.fastq	23,159	barcode08_22_Blue_all_chop.q9.fastq	16,623
barcode09_23_Blue_all.fastq	16,754	barcode09_23_Blue_all_chop.q9.fastq	12,039
barcode10_24_Blue_all.fastq	14,690	barcode10_24_Blue_all_chop.q9.fastq	10,265
barcode11_25_Blue_all.fastq	22,771	barcode11_25_Blue_all_chop.q9.fastq	15,944
barcode12_26_Blue_all.fastq	24,650	barcode12_26_Blue_all_chop.q9.fastq	17,460
barcode13_19_Red_all.fastq	14,110	barcode13_19_Red_all_chop.q9.fastq	10,034
barcode14_20_Red_all.fastq	11,863	barcode14_20_Red_all_chop.q9.fastq	8,379
barcode15_21_Red_all.fastq	14,948	barcode15_21_Red_all_chop.q9.fastq	10,682
barcode16_22_Red_all.fastq	21,679	barcode16_22_Red_all_chop.q9.fastq	15,458
barcode17_23_Red_all.fastq	19,794	barcode17_23_Red_all_chop.q9.fastq	14,149
barcode18_24_Red_all.fastq	16,333	barcode18_24_Red_all_chop.q9.fastq	11,534
barcode21_25_Red_all.fastq	11,352	barcode21_25_Red_all_chop.q9.fastq	7,979
barcode22_26_Red_all.fastq	11,610	barcode22_26_Red_all_chop.q9.fastq	8,343
barcode23_27_Red_all.fastq	16,575	barcode23_27_Red_all_chop.q9.fastq	11,848
barcode24_28_Red_all.fastq	19,500	barcode24_28_Red_all_chop.q9.fastq	13,963

Supplemental Table 3. Plasma lipid analysis

Exposure		Plasma lipid (mg/dL)			
size	**dose**	**HDL**	**LDL**	**Total cholesterol**	**Triglycerides**
-	-	35.7 (2.2)	24.2 (1.3)	71.3 (3.2)	57.2 (4.7)
5 μm	0.1μg/ml	37.4 (2.0)	19.5 (1.5)	70.2 (2.8)	66.2 (4.4)
5 μm	1.0 μg/ml	36.8 (2.4)	21.0 (2.1)	71.0 (4.1)	65.9 (5.0)
0.5 μm	0.1 μg/ml	37.5 (1.6)	24.7 (0.7)	73.8 (2.3)	58.0 (4.0)
0.5 μm	1.0 μg/ml	43.7 (2.0)*	26.2 (1.0)	81.3 (2.9)	56.8 (3.0)

Listed are the levels of fasting plasma lipids in blood samples obtained from the experimental groups at termination. Values are presented as average (SE).
*: $p<0.05$ vs control.

Supplemental Table 4. Metabolic activity

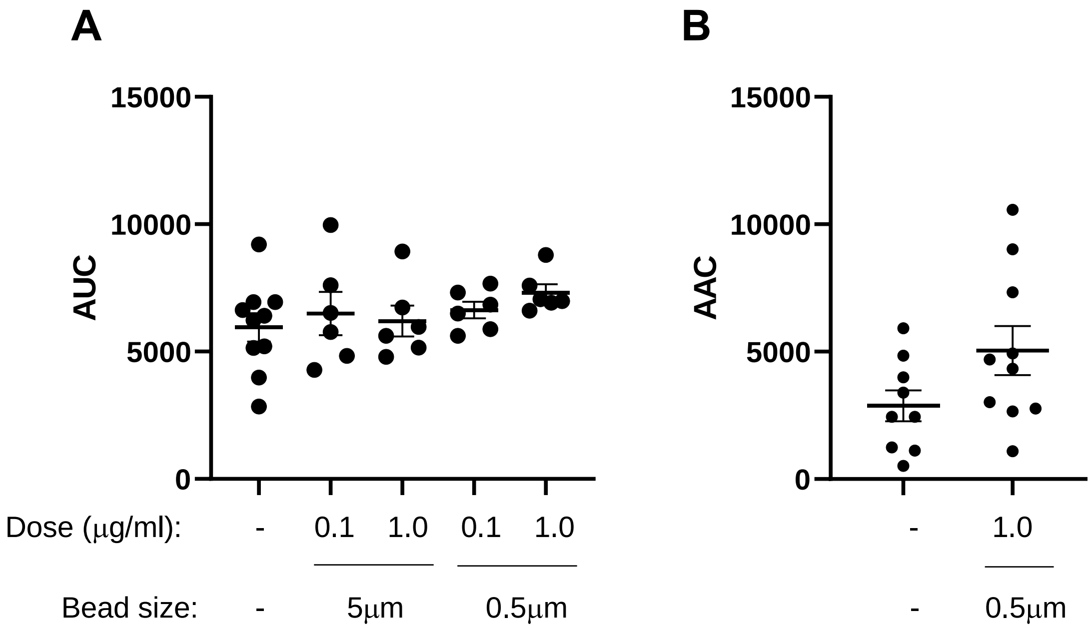
Parameter	**Control**	**Exposed (0.5μm; 1.0μg/ml)**
Intake		
Food / body wt ratio (g/kg)	90.3 (2.8)	76.1 (6.8)
Water / body wt ratio (ml/kg)	107.9 (4.7)	90.8 (8.9)
Respiration		
VO2 (ml/h/kg)	3723 (41)	3713 (86)
VCO2 (ml/h/kg)	3274 (58)	3214 (96)
RER	0.881 (0.011)	0.869 (0.009)
Activity		
Heat (kcal/h/kg)	18.3 (0.2)	18.2 (0.5)
Total activity	677.0 (38.4)	698.3 (42.4)
Gross movements	495.2 (32.4)	518.7 (34.0)
Fine movements	181.8 (7.0)	179.6 (9.1)

Listed are those parameters measured during the dark phase (6PM-6AM) of housing in metabolic cages. Values are expressed as avg (SE). RER: respiratory exchange ratio

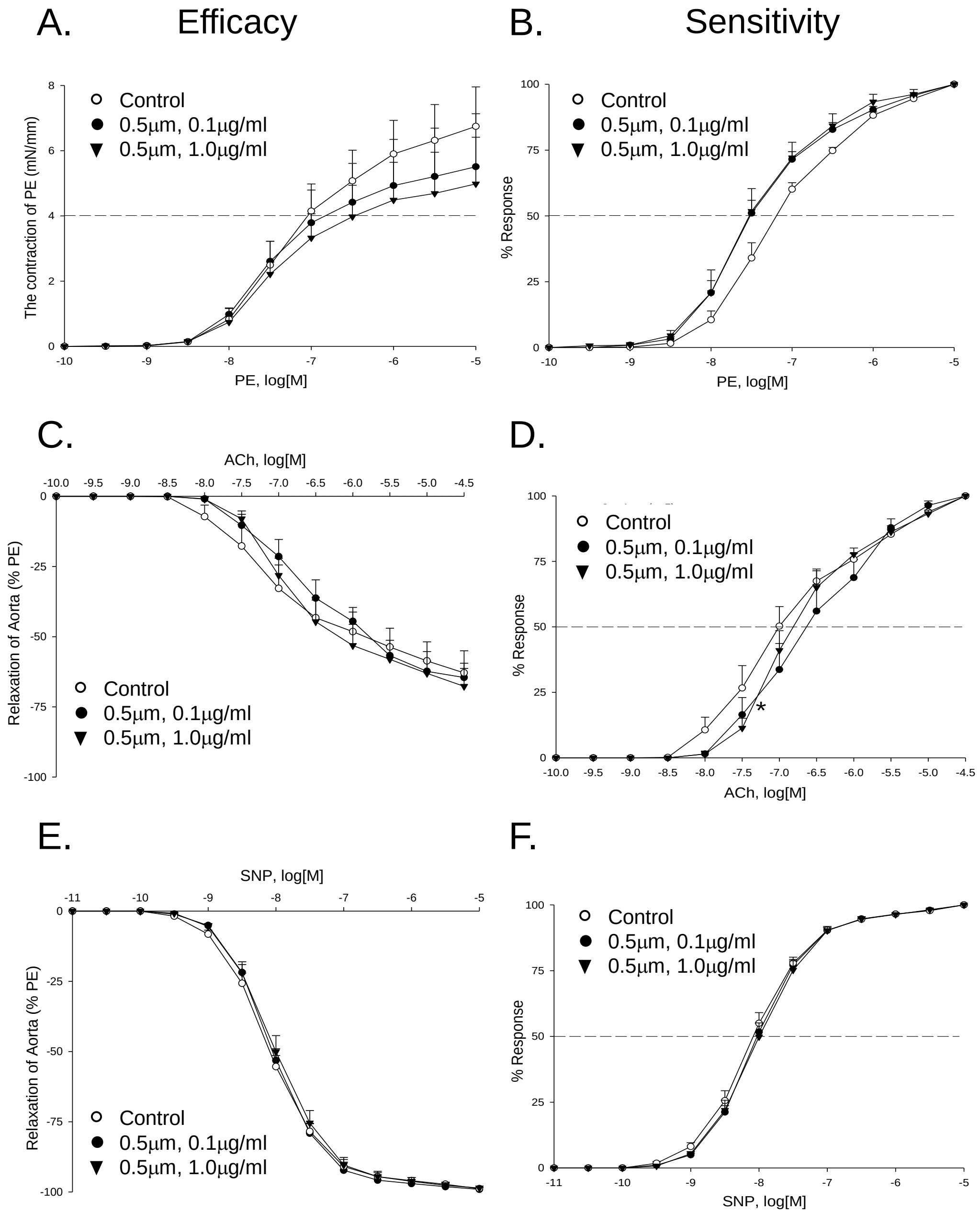
Supplemental Table 5: Effects of 12-week PS consumption (0.5μm) on aorta function *ex vivo*.

	Treatment Group			
Measurement	**Control**	**0.1μg/ml**	**1.0μg/ml**	**Combined**
[1]PE (10 μM)	6.75±1.21	5.51±1.62	4.98±1.43	5.25±1.02
[2]PE EC_{50} (nM)	61.6±10.7	32.7±5.4	37.7±10.3	35.2±5.5*
[3]PE pD_2	7.24±0.09	7.52±0.08	7.51±0.15	7.51±0.08
[4]PE Contraction Ratio	1.35±0.07	1.28±0.04	1.37±0.09	1.33±0.05
[5]ACh (%, PE)	-62.9±7.9	-64.6±3.2	-67.7±8.2	-66.1±4.2
[2]ACh EC_{50} (nM)	121±27	389±169	182±70	286±93
[3]ACh pD_2	7.00±0.17	6.61±0.22	6.83±0.13	6.72±0.13
[5]SNP (%, PE)	-98.8±0.4	-99.1±0.6	-98.6±0.6	-98.8±0.4
[2]SNP EC_{50} (nM)	8.6±1.4	9.7±1.2	10.7±2.0	10.2±1.1
[3]SNP pD_2	8.09±0.07	8.03±0.05	8.00±0.09	8.01±0.05

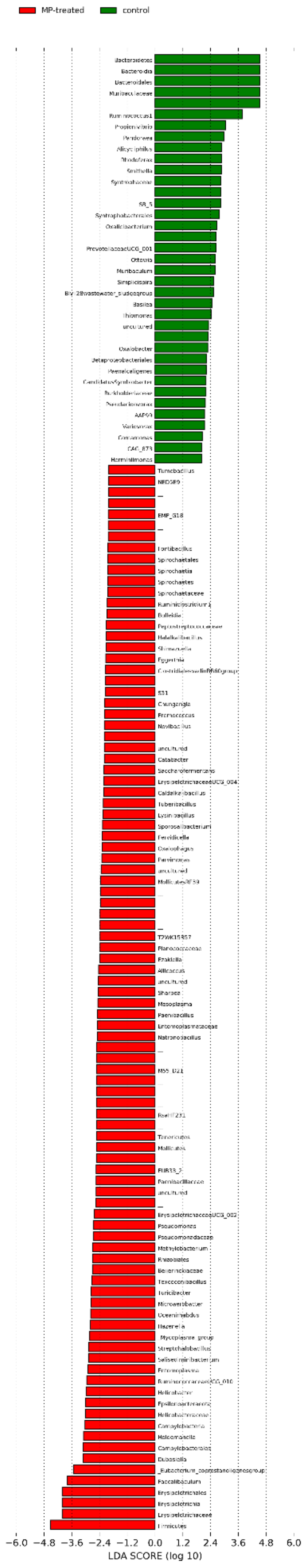
Data are mean ± SEM; n=5 mice per group or n=10 mice in “Combined” group. **Abbr.** PE, phenylephrine; ACh, acetylcholine; SNP, sodium nitroprusside; [1]mN/mm, [2]EC_{50}, effective concentration producing 50% response (in nM); [3]pD_2, -log [EC_{50}]; [4]L-NAME+PE Tension/PE Tension; [5]agonist-induced relaxation as a percentage of PE-induced tension. * $P<0.05$ vs. Control.



Supplemental Figure 1. Glucose homeostasis. A) Illustrated are the areas under the curve (AUC) calculated from glucose tolerance tests using mice from the 5 treatment groups after 9 weeks of exposure. B) Illustrated are areas above the curve (AAC) calculated from an insulin tolerance test using control mice and those mice ingesting 0.5µm beads at a dose of 1µg/ml for 12 weeks.



Supplemental Figure 2. Effects of PS consumption on aortic function *ex vivo*. Aortae were collected from control mice and those drinking PS-containing water of the indicated size and dose and used to analyze functional reactivity. A, B) Summary data of cumulative concentration-dependent phenylephrine- (PE) induced increase in isometric tension (mN/mm) in aortic rings (Efficacy) and as a % of the total response (Sensitivity). C, D) Summary data of cumulative concentration-dependent acetylcholine- (ACh) induced relaxation as a % of PE-induced tension in aortic rings (Efficacy) or as a % of the total response (Sensitivity). E, F) Summary data of cumulative concentration-dependent sodium nitroprusside- (SNP) induced relaxation as a % of PE-induced tension in aortic rings (Efficacy) or as a % of the total response (Sensitivity). Data are mean ± SE. n=5 aorta per group.



Supplemental Figure 3. Genus level differences. Illustrated are changes in gut microbiota at the genus level in mice drinking normal water (green) and that containing the PS beads (red).