Table S1. Adverse clinical biomarkers

	Lean (n=26)	NWO (n=43)	Overweight/ Obese (n=110)	p-value
Plasma glucose >125 mg/dL	1 (4)	-	3 (3)	0.47
HDL cholesterol <50 mg/dL (females) or <40 mg/dL (males)	1 (4)	5 (12)	18 (17)*	0.16
Triglycerides >150 mg/dL	-	5 (12)	25 (23)	0.006
Systolic Blood Pressure >140 mmHg	3 (12)	3 (7)	17 (15)	0.33
Diastolic Blood Pressure >90 mmHg	2 (8)	-	18 (16)	0.004

All data is presented as n (%).
- indicates no subjects had adverse biomarkers
* 109 subjects

Table S2. Significantly enriched pathways and putative annotation of metabolic features within each pathway produced from *Mummichog* analyses

Significantly Enriched Pathway	Individual Metabolites	P-value
Linoleic metabolism	Linoleic acid, 13(S)-HODE, 13-OxoODE, 9,10-DHOME, 12(13)-EpOME, 9(S)-HPODE, 13(S)-HPODE	0.001
Beta-alanine metabolism	Glutamate, Beta-alanine, Histidine, Ornithine, 5-oxoproline	0.002
Histidine metabolism	Glutamate, Histidine, Beta-alanine, 5-oxoproline, Uric acid, Ornithine	0.002
Aspartate and asparagine metabolism	Glutamate, 5-oxoproline, Proline, Putrescine, Carnitine, Ornithine, Lysine, Gamma-L-glutamyl cysteine, Acetamidopropanal, Acetyalaminobutanal, 4-Guanidinobutanoate, Pyrroline-hydroxy-carboxylate	0.002
Glutathione metabolism	5-oxoproline, Glutamate, Alanine, Gamma-L-glutamyl cysteine	0.002
Glutamate metabolism	Glutamate, Alanine, Gamma-L-glutamyl cysteine, Pyruvate	0.003
Lysine metabolism	Glutamate, Carnitine, Lysine, Pipecolinic acid, 2-oxoadipate, Unknown	0.003
Glycine, serine, alanine, threonine metabolism	Glutamate, Choline, Betaine, Pyruvate, Glycerate, Allotheronine, Alanine, Ornithine, Threonine	0.009
Aminosugars metabolism	Glutamate, Inosine diphosphate, Glucosamine-6-phosphate, Pyruvate, CMP-N-glycolyneuraminate	0.02
Urea cycle/amino group metabolism	Glutamate, Proline, Ornithine, Thiopurine, N-acetyl-glutamate, Sarcosine, N4-Acetylamino-butanal	0.03

Metabolic feature annotation is based on output from *Mummichog* analyses. *Mummichog* utilizes the collective power of mapping statistically significant metabolic features to biological pathways to detect the most likely match for metabolites. Importantly, one mass to charge ratio (*mz*) may match to several metabolites. *Mummichog* maps all possible identifications for an *m/z* and then bases the final output on what pathway is enriched in a significant manner. The possible matches outside of the enriched pathway are distributed at random, eliminating the possibility of additional pathways.