Supplemental file for online publication

Table S1. Amount (in mg) of organic acids and phenolic compounds from *Hibiscus sabdariffa* administered orally to each participant.

Organic acids (74.2%)	
Hibiscicus acid	248.98
Hydroxycitric acid	66.31
Hydroxycinnamic acids (11.3%)	
Chlorogenic acid	45.76
5-O-Caffeoylshikimic acid	1.37
N-Feruloyltyramine	0.79
Anthocyanins (8.7%)	
Delphinidin 3-sambubioside	21.61
Cyanidin 3-sambubioside	15.51
Coumarins (3.5%)	
Umbelliferone	14.71
Flavonols (2.3%)	
Quercetin 3-rutinoside	3.97
Quercetin 3-sambubioside	2.43
Quercetin 3-glucoside	1.15
Quercetin	0.97
Kaempferol 3-O-rutinoside	0.74
Myricetin 3-arabinogalactose	0.46
Kaempferol 3-(p-coumarylglucoside)	0.23
Total amount	424.99

Table S2. Arbitrarily selected information on differentially expressed genes involved in molecular function and biological process GO terms according to a higher likelihood to be influential according to the Genome Set Enrichment Analysis

MOLECULAR FUNCTION GO TERMS

GO	Term Name	Gene Size	False Discovery Rate
0003712	transcription cofactor activity	445	0.152
0000989	transcription factor binding transcription factor activity	459	0.122
0000988	protein binding transcription factor activity	474	0.155

Common genes significantly involved (in order from major to minor contribution):

ID3, ZNF593, UTF1, MXI1, TBPL1, SRSF2, DDX5, ENY2, NFE2, CRYM, WDR77, E4F1, JUNB, CBX4, RLIM, HDAC4, PCBD1, MED21, MED9, RCOR2.

GO	Term Name	Gene Size	False Discovery Rate
0042809	vitamin D receptor binding	17	0.124

Common genes significantly involved (in order from major to minor contribution):

MED17, TAF7, MED13, MED16, TOB2, RXRB, MED14, HR, THRAP3, MED12, MED24, BAZ1B, MED1, MED30, TAF11.

BIOLOGICAL PROCESS GO TERMS

GO	Term Name	Gene Size	False Discovery Rate
0071222	cellular response to lipopolysaccharide	85	0.096
0071219	cellular response to molecule of bacterial origin	90	0.110
0071216	cellular response to biotic stimulus	101	0.036
0009607	response to biotic stimulus	558	0.251

Common genes significantly involved (in order from major to minor contribution):

IL8, CCL3, TLR2, CD36, CCL2, TNFAIP3, IRF8, IFNG, CMPK2, NR1D1, IRAK1, PAF1, IL18, GFI1, RARA, CX3CR1, IL10, TNFSF4, TNFRSF1B, CEBPE, VLDLR, NR1H3.

GO	Term Name	Gene Size	False Discovery Rate
0072595	maintenance of protein localization in organelle	23	0.124

Common genes significantly involved (in order from major to minor contribution):

TAF8, ORC3, TOPORS, GRIK5, SUN1, GPAA1, BBS4, BCL3, NR5A1, PDIA3, KDELR3, SYNE1, ANKRD13C, SUPT7L, PDIA2, SUN2, PML.

Fig. S1 The graphical representation in the human metabolic network highlighted the notion that alterations in metabolites were not concentrated in a defined region (green decreased, red increased, black without appreciable changes).

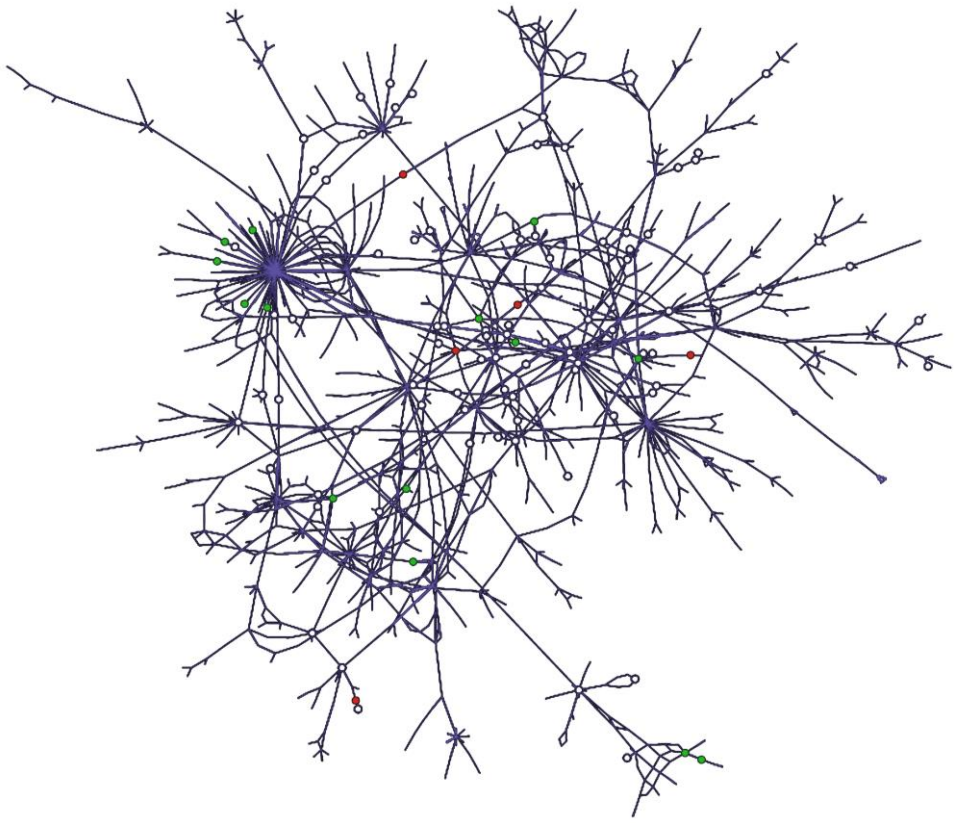

Fig. S2 The ingestion of the HS extract elicited a significant decrease in metabolites derived from leucine, valine and isoleucine. The apparent net effect is a decreased capacity to release glucose and to form triglycerides as well as an increased capacity for mitochondrial oxidation.

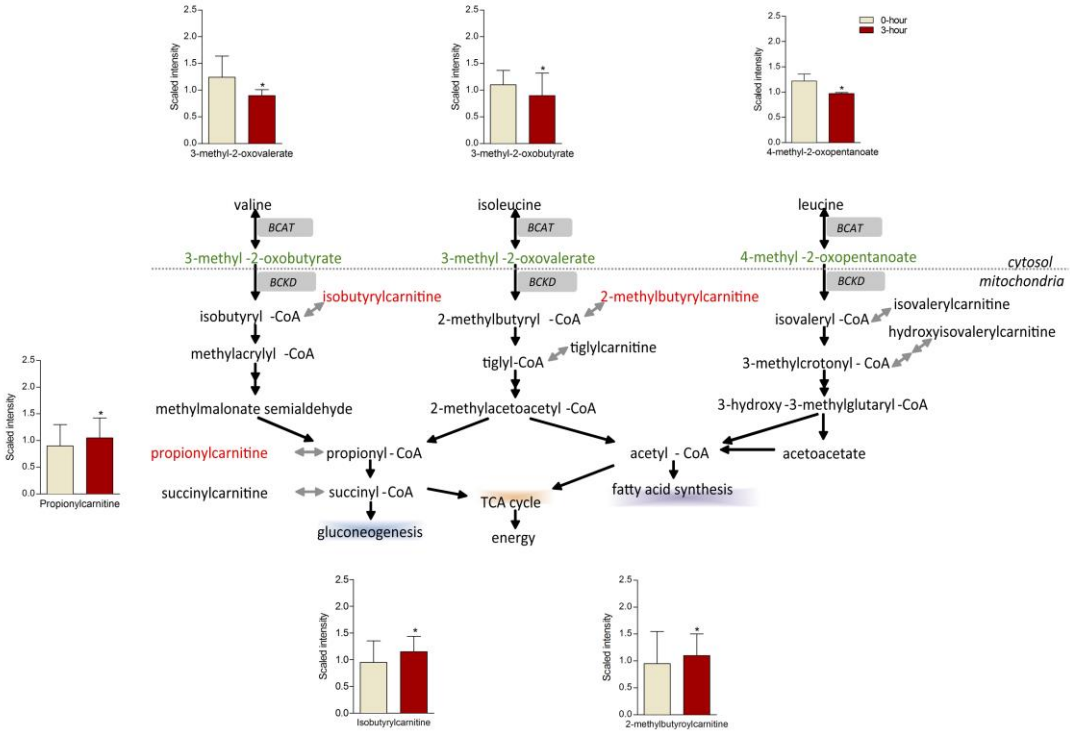

Fig. S3 The HS extract elicited an acute decrease in concentration of long chain fatty acids confirming the increased capacity for mitochondrial oxidation.

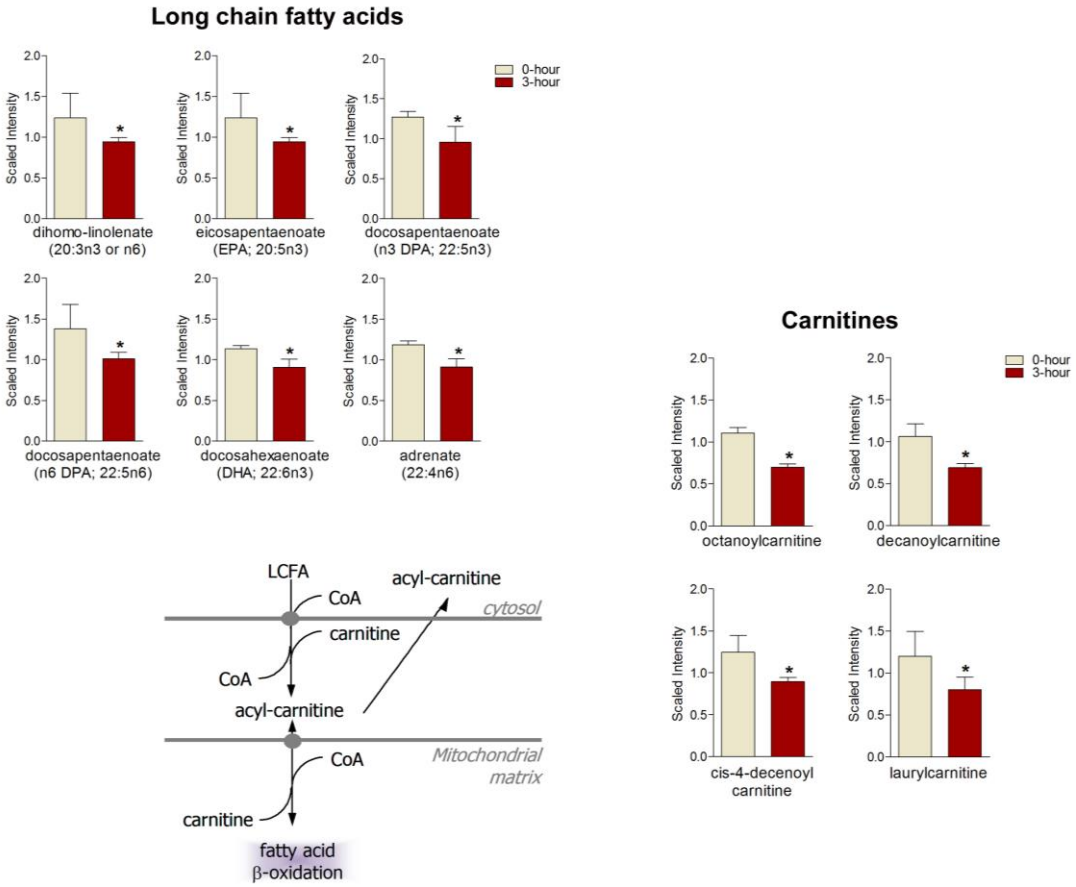

Fig. S4 Using significant metabolites in the univariate analysis, principal component analysis (A, B) and the linear discriminant analysis (C, D) confirmed the group clustering and pattern recognition.

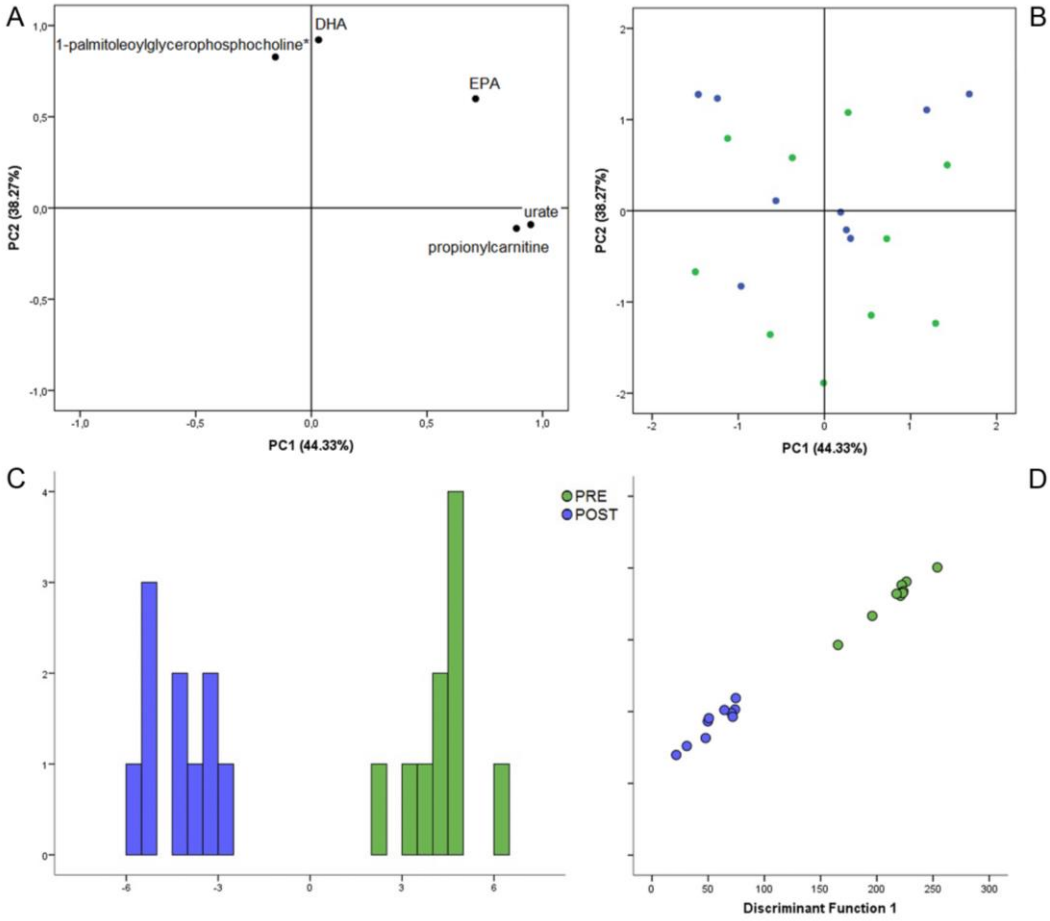

Fig. S5 Cortisol is the most common glucocorticoid found in the blood and cortisone is the inactive form. The acute decrease in these metabolites was the primary differentiator according to the random forest analysis and probably represents beneficial effects in metabolism.

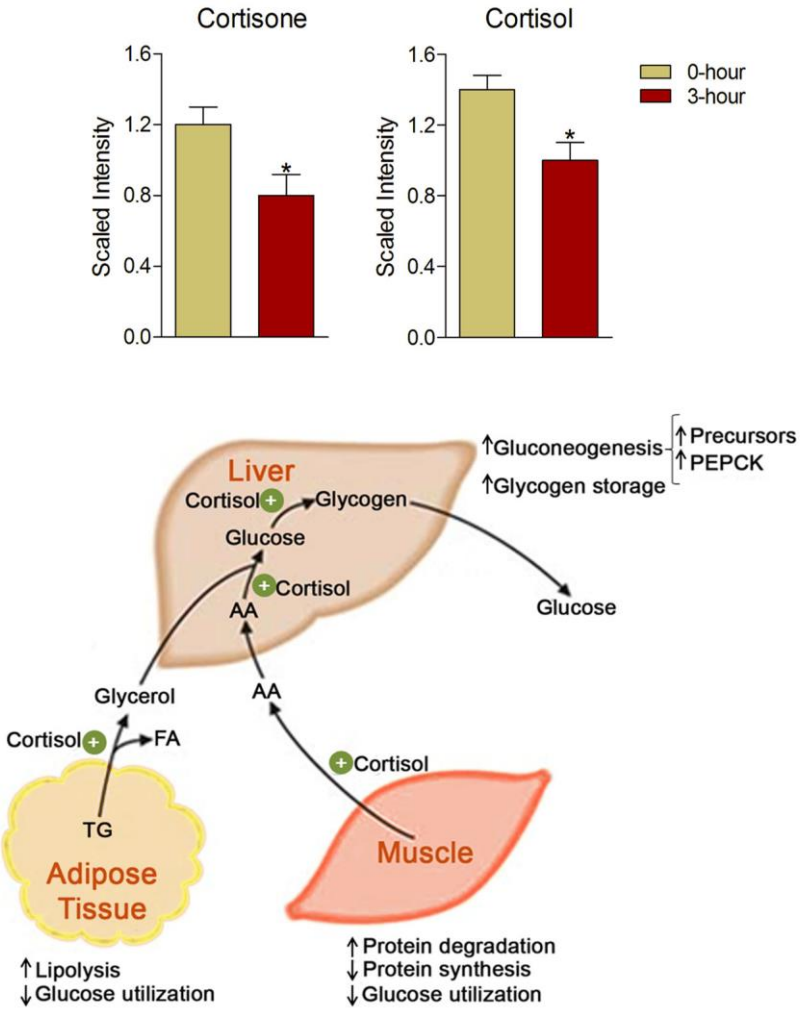

Fig. S6 Significant overrepresentation of GO terms corresponding to different biological processes according to the Gene Set Enrichment Analysis. The nodes are colored according to their FDR value following the scheme at the bottom. Grey nodes correspond to processes without gene representation in the array and dashed lines denote missing intermediate terms between connections.