

Supplemental Data S1. qPCR analysis of 6 randomly chosen genes affected in NW individuals by PUFA treatments. Results are expressed as the fold change (FC) with respect to the corresponding untreated control. p-values ≤ 0.05 are in bold; Cells colored in light red or blue indicate the concordance with up- or down-regulation in RNASeq data, respectively.

Gene	NW-AA		NW-DHA		OB-AA		OB-DHA		CRC-AA		CRC-DHA	
	FC	p-value	FC	p-value	FC	p-value	FC	p-value	FC	p-value	FC	p-value
ACTB	1.92	0.042	2.17	0.095	3.24	0.934	0.51	0.130	1.95	0.186	0.96	0.517
CAST	2.01	0.002	1.84	0.110	1.67	0.007	1.10	0.916	1.30	0.374	1.20	0.882
DDR1	1.42	0.206	1.56	0.017	0.60	0.333	0.55	0.007	1.79	0.397	1.38	0.725
FAT1	1.58	0.001	1.55	0.019	1.71	0.148	0.79	0.270	1.92	0.392	1.52	0.754
LIPE	0.39	0.002	0.50	0.009	2.30	0.977	1.13	0.627	0.56	0.022	0.39	0.045
SLC2A5	6.58	0.005	7.02	0.0014	1.85	0.82	0.74	0.331	9.04	0.066	6.08	0.058

Supplemental Data S3. Anthropometric characteristics of subjects included in the study. Data are mean ±Standard Error. BMI, body mass index.

	Lean	Obese	Cancer
N (Male/Female)	3 (0M, 3F)	3 (2M, 1F)	3 (2M, 1F)
Age (years)	36,3±4,4	44,7±8,8	57,7±4,7
Body weight (Kg)	60,3±5,7	104,3±33,5	70±12,2
BMI (Kg/m ²)	23±1,4	35,2±5	23,3±1,4

Supplemental Data S4: List of genes and probes selected for real time qPCR analysis.

Gene Symbol	Gene Name	Assay ID
ACTB	actin b	Hs99999903_m1
CAST	calpastatin	Hs00156280_m1
DDR1	discoidin domain receptor tyrosine kinase 1	Hs01058430_m1
FAT1	FAT atypical cadherin 1	Hs00170627_m1
LIPE	lipase E, hormone sensitive type	Hs00943410_m1
SLC2A5	solute carrier family 2 member 5	Hs01086390_m1