

Supplementary Table 1. Pre-exercise mRNA expression of selected metabolic genes following LOW, MOD and HIGH.

Gene (Quiagen catalogue number; Refseq#)	LOW (n = 11)	MOD (n = 11)	HIGH (n = 12)
ACACA (Acetyl-CoA Carboxylase Alpha) (PPH02316A; NM_000664)	1.108 (0.560, 1.657)	1.275 (0.742, 1.807)	1.135 (0.588, 1.682)
ACACB (Acetyl-CoA Carboxylase Beta) (PPH02301A; NM_001093)	1.304 (0.757, 1.852)	1.187 (0.666, 1.709)	1.017 (0.475, 1.559)
ACSL1 (Acyl-CoA Synthetase Long Chain Family Member 1) (PPH19272A; NM_001995)	2.057 (1.137, 2.978)	1.321 (0.433, 2.209)	1.075 (0.156, 1.994)
ACSL6 (Acyl-CoA Synthetase Long Chain Family Member 6)	0.942 (0.432, 1.451)	0.918 (0.424, 1.411)	1.091 (0.582, 1.599)

(PPH08013A; NM_001009185)			
AKT2 (AKT Serine/Threonine kinase 2) (PPH00289F; NM_001243027)	1.119 (0.777, 1.462)	1.106 (0.771, 1.441)	1.073 (0.731, 1.414)
CD36 (Cluster of Differentiation 36) (PPH01356A; NM_000072)	1.758 (1.213, 2.303)	1.425 (0.901, 1.949)	1.199 (0.655, 1.744)
CPT1B (Carnitine Palmitoyltransferase 1B) (PPH20905B; NM_001145134)	1.223 (0.716, 1.749)	0.974 (0.480, 1.469)	0.764 (0.246, 1.282)
CPT2 (Carnitine Palmitoyltransferase 2) (PPH15572A; NM_000098)	1.283 (0.878, 1.688)	1.315 (0.914, 1.691)	1.101 (0.696, 1.506)
DGAT1 (Diacylglycerol O- Acyltransferase 1) (PPH23420F; NM_012079)	1.308 (-0.593, 3.210)	1.415 (-0.497, 3.327)	1.278 (-0.623, 3.179)
FABP3	2.655 (1.867, 3.442)	1.536 (0.777, 2.295)	1.194 (0.407, 1.980)

(Fatty Acid Binding Protein 3) (PPH02460C; NM_004102)			
FABP4 (Fatty Acid Binding Protein 4) (PPH02382F; NM_001442)	1.346 (0.854, 1.838)	1.081 (0.605, 1.557)	1.029 (0.538, 1.520)
GPAM (Glycerol-3-Phosphate Acyltransferase) (PPH06361A; NM_001244949)	1.070 (0.672, 1.467)	1.115 (0.735, 1.495)	1.077 (0.678, 1.477)
GYG1 (Glycogenin 1) (PPH13614A; NM_001184720)	0.919 (0.639, 1.199)	0.947 (0.675, 1.220)	1.008 (0.729, 1.287)
GYS1 (Glycogen Synthase 1) (PPH00988C; NM_001161587)	0.857 (0.491, 1.222)	0.809 (0.446, 1.172)	0.852 (0.487, 1.217)
HADHA (Hydroxyacyl-CoA Dehydrogenase) (PPH10000B; NM_000182)	1.550 (1.208, 1.893)	1.270 (0.943, 1.598)	1.124 (0.780, 1.469)
IL6 (Interleukin 6)	0.676 (-0.103, 1.455)	0.781 (0.015, 1.546)	0.784 (0.006, 1.561)

(PPH00560C; NM_000600)			
IRS1 (Insulin Receptor Substrate-1) (PPH02328A; NM_005544)	0.791 (0.434, 1.148)	0.697 (0.347, 1.048)	0.719 (0.363, 1.075)
IRS2 (Insulin Receptor Substrate-2) (PPH02297A; NM_003749)	0.782 (0.437, 1.126)	0.720 (0.386, 1.054)	0.713 (0.369, 1.057)
LIPE (lipase E, hormone sensitive type) (PPH02383A; NM_005357)	1.733 (0.547, 2.918)	1.345 (0.182, 2.508)	1.081 (-0.056, 2.218)
MLYCD (Malonyl-CoA Decarboxylase) (PPH12795A; NM_012213)	2.220 (1.620, 2.820)	1.345 (0.771, 1.918)	0.912 (0.311, 1.513)
PDK2 (Pyruvate dehydrogenase Kinase Isoform 2) (PPH00810A; NM_001199898)	1.374 (0.890, 1.858)	0.973 (0.507, 1.438)	0.996 (0.513, 1.480)
PDK4 (Pyruvate dehydrogenase Kinase Isoform 4)	3.202 (-0.747, 7.151)	1.936 (-1.997, 5.870)	1.714 (-2.230, 5.659)

(PPH07615A; NM_002612)			
PNPLA2 (Patatin Like Phospholipase Domain Containing 2) (PPH11403B; NM_020376)	1.363 (0.862, 1.864)	1.089 (0.594, 1.584)	0.969 (0.469, 1.469)
PPARA (Peroxisome Proliferator Activated Receptor Alpha) (PPH01281B; NM_001001928)	1.023 (0.634, 1.412)	0.989 (0.613, 1.364)	0.945 (0.557, 1.333)
PPARD (Peroxisome Proliferator Activated Receptor Delta) (PPH00455A; NM_001171818)	1.172 (0.698, 1.645)	1.113 (0.659, 1.567)	1.048 (0.575, 1.522)
PPARGC1A (Peroxisome Proliferator Activated Receptor Gamma Coactivator 1-Alpha) (PPH00461F; NM_013261)	1.202 (0.624, 1.781)	1.148 (0.582, 1.714)	1.065 (0.488, 1.642)
PRKAA1 (Protein Kinase AMP-Activated Catalytic Subunit Alpha 1)	1.042 (0.711, 1.372)	1.155 (0.839, 1.470)	1.004 (0.672, 1.336)

(PPH00043B; NM_206907)			
PRKAA2 (Protein Kinase AMP-Activated Catalytic Subunit Alpha 2) (PPH15207A; NM_006252)	1.027 (0.708, 1.364)	1.080 (0.762, 1.399)	0.969 (0.642, 1.297)
PRKAB2 (Protein Kinase AMP-Activated Catalytic Subunit Beta 2) (PPH09415B; NM_005399)	0.955 (0.717, 1.193)	1.075 (0.847, 1.302)	0.994 (0.755, 1.234)
PRKAG1 (Protein Kinase AMP-Activated Catalytic Subunit Gamma 1) (PPH07190A; NM_001206709)	1.087 (0.774, 1.400)	1.024 (0.720, 1.328)	1.096 (0.784, 1.408)
SLC27A1 (Fatty Acid Transporter Protein 1) (PPH17902A; NM_198580)	1.056 (0.730, 1.383)	0.929 (0.615, 1.243)	0.804 (0.478, 1.130)
SLC27A4 (Fatty Acid Transporter Protein 4) (PPH00471A; NM_005094)	1.117 (0.520, 1.715)	1.115 (0.527, 1.704)	1.015 (0.419, 1.611)

SLC2A4 (Glucose Transporter Type 4) (PPH02326A; NM_001042)	1.194 (0.892, 1.497)	1.100 (0.811, 1.389)	1.115 (0.812, 1.418)
UCP3 (Uncoupling Protein 3) (PPH06066A; NM_003356)	1.524 (0.805, 2.243)	0.957 (0.244, 1.669)	0.854 (0.136, 1.571)

Data are fold change relative to baseline and are expressed as adjusted means (lower, upper 99.95 % CI).

Supplementary Table 2. Between-intervention differences in pre-exercise mRNA expression of selected metabolic genes following LOW, MOD and HIGH.

Gene	HIGH vs. MOD	MOD vs. LOW	HIGH vs. LOW
	Diff. in means (99.95% CI) P-value	Diff. in means (99.95% CI) P-value	Diff. in means (99.95% CI) P-value
ACACA (Acetyl-CoA Carboxylase Alpha)	-0.140 (-0.724, 0.445) P = 0.318	0.166 (-0.406, 0.739) P = 0.229	0.027 (-0.563, 0.616) P = 0.846
ACACB (Acetyl-CoA Carboxylase Beta)	-0.170 (-1.020, 0.679) P = 0.306	-0.117 (-0.942, 0.708) P = 0.467	-0.287 (-1.156, 0.581) P = 0.103
ACSL1 (Acyl-CoA Synthetase Long Chain Family Member 1)	-2.246 (-1.315, 0.823) P = 0.335	-0.736 (-1.782, 0.310) P = 0.008	-0.982 (-2.062, 0.098) P = 0.001
ACSL6 (Acyl-CoA Synthetase Long Chain Family Member 6)	0.173 (-0.390, 0.736) P = 0.202	-0.024 (-0.576, 0.527) P = 0.852	0.149 (-0.420, 0.718) P = 0.272
AKT2 (AKT Serine/Threonine Kinase 2)	-0.033 (-0.363, 0.297) P = 0.669	-0.013 (-0.337, 0.310) P = 0.861	-0.047 (-0.379, 0.286) P = 0.553
CD36	-0.226 (-0.886, 0.435)	-0.333 (-0.979, 0.313)	-0.559 (-1.227, 0.109)

(Cluster of Differentiation 36)	P = 0.160	P = 0.041	P = 0.002
CPT1B (Carnitine Palmitoyltransferase 1B)	-0.210 (-0.911, 0.490) P = 0.215	-0.258 (-0.942, 0.426) P = 0.124	-0.469 (-1.178, 0.241) P = 0.011
CPT2 (Carnitine Palmitoyltransferase 2)	-0.201 (-0.725, 0.322) P = 0.113	0.019 (-0.492, 0.531) P = 0.871	-0.182 (-0.712, 0.348) P = 0.153
DGAT1 (Diacylglycerol O-Acyltransferase 1)	-0.137 (-0.970, 0.697) P = 0.476	0.106 (-0.714, 0.926) P = 0.572	-0.030 (-0.866, 0.805) P = 0.873
FABP3 (Fatty Acid Binding Protein 3)	-0.343 (-1.266, 0.580) P = 0.129	-1.118 (-2.021, -0.215) P < 0.0001	-1.461 (-2.394, -0.528) P < 0.0001
FABP4 (Fatty Acid Binding Protein 4)	-0.052 (-0.606, 0.501) P = 0.691	-0.265 (-0.807, 0.277) P = 0.051	-0.317 (-0.876, 0.242) P = 0.026
GPAM (Glycerol-3-Phosphate Acyltransferase)	-0.038 (-0.596, 0.520) P = 0.776	0.045 (-0.499, 0.590) P = 0.726	0.008 (-0.558, 0.574) P = 0.954
GYG1 (Glycogenin 1)	0.061 (-0.232, 0.353) P = 0.381	0.028 (-0.258, 0.315) P = 0.672	0.089 (-0.206, 0.384) P = 0.207
GYS1 (Glycogen Synthase 1)	0.043 (-0.231, 0.317) P = 0.505	-0.047 (-0.317, 0.222) P = 0.455	-0.005 (-0.280, 0.271) P = 0.944

HADHA (Hydroxyacyl-CoA Dehydrogenase)	-0.146 (-0.648, 0.357) P = 0.218	-0.280 (-0.770, 0.210) P = 0.023	-0.426 (-0.936, 0.085) P = 0.002
IL6 (Interleukin 6)	0.003 (-0.684, 0.690) P = 0.985	0.105 (-0.569, 0.778) P = 0.512	0.108 (-0.583, 0.799) P = 0.509
IRS1 (Insulin Receptor Substrate-1)	0.021 (-0.311, 0.354) P = 0.781	-0.094 (-0.420, 0.232) P = 0.226	-0.072 (-0.407, 0.262) P = 0.355
IRS2 (Insulin Receptor Substrate-2)	-0.007 (-0.384, 0.369) P = 0.937	-0.062 (-0.430, 0.307) P = 0.479	-0.069 (-0.449, 0.311) 0.443
LIPE (lipase E, hormone sensitive type)	-0.264 (-3.071, 2.544) P = 0.336	-0.388 (-3.059, 2.284) P = 0.180	-0.651 (-3.625, 2.232) P = 0.059
MLYCD (Malonyl-CoA Decarboxylase)	-0.433 (-1.260, 0.394) P = 0.036	-0.875 (-1.682, -0.068) P = 0.0002	-1.308 (-2.147, -0.0469) P < 0.0001
PDK2 (Pyruvate dehydrogenase Kinase Isoform 2)	0.024 (-0.559, 0.606) P = 0.863	-0.401 (-0.971, 0.168) P = 0.008	-0.378 (-0.967, 0.211) P = 0.013
PDK4 (Pyruvate dehydrogenase Kinase Isoform 4)	-0.222 (-2.772, 2.328) P = 0.711	-1.266 (-3.772, 1.240) P = 0.044	-1.488 (-4.048, 1.072) P = 0.023
PNPLA2	-0.120 (-0.518, 0.278)	-0.274 (-0.665, 0.117)	-0.394 (-0.794, 0.006)

(Patatin Like Phospholipase Domain Containing 2)	P = 0.211	P = 0.008	P = 0.0006
PPARA (Peroxisome Proliferator Activated Receptor Alpha)	-0.044 (-0.486, 0.399) P = 0.674	-0.034 (-0.467, 0.399) P = 0.740	-0.078 (-0.525, 0.369) P = 0.461
PPARD (Peroxisome Proliferator Activated Receptor Delta)	-0.065 (-0.664, 0.536) P = 0.649	-0.059 (-0.646, 0.528) P = 0.673	-0.124 (-0.732, 0.484) P = 0.393
PPARGC1A (Peroxisome Proliferator Activated Receptor Gamma Coactivator 1-Alpha)	-0.083 (-0.638, 0.472) P = 0.524	-0.055 (-0.599, 0.490) P = 0.668	-0.137 (-0.697, 0.422) P = 0.298
PRKAA1 (Protein Kinase AMP-Activated Catalytic Subunit Alpha 1)	-0.151 (-0.641, 0.340) P = 0.191	0.113 (-0.365, 0.591) P = 0.310	-0.038 (-0.536, 0.461) P = 0.740
PRKAA2 (Protein Kinase AMP-Activated Catalytic Subunit Alpha 2)	-0.111 (-0.462, 0.240) P = 0.188	0.044 (-0.300, 0.388) 0.585	-0.067 (-0.421, 0.287) P = 0.422
PRKAB2 (Protein Kinase AMP-Activated Catalytic Subunit Beta 2)	-0.080 (-0.426, 0.266) P = 0.332	0.120 (-0.218, 0.457) P = 0.147	0.039 (-0.312, 0.391) P = 0.637

PRKAG1 (Protein Kinase AMP-Activated Catalytic Subunit Gamma 1)	0.072 (-0.257, 0.401) P = 0.353	-0.063 (-0.386, 0.259) P = 0.405	0.009 (-0.324, 0.341) P = 0.909
SLC27A1 (Fatty Acid Transporter Protein 1)	-0.125 (-0.520, 0.269) P = 0.187	-0.127 (-0.513, 0.259) P = 0.174	-0.253 (-0.652, 0.146) P = 0.014
SLC27A4 (Fatty Acid Transporter Protein 4)	-0.101 (-0.603, 0.402) P = 0.399	-0.002 (-0.495, 0.491) P = 0.986	-0.103 (-0.608, 0.403) P = 0.391
SLC2A4 (Glucose Transporter Type 4)	0.015 (-0.392, 0.423) P = 0.876	-0.094 (-0.492, 0.304) P = 0.325	-0.079 (-0.492, 0.334) P = 0.420
UCP3 (Uncoupling Protein 3)	-0.103 (-0.647, 0.441) P = 0.423	-0.567 (-1.101, -0.033) P = 0.0003	-0.670 (-1.217, -0.123) P = <0.0001

Data differences in means between respective diets and expressed as mean (lower, upper 99.95% CI).

Green = significant difference between diets when adjusted for multiple comparisons (N = 102).