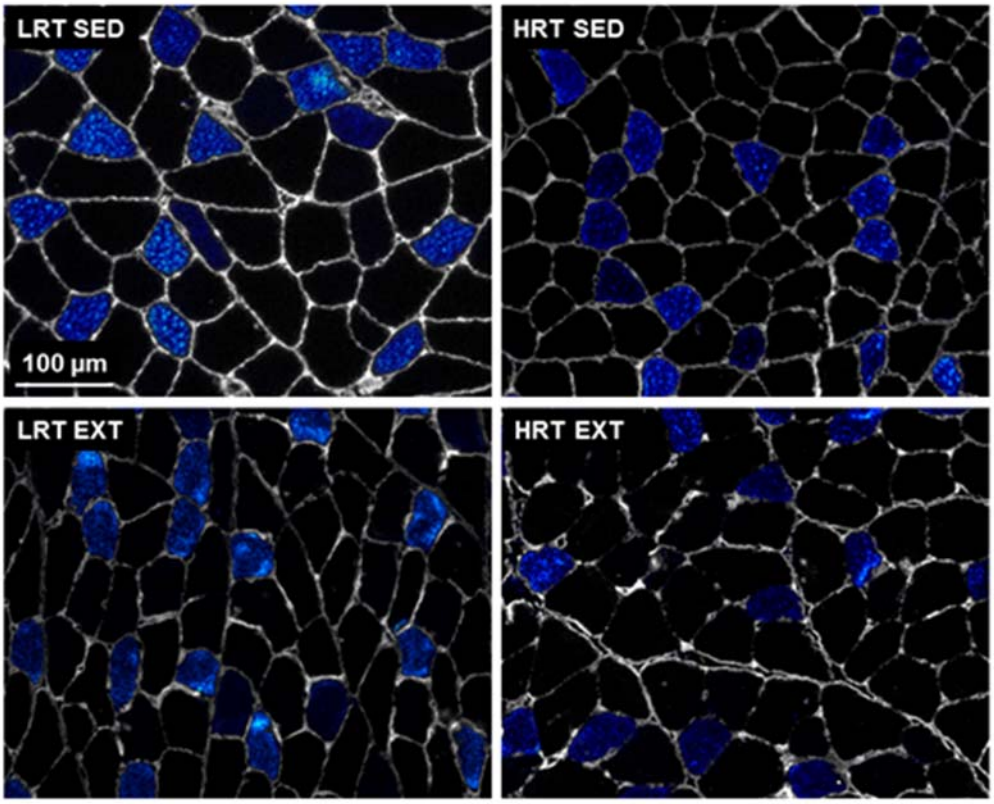
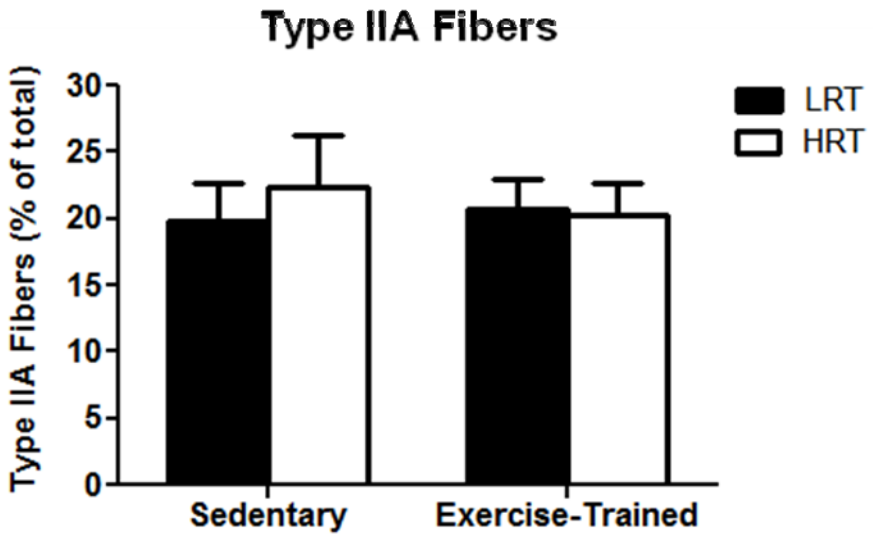
SUPPLEMENTARY DATA

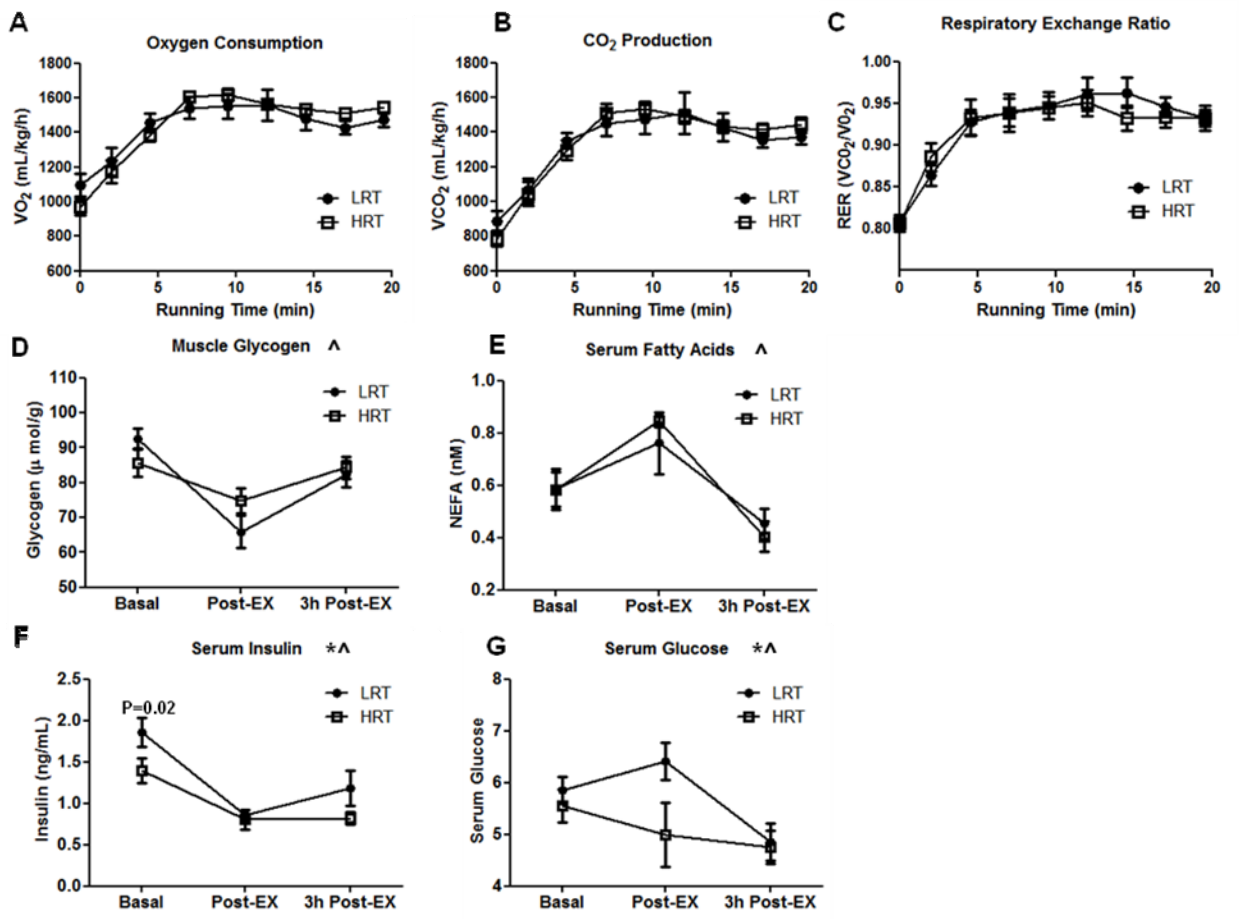
Supplementary Figure 1. Type IIA fiber content. Plantaris muscles from sedentary (SED) and exercise-trained (EXT) rats were frozen in N2-cooled isopentane and cut into 6 µm cross-sections. (A) Sections were stained with antibodies against laminin (white) and Myosin Heavy Chain IIA (blue), and visualized using fluorescent secondary antibodies under 100 x magnification. Type IIA fiber content was expressed as % of total muscle fibers counted. n=5/group.





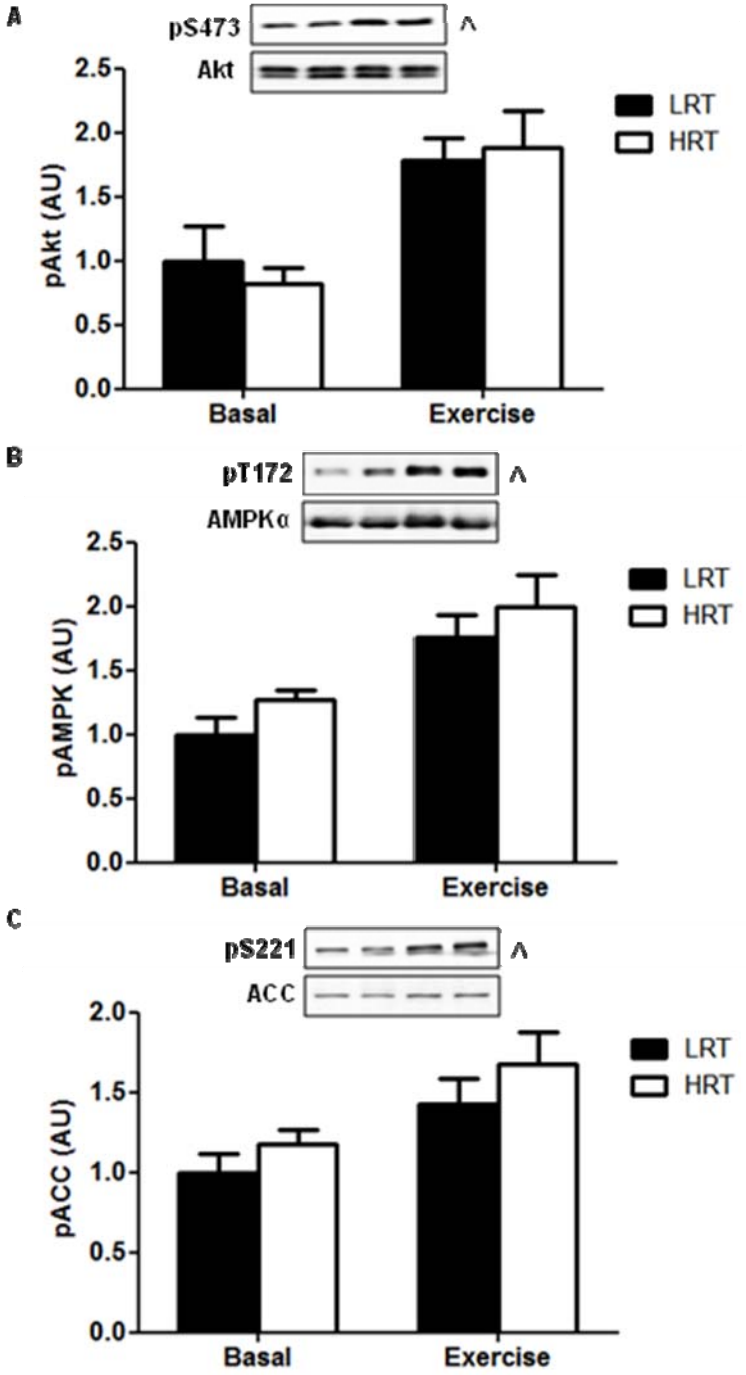
SUPPLEMENTARY DATA

Supplementary Figure 2. Whole-body metabolic effect of acute exercise in LRT/HRT. (A) Rats underwent a bout of exercise in a metabolic treadmill equipped for the measurement of respiratory gasses. (A) Oxygen consumption (VO2) and (B) Carbon Dioxide production (VCO2) were measured under resting conditions (Time 0) and over the course of the 20 min exercise session (15 m/min, 15% incline). (C) The respiratory exchange ratio (RER) was calculated (VO2/VCO2) as an indicator of substrate metabolism and exercise intensity. (D) Gastrocnemius muscles were collected from rats under resting conditions (Basal), immediately following acute exercise (Post-EX), or 3h following exercise (3h Post-EX), frozen and pulverized in liquid N2, and an aliquot of muscle was used for the analysis of muscle glycogen. Blood samples were collected at the same time points, and serum was used for the analysis of (E) non-esterified fatty acids (NEFA), (F) insulin, and (G) glucose. N=7-8.



SUPPLEMENTARY DATA

Supplementary Figure 3. Metabolic signaling in skeletal muscle in response to acute exercise in LRT/HRT. Phosphorylation of proteins involved in insulin and AMPK signaling were measured by Western Blotting in lysates from Gastrocnemius muscle under resting conditions (Basal), or immediately following an acute bout of exercise (Exercise). N=6-7/group. AMPK, AMP-activated protein kinase; ACC, acetyl-CoA carboxylase. ^P<0.05 Exercise main effect by 2-way ANOVA. P-values obtained by Tukey post-hoc testing are displayed.



SUPPLEMENTARY DATA

Supplementary Figure 4. Divergent transcriptomic responses to acute exercise identified by microarray analysis in LRT/HRT. RNA was extracted from the soleus muscles of rats under resting conditions, or 3-hours following an acute bout of treadmill running exercise. Genes that were significantly up-regulated or down-regulated in response to exercise in LRT/HRT were identified using Affymetrix Rat ST 1.0 chips and analyzed using Ingenuity Pathway Analysis (IPA). (A) In LRT, 193 genes were up-regulated and in HRT, 122 genes were up-regulated in response to acute exercise, with 63 of these genes being commonly upregulated in both phenotypes (FDR=5%, no fold-change filter). (B) In LRT, 133 genes were down-regulated in response to acute exercise (FDR=5%, no fold-change filter), while no genes were significantly down-regulated in response to exercise in HRT. (C) Gene ontology (GO) analysis revealed that genes uniquely regulated by exercise in LRT belonged to the functional categories of gene expression, development and cell cycle regulation. (D) In contrast, genes uniquely regulated by exercise in HRT belonged to the function categories of cellular growth, proliferation and movement, as well as skeletal and muscular development. No ontological or pathway overlap was observed between the LRT and HRT transcriptional responses to exercise. N=5-6 chips/group.