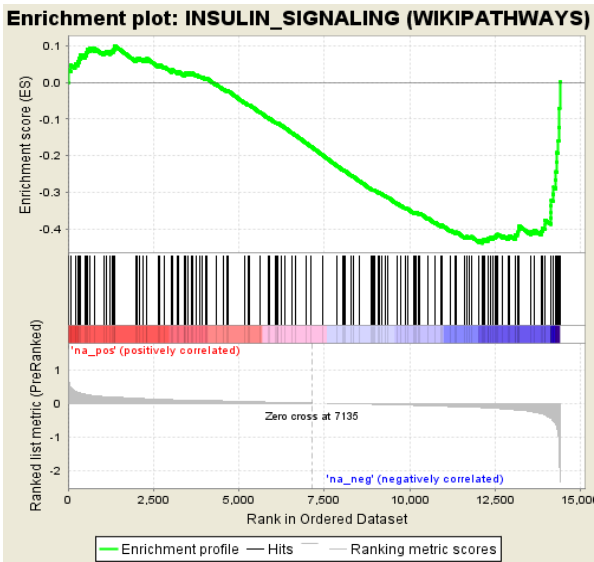


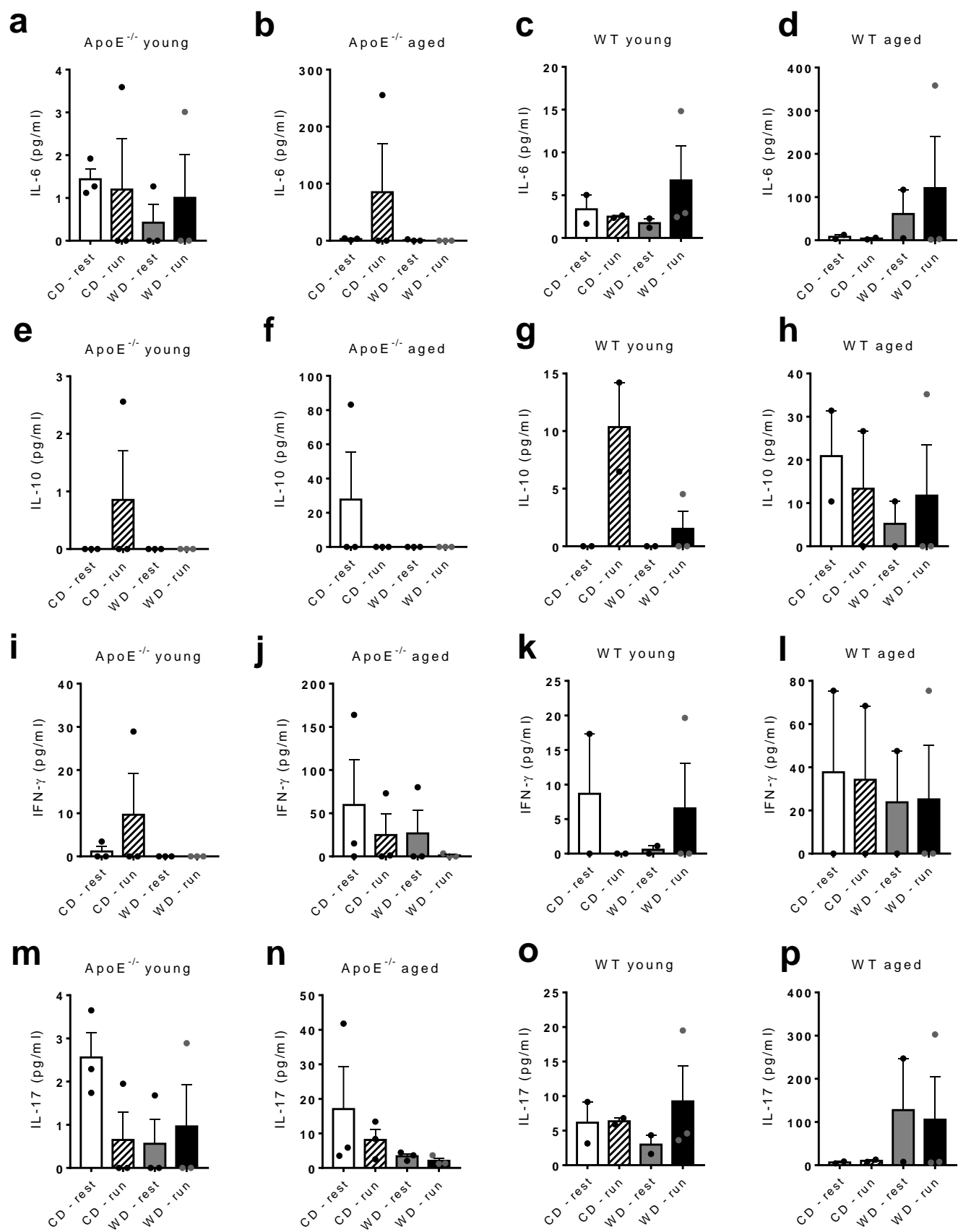
Supplementary figure 1



NES=-1.69
FDR=0.011

Supplementary Figure 1. Gene Set Enrichment Analysis (GSEA) of the insulin signaling pathway gene set. Enrichment plot indicating that genes within the insulin signaling pathway were significantly associated with downregulated genes in skeletal muscle of running aged ApoE^{-/-} on CD compared to running aged ApoE^{-/-} on WD based on ranking of genes by their descending log₂ fold change. NES = Normalized enrichment score, FDR = False discovery rate

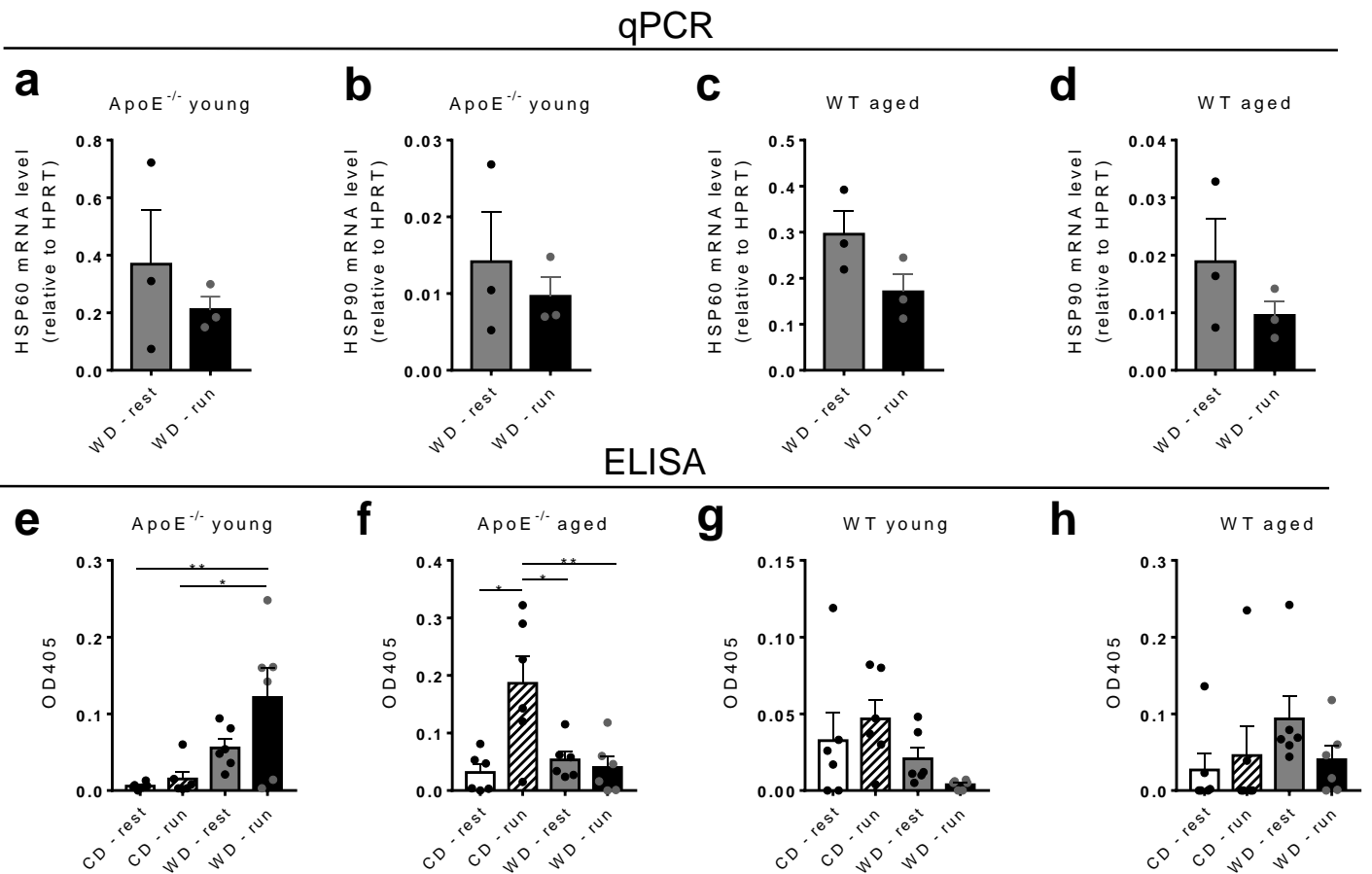
Supplementary figure 2



Supplementary Figure 2. Plasma cytokine levels

Plasma samples were collected at the time of sacrifice and the cytokines IL-6, IL-10, IFN-γ and IL-17 were measured in ApoE^{-/-} (a-b, e-f, i-j, m-n) and WT mice (c-d, g-h, k-l, o-p). One-way ANOVA test was used, followed by Bonferroni's Multiple Comparison test. Results are shown as pg/ml ± SEM, n=2-3 per group.

Supplementary figure 3



Supplementary Figure 3. HSP60 and HSP90 qPCR and anti-HSP60 antibody titers
(a-d) qPCR of HSP60 and HSP90 from skeletal muscle mRNA, normalized to HPRT. Plasma samples were collected at the time of sacrifice and anti-HSP60 antibody titers were measured in young and aged ApoE^{-/-} (e-f) and WT (g-h) mice. One-way ANOVA test was used, followed by Bonferroni's Multiple Comparison test. Results shown as OD405 values ± SEM. p<0.05 = *, p<0.01 = **, n=2-6 per group.