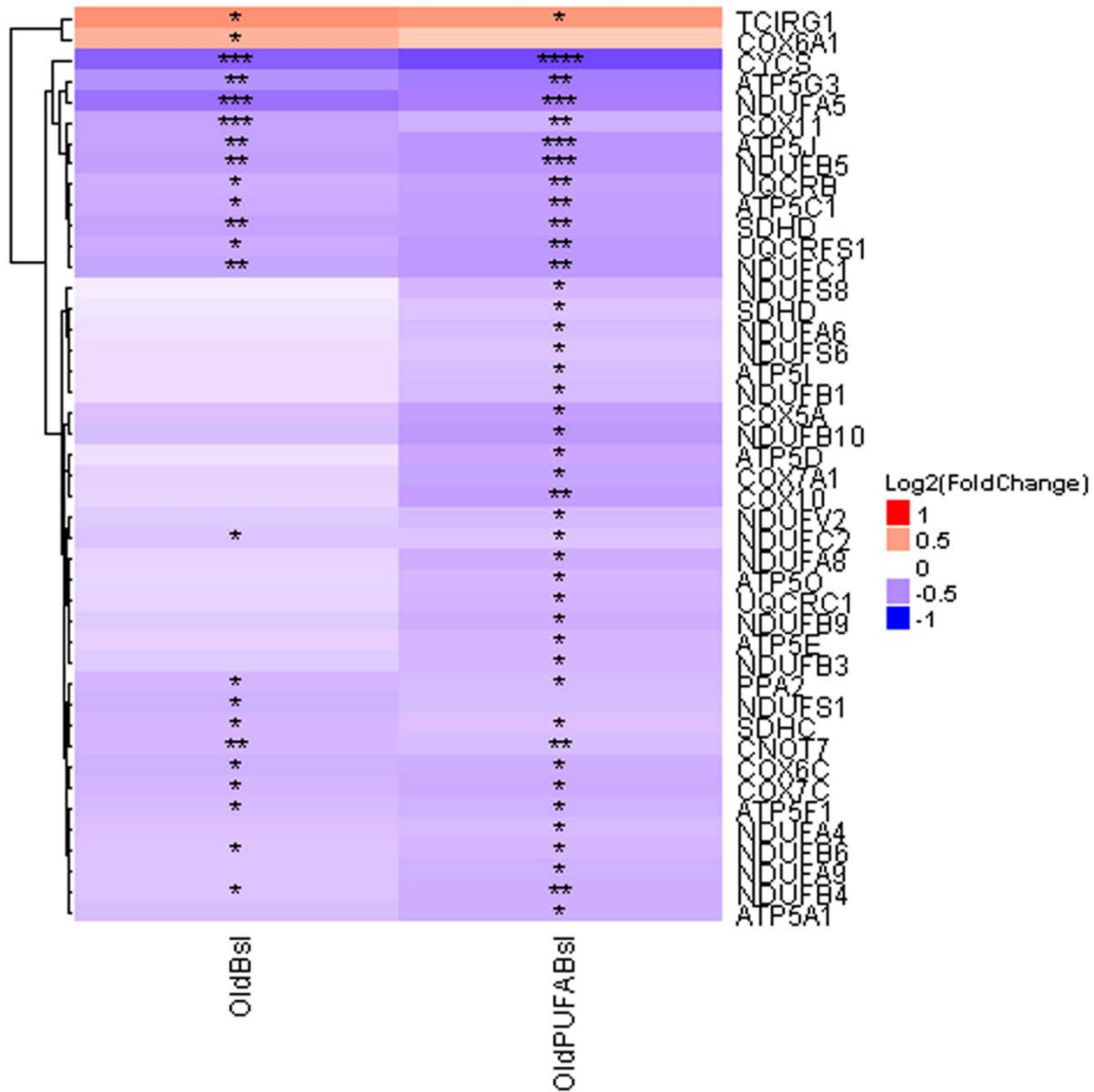
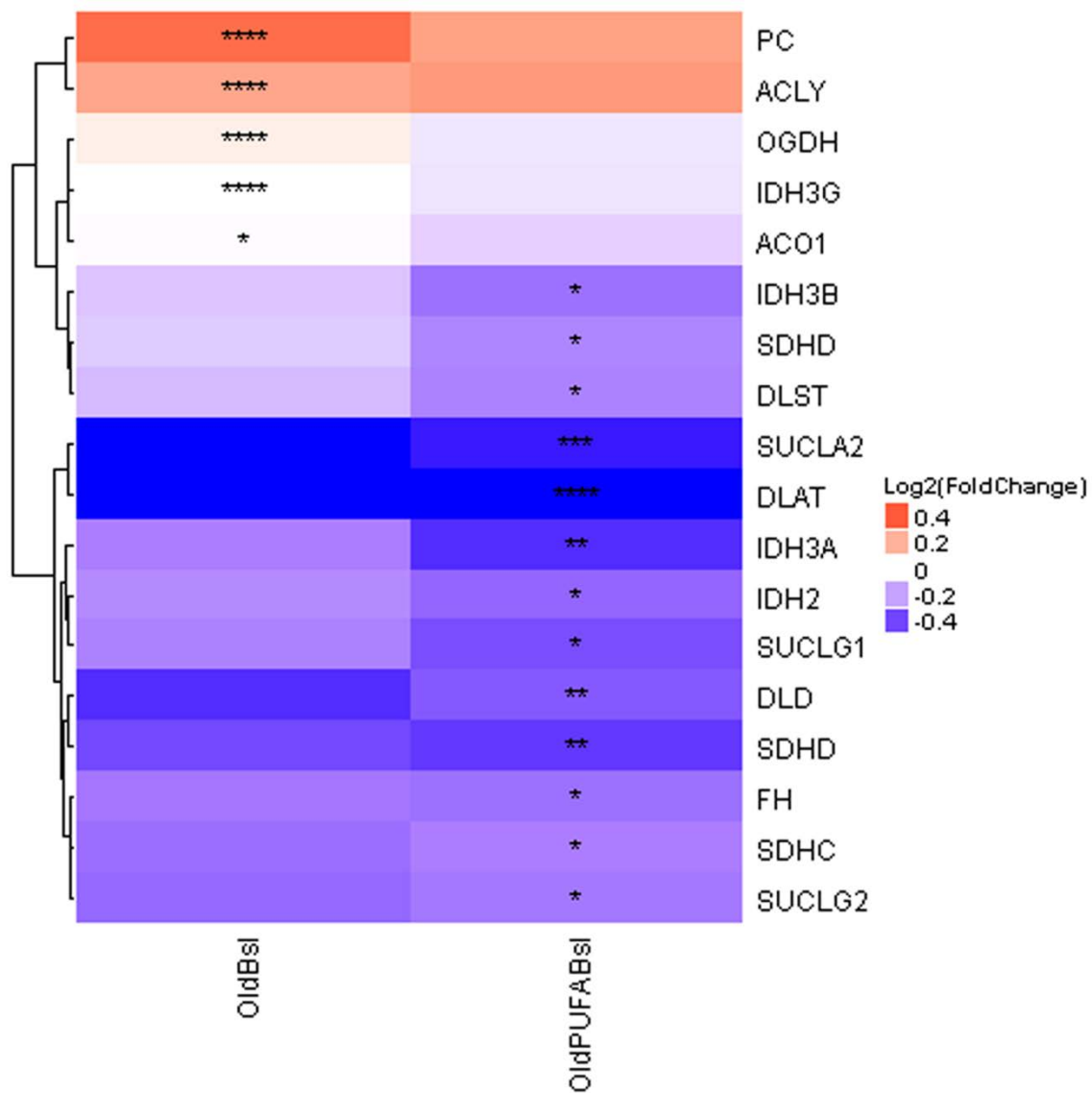


SUPPLEMENTARY MATERIALS

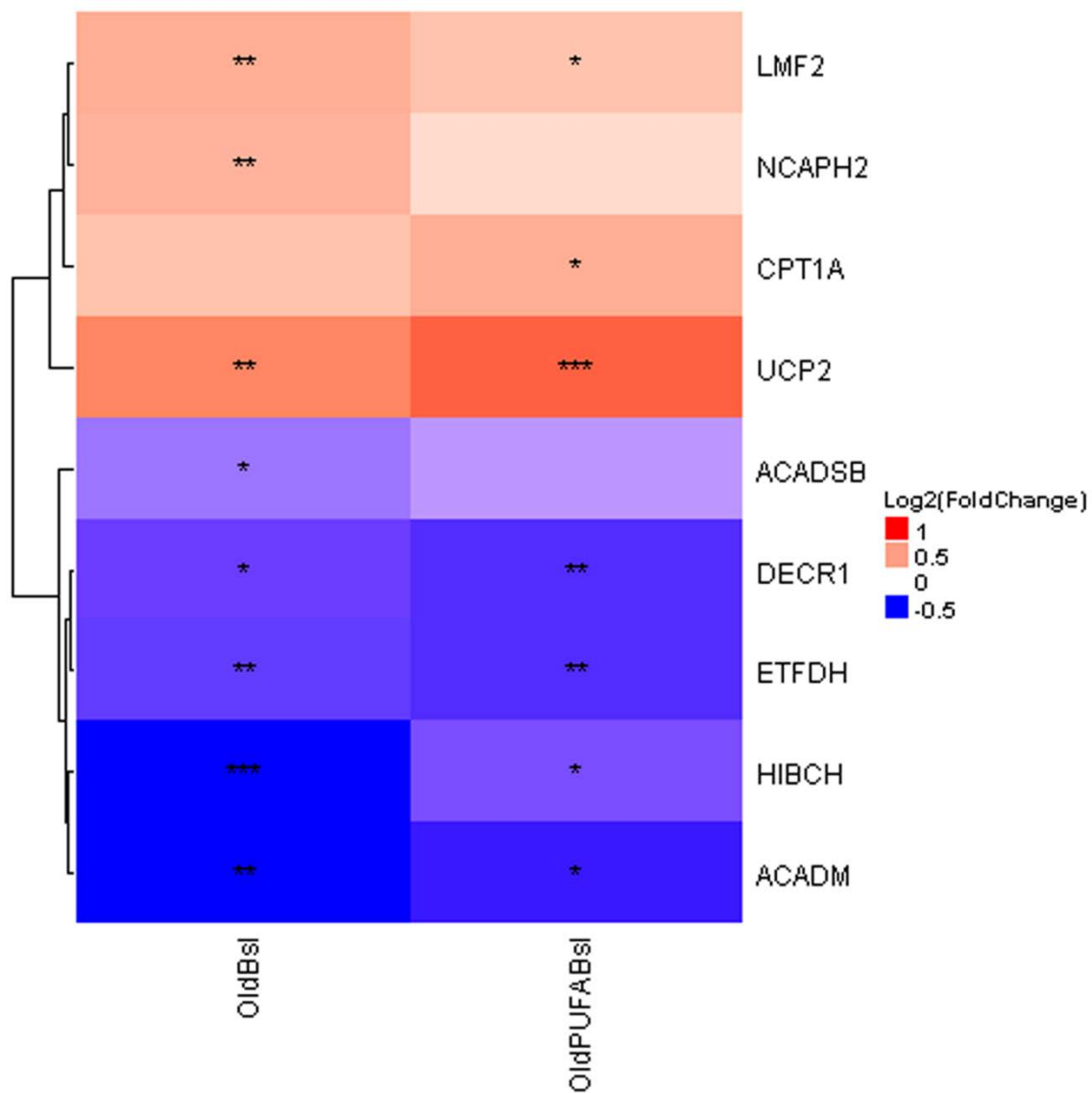
Supplemental Figures



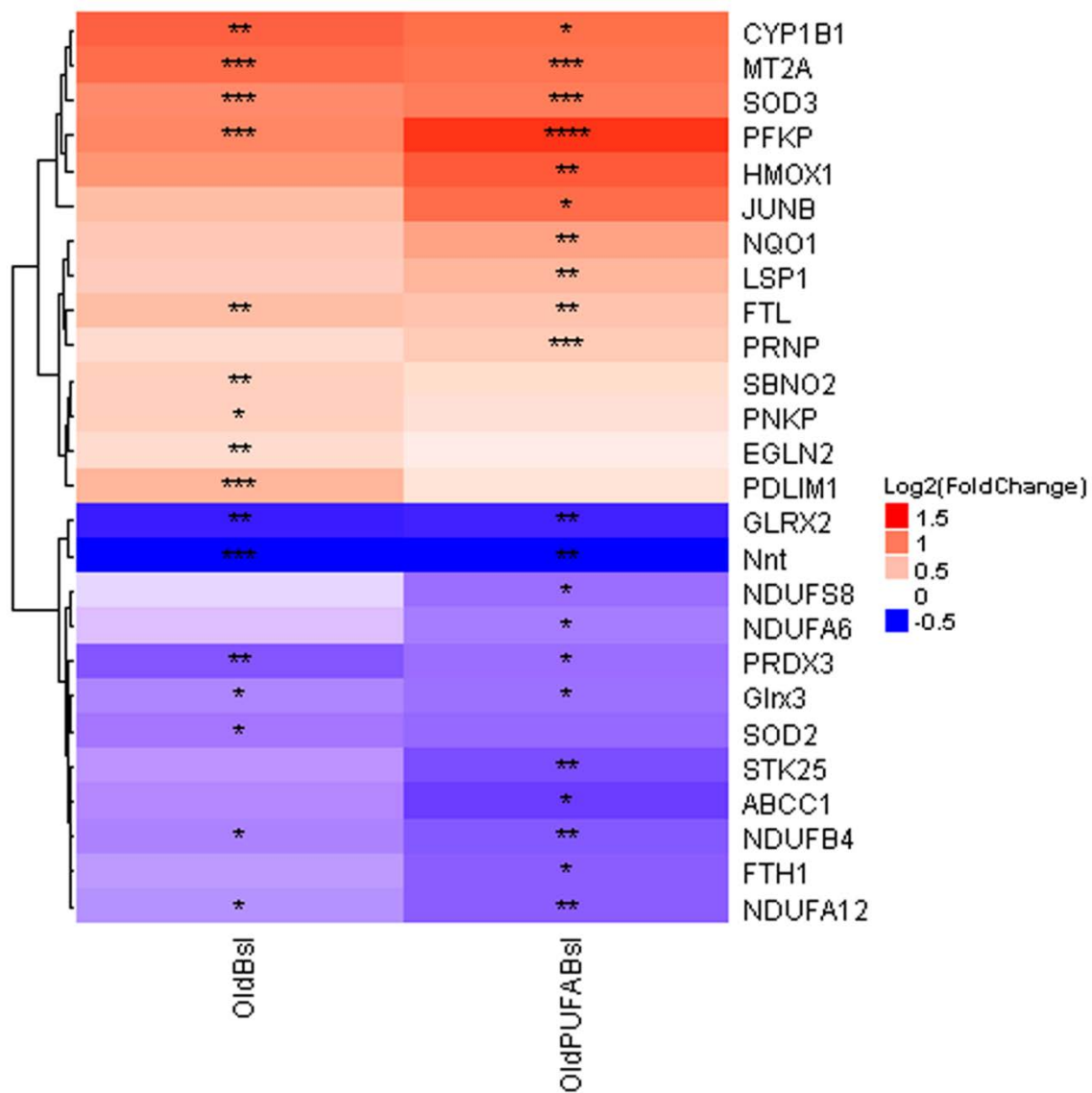
**Supplemental Figure 1.** The heatmap shows fold changes for genes related to oxidative phosphorylation in old baseline preintervention and old baseline postintervention relative to young baseline. A positive fold change (red) indicates upregulated in old compared to young, and a negative fold change (blue) indicated downregulated in old compared to young. \* denotes where the fold change was statistically significant (p ≤ 0.05).



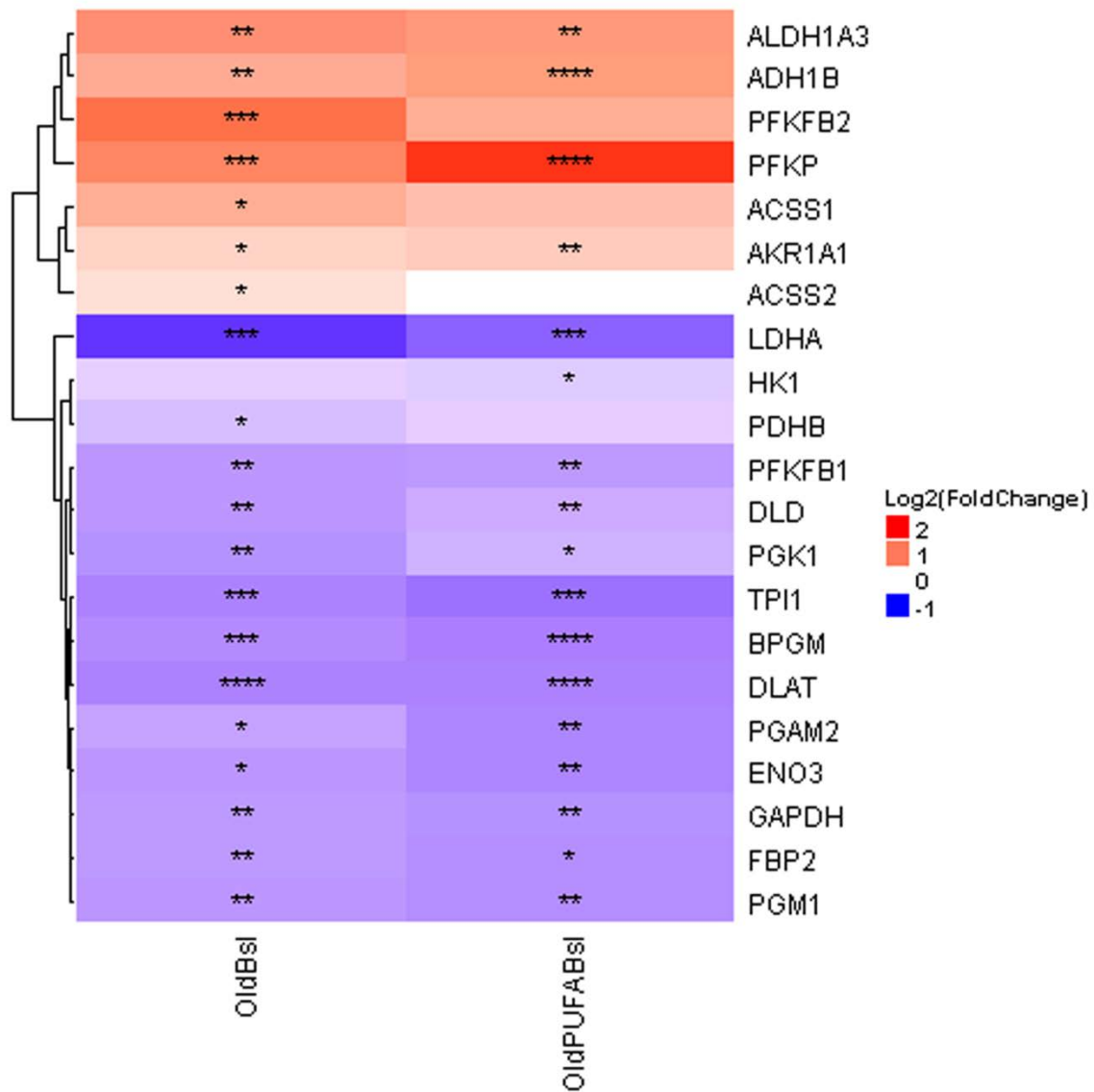
**Supplemental Figure 2.** The heatmap shows fold changes for genes related to tricarboxylic acid cycle in old baseline preintervention and old baseline postintervention relative to young baseline. A positive fold change (red) indicates upregulated in old compared to young, and a negative fold change (blue) indicated downregulated in old compared to young. \* denotes where the fold change was statistically significant ( $p \leq 0.05$ ).



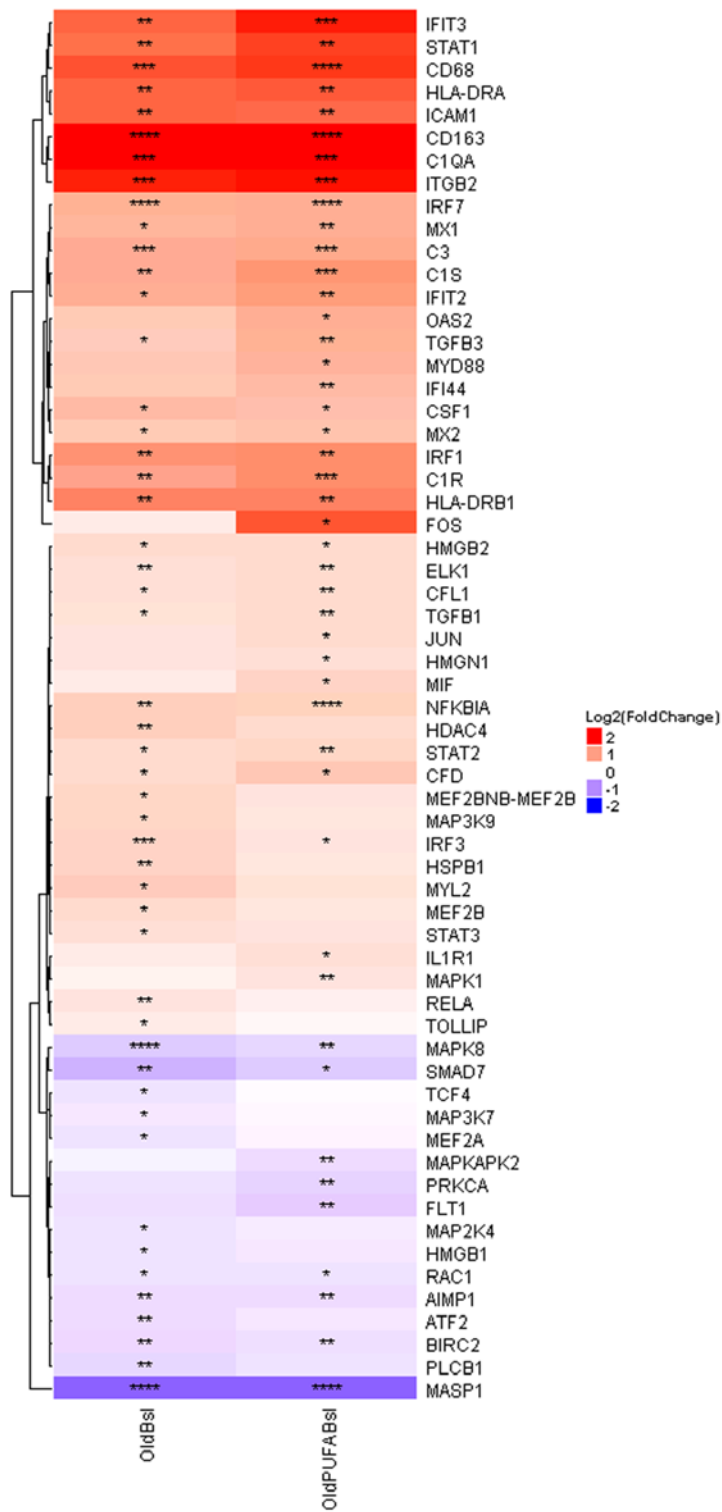
**Supplemental Figure 3.** The heatmap shows fold changes for genes related to lipid metabolism in old baseline preintervention and old baseline postintervention relative to young baseline. A positive fold change (red) indicates upregulated in old compared to young, and a negative fold change (blue) indicated downregulated in old compared to young. \* denotes where the fold change was statistically significant ( $p \leq 0.05$ ).



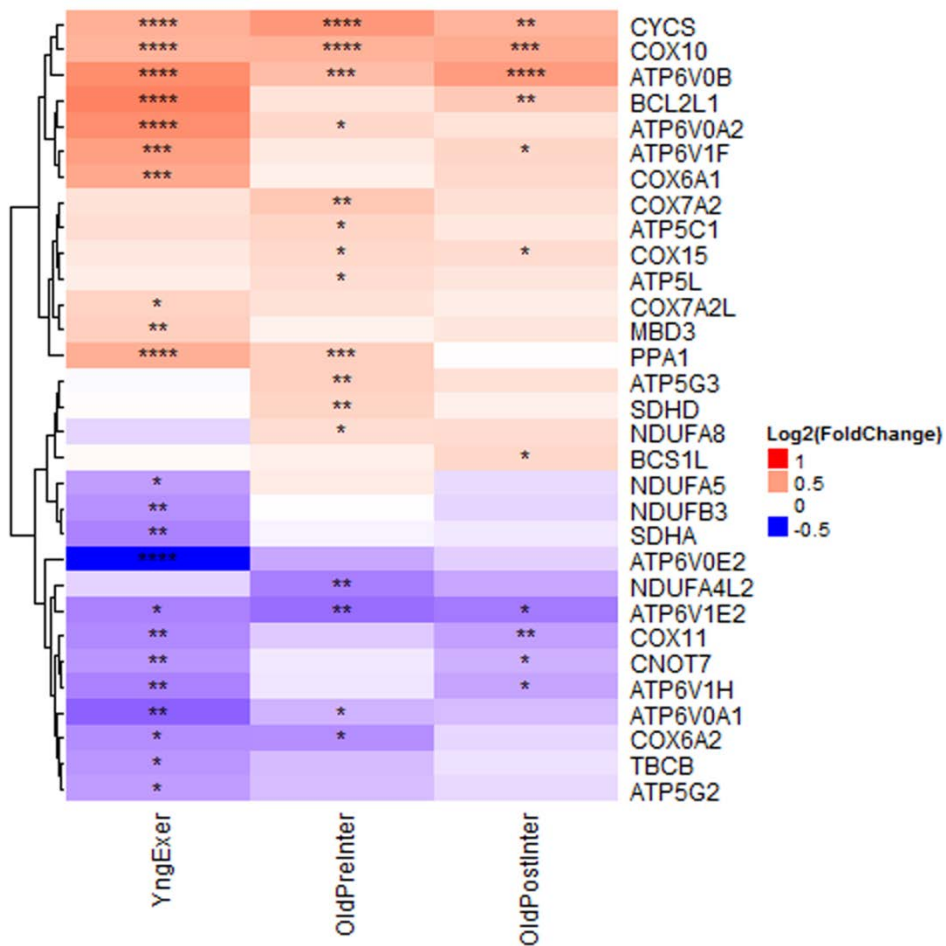
**Supplemental Figure 4.** The heatmap shows fold changes for genes related to oxidative stress in old baseline preintervention and old baseline postintervention relative to young baseline. A positive fold change (red) indicates upregulated in old compared to young, and a negative fold change (blue) indicated downregulated in old compared to young. \* denotes where the fold change was statistically significant ( $p \leq 0.05$ ).



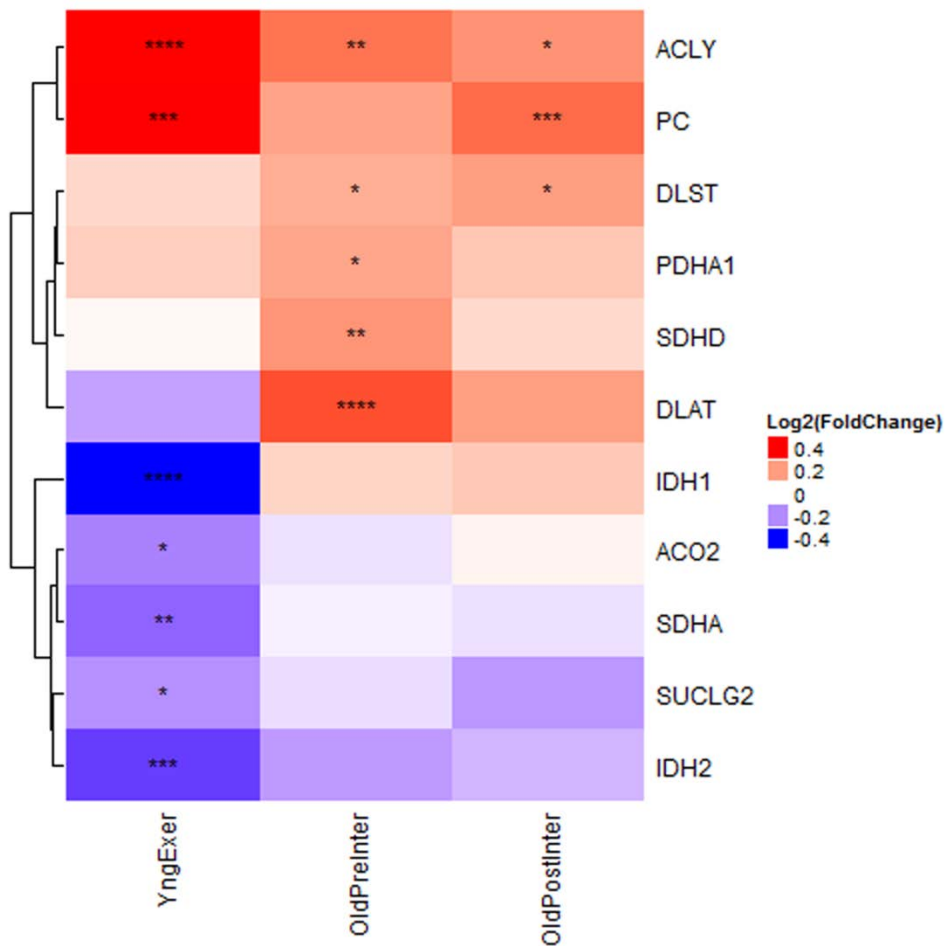
**Supplemental Figure 5.** The heatmap shows fold changes for genes related to glycolysis in old baseline preintervention and old baseline postintervention relative to young baseline. A positive fold change (red) indicates upregulated in old compared to young, and a negative fold change (blue) indicated downregulated in old compared to young. \* denotes where the fold change was statistically significant ( $p \leq 0.05$ ).



**Supplemental Figure 6.** The heatmap shows fold changes for genes related to inflammation in old baseline preintervention and old baseline postintervention relative to young baseline. A positive fold change (red) indicates upregulated in old compared to young, and a negative fold change (blue) indicated downregulated in old compared to young. \* denotes where the fold change was statistically significant ( $p \leq 0.05$ ).

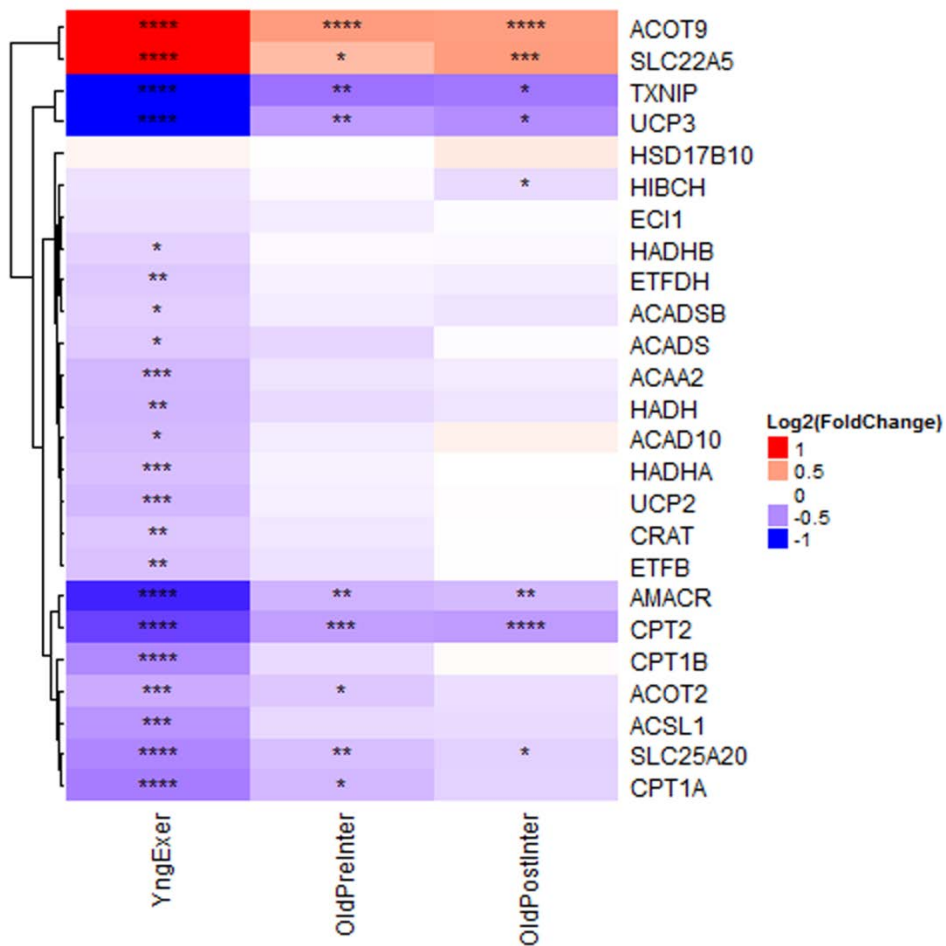


**Supplemental Figure 7.** The heatmap shows post exercise fold changes for genes related to oxidative phosphorylation in young, old, and old post-supplementation relative to their respective baseline transcript levels. A positive fold change (red) indicates upregulated after exercise, and a negative fold change (blue) indicated downregulated after exercise. \* denotes where the fold change was statistically significant from pre-exercise ( $p \leq 0.05$ ).

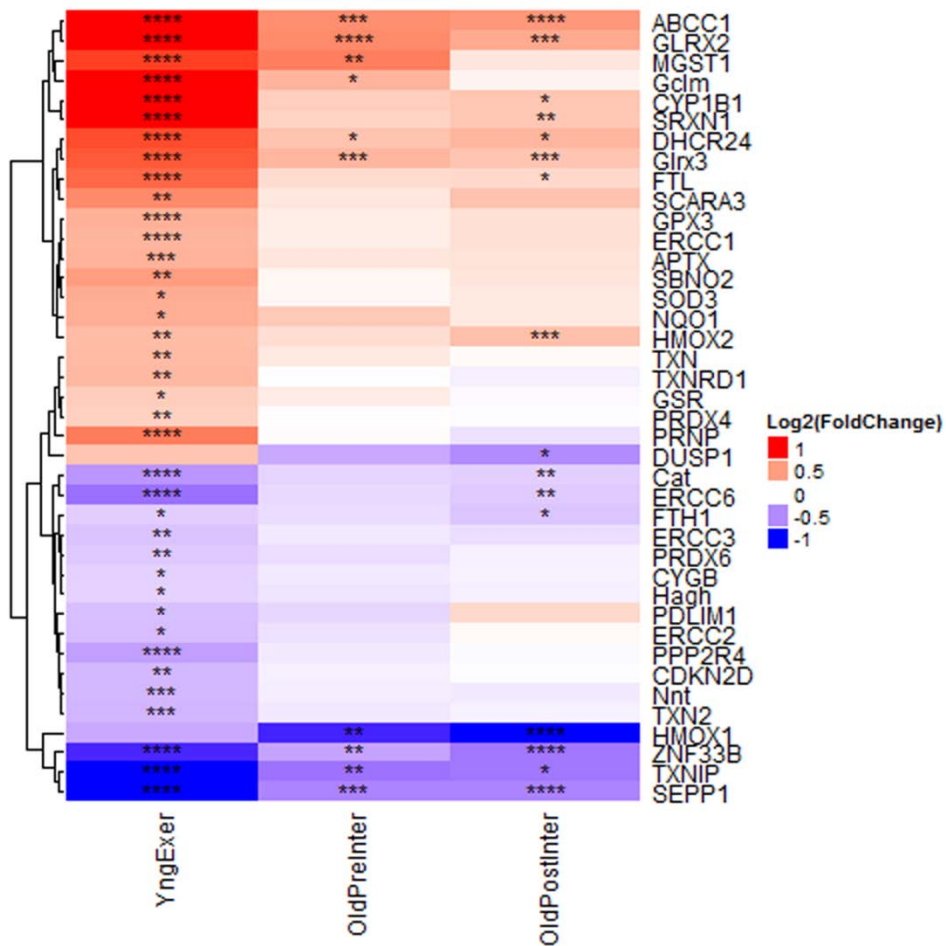


**Supplemental Figure 8.** The heatmap shows post exercise fold changes for genes related to tricarboxylic acid cycle in young, old, and old post-supplementation relative to their respective baseline transcript levels. A positive fold change (red) indicates upregulated after exercise, and a negative fold change (blue) indicated downregulated after exercise. \* denotes where the fold change was statistically significant from pre-exercise ( $p \leq 0.05$ ).

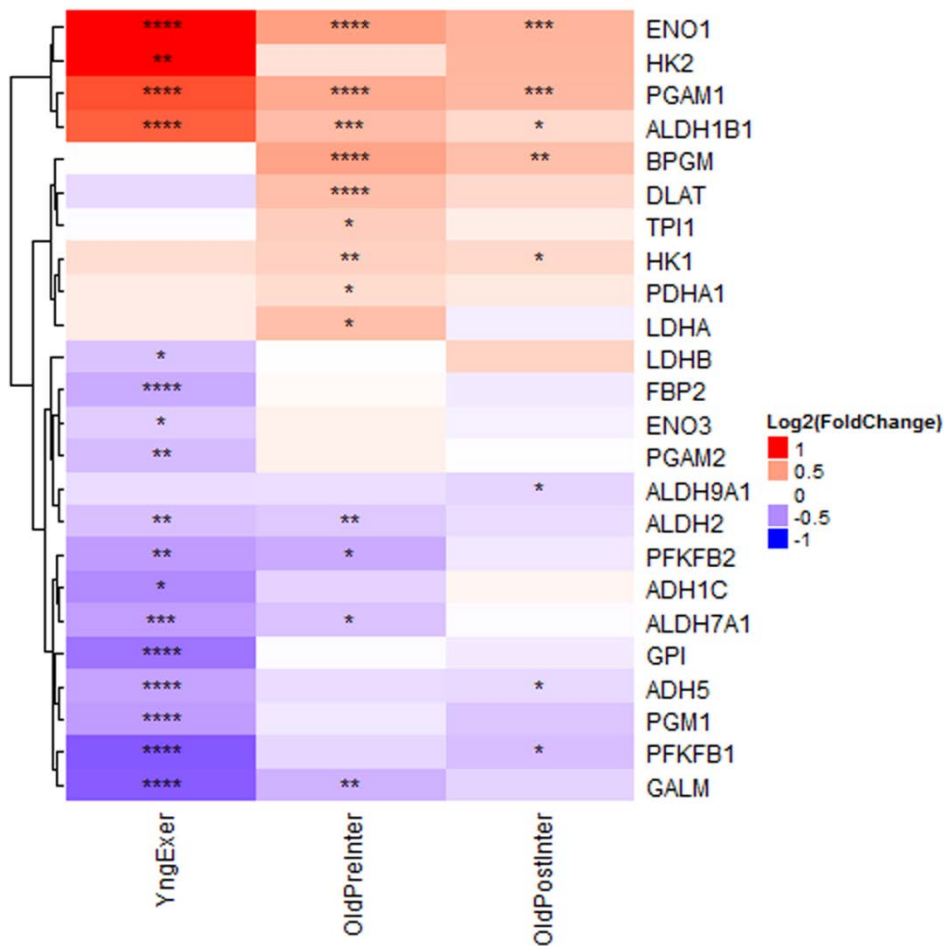




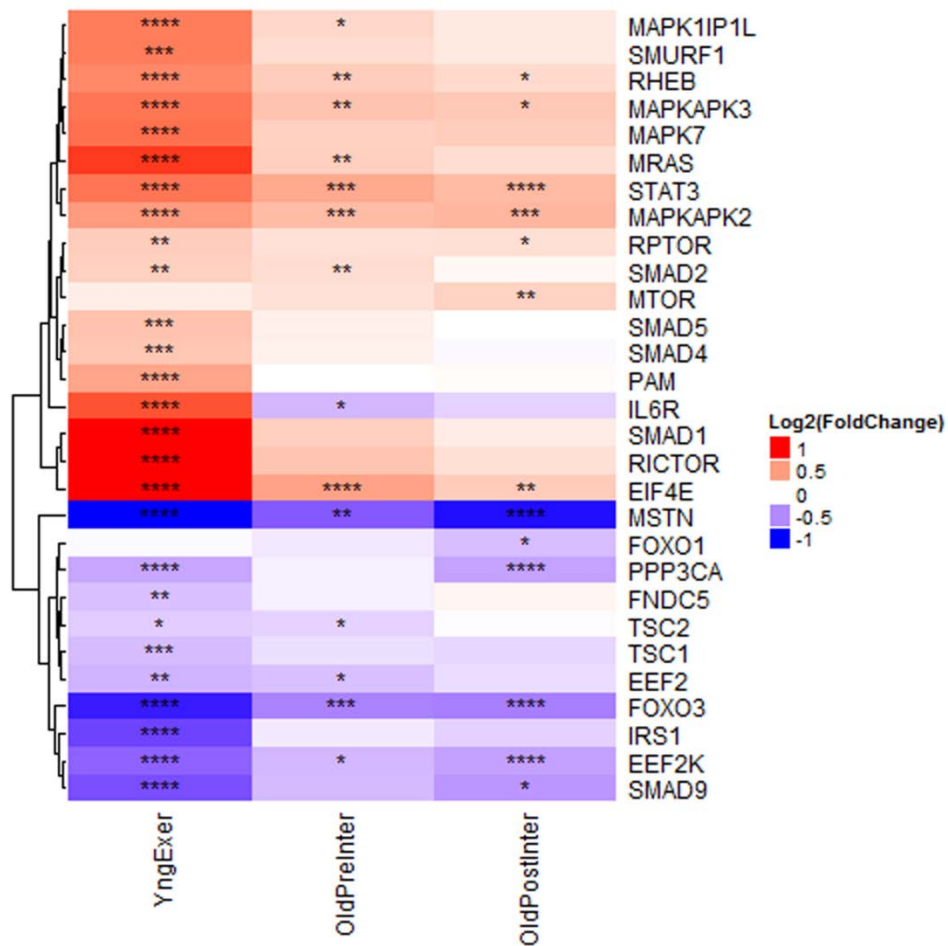
**Supplemental Figure 9.** The heatmap shows post exercise fold changes for genes related to lipid metabolism in young, old, and old post-supplementation relative to their respective baseline transcript levels. A positive fold change (red) indicates upregulated after exercise, and a negative fold change (blue) indicated downregulated after exercise. \* denotes where the fold change was statistically significant from pre-exercise ( $p < 0.05$ ).



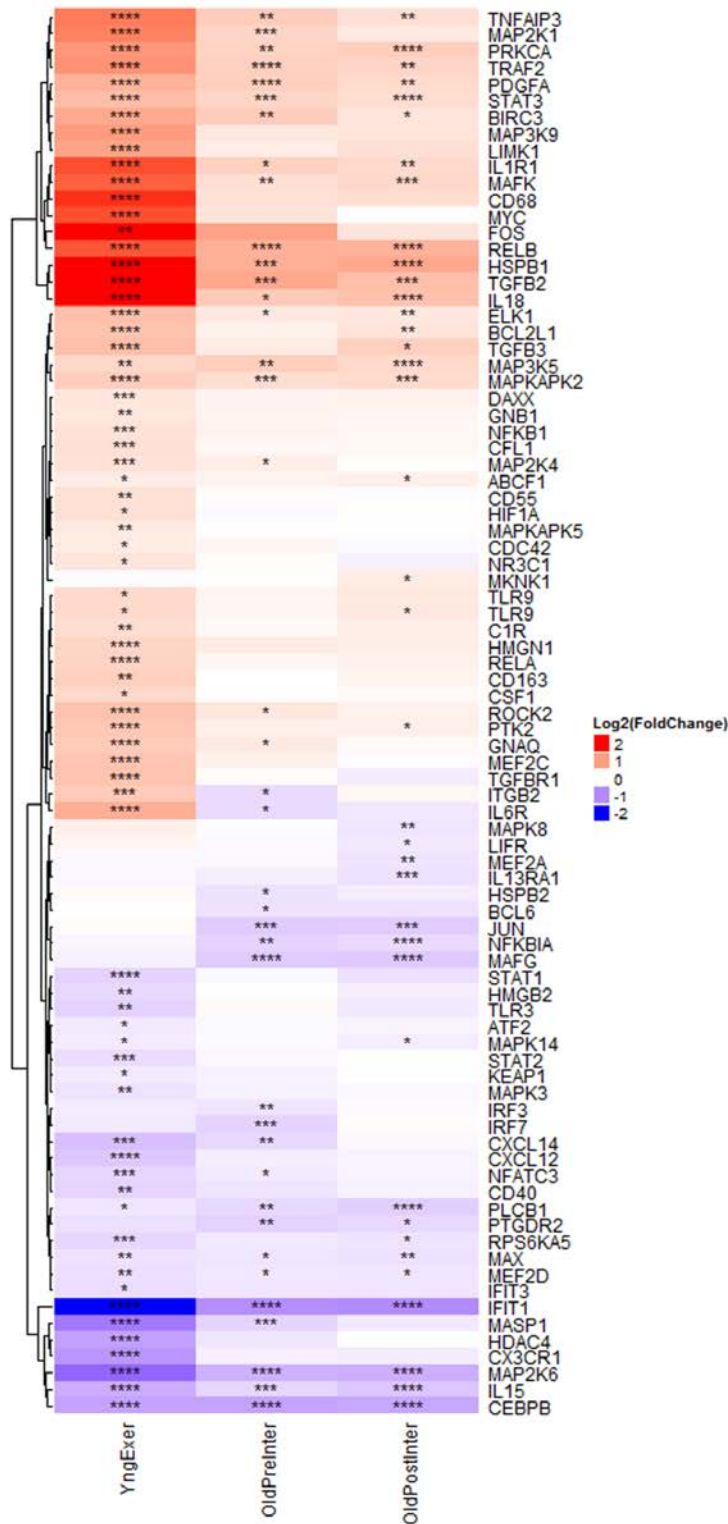
**Supplemental Figure 10.** The heatmap shows post exercise fold changes for genes related to oxidative stress in young, old, and old post-supplementation relative to their respective baseline transcript levels. A positive fold change (red) indicates upregulated after exercise, and a negative fold change (blue) indicated downregulated after exercise. \* denotes where the fold change was statistically significant from pre-exercise ( $p < 0.05$ ).



**Supplemental Figure 11.** The heatmap shows post exercise fold changes for genes related to glycolysis in young, old, and old post-supplementation relative to their respective baseline transcript levels. A positive fold change (red) indicates upregulated after exercise, and a negative fold change (blue) indicated downregulated after exercise. \* denotes where the fold change was statistically significant from pre-exercise ( $p \leq 0.05$ ).



**Supplemental Figure 12.** The heatmap shows post exercise fold changes for genes related to protein turnover in young, old, and old post-supplementation relative to their respective baseline transcript levels. A positive fold change (red) indicates upregulated after exercise, and a negative fold change (blue) indicated downregulated after exercise. \* denotes where the fold change was statistically significant from pre-exercise ( $p \leq 0.05$ ).



**Supplemental Figure 13.** The heatmap shows post exercise fold changes for genes related to inflammation in young, old, and old post-supplementation relative to their respective baseline transcript levels. A positive fold change (red) indicates upregulated after exercise, and a negative fold change (blue) indicated downregulated after exercise. \* denotes where the fold change was statistically significant from pre-exercise ( $p < 0.05$ ).

## Supplemental Tables

**Supplemental Table 1. Gene expression assays.**

Gene Symbol	Gene Name	Assay ID	Context Sequence	Probe Dye
<ul style="list-style-type: none"> <li><b>Gene targets with HPRT1 reference gene (4326321E, VIC probe)</b></li> </ul>				
SLN	sarcolipin	Hs01888464_s1	ACACGGTCTGCAACC AAACTCTAAT	FAM
FST	follistatin	Hs00246256_m1	TGCCCAGGCTGGGAA CTGCTGGCTC	FAM
CAPN1	calpain 1, (mu/I) large subunit	Hs00559804_m1	AACTACCCAGCCACC TTCTGGGTGA	FAM
TRIM63	tripartite motif containing 63, E3 ubiquitin protein ligase	Hs00822397_m1	GTCGAGTGACCAAGG AGAACAGTCA	FAM
MYOD1	myogenic differentiation 1	Hs02330075_g1	CGACGGCATGATGGA CTACAGCGGC	FAM
<ul style="list-style-type: none"> <li><b>Gene targets with B2M reference gene (4326319E, VIC probe)</b></li> </ul>				
B2M	Beta 2 microglobulin			
MSTN	myostatin	Hs00976237_m1	ATGCCTACAGAGTCT GATTTTCTAA	FAM
CAPN2	calpain 2, (m/II) large subunit	Hs00965097_m1	CGGAGCCGAGGAGGT TGAAAGTAAC	FAM
FBXO32	F-box protein 32	Hs01041408_m1	TCCGAGCGGCAGATC CGCAAACGAT	FAM
FOXO3B, FOXO3	forkhead box O3B pseudogene, forkhead box O3	Hs00921424_m1	GGGCAAAGCAGACCC TCAAACGTGAC	FAM

**Supplemental Table 2. Gene identities of elements in each section of the Venn Diagram in Figure 5.**

See Supplemental File 2.