

Data supplement

Transcriptional changes associated with long-term left ventricle volume overload in rats: impact on enzymes related to myocardial energy metabolism.

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Table S1. Primer Assays used in Q-PCR analysis of gene expression (Figure S1).

mRNA	Symbol	Cat. No.	Amplicon (bp)
Connective tissue growth factor	Ctgf	QT00182021	102
Cathepsin K	Ctsk	QT00375599	80
Fibronectin 1	Fn1	QT00179333	92
Follistatin-like 1	Fstl1	QT00195762	131
Hepcidin antimicrobial peptide	Hamp	QT00372876	120
Integrin beta 1	Itgb1	QT00187656	117
Natriuretic peptide precursor type A	Nppa	QT00366170	94
Natriuretic peptide precursor type B	Nppb	QT00183225	89
Peripheral myelin protein 22	Pmp22	QT00175938	89
Transforming growth factor beta 2	Tgfb2	QT00187320	139
Tissue inhibitor of metalloproteinase 1	Timp1	QT00185304	113

Table S2. Significant up-regulated gene categories based on gene ontology annotation system.

System	Gene Category	No. of genes	EASE score ^a
GO Biological Process	regulation of cell cycle	16	4.29E-04
GO Biological Process	cell growth	9	5.59E-04
GO Biological Process	transition metal ion homeostasis	5	6.27E-04
GO Biological Process	di-, tri-valent inorganic cation homeostasis	7	7.50E-04
GO Biological Process	response to biotic stimulus	23	8.05E-04
GO Molecular Function	calcium ion binding	25	6.90E-06
GO Molecular Function	metal ion binding	36	8.01E-05
GO Molecular Function	cell adhesion molecule activity	15	2.11E-04
GO Molecular Function	calcium-dependent phospholipid binding	5	6.74E-04
GO Cellular Component	extracellular	70	2.70E-11
GO Cellular Component	extracellular matrix	22	6.04E-08
GO Cellular Component	extracellular space	42	3.80E-06

a: Ease Probability score. E: exponent, power of 10.

Table S3. Significant down-regulated gene categories based on gene ontology annotation system.

System	Gene Category	No. of genes	EASE score ^a
GO Biological Process	organic acid metabolism	18	2.49E-07
GO Biological Process	carboxylic acid metabolism	18	2.49E-07
GO Biological Process	fatty acid metabolism	11	4.64E-06
GO Biological Process	energy derivation by oxidation of organic compounds	10	2.75E-05
GO Biological Process	energy pathways	11	2.89E-05
GO Molecular Function	oxidoreductase activity	26	1E-10
GO Molecular Function	transferase activity	26	3.06E-04
GO Cellular Component	mitochondrion	54	4.8E-24

a: Ease Probability score. E: exponent, power of 10.

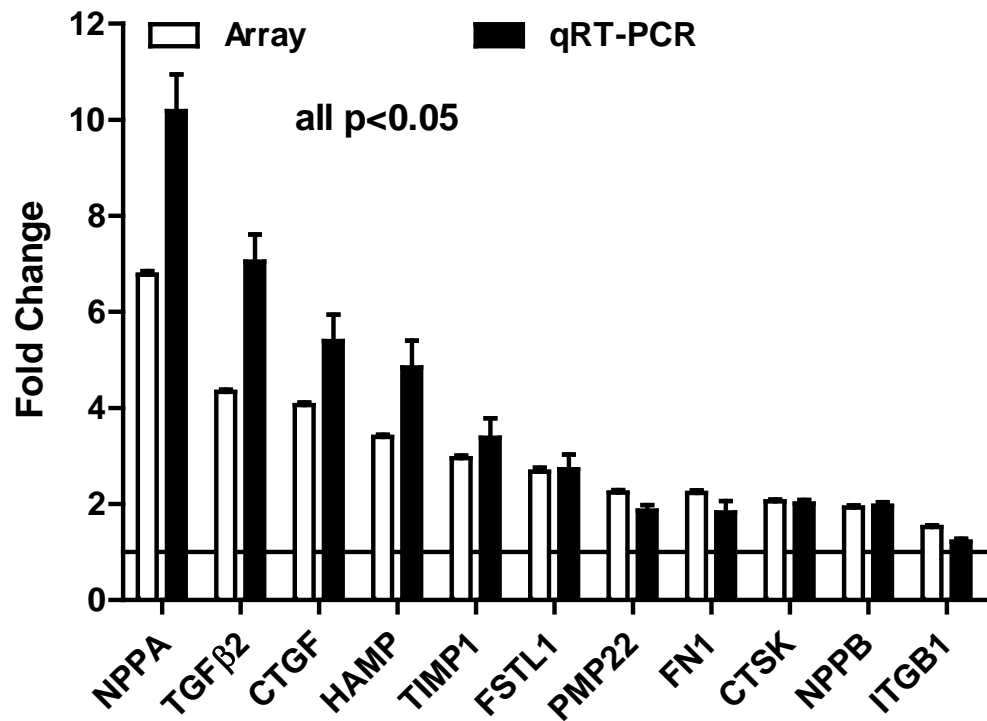


Figure S1. Comparison between fold change results obtained from the microarray and by quantitative RT-PCR for a subset of 11 up-regulated genes as determined in the array study. Results are reported in as mean \pm SEM ($n = 5$ per group for array and $n=6$ for qRT-PCR). Levels in sham animals were fixed to 1.

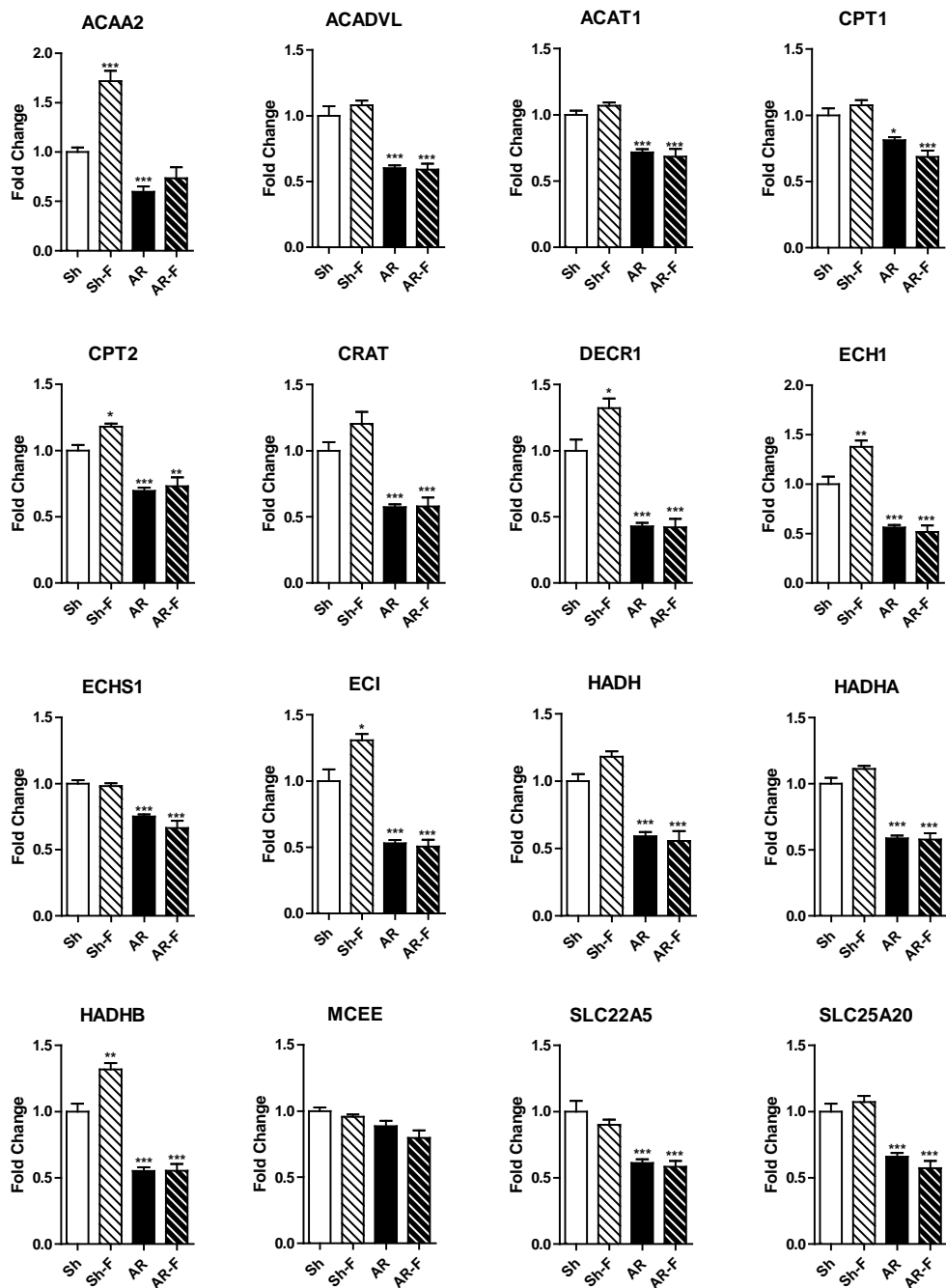


Figure S2. Impact of an 8-week fenofibrate (F) treatment on LV expression of 16 FAO genes in Sham (Sh) and AR rats. Levels in sham animals were fixed to 1 (Line). *: $p < 0.05$, **: $p < 0.01$ and ***: $p < 0.001$ vs. untreated sham animals.