Metabolomics and the pig model reveal aberrant myocardial energy metabolism in metabolic syndrome

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TABLE S1 (related to Fig 2a) Metabolites that are overrepresented in LD vs MS as identified by UML based on the weight of the metabolite in the individual signatures. Probability in LD is higher than in MS (100 means MS, S3=0)

glyoxylate	NADH	fructose-1,6-bisphosphate
pyruvate	acetyl-CoA	NADPH
ribose-phosphate	succinyl-CoA	N-acetyl-glutamine
uridine	acetoacetate	Glucose-3-phosphate
glucose-1-phosphate	2-oxobutanoate	UDP
biotin	anthranilate	ATP
guanosine	glucose-6-phosphate	3-hydroxybutirate
7-methylguanosine	fructose-6-phosphate	Malonyl-CoA
AMP	FAD	glutathione glyoxylate

Figure S1 (related to Fig 4b) (a) Western blot with protein specific antibodies against IDH2, SDHB, FH, MAOB, GAPDH as shown on top of the panels. Each gel received total tissue lysate (50 μg/lane) from four of the LD pigs (lanes 1, 2, 3, 4) and four of the MS pigs (5, 6, 7, 8). The migration position and the molecular mass of the protein that is recognized by the antibody is shown on left. (b) Ponceau staining of the membranes confirmed equal lysate loading and transfer.

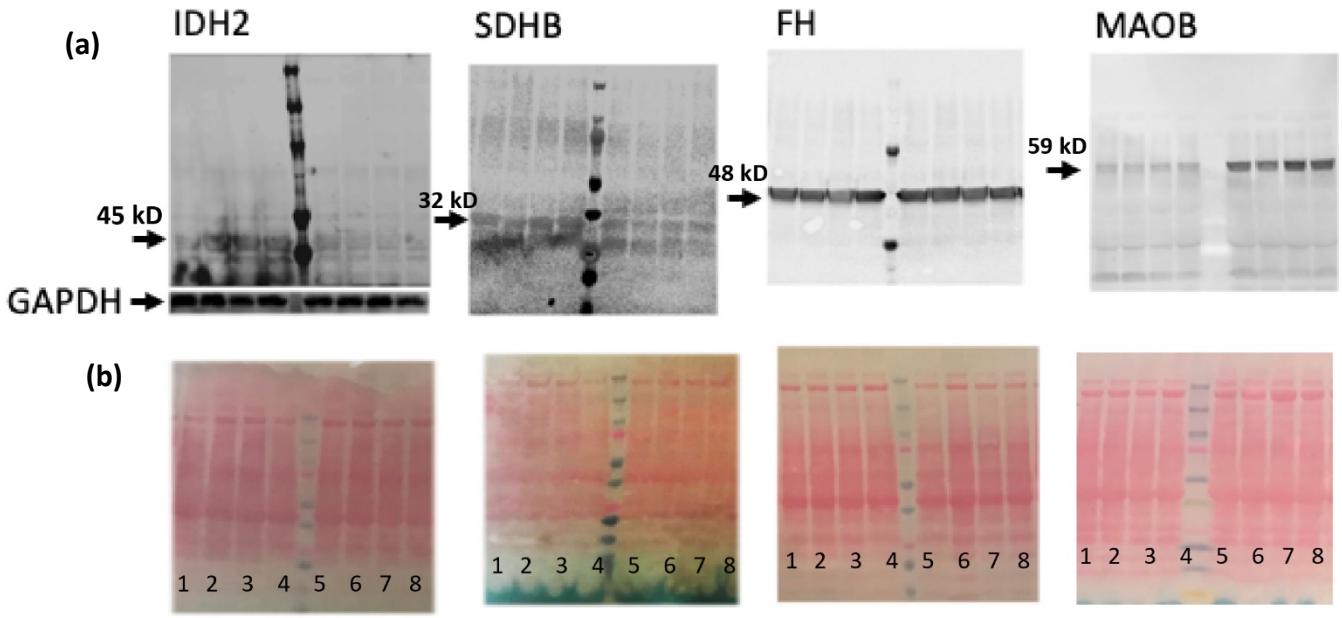

Figure S2 (related to Fig 4a) mRNA content of phenylalainine hydroxylase (*PAH*) (n=4, p=0.028) and Fumarylacetoacetase (*FAH*) (n=4, p=0.059)