



Supplementary Material

Multiparametric evaluation of post-MI small animal models using metabolic ([¹⁸F]FDG) and perfusion-based ([¹⁸F]Fkardio) heart viability markers

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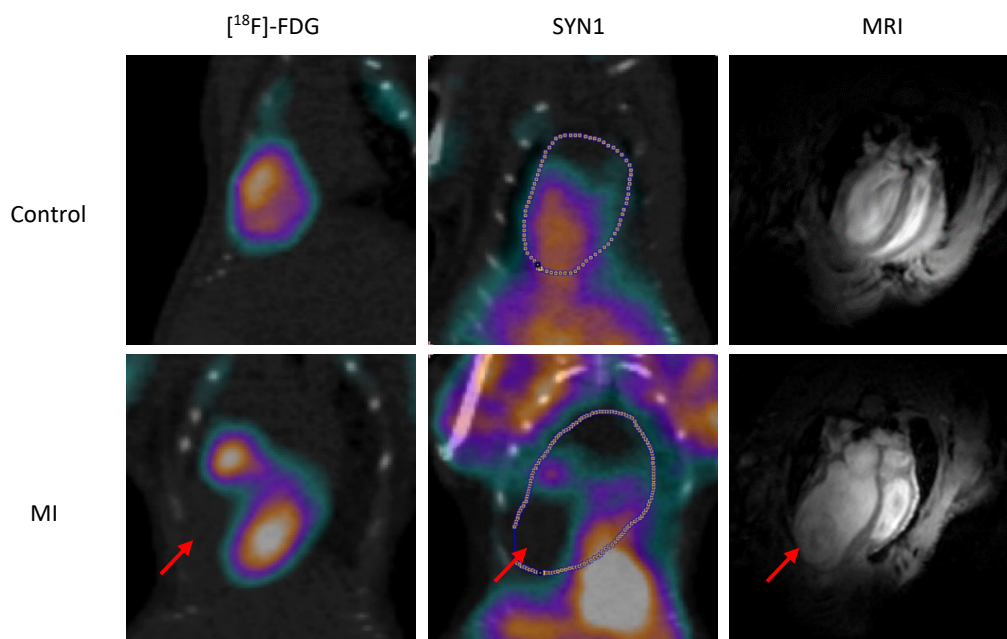
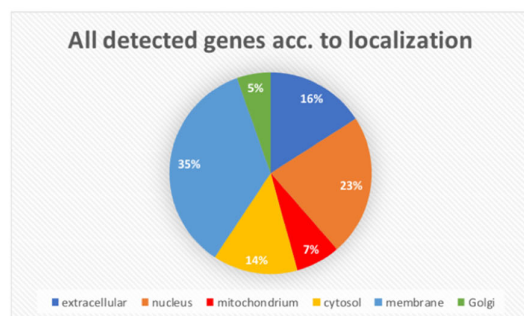


Figure S1. Comparison of molecular imaging of control and MI mice.

Control mouse (top row) and post MI mouse (bottom row). Note the difference in the loss of [¹⁸F]-FDG and SYN1 uptake in the apex region. MRI imaging confirms the damage of the heart muscle left ventricle, which is also visible in the images. The size of post MI heart is bigger due to the organ remodeling.

A

Upregulated genes signalling pathways ranking (based on KEGG pathways)

	p-value
HIF-1 signaling pathway	0.0003651
ECM-receptor interaction	0.002581
Protein digestion and absorption	0.004025
PI3K-Akt signaling pathway	0.06896
Apelin signaling pathway	0.008858
Cytokine-cytokine receptor interaction	0.02863
Hippo signaling pathway	0.01415
Wnt signaling pathway	0.004788
Chemokine signaling pathway	0.01485
Focal adhesion	0.03855

Downregulated genes signalling pathways ranking (based on KEGG pathways)

	p-value
Pentose phosphate pathway	0.02227
Fructose and mannose metabolism	0.02447
Vasopressin-regulated water reabsorption	0.03251
Mineral absorption	0.04408
Glycolysis / Gluconeogenesis	0.04911
Pancreatic secretion	0.07385
HIF-1 signaling pathway	0.07873
Vascular smooth muscle contraction	0.09527
Phospholipase D signaling pathway	0.1055
Neuroactive ligand-receptor interaction	0.2274

Figure S2. Summary of the expression data between MI and control groups

- A. Localization of the differentially expressed genes (DEG) shows that the major changes occur in the extracellular and membrane compartments, accompanied with the nuclei expression changes.
- B. Major up- and downregulated signaling pathways in post MI group. Signaling pathway ranking is based on reversed p-values. P-values are presented next to the chart.