Figure S1. GO term analysis in the categories BP, MF and CC for the differentially expressed genes in acute myocardial infarction. The negative logarithm of the P-value (x-axis) indicates the significance of the gene set belonging to predefined categories under the 52-gene background. The y-axis represents each GO category. The gene number and EC value of the category in the subnetwork are presented in brackets. GO, Gene Ontology; BP, biological process; MF, molecular function; CC, cellular component; EC, expression coherence.
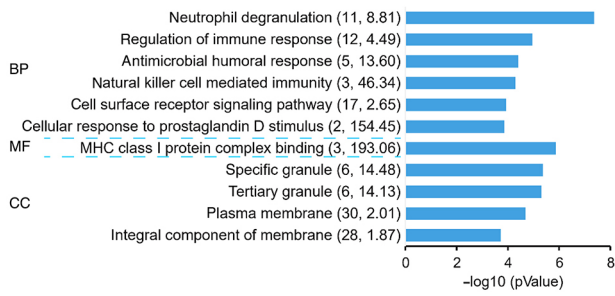
Figure S2. mRNA expression of differentially expressed genes in AMI. Expression of three upregulated genes (A) AKR1C3, (B) P2RY12 (C) RPS24 and three downregulated genes (D) ACSL1, (E) B3GNT5 and (F) MGAM in AMI vs. Ctrl was validated via reverse transcription-quantitative PCR. **$P<0.01$. AMI, acute myocardial infarction; Ctrl, control; AKR1C3, aldo-keto reductase 1 C3; RPS24, ribosomal protein S24; P2RY12, purinergic receptor P2Y12; ACSL1, acyl-CoA synthetase long chain family member 1; B3GNT5, UDP-GlcNAc: βGal β-1,3-N-acetylglucosaminyltransferase 5; MGAM, maltase-glucoamylase.