

Figure S1. ROC analysis of analyzed miRNAs for hepatic injury in autologous hematopoietic stem cell transplantation recipients. (A) miR-122-5p. (B) miR-122-3p. (C) miR-99b-5p. (D) miR-125a-5p. (E) miR-15b-5p.

Figure S2. Target prediction analysis of miRNAs included in the model predicting hepatotoxicity occurrence in AHSCT recipients—miR-122-5p and miR-125a-5p. Genes involved in the Hepatitis C KEGG pathway were annotated.

Figure S3. Functional enrichment analysis of identified targets of miR-122-5p and miR-125a-5p using the KEGG database.

Supplementary File S1. Normalized miRNA expression data with clinical variables.

Supplementary File S2. Predicted target genes of miR-122-5p and miR-125a-5p using miRNet and miRTarBase v 8.0.

Supplementary Table S1. Multivariate logistic regression analysis for hepatic toxicity (HT) during hospitalization after ASCT—MM patients only.