**Plasma-derived exosomal sncRNAs as a promising diagnostic biomarker for early dectection of HBV-related acute-on-chronic liver failure**

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***Supplementary Material***

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**Figure S9: The KEGG pathway analysis for the MTR-RNA signature including hsa-miR-23b-3p, hsa-miR-223-3p and hsa-miR-339-5p (A), and tsRNA-20 and tsRNA-46 (B)………………………………………………………………………...11**

**Table S1: Transcripts differentially expressed identified by the sncRNA-seq analysis.**

**Table S2: The differentially expressed miRNAs were analyzed by sncRNA-seq.**

**Table S3: Using miRanda and TargetScan softwares to predicte miRNA potential targets.**

**Table S4:** **The differentially expressed tsRNAs were analyzed by sncRNA-seq.**

**Table S5: Using miRanda and TargetScan softwares to predicte tsRNA potential targets.**

**Table S6: The differentially expressed rsRNAs were analyzed by sncRNA-seq.**

**Table S7: List of 20 sncRNA candidates used in this study.**

**Table S8: Sequences of primers used in this study.**

**Supplementary Figures**

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**Figure S1:** Mapping of overall length displaying relative sncRNA reads distributions in 13 exosome samples in small RNA-seq.

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**Figure S2:** Results presenting the dynamic sncRNAs landscape measured through 13 exosome samples in small RNA-seq.

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**Figure S3:** Results showing the dynamic tsRNAs landscape measured in discovery cohort.

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**Figure S4:** Mapping of overall length displaying relative rsRNA read distributions in 13 exosome samples in small RNA-seq.

**G:\2022年5月5日=回答审稿人的意见\2022年4月18日=frotier投稿\Figure.S5=new-01.tifFigure S5:** Results revealing the dynamic rsRNAs landscape measured in discovery cohort.

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**Figure S6:** Results showing the dynamic rsRNAs landscape derived from rRNA-28s and rRNA-18s detected in discovery cohort.

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**Figure S7:** The construction of a molecule signature model for candidate sncRNAs in the RNA-seq data from the discovery cohort. **(A)** Schematic diagram of LR screening in three different RNA sequencing groups. **(B)** The misclassification error diagram for the RNA-seq model in discovery cohort. **(C)** AUC curve for candidate sncRNAs in the RNA-seq model. **(D)** The Model evaluation for candidate sncRNAs in the RNA-seq model.

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**Figure S8:** Comparison of MTA-RNA signature molecules with current traditional clinical guidelines for TB and PTA, respectively.

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**Figure S9:** The KEGG pathway analysis for the MTR-RNA signature including hsa-miR-23b-3p, hsa-miR-223-3p and hsa-miR-339-5p **(A)**, and tsRNA-20 and tsRNA-46 **(B)**.