SUPPLEMENTAL MATERIAL

Supplemental Methods

Platelet Aggregation Test

The platelet aggregation test was performed using lighttransmission aggregometry (LTA) by one appointed researcher who was blinded for the subject's conditions. Two milliliter of blood sample from each subject was collected into a vacuum tube containing 3.8% sodium citrate anticoagulant (9NC; Greiner Bio-One, Thailand), and then centrifuged at 1,000 revolutions per minute (rpm) for 10 minutes at room temperature (24±2°C) to obtain plate let-rich plasma (PRP). After pipetting 300μL of PRP into a cuvette containing a metal stir bar, the remaining blood sample was centrifuged at 3000 rpm for 10 minutes at room temperature to obtain the same quantity of platelet-poor plasma (PPP). According to the manufacturer's instruction, cuvettes containing PRP and PPP were put into the test holes of a four-channel platelet aggregometer (Precil Corp., China), respectively. After adding 3 μL adenosine diphosphate (ADP) (concentration of 20 μmol/L; Chrono-Log, United States) as the agonists into PRP, the platelet aggregation curve and MPAR were calculated automatically.

Nailfold Capillaroscopy

Nailfold capillaroscopy was performed using Microcirculation Monitor (XW-880, China). Before the examination, subjects were asked to take off their watches and rings and sit quietly for 20 minutes at room temperature to eliminate the influence caused by movement and temperature on NM. The right ring finger was positioned on the microscope stage. Immersion oil was applied to the nailfold bed to maximize stratum-corneum transparency. Capillaroscopy images were captured and subsequently evaluated by a trained and experienced researcher who was blinded for the subject's allocation. An integrated score, including the morphology, blood flow, and peripheral status of capillary loops, was assessed for evaluating the condition of NM. The Nailfold microcirculation score table was showed in Supplementary Table 1

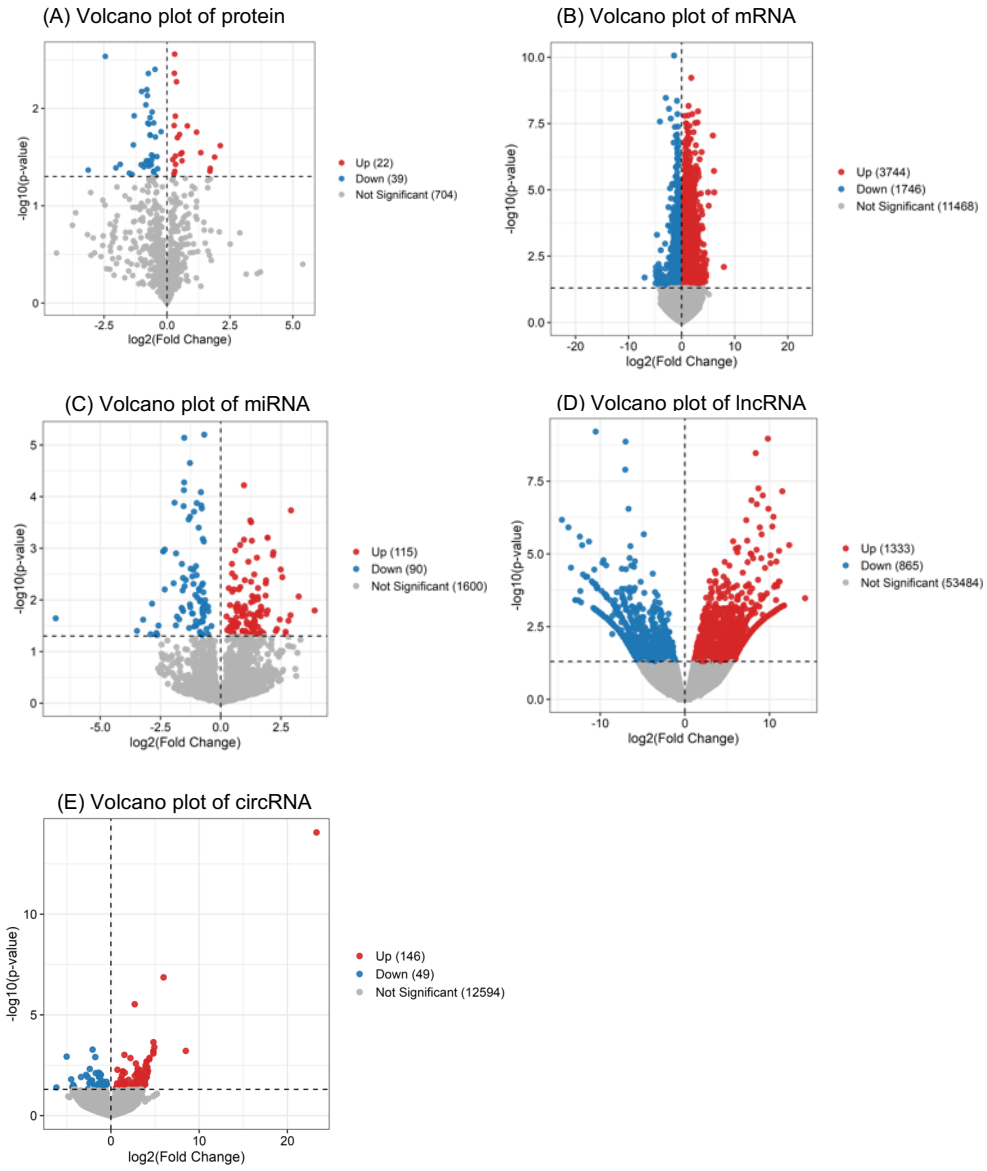

Fig. 1. Volcano plots of differentially expressed molecules between PTS and HEALTH groups. (A) DEproteins, (B) DEmRNAs, (C) DEmiRNAs, (D) DElncRNAs, and (E) DEcircRNAs.

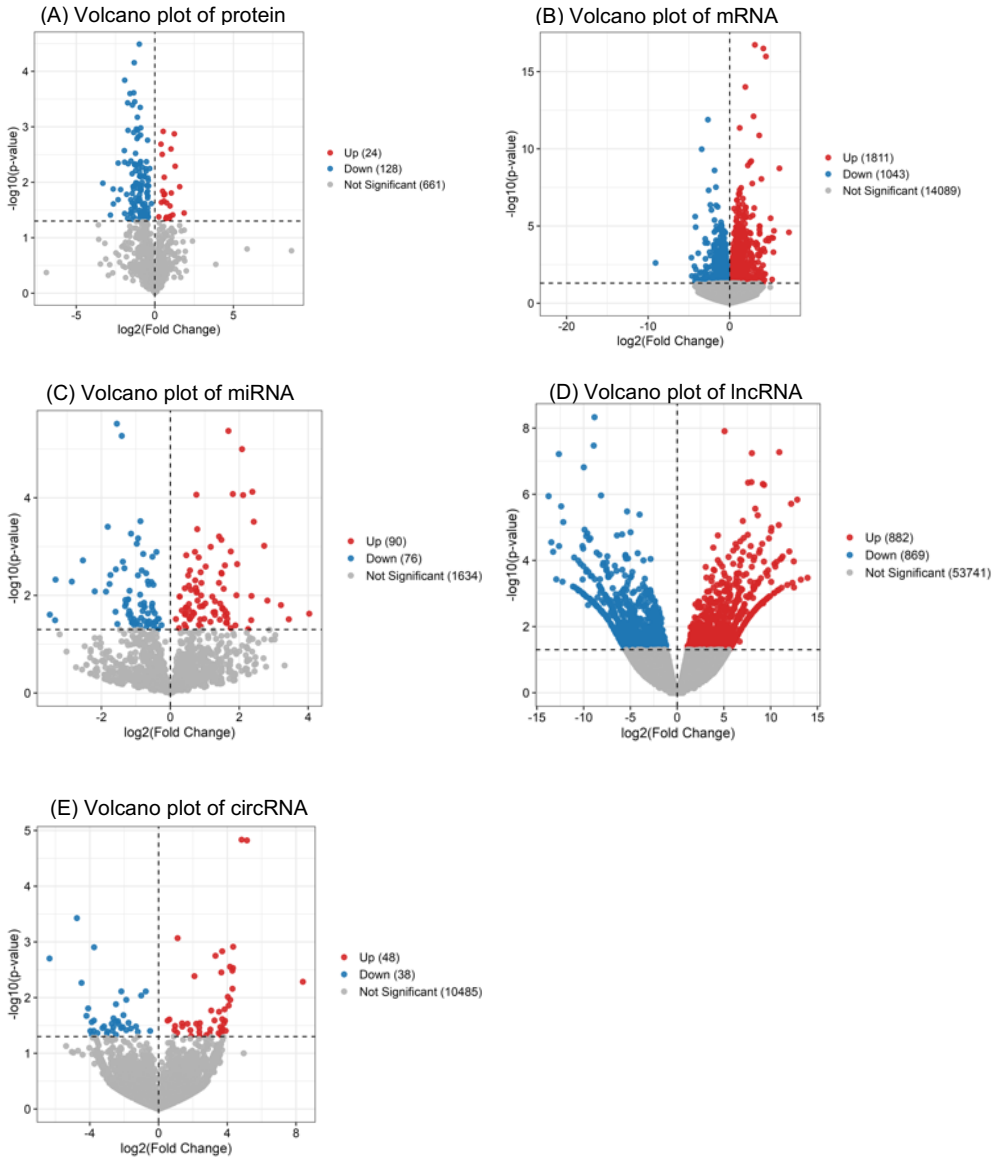

Fig. 2. Volcano plots of differentially expressed molecules between AMI and HEALTH groups. (A) DEproteins, (B) DEmRNAs, (C) DEmiRNAs, (D) DElncRNAs, and (E) DEcircRNAs.

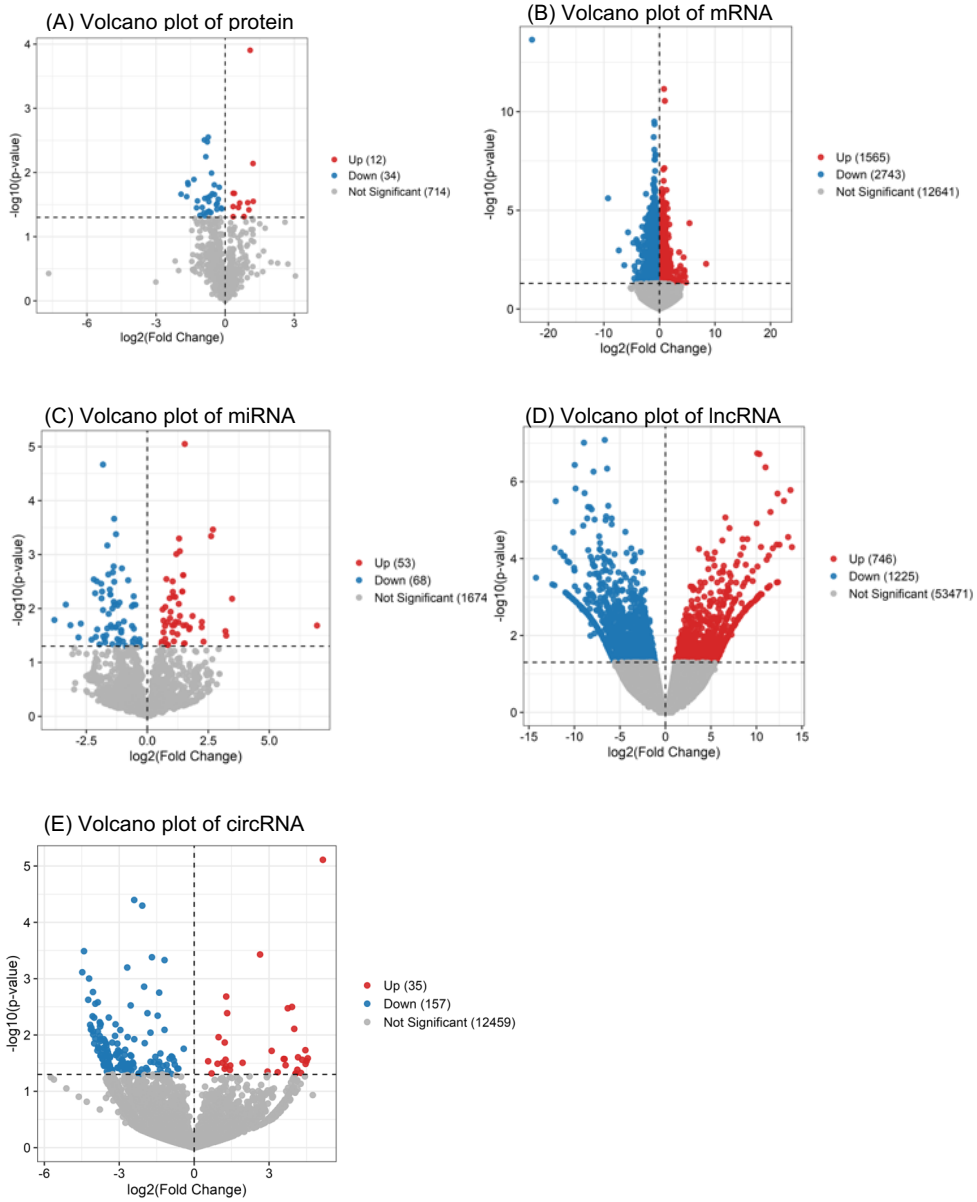

Fig. 3. Volcano plots of differentially expressed molecules between PTS and NPTS groups. (A) DEproteins, (B) DEmRNAs, (C) DEmiRNAs, (D) DElncRNAs, and (E) DEcircRNAs.

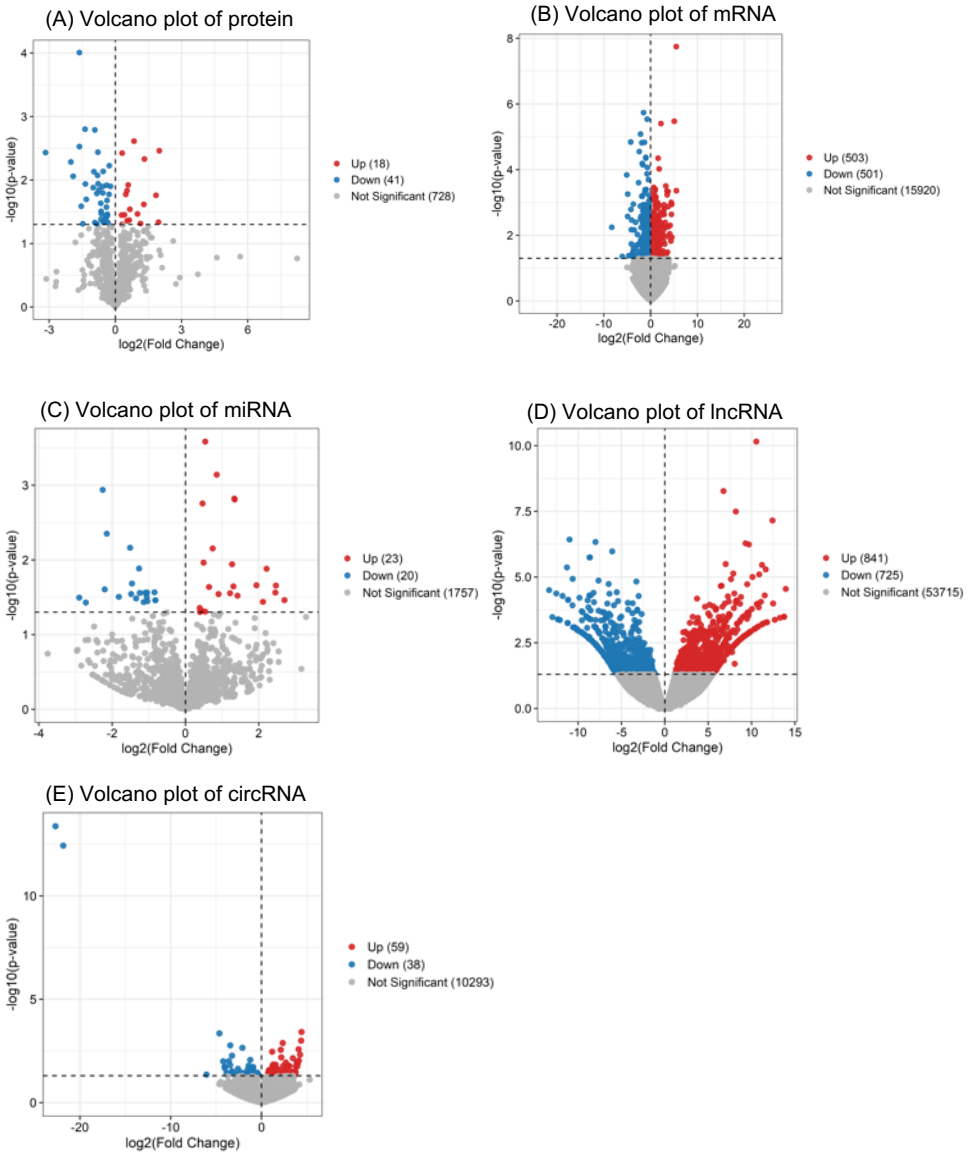

Fig. 4. Volcano plots of differentially expressed molecules between AMI and PTS groups. (A) DEproteins, (B) DEmRNAs, (C) DEmiRNAs, (D) DElncRNAs, and (E) DEcircRNAs.

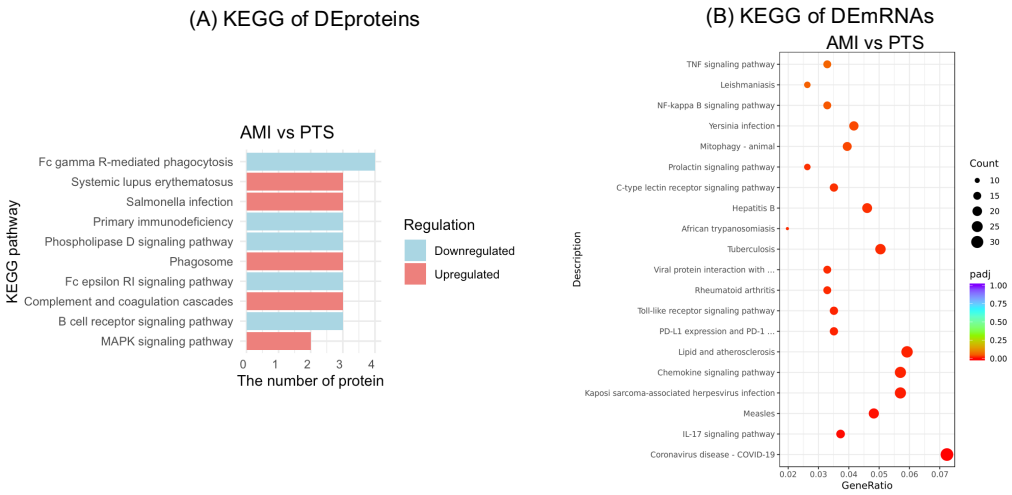

Fig. 5. KEGG pathway enrichment analysis of DEproteins and DEmRNAs between AMI and PTS group.

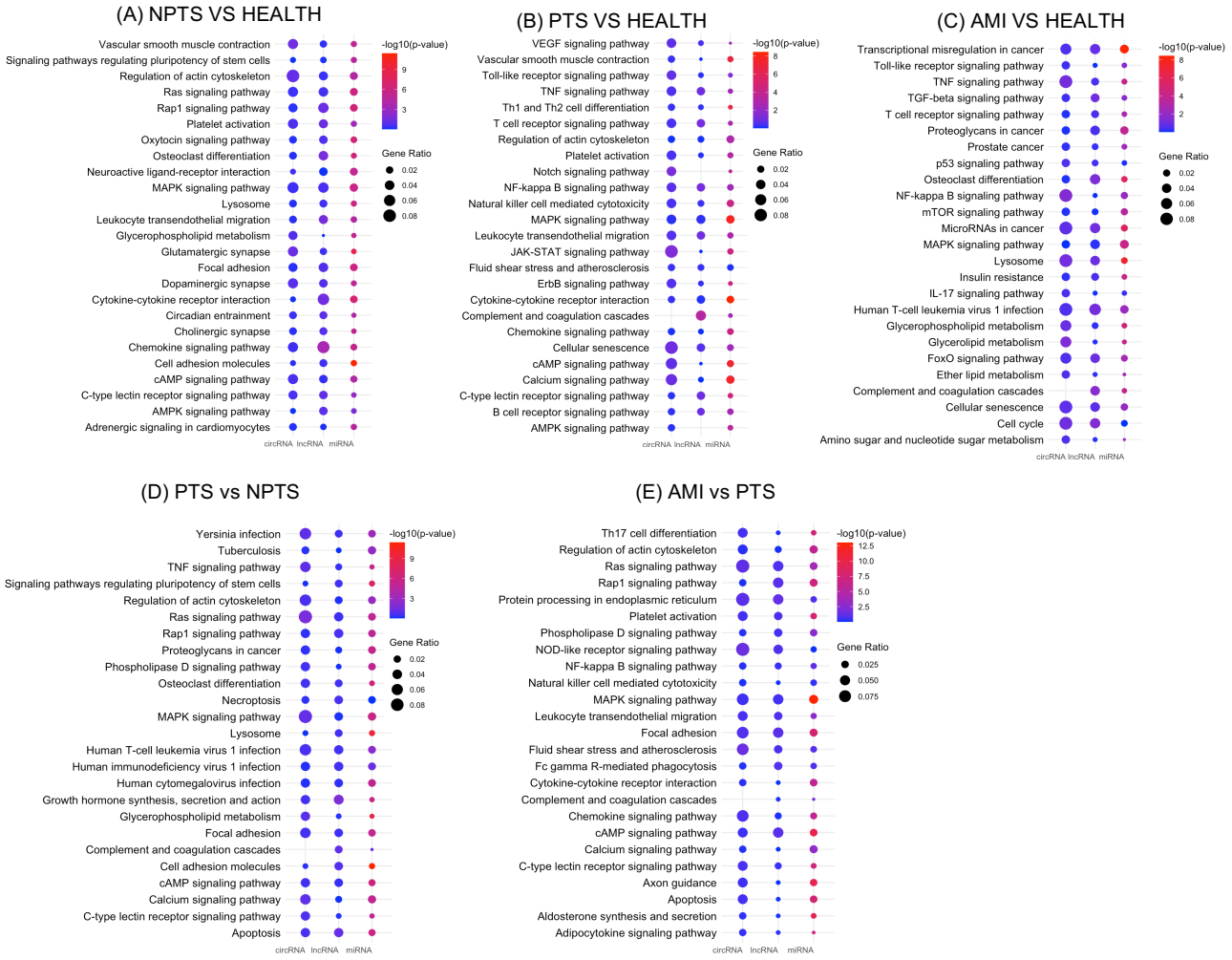

Fig. 6. KEGG pathway enrichment analysis of DEncRNA across different groups comparison. (A) NPTS vs HEALTH, (B) PTS vs HEALTH, (C) AMI vs HEALTH, (D) PTS vs NPTS, and (E) AMI vs PTS.

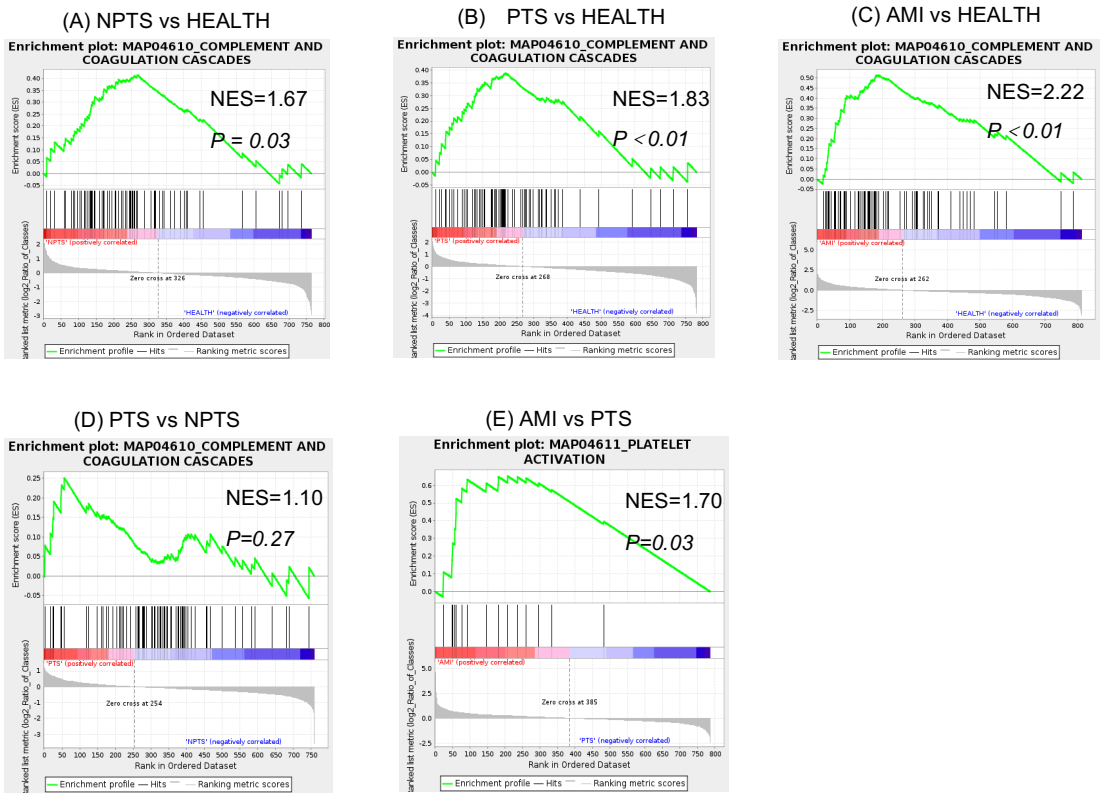

Fig. 7. GSEA of DEproteins across different groups comparison. (A) NPTS vs HEALTH, (B) PTS vs HEALTH, (C) AMI vs HEALTH, (D) PTS vs NPTS, and (E) AMI vs PTS. The normalized enrichment scores (NES) and *p*-values are indicated in each panel.

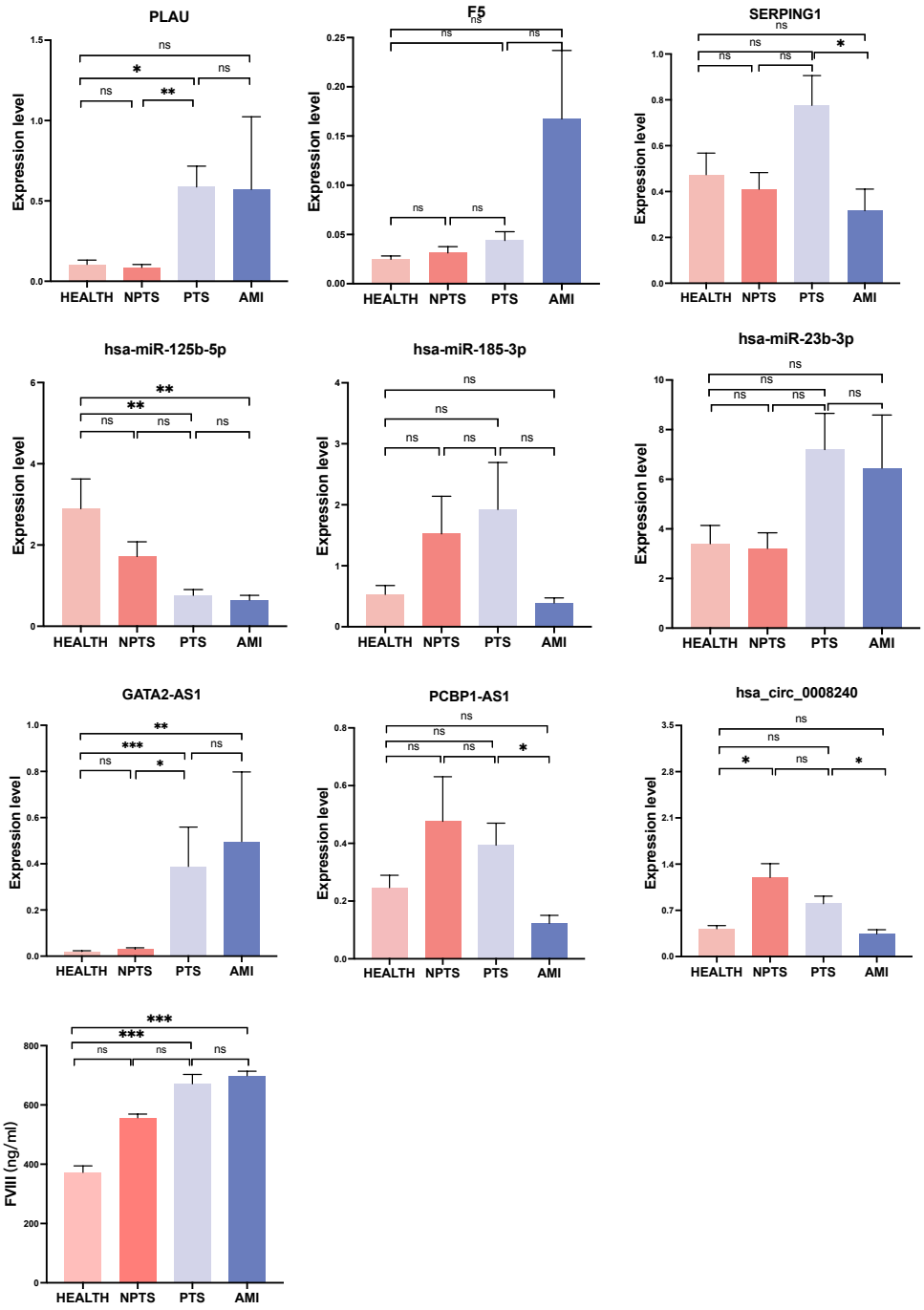

Fig. 8. Sensitivity analysis of candidate PTS biomarkers. Extreme outliers were defined as values greater than 3 times the interquartile range (IQR) and were excluded from the analysis to avoid distortion of statistical results.