

High-throughput DeepPRM-Stellar proteomics coupled with machine learning enables precise quantification of atherosclerosis-stroke progression biomarkers and risk prediction

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[‡]: This study is dedicated to the memory of Professor Pengyuan Yang (1949-2021)

[†]: Electronic Supplementary Information (ESI) available. See DOI:

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Appendix Figures S1-3

Figure S1

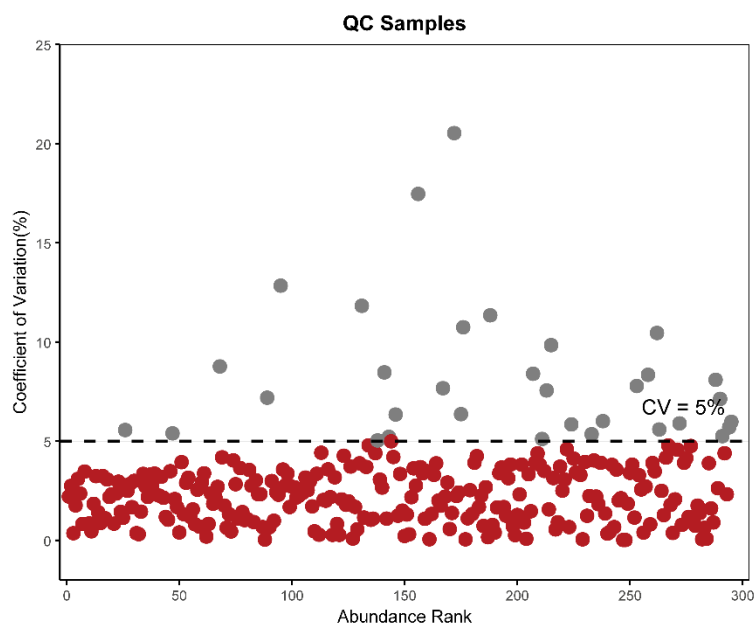
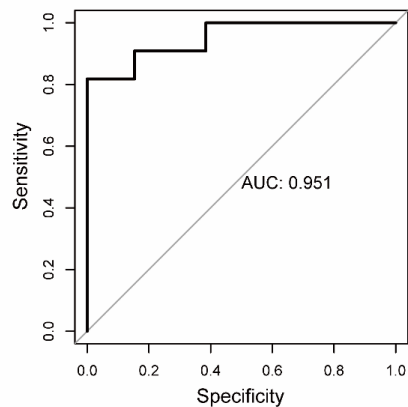


Figure S1. Quality control assessment of peptide measurements in PRM assays.

Scatter plot showing coefficient of variation (CV) versus abundance rank for all QC sample measurements ($n = 3$ technical replicates per peptide). Each point represents an individual peptide measurement, with red points indicating high reproducibility ($CV < 5\%$) and gray points showing greater variability ($CV \geq 5\%$). The dashed line at $CV = 5\%$ marks the acceptable variation threshold, with 90% of measurements demonstrating high reproducibility (red points clustered below the threshold line). The stable CV distribution across the full abundance range (0-300) confirms consistent instrument performance.

Figure S2

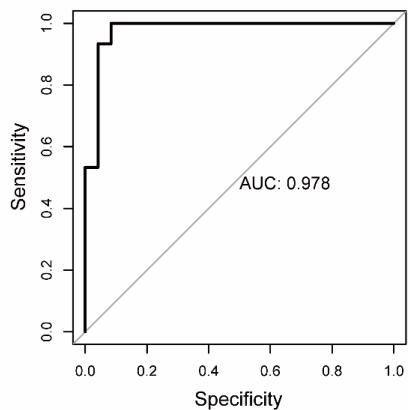
A



P3

Mean_AUC	0.951
Median_AUC	0.947
SD_AUC	0.009
Min_AUC	0.946
Max_AUC	0.984

B



P6

Mean_AUC	0.978
Median_AUC	0.977
SD_AUC	0.003
Min_AUC	0.976
Max_AUC	0.997

Figure S2. Model performance evaluation using Leave-One-Out Cross-Validation (LOOCV).

A). ROC curve for AIS vs LAA classification ($n = 24$). The black solid line shows the model performance ($AUC = 0.951$), with the diagonal representing random guessing ($AUC = 0.5$). The right-side table summarizes AUC statistics from LOOCV iterations: Mean_AUC = 0.951, Median_AUC = 0.947, SD_AUC = 0.009, Min_AUC = 0.946, Max_AUC = 0.984.

B). ROC curve for AIS&LAA vs HC classification ($n = 39$, $AUC = 0.978$). The table lists LOOCV results: Mean_AUC = 0.978, Median_AUC = 0.977, SD_AUC = 0.003, Min_AUC = 0.976, Max_AUC = 0.997. All models were trained using XGBoost .

Figure S3

A



B

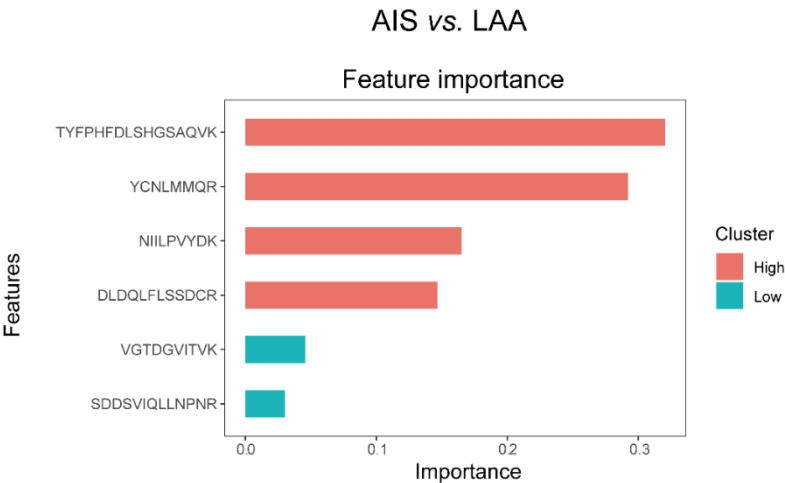


Figure S3. Feature importance analysis of candidate biomarkers.

A). Feature importance ranking for distinguishing AIS&LAA from healthy controls (HC). Proteins are sorted by their Cover-based importance scores from XGBoost.

B). Feature importance ranking for distinguishing AIS from LAA subtypes. In both panels, features are color-coded by their relative importance (red: high; blue-green: low).