



Shaping Tomorrow's Nephrology: Insight-Driven Kidney Care

KSN SEOUL, KOREA
2026

The 46th Annual Meeting of the Korean Society of Nephrology



Jun 11 (Thu) – 14 (Sun), 2026

COEX, Seoul, Korea

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Abstract Topic : Hypertensive Kidney Disease + Vascular Biology in CKD

Proteome-wide Association Study Identifies Plasma Protein Signatures for Incident Acute Myocardial Infarction across eGFR Strata in the UK Biobank

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Objectives : To identify plasma proteins associated with incident AMI across eGFR strata using a proteome-wide association study (PWAS), and to evaluate whether proteomic features improve AMI prediction in individuals with reduced eGFR.

Methods : Among 31,436 UK Biobank participants with 2,923 plasma proteins (Olink Explore), Cox models were applied in three strata: overall cohort, reduced eGFR subgroup (eGFR <60; N=744), and sensitivity cohort (eGFR <75; N=3,719), adjusting for age, sex, BMI, eGFR, diabetes, hypertension, SBP, cholesterol, CRP, and smoking. FDR $q < 0.05$ was applied overall; nominal $p < 0.05$ in reduced eGFR strata. Pathway enrichment used clusterProfiler. Machine learning compared clinical-only (Model A) versus clinical plus LASSO-selected proteins (Model B).

Results : Over 13.15 years median follow-up, 1,649 AMI events occurred. After full adjustment, 362 proteins were associated with AMI (FDR $q < 0.05$), with cytokine-cytokine receptor interaction as the top KEGG pathway (59 genes, $q = 1.9 \times 10^{-9}$). Sixteen proteins were significant across all eGFR strata, including EDA2R (HR 3.59), MMP12 (HR 1.87), IGFBP4 (HR 2.22), and EGFR (HR 0.22). Two dose-response patterns emerged: monotonically increasing HRs with declining eGFR (e.g., RBFOX3: HR 1.21 to 4.51 from eGFR ≥ 90 to 30–44), and non-monotonic trajectories peaking at eGFR 60–89. PLA2G7-AMI association was markedly attenuated at eGFR <60 (interaction HR 0.035, $p = 0.0009$). Proteomic features improved AUC by 13.5% (0.691 to 0.783; validation AUC 0.798–0.835).

Conclusions : This PWAS identifies 362 AMI-associated proteins and 16 cross-strata consensus biomarkers driven by cytokine signaling. eGFR-dependent dose-response patterns and PLA2G7 interaction offer mechanistic insights into cardiorenal risk. Proteomic profiling substantially improves AMI prediction beyond clinical variables in individuals with reduced kidney function.

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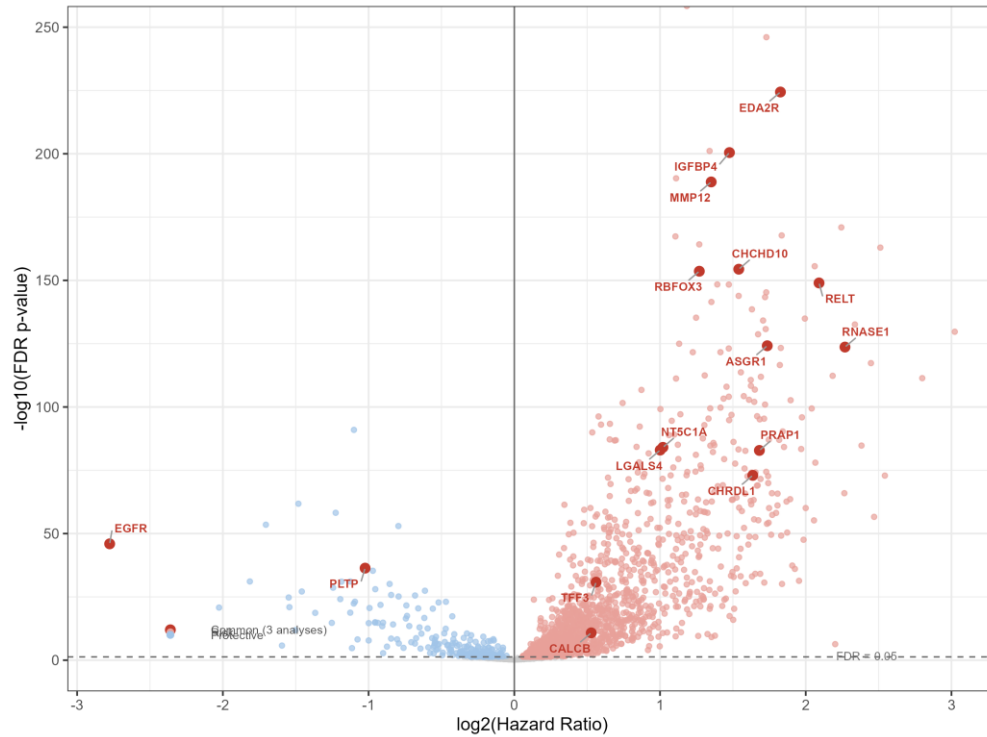


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Proteome-wide Association with Incident AMI

N=31436 | AMI events=1649 | 2,923 proteins | FDR-adjusted



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Protein-AMI Association by eGFR Grade

16 proteins significant across all analyses | * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$

