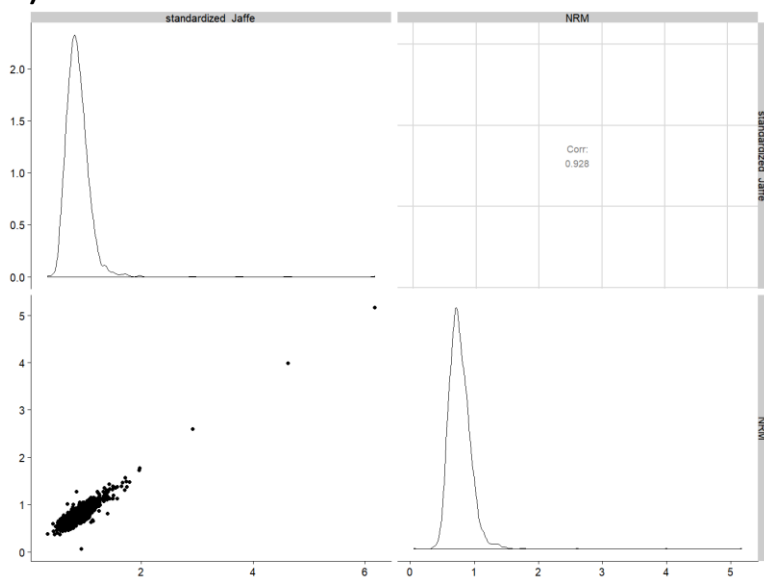# Plasma proteomics of renal function: a trans-ethnic meta-analysis and Mendelian randomization study
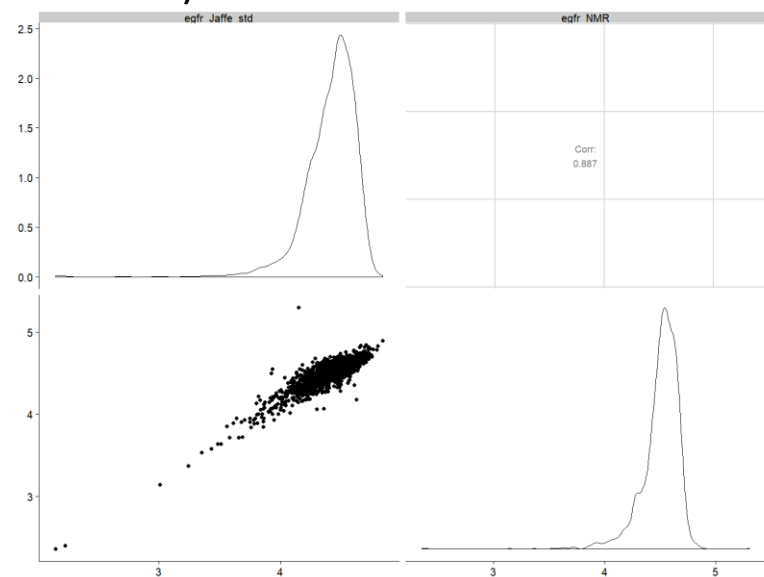
Supplementary Figures

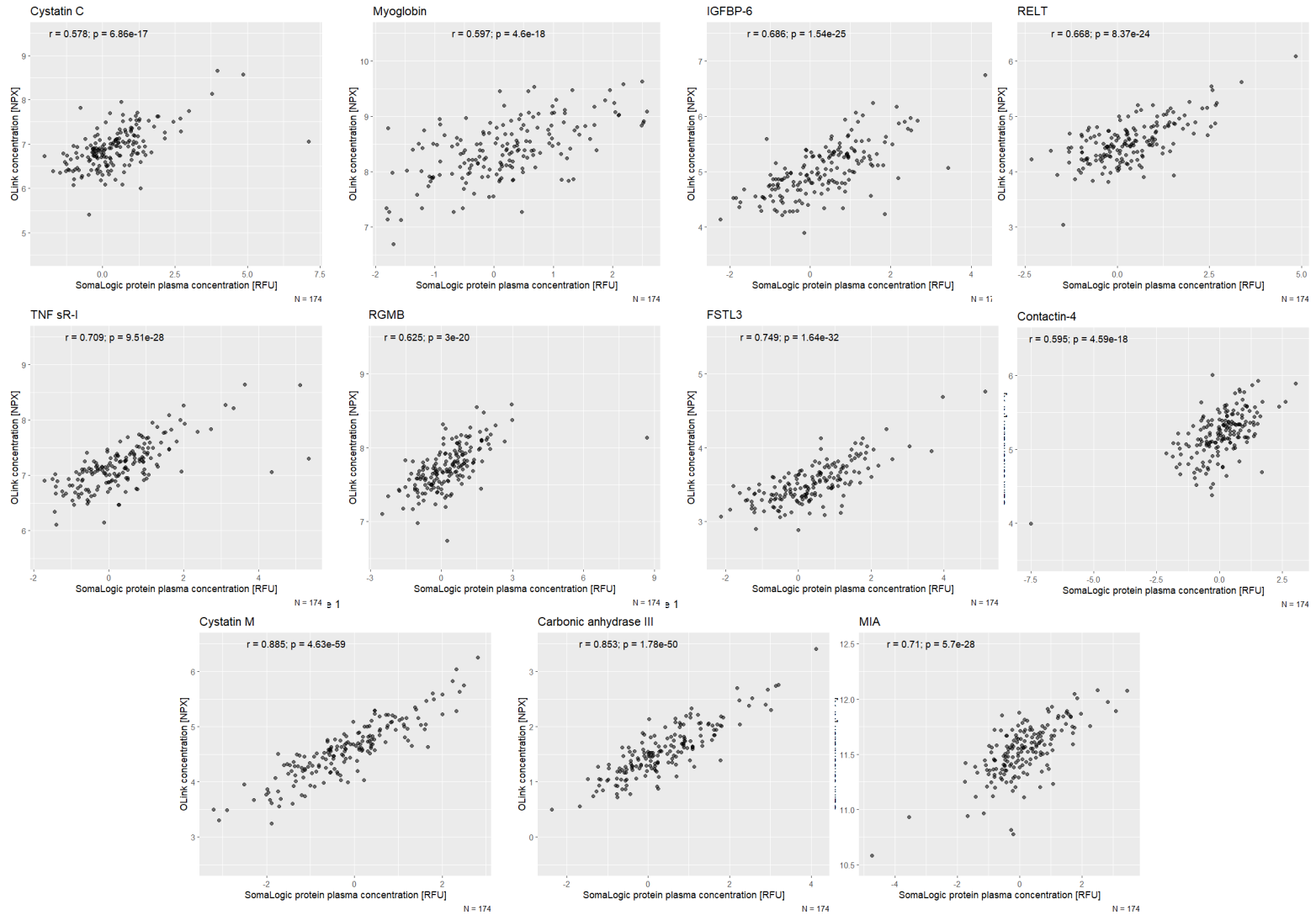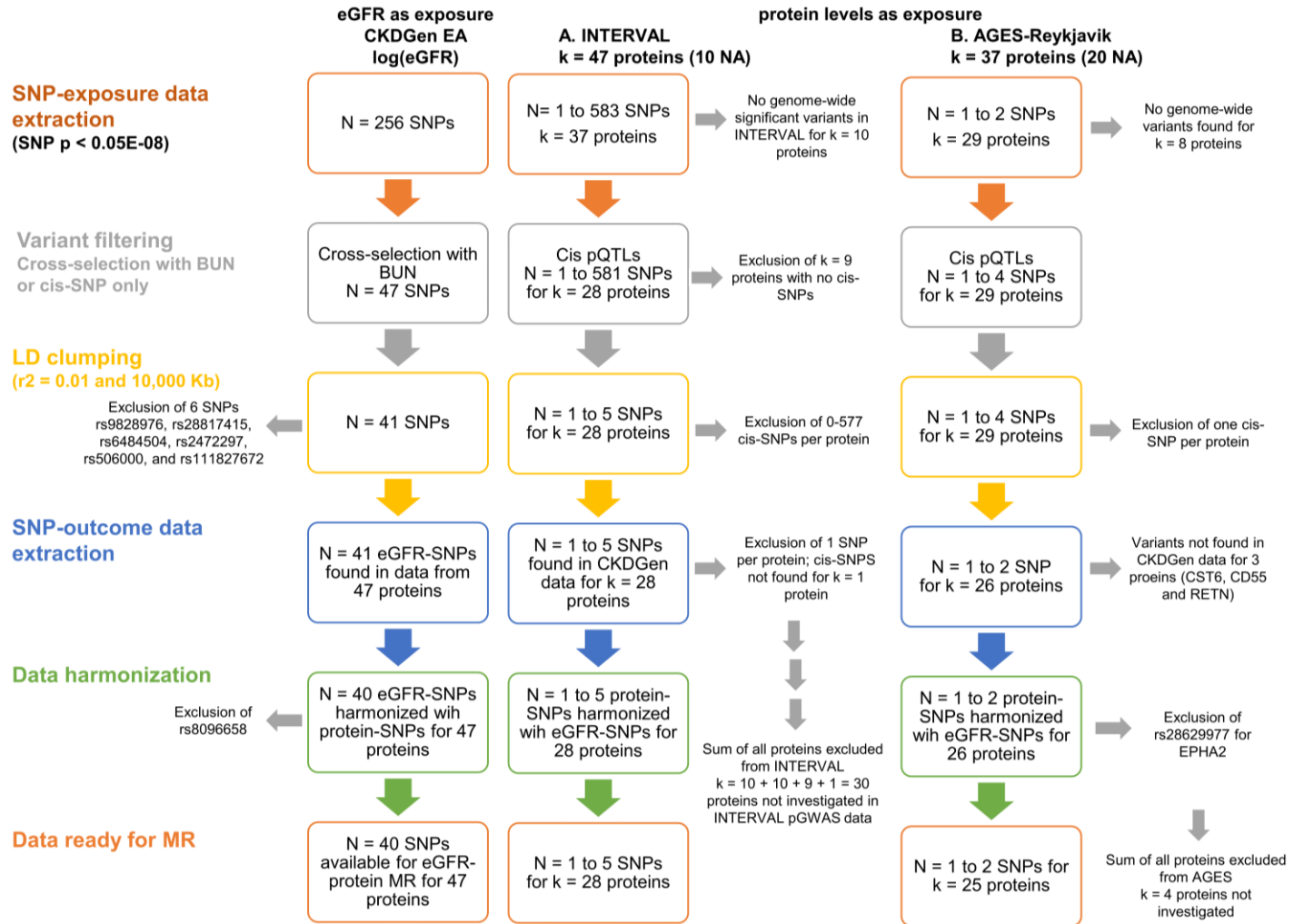# Suppl. Fig. 1. Correlation of serum creatinine variables in KORA F4

Suppl. Fig. 2. Correlation between plasma proteomic measurements in KORA F4
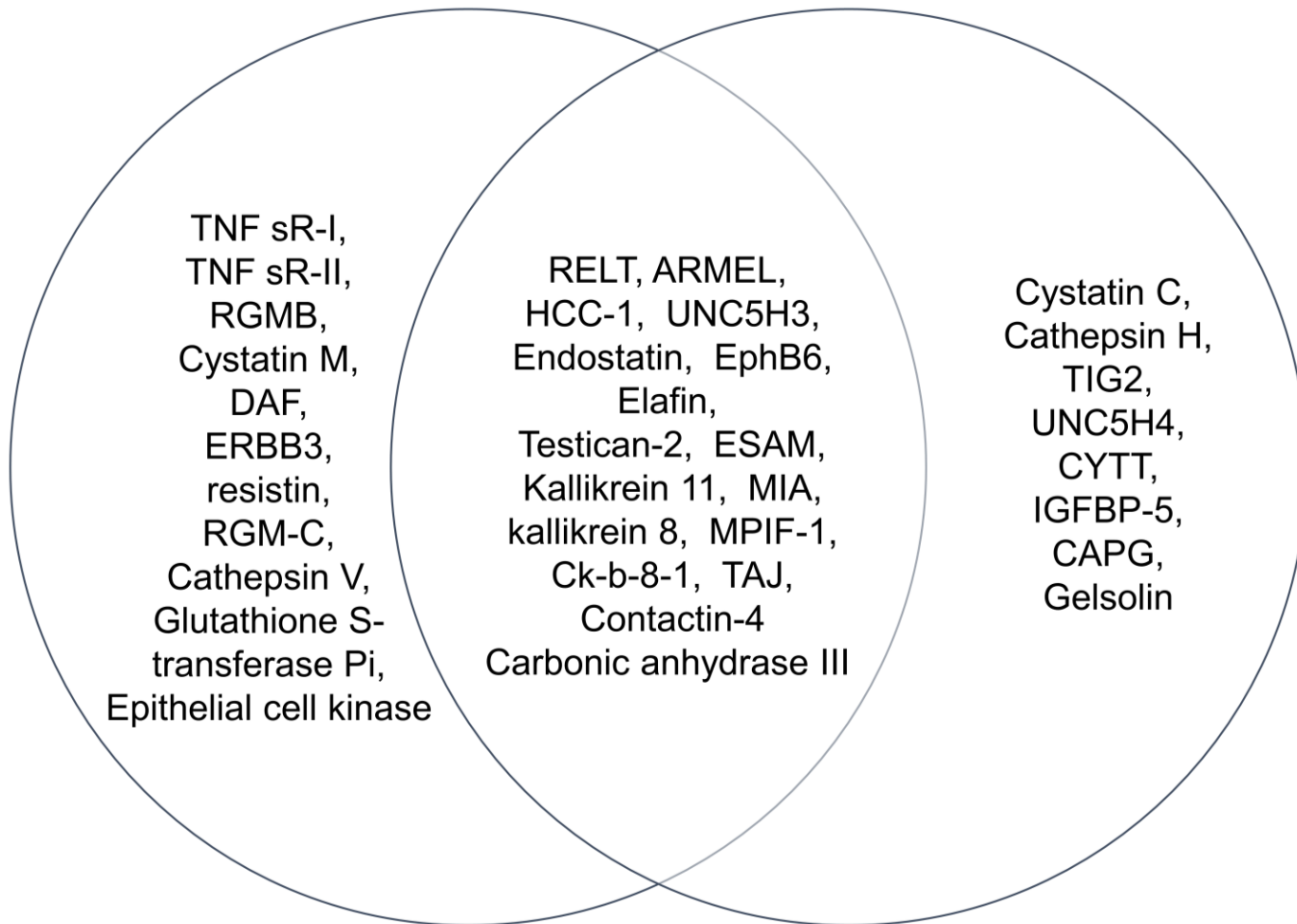
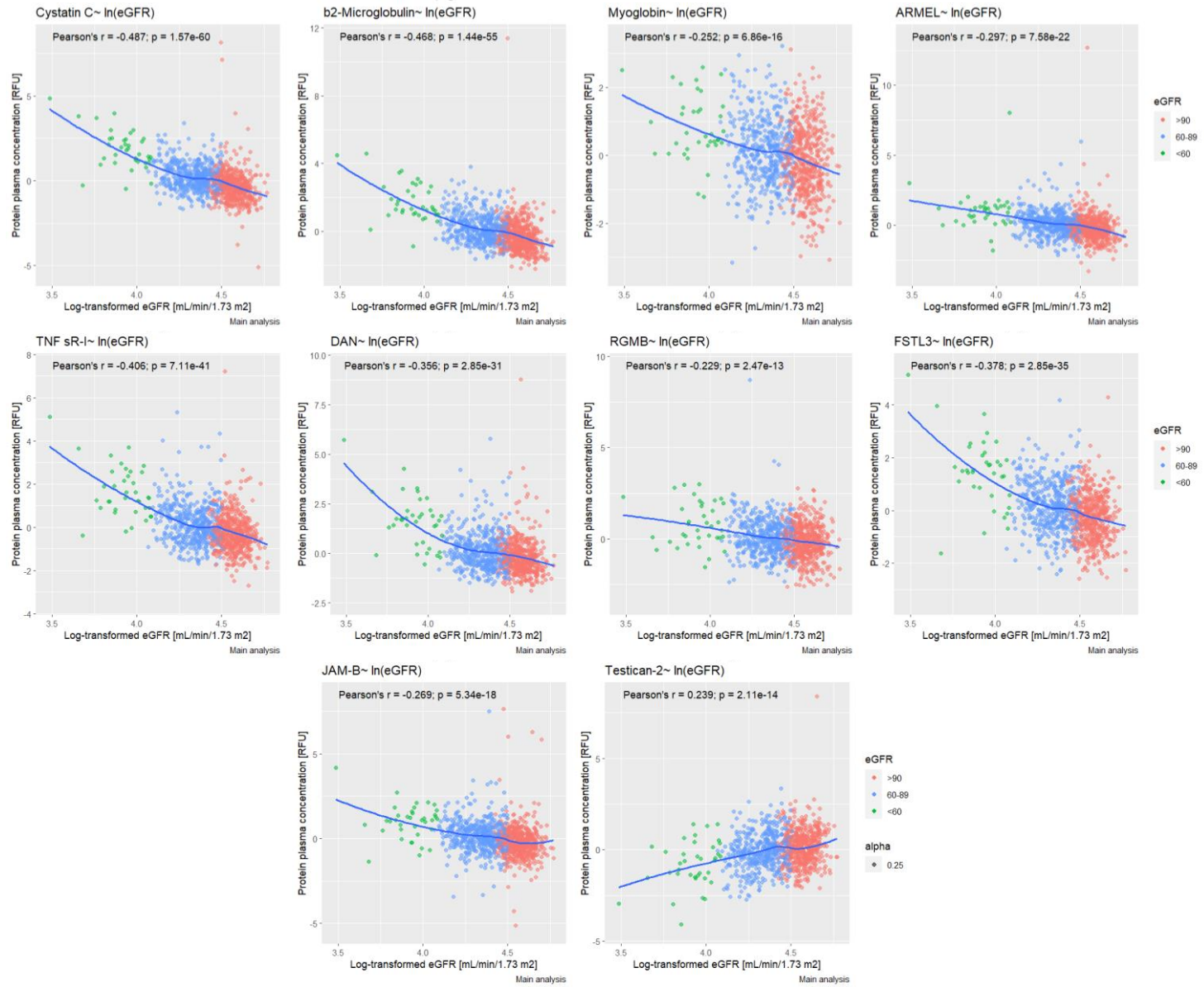# Suppl. Fig. 3. Genetic instrument selection and data harmonization for MR

Suppl. Fig. 4. Protein overlap in pGWAS datasets used in reverse direction of MR

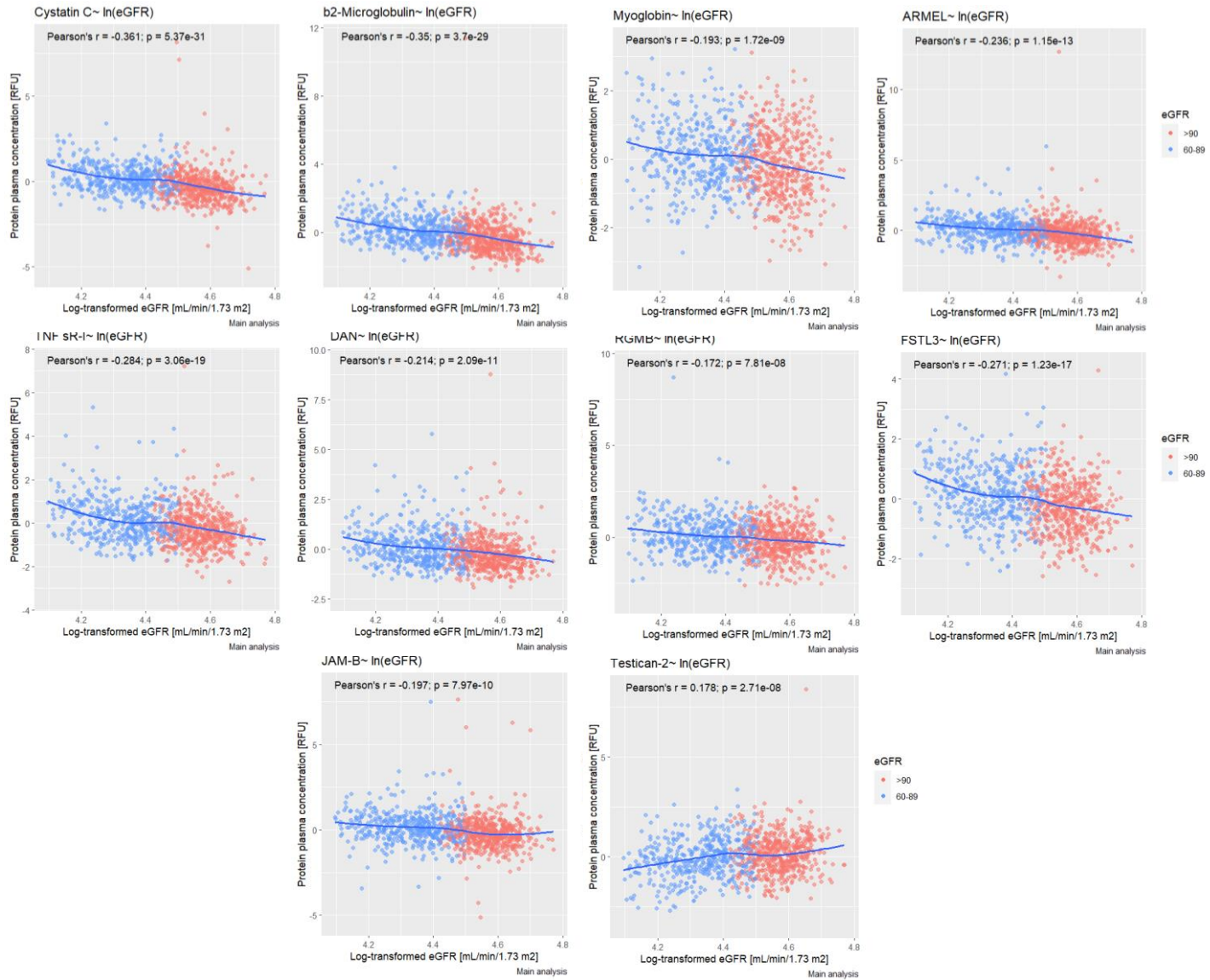Proteins for which the MR analysis was performed using **INTERVAL pGWAS** summary statistics

Proteins for which the MR analysis was performed using **AGES-Reykjavik pGWAS** summary statistics
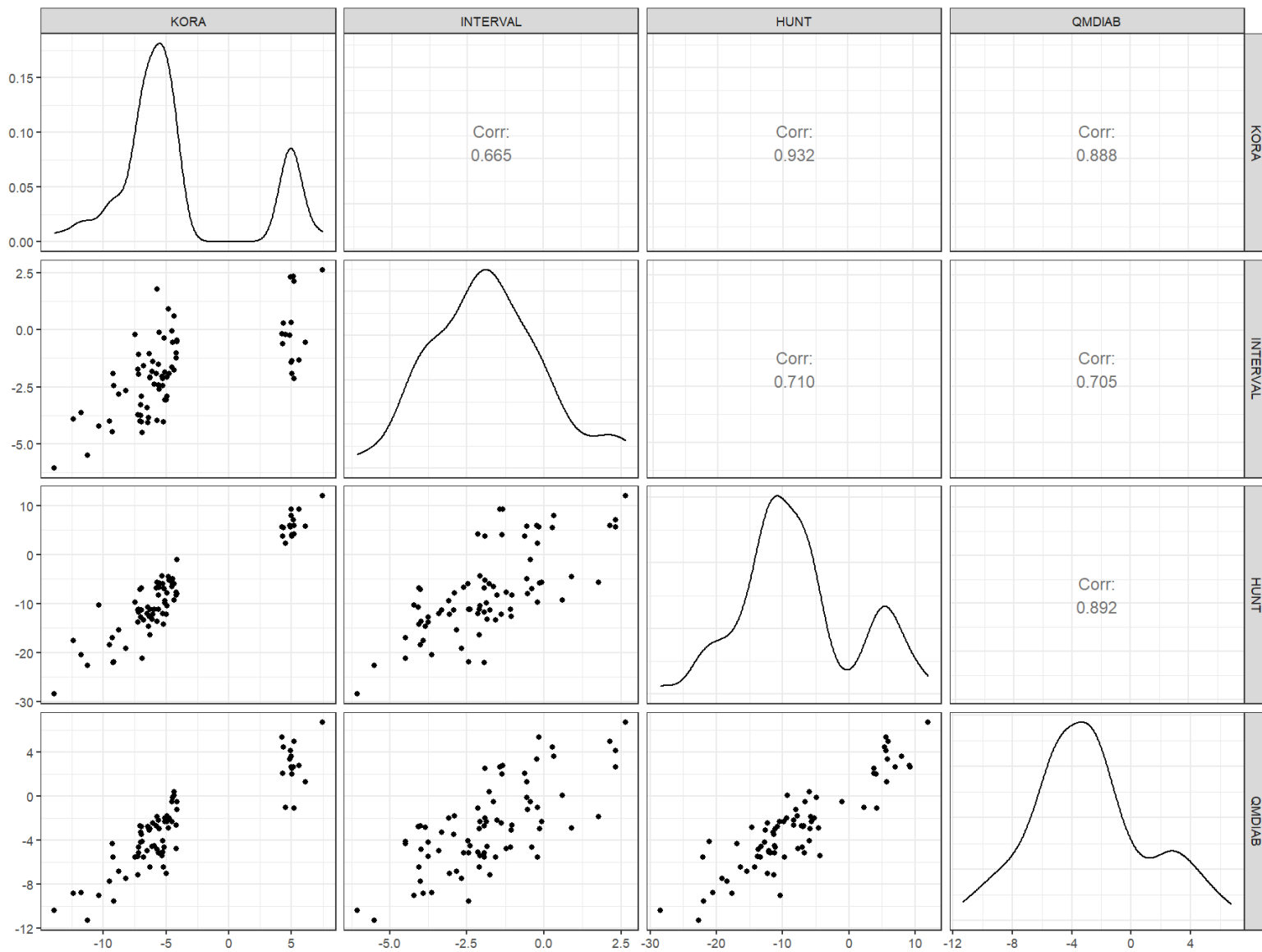
TNF sR-I,
TNF sR-II,
RGMB,
Cystatin M,
DAF,
ERBB3,
resistin,
RGM-C,
Cathepsin V,
Glutathione S-transferase Pi,
Epithelial cell kinase

RELT, ARMEL,
HCC-1, UNC5H3,
Endostatin, EphB6,
Elafin,
Testican-2, ESAM,
Kallikrein 11, MIA,
kallikrein 8, MPIF-1,
Ck-b-8-1, TAJ,
Contactin-4
Carbonic anhydrase III

Cystatin C,
Cathepsin H,
TIG2,
UNC5H4,
CYTT,
IGFBP-5,
CAPG,
Gelsolin

Suppl. Fig. 5. Cross sectional results for eGFR-protein associations across studies

Suppl. Fig. 6. Proteins and log(eGFR) distribution in discovery dataset
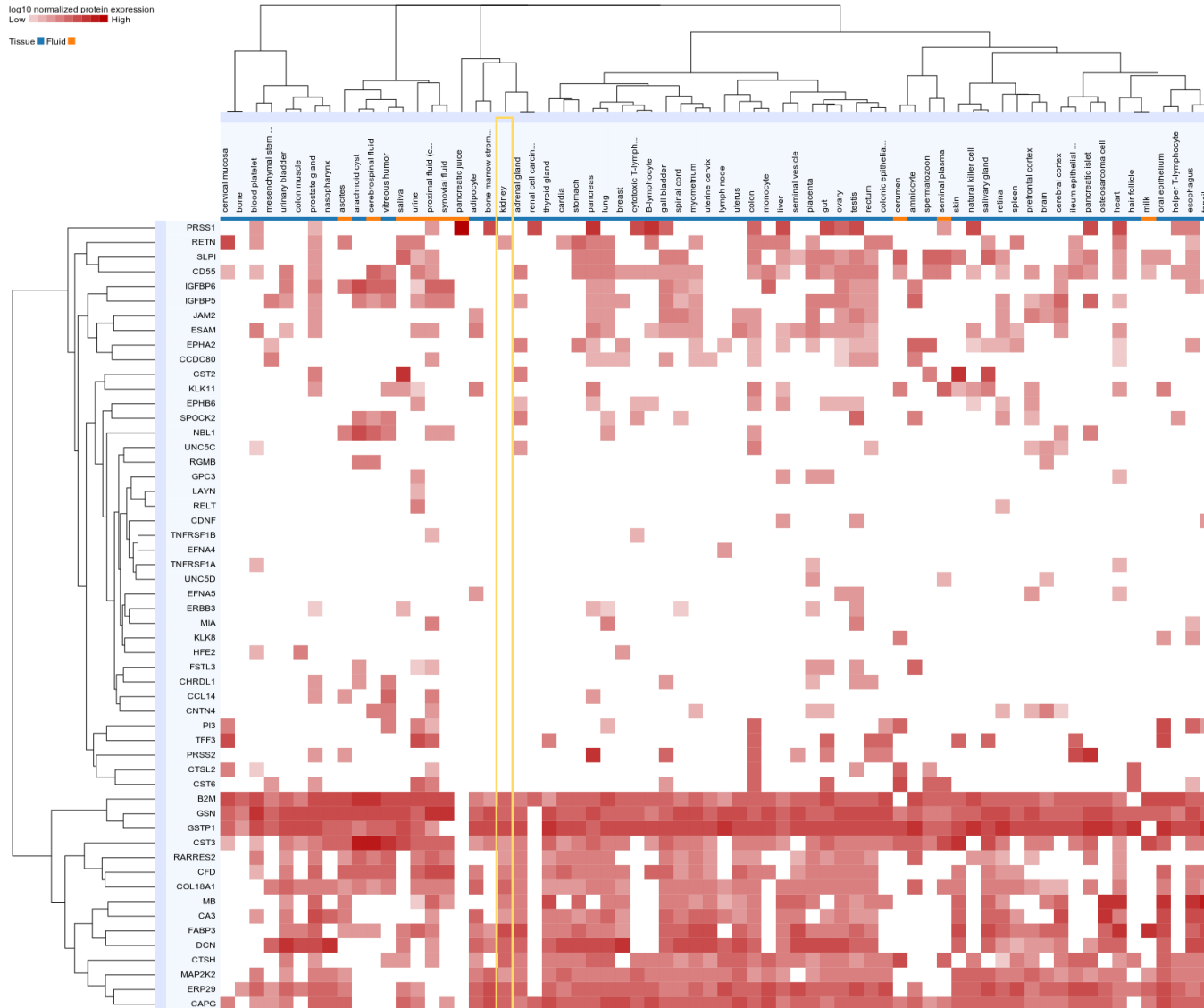
Suppl. Fig. 7. Proteins and log(eGFR) distribution in discovery dataset after CKD exclusion
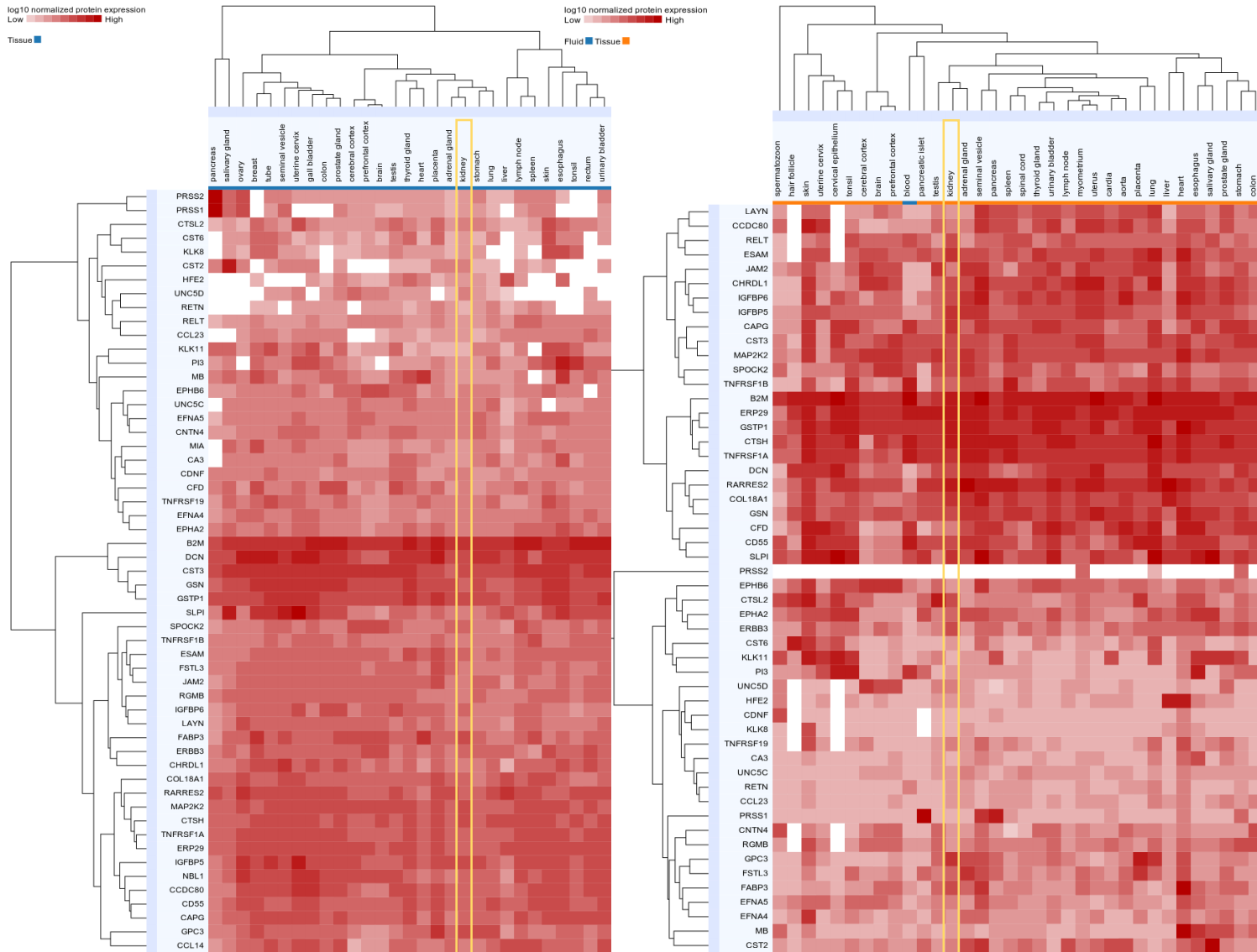
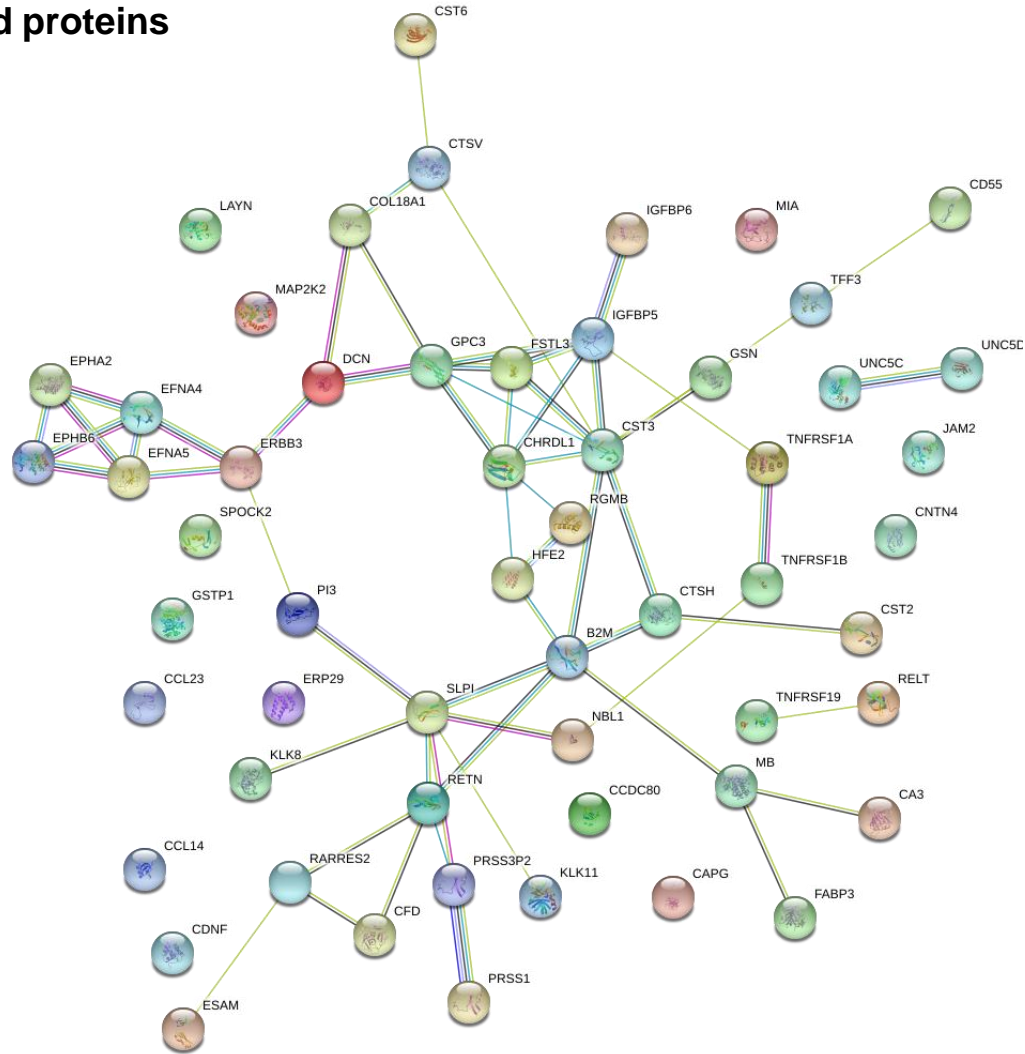**Suppl. Fig. 8. Correlation between Z-values for eGFR-protein associations across studies**

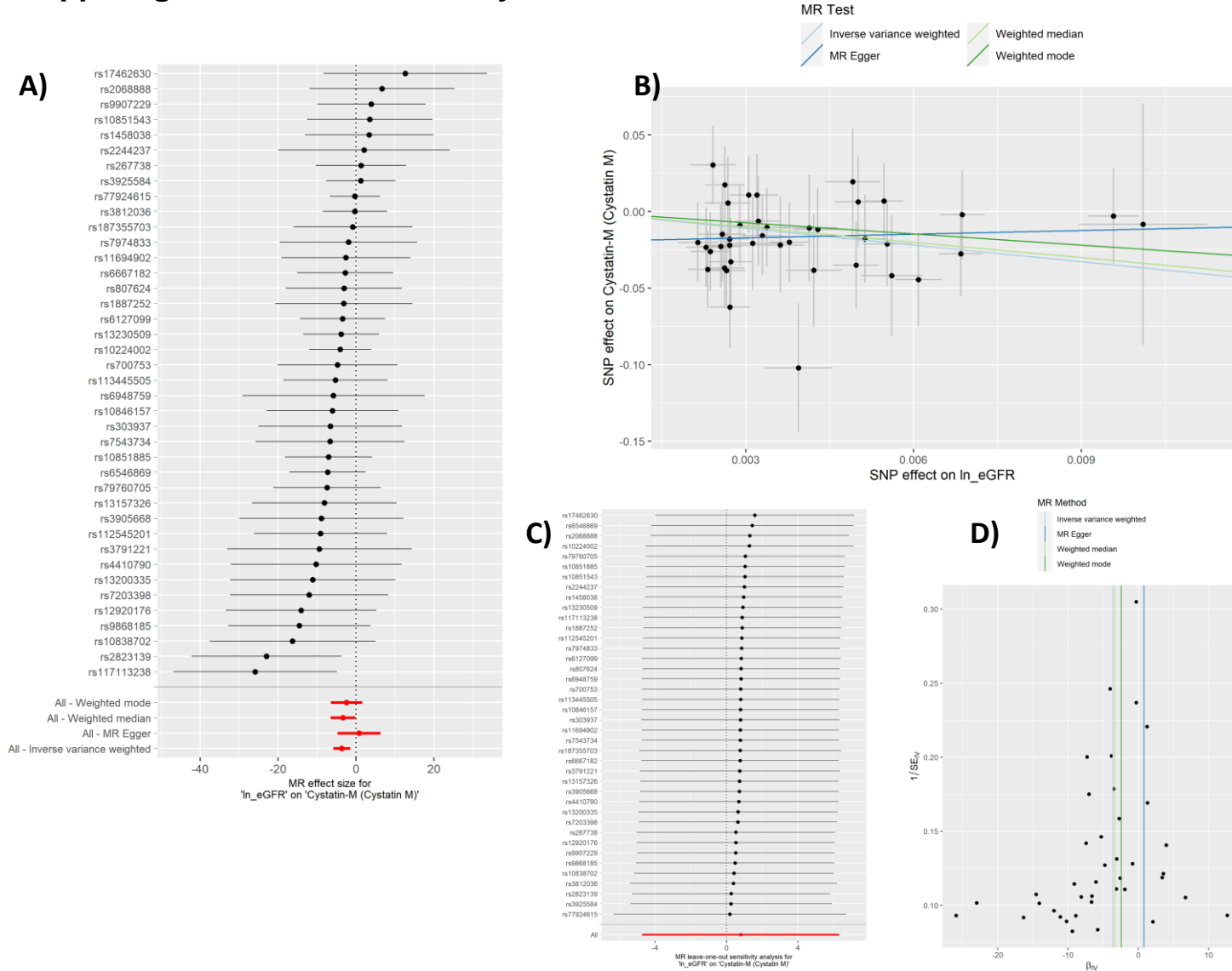**Suppl. Fig. 9. Tissue expression of 56 eGFR-associated proteins (ProteomeDB)**

Suppl. Fig. 10. Tissue expression of 56 eGFR-associated protein coding genes (ProteomeDB)
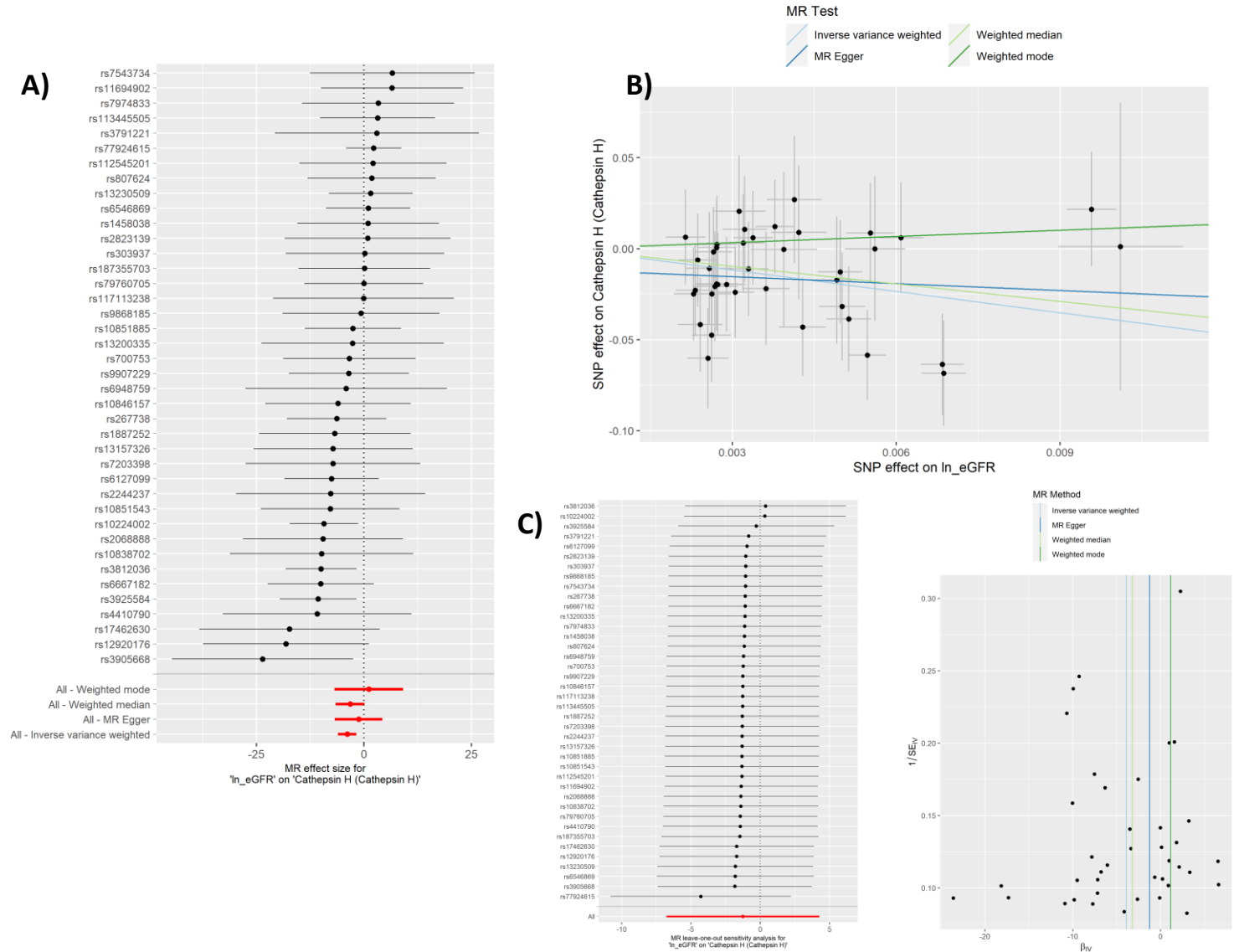
Suppl. Fig. 11. Tissue expression of 56 eGFR-associated proteins (GTEx, transcriptomics)

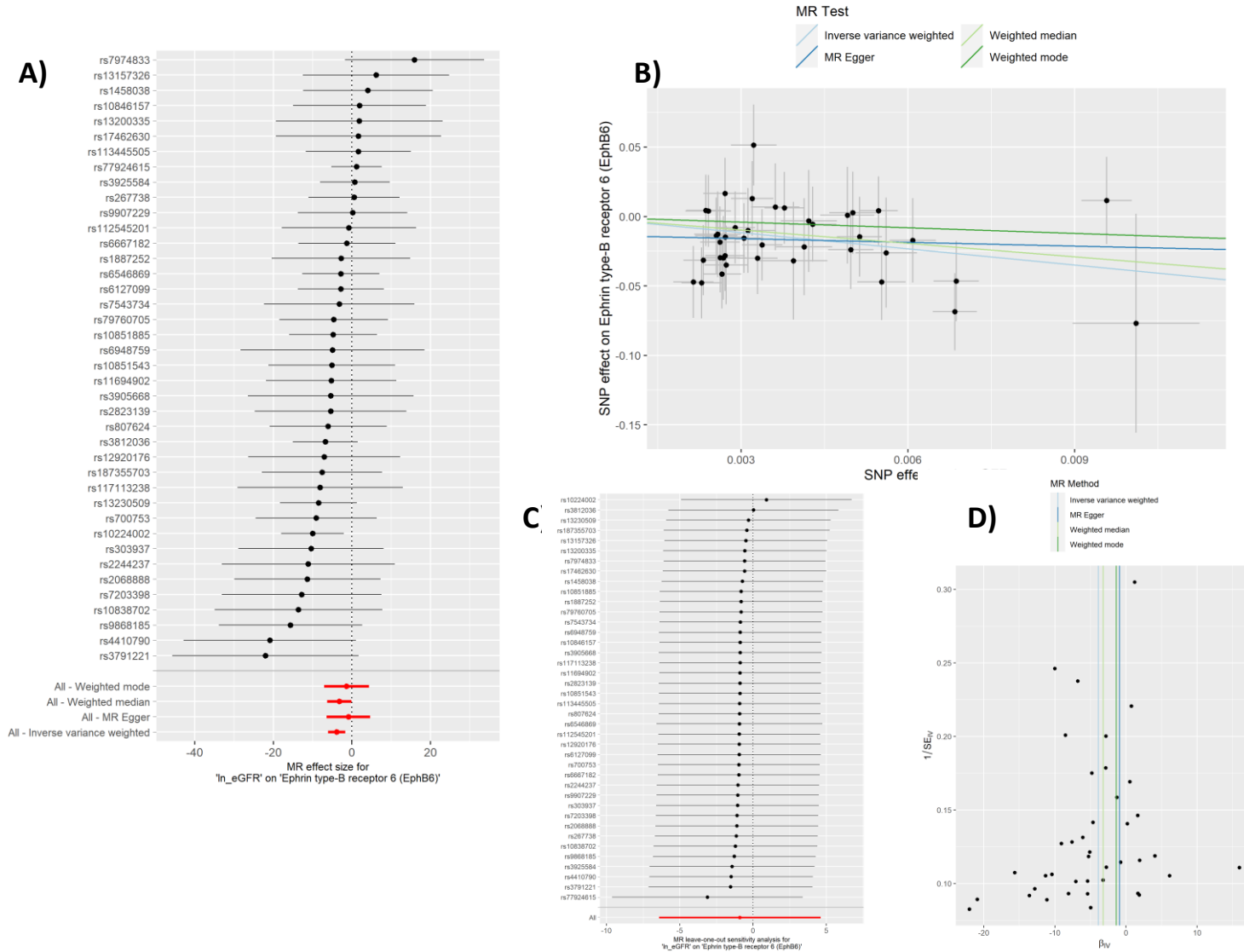**Suppl. Fig. 12. Protein-protein interaction network of 57 replicated eGFR-associated proteins**
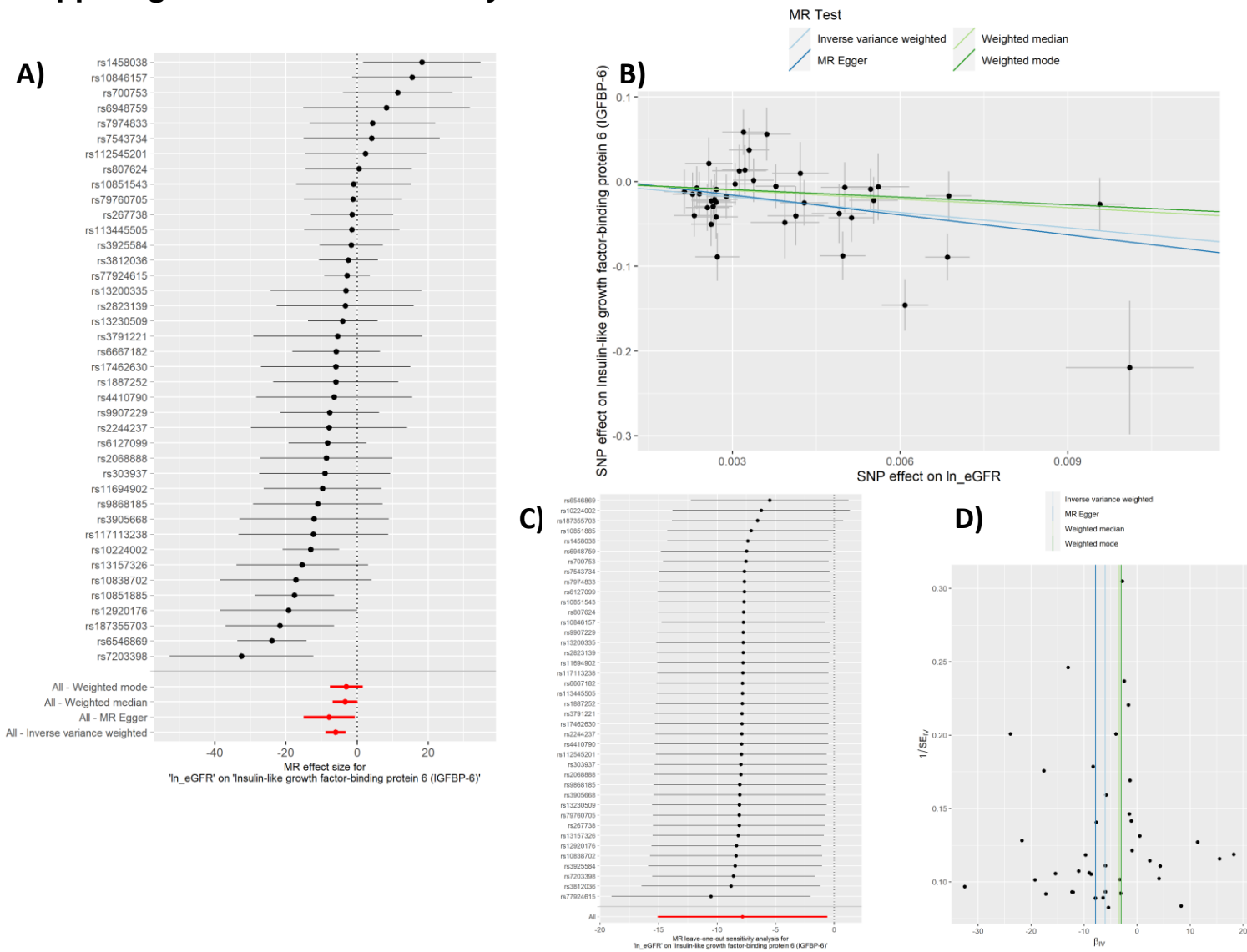
Suppl. Fig. 13. Forward MR analysis for eGFR-CST6
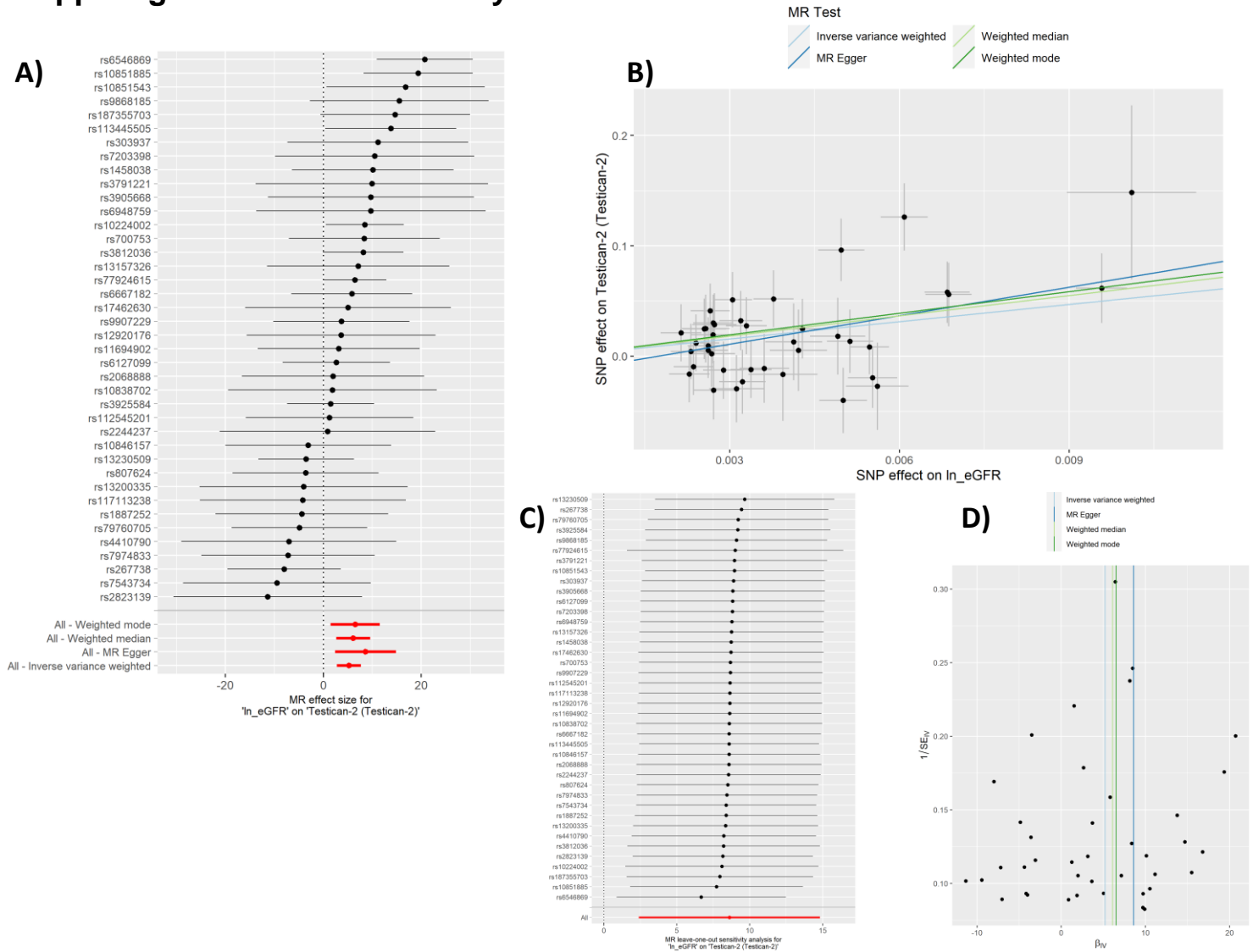
Suppl. Fig. 14. Forward MR analysis for eGFR-Cathepsin H
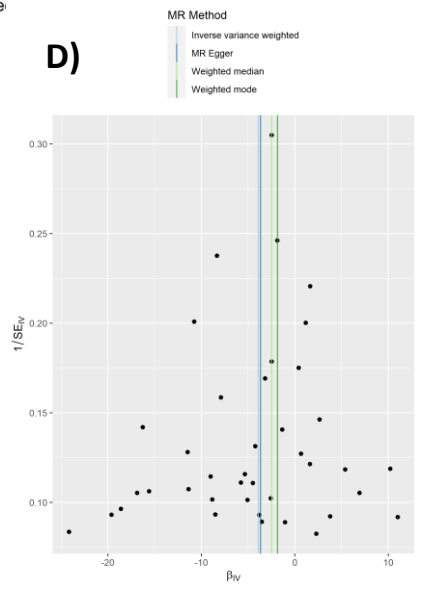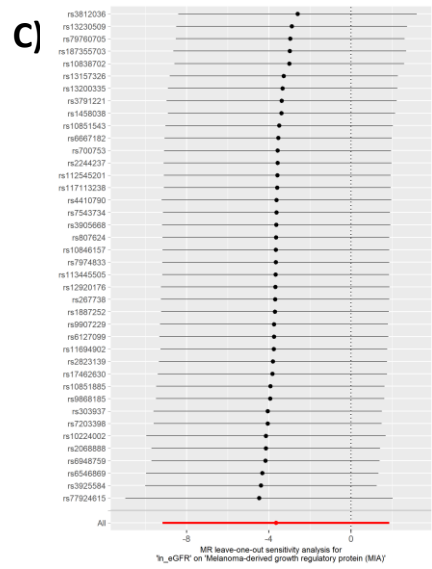
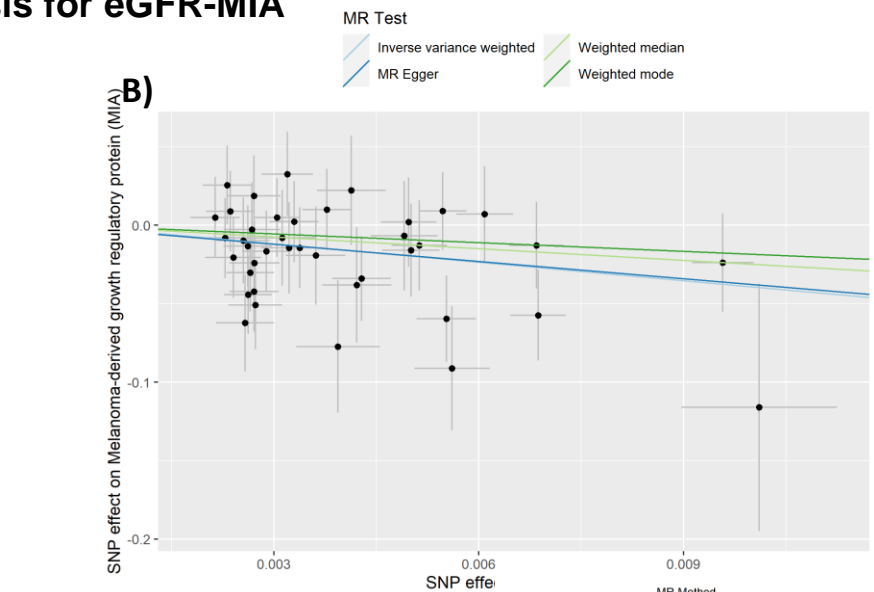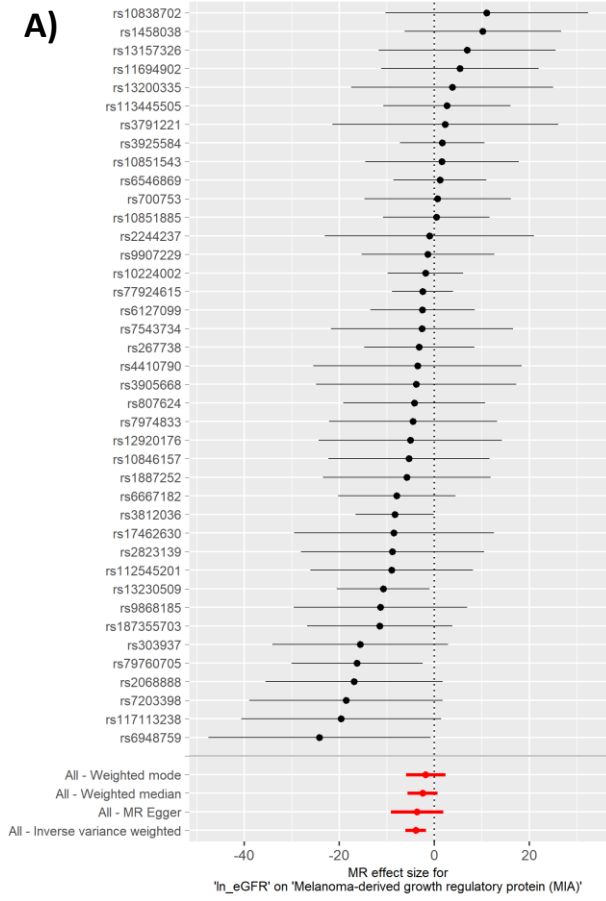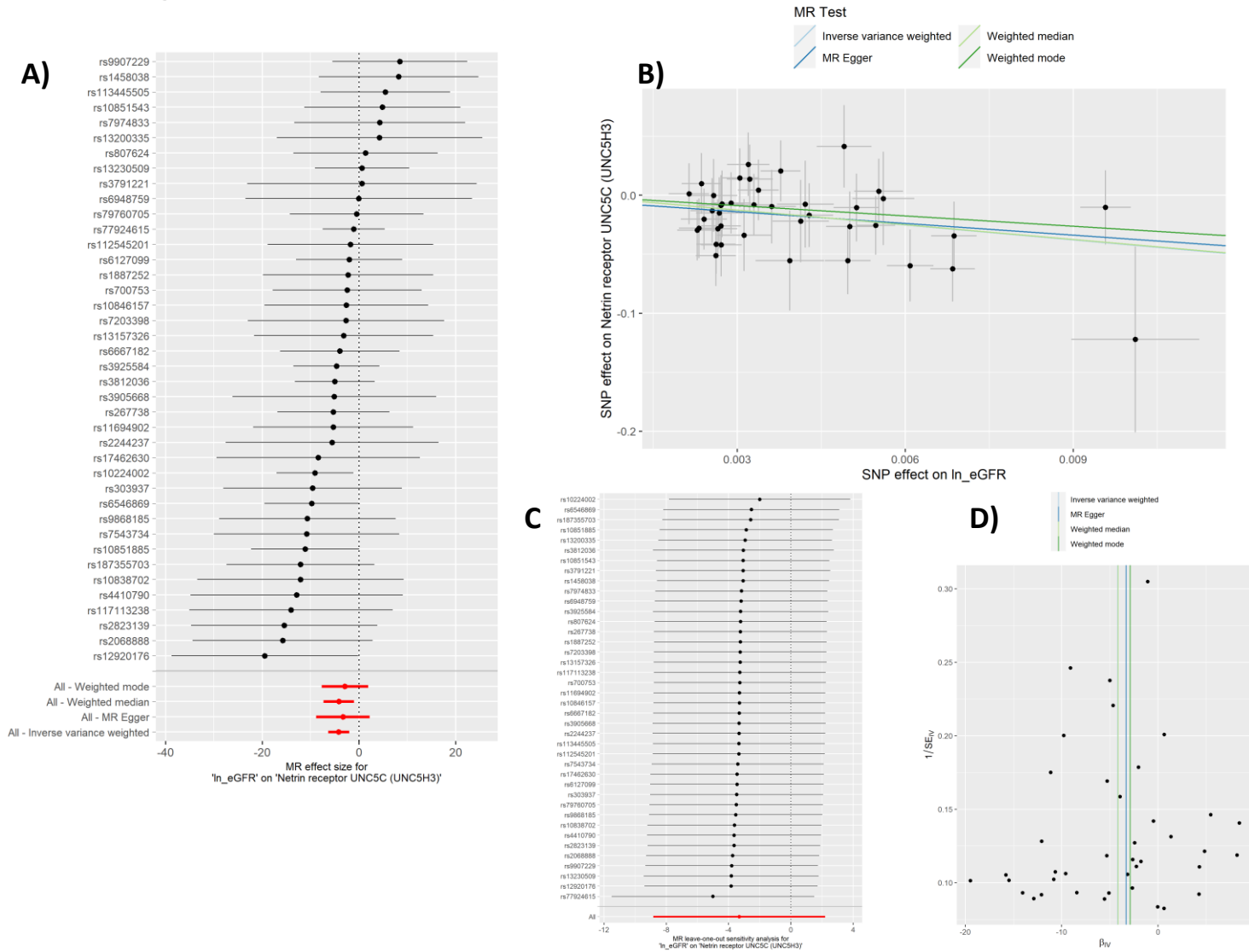# Suppl. Fig. 15. Forward MR analysis for eGFR-EphB6

Suppl. Fig. 16. Forward MR analysis for eGFR-IGFBP-6

Suppl. Fig. 17. Forward MR analysis for eGFR-SPOCK2
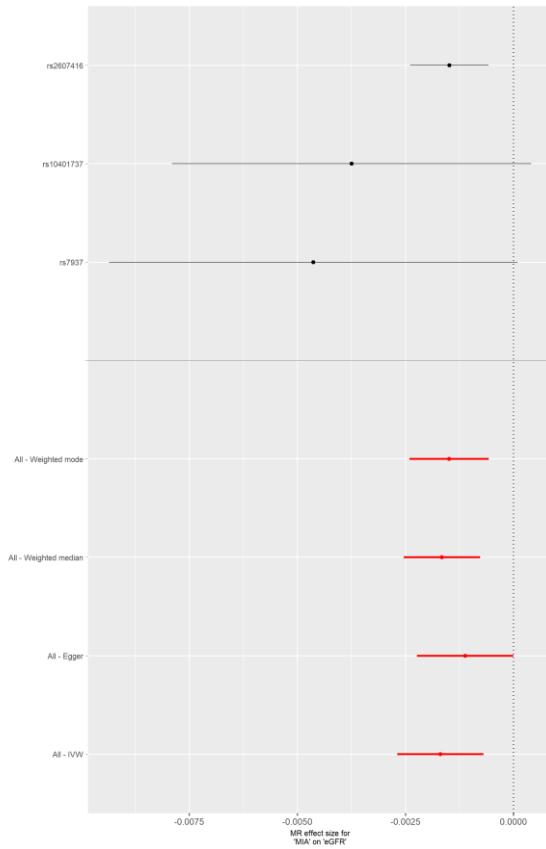
Suppl. Fig. 18. Forward MR analysis for eGFR-MIA
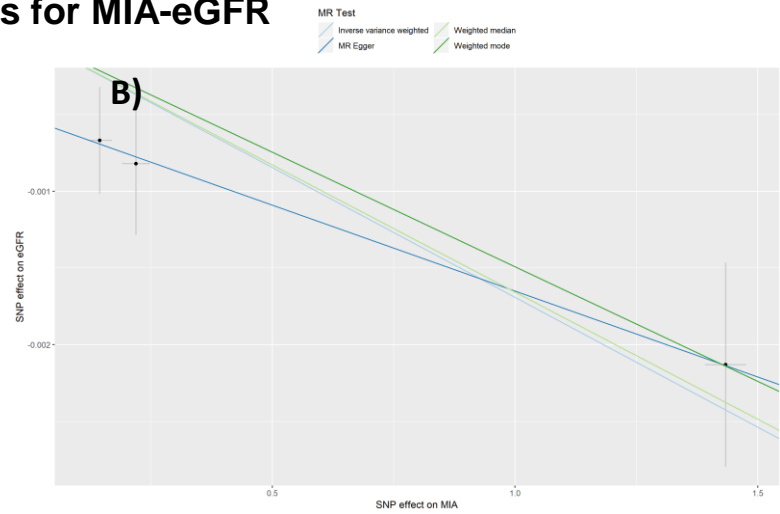
Suppl. Fig. 19. Forward MR analysis for eGFR-UNC5H3

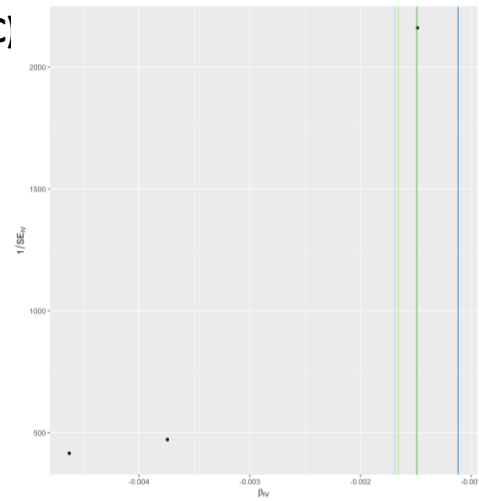# Suppl. Fig. 20. Reverse MR analysis for MIA-eGFR

Suppl. Fig. 21. *SPOCK2* **gene expression in renal tissue from 26 CKD patients**

Pearson's r = 0.25, p = 0.22, N = 26