A Metabolome-Wide Association Study of Kidney Function and Disease

in the General Population

Peggy Sekula, Oemer-Necmi Goek, Lydia Quaye, Clara Barrios, Andrew S. Levey, Werner Römisch–Margl, Cristina Menni, Idil Yet, Christian Gieger, Lesley A. Inker, Jerzy Adamski, Wolfram Gronwald, Thomas Illig, Katja Dettmer, Jan Krumsiek, Peter Oefner, Ana M. Valdes, Christa Meisinger, Josef Coresh, Tim D. Spector, Robert P. Mohney, Karsten Suhre, Gabi Kastenmüller, Anna Köttgen

SUPPLEMENTAL MATERIAL

Supplemental Figure 1: Analytical Workflow

Supplemental Figure 2: Receiver operating characteristic curves of different models comparing the area under the curve for the ability to predict incident CKD.

Supplemental Table 1: All metabolites evaluated at the KORA S4 and F4 Study

Supplemental Table 2: Association between all tested metabolites and eGFRcrea, eGFRcys and CKD at the KORA F4 visit as well as all corresponding results from the TwinsUK Study and the combined datasets for metabolites selected for replication

Supplemental Table 3: Significant association between tested metabolite ratios and eGFRcrea, eGFRcys and CKD at the KORA F4 visit

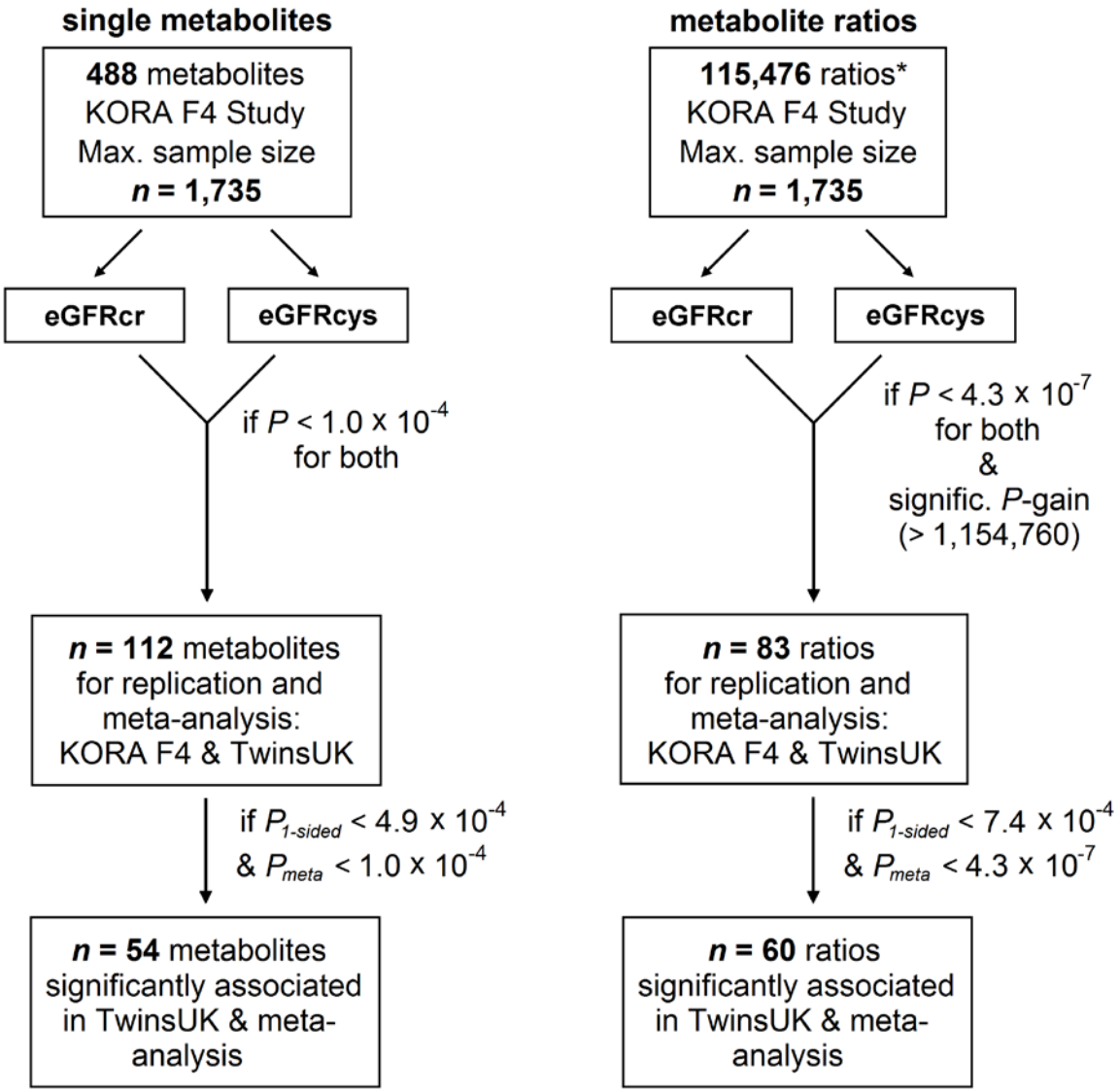
Supplemental Table 4: Association between all tested metabolites with annual eGFR decline and incident CKD

Supplemental Table 5: Characterization of significant kidney function associated metabolites in the KORA F4 study population

Supplemental Table 6: Clinical information and metabolites selected for prediction of incident CKD

Supplemental Table 7: Significant genetic associations of the highlighted metabolites (Tables 2 and 3) from previous genome-wide association studies of blood metabolite concentrations

Supplemental Figure 1. Analytical Workflow



Supplemental Figure 2. Receiver operating characteristic curves of different models comparing the area under the curve for the ability to predict incident CKD.