

Metabolomic Insights into Kidney Disease Progression

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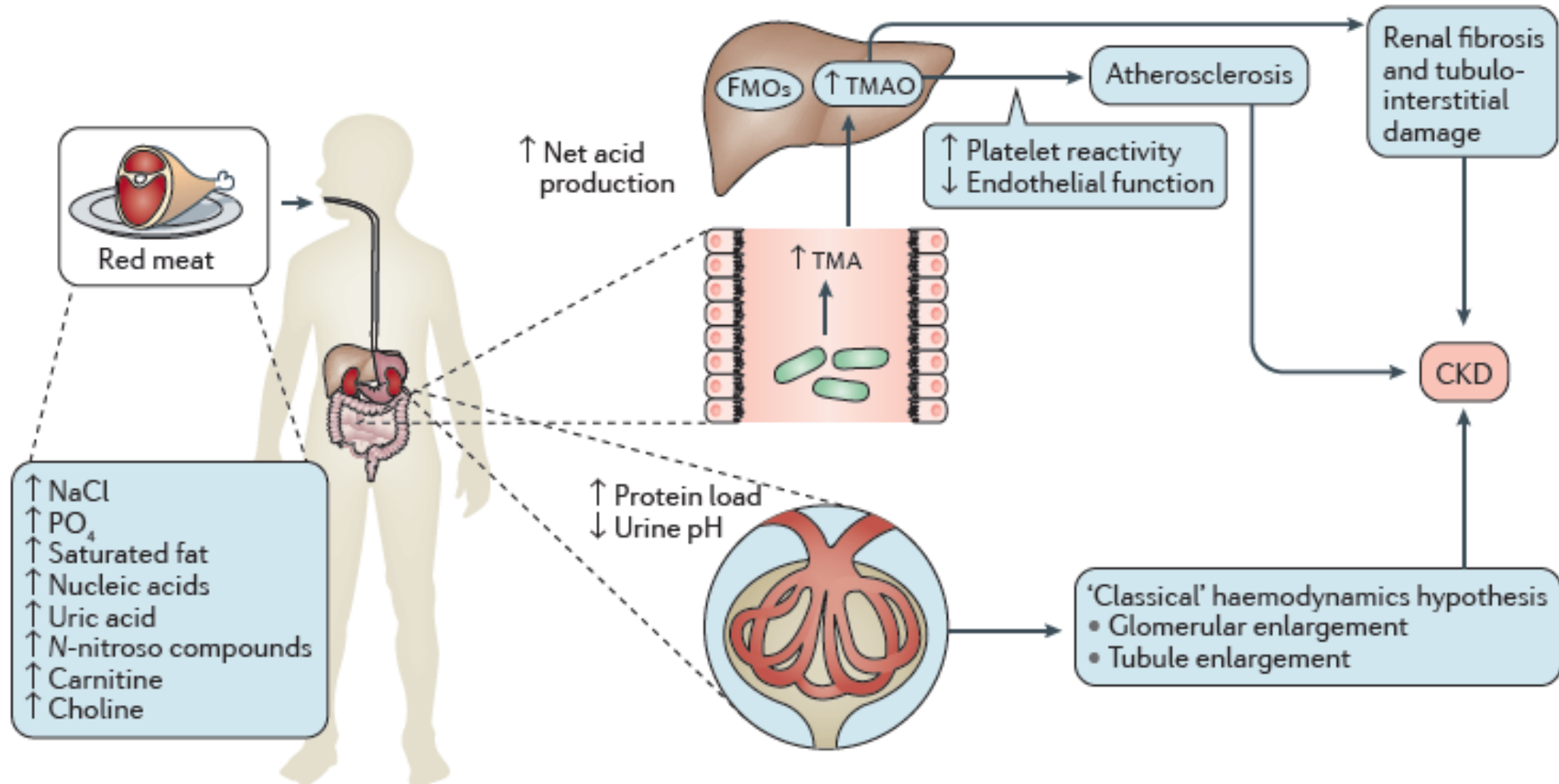


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Disclaimers

- Participate in advisory board with Gilead Sciences, Baxter Healthcare
- Participate in research with Traverre Therapeutics, Alpine Immune Sciences, Vera Therapeutics, Novartis, AstraZeneca, Boehringer Ingelheim, Bayer, Otsuka
- Speaker for AstraZeneca, Boehringer Ingelheim, Otsuka Pharmaceutical, Baxter, Fresenius Medical Care
- Research grant from AstraZeneca, Boehringer Ingelheim

Early observation: effect of red meat intake on kidney function

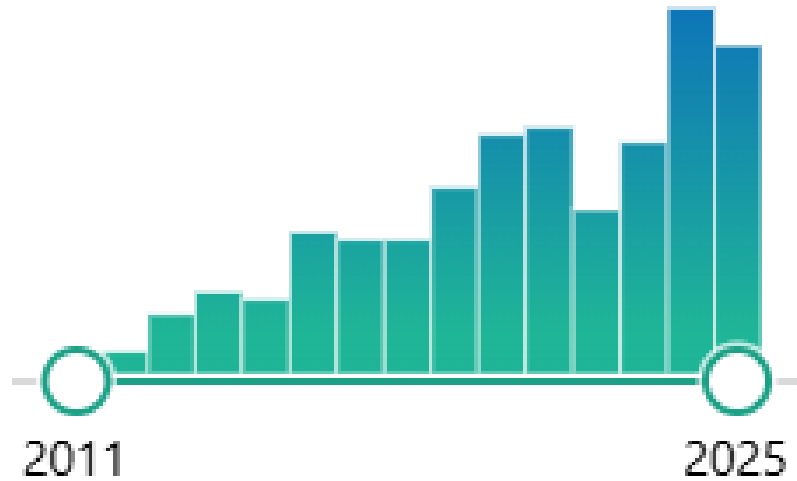


Peter Stenvinkel. Nat Rev Nephrol 2018; 265.

*FMO: Flavin-containing monooxygenase (enzyme for the generation of TMAO)

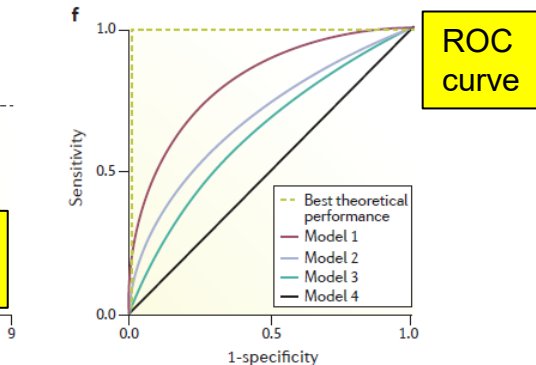
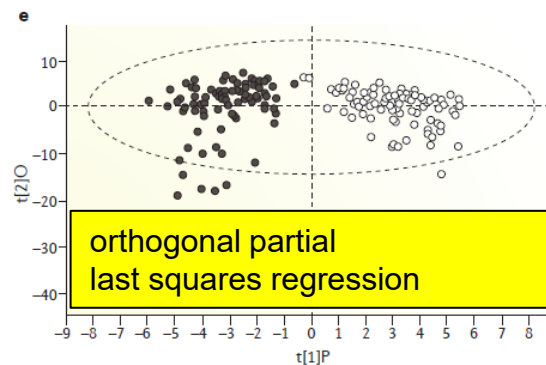
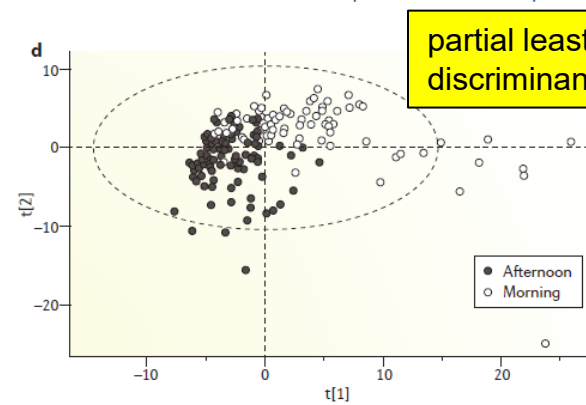
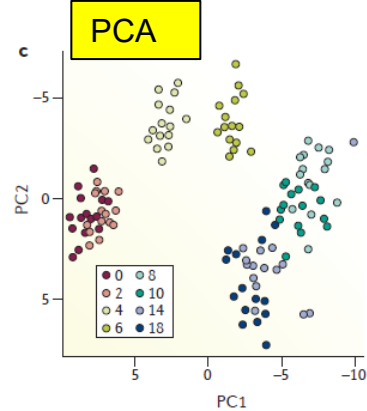
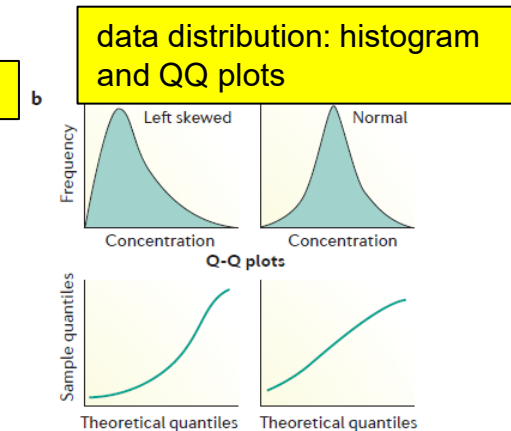
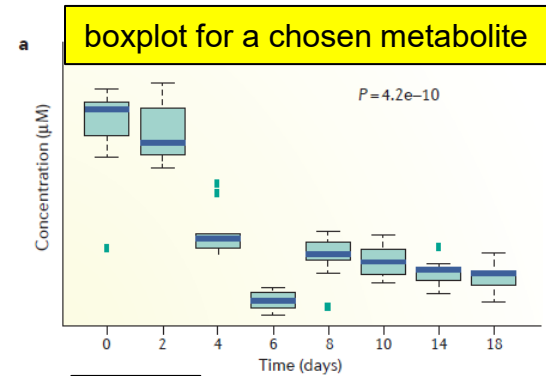
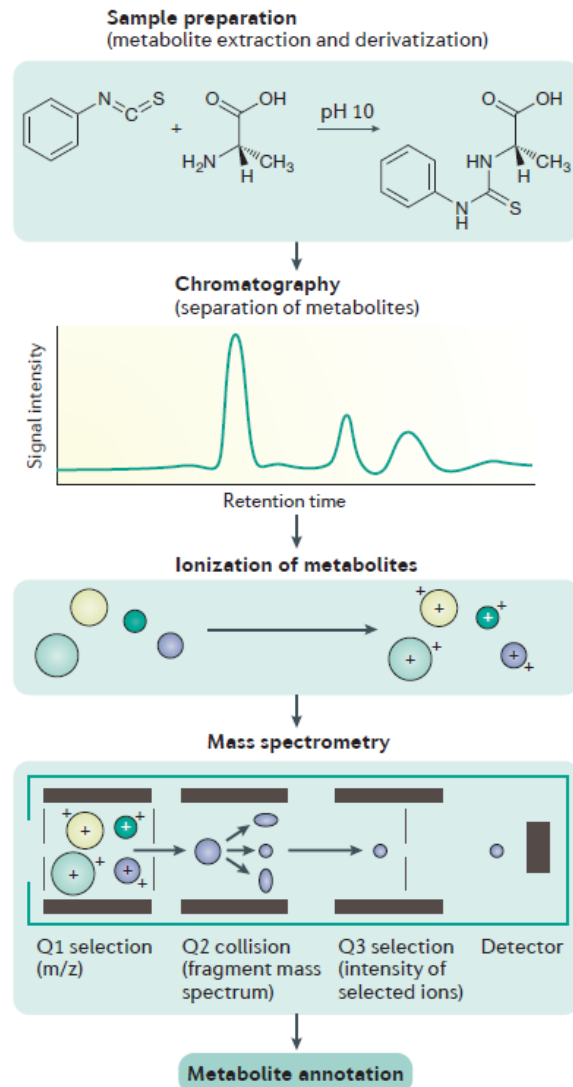
Metabolomic study and CKD: some questions

no. of publications in PubMed on
“chronic kidney disease” and “metabolomic”



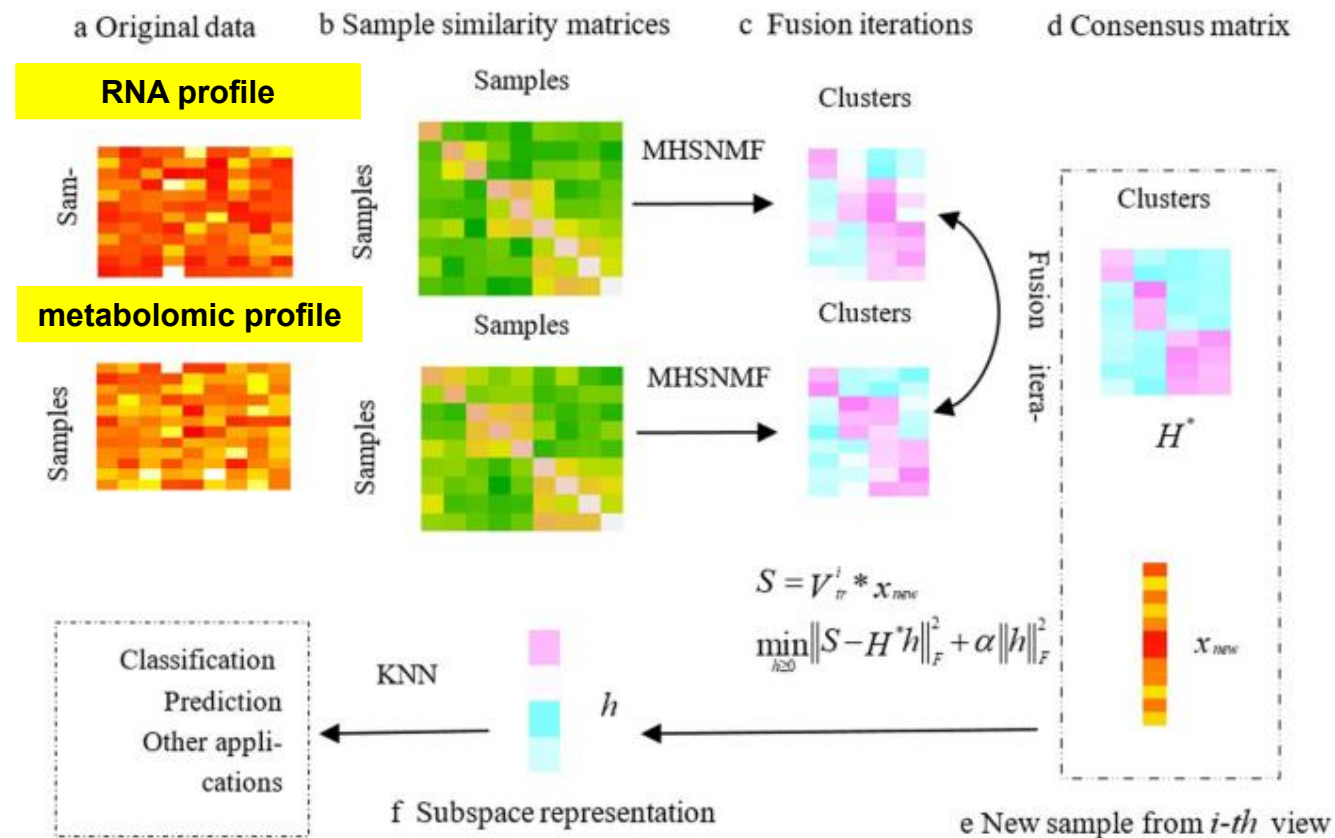
- How ? method of study
- Which ? metabolite species of interest
- What ? clinical implications
- Why ? mechanism of the effect

Metabolomics: methods in a nutshell

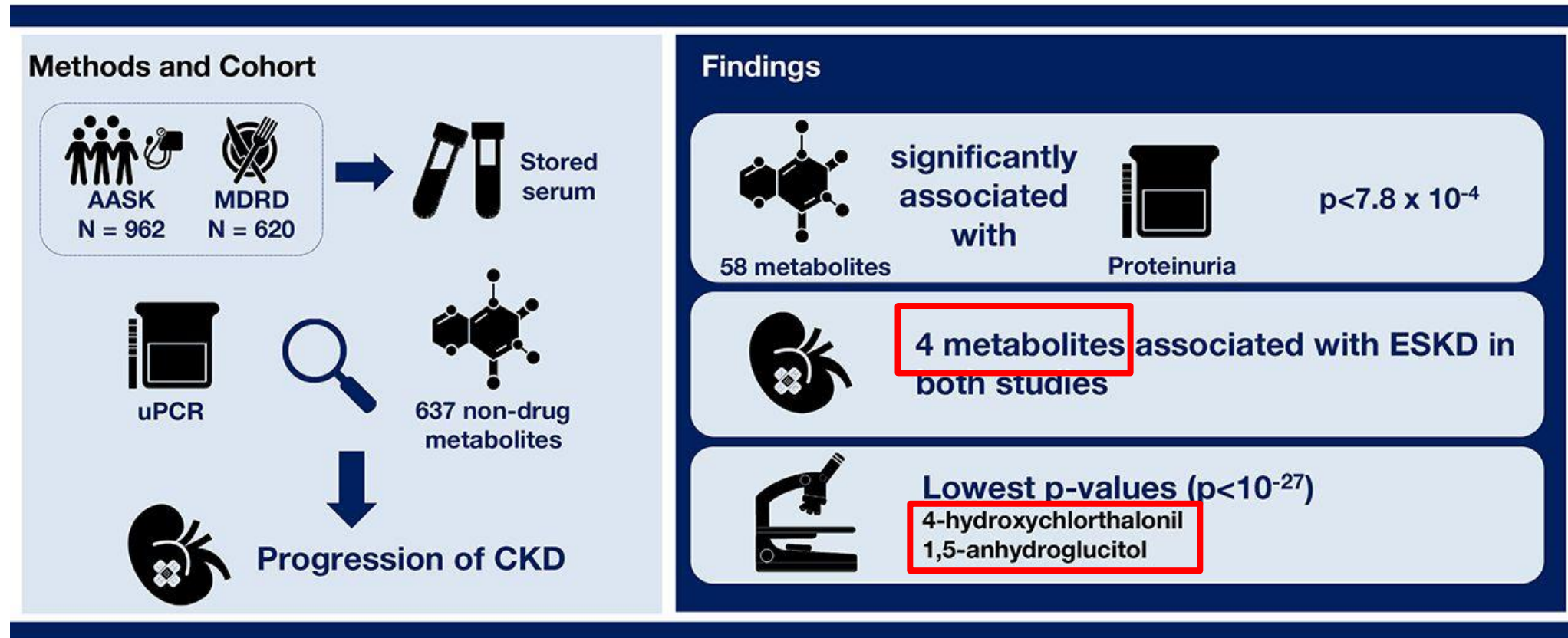


From metabolomic to multi-omic study

non-negative matrix factorization (NMF) clusters for molecular subgroups

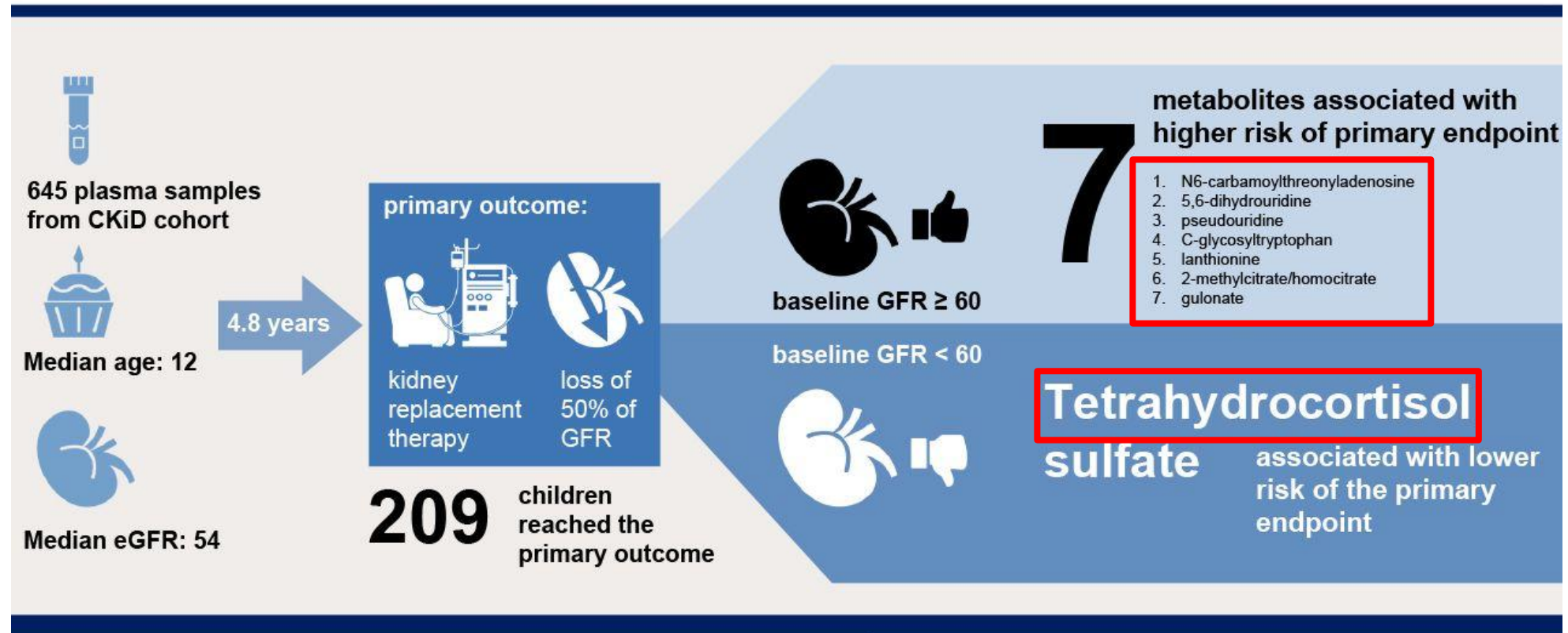


Serum metabolomic alterations a/w proteinuria in CKD



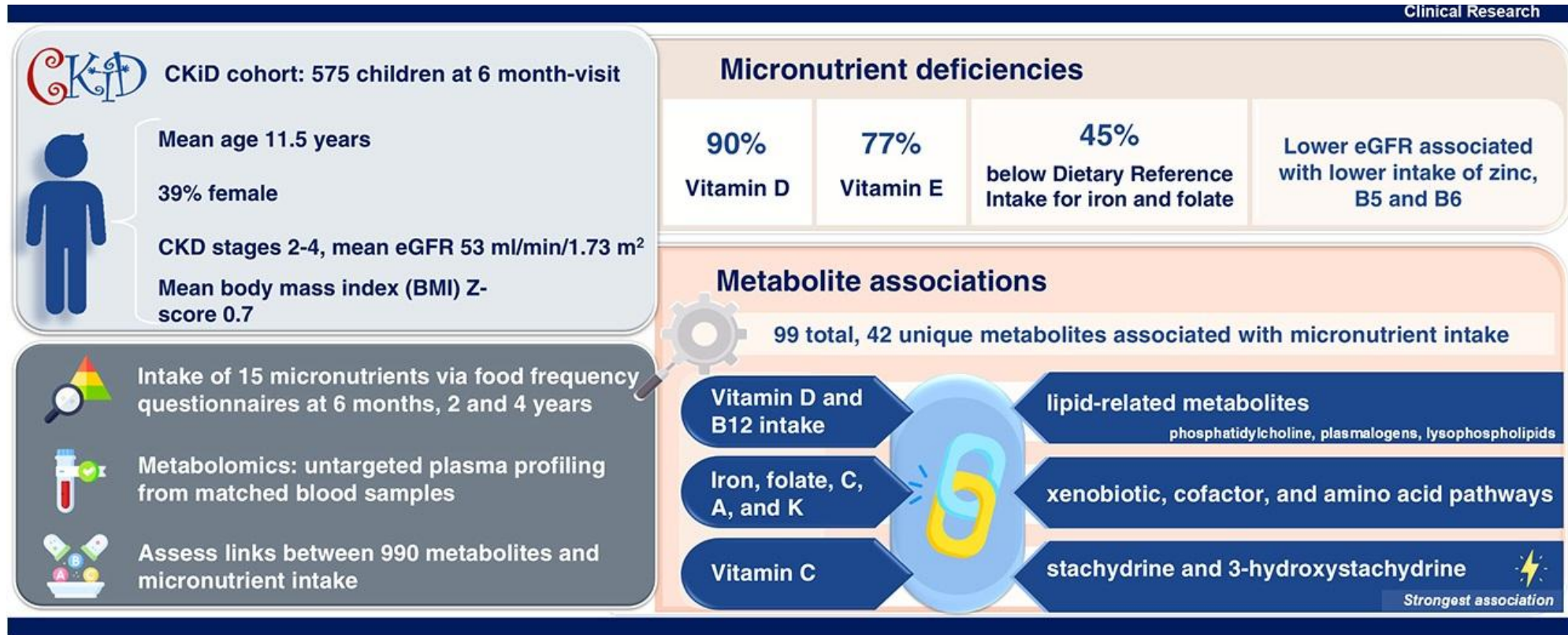
Conclusions We identified 58 serum metabolites with cross-sectional associations with **proteinuria**, some of which were also associated with **CKD progression**.

Metabolite biomarkers of CKD progression in children



Conclusion: Untargeted plasma metabolomic profiling facilitated discovery of novel metabolite associations with CKD progression in children that were independent of established clinical predictors and highlight the role of select biological pathways.

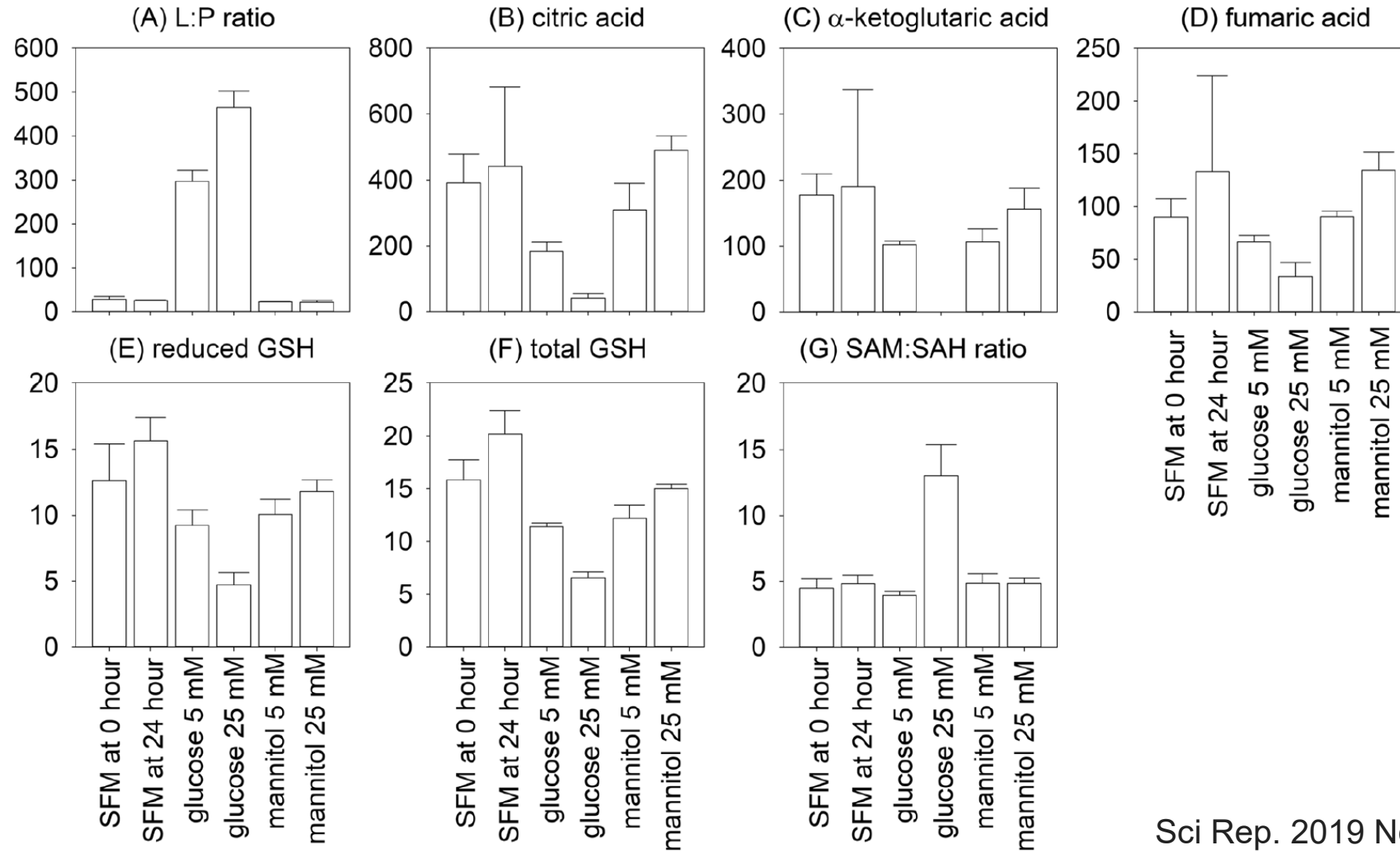
Dietary Micronutrient Intake and Metabolome in CKD



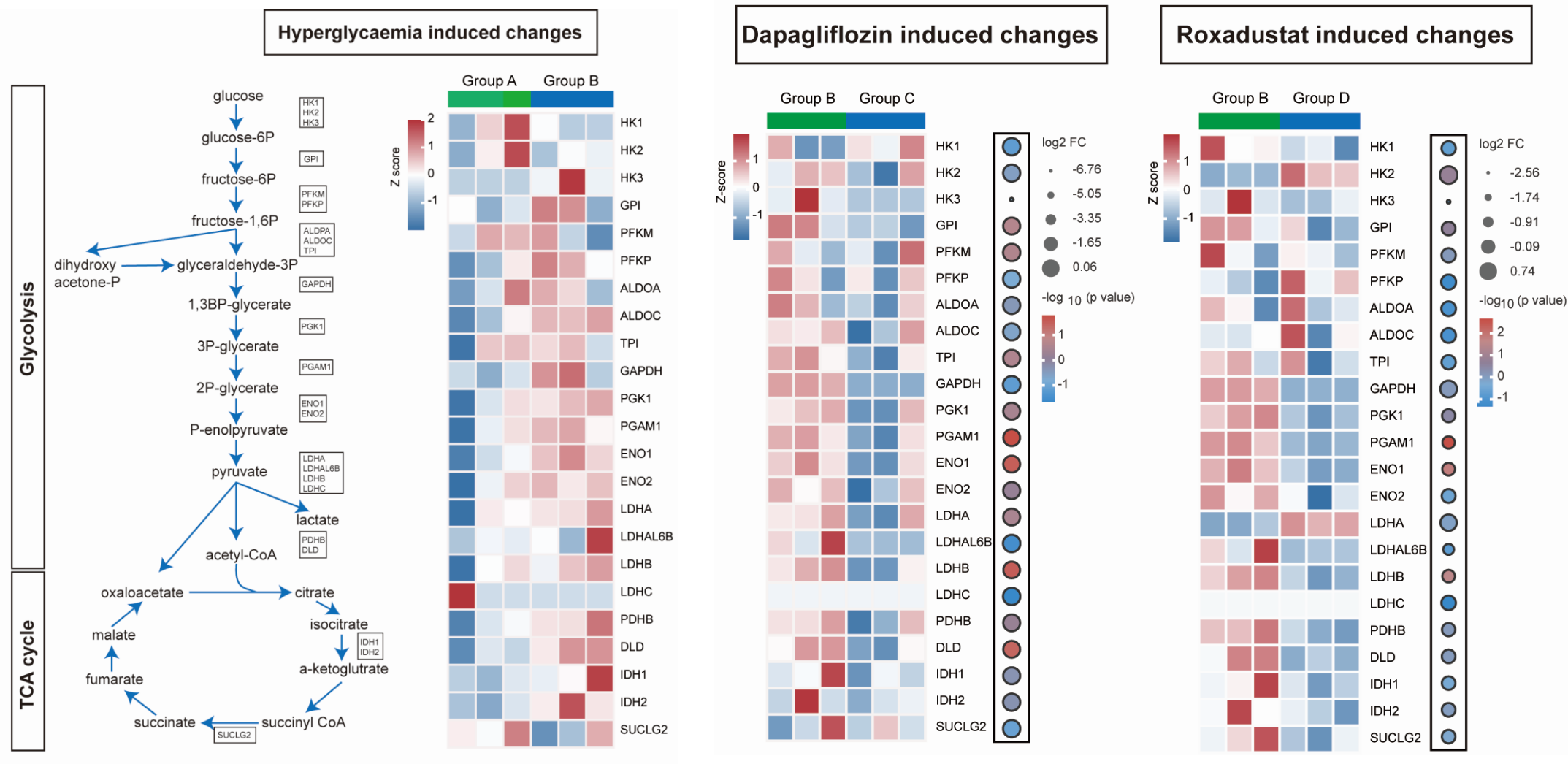
Conclusions: The majority of children with CKD have intake below dietary reference intake of at least one micronutrient despite normal BMI, which was associated with alterations in lipid metabolism.

Denise C. Hasson.
Clin J Am Soc Nephrol 2025; 20:1536

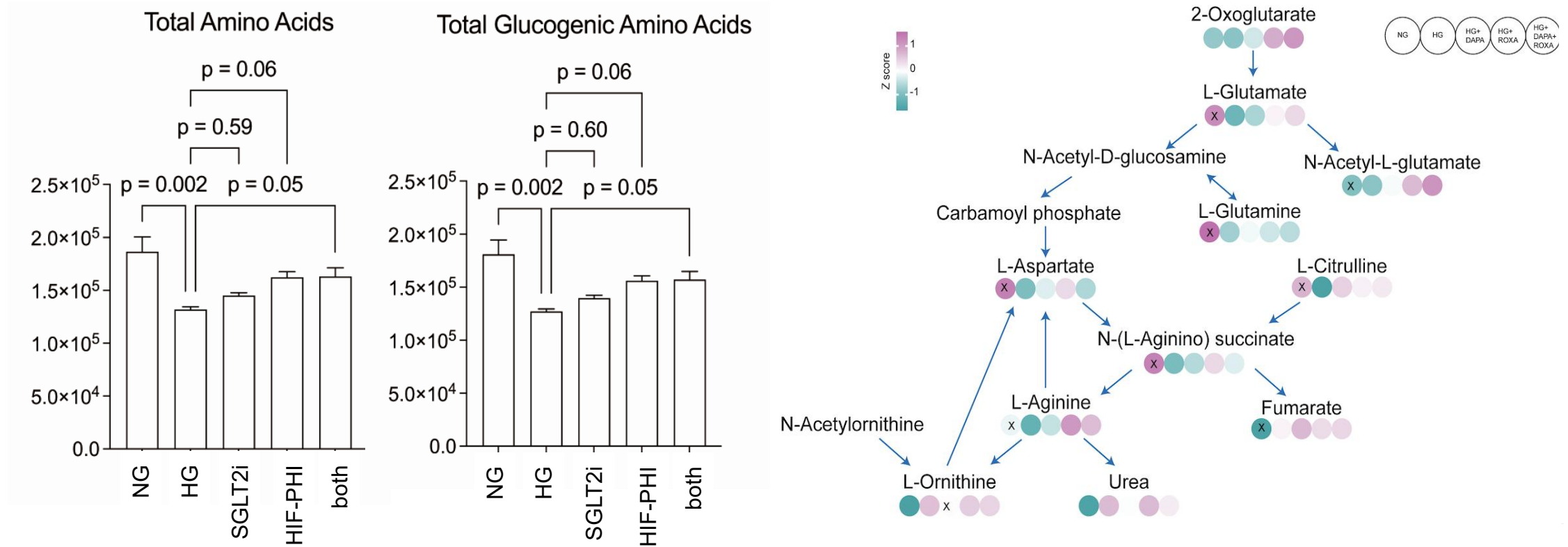
Cell specific metabolomic change: PTC in high glucose



cf. metabolomic change of podocyte



Change in amino acid profile and arginine / NO pathway



*HIF hydroxylation require alpha ketoglutarate as co-substrate

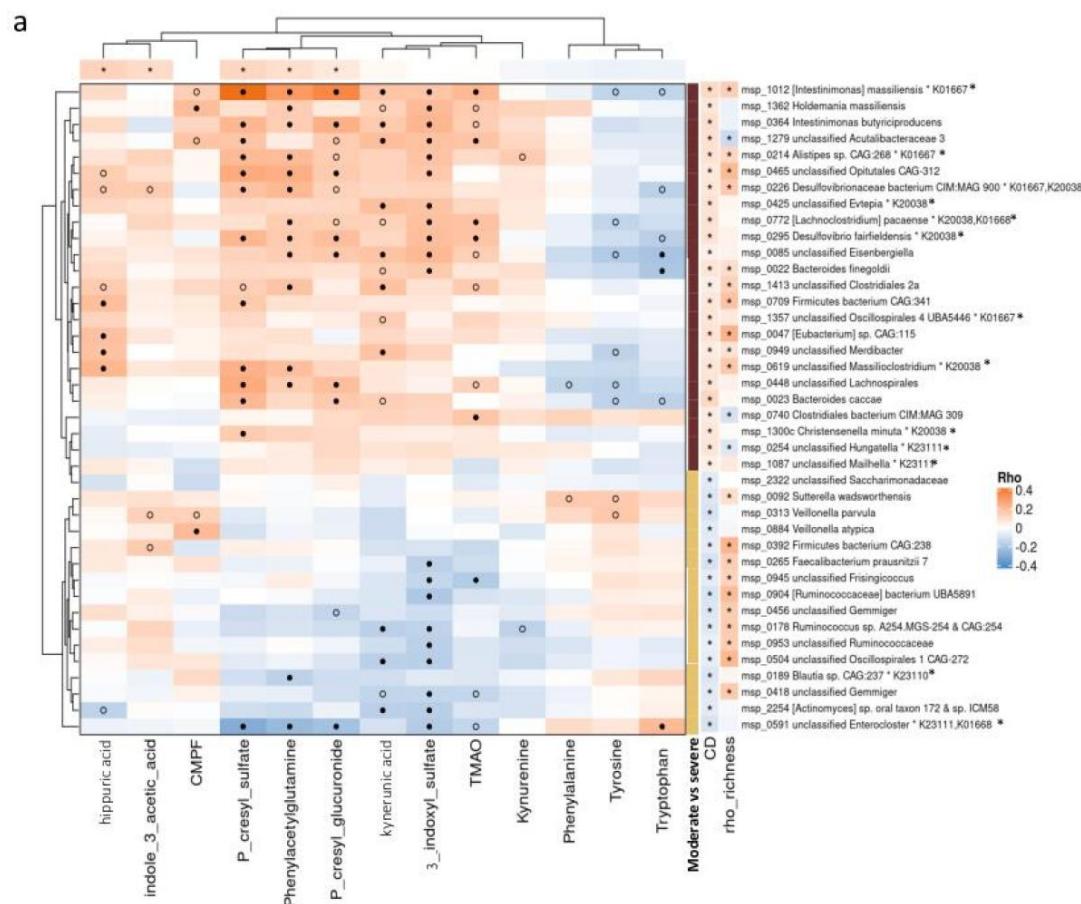
Li CL. manuscript under review

Metabolome: not only our own metabolites

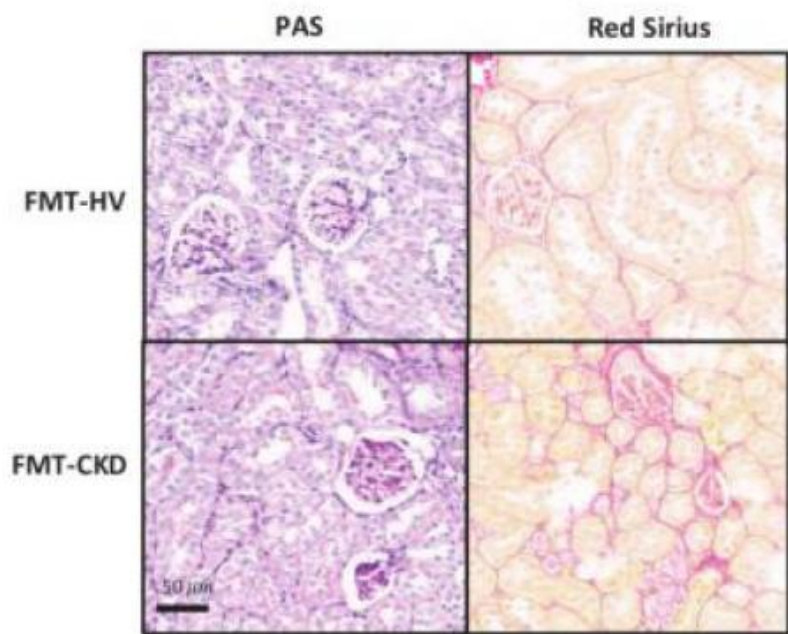
- MASLD and CKD are linked through mechanisms like lipid accumulation and oxidative stress
- gut dysbiosis leads to harmful metabolites that affect kidney function
 - toxins from the gut can cause systemic inflammation and kidney damage
 - liver processes gut-derived metabolites → further effects on kidney
 - liver also secretes molecules that influence gut microbiota and barrier integrity

Microbiome contribution to metabolome

- 2 CKD cohorts and 1 healthy cohort



FMT from patients with CKD to antibiotic-treated CKD model mice increased serum UT levels and exacerbated kidney fibrosis.



Uremic toxins and microbiota-derived metabolites tested

Compound	Origin	Role in diseases
TMAO	metabolic product of ingested meat	association with proteinuria, CKD decline, all-cause mortality and CVD
kynurenine	metabolite of tryptophan	increased production associated with worsen depressive symptoms and cognitive dysfunction
kynurenic acid	metabolite of tryptophan	antagonist of glutamate receptors and NMDA receptor; affect synaptic function
hippuric acid	formed from gut microbiota; also produced in the liver and kidneys	a marker for Parkinson's disease
phenyl-acetyl-glutamine	metabolite of phenylacetate in the liver; also produced by gut microbiota	possible marker for cardiovascular disease
indoxyl sulfate	metabolite of tryptophan from gut microbiota	stimulates glomerular sclerosis and renal interstitial fibrosis; contribute to CKD progression; also a predictor of CVD
p-cresyl sulfate	metabolite of aromatic amino acids from gut microbiota	contribute to CKD progression
p-cresyl glucuronide	metabolite of aromatic amino acids from gut microbiota	none reported
indole-3-acetic acid	plant hormone, also produced by some bacterial species	developmental toxicity and immunotoxin in animals
CMPF	endogenous metabolite of furan fatty acids in diet; also produced from gut microbiota	may induce kidney cell apoptosis or ferroptosis

TMAO and kidney function decline

Methods and Cohort



Two community-based Prospective cohorts*



eGFR ≥ 60 mL/min/1.73m²
N= 10,564



Serial plasma TMAO level
Baseline and one follow-up



Creatinine and Cystatin C
4 times during follow-up



Incident CKD: eGFR decline $\geq 30\%$ from baseline and a resulting eGFR < 60 mL/min/1.73 m²
N= 979

*Median follow-up 9.4 years

Higher TMAO levels associated with higher relative risk of incident CKD



2.24

1.68, 2.98

and greater annualized eGFR decline (mL/min/1.73m²)



-0.43

-0.56, -0.30



These associations were consistent across different racial/ethnic groups examined



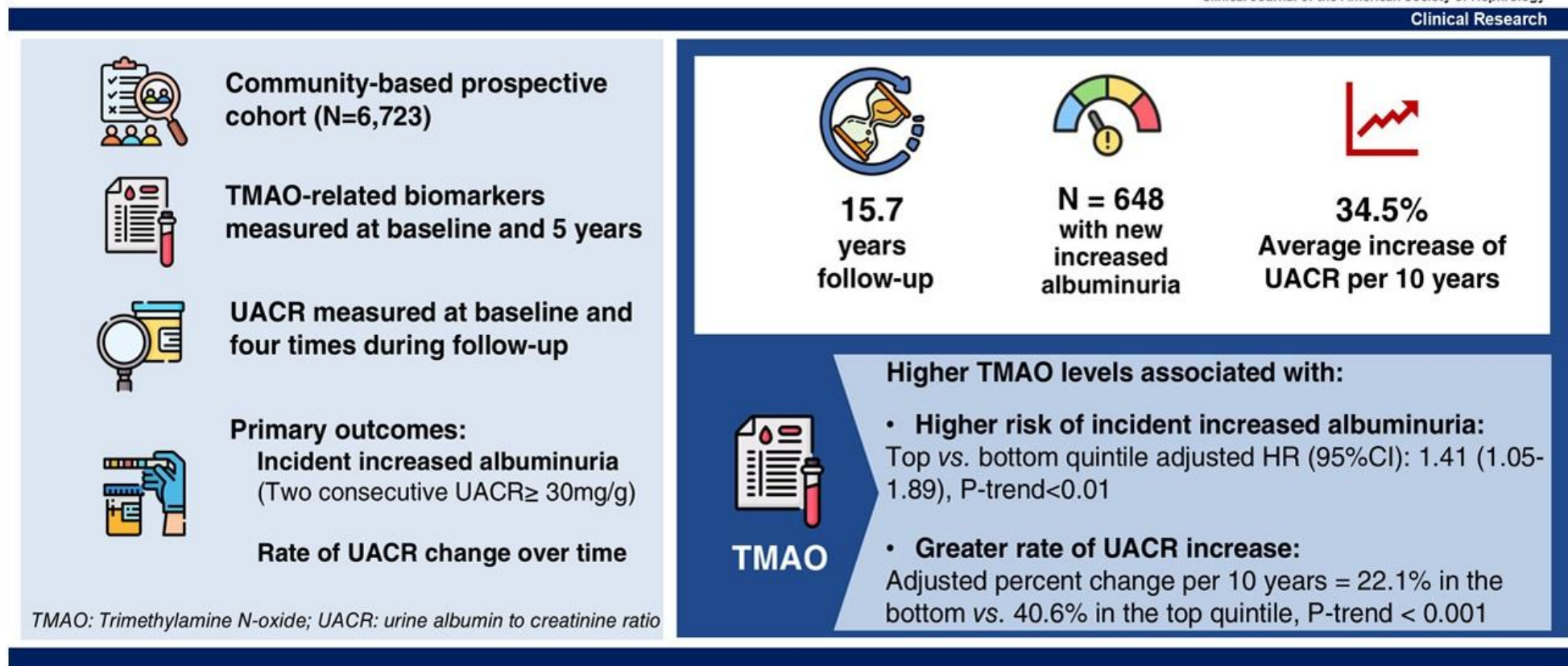
Association with eGFR decline \geq that of established CKD risk factors (DM, black race, age per 10 yr, SBP per 10mmHg)

Effect estimates are for top vs. bottom TMAO quintile

TMAO, Trimethylamine N-oxide; DM, diabetes; SBP, systolic blood pressure

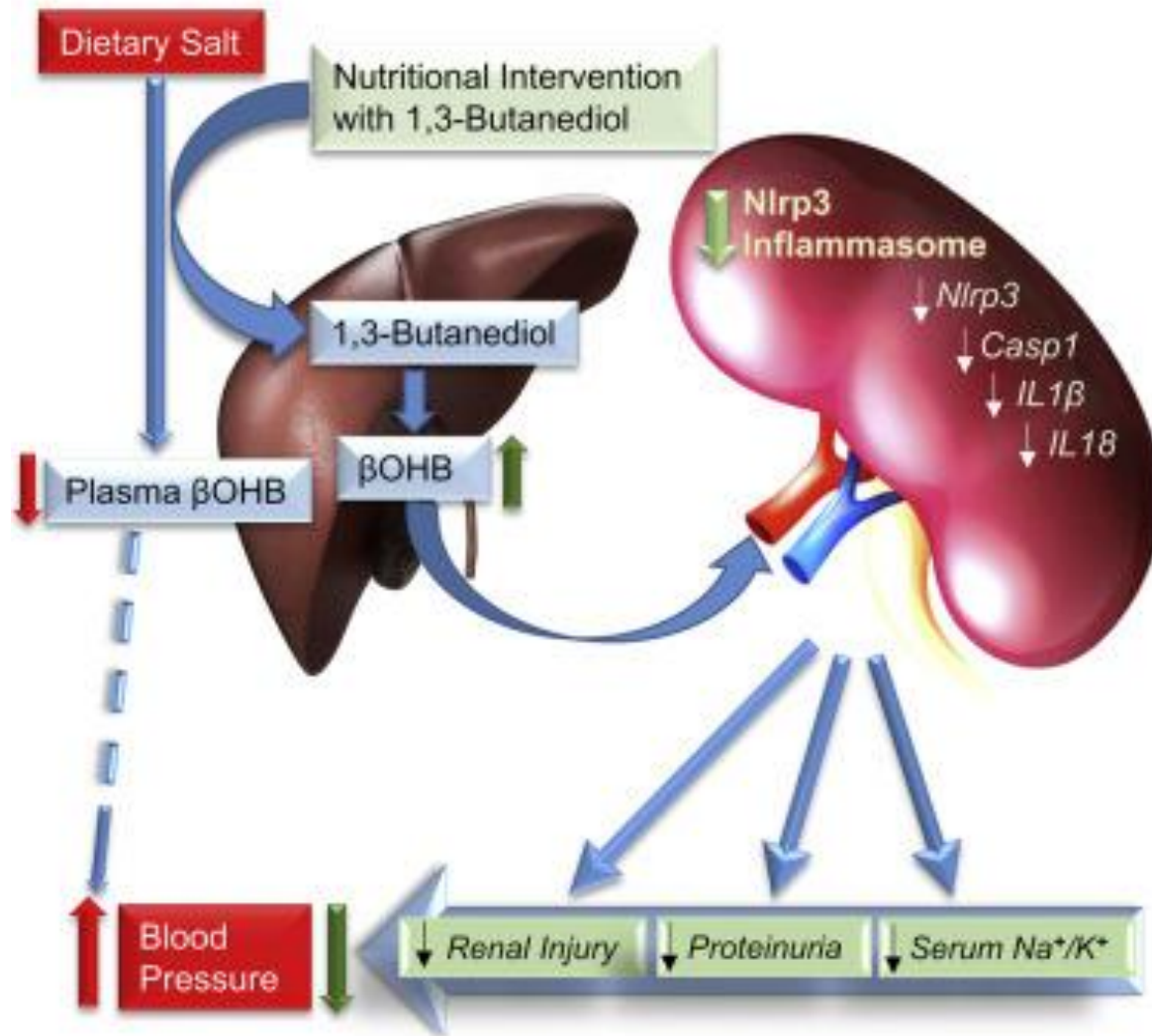
Conclusions: In community-based US adults, higher serial measures of plasma TMAO were associated with higher risk of incident CKD and greater annualized kidney function decline.

TMAO and albuminuria



Conclusions: TMAO-related gut microbial metabolites appears to be a novel risk factor for albuminuria and its progression, raising the need to investigate the role of targeting the TMAO pathway on albuminuria.

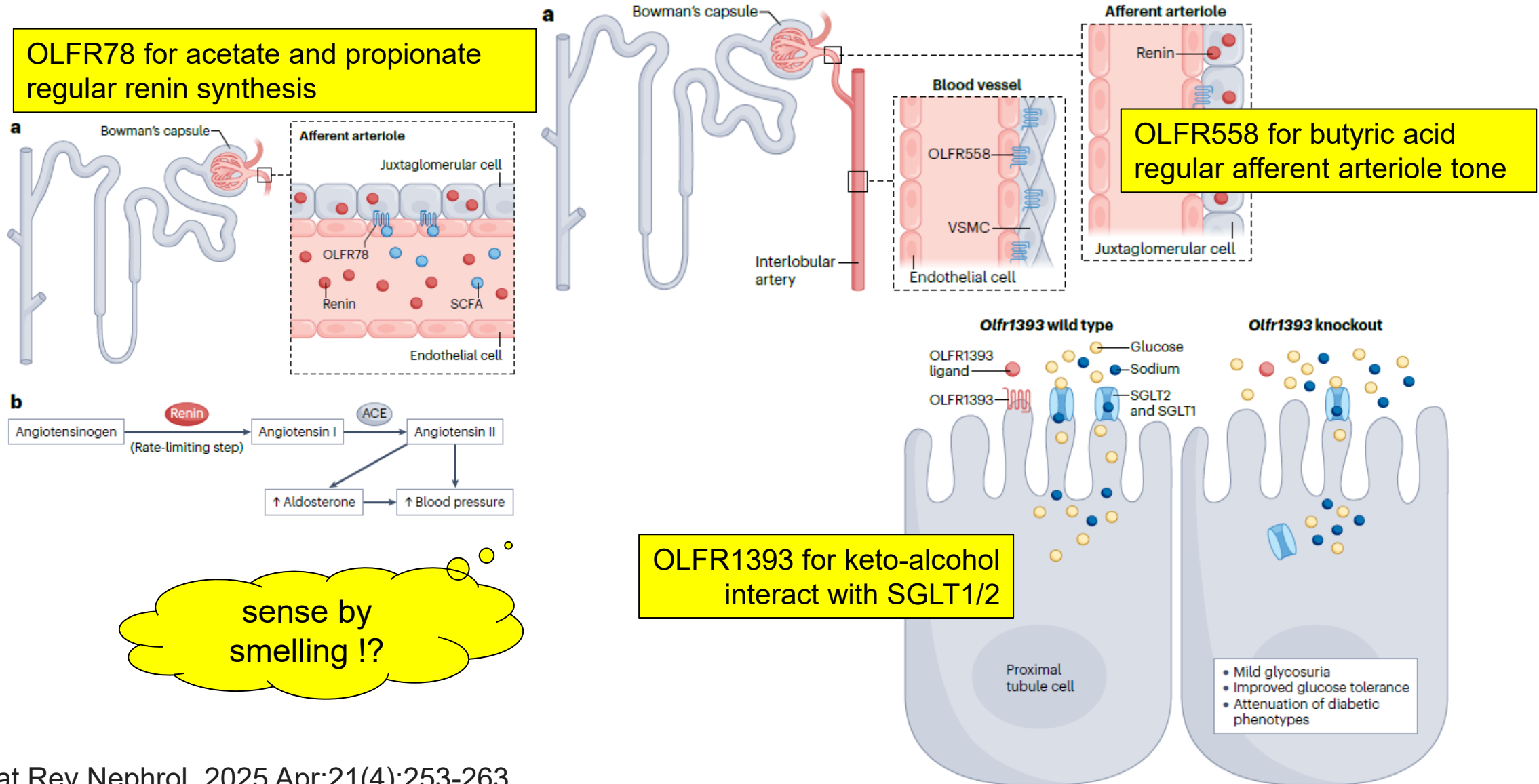
Mechanistic exploration: β -hydroxybutyrate and BP



Short term
 β HB
 \downarrow
 SK_{Ca} and IK_{Ca} and Na^+/K^+ -ATPase
 \downarrow
 \uparrow Hyperpolarization
 \downarrow
Vasodilation and reduced vascular load

Long term
 β HB
 \downarrow
 \uparrow NO bioavailability
 \downarrow
 \downarrow Hypertension

Can the kidney sense specific metabolites?



Conclusion

- advance in methodologies
- metabolomic changes are context and cell-type specific
- contribution of gut microbiota to metabolomic alterations
- kidney can “sense” many metabolites at low concentrations