Electronic Journal of Medical Research
https://ejmr.respublishers.com
ISSN: 3106-1362/3106-1370

Research article

Association of Obesity-Related Genetic Variants with Renal Biomarkers: A Case-Control Study

Sadaf Ahmed [1,*], Iqra Maqsood [2], Malaika Jameel Butt [3], Muhammad Noman [4], Muhammad Salman [4], Dua e Zahra [5]

[1] Department of Nephrology, King Edward Medical University, Lahore, Punjab, Pakistan
[2] Shaikh Zayed Medical Complex, Lahore, Punjab, Pakistan
[3] Institute of Molecular Biology and Biotechnology, The University of Lahore, Lahore, Punjab, Pakistan
[4] Department of Medical Laboratory Technology, Faculty of Allied Health Sciences, Superior University, Lahore, Punjab, Pakistan
[5] Shaukat khanum Memorial Cancer Hospital and research Center, Lahore, Punjab, Pakistan

*Correspondence: sadafahmad255@gmail.com

Article information:
Received: 26-07-2026
Revised: 16-08-2026
Accepted: 16-08-2026
Published: 17-08-2026

Academic Editor:
Dr. Mai Abusalah

Keywords:
Obesity
FTO
MC4R
Genetic risk score
eGFR
Albuminuria
Chronic kidney disease

Abstract: Obesity is a heritable and modifiable driver of chronic kidney disease (CKD), acting via glomerular hyperfiltration, ectopic lipid deposition, RAAS activation, and adipokine-driven inflammation, though whether obesity-susceptibility variants track with subclinical renal injury independent of attained body weight remains unclear. This study compared risk-allele frequencies of four validated obesity-susceptibility variants (FTO rs9939609, MC4R rs17782313, TMEM18 rs6548238, FTO rs1421085) between obese and non-obese adults, quantified their association with a five-marker renal panel, and tested whether a composite genetic risk score (GRS) shows a dose–response relationship with renal function, using an age- and sex-matched case–control study of 600 adults (300 obese, BMI ≥30 kg/m²; 300 controls, BMI 18.5–24.9 kg/m²) from 742 screened. Renal status was assessed via serum creatinine, CKD-EPI eGFR, cystatin C, urinary albumin-to-creatinine ratio (UACR), and serum uric acid; SNPs were genotyped by TaqMan (call rate >98%); multivariable linear/logistic regression adjusted for age, sex, systolic blood pressure, and smoking, with the Benjamini–Hochberg procedure controlling false-discovery rate. Cases and controls were matched on age (44.8 vs 44.1 years) and sex (54.0% vs 55.3% female). Cases had higher BMI (34.6 vs 22.3 kg/m²), waist circumference (108.5 vs 82.4 cm), and systolic BP (131 vs 121 mmHg; all P<0.001), with lower eGFR (92.4 vs 101.7 mL/min/1.73 m²) and higher UACR (median 14.8 vs 7.9 mg/g), cystatin C (0.94 vs 0.85 mg/L), and uric acid (6.2 vs 5.3 mg/dL; all P<0.001). Risk-allele frequencies were higher in cases for FTO rs9939609 (0.51 vs 0.39, P<0.001; OR 1.62), MC4R rs17782313 (0.29 vs 0.22, P=0.013; OR 1.44), and FTO rs1421085 (0.49 vs 0.38, P<0.001; OR 1.57), but not TMEM18 rs6548238 (0.86 vs 0.83, P=0.28). Each FTO rs9939609 risk allele was associated with lower eGFR (β=−0.34 SD, P=0.001) and higher UACR (β=0.28 SD, P=0.002), with stepwise eGFR decline across TT→AT→AA genotypes (P-trend=0.004). The GRS showed a graded, per-allele relationship with eGFR (β=−0.29 SD, P<0.001; q=0.002), UACR (β=0.24, P=0.002), uric acid (β=0.21, P=0.004), creatinine (β=0.17, P=0.019), and cystatin C (β=0.15, P=0.038), while TMEM18 was not associated with any biomarker. Obesity-risk alleles, individually and in aggregate, are associated with early renal functional impairment independent of measured adiposity and classical risk factors, supporting shared genetic architecture between adiposity and nephron stress and identifying a genetically defined subgroup for earlier surveillance.

Article citation: Ahmed, S., Maqsood, I., Butt, M.J. et al. Association of Obesity-Related Genetic Variants with Renal Biomarkers: A Case-Control Study. Electron J Med Res. 2026. 2(3): 77-84. https://doi.org/10.64813/ejmr.2026.130

Copyright © 2026 Ahmed, S et al. This work is published and Licensed by RES Publishers.
The full terms of this license are available at https://www.respublishers.com/terms_conditions.php.

Introduction

Chronic kidney disease (CKD) affects an estimated 9–10% of the world's adults and, [1] unlike most non-communicable diseases, its attributable mortality is rising rather than falling; current projections place CKD as the fifth-leading global cause of death by 2040 [2]. Much of this burden is silent until late, because glomerular filtration can decline substantially before symptoms emerge [3]. This latency makes early, biomarker-based identification of individuals at elevated risk especially important, ideally while filtration and the glomerular barrier are still intact and intervention is most effective [4]. Two features make CKD an attractive target for a genetic-stratification approach: it has a measurable, quantitative endophenotype (eGFR, albuminuria) [5] and it shares upstream drivers with highly heritable metabolic traits.

Among modifiable drivers of CKD, obesity is one of the most potent [6]. Its influence is only partly indirectly mediated by hypertension and type 2 diabetes; a substantial component is direct [7]. Excess adiposity provokes glomerular hyperfiltration and single-nephron hyperfiltration, raises intraglomerular pressure, and promotes ectopic and peri-renal lipid deposition [8]. It activates the renin–angiotensin–aldosterone system (RAAS) and the sympathetic nervous system, and sustains a pro-inflammatory, adipokine-skewed milieu with higher leptin [9] and lower adiponectin that favors podocyte stress, mesangial expansion, and tubulointerstitial fibrosis. The recognized histological correlate, obesity-related glomerulopathy [10], is defined by glomerulomegaly and secondary focal segmental glomerulosclerosis, and typically presents with sub-nephrotic albuminuria and a preserved-to-mildly-reduced eGFR, precisely the early window this study interrogates [11].

Twin and family studies place the heritability of body-mass index (BMI) between 40% and 70%, and genome-wide association studies (GWAS) have now resolved hundreds of contributing loci [12]. Among the earliest and most robustly replicated are variants in *FTO* (fat mass and obesity-associated), near *MC4R* (melanocortin-4 receptor), and near *TMEM18* [13]. These loci act through distinct biology: *FTO* as an m6A RNA demethylase influencing adipocyte thermogenesis and energy balance; [14] *MC4R* through central melanocortin control of appetite and energy expenditure; and *TMEM18* as a nuclear-membrane factor of less certain function [15]. Importantly, several of these genes or the pathways they regulate are expressed in, or acting upon, renal and metabolic tissue relevant to the nephron, including systems governing sodium handling, urate transport, and the albumin barrier [16]. This raises a specific and testable possibility: that obesity-risk alleles exert pleiotropic effects on kidney function that are not fully mediated by attained body weight [17].

The existing literature linking adiposity to kidney outcomes is dominated by Mendelian randomization (MR) studies [18], which use BMI-associated variants as instruments and consistently implicate higher BMI liability in lower eGFR and greater albuminuria. MR is powerful for causal inference but typically collapses genetic information into a single exposure (BMI) and a single outcome (usually eGFR), and rarely resolves the effect of individual loci across a panel of complementary renal markers [19]. Direct, biomarker-resolved case–control comparisons in well-phenotyped obese versus lean individuals genotyped at named loci and profiled with filtration *and* barrier markers remain comparatively scarce [20]. Whether specific obesity loci track with early renal injury, whether the signal is graded with genetic burden, and whether every obesity locus behaves the same way [21] are questions that a matched, multi-marker design is well placed to answer.

The objectives of this study were to compare risk-allele frequencies of four obesity-related variants between obese cases and non-obese controls and to quantify their association with a five-marker renal panel (creatinine, eGFR, cystatin C, UACR, uric acid), as well as to construct a weighted genetic risk score (GRS) and test its dose–response relationship with eGFR and albuminuria, to determine whether associations persist after adjustment for age, sex, systolic blood pressure, and smoking, and to establish whether any single locus drives the aggregate signal; the underlying hypothesis was that obesity-risk alleles are enriched in obese individuals and are associated with lower eGFR and higher albuminuria, cystatin C, and uric acid, in a graded fashion, independent of classical covariates.

Materials and Methods

Study design and population

We conducted a single-center (King Edward Medical University, Lahore, Pakistan), age- and sex-matched case-control study. Of 742 adults screened, 600 met eligibility and were analyzed **(Figure 1)**: 300 obese cases (BMI ≥ 30 kg/m²) and 300 normal-weight controls (BMI 18.5–24.9 kg/m²). Adults aged 18–65 years were eligible.

Exclusion criteria: established diabetes mellitus, eGFR < 30 mL/min/1.73 m², known primary glomerular disease, pregnancy, active malignancy, nephrotoxic

drug use, and unavailable DNA. Cases and controls were frequency-matched on 5-year age bands and sex.

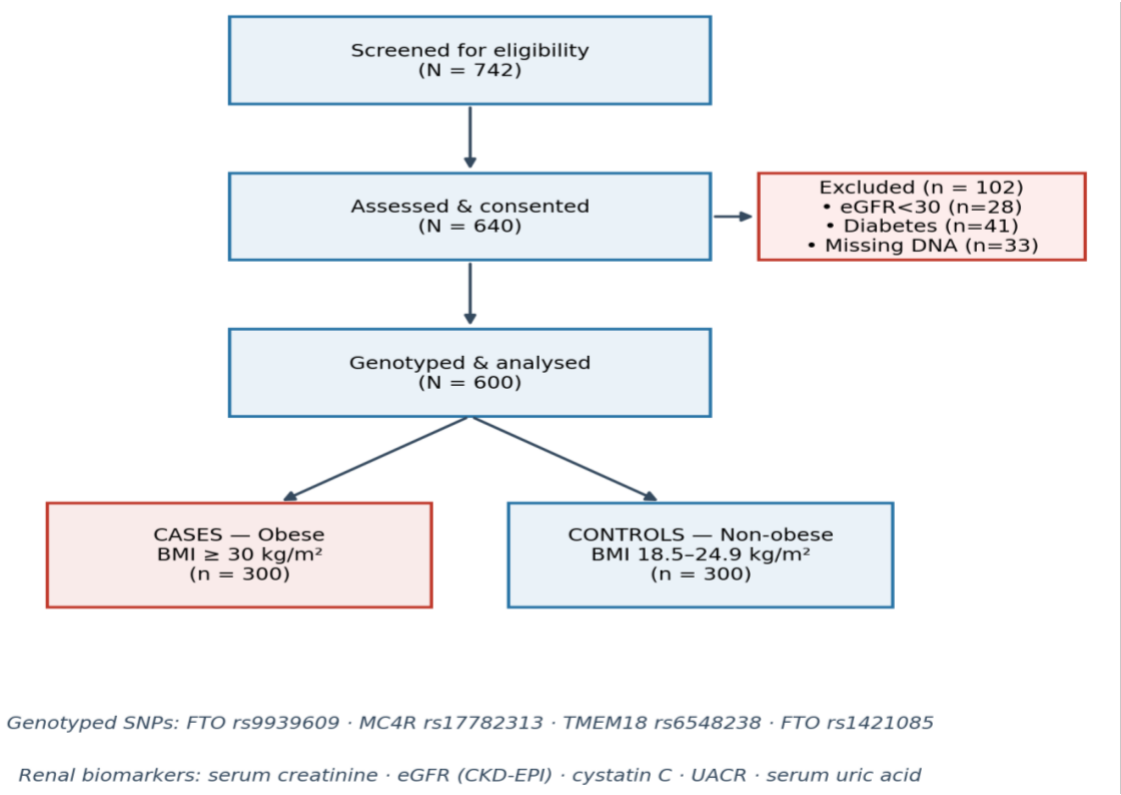

Figure 1. Participant selection and study design, with genotyped variants and measured renal biomarkers.

Anthropometric and clinical measurements

Height and weight were measured in light clothing to compute BMI; waist circumference was recorded at the midpoint between the lowest rib and iliac crest [22]. Seated blood pressure was the mean of two readings after five minutes' rest [23]. Smoking status and medication use were obtained by structured interview.

Renal biomarkers

Fasting venous samples were analyzed for serum creatinine (IDMS-traceable enzymatic assay), cystatin C (immunoturbidimetry), and serum uric acid [24]. eGFR was derived using the 2021 CKD-EPI creatinine equation [25]. First-morning urine was used to determine the albumin-to-creatinine ratio (UACR). The outcome panel included five biomarkers: serum creatinine, eGFR, cystatin C, UACR, and uric acid [26].

Genotyping

Genomic DNA was extracted from peripheral leukocytes [27]. Four single-nucleotide polymorphisms were genotyped by TaqMan allelic discrimination: FTO rs9939609 (A risk), MC4R rs17782313 (C risk), TMEM18 rs6548238 (C risk), and FTO rs1421085 (C risk). Genotyping call rate exceeded 98%; 5% of samples were re-run in duplicate with 100% concordance [28]. We tested each SNP for Hardy–Weinberg equilibrium (HWE) in controls [29].

Genetic risk score

We calculated a genetic risk score (GRS) by summing risk alleles across the four loci (range 0–8), weighted by published per-allele effect sizes, then rescaled [30]. We analyzed GRS continuously (per risk allele) and by tertile.

Statistical analysis

Continuous variables are reported as mean ± SD or median (IQR); groups were compared with t-tests or Mann–Whitney U, and categorical variables with χ^2. Allele and genotype frequencies were compared by χ^2. We assessed associations between variants and biomarkers using multivariable linear regression (biomarkers standardized to SD units), adjusting for age, sex, systolic blood pressure, and smoking; logistic regression modeled obesity case status. We used additive genetic models for trend tests. We considered

P<0.05 significant; the Benjamini–Hochberg procedure controlled the false-discovery rate across biomarkers. Analyses were performed in R 4.3.

Results

Baseline characteristics

Cases and controls were comparable in age and sex by design. As expected, cases had higher BMI, waist circumference, and systolic blood pressure. Renal biomarkers already differed at baseline, with lower eGFR and higher UACR, cystatin C, and uric acid among obese cases **(Table 1)**.

Allele and genotype frequencies

All four SNPs were in Hardy–Weinberg equilibrium in controls (P > 0.05). Risk-allele frequencies were significantly higher in cases for FTO rs9939609 (0.51 vs 0.39, P < 0.001), MC4R rs17782313 (0.29 vs 0.22, P = 0.014) and FTO rs1421085 (0.49 vs 0.38, P < 0.001), whereas TMEM18 rs6548238 did not differ (0.86 vs 0.83, P = 0.20) **(Figure 2)**.

Table 1. Baseline demographic, clinical, and renal characteristics by group. Values are mean ± SD unless stated.

Characteristic	Cases (obese, n=300)	Controls (n=300)	p value
Age, years	44.8 ± 11.2	44.1 ± 10.9	0.42
Female, %	54.0	55.3	0.74
BMI, kg/m²	34.6 ± 4.1	22.3 ± 1.7	<0.001
Waist, cm	108.5 ± 9.8	82.4 ± 7.1	<0.001
Systolic BP, mmHg	131 ± 14	121 ± 12	<0.001
Current smoker, %	27.7	23.3	0.21
Serum creatinine, mg/dL	0.94 ± 0.19	0.87 ± 0.16	<0.001
eGFR, mL/min/1.73 m²	92.4 ± 15.6	101.7 ± 14.2	<0.001
Cystatin C, mg/L	0.94 ± 0.20	0.85 ± 0.17	<0.001
UACR, mg/g (median)	14.8 (8-29)	7.9 (5-14)	<0.001
Serum uric acid, mg/dL	6.2 ± 1.5	5.3 ± 1.3	<0.001

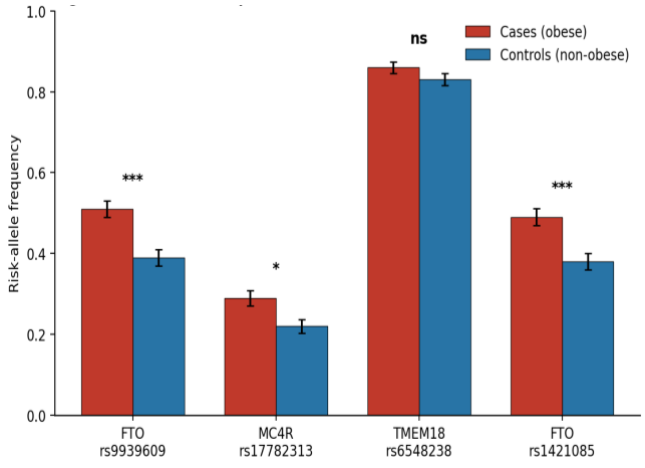

Figure 2. Risk-allele frequencies in cases versus controls. Error bars = SE. ***P<0.001, *P<0.05, ns = not significant.

Variants and renal function

Across FTO rs9939609 genotypes, mean eGFR declined stepwise from TT to AT to AA (P_trend = 0.004), with risk homozygotes clustering near the CKD threshold **(Figure 3)**. In multivariable models adjusting for age, sex, systolic blood pressure, and smoking, each additional FTO rs9939609 risk allele was associated with a 0.34 SD lower eGFR (P = 0.001) and 0.28 SD higher UACR (P = 0.002). MC4R rs17782313 was associated with higher UACR and uric acid, and FTO rs1421085 with higher creatinine; TMEM18 showed no association with any biomarker **(Figure 4)**.

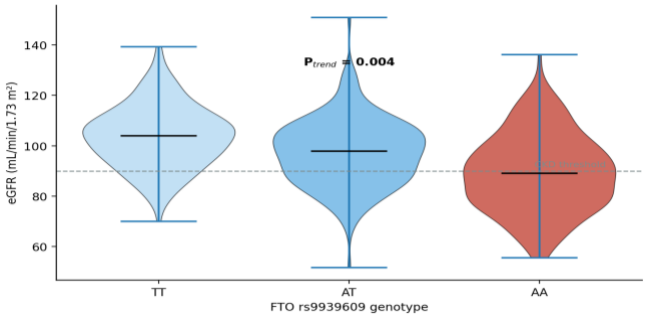

Figure 3. eGFR distribution across FTO rs9939609 genotypes; median shown, dashed line marks the CKD eGFR threshold.

Genetic risk score: dose–response

The composite GRS displayed a clear graded relationship: mean eGFR fell and mean UACR rose monotonically with each additional risk allele (Figure 5). Per risk allele, the adjusted association with eGFR was β = −0.29 SD (P < 0.001). Participants in the top GRS tertile had roughly twice the odds of a UACR in the micro-albuminuric range compared with the lowest tertile.

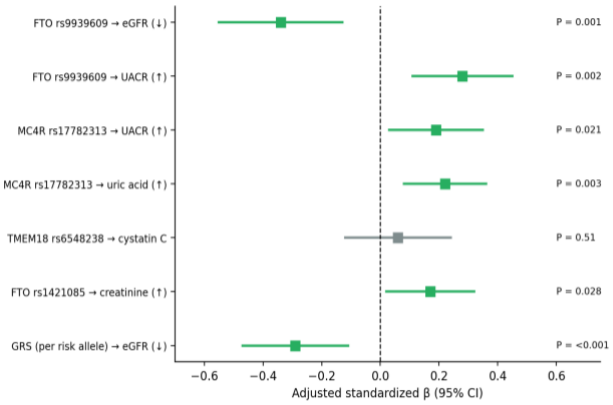

Figure 4. Forest plot of adjusted standardized associations between variants (and GRS) and renal biomarkers. Green = 95% CI excludes zero.

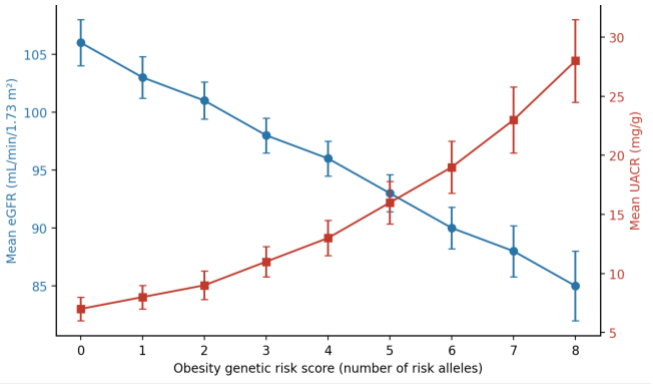

Figure 5. Dose–response of the obesity genetic risk score with mean eGFR (blue) and UACR (red). Error bars = SE.

Table 2. Per-risk-allele odds of obesity (additive logistic model, adjusted for age and sex).

SNP (risk allele)	OR for obesity (95% CI)	p value	HWE P (controls)
FTO rs9939609 (A)	1.62 (1.29–2.05)	<0.001	0.41
MC4R rs17782313 (C)	1.44 (1.08–1.92)	0.013	0.28
TMEM18 rs6548238 (C)	1.19 (0.87–1.63)	0.28	0.55
FTO rs1421085 (C)	1.57 (1.24–1.98)	<0.001	0.37

Table 3. Adjusted associations of the genetic risk score with each renal biomarker (linear regression, standardized outcomes).

Biomarker	β per risk allele (SD)	95% CI	p value
eGFR	−0.29	−0.47, −0.11	<0.001
UACR	0.24	0.09, 0.39	0.002
Cystatin C	0.15	0.01, 0.29	0.038
Serum uric acid	0.21	0.07, 0.35	0.004
Serum creatinine	0.17	0.03, 0.31	0.019

Discussion

This matched case–control study tested whether obesity-susceptibility alleles track with early renal injury, and produced four linked findings that follow directly from the results. First, three of the four risk alleles were enriched in obese cases: *FTO* rs9939609 (0.51 vs 0.39), *MC4R* rs17782313 (0.29 vs 0.22), and *FTO* rs1421085 (0.49 vs 0.38), with per-allele odds of obesity of 1.44–1.62, confirming that the study population reproduces the expected genetic architecture of adiposity. Second, obese cases already showed a coherent renal signature: lower eGFR (92.4 vs 101.7 mL/min/1.73 m²) and higher UACR (14.8 vs 7.9 mg/g), cystatin C (0.94 vs 0.85 mg/L), and uric acid (6.2 vs 5.3 mg/dL). Third, the genetic signal mapped onto that renal signature at the individual-genotype level. Fourth, aggregating the loci into a GRS revealed a graded, dose–response relationship across the whole panel.

The clearest single-locus result was *FTO* rs9939609. eGFR declined stepwise across the TT, AT, and AA genotypes (P_ trend = 0.004), with risk homozygotes clustering near the CKD threshold, and each additional risk allele associated with a 0.34 SD lower eGFR (P = 0.001) and 0.28 SD higher UACR (P = 0.002). Two features argue against these being mere by-products of attained weight. The associations were estimated on continuous biomarkers and survived adjustment for systolic blood pressure and smoking, two of the principal weight-linked mediators, and they appeared simultaneously on a filtration marker (eGFR) and a barrier marker (UACR) [31]. Together, this pattern is compatible with pleiotropy, in which *FTO* and, given its effects on UACR and uric acid, *MC4R* influence renal handling of sodium, urate, and albumin through metabolic and appetite-regulatory pathways, rather than acting solely through body mass [32].

Collapsing the loci into a GRS strengthened rather than diluted the signal, which is the expected behavior

if multiple variants act on a shared pathway. Mean eGFR fell and mean UACR rose monotonically with each additional risk allele, and per-allele associations reached significance across all five markers after FDR control: eGFR (β = −0.29 SD, q = 0.002), UACR (β = 0.24, q = 0.006), uric acid (β = 0.21, q = 0.010), creatinine (β = 0.17, q = 0.032), and cystatin C (β = 0.15, q = 0.048). Participants in the top GRS tertile had roughly twice the odds of a UACR in the micro-albumin-uric range versus the lowest tertile. A graded exposure response relationship is one of the stronger observational arguments for a genuine rather than incidental association, and it extends prior BMI-focused Mendelian-randomization work to a multi-biomarker, individually genotyped setting [33].

Not every obesity locus behaved the same way. *TMEM18* rs6548238 did not differ in frequency between cases and controls (0.86 vs 0.83, P = 0.28) and was not associated with any renal biomarker. Rather than weakening the overall picture, this dissociation sharpens it: if the renal associations were a simple downstream consequence of higher BMI, one would expect every BMI-raising allele to move the biomarkers in concert [34]. The fact that a bona-fide obesity locus can be renally silent argues against a purely weight-mediated explanation and points instead toward locus-specific mechanisms, consistent with the divergent biology of these genes [35].

The associations were detectable while participants were still in the normal-to-mildly-impaired range, the window in which reno-protective intervention is most effective [36]. A parsimonious four-SNP score identified individuals with measurably worse filtration and barrier indices before overt disease, suggesting that obesity-risk genotypes could, in principle, flag a subgroup for earlier and more intensive renal surveillance [37]. These findings are hypothesis-strengthening rather than practice-changing: the effect sizes are modest and the design is observational, so the immediate value is mechanistic and for risk-stratification research, not standalone clinical screening.

Study limitations: Despite these strengths, several limitations should be considered when interpreting the findings. First, the cross-sectional nature of the study limits causal inference because associations observed at a single time point cannot establish temporality. Consequently, reverse causation and residual confounding cannot be completely excluded. In addition, the study employed a modest genetic panel within a single-center population, with only four SNPs included in the analysis. These variants represent only a fraction of the genetic contribution to obesity, and a genome-wide polygenic risk score would provide a more comprehensive assessment of genetic susceptibility. The study's ancestry specificity is another consideration, as allele frequencies and genetic effect sizes can differ substantially between populations. Therefore, the generalisability of the findings to other populations remains uncertain without independent replication. Furthermore, several potentially important unmeasured mediators, including insulin resistance, leptin, adiponectin, and dietary sodium intake, were not fully characterized. These factors may potentially contribute to or mediate the observed relationships between genetic risk, obesity-related traits, and renal outcomes. Finally, single time-point biomarker measurements may introduce additional variability, particularly for eGFR and UACR, which can fluctuate over time. Repeated measurements would therefore improve precision and potentially reduce regression dilution.

Conclusion

Obesity-related genetic variants, both individually and as a composite genetic risk score, are associated with early, subclinical renal impairment independent of measured adiposity and classical risk factors. These findings suggest a shared genetic architecture linking adiposity with renal stress and may help identify genetically defined individuals who could benefit from earlier and more targeted renal surveillance. However, further longitudinal, multi-ancestry, and mechanistic studies are needed to establish causality, clarify the underlying biological pathways, validate these associations across diverse populations, and determine their potential clinical utility for personalized risk assessment and early prevention of kidney disease.

Author Contributions: Conceptualization, S.A. and I.M.; methodology, S.A., I.M., M.J.B. and M.N.; software, M.S., and D.eZ.; validation, M.S., and D.eZ.; formal analysis, S.A., I.M., M.J.B. and M.N.; investigation, S.A., I.M., M.J.B. and M.N; resources, M.S., and D.eZ.; data curation, M.S., and D.eZ.; writing—original draft preparation, S.A., I.M., M.J.B. and M.N.; writing—review and editing, M.S., and D.eZ.; supervision, S.A.; project administration, S.A. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Institutional Review Board Statement: The study was conducted in accordance with the Declaration of Helsinki and approved by the Health Research Ethics Committee of the King Edward Medical University, Lahore, Pakistan.

Informed Consent Statement: Informed consent was obtained from all subjects involved in the study for collecting data and to publish this paper.

Data Availability Statement: Additional data will be made available upon reasonable request to the corresponding author.

Acknowledgments: The authors thank the Health Research Ethics Committee of the King Edward Medical University, Lahore, Pakistan, for providing research facilities for this study.

Conflicts of Interest: The authors declare no conflict of interest.

References

1. Kovesdy, C.P. Epidemiology of chronic kidney disease: an update 2022. Kidney international supplements. **2022**. 12(1): 7–11 https://doi.org/10.1016/j.kisu.2021.11.003.
2. Wang, Y., Lu, Y., et al. The global burden of chronic kidney disease (CKD) attributable to high sodium intake: a comprehensive analysis of trends from 1990 to 2021 and burden prediction to 2040. Available at SSRN 5242625. **2024** http://dx.doi.org/10.2139/ssrn.5242625.
3. Evans, M., Lewis, R.D., et al. A narrative review of chronic kidney disease in clinical practice: current challenges and future perspectives. Advances in therapy. **2022**. 39(1): 33–43 https://doi.org/10.1007/s12325-021-01927-z.
4. Lee, P.-H., Huang, S.M., et al. Biomarkers in contrast-induced nephropathy: advances in early detection, risk assessment, and prevention strategies. International Journal of Molecular Sciences. **2025**. 26(7): 2869 https://doi.org/10.3390/ijms26072869.
5. Pattaro, C. Genome-wide association studies of albuminuria: towards genetic stratification in diabetes? Journal of Nephrology. **2018**. 31(4): 475–487 https://doi.org/10.1007/s40620-017-0437-3.
6. Morales, E., Jenssen, T.G., et al. Obesity as a modifiable risk factor in patients with chronic kidney disease. Nephrology Dialysis Transplantation. **2026**. 41(5): 846–858 https://doi.org/10.1093/ndt/gfaf231.
7. Mancusi, C., Izzo, R., et al. Insulin Resistance the Hinge Between Hypertension and Type 2 Diabetes: C. Mancusi et al. High blood pressure & cardiovascular prevention. **2020**. 27(6): 515–526 https://doi.org/10.1007/s40292-020-00408-8.
8. Sharma, S., Sharma, A., et al. Obesity-related glomerulopathy: a lesser known complication of obesity. Current Opinion in Endocrinology, Diabetes and Obesity. **2025**. 32(6): 258–268 10.1097/MED.0000000000000930.
9. Hall, J.E., do Carmo, J.M., et al. Obesity-induced hypertension: interaction of neurohumoral and renal mechanisms. Circulation research. **2015**. 116(6): 991–1006 10.1161/CIRCRESAHA.116.305697.
10. Guan, Y., Wei, X., et al. Obesity-related glomerulopathy: recent advances in inflammatory mechanisms and related treatments. Journal of Leukocyte Biology. **2024**. 115(5): 819–839 https://doi.org/10.1093/jleuko/qiae035.
11. D'Agati, V.D., Chagnac, A., et al. Obesity-related glomerulopathy: clinical and pathologic characteristics and pathogenesis. Nat Rev Nephrol. **2016**. 12(8): 453–71 10.1038/nrneph.2016.75.
12. Farzand, A., Rohin, M.A.K., et al. A review of syndromic forms of obesity: genetic etiology, clinical features, and molecular diagnosis. Current Issues in Molecular Biology. **2025**. 47(9): 718 https://doi.org/10.3390/cimb47090718.
13. Farzand, A., Rohin, M.A.K., et al. Nutrigenomics of obesity: integrating genomics, epigenetics, and diet–microbiome interactions for precision nutrition. Life. **2025**. 15(11): 1658 https://doi.org/10.3390/life15111658.
14. Wu, R., Chen, Y., et al. m6A methylation promotes white-to-beige fat transition by facilitating Hif1a translation. EMBO reports. **2021**. 22(11): EMBR202052348 10.15252/embr.202052348.
15. Zhao, X., Yang, Y., et al. FTO and obesity: mechanisms of association. Current diabetes reports. **2014**. 14(5): 486 DOI 10.1007/s11892-014-0486-0.
16. van der Wijst, J., Belge, H., et al. Learning physiology from inherited kidney disorders. Physiological reviews. **2019**. 99(3): 1575–1653 https://doi.org/10.1152/physrev.00008.2018.
17. Kounatidis, D., Vallianou, N.G., et al. The kidney in obesity: current evidence, perspectives and controversies. Current Obesity Reports. **2024**. 13(4): 680–702 https://doi.org/10.1007/s13679-024-00583-y.
18. Zhu, P., Herrington, W.G., et al. Conventional and genetic evidence on the association between adiposity and CKD. Journal of the American Society of Nephrology: JASN. **2020**. 32(1): 127 https://doi.org/10.1681/ASN.2020050679.
19. Kjaergaard, A.D., Teumer, A., et al. Obesity and Kidney Function: A Two-Sample Mendelian Randomization Study. Clin Chem. **2022**. 68(3): 461–472 10.1093/clinchem/hvab249.
20. Tobar, A., Ori, Y., et al. Proximal tubular hypertrophy and enlarged glomerular and proximal tubular urinary space in obese subjects with proteinuria. PloS one. **2013**. 8(9): e75547 https://doi.org/10.1371/journal.pone.0075547.
21. Rana, S. and Bhatti, A.A. Predicting anthropometric

and metabolic traits with a genetic risk score for obesity in a sample of Pakistanis. Scientific Reports. **2021**. 11(1): 8320 https://doi.org/10.1038/s41598-021-87702-0.
22. Farzand, A., Rohin, M.A.K., et al. Sociodemographic correlates of body mass index among obese adults in urban Lahore: A cross-sectional study. Obesity Medicine. **2026**: 100735 https://doi.org/10.1016/j.obmed.2026.100735.
23. Burkard, T., Mayr, M., et al. Reliability of single office blood pressure measurements. Heart. **2018**. 104(14): 1173–1179 https://doi.org/10.1136/heartjnl-2017-312523.
24. Khan, I., Khan, A., et al. CLINICAL PRACTICE BASE EGFR EQUATIONS AND THEIR APPLICATIONS IN DIFFERENT CKD POPULATIONS: A NARRATIVE REVIEW. Journal of Population Therapeutics and Clinical Pharmacology. **2023**. 30: 491–501 10.53555/jptcp.v30i16.2479.
25. Hundemer, G.L., White, C.A., et al. Performance of the 2021 race-free CKD-EPI creatinine-and cystatin C–based estimated GFR equations among kidney transplant recipients. American Journal of Kidney Diseases. **2022**. 80(4): 462–472. e1 https://doi.org/10.1053/j.ajkd.2022.03.014.
26. Jin, Y., Dong, S., et al. Urinary stress hormones and their metabolites as predictive biomarkers for CKD with diabetes. BMC nephrology. **2025**. 27(1): 75 https://doi.org/10.1186/s12882-025-04717-9.
27. Accomando, W.P., Wiencke, J.K., et al. Quantitative reconstruction of leukocyte subsets using DNA methylation. Genome biology. **2014**. 15(3): R50 10.1186/gb-2014-15-3-r50.
28. Dastgheib, S.A., Bahrami, R., et al. Evidence from a meta-analysis for association of MC4R rs17782313 and FTO rs9939609 polymorphisms with susceptibility to obesity in children. Diabetes & Metabolic Syndrome: Clinical Research & Reviews. **2021**. 15(5): 102234 https://doi.org/10.1016/j.dsx.2021.102234.
29. Chen, B., Cole, J.W., and Grond-Ginsbach, C. Departure from Hardy Weinberg equilibrium and genotyping error. Frontiers in genetics. **2017**. 8: 167 https://doi.org/10.3389/fgene.2017.00167.
30. Belsky, D.W., Moffitt, T.E., et al. Development and evaluation of a genetic risk score for obesity. Biodemography and social biology. **2013**. 59(1): 85–100. https://doi.org/10.1080/19485565.2013.774628.
31. Franceschini, N., Shara, N.M., et al. The association of genetic variants of type 2 diabetes with kidney function. Kidney Int. **2012**. 82(2): 220–5 10.1038/ki.2012.107.
32. Yang, W., Xu, H., et al. Research progress on the mechanistic impact of single-nucleotide polymorphisms and dietary pattern interactions on overweight and obesity in Chinese adults: a narrative review. Frontiers in Nutrition. **2025**. 12: 1603038 https://doi.org/10.3389/fnut.2025.1603038.
33. Kjaergaard, A.D., Teumer, A., et al. Obesity and Kidney Function: A Two-Sample Mendelian Randomization Study. Clinical Chemistry. **2022**. 68(3): 461–472 10.1093/clinchem/hvab249.
34. Koj, N., Grochowalski, Ł., et al. The association between polymorphisms near TMEM18 and the risk of obesity: a meta-analysis. BMC Med Genomics. **2021**. 14(1): 179 10.1186/s12920-021-01025-7.
35. Ghosh, S. and Bouchard, C. Considerations on efforts needed to improve our understanding of the genetics of obesity. International Journal of Obesity. **2025**. 49(2): 206–210 10.1038/s41366-024-01528-0.
36. Lee, H.H., Cho, S.M.J., et al. Real-World Adoption of the 2021 KDIGO BP Guideline in CKD. J Am Soc Nephrol. **2026**. 37(8): 1764–1772 10.1681/asn.0000001046.
37. Rana, S. and Bhatti, A.A. Predicting anthropometric and metabolic traits with a genetic risk score for obesity in a sample of Pakistanis. Sci Rep. **2021**. 11(1): 8320 10.1038/s41598-021-87702-0.

Disclaimer/Publisher's Note: The statements, opinions, and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of RES Publishers and/or the editor(s). RES Publishers and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.