Supplemental Material

STROBE Statement

	Item No.	Recommendation	Page No.	Relevant text from manuscript
Title and abstract	1	(*a*) Indicate the study's design with a commonly used term in the title or the abstract	1	
		(*b*) Provide in the abstract an informative and balanced summary of what was done and what was found	1	
Introduction				
Background/rationale	2	Explain the scientific background and rationale for the investigation being reported	2	
Objectives	3	State specific objectives, including any prespecified hypotheses	2	
Methods				
Study design	4	Present key elements of study design early in the paper	2	
Setting	5	Describe the setting, locations, and relevant dates, including periods of recruitment, exposure, follow-up, and data collection	2	
Participants	6	(*a*) *Cohort study*—Give the eligibility criteria, and the sources and methods of selection of participants. Describe methods of follow-up *Case-control study*—Give the eligibility criteria, and the sources and methods of case ascertainment and control selection. Give the rationale for the choice of cases and controls *Cross-sectional study*—Give the eligibility criteria, and the sources and methods of selection of participants	2	
		(*b*) *Cohort study*—For matched studies, give matching criteria and number of exposed and unexposed *Case-control study*—For matched studies, give matching criteria and the number of controls per case	NA	
Variables	7	Clearly define all outcomes, exposures, predictors, potential confounders, and effect modifiers. Give diagnostic criteria, if applicable	NA	

Data sources/ measurement	8*	For each variable of interest, give sources of data and details of methods of assessment (measurement). Describe comparability of assessment methods if there is more than one group	3
Bias	9	Describe any efforts to address potential sources of bias	2
Study size	10	Explain how the study size was arrived at	2

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Quantitative variables	11	Explain how quantitative variables were handled in the analyses. If applicable, describe which groupings were chosen and why	2
Statistical methods	12	(*a*) Describe all statistical methods, including those used to control for confounding	2
		(*b*) Describe any methods used to examine subgroups and interactions	2
		(*c*) Explain how missing data were addressed	2
		(*d*) *Cohort study*—If applicable, explain how loss to follow-up was addressed *Case-control study*—If applicable, explain how matching of cases and controls was addressed *Cross-sectional study*—If applicable, describe analytical methods taking account of sampling strategy	NA
		(*e*) Describe any sensitivity analyses	NA
Results			
Participants	13*	(a) Report numbers of individuals at each stage of study—eg numbers potentially eligible, examined for eligibility, confirmed eligible, included in the study, completing follow-up, and analysed	3
		(b) Give reasons for non-participation at each stage	NA
		(c) Consider use of a flow diagram	Supplemental material
Descriptive data	14*	(a) Give characteristics of study participants (eg demographic, clinical, social) and information on exposures and potential confounders	3
		(b) Indicate number of participants with missing data for each variable of interest	
		(c) *Cohort study*—Summarise follow-up time (eg, average and total amount)	
Outcome data	15*	*Cohort study*—Report numbers of outcome events or summary measures over time	*3*
		Case-control study—Report numbers in each exposure category, or summary measures of exposure	
		Cross-sectional study—Report numbers of outcome events or summary measures	
Main results	16	(*a*) Give unadjusted estimates and, if applicable, confounder-adjusted estimates and their precision (eg, 95% confidence interval). Make clear which confounders were adjusted for and why they were included	3-4
		(*b*) Report category boundaries when continuous variables were categorized	NA
		(*c*) If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period	NA

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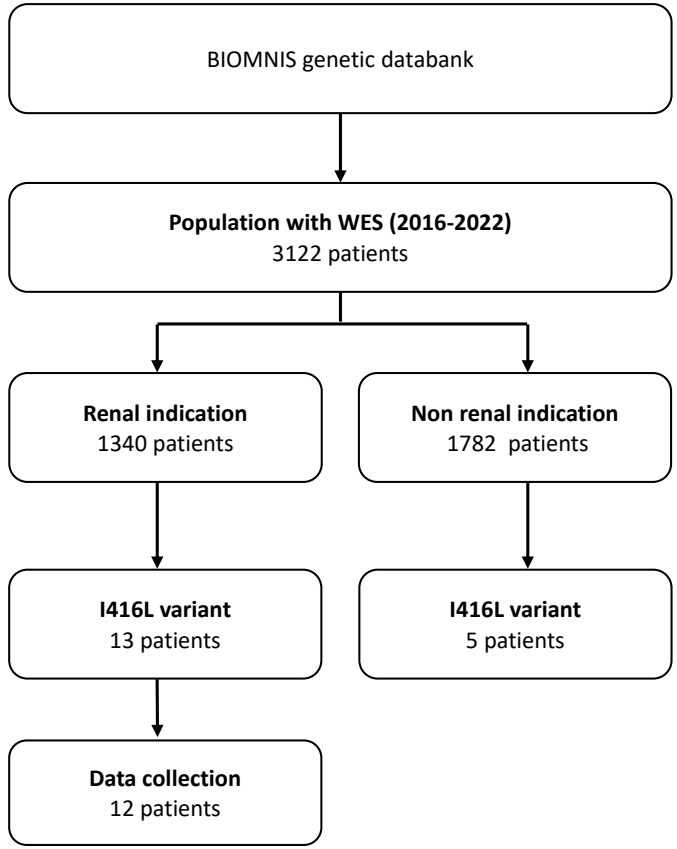
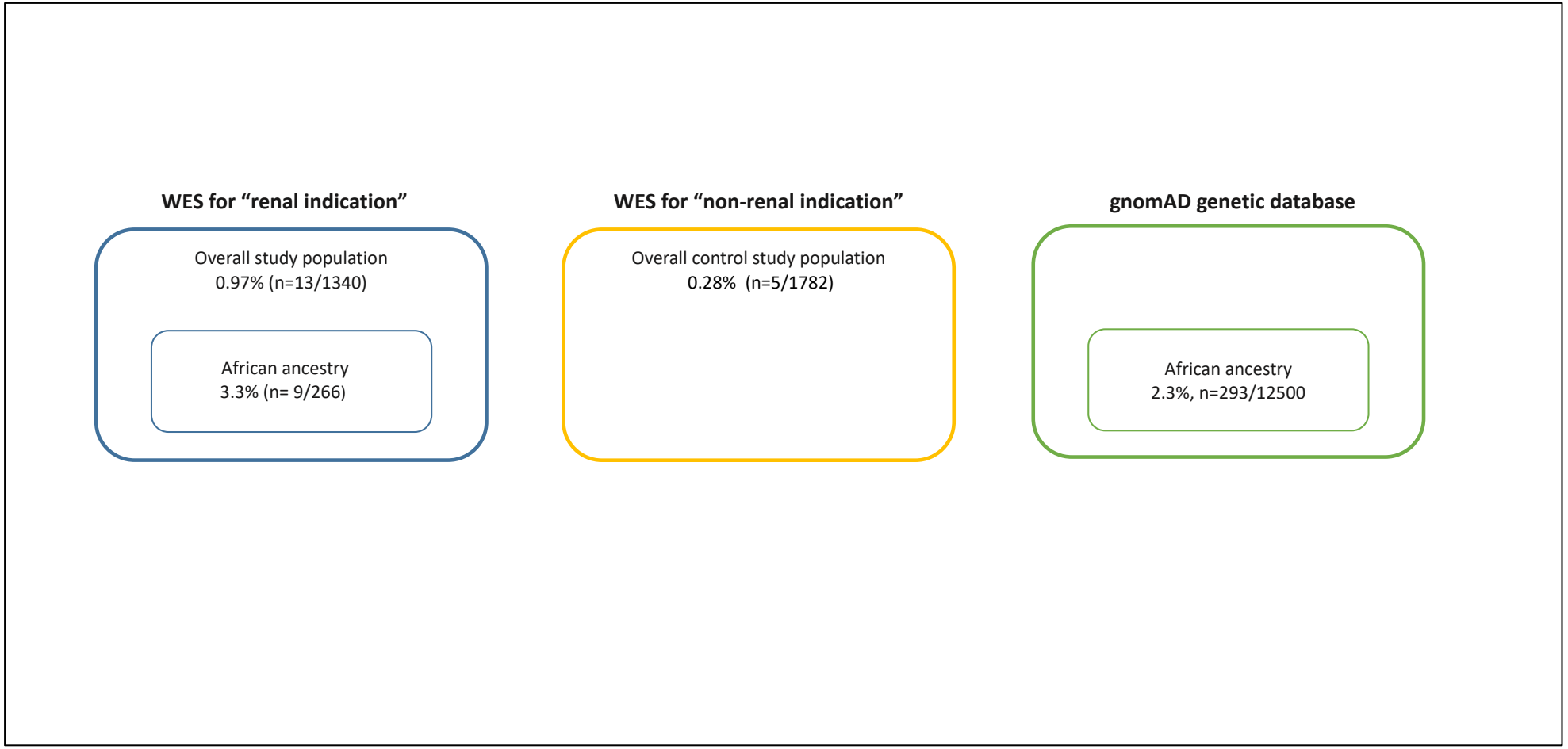
Other analyses	17	Report other analyses done—eg analyses of subgroups and interactions, and sensitivity analyses	4
Discussion			
Key results	18	Summarise key results with reference to study objectives	4
Limitations	19	Discuss limitations of the study, taking into account sources of potential bias or imprecision. Discuss both direction and magnitude of any potential bias	5
Interpretation	20	Give a cautious overall interpretation of results considering objectives, limitations, multiplicity of analyses, results from similar studies, and other relevant evidence	5
Generalisability	21	Discuss the generalisability (external validity) of the study results	6
Other information			
Funding	22	Give the source of funding and the role of the funders for the present study and, if applicable, for the original study on which the present article is based	6



Supplementary Figure S1: Selection of participants



Supplementary Figure S2: Prevalence of the CFI I416L variant in the different study populations and other genomic databanks (ppt)

Supplementary references

S1. Richards S, Aziz N, Bale S, et al. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. *Genet Med Off J Am Coll Med Genet*. 2015;17(5):405-424. doi:10.1038/gim.2015.30

S2. Jlajla H, Dehman F, Jallouli M, et al. Molecular basis of complement factor I deficiency in Tunisian atypical haemolytic and uraemic syndrome patients. *Nephrology*. 2019;24(3):357-364. doi:10.1111/nep.13217

S3. Larsen CP, Wilson JD, Best-Rocha A, Beggs ML, Hennigar RA. Genetic testing of complement and coagulation pathways in patients with severe hypertension and renal microangiopathy. *Mod Pathol Off J U S Can Acad Pathol Inc*. 2018;31(3):488-494. doi:10.1038/modpathol.2017.154

S4. rs61733901 RefSNP Report - dbSNP - NCBI. Accessed September 4, 2022. https://www.ncbi.nlm.nih.gov/snp/rs61733901#frequency_tab

S5. 4-110667561-T-G | gnomAD v2.1.1 | gnomAD. Accessed September 9, 2022. https://gnomad.broadinstitute.org/variant/4-110667561-T-G?dataset=gnomad_r2_1

S6. Zhang Y, Goodfellow RX, Ghiringhelli Borsa N, et al. Complement Factor I Variants in Complement-Mediated Renal Diseases. *Front Immunol*. 2022;13:866330. doi:10.3389/fimmu.2022.866330

S7. Leon J, LeStang MB, Sberro-Soussan R, et al. Complement-driven hemolytic uremic syndrome. *Am J Hematol*. 2023;98 Suppl 4:S44-S56. doi:10.1002/ajh.26854

S8. Fakhouri F, Frémeaux-Bacchi V. Thrombotic microangiopathy in aHUS and beyond: clinical clues from complement genetics. *Nat Rev Nephrol*. 2021;17(8):543-553. doi:10.1038/s41581-021-00424-4

S9. Ruhl AP, Jeffries N, Yang Y, et al. Alpha Globin Gene Copy Number Is Associated with Prevalent Chronic Kidney Disease and Incident End-Stage Kidney Disease among Black Americans. *J Am Soc Nephrol JASN*. 2022;33(1):213-224. doi:10.1681/ASN.2021050653

S10. Grams ME, Rebholz CM, Chen Y, et al. Race, APOL1 Risk, and eGFR Decline in the General Population. *J Am Soc Nephrol JASN*. 2016;27(9):2842-2850. doi:10.1681/ASN.2015070763

S11. Timmermans SAMEG, Damoiseaux JGMC, Werion A, Reutelingsperger CP, Morelle J, van Paassen P. Functional and Genetic Landscape of Complement Dysregulation Along the Spectrum of Thrombotic Microangiopathy and its Potential Implications on Clinical Outcomes. *Kidney Int Rep*. 2021;6(4):1099-1109. doi:10.1016/j.ekir.2021.01.034

Supplementary information is available at *KI Report's* **website.**