Supplemental Appendix

For the paper titled:

Apolipoprotein L1 high-risk genotypes and albuminuria in Sub-Saharan African populations

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Supplemental Table 1: *APOL1* haplotypes (referred to as alleles G0, G1 and G2 for ease of comparison to other literature) based on three polymorphic loci on chromosome 22

***APOL1* alleles**	**rs73885319 (36661906)***	**rs60910145 (36662034)***	**rs71785313 (36662041)***
G0	A	T	I : AATAATT
G1	G	G	I : AATAATT
	G	T	I : AATAATT
G2	A	T	A

* nucleotide positions based on build hg19

Supplemental Table 2: Quality of imputation for the three variant positions and *APOL1* G0, G1 and G2 risk alleles on chromosome 22

			Risk alleles	Risk alleles	rs73885319			rs60910145			rs71785313			Risk alleles			
[1]Dataset	[2]Ancestry	Population	[3]N (WGS)	[4]N (Imp)	[5] % Diff	[6]Freq (Imp)	[7]Freq (WGS)	% Diff	Freq (Imp)	Freq (WGS)	% Diff	Freq (Imp)	Freq (WGS)	G0	G1	G2	[8]% Diff
1000G	AFR	Esan, Nigeria	198	198	0	50.5	50.5	0.0	49.5	49.5	2.0	12.6	11.6	37.9	49.5	12.6	2.0
1000G	AFR	Yoruba, Ibadan, Nigeria	216	216	0	62.5	62.5	0.0	37.5	37.5	0.0	7.9	7.9	54.6	37.5	7.9	0.0
1000G	AFR	Gambia, Western Divisions	226	226	0	75.7	75.7	0.0	24.3	24.3	0.9	19.9	19.5	55.8	24.3	19.9	0.9
1000G	AFR	Afro-Caribbean, Barbados	192	192	0	74.0	74.0	0.0	25.5	25.5	0.0	13.0	13.0	60.9	26.0	13.0	0.0
1000G	SAS	Bengali, Bangladesh	172	172	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
1000G	EUR	British, United Kingdom	182	182	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
1000G	EAS	Dai, Xishuangbanna, China	186	186	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
1000G	AMR	Colombian, Medellin, Colombia	188	188	0	100.0	100.0	0.0	0.0	0.0	0.0	0.5	0.5	99.5	0.0	0.5	0.0
1000G	EUR	Finnish, Finland	198	198	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
1000G	SAS	Gujarati Indian, Houston, Texas	206	206	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
1000G	EAS	Han, Beijing, China	206	206	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
1000G	SAS	Indian Telugu, United Kingdom	204	204	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
1000G	EAS	Japanese, Tokyo, Japan	208	208	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
1000G	EAS	Kinh, Ho Chi Minh City, Vietnam	198	198	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
1000G	AFR	African Ancestry, South-West USA	122	122	0	77.9	77.9	0.0	22.1	22.1	0.0	9.8	9.8	68.0	22.1	9.8	0.0
1000G	AMR	Mexican Ancestry, Los Angeles, USA	128	128	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
1000G	AFR	Mende, Sierra Leone	170	170	0	87.6	87.6	0.0	12.4	12.4	0.0	18.2	18.2	69.4	12.4	18.2	0.0
1000G	AMR	Peruvian, Lima, Peru	170	170	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
1000G	AMR	Puerto Rican, Puerto Rico	208	208	0	97.1	97.1	0.0	2.9	2.9	0.0	2.4	2.4	94.7	2.9	2.4	0.0
1000G	SAS	Punjabi, Lahore, Pakistan	192	192	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
AWIWGS	AFR	Agincourt, South Africa	48	48	0	95.8	95.8	0.0	4.2	4.2	0.0	25.0	25.0	70.8	4.2	25.0	0.0
1000G	EAS	Southern Han, China	210	210	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
1000G	SAS	Sri Lankan Tamil, United Kingdom	204	204	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
1000G	EUR	Toscani, Italy	214	214	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0

			Risk alleles	Risk alleles	rs73885319			rs60910145			rs71785313			Risk alleles			
[1]Dataset	[2]Ancestry	Population	[3]N (WGS)	[4]N (Imp)	[5] % Diff	[6]Freq (Imp)	[7]Freq (WGS)	% Diff	Freq (Imp)	Freq (WGS)	% Diff	Freq (Imp)	Freq (WGS)	G0	G1	G2	[8]% Diff
1000G	EUR	Utah, USA	198	198	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
AWIWGS	AFR	Soweto, South Africa	100	100	0	89.0	89.0	0.0	11.0	11.0	2.0	17.0	16.0	72.0	11.0	17.0	2.0
AGVP	AFR	Zulu, South Africa	200	200	0	87.5	87.5	1.0	12.5	12.0	2.0	15.0	15.0	72.5	12.5	15.0	2.0
AWIWGS	AFR	Dikgale, South Africa	52	52	0	92.3	92.3	0.0	7.7	7.7	0.0	17.3	17.3	75.0	7.7	17.3	0.0
1000G	EUR	Iberian, Spain	214	214	0	100.0	100.0	0.0	0.0	0.0	0.9	0.5	0.0	99.5	0.0	0.5	0.9
1000G	AFR	Luhya, Webuye, Kenya	198	198	0	94.4	94.4	0.0	5.6	5.6	1.0	8.6	9.1	85.9	5.6	8.6	1.0
AGVP	AFR	Baganda, Uganda	200	200	0	94.5	94.5	0.0	5.5	5.5	3.0	8.0	7.5	86.5	5.5	8.0	3.0
AGVP	AFR	Somali, Somalia	48	48	0	100.0	100.0	0.0	0.0	0.0	0.0	2.1	2.1	97.9	0.0	2.1	0.0
AGVP	AFR	Gumuz, Ethiopia	48	48	0	100.0	100.0	0.0	0.0	0.0	4.2	2.1	4.2	97.9	0.0	2.1	4.2
AGVP	AFR	Amhara, Ethiopia	48	48	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
AGVP	AFR	Oromo, Ethiopia	48	48	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
AGVP	AFR	Wolayta, Ethiopia	48	48	0	100.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0
AGVP/ 1000G/ AWI-WGS	AFR	-	1081	1081	0	81.6	81.6	0.1	18.2	18.2	1.0	11.9	11.9	69.8	18.3	11.9	1.0

[1]Dataset - Dataset of populations (1000G - 1000 Genomes Project; AWIWGS - AWI-GEN whole genome sequencing; AGVP - African Genome Variation Project).
[2]Ancestry - ancestry of sample, AFR - African, SAS - South Asian, EAS - East Asian, AMR - Add Mixed American, EUR – European.
[3]N (WGS) - individual number extracted from whole genome sequencing.
[4]N (Imp) - individual number extracted from imputation.
[5]% Diff - percent difference between frequencies using whole genome sequencing and frequencies after imputation of 36661906, 36662034, 36662034.
[6]Freq (Imp) - frequencies after imputation of 36661906, 36662034, 36662034.
[7]Freq (WGS) - frequencies from whole genome sequencing of 36661906, 36662034, 36662034.
[8]% Diff - percent difference between frequencies using whole genome sequencing and from imputation of G0, G1 and G2.

Supplemental Table 3: *APOL1* alleles and high-risk genotypes using recessive models by ethnicity (data used for Figure 1 in the manuscript)

Ethnicity	N	G0 (%)	G1 (%)	G2 (%)	High-risk* Genotypes (%)	African Region
Kamba	656	86	5	9	1	East
Kikuyu	1292	90	4	6	1	East
Kisii	94	87	4	9	0.0	East
Luhya	554	87	7	7	1	East
Luo	714	85	7	9	2	East
Somali	96	100	0	0	0	East
Bapedi	2314	76	7	17	5	South
Ndebele	72	75	10	15	6	South
Sotho	762	77	8	16	6	South
Swati	298	70	11	20	7	South
Tsonga	4188	66	10	24	12	South
Tswana	480	78	9	14	7	South
Venda	158	68	10	22	17	South
Xhosa	348	76	14	10	8	South
Zulu	1272	74	10	16	8	South
Bulsa	84	70	10	20	7	West
Gourounsi	204	75	12	13	3	West
Kassena	1962	75	13	12	5	West
Mossi	3700	78	13	9	5	West
Nankana	1540	77	11	13	5	West

*Kidney disease risk was determined by the number of risk alleles carried: high-risk genotypes comprised 2 risk alleles in any combination (G1/G1; G1/G2; G2/G2);
Categories reported as number (N) and percent (%); percentages may sum to +/- 100 from rounding up

Supplemental Table 4: *APOL1* risk alleles and associated risk factors for kidney disease across the combined dataset of the Africa Wits-International Network for the Demographic Evaluation of Populations and their Health Partnership for Genomic Studies (AWI-Gen)

Variable[1]	Overall	*APOL1* risk alleles		
		0	1	2
Sample size[2]	**N=10,769**	**N=6,275**	**N=3,844**	**N=650**
Age - years	52 (8)	51 (8)	52 (9)	53 (9)
Male N (%)	4,876 (45)	2,847 (45)	1,743 (45)	286 (44)
Female N (%)	5,893 (55)	3,428 (55)	2,101 (55)	364 (56)
Diabetes mellitus N (%)	695/10,642 (7)	403/6,204 (6)	246/3,796 (6)	46/642 (7)
Hypertension N (%)	3,992/10,769 (37)	2,209/6,275 (35)	1,501/3,844 (39)	282/650 (43)
HIV infection N (%)	1,318/9,970 (13)	754/5,812 (13)	471/3,552 (13)	93/606 (15)
BMI (kg/m^2)[3,4]	**N=10,313**	**N=6,011**	**N=3,680**	**N=622**
Underweight (<18.5)	1,175 (11)	708 (12)	410 (11)	57 (9)
Normal (18.5-24.9)	5,055 (49)	3,014 (50)	1,783 (49)	258 (43)
Overweight (25.0-29.9)	1,961 (19)	1,172 (19)	681 (19)	108 (18)
Obese (30.0 +)	2,122 (21)	1,174 (19)	765 (21)	183 (30)
Socioeconomic status as quintiles[5,6]	**N=10619**	**N=6205**	**N=3771**	**N=643**
1	1,572 (15)	883 (14)	576 (15)	113 (18)
2	2,322 (22)	1,347 (22)	834 (22)	141 (22)
3	1,846 (17)	1,105 (18)	638 (17)	103 (16)
4	2,250 (21)	1,320 (21)	804 (21)	126 (20)
5	2,629 (25)	1,550 (25)	919 (24)	160 (25)

[1]All data reported as mean (SD) unless stated otherwise; categories reported as number (N) and percent (%); percentages may sum to +/- 100 due to rounding up

[2]Where sample sizes differed from what is represented for the variable, the sample size was included as a denominator

[3]BMI: WHO classification for body ass index (https://www.euro.who.int/en/health-topics/disease-prevention/nutrition/a-healthy-lifestyle/body-mass-index-bmi).

[4]BMI: missing data N=456/10,769 (4%)

[4]Socioeconomic status: assessed using a validated tool appropriate for assessing wealth in low income settings, household assests are scored, and based on the score, data a represented by quintile, with the poorest in the first quintile[1].

[5]Socioeconomic status: missing data N=150/10,769 (1%)

Reference:
1. Ali SA, Soo C, Agongo G, Alberts M, Amenga-Etego L, Boua RP, Choudhury A, Crowther NJ, Depuur C, Gómez-Olivé FX: Genomic and environmental risk factors for cardiometabolic diseases in Africa: methods used for Phase 1 of the AWI-Gen population cross-sectional study. *Global Health Action*, 11: 1507133, 2018.

Supplemental Table 5: *APOL1* associations with albuminuria across the Africa Wits-International Network for the Demographic Evaluation of Populations and their Health Partnership for Genomic Studies (AWI-Gen) study sites

Site	Recessive OR (95% CI)	Dominant OR (95% CI)	Additive OR (95% CI)
Agincourt South Africa	**1.75 (1.12 – 2.56)**	1.03 (0.79 – 1.37)	1.18 (0.96 – 1.44)
Soweto South Africa	1.07 (0.43 – 2.68)	1.15 (0.74 – 1.79)	1.10 (0.77 – 1.58)
Digkale South Africa	1.12 (0.54 – 2.66)	1.13 (0.76 – 1.71)	1.12 (0.81 – 1.54)
Nairobi Kenya	2.78 (0.75 – 10.39)	1.10 (0.73 – 1.65)	1.16 (0.80 – 1.68)
Nanoro Burkina Faso	**2.37 (1.21 – 4.62)**	1.74 (1.19 – 2.54)	**1.64 (1.22 – 2.22)**
Navrongo Ghana	1.68 (0.78 – 3.63)	0.95 (0.64 – 1.42)	1.05 (0.75 – 1.46)

For each model (recessive, dominant, additive) the associations between *APOL1* risk alleles and albuminuria are presented as the odd ratio (95% confidence interval).
Models were adjusted for age, sex, BMI, diabetes mellitus status, hypertension status, and HIV status.

Supplemental Table 6: Association (OR (95% CI) between *APOL1* using additive, dominant, and recessive models and albuminuria alone, or as a composite endpoint

	Albuminuria[1]		Composite endpoint[2]	
Model*	BMI[3] adjusted	BMI unadjusted	BMI adjusted	BMI unadjusted
Additive	1.39 (1.09-1.76)	1.37 (1.08-1.74)	1.16 (0.93-1.45)	1.16 (0.93-1.45)
Dominant	1.12 (0.97-1.31)	1.12 (0.97-1.30)	1.03 (0.90-1.19)	1.03 (0.90-1.19)
Recessive	1.63 (1.25-2.12)	1.59 (1.22-2.08)	1.37 (1.06-1.78)	1.36 (1.05-1.76)

*adjusted for site as a random variable; and age, sex, diabetes mellitus status, hypertension status, and HIV status as fixed variables

[1]Albuminuria: defined as albumin:creatinine ratio >30mg/g

[2]Composite endpoint: defined as low eGFR (eGFR <60ml/min/1.73m^2) and/or albuminuria

[3]BMI: body mass index

Supplemental Table 7: Association (OR (95% CI) between *APOL1* using additive, dominant, and recessive models and albuminuria, low eGFR, and the composite endpoint

	Albuminuria[1]		Composite endpoint[2]		Low eGFR[3]	
Model*	SES[4] adjusted	SES unadjusted	SES adjusted	SES unadjusted	SES adjusted	SES unadjusted
Additive	1.39 (1.09-1.76)	1.39 (1.09-1.76)	1.16 (0.93-1.45)	1.16 (0.93-1.45)	0.78 (0.52-1.19)	0.79 (0.52-1.19)
Dominant	1.12 (0.97-1.31)	1.13 (0.97-1.31)	1.03 (0.90-1.19)	1.03 (0.90-1.19)	0.86 (0.67-1.11)	0.86 (0.67-1.11)
Recessive	1.63 (1.25-2.12)	1.63 (1.25-2.12)	1.37 (1.06-1.78)	1.37 (1.06-1.78)	0.87 (0.52-1.47)	0.87 (0.52-1.48)

*adjusted for site as a random variable; and age, sex, diabetes mellitus status, hypertension status, and HIV status as fixed variables

[1]Albuminuria: defined as albumin:creatinine ratio >30mg/g

[2]Composite endpoint: defined as low eGFR and/ or albuminuria

[3]low eGFR: defined as eGFR <60ml/min/1.73m^2

[4]SES: socioeconomic status

Supplemental Table 8: Effect of genotypes (G1/G1 compared to G2/G2) on biomarkers of kidney disease

Biomarkers of kidney disease	Odds ratio (95% CI); p-value
Albuminuria (ACR >30mg/g)	2.19 (1.01-4.76); p=0.047
Low eGFR (eGFR<60ml/min/1.73m^2)	0.44 (0.05-3.93); p=0.46
Composite endpoint (albuminuria and/or low eGFR)	1.8 (0.83-3.9); p=0.137

Logistic mixed models were adjusted for site as a random variable and age, sex, BMI, diabetes mellitus status, hypertension status and HIV status as fixed variables

Supplemental Table 9: APOL1 associations with low eGFR[1] stratified by diabetes, hypertension, and HIV status

Comorbidity Status	Low eGFR[1] n/N (%)	Low eGFR[1] (OR (95% CI) (age + sex adjusted model)[2]	Low eGFR[1] (OR 95% CI) (fully-adjusted model)[3]	P interaction term (age +sex adjusted model)[2]
Diabetes				
Absent	285/9,861 (2.9)	1.19 (0.76-1.86)	1.05 (0.62-1.77)	0.10
Present	58/687 (8.4)	0.20 (0.03-1.49)	N/A[4]	
Hypertension				
Absent	141/6,708 (2.1)	0.76 (0.33-1.75)	0.43 (0.13-1.37)	0.39
Present	206/3,934 (5.2)	1.07 (0.64-1.81)	1.15 (0.63-2.08)	
HIV				
Negative	255/8,582 (3.0)	0.78 (0.45-1.36)	0.66 (0.35-1.27)	0.11
Positive	54/1,290 (4.2)	1.80 (0.73-4.43)	1.8 (0.72-4.48)	

[1] Low eGFR: eGFR <60ml/min/1.73m^2

[2] Logistic mixed models were adjusted for age and sex as fixed variables

[3] Logistic mixed models were adjusted for site as a random variable and age, sex, BMI, diabetes mellitus status, hypertension status and HIV status as fixed variables. Some participants were excluded from the fully adjusted model due to missing data.

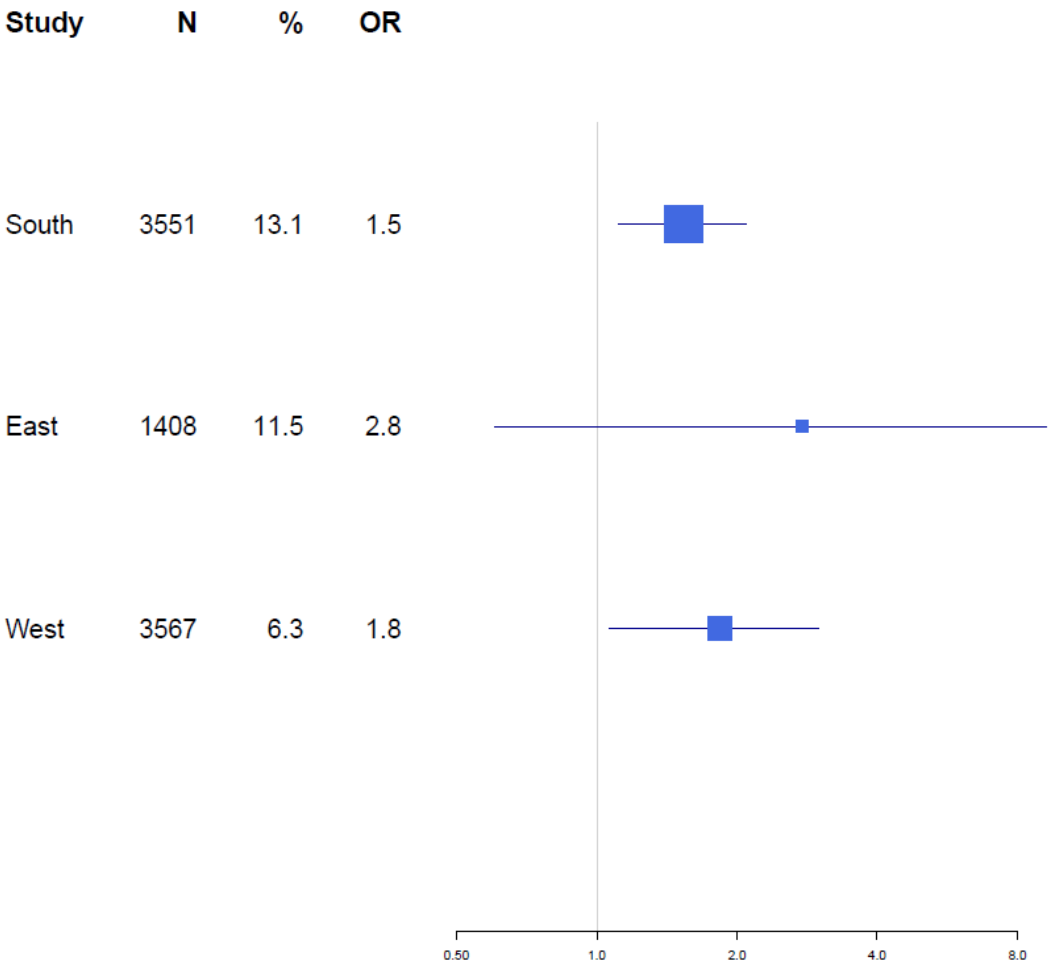
[4] N/A: not applicable as data too few for statistical analysis

Supplemental Table 10: APOL1 associations with the composite endpoint[1] stratified by diabetes, hypertension, and HIV status

Comorbidity Status	Composite endpoint[1] n/N (%)	Composite endpoint[1] (OR (95% CI) (age + sex adjusted model)[2]	Composite endpoint[1] (OR 95% CI) (fully-adjusted model)[3]	P interaction term (age +sex adjusted model)[2]
Diabetes				
Absent	910/8,222 (11.1)	1.49 (1.15-1.93)	1.47 (1.12-1.92)	0.14
Present	150/520 (28.8)	0.81 (0.35-1.88)	0.69 (0.28-1.67)	
Hypertension				
Absent	474/5,744 (8.3)	1.57 (1.08-2.26)	1.61 (1.11-2.34)	0.23
Present	600/3,071 (19.5)	1.24 (0.88-1.74)	1.18 (0.83-1.69)	
HIV				
Negative	808/7,465 (10.8)	1.34 (1.01-1.79)	1.36 (1.01-1.82)	0.99
Positive	223/1,105 (20.2)	1.39 (0.8-2.38)	1.4 (0.81-2.42)	

[1] Composite endpoint: low eGFR and/or albuminuria
[2] Logistic mixed models were adjusted for age and sex as fixed variables
[3] Logistic mixed models were adjusted for site as a random variable and age, sex, BMI, diabetes mellitus status, hypertension status and HIV status as fixed variables. Some participants were excluded from the fully adjusted model due to missing data.

Supplemental Figure 1: Forest plot: association between high-risk *APOL1* genotypes (OR (95%CI)) and albuminuria by region



Regions: **East**: East Africa (Kenya); **West**: West Africa (Burkina Faso and Ghana); **South**: South Africa.
OR (odds ratio) with 95% CI (confidence interval).

Supplemental Appendix 1: Comparison of models between eGFR using CKD-EPI 2009 and CKD-EPI 2021

Objectives

We have compared the CKD-EPI (creatinine) equation (2009)[1] with the CKD-EPI (creatinine) equation (2021)[2]. From our perspective, race-based coefficients for the MDRD and CKD-EPI equations have only been validated in a handful of small studies in Africa and are known to overestimate GFR in continental African populations[3-7]. As such, we exclude adjustments for race (based on African Americans) in the estimation of GFR in Africa. Even without race-based adjustments, the eGFR equations still appear to overestimate GFR, thus underdiagnosing CKD.

Results

As a case in point in our dataset, when we used the CKD-EPI(creatinine) equation (2009) without race-based adjustment, the prevalence of CKD (defined as eGFR <60ml/min/1.73m^2) was 347/10,642 (3.3%). However, when we used the CKD-EPI (creatinine) 2021 equation, CKD prevalence was reduced to 2.5% with 81 individuals reclassified by CKD stage. In the absence of a comparison to a gold standard measured GFR, we have no way to ascertain whether the observed changes are true or reflect an artefact of the modelling.

We have included the comparison of the two CKD-EPI equations for your perusal (see below):

1. **Figure A** demonstrates the correlation with a coefficient of determination $R^2 = 0.996$
2. **Figure B** demonstrates the associations between eGFR and additive, dominant, and recessive models for *APOL1* risk alleles for each equation

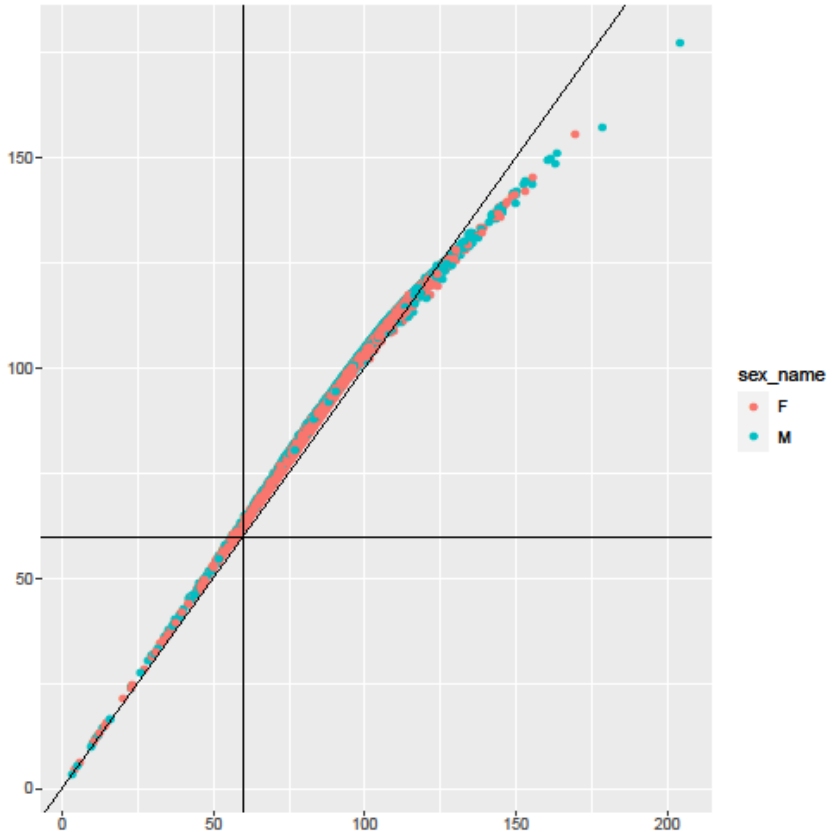


Figure A Correlation between CKD-EPI (creatinine) 2021 equation (y-axis) and CKD-EPI (creatinine) 2009 equation (x-axis)

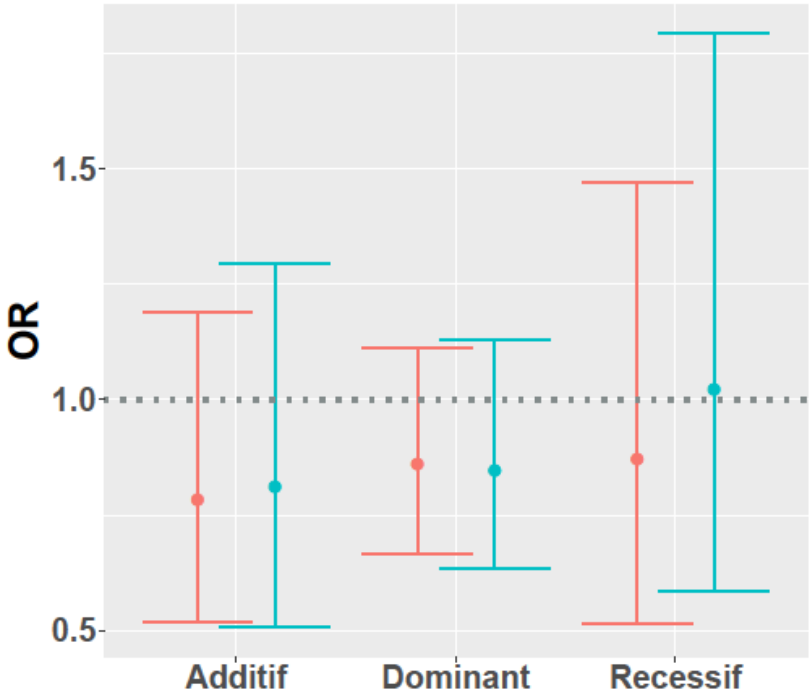


Figure B Association between eGFR calculated using CKD-EPI (creatinine) 2009 (orange) and CKD-EPI (creatinine) 2021 (blue) and additive, dominant, and recessive models for *APOL1* risk alleles; OR (odds ratio) with 95% CI (confidence interval)

Conclusion

Since the differences between both CKD-EPI equations are so small, we would prefer to use the CKD-EPI (creatinine) 2009 equation so our results can be compared to other published results using the CKD-EPI (2009) equation.

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Supplemental Appendix 2: H3Africa Consortium AWI-Gen Study

Core AWI-Gen group to be acknowledged in publications

The table below shows the members of the AWI-Gen Study who contributed significantly to the work of the study. Authors of specific papers are solely responsible for the papers to which their names are attached; membership of the study does not in itself imply that the person takes responsibility for any paper.

Key AWI-Gen contributors over extended period

Centre	Names	Affiliation	AWI-Gen 1	AWI-Gen 2
Agincourt	Stephen Tollman	7, 8	√	√
	Alisha Wade	7	√	√
	Chodziwadziwa Kabudula	7	√	√
	Daniel Ohene-Kwofie	7	√	√
	F. Xavier Gómez-Olivé	7, 8	√	√
	Floidy Wafawanaka	7	√	√
	Kathleen Kahn	7, 8	√	√
	Mwawi Gondwe	7		√
	Rhian Twine	7	√	√
	Ryan Wagner	7, 8	√	√
APHRC	Catherine Kyobutungi	12	√	√
	Christopher Khayeka-Wandabwa	12	√	
	Gershim Asiki	12	√	√
	Isaac Kisiangani	12	√	√
	Shukri Mohamed	12	√	√
DIMAMO	Marianne Alberts **§**	14	√	√
	Solomon Choma	14		√
	Felistas Mashinya	14	√	
	Given Mashaba	14		√
Nanoro	Halidou Tinto	13	√	√
	Herman Sorgho	13	√	√
	Palwendé Romuald Boua	13	√	√
Navrongo	Abraham R Oduro	11	√	√
	Godfred Agongo	11	√	√
	Cornelius Debpuur	11	√	√
	Engelbert Nonterah	11	√	√
Soweto	Shane A Norris	5, 6	√	√
	Lisa Micklesfield	5	√	√
	Vukosi Baloyi	5	√	√
Wits/WHC	Michèle Ramsay	2, 4	√	√
	Ananyo Choudhury	2	√	√
	Busisiwe Mthembu	2		√
	Cassandra Soo	2	√	√
	Dhriti Sengupta	2	√	√
	Ernest Tambo	2	√	
	Francisco Camiña Ceballos	2	√	

	Freedom Mukomana	2	√	√
	Furahini Tluway	2		√
	Henry Wandera	2	√	√
	Himla Soodyall	4	√	
	Jean-Tristan Brandenburg	2	√	
	Natalie Smyth	2	√	√
	Nigel Crowther	16	√	√
	Ovokeraye Oduaran	2	√	√
	Scott Hazelhurst	2, 9	√	√
	Stuart Ali	2	√	√
	Theo Mathema	2	√	√
	Tinashe Chikowore	2	√	
	Yaniv Swiel	2, 9	√	√
	Zané Lombard	4	√	
INDEPTH	Osman Sankoh	8	√	
UG	Pauline Tindana	11, 15	√	√

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