# Genetic Association and Transferability for Urinary Albumin-Creatinine Ratio as a Marker of Kidney Disease in four Sub-Saharan African Populations and non-continental Individuals of African Ancestry

## Jean-Tristan Brandenburg April 4, 2024

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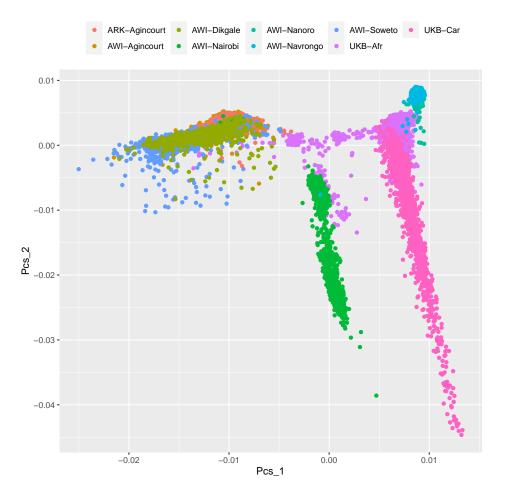


Figure S1: Genetic Diversity of pooled samples using PC1 and 2

AWIGEN: Africa Wits-INDEPTH partnership for Genomic Studies ; ARK: African Research on Kidney Disease Study; UKB: UK Biobank

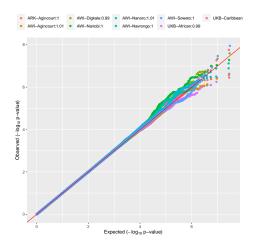


Figure S2a: QQ plot and lambda value for UKB-African, UKB-Caribbean, AWI-Agincourt, ARK-Agincourt, AWI-Dikgale, AWI-Navrongo, AWI-Nanoro, AWI-Soweto and AWI-Nairobi

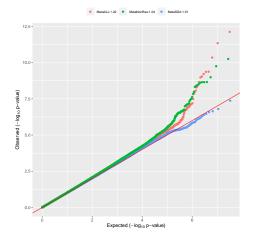


Figure S2b: QQ plot and lambda value for  $\rm Meta_{SSA},\, Meta_{ALL}$  and  $\rm Meta_{NONRES}$ 

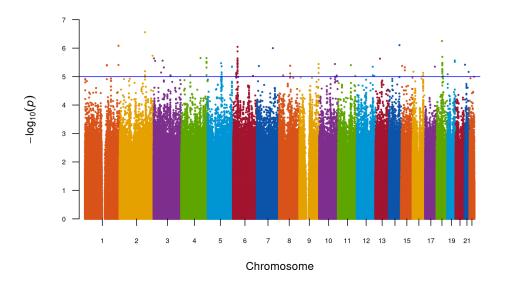


Figure S3a: Manhattan plot for UKB-African

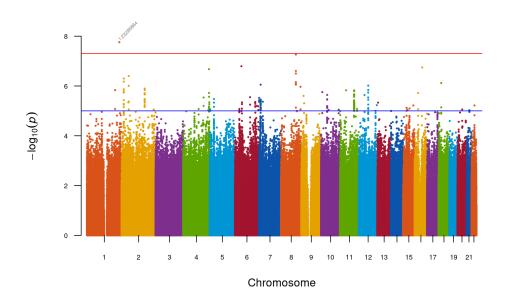


Figure S3b: Manhattan plot for UKB-Caribbean

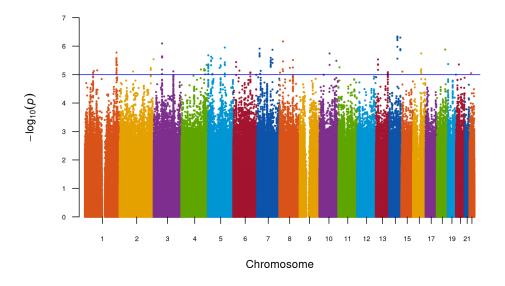


Figure S3c: Manhattan plot for ARK-Agincourt

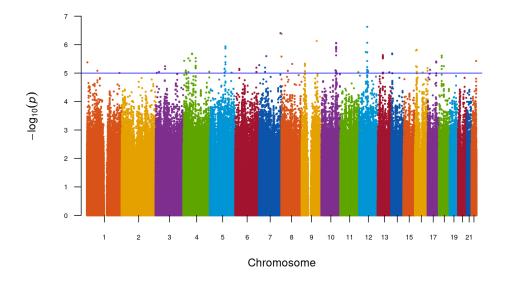


Figure S3d: Manhattan plot for AWI-Agincourt

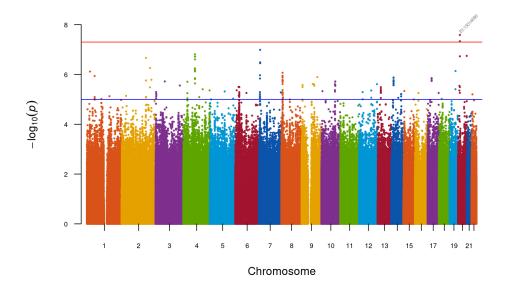


Figure S3e: Manhattan plot for AWI-Dikgale

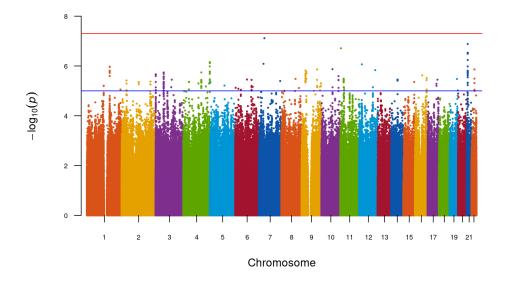


Figure S3f: Manhattan plot for AWI-Nanoro

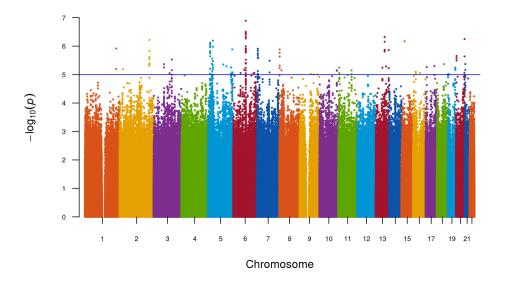


Figure S3g: Manhattan plot for AWI-Navrongo

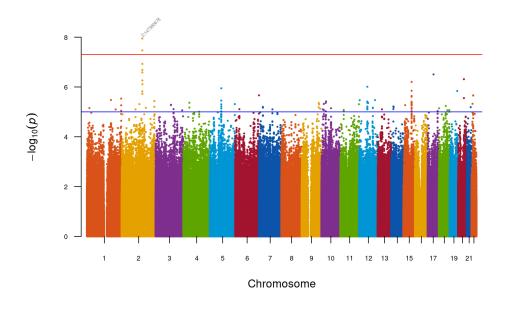


Figure S3h: Manhattan plot for AWI-Soweto

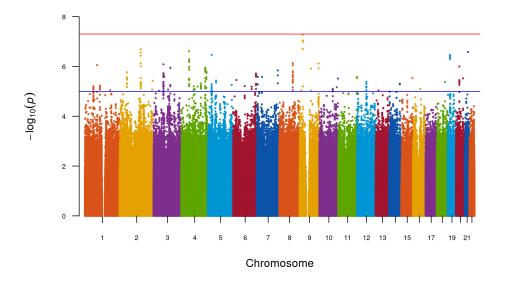


Figure S3i: Manhattan plot for AWI-Nairobi

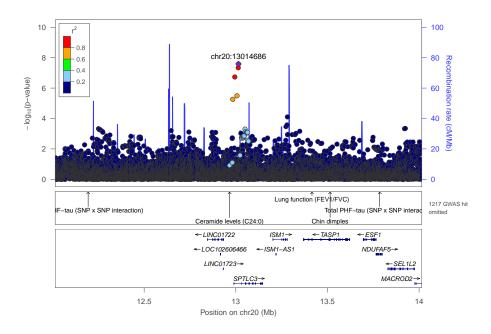


Figure S4a: Regional plot around rs2052976 (20-13014686) using AWI-Dikgale results

rs 2052976 found significant in AWI-Dikgale, regional plot had been done using locus zoom with a windows of 1MB around and LD had been estimated using sample from AWI-Dikgale

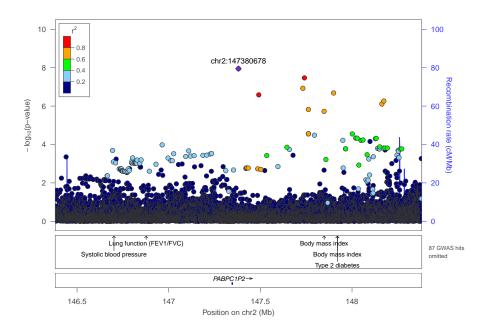


Figure S4b: Regional plot around  ${\rm rs}147938214$  (2-147380678) using AWI-Soweto results

 ${\rm rs} 147938214 \ {\rm found \ significant \ in \ AWI-Soweto, \ regional \ plot \ had \ been \ done}$  using locuszoom with a windows of 1MB around and LD had been estimated using sample from AWI-Soweto

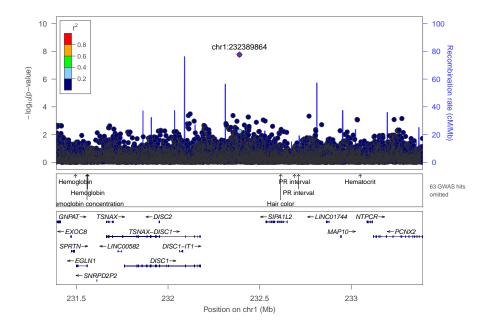


Figure S4c: Regional plot around  ${\rm rs}12067862$  (1-232,389,864) using UKB-Caribbean results

rs 12067862 found significant in UKB-Caribbean, regional plot had been done using locus zoom with a windows of 1MB around and LD had been estimated using sample from UKB-Caribbean

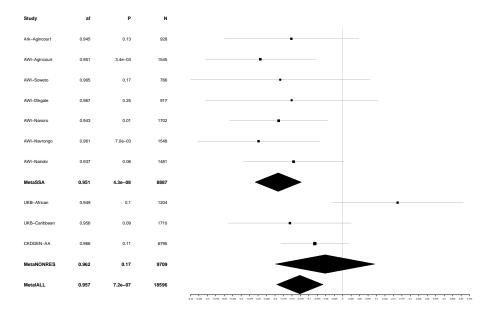


Figure S5: Forest plot (beta, se) and af, p-value and N for each dataset and meta analysis result of rs9505286 (chr6,7820353) found significant in Meta\_{SSA}

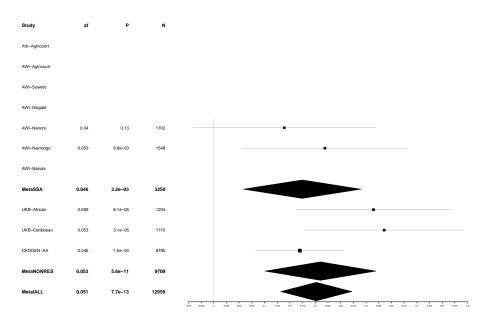
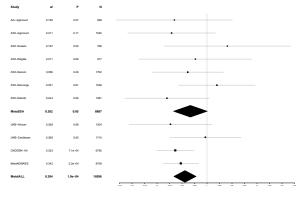
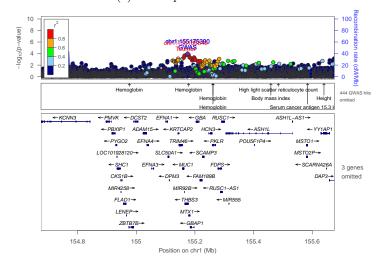


Figure S6: Forest plot (beta, se) and af, p-value and N for each dataset and meta analysis of rs73404549 (chr11,5320654) found significant in  $\rm Meta_{NONRES}$ ,  $\rm Meta_{ALL}$ 



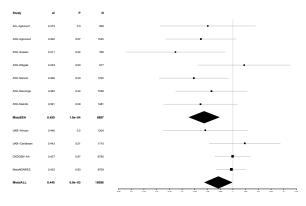




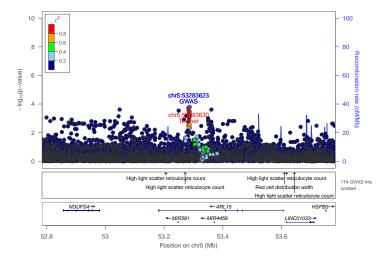
(b) Regional plot around rs370545 in  $Meta_{ALL}$ 

Figure S7: Replication of THBS3 regions identified in CKDGEN-EA : forest plot of lead SNPs identified in Meta\_SSA rs370545 (a) and regional plot around (b)

regional plot had been perforned using locus zoom, using  $LD_{ALL}$ , lead SNPs identified in Meta<sub>ALL</sub> are annotated in blue and Significant SNPs identified in CKDGEN-EA are highligth in red (b)



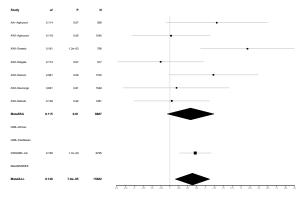
### (a) Forest plot of rs1694067



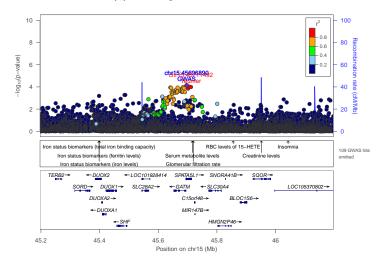
(b) Regional plot using Metassa and CKDGEN-MA

Figure S8: Replication of ARL15 regions identified in CKDGEN-EA and CKDGEN-MA : forest plot of lead SNPs identified in Meta<sub>SSA</sub> rs1694067 (a) and regional plot around (b)

regional plot had been perforned using locus zoom, using  $LD_{SSA}$ , lead SNPs identified in Meta<sub>SSA</sub> are annotated in blue and Significant SNPs identified in CKDGEN-MA are highligth in red (b)



#### (a) Forest plot of rs1153847



(b) Regional plot around rs1153847 using Meta\_ALL and CKD-GENEA

Figure S9: replication of GATM/SPATA5L1 regions identified in CKDGEN-EA: forest plot of lead SNPs identified in Meta\_ALL rs1153847 (15-45696890) (a) and regional plot around (b)

regional plot had been perforned using locus zoom, using  $LD_{ALL}$ , lead SNPs identified in Meta<sub>ALL</sub> are annotated in blue and Significant SNPs identified in CKDGEN-EA are highligth in red (b)

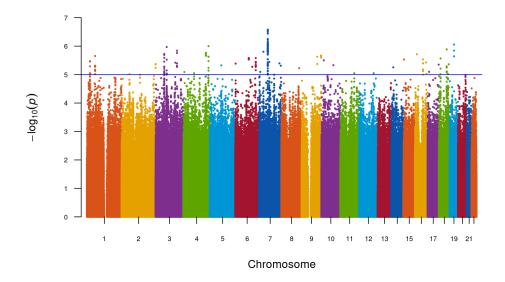


Figure S10a: Manhattan plot of Meta Analysis using South resident using Fixed effect method

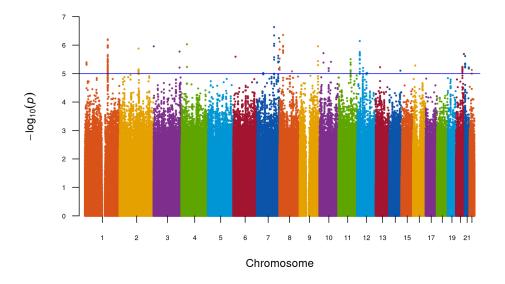


Figure S10b: Manhattan plot of Meta Analysis using West resident using Fixed effect method

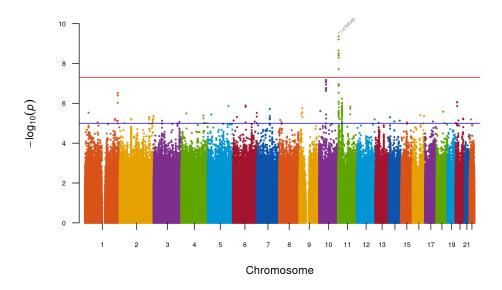


Figure S11: Manhattan plot of Meta Analysis using all dataset using Random effect