Table S3. Adjusted associations[1] of *APOL1* risk alleles with biomarkers among HIV-infected African-American women (N=795) using multiple imputation to include participants with missing *APOL1* genotype or urine biomarker measurements

		Models of inheritance		
		Recessive[2]	Dominant[3]	Additive[4]
	% Estimate[5] (95% CI)	P-value	P-value	P-value
Continuous outcomes				
ACR (mg/g)	81 (16, 181)	0.0087	0.69	0.23
IL-18/Cr (pg/mg)	-1 (-20, 23)	0.92	0.78	0.31
KIM-1/Cr (pg/mg)	-13 (-29, 6)	0.17	0.77	0.098
NGAL/Cr (ng/mg)	11 (-24, 63)	0.58	0.54	0.25
	Prevalence Ratio[6] (95% CI)	**P-value**	**P-value**	**P-value**
Dichotomous outcomes				
ACR >30mg/g	1.95 (1.17, 3.25)	0.011	0.82	0.16
Detectable α1m	0.96 (0.65, 1.43)	0.85	0.68	0.53

[1]Multivariable models adjust for age, hypertension, diabetes mellitus, body mass index, HCV infection, HIV viral load, CD4 cell count, current HAART, eGFR, PC1, PC3, and PC5.
[2]P-value compares 2 vs 0/1 *APOL1* risk alleles
[3]P-value compares 2/1 vs 0 *APOL1* risk alleles
[4]P-value for trend, 2 vs 1 vs 0 *APOL1* risk alleles
[5]Estimated percentage difference attributable to having 2 vs 0/1 *APOL1* risk alleles.
[6]Adjusted prevalence ratio among individuals with 2 vs 0/1 *APOL1* risk alleles.
Abbreviations: ACR, albumin-creatinine ratio; α1m, α1-microglobulin; CI, confidence interval; Cr, creatinine; IL-18, interleukin-18; KIM-1, kidney injury molecule-1; NGAL, neutrophil gelatinase-associated lipocalin; PC, principal component.