Table S6. Adjusted associations[1] of *APOL1* risk alleles with biomarkers among HIV-infected African-American women with eGFR>60ml/min/1.73m^2 (N=408)

		Models of inheritance		
		Recessive[2]	Dominant[3]	Additive[4]
	% Estimate[5] (95% CI)	P-value	P-value	P-value
Continuous outcomes				
ACR (mg/g)	69 (8, 163)	0.020	0.55	0.071
IL-18/Cr (pg/mg)	-7 (-26, 16)	0.52	0.69	0.49
KIM-1/Cr (pg/mg)	-12 (-29, 10)	0.28	0.57	0.26
NGAL/Cr (ng/mg)	-10 (-37, 29)	0.57	0.68	0.54
	Prevalence Ratio[6] (95% CI)	**P-value**	**P-value**	**P-value**
Dichotomous outcomes				
ACR >30mg/g	2.10 (1.14, 3.89)	0.018	0.83	0.079
Detectable α1m	0.94 (0.60, 1.48)	0.80	0.63	0.96

[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; eGFR, estimated glomerular filtration rate; IL-18, interleukin-18; KIM-1, kidney injury molecule-1; NGAL, neutrophil gelatinase-associated lipocalin; PC, principal component.