SUPPLEMENTAL MATERIAL

Table S1. *ARMC5* variants and risk of hypertension in African Americans: Minority Health-GRID study. Minority Health Genomics and Translational Research Bio-Repository Database (MH-GRID) study: inclusion and exclusion criteria.

Inclusion Criteria
• Self-identified African-Americans males or females ages 30-55 years. • Cases: Severe-Controlled Hypertension (SCH): SBP ≤ 140 and/or DBP ≤ 90 mmHg on a stable regimen (≥6 months) with ≥ 2 anti-hypertensive drugs (must include a diuretic). • Cases: Severe-Resistant Hypertension (SRH): SBP > 140 and/or DBP > 90 mmHg on a stable regimen (≥3 months) of ≥ 3 drugs (must include a diuretic). • Controls: Individuals with optimal blood pressure: ≤ 120/80 mmHg and normal kidney function (eGFR > 90 ml/min).
Exclusion Criteria
• Failure to meet the inclusion criteria. • Primary chronic kidney disease or proteinuria unrelated to hypertension. • Secondary forms of hypertension*. • Chronic diseases that may secondarily compromise renal function such as diabetes, chronic congestive heart failure, HIV or liver disease. • Patients with recent hospitalizations (< 3 months). • Unable to give informed consent. • Pregnant or lactating women.

SBP: Systolic blood pressure, DBP: Diastolic Blood Pressure, eGFR: estimated glomerular filtration rate.*no aldosterone or plasma renin activity data was available

Table S2. Gene-based analysis results, in MH-GRID.

SNP	P-Value	Number of variants in SNP set
Rare variants	0.0011	16
Low frequency variants	0.1656	4
Rare + Low frequency variants	0.0070	20
Rare variants + rs116201073	0.0003	17
Low frequency variants + rs116201073	0.1090	5
Rare + Low + rs116201073	0.0057	21

MH-GRID: Minority Health Genomics and Translational Research Bio-Repository Database; SNP: Single nucleotide polymorphisms.

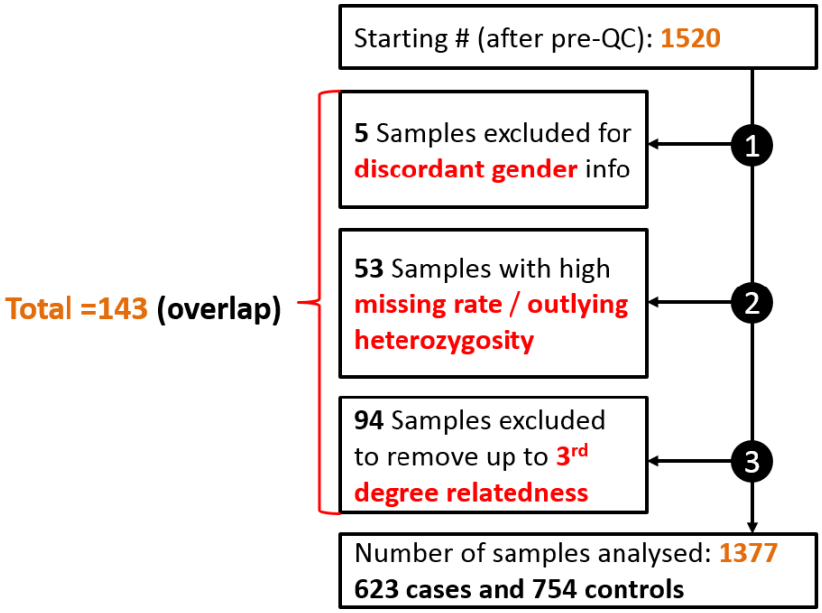
Table S3. Minor Allele Frequency of rs116201073, rs141923065 and rs367810854 in the 1000 Genomes Project populations.

Population	Population	rs116201073	rs141923065	rs367810854
African	ACB	0.0469	0.0012	0
	ASW	0.0984	0.0052	0
	YRI	0.1019	0	0
	ESN	0.0758	0	0
	LWK	0.101	0	0
	GWD	0.1018	0	0
	MSL	0.1	0	0
Admix American	MXL	0	0	0
	PUR	0.0144	0	0
	CLM	0	0	0
	PEL	0.0059	0	0
South Asian	GIH	0	0	0.0631
	PJL	0	0	0.0938
	BEB	0	0	0.0581
	STU	0	0	0.0735
	ITU	0	0	0.0784
European	CEU	0	0	0
	TSI	0	0	0
	FIN	0	0	0
	GBR	0	0	0
	IBS	0	0	0
East Asian	JPT	0	0	0
	KHV	0	0	0
	CHB	0	0.0097	0
	CDX	0	0	0
	CHS	0	0	0

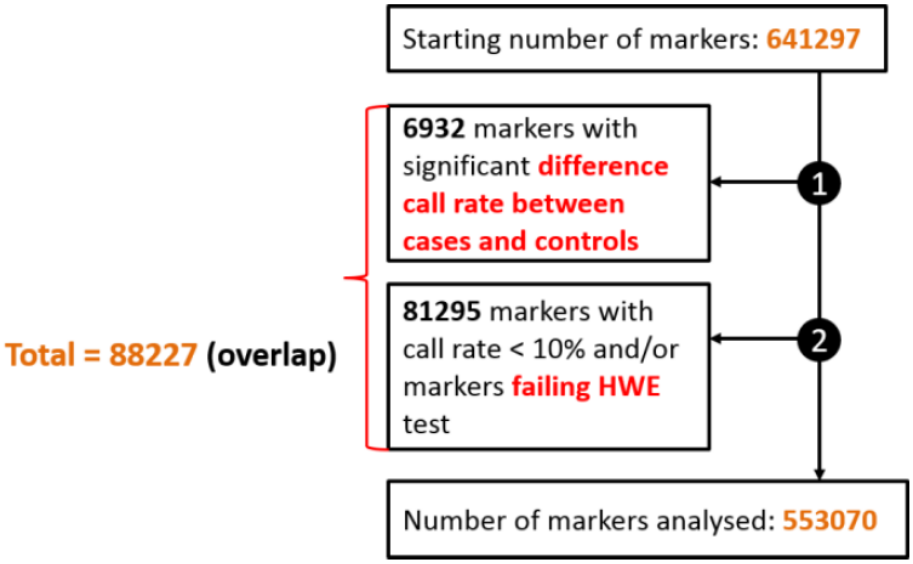
ASW: African ancestry in SW USA; ACB: African Caribbean in Barbados; BEB: Bengali in Bangladesh; GBR: British from England and Scotland; CDX: Chinese Dai in Xishuangbanna, China; CLM: Colombian in Medellín, Colombia; ESN: Esan in Nigeria; FIN: Finnish in Finland; GWD: Gambian in Western Division – Mandinka; GIH: Gujarati Indians in Houston, Texas, United States; CHB: Han Chinese in Beijing, China; CHS: Han Chinese South, China; IBS: Iberian populations in Spain; ITU: Indian Telugu in the U.K.; JPT: Japanese in Tokyo, Japan; KHV: Kinh in Ho Chi Minh City, Vietnam; LWK: Luhya in Webuye, Kenya; MS: Mende in Sierra Leone; MXL: Mexican Ancestry in Los Angeles CA United States; PEL: Peruvian in Lima, Peru; PUR: Puerto Rican in Puerto Rico; PJL: Punjabi in Lahore, Pakistan; STU: Sri Lankan Tamil in the UK; TSI: Toscani in Italy; YRI: Yoruba in Ibadan, Nigeria; CEU: Utah residents with Northern and Western European ancestry from the CEPH collection.

Figure S1. Summary of Quality Controls (QC) for MH-GRID Exome-Wide Sequencing Data.

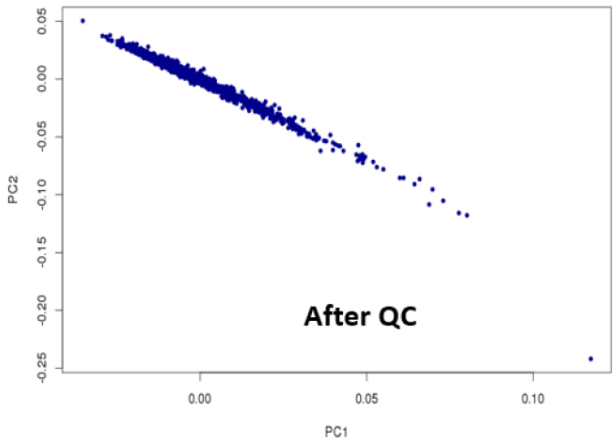
A. Sample QC



B. Markers QC

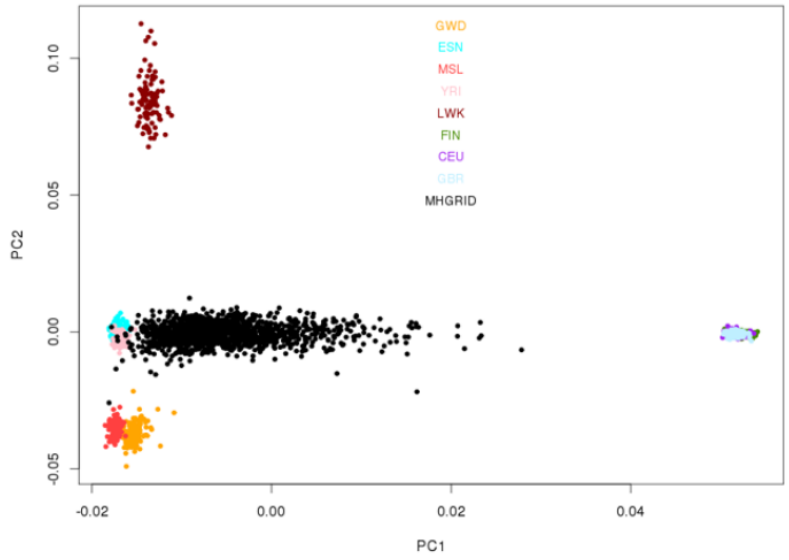


C. Principal component analysis graph after all QC show homogeneous sample set



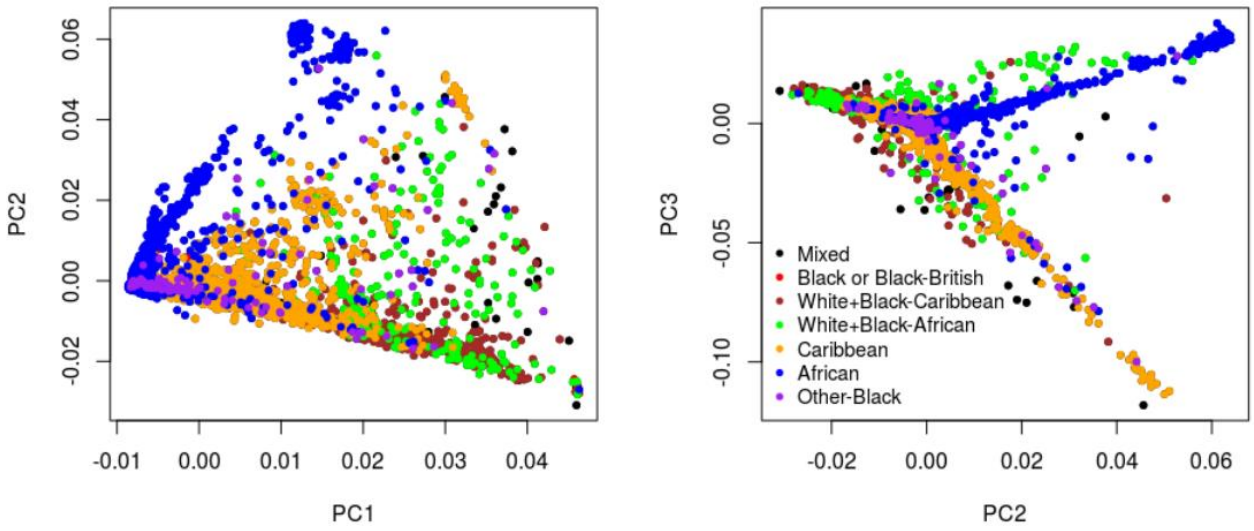
A. After excluding samples failing quality control filters 1377 samples remained for analysis. **B.** 44 variants between the start and end position of the *ARMC5* gene are among the 553070 variants that passed quality control. The Ti/Tv ratio after quality control is 3.31 indicating good quality data with regards to sequencing errors. **C.** There was no evidence of batch effect after quality control as shown by the homogenous cluster where the smear shape just reflects admixture from West-African to European ancestry shown in.

Figure S2. Principal component analyses of MH-GRID data with 1000 Genomes Project samples.



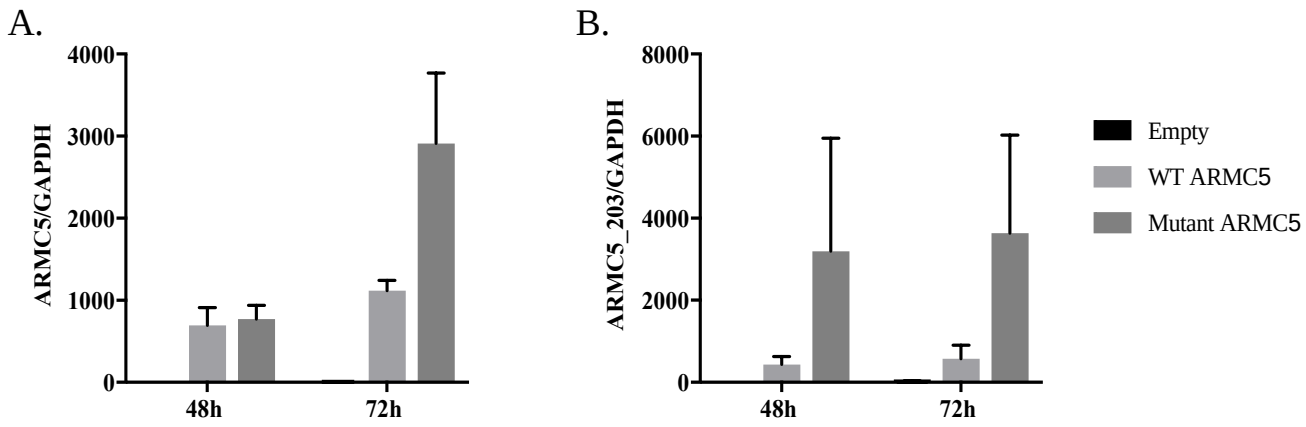
MH-GRID: Minority Health Genomics and Translational Research Bio-Repository Database; Optimal model is adjusted for age, sex, HDL, LDL, smoking and the first principal component (PC1) of the principal component analysis carried out to investigate admixture. PC1 separates the 2 continental ancestries relevant for this analysis. The graph represents a PCA plot of 1377 MH-GRID samples with eight 1000 Genome populations: 5 African, GWD (Gambian in Western Division), ESN (Esan in Nigeria), MSL (Mende in Sierra Leone), YRI (Yoruba in Ibadan, Nigeria) and LWK (Luhya in Webuye, Kenya) and 3 European, FIN (Finnish in Finland), CEU (Utah Residents with Northern and Western European Ancestry) and GBR(British from England and Scotland).

Figure S3. Graphs of principal component analyses (PCA) of UK Biobank genotype data.



PCA analyses of UK Biobank genotype data to determine principal components (PC)s to consider adjusting for ancestry. In the below figure the plots of PC1 vs. PC2 and PC2 vs. PC3 PC2 and PC3 are the relevant PC for the analysis restricted to the African populations (in blue). Therefore, PC2 and PC3 were added to the model described in the manuscript.

Figure S4. Comparison of wild type (WT) and mutant ARMC5 (rs116201073) expression in HEK293 cell line.



Expression of wild type (WT) and mutant *ARMC5* variant (rs116201073) after transfection in the adrenocortical cell line, H295R. The *ARMC5* expression is analyzed by RTqPCR using primers targeting all *ARMC5* isoforms (A) or only the transfected 203 isoforms (B). The graph represents the means of at least 2 independent experiments ± SEM.