



Correction

Correction: Udosen et al. Meta-Analysis and Multivariate GWAS Analyses in 80,950 Individuals of African Ancestry Identify Novel Variants Associated with Blood Pressure Traits. *Int. J. Mol. Sci.* 2023, 24, 2164

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In the original publication [1], the funding from United States' Veteran Health Administration with grant numbers 5I01BX003360 and 1I01CX001897 awarded to Adriana M. Hung was not included. There was an error in the sample size stated in Figure 1 for the Million Veteran Program cohort. The sample size listed is 56,833 but the correct sample size is 59,933. The total sample size of the meta-analysis consequently increases to 80,950. Thus, all instances of the number 77,850 in the title, abstract, text, Table 1 and Figure 1 should be 80,950. The corrected Figure 1 and Table 1 appear below. The authors state that the scientific conclusions are unaffected. In the Acknowledgments, the authors would like to add an acknowledgment of the contributions of Jacklyn N. Hellwege, Ayush Giri, Adriana M. Hung and Todd L. Edwards of the Nashville VA and Vanderbilt University Medical Centers for leading the effort that generated the GWAS summary statistics of blood pressure in the Million Veteran Program included in this report. This correction was approved by the Academic Editor. The original publication has also been updated.

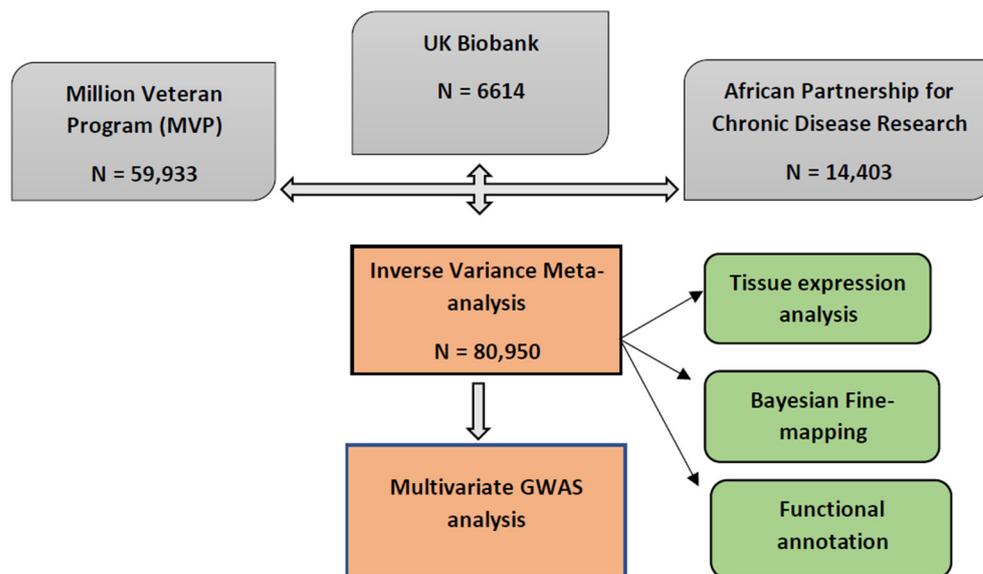


Figure 1. Study design schematic for discovery and validation of loci. APCDR; African Partnership for Control of Disease Research, UKB; United Kingdom Biobank, MVP; Million Veteran Program.

Table 1. Description of cohorts used in this study.

Cohort	Continent	Country	Sample Size (N)	Phenotype	Imputation Panel and Genome Build
APCDR-UGR (27)	Africa	Uganda	6407	SBP/DBP	African genome panel, hg19
APCDR-DCC (27)	Africa	South Africa	1600	SBP/DBP	African genome panel, hg19
APCDR-DDS (27)	Africa	South Africa	1165	SBP/DBP	African genome panel, hg19
APCDR-AADM (27)	Africa	Nigeria, Ghana, and Kenya	5231	SBP/DBP	African genome panel, hg19
MVP-AFR	N. America	USA	59,933	SBP/DBP	1k Genome, hg19
UKB-AFR (28)	Europe	UK	6614	SBP/DBP	1k Genome, hg19

Reference

1. Udosen, B.; Soremekun, O.; Kamiza, A.; Machipisa, T.; Cheickna, C.; Omotuyi, O.; Soliman, M.; Wélé, M.; Nashiru, O.; Chikowore, T.; et al. Meta-Analysis and Multivariate GWAS Analyses in 80,950 Individuals of African Ancestry Identify Novel Variants Associated with Blood Pressure Traits. *Int. J. Mol. Sci.* **2023**, *24*, 2164. [[CrossRef](#)] [[PubMed](#)]

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