SUPPLEMENTAL MATERIAL

FIGURE LEGENDS

Supplemental Figure 1. Plot of the principal component analysis of CARDIA AA cases along with individuals from the 1,000 Genomes Project.

AMR-Ad Mixed American; SAS-South Asian; EAS-East Asian; EUR-European; ACB-African Caribbeans in Barbados; ASW-Americans of African Ancestry in SW USA; AFR-African.

Supplemental Figure 2. Plot of the principal component analysis of BioVU AA cases along with individuals from the 1,000 Genomes Project.

AMR-Ad Mixed American; SAS-South Asian; EAS-East Asian; EUR-European; ACB-African Caribbeans in Barbados; ASW-Americans of African Ancestry in SW USA; AFR-African.

Supplemental Figure 3. Plot of the principal component analysis of CARDIA AA cases along with individuals from the 1,000 Genomes Project.

AMR-Ad Mixed American; SAS-South Asian; EAS-East Asian; AFR-African; EUR-European.

Supplemental Figure 4. Plot of the principal component analysis of BioVU AA cases along with individuals from the 1,000 Genomes Project.

AMR-Ad Mixed American; SAS-South Asian; EAS-East Asian; AFR-African; EUR-European.

Supplemental Figure 5. The QQ plot for the meta-analysis results from the GWAS for number of fibroids (single vs multiple) for BioVU and CARDIA AAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 6. The QQ plot for the meta-analysis results from the GWAS for $\log_{10}$ transformed largest dimension of all fibroids for BioVU and CARDIA AAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 7. The QQ plot for the meta-analysis results from the GWAS for $\log_{10}$ transformed fibroid volume for BioVU and CARDIA AAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 8. The QQ plot for the meta-analysis results from the GWAS for number of fibroids (single vs multiple) for BioVU and CARDIA EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 9. The QQ plot for the meta-analysis results from the GWAS for $\log_{10}$ transformed largest dimension of all fibroids for BioVU and CARDIA EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 10. The QQ plot for the meta-analysis results from the GWAS for $\log_{10}$ transformed fibroid volume for BioVU and CARDIA EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 11. The QQ plot for the transethnic meta-analysis results from the GWAS for number of fibroids (single vs multiple) for BioVU and CARDIA AAs and EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 12. The QQ plot for the transethnic meta-analysis results from the GWAS for $\log_{10}$ transformed largest dimension of all fibroids for BioVU and CARDIA AAs and EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 13. The QQ plot for the transethnic meta-analysis results from the GWAS for $\log_{10}$ transformed fibroid volume for BioVU and CARDIA AAs and EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 14. The manhattan plot for the meta-analysis results from the GWAS for number of fibroids (single vs multiple) for BioVU and CARDIA AAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 15. The manhattan plot for the meta-analysis results from the GWAS for $\log_{10}$ transformed largest dimension of all fibroids for BioVU and CARDIA AAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 16. The manhattan plot for the meta-analysis results from the GWAS for $\log_{10}$ transformed fibroid volume for BioVU and CARDIA AAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 17. The manhattan plot for the meta-analysis results from the GWAS for number of fibroids (single vs multiple) for BioVU and CARDIA EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 18. The manhattan plot for the meta-analysis results from the GWAS for $\log_{10}$ transformed largest dimension of all fibroids for BioVU and CARDIA EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 19. The manhattan plot for the meta-analysis results from the GWAS for $\log_{10}$ transformed fibroid volume for BioVU and CARDIA EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 20. The manhattan plot for the transethnic meta-analysis results from the GWAS for number of fibroids (single vs multiple) for BioVU and CARDIA AAs and EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 21. The manhattan plot for the transethnic meta-analysis results from the GWAS for $\log_{10}$ transformed largest dimension of all fibroids for BioVU and CARDIA AAs and EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 22. The manhattan plot for the transethnic meta-analysis results from the GWAS for $\log_{10}$ transformed fibroid volume for BioVU and CARDIA AAs and EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 23. The MetaXcan plot for the meta-analysis results from the GWAS for number of fibroids (single vs multiple) for BioVU and CARDIA AAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 24. The MetaXcan plot for the meta-analysis results from the GWAS for $\log_{10}$ transformed largest dimension of all fibroids for BioVU and CARDIA AAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 25. The MetaXcan plot for the meta-analysis results from the GWAS for $\log_{10}$ transformed fibroid volume for BioVU and CARDIA AAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 26. The MetaXcan plot for the meta-analysis results from the GWAS for number of fibroids (single vs multiple) for BioVU and CARDIA EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 27. The MetaXcan plot for the meta-analysis results from the GWAS for $\log_{10}$ transformed largest dimension of all fibroids for BioVU and CARDIA EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 28. The MetaXcan plot for the meta-analysis results from the GWAS for $\log_{10}$ transformed fibroid volume for BioVU and CARDIA EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 29. The MetaXcan plot for the transethnic meta-analysis results from the GWAS for number of fibroids (single vs multiple) for BioVU and CARDIA AAs and EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 30. The MetaXcan plot for the transethnic meta-analysis results from the GWAS for $\log_{10}$ transformed largest dimension of all fibroids for BioVU and CARDIA AAs and EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Supplemental Figure 31. The MetaXcan plot for the transethnic meta-analysis results from the GWAS for $\log_{10}$ transformed fibroid volume for BioVU and CARDIA AAs and EAs.

The regression analyses were adjusted for age, BMI, and five principal components. Markers with a MAF of at least 5% were used in the analyses.

Figure 32. Regional association plot of the most significant marker from the EA meta-analyses.

The index SNP from this regional plot is rs141745233 from the EA meta-analysis of fibroid volume. European individuals from the 1000 genomes was used to estimate linkage disequilibrium (LD) for this plot. The X-axis represents the genomic position along each chromosome in megabases (Mb). The Y-axis represents both the $-\log_{10}$ P-values for each SNP as well as the recombination rate. The color of each SNP represents the strength of the correlation (r^2) to the index SNP (purple). Nearby genes are listed below the regional plots.

Figure 33. Regional association plot of the most significant marker from the transethnic meta-analyses using African individuals from the 1000 genomes to estimate linkage disequilibrium (LD).

(a) The index SNP from this regional plot is rs6605005 from the transethnic meta-analysis of fibroid volume. The X-axis represents the genomic position along each chromosome in megabases (Mb). The Y-axis represents both the $-\log_{10}$ P-values for each SNP as well as the recombination rate. The color of each SNP represents the strength of the correlation (r^2) to the index SNP (purple). Nearby genes are listed below the regional plots.

Figure 34. Regional association plot of the most significant marker from the transethnic meta-analyses using European individuals from the 1000 genomes to estimate linkage disequilibrium (LD).

The index SNP from this regional plot is rs6605005 from the transethnic meta-analysis of fibroid volume. The X-axis represents the genomic position along each chromosome in megabases (Mb). The Y-axis represents both the $-\log_{10}$ P-values for each SNP as well as the recombination rate. The color of each SNP represents the strength of the correlation (r^2) to the index SNP (purple). Nearby genes are listed below the regional plots.

Supplemental Table 1. Quality control (QC) details for each study

Cohort	**Race**	**Genotyping Platform**	**Post-QC, Pre-imputation SNPs**	**Outcome**	**Post Imputation SNPs**
BioVU	AA	Affymetrix Axiom Biobank Array & Axiom World Array 3 Platform	1,345,099	Number	9,530,809
				Max Dimension	9,526, 536
				Volume	9,540,688
	EA	Affymetrix Axiom Biobank Array	602,522	Number	6,942,486
				Max Dimension	6,945,186
				Volume	6,949,297
CARDIA	AA	Affymetrix 6.0 Array	784,270	Number	9,627,525
				Max Dimension	9,596,033
				Volume	9,597,202
	EA	Affymetrix 6.0 Array	562,358	Number	6,938,376
				Max Dimension	6,953,394
				Volume	6,956,705

AA - African American; EA - European American

Supplemental Table 2. Summary of cohort-specific single SNP signals from the meta-analyses between BioVU and CARDIA blacks for each fibroid outcome

Number				
rs35322806 in 4q32.1				
Cohort	**OR [95% CI]**	**P-value**	**EAF**	**Info**
BioVU AA	0.49 [0.34, 0.70]	$9.85x10^{-5}$	0.21	0.97
CARDIA AA	0.31 [0.17, 0.59]	$3.31x10^{-4}$	0.20	0.99
rs735658 in 17q25.3				
Cohort	**OR [95% CI]**	**P-value**	**EAF**	**Info**
BioVU AA	0.39 [0.23, 0.67]	$7.23x10^{-4}$	0.09	0.83
CARDIA AA	0.09 [0.03, 0.27]	$1.29x10^{-5}$	0.08	0.67
rs7625080 in 3p26.1				
Cohort	**OR [95% CI]**	**P-value**	**EAF**	**Info**
BioVU AA	0.52 [0.38, 0.69]	$1.11x10^{-5}$	0.34	0.98
CARDIA AA	0.56 [0.34, 0.93]	0.0257	0.34	0.97
rs62203867 in 20p12.3				
Cohort	**OR [95% CI]**	**P-value**	**EAF**	**Info**
BioVU AA	0.48 [0.34, 0.67]	$1.82x10^{-5}$	0.24	0.97
CARDIA AA	0.41 [0.20, 0.85]	0.0169	0.22	0.81
Max Dimension				
rs57542984 in 5q34				
Cohort	**Beta [95% CI]**	**P-value**	**EAF**	**Info**
BioVU AA	0.13 [0.08, 0.19]	$1.66x10^{-6}$	0.80	0.91
CARDIA AA	0.12 [0.05, 0.18]	$3.37x10^{-4}$	0.83	0.91
rs62484733 in 7q22.3				
Cohort	**Beta [95% CI]**	**P-value**	**EAF**	**Info**
BioVU AA	0.11 [0.04, 0.18]	$1.94x10^{-3}$	0.10	0.92
CARDIA AA	0.17 [0.09, 0.25]	$3.14x10^{-5}$	0.09	0.88
rs13183849 in 5q14.3				
Cohort	**Beta [95% CI]**	**P-value**	**EAF**	**Info**
BioVU AA	-0.10 [-0.15, -0.06]	$1.59x10^{-5}$	0.31	0.97
CARDIA AA	-0.07 [-0.12, -0.02]	0.0105	0.27	0.99
Volume				
rs6938199 in 6q22.33				
Cohort	**Beta [95% CI]**	**P-value**	**EAF**	**Info**
BioVU AA	-0.35 [-0.55, -0.14]	$8.39x10^{-4}$	0.10	1.00
CARDIA AA	-0.49 [-0.74, -0.25]	$8.86x10^{-5}$	0.11	1.00

OR-odds ratio; CI-confidence interval; EAF-effect allele frequency.

Supplemental Table 3. Summary of most significant SNPs from the meta-analyses between BioVU and CARDIA EAs for each fibroid outcome

Number

SNP	**Region**	**BP**	**Genes**	**A2/A1**	**EAF**	**OR [95% CI]**	**P-value**	**Het. P**	**Dir.**
rs35071394	14q21.1	41,837,615	*FBXO33*||*LRFN5*	C/CCT	0.92	2.93 [1.92, 4.48]	6.56x10^{-7}	0.308	++
rs1392505	16q21	59,746,130	*GOT2*||*CDH8*	A/G	0.80	1.89 [1.46,2.44]	1.00x10^{-6}	0.291	++

Volume

SNP	**Region**	**BP**	**Genes**	**A2/A1**	**EAF**	**Beta [95% CI]**	**P-value**	**Het. P**	**Dir.**
rs141745233	7q36.1	148,269,774	*CNTNAP2*||*CUL1*	T/TG	0.09	-0.46 [-0.64, -0.29]	3.97x10^{-7}	0.227	--
rs17506409	5q22.1	110,089,908	*SLC25A46*	G/A	0.08	0.46 [0.28, 0.64]	8.10x10^{-7}	0.339	++

SNP-single nucleotide polymorphism; BP-base pairs; A2-effect allele; A1-reference allele; OR-odds ratio; CI-confidence interval; Het. P-heterogeneity p-value; Dir.-direction.

Supplemental Table 4. Summary of cohort-specific single SNP signals from the meta-analyses between BioVU and CARDIA whites for each fibroid outcome

Number

rs35071394 in 14q21.1

Cohort	OR [95% CI]	P-value	EAF	Info
BioVU EA	3.17 [2.02, 4.97]	$4.93\text{x}10^{-7}$	0.91	0.74
CARDIA EA	1.57 [0.44, 5.60]	0.484	0.94	0.66

rs1392505 in 16q21

Cohort	OR [95% CI]	P-value	EAF	Info
BioVU EA	1.78 [1.35, 2.35]	$4.55\text{x}10^{-5}$	0.80	0.95
CARDIA EA	2.60 [1.36, 4.97]	$3.73\text{x}10^{-3}$	0.80	0.94

Volume

rs141745233 in 7q36.1

Cohort	Beta [95% CI]	P-value	EAF	Info
BioVU EA	-0.54 [-0.75, -0.32]	$9.60\text{x}10^{-7}$	0.09	1.00
CARDIA EA	-0.30 [-0.62, 0.03]	0.0755	0.09	0.66

rs17506409 in 5q22.1

Cohort	Beta [95% CI]	P-value	EAF	Info
BioVU EA	0.53 [0.30, 0.77]	$1.04\text{x}10^{-5}$	0.07	0.99
CARDIA EA	0.35 [0.07, 0.64]	0.0159	0.08	1.00

OR-odds ratio; CI-confidence interval; EAF-effect allele frequency.

Table 5. Summary of cohort-specific single SNP signals from the transethnic meta-analyses between all BioVU and CARDIA women for each fibroid outcome

Number				
rs55964111 in 15q15.3				
Cohort	**OR [95% CI]**	**P-value**	**EAF**	**Info**
BioVU AA	1.88 [1.39, 2.55]	4.14x10^{-5}	0.60	0.98
CARDIA AA	1.99 [1.18, 3.37]	0.0104	0.63	0.98
BioVU EA	1.32 [0.85, 2.04]	0.215	0.92	0.85
CARDIA EA	3.20 [1.23, 8.35]	0.0173	0.91	0.80
rs1419784 in 7p14.3				
Cohort	**OR [95% CI]**	**P-value**	**EAF**	**Info**
BioVU AA	1.50 [1.11, 2.02]	8.44x10^{-3}	0.68	0.99
CARDIA AA	1.06 [0.61, 1.82]	0.847	0.67	0.97
BioVU EA	1.57 [1.23, 2.01]	2.73x10^{-4}	0.77	0.99
CARDIA EA	2.31 [1.29, 4.11]	4.61x10^{-3}	0.77	0.97
Max Dimension				
rs7751006 in 6q27				
Cohort	**Beta [95% CI]**	**P-value**	**EAF**	**Info**
BioVU AA	0.06 [0.00, 0.12]	0.0467	0.84	0.89
CARDIA AA	0.07 [0.00, 0.15]	0.0622	0.87	0.73
BioVU EA	0.07 [0.02, 0.11]	2.31x10^{-3}	0.66	0.95
CARDIA EA	0.09 [0.03, 0.14]	1.47x10^{-3}	0.68	0.94
rs111855550 in 4p16.1				
Cohort	**Beta [95% CI]**	**P-value**	**EAF**	**Info**
BioVU AA	-0.04 [-0.10, 0.01]	0.138	0.13	0.98
CARDIA AA	-0.10 [-0.17, -0.03]	2.73x10^{-3}	0.12	0.99
BioVU EA	-0.06 [-0.12, 0.00]	0.0605	0.13	0.95
CARDIA EA	-0.14 [-0.21, -0.07]	1.54x10^{-4}	0.13	1.00
Volume				
rs6605005 in 1q31.1				
Cohort	**Beta [95% CI]**	**P-value**	**EAF**	**Info**
BioVU AA	0.30 [0.16, 0.44]	1.96x10^{-6}	0.75	1.00
CARDIA AA	0.17 [0.01, 0.33]	0.0419	0.74	0.95
BioVU EA	0.40 [0.19, 0.62]	2.76x10^{-4}	0.91	1.00
CARDIA EA	0.02 [-0.23, 0.27]	0.886	0.87	0.75
rs10024805 in 4q35.1				
Cohort	**Beta [95% CI]**	**P-value**	**EAF**	**Info**
BioVU AA	0.22 [0.09, 0.35]	9.12x10^{-4}	0.36	1.00
CARDIA AA	0.16 [0.02, 0.29]	0.0222	0.39	1.00
BioVU EA	0.12 [-0.03, 0.26]	0.113	0.29	0.99
CARDIA EA	0.29 [0.13, 0.46]	3.52x10^{-4}	0.26	1.00
rs7968890 in 12p12.1				
Cohort	**Beta [95% CI]**	**P-value**	**EAF**	**Info**
BioVU AA	0.12 [-0.01, 0.24]	0.0743	0.44	1.00
CARDIA AA	0.29 [0.15, 0.44]	7.46x10^{-5}	0.43	0.90
BioVU EA	0.16 [0.04, 0.29]	0.0120	0.44	1.00
CARDIA EA	0.14 [-0.01, 0.30]	0.0710	0.45	1.00

OR-odds ratio; CI-confidence interval; EAF-effect allele frequency.

Supplemental Table 6. Predicted gene expression summary from MetaXcan

Number

Meta-analysis	**Tissue**	**Gene**	**Chr**	**Z-Score**	**P-value**	**R^{2a}**	**Variance[b]**	**N SNPs[c]**	**Model N[d]**
Transethnic	Thyroid	*EDEM2*	20	-4.51	6.34×10^{-6}	0.148	0.053	14	24
EAs	Pituitary	*C2orf73*	2	4.45	8.48×10^{-6}	0.342	0.229	24	25

[a] Predicted performance R^2.

[b] Variance of predicted gene expression.

[c] Number of SNPs in the prediction model that were present in the GWAS summary statistics.

[d] Number of SNPs in the tissue-specific gene expression prediction model using GTEx data.

Supplemental Table 7. Examining cross phenotype associations for transethnic meta-analyses between all BioVU and CARDIA women

				S_{Hom}				
SNP	**Region**	**BP**	**Genes**	**A2/A1**	**P-value**	**Number Z-Score**	**Max Dimension Z-Score**	**Volume Z-Score**
rs200348	14q32.2	99,380,544	*VRK1*||*BCL11B*	G/A	7.13×10^{-7}	-4.26	-3.12	-1.69
rs11691049	2q24.3	168,615,362	*B3GALT1*	C/A	7.48×10^{-7}	-3.83	-3.61	-3.38

SNP-single nucleotide polymorphism; BP-base pairs; A2-effect allele; A1-reference allele.