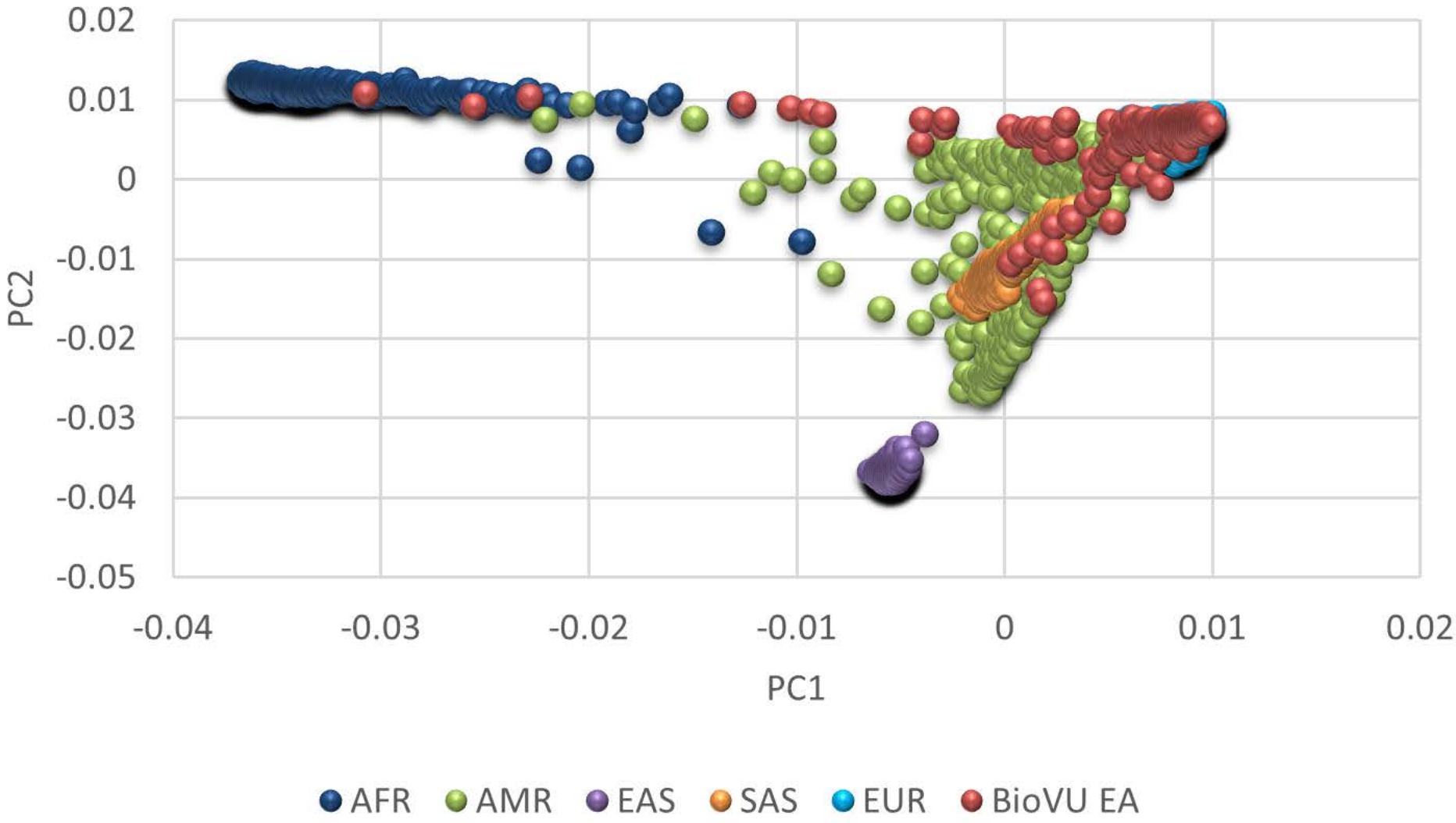
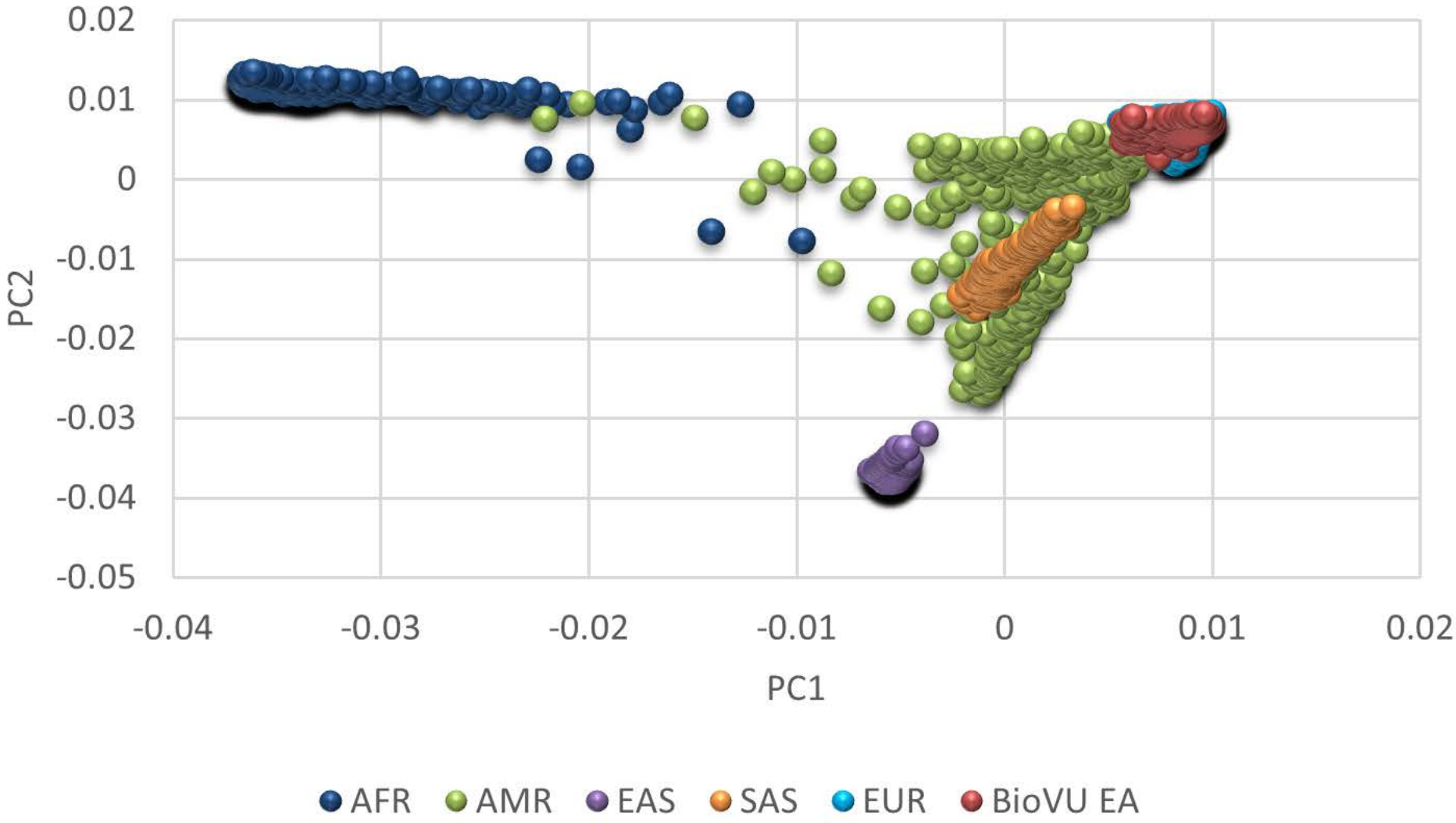
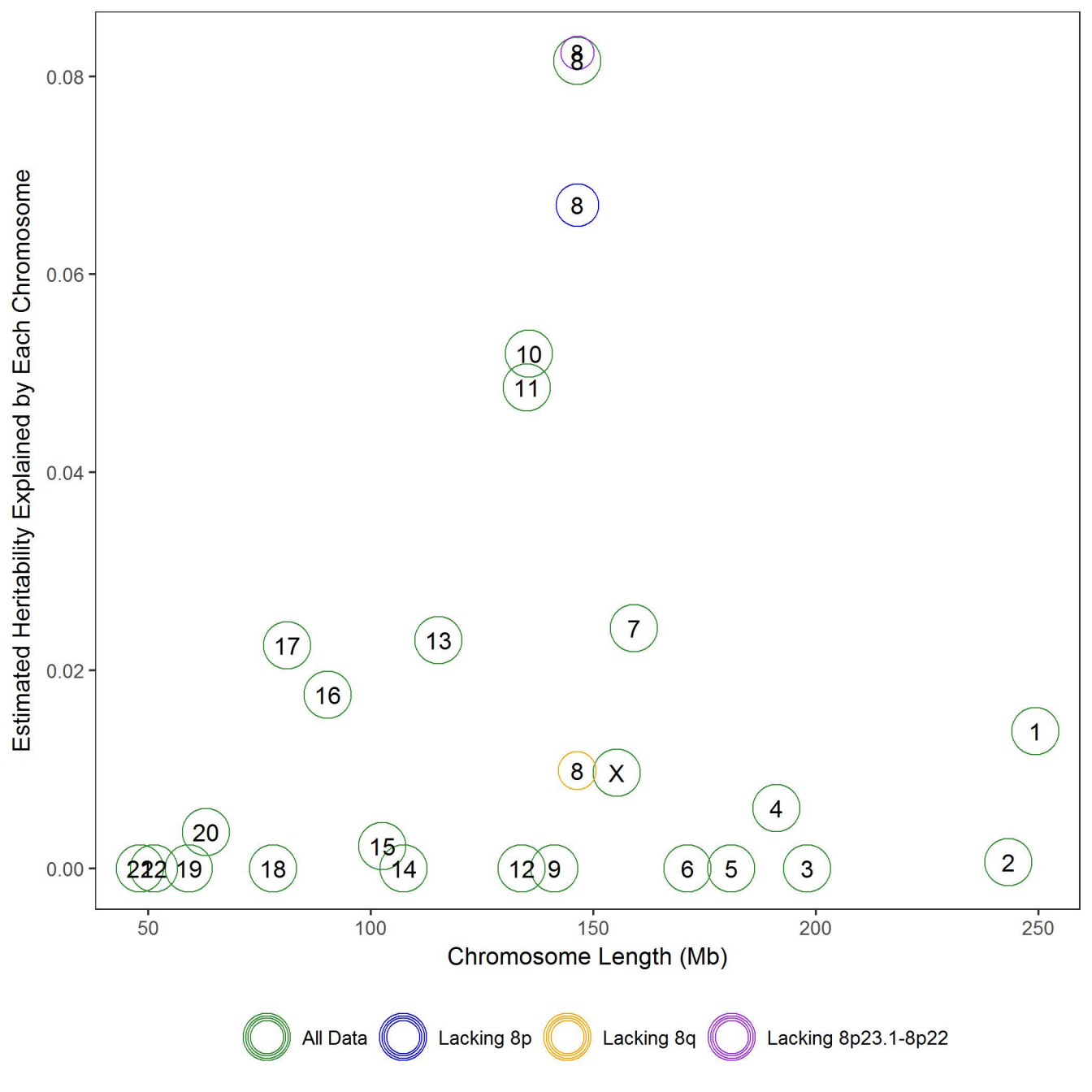

0.02
0.01
0
-0.01
-0.02
-0.03
-0.04
-0.05
PC2
-0.04
-0.03
-0.02
-0.01
0
0.01
0.02
PC1
AFR
AMR
EAS
SAS
EUR
BioVU EA


0.02
0.01
0
-0.01
-0.02
-0.03
-0.04
-0.05
PC2
-0.04
-0.03
-0.02
-0.01
0
0.01
0.02
PC1
AFR
AMR
EAS
SAS
EUR
BioVU EA


Estimated Heritability Explained by Each Chromosome
0.08
0.06
0.04
0.02
0.00
50
100
150
200
250
Chromosome Length (Mb)
All Data
Lacking 8p
Lacking 8q
Lacking 8p23.1-8p22

SUPPLEMENTAL INFORMATION

FIGURE LEGENDS

Supplemental Figure-1. Principal components plot of BioVU EAs with reference population before pruning outliers. AFR-African; AMR-Ad Mixed American; EAS-East Asian; SAS-South Asian; EUR-European.

Supplemental Figure-2. Principal components plot of BioVU EAs with reference population after pruning outliers. AFR-African; AMR-Ad Mixed American; EAS-East Asian; SAS-South Asian; EUR-European.

Supplemental Figure-3. Estimated SNP- based heritability of each chromosome by chromosome length in Mb with sections of chromosome 8 removed. To help all models converge, the model used to produce this figure adjusted for age, BMI, and 7 PCs with a prevalence estimate at 70%.

Supplemental Table 1. Heritability estimates for fibroid risk using European Americans within BioVU.

Heritability Estimate ± (Std. Err.)	P-value	PC Adjustments
0.38 ± (0.18)	0.013[a]	0
0.34 ± (0.18)	0.031[a]	1
0.35 ± (0.18)	0.027[a]	2
0.33 ± (0.18)	0.037[a]	3
0.33 ± (0.18)	0.038[a]	4
0.33 ± (0.18)	0.040[a]	5
0.33 ± (0.18)	0.040[a]	6
0.29 ± (0.18)	0.064	7
0.29 ± (0.18)	0.058	8
0.30 ± (0.18)	0.053	9
0.30 ± (0.18)	0.056	10

Model: Adjusted for age and BMI and noted PC number in table.
SNPs are limited to ≥5% MAF.
Prevalence estimates of fibroids are set at 70%.
[a]Statistically significant

Supplemental Table 2. Heritability estimates for largest fibroid dimension using European Americans within BioVU.

Heritability Estimate ± (Std. Err.)	P-value	PC Adjustments
0.34 ± (0.47)	0.246	0
0.40 ± (0.47)	0.209	1
0.40 ± (0.47)	0.209	2
0.40 ± (0.47)	0.209	3
0.39 ± (0.47)	0.212	4
0.35 ± (0.47)	0.238	5
0.36 ± (0.48)	0.233	6
0.38 ± (0.48)	0.224	7
0.39 ± (0.48)	0.214	8
0.43 ± (0.48)	0.195	9
0.44 ± (0.48)	0.190	10

Model: Adjusted for age and BMI and noted PC number in table.
SNPs are limited to ≥5% MAF.

Supplemental Table 3. Heritability estimates for largest fibroid volume using European Americans within BioVU.

Heritability Estimate ± (Std. Err.)	P-value	PC Adjustments
0.12 ± (0.65)	0.426	0
0.18 ± (0.65)	0.391	1
0.18 ± (0.65)	0.389	2
0.12 ± (0.66)	0.427	3
0.13 ± (0.66)	0.423	4
0.14 ± (0.66)	0.417	5
0.16 ± (0.65)	0.404	6
0.17 ± (0.67)	0.399	7
0.24 ± (0.67)	0.355	8
0.28 ± (0.67)	0.334	9
0.35 ± (0.67)	0.300	10

Model: Adjusted for age and BMI and noted PC number in table.
SNPs are limited to ≥5% MAF.

Supplemental Table 4. Heritability estimates of fibroid risk with suggestive to significant regions of the genome removed from prior studies.

Studies	Heritability Estimate ± (Std. Err.)
No Studies	0.33 ± (0.18)
[1]	0.33 ± (0.18)
[2]	0.33 ± (0.18)
All Studies	0.34 ± (0.18)

Model: Adjusted for age, BMI, and 5 PCs.
SNPs are limited to ≥5% MAF.
Prevalence estimates of fibroids are set at 70%.

References

1 Cha, P. C. *et al.* A genome-wide association study identifies three loci associated with susceptibility to uterine fibroids. *Nature genetics* **43**, 447-450, doi:10.1038/ng.805 (2011).

2 Hellwege, J. N. *et al.* A multi-stage genome-wide association study of uterine fibroids in African Americans. *Human genetics*, doi:10.1007/s00439-017-1836-1 (2017).

Supplemental Table 5. Final sample size and SNP count for each outcome.

Outcome	Sample Size	Post QC SNP Number - MAF 5%[a]
Fibroid Risk		4,500,362
Case	1,042	
Control	1,067	
Volume	373	4,522,829
Max Dimension	551	4,518,340

[a]Post QC SNP Numbers - These are slightly different between studies because we removed SNPs out of HWE at the end for each outcome independently.

Supplemental Table 6. Heritability estimates for fibroid risk using European Americans within BioVU.

Heritability Estimate ± (Std. Err.)	P-value	Prevalence
0.24 ± (0.13)	0.040[a]	0.10
0.29 ± (0.16)	0.040[a]	0.20
0.33 ± (0.18)	0.040[a]	0.30
0.35 ± (0.19)	0.040[a]	0.40
0.35 ± (0.20)	0.040[a]	0.50
0.35 ± (0.19)	0.040[a]	0.60
0.33 ± (0.18)	0.040[a]	0.70
0.29 ± (0.16)	0.040[a]	0.80
0.24 ± (0.13)	0.040[a]	0.90

Model: Adjusted for age, BMI, and 5 PCs.
SNPs are limited to ≥5% MAF.
[a]Statistically significant