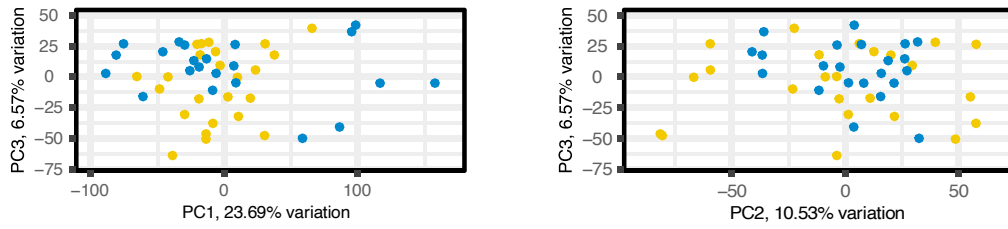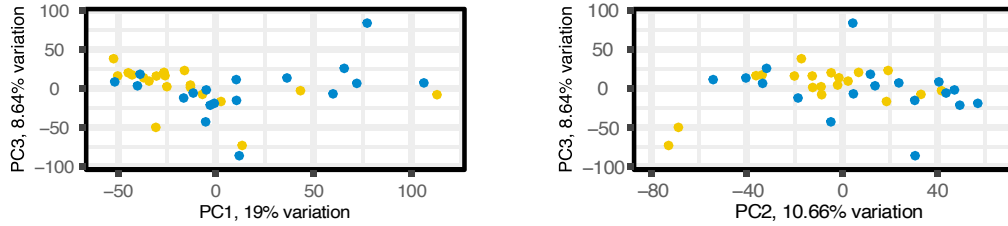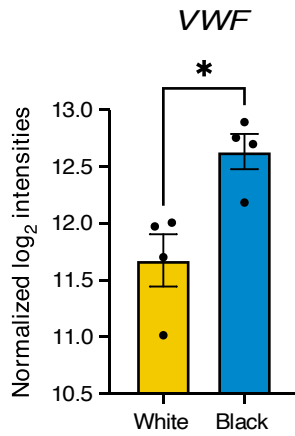# Figure S1

A

B

B
W

C

VWF

Figure S1. Principal component analyses of RNA-seq results from Fibroids (**A**) and Myometrial (**B**) samples from Black and White women. (**C**) Microarray results (GSE193320; Chuang, T.D., et al., *Differential Expression of Super-Enhancer-Associated Long Non-coding RNAs in Uterine Leiomyomas.* Reprod Sci, 2022.) for *VWF* expression in myometrial samples from Black and White women. *$p<0.05$ by two-tailed student t test.
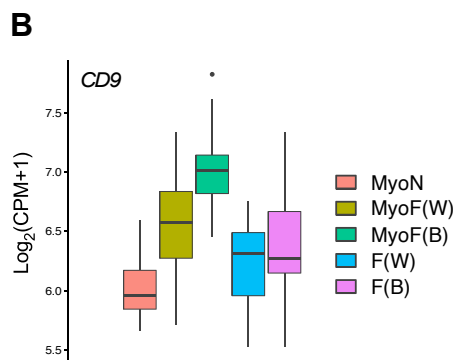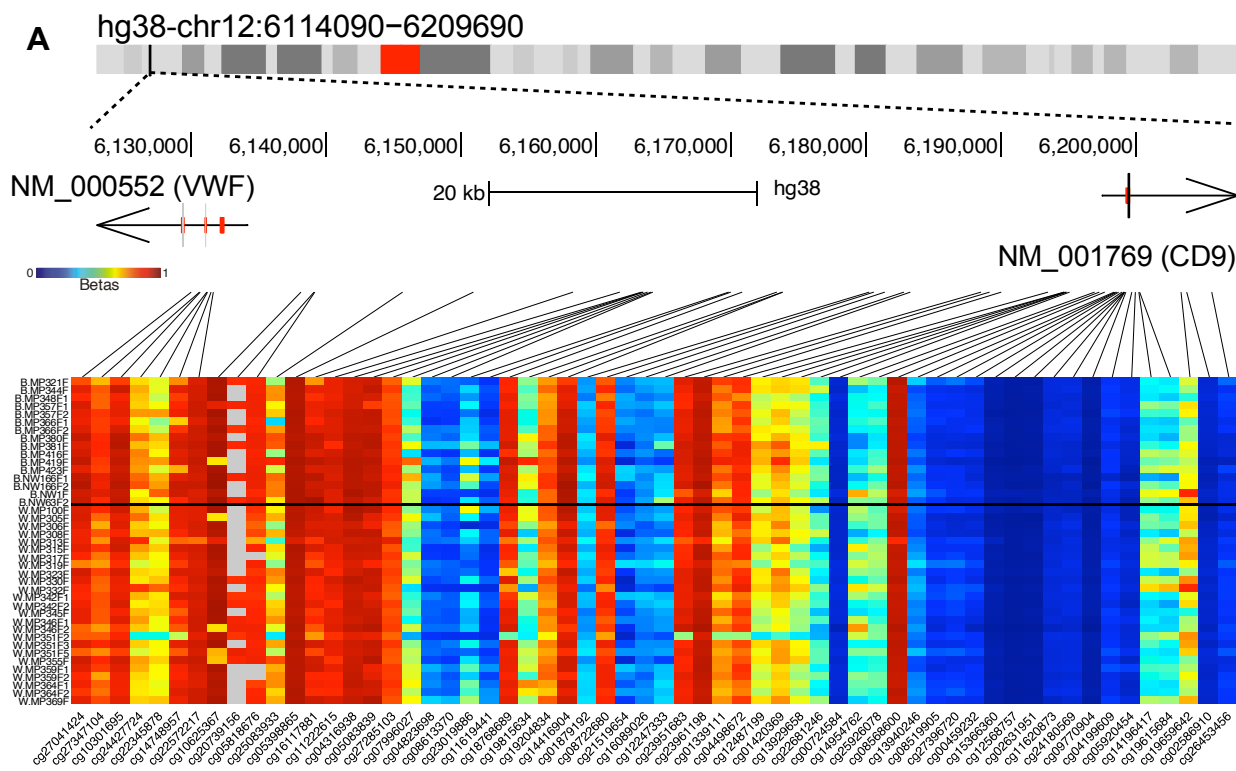
Figure S2

Figure S2. DNA methylation at the VWF and CD9 genes. **(A)** Heatmap of the CpG probes methylation beta values in fibroids. The white box indicates the position of the 2 CpG probes that are differentially methylated in myometrial samples (Fig 5). The black line separates fibroid samples from Black and White women. **(B)** Box and wisker plot for CD9 expression.

Figure S3

A

B

Race Check of Myometrium

C

Cell Composition Check

Figure S3. Sample quality control. (A) SNPs were determined from the EPIC Array data and used to generate a heatmap in tissues. Samples from the same patient a found in a single branch. (B) Principal component analysis of race-specific SNPs were used to ensure that only samples with congruent self-reported race and SNPs were subsequently analyzed. (C) Cell composition by beta values for aSMA (smooth muscle-specific gene) and miR-200 (epithelial-specific).