**Supplementary Fig 1.** Exosome-induced vascular smooth muscle cell (VSMC) and endothelial cell (EC) migration does not significantly differ by diabetic or smoking status. Fold change in VSMC **(A)** and EC **(B)** migration when treated with exosomes from nondiabetic (*non-DM*) vs diabetic (*DM*) patients did not differ significantly between the two groups. Fold change in VSMC **(C)** and EC **(D)** migration when treated with exosomes from nonsmokers vs former smokers vs current smokers also did not differ significantly between the two groups. *FBS,* Fetal bovine serum; *NC,* negative control; *PDGF,* platelet-derived growth factor; *Veh,* vehicle. Data are reported as mean $+/-$ standard error of the mean. $P > .05$ for all comparisons (one-way analysis of variance with Tukey post hoc test).
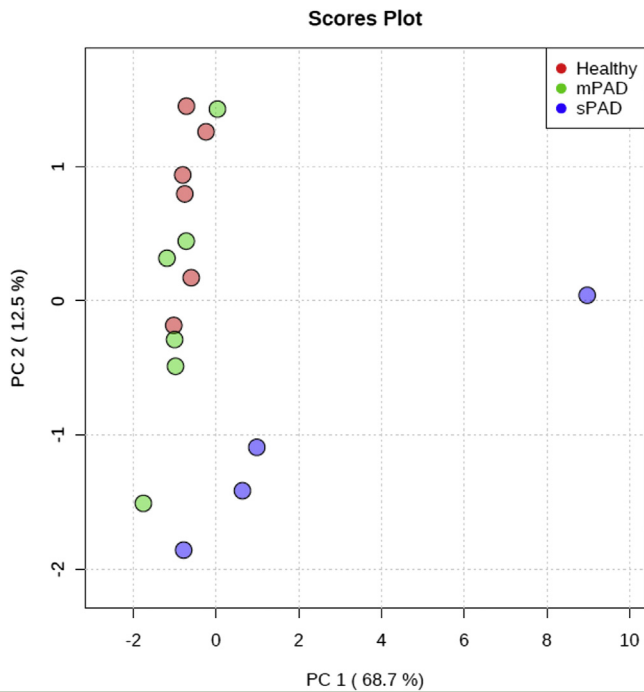
Supplementary Fig 2. Principal component (*PC*) analysis reveals distinct clusters of microRNA (miRNA) based on severity of peripheral artery disease (PAD). After normalization to a spike-in control, quantitative polymerase chain reaction (PCR) data from tested miRNA with cycle threshold values <35 were used to perform a principal component analysis, which reveals distinct clustering of patients with mild PAD (*mPAD*) and severe PAD (*sPAD*) based on their miRNA content.

Supplementary Table. Primer sequences for monocyte-derived macrophage (MDM) gene polymerase chain reaction (PCR) and exosome microRNA (*miRNA*) PCR

Gene	Primer sequence/assay ID (F = Forward, R = Reverse)
TNFa	F: AGAGGGCCTGTACCTCATCTACTC R: GGTTGACCTTGGTCTGGTAGGA
MCP1	F: CAGCAGCAAGTGTCCCAAAG R: GAATCCTGAACCCACTTCTGCTT
CXCL10	ID: Hs.58.39328322.gs (IDT Technologies)
IL10	F: GGCGCTGTCATCGATTTCTT R: GTAGATGCCTTTCTCTTGGAGCTT
CCL17	ID: Hs.PT.58.159549 (IDT Technologies)
MRC1	ID: Hs.PT.58.15093573 (IDT Technologies)
UBC	F: ATTTGGGTCGCGGGTTCTTG R: TGCCTTGACATTCTCGATGGT
HPRT	F: CAAGCTTGCTGGTGAAAAGGA R: TGAAGTACTTATAGTCAAGGGCATATC

miRNA	Primer sequence/catalog No. (Qiagen)
hsa-miR-21-5p	Sequence: 5'UAGCUUAUCAGACUGAUGUUGA Cat #: YP00204230
hsa-miR-23b-3p	Sequence: 5'AUCACAUUGCCAGGGAUUACC Cat #: YP00204790
hsa-miR-122-5p	Sequence: 5'UGGAGUGUGACAAUGGUGUUUG Cat #: YP00205664
hsa-miR-126-3p	Sequence: 5'UCGUACCGUGAGUAAUAAUGCG Cat #: YP00204227
hsa-miR-143-3p	Sequence: 5'UGAGAUGAAGCACUGUAGCUC Cat #: YP00205992
hsa-miR-145-5p	Sequence: 5'GUCCAGUUUUCCCAGGAAUCCCU Cat #: YP00204483
hsa-miR-146a-5p	Sequence: 5'UGAGAACUGAAUUCCAUGGGUU Cat #: YP00204688
hsa-miR-146b-5p	Sequence: 5'UGAGAACUGAAUUCCAUAGGCU Cat #: YP00204553
hsa-miR-155-5p	Sequence: 5'UUAAUGCUAAUCGUGAUAGGGGU Cat #: YP00204308
hsa-miR-181b-5p	Sequence: 5'AACAUUCAUUGCUGUCGGUGGGU Cat #: YP00204530
hsa-miR-195-5p	Sequence: 5'UAGCAGCACAGAAAUAUUGGC Cat #: YP00205869
hsa-miR-208a-3p	Sequence: 5'AUAAGACGAGCAAAAAGCUUGU Cat #: YP00205619
hsa-miR-219-5p	Sequence: 5'UGAUUGUCCAAACGCAAUUCU Cat #: YP00204780
hsa-miR-221-3p	Sequence: 5'AGCUACAUUGUCUGCUGGGUUUC Cat #: YP00204532
hsa-miR-222-3p	Sequence: 5'AGCUACAUCUGGCUACUGGGU Cat #: YP00204551
hsa-miR-1202	Sequence: 5'GUGCCAGCUGCAGUGGGGGAG Cat #: YP00206001