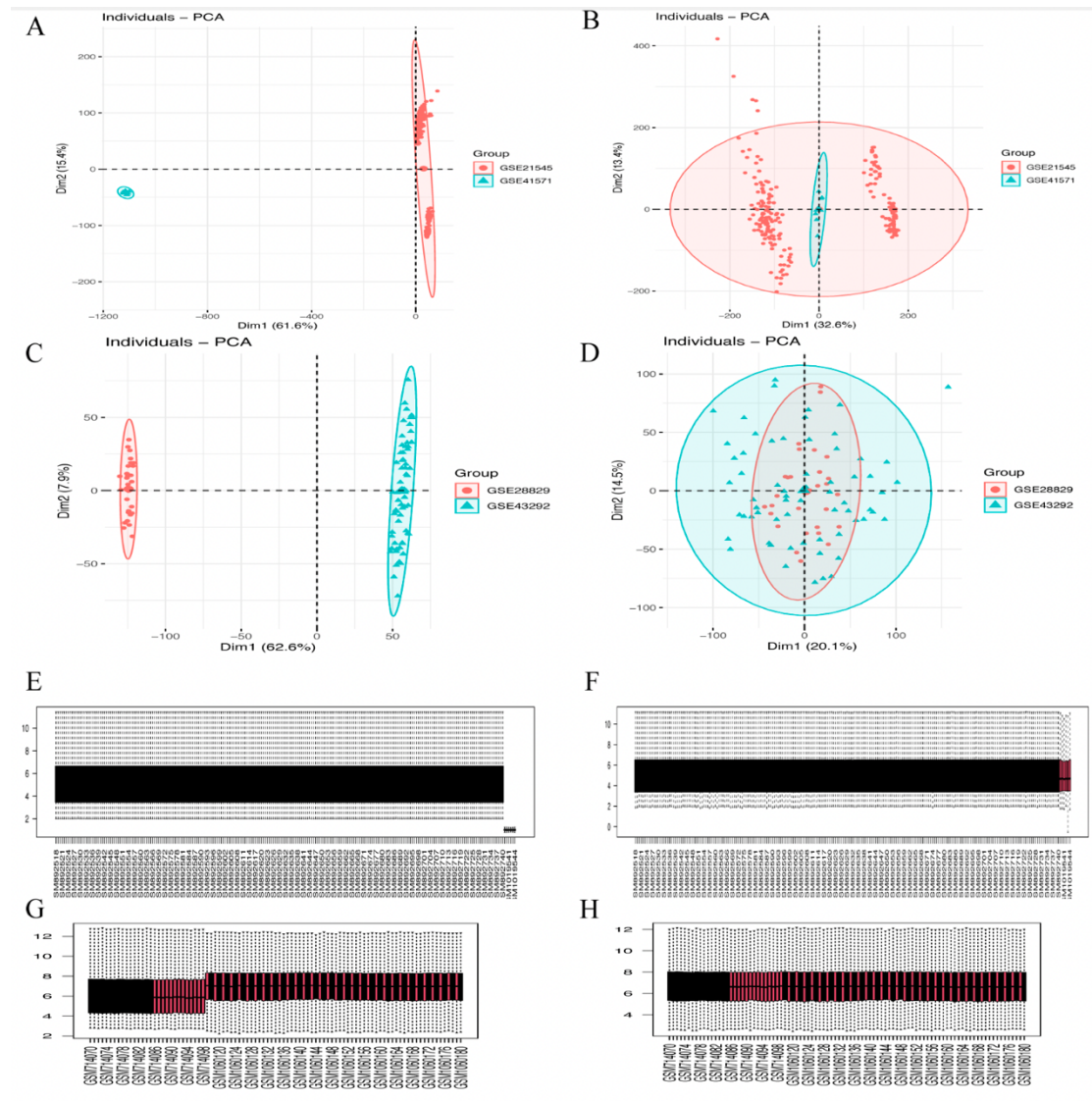
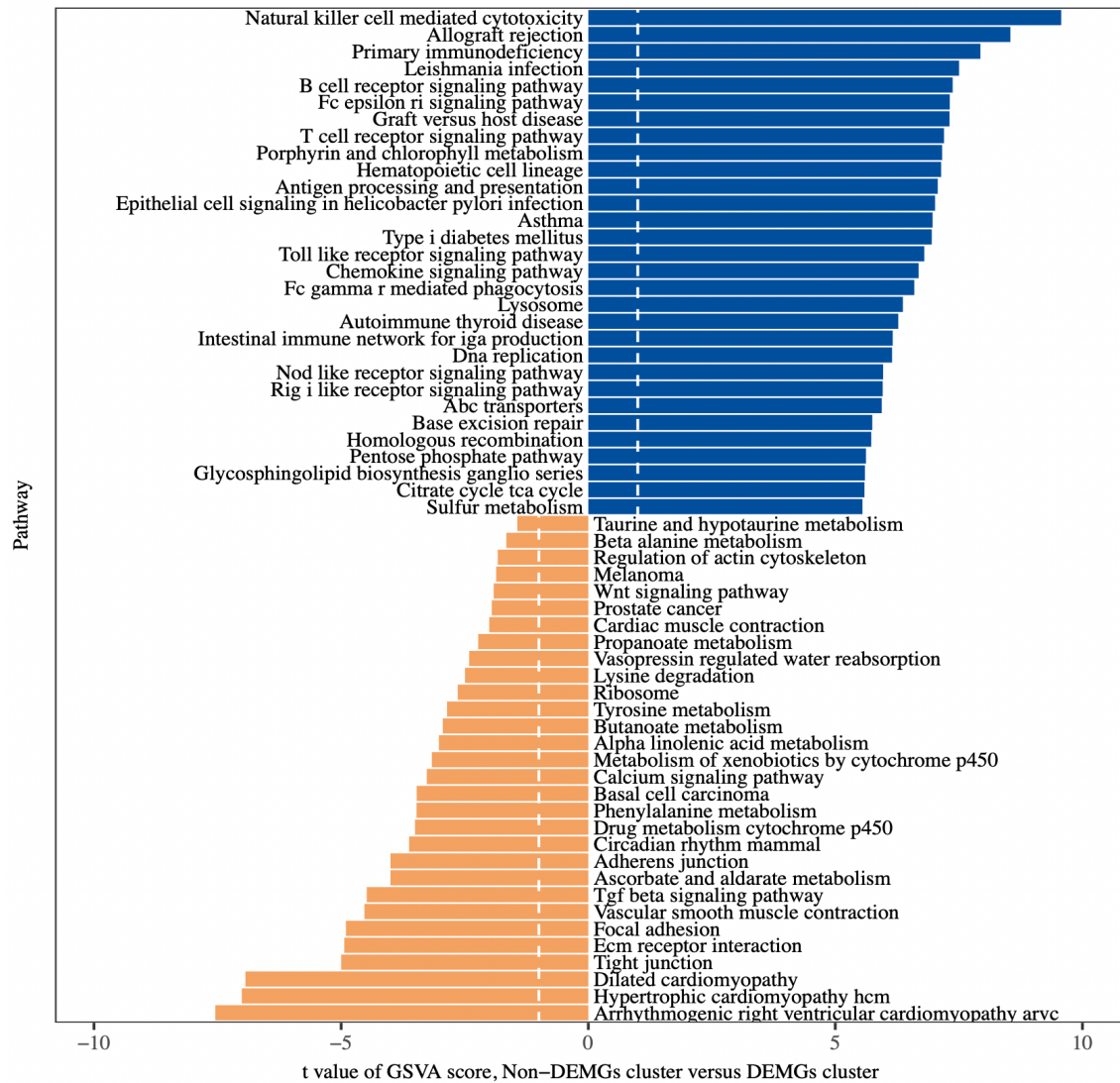


Supplementary Figure 1



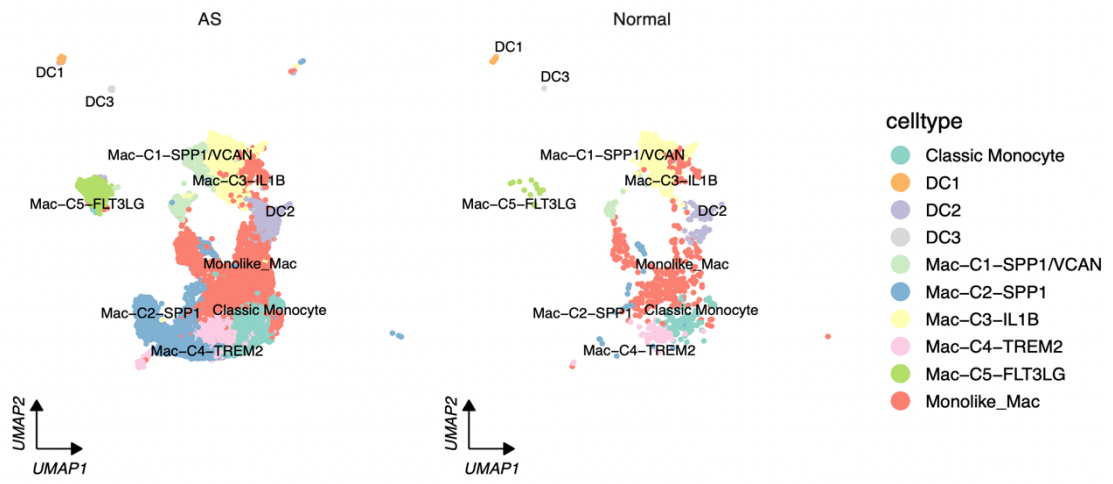
The merged matrix was standardized and processed. (A-B) The figure shows two-dimensional PCA cluster plots before and after correcting for inter-batch differences removed for GSE21545 and GSE41571. (C-D) The figure shows two-dimensional PCA cluster plots before and after correcting for inter-batch differences removed for GSE28829 and GSE43292. (E-F) The figure shows box plots before and after normalization for GSE21545 and GSE41571. (G-H) The figure shows box plots before and after normalization for GSE28829 and GSE43292.

Supplementary Figure 2



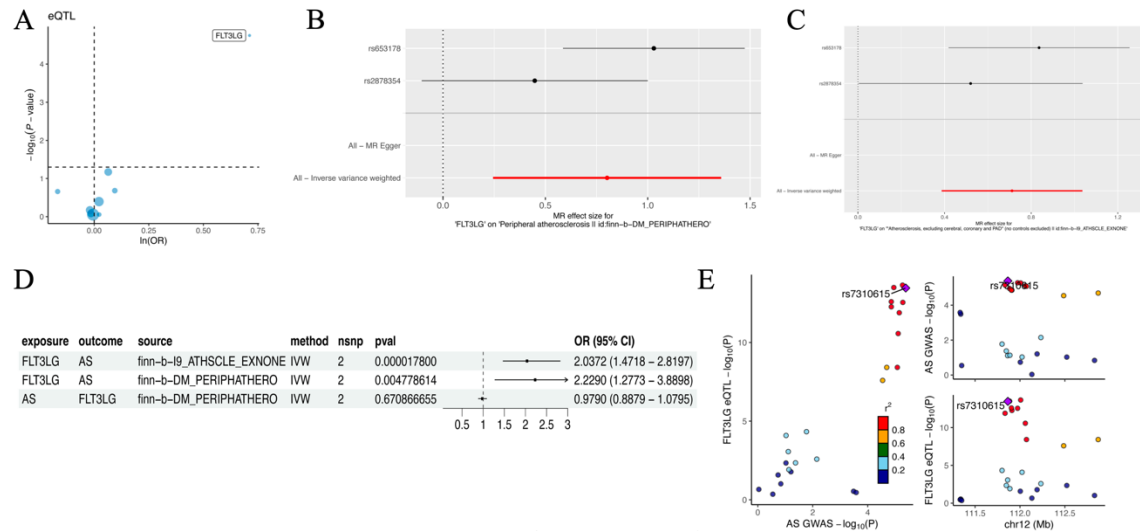
Top 30 KEGG pathways ranked by GSVA score differences between non-DEMGs cluster vs. DEMGs cluster.

Supplementary Figure 3



UMAP plot visualizing 10 myeloid subtypes identified from scRNA-seq in AS vs. normal groups.

Supplementary Figure 4



The MR analysis indicated a significant causal association between the eQTL of FLT3LG and AS. (A) Dot plot shows a significant causal association between the eQTL of FLT3LG and AS. (B-C) Forest plot of MR effect size FLT3LG on AS in different datasets, respectively. (D) Forest plot shows results of forward and reverse MR Analysis in AS. (E) Left: Scatter plot shows the relationship between the significance of eQTLs for the FLT3LG gene and the significance of GWAS. Each dot represents a single nucleotide polymorphism (SNP). The color coding (referenced in the legend as r^2) indicates the degree of linkage disequilibrium (LD) between the SNPs, with warmer colors like red indicating higher LD. Right: Regional association plot in on a specific region of chromosome 12 (chr12), where the FLT3LG gene is located. It shows the $-\log_{10}$ p-values of the association between SNPs in this region and the gene expression levels (eQTLs) and their association with AS.

Supplementary Table 1

GSEseries number	Data source	Group	Type	date	patient	sample	platforms	manufacturer
GSE159677	Carotid artery plaque	3AS:3non-AS	scRNA	10/2020	3	6	GPL18573	Illumina NextSeq 500 (Homo sapiens)
GSE155512	Carotid artery plaque	1AS:2non-AS	scRNA	08/2020	3	3	GPL24676	Illumina NovaSeq 6000 (Homo sapiens)
GSE43292	Carotid artery plaque	32AS:32non-AS	bulk	04/2013	32	64	GPL6244	Affymetrix Human Gene 1.0 ST Array
GSE28829	Carotid artery plaque	13EAS:16AAS	bulk	04/2011	29	29	GPL570	Affymetrix Human Genome U133 Plus 2.0 Array
GSE21545	Carotid artery plaque	126AS (carotid plaque):97AS (PBMC)	bulk	03/2012	223	126	GPL570	Affymetrix Human Genome U133 Plus 2.0 Array
GSE163154	Carotid artery plaque	16EAS:27AAS	bulk	12/2020	43	43	GPL6104	Illumina humanRef-8 v2.0 expression beadchip
GSE41571	Carotid artery plaque	6EAS:5AAS	bulk	12/2012	11	11	GPL570	Affymetrix Human Genome U133 Plus 2.0 Array

EAS, early atherosclerotic plaque; AAS, advanced atherosclerotic plaque

The source of the datasets.

Supplementary Table 2

Items	Identification of Hub Genes in AS Based on Bioinformatics Analysis		
	Our Findings	Cell Paper (PMID:36855107)	Cell Paper (PMID:36061826)
Years	2024	2023	2022
Atherosclerotic plaque subtypes with prognostic significance	cluster3 AS plaques	-	-
A subtype of macrophage with prognostic significance	SPP1 ⁺ /VCAN ⁺ macrophages, IL1B ⁺ macrophages, FLT3LG ⁺ macrophages	SPP1 ⁺ macrophages	-
Single cell analysis strategies	Monocle2, PySCENIC, scMetabolism, CellChart, BayesPrism	Monocle2, SCENIC, scMetabolism, NicheNet, CIBERSORTX	-
Mendelian Randomization (MR) analysis	use	-	-
Machine learning algorithms	10 algorithms	-	3 algorithms
Bulk datasets use	GSE21545, GSE41571, GSE163154, GSE28829, GSE43292	GSE21545, GSE100927, GSE163154, GSE43292	GSE28829, GSE43292, GSE100927
Verification	Mice Atherosclerotic plaque: qPCR, WB, mIF	-	Mice Atherosclerotic plaque: WB, mIF

qPCR, quantitative real-time polymerase chain reaction; WB, western blot; mIF, multiplex immunofluorescence

Several findings in this study are significantly novel in comparing to what is published.