

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: The list of genes differentially expressed in the aortic CFU-M progenitor cell clusters identified by scRNA-seq. Cluster identity and fold changes in expression with adjusted p -values for the genes are listed.

File Name: Supplementary Data 2

Description: Pathways in which genes differentially expressed in the aortic CFU-M progenitor cluster 1 identified by scRNA-seq are over-represented. Significantly over-represented pathways are those with corrected $p < 0.05$.

File Name: Supplementary Data 3

Description: List of pathways in which genes differentially expressed in the aortic CFU-M progenitor cluster 2 identified by scRNA-seq are over-represented. Pathways with corrected $p < 0.05$ are significantly over-represented.

File Name: Supplementary Data 4

Description: Pathways in which genes differentially expressed in the aortic CFU-M progenitor cluster 3 identified by scRNA-seq are over-represented. Significantly over-represented pathways are the ones with corrected $p < 0.05$.

File Name: Supplementary Data 5

Description: List of pathways in which genes differentially expressed in the aortic CFU-M progenitor cluster 4 identified by scRNA-seq are over-represented. Pathways with corrected $p < 0.05$ are significantly over-represented.

File Name: Supplementary Data 6

Description: Pathways in which genes differentially expressed in the aortic CFU-M progenitor cluster 5 identified by scRNA-seq are over-represented. Significantly over-represented pathways are those with corrected $p < 0.05$.

File Name: Supplementary Data 7

Description: List of pathways in which genes differentially expressed in the aortic CFU-M progenitor cluster 6 identified by scRNA-seq are over-represented. Pathways with corrected $p < 0.05$ are significantly over-represented.

File Name: Supplementary Data 8

Description: Pathways in which genes differentially expressed in the aortic CFU-M progenitor cluster 7 identified by scRNA-seq are over-represented. Significantly over-represented pathways are those with corrected $p < 0.05$.

File Name: Supplementary Data 9

Description: List of pathways in which genes differentially expressed in the aortic CFU-M progenitor Proliferative cluster 1 identified by scRNA-seq are over-represented. Pathways with corrected $p < 0.05$ are significantly over-represented.

File Name: Supplementary Data 10

Description: Pathways in which genes differentially expressed in the aortic CFU-M progenitor Proliferative cluster 2 identified by scRNA-seq are over-represented. Significantly over-represented pathways are those with corrected $p < 0.05$.

File Name: Supplementary Data 11

Description: Significantly over-represented transcription factor binding sites in genes differentially expressed in the aortic CFU-M progenitor clusters identified by scRNA-seq. Cluster identity, transcription factors, numbers of differentially expressed genes and numbers of genes in InnateDB with binding sites for the transcription factors and corresponding corrected p -values are indicated.

File Name: Supplementary Data 12

Description: A list of antibodies, important chemicals, including pharmacological agents, peptides, recombinant proteins, assays, mouse strains and software used in this study.

File Name: Supplementary Data 13

Description: A list of primers used for qRT-PCR analyses of indicated genes in this study.