

## **Descriptions of additional Supplementary files**

### **Supplementary Dataset 1: SMC dataset**

Zipped .h5ad object for the aortic smooth muscle cells which can be loaded using the AnnData or ScanPy libraries in Python. The object contains cell information in the .obs slot. In particular, cell collection times and cell library sizes can be viewed in the 'zt' and 'lib\_size' columns of the .obs slot. Gene information can be found in the .var slot. The object contains UMI counts in the .X slot ([cells x genes] matrix of the raw counts).

### **Supplementary Dataset 2: Fibroblast dataset**

Zipped .h5ad object for the aortic fibroblasts which can be loaded using the AnnData or ScanPy libraries in Python. The object contains cell information in the .obs slot. In particular, cell collection times and cell library sizes can be viewed in the 'zt' and 'lib\_size' columns of the .obs slot. Gene information can be found in the .var slot. The object contains UMI counts in the .X slot ([cells x genes] matrix of the raw counts).

### **Supplementary Dataset 3: Endothelial dataset**

Zipped .h5ad object for the aortic endothelial cells which can be loaded using the AnnData or ScanPy libraries in Python. The object contains cell information in the .obs slot. In particular, cell collection times and cell library sizes can be viewed in the 'zt' and 'lib\_size' columns of the .obs slot. Gene information can be found in the .var slot. The object contains UMI counts in the .X slot ([cells x genes] matrix of the raw counts).

### **Supplementary Dataset 4: Macrophage dataset**

Zipped .h5ad object for the aortic macrophages which can be loaded using the AnnData or ScanPy libraries in Python. The object contains cell information in the .obs slot. In particular, cell collection times and cell library sizes can be viewed in the 'zt' and 'lib\_size' columns of the .obs slot. Gene information can be found in the .var slot. The object contains UMI counts in the .X slot ([cells x genes] matrix of the raw counts).