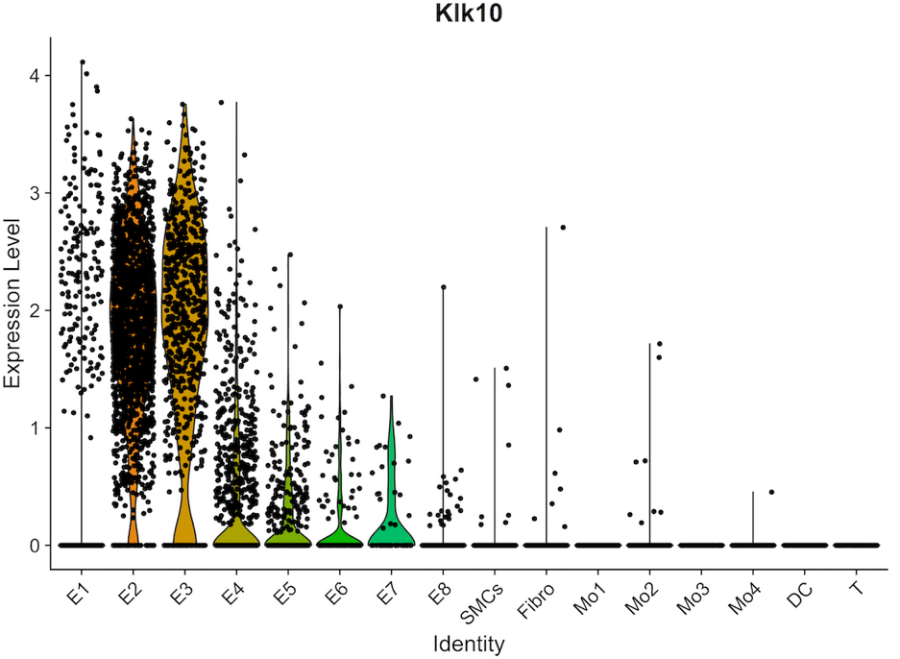
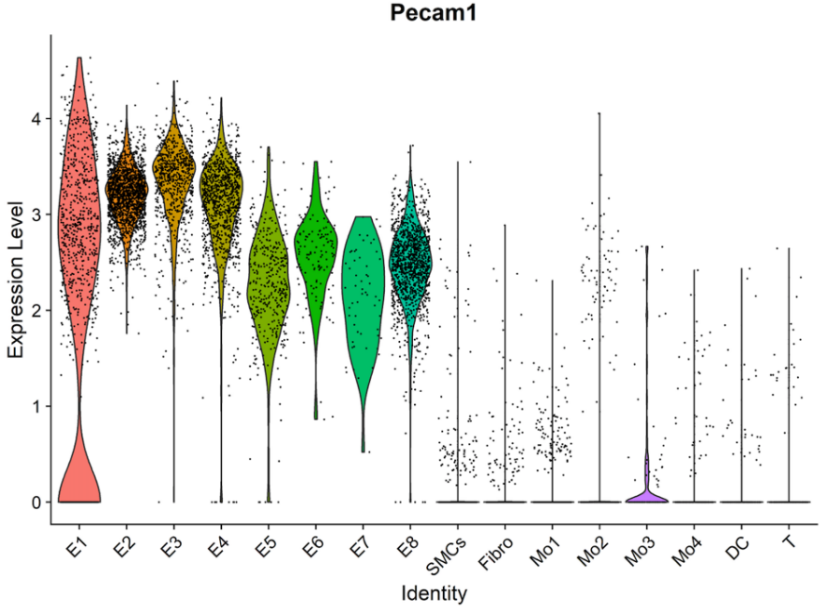
**Figure 1- Figure Supplement 1. scRNAseq analysis of *Klk10* and *Pecam1* from the PCL mouse model.** Violin plots show single cell expression of (a) *Klk10* and (b) CD31 (*Pecam1*) gene transcripts in 8 endothelial cell clusters (E1-E8), smooth muscle cells (SMCs), fibroblasts (Fibro), 4 monocytes/macrophages clusters (Mo1-4), dendritic cells (DC), and T cells (T) in the mouse carotid arteries following 2 days or 2 weeks of the PCL surgery as we recently reported38. The published scRNAseq data38 were re-analyzed here for *Klk10* and *Pecam1* genes. E1–E4 clusters represent ECs exposed to *s-flow* conditions in the RCA. E5 and E7 clusters represent ECs exposed to acute (2 days) *d-flow* in the LCA*.* E6 and E8 clusters represent ECs exposed to chronic (2 weeks) *d-flow* in the LCA*.*



**a**

*Klk10*



*Pecam1*

**b**