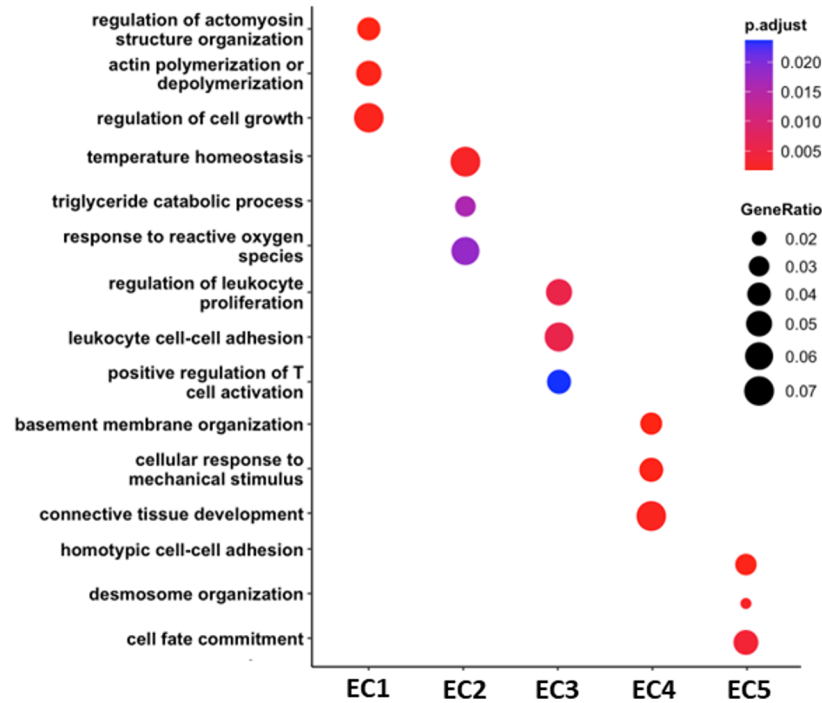
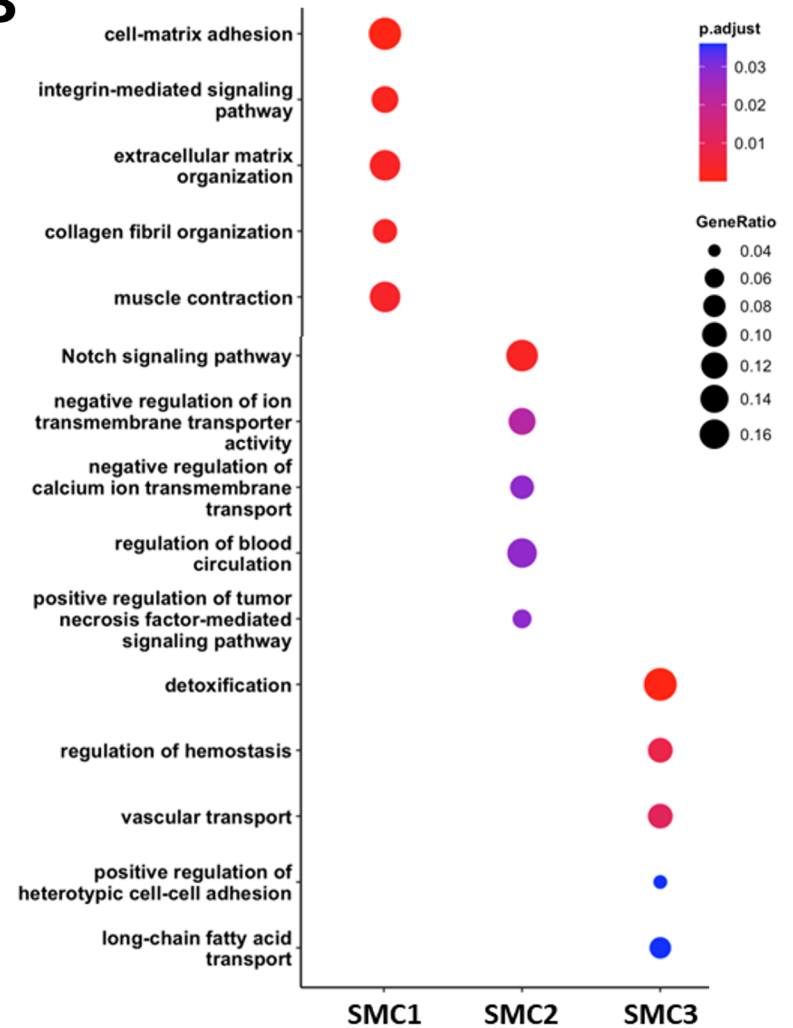


A**B**

S5 Fig. Predicted functional differences among cell populations in veins. Gene ontology pathway analysis of genes expressed in endothelial cell (A) and smooth muscle cell (B) populations in veins. EC1: arteriolar-like, EC2: capillary-like, EC3: venous-like, EC4: valvular-like, EC5: lymphatic-like, SMC1: *MYH11*^{hi}*DES*^{hi}, SMC2: *MYH11*^{lo}*DES*^{lo}, SMC3: pericyte-like.