SUPPLEMENTARY FIG. S2. Distribution curves reflecting the likelihood of obtaining clusters with specific Lewis-X (LeX)[+]/C1qR1[+] to LeX[+]/C1qR1^{−} cells ratio. **(A)** Single-cell mRNA data from passage 2 LeX[+]/C1qR1[+] and LeX[+]/C1qR1^{−} cells were pooled and 100 cells (number of cells in cluster L1) were randomly selected to form a cluster and the ratio of LeX[+]/C1qR1[+] to LeX[+]/C1qR1^{−} cells was calculated. This procedure was repeated 1,000 times to construct the distribution curve. Values, 0.75 and 1.33, on the *x*-axis are the boundaries at 90% significance level. Similarly, distribution curves for **(B)** cluster L2 and **(C)** cluster L3 were also constructed. The boundaries at 90% significance level for cluster L2 are at 0.72 and 1.39 and for cluster L3 are at 0.83 and 1.21. The ratios for clusters L1, L2, and L3 at 4.26, 0.64, and 0.57, respectively, indicate that these clusters are not formed by chance.