Supplementary Data 1: Differential expression analysis. Table (excel format) showing data obtained by the Model-based Analysis of Single-cell Transcriptomics (MAST) method. Each cluster was compared versus the rest using a p adjusted value of <0.01.

Supplementary Data 2: Differential expression analysis. Table (excel format) showing data obtained by the Model-based Analysis of Single-cell Transcriptomics (MAST) method comparing specific clusters.

Supplementary Data 3: Source data underlying Figures 1 and 2.