Suppl 1. scRNA-seq profiling of cells from the healthy human and AIS vertebra tissues. a. Overview of the single-cell isolation and analysis workflow.

b. Workflows of the the dissociation of vertebra tissues and the preparation of single-cell solutions for scRNA-seq.

c. The generation of scRNA-seq cDNA expression libraries using BD Rhapsody system.

d. Data analysis, including cell clustering and cell counts analysis, pseudotime analysis and cell communication analysis.