

We used Cell Ranger to complete gene and expression identification, transferred the obtained expression matrix to Seurat for subsequent analysis, and used DoubletFinder to perform polycellular filtering, thus the result of single cell subcluster classification can be visualized. Monocle2, Monocle3, PAGA, and scVelo were used for pseudotime analysis of single cell subclusters. We used CopyKAT to identify malignant cells. CellphoneDB was used to analyze cell communication. The 10 × Genomics datasets generated during this study is publicly available via Genome Sequence Archive (GSA), under the **Accession number: HRA002151**.

The software we used is open source software. The software list is as follows:

1. **Software:** Cell Ranger  
**Version number:** cellranger-5.0.0  
**Download address:** <http://support.10xgenomics.com/single-cell/software/overview/welcome>
2. **Software:** Seurat  
**Version number:** V3.1.1  
**Download address:** <https://satijalab.org/seurat/index.html>
3. **Software:** DoubletFinder  
**Version number:** v2.0.3  
**Download address:** <https://github.com/ddiez/DoubletFinder>
4. **Software:** Monocle2  
**Version number:** V2.10.1  
**Download address:** <http://cole-trapnell-lab.github.io/monocle-release/>
5. **Software:** Monocle3  
**Version number:** 0.2.1  
**Download address:** <https://cole-trapnell-lab.github.io/monocle3/docs/installation/>
6. **Software:** PAGA  
**Version number:** Scanpy (v1.6.0)  
**Download address:** <https://github.com/theislab/paga>
7. **Software:** scVelo  
**Version number:** 0.2.2 (python 3.7.3)  
**Download address:** <https://scvelo.readthedocs.io/>
8. **Software:** CopyKAT  
**Version number:** 1.0.4  
**Download address:** <https://github.com/navinlabcode/copykat>
9. **Software:** cellphoneDB  
**Version number:** v2.1.2  
**Download address:** <https://github.com/Teichlab/cellphonedb>