1 Methods

We obtained single-cell sequencing data. [1] The pre-processed gene counts are accessible through GEO (accession no. GSE147082). To obtain the spliced-unspliced ratios required for cell velocity calculation, we retrieved the full sequences from SRA (accession no. PRJNA612966)

References

[1] Susan Olalekan, Bingqing Xie, Rebecca Back, Heather Eckart, and Anindita Basu. Characterizing the tumor microenvironment of metastatic ovarian cancer by single-cell transcriptomics. *Cell reports*, 35(8), 2021.