

The Maehr Lab recently published a paper on single-cell RNA mapping of mouse thymus development. (You can find it [here](#).) We performed single-cell RNA sequencing on thymi from mouse embryos from 12.5 dpc (when the thymus forms) to birth (8 days later). The idea was to produce a resource for any lab studying thymus development or thymocyte development.

There is a ton you could dig into in this type of dataset: you could look for new cell subpopulations, find transcription factors that are subset-specific or dynamically expressed, or look for instances of "thymic crosstalk". One of my favorite aspects of the paper was that in a couple of places, we were able to cross-reference the expression data with GWAS hits. Although there are advantages of working in a developmental biology lab rather than doing on genetic epidemiology (with no access to wet-lab resources), this experience really showed me the importance of GWAS and similar research.

This was my first major project in my job, and I learned a ton. I hope to write some follow-up posts on specific technical topics. One of the biggest challenges was keeping everything organized and making sure the analyses were reproducible. I worked really hard at that, and you can find [the code](#) on Github.