In this project, I analyzed MiSeq data using R for my paper "Diverse mucosal-associated invariant T cell receptor usage and phenotype in HIV infection." We isolated peripheral blood mononuclear cells (PBMCs) from healthy donors (denoted as HD), HIV-1-infected individuals (denoted as HIV or PR) and elite controllers (denoted as EC) and stimulated with E.coli. We sorted MAIT cells using flow cytometry and used a high-throughput sequencing method (MiSeq) with bar coding to link the expression of TCRα, TCRβ, and functional genes of interest at the single cell level.