

T cell responses at diagnosis of amyotrophic lateral sclerosis predict disease progression

ID: 2022-113

Data documentation

The data set contains information from 9 individuals. As described, we used single cell RNA sequencing in combination with V(D)J sequencing to study the immune profile of the central nervous compartment.

File format: .fastq.gz

File naming: [NGI ID]_S1_L00[Lane Number]_[Read Type]_001.fastq.gz

Lane Number: 1 or 2

Read Type: R: Read or I: Index

Variable name	participant	NGI ID	group	experiment	batch
Format	Case #, Control #	Pxxxxx_xxxx	MND, NPH, cervical radiculopathy, healthy control	scRNAseq, TCR seq	Batch #
Description	We have information on 5 ALS patients (Case #) and 4 controls (control #)	Folder names	Information on the health status of participants. Cases: Motor neuron disease (MND). Controls: normal pressure hydrocephalus (NPH), radiculopathy, healthy control	Per individual we collected data on single cell RNA sequencing (scRNAseq) and V(D)J sequencing (TCR seq)	Samples were collected and run on different days. Samples in the same batch share the same batch number.