

# Extracting information from omics data

2pm Tuesday 9 April 2024; Data-driven approaches to understanding dementia

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# Practical session

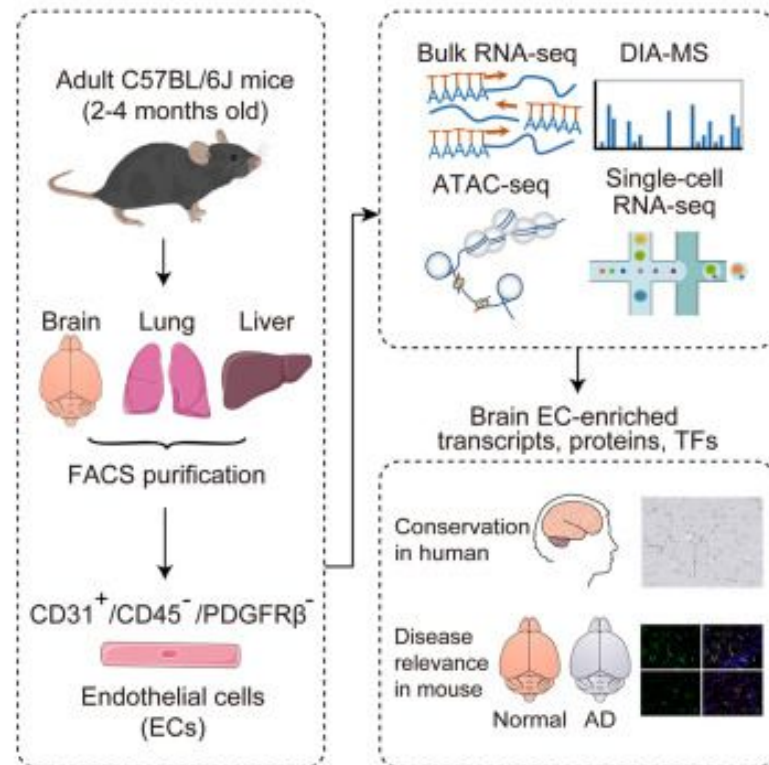
# Integrative multi-omic profiling of adult mouse brain endothelial cells and potential implications in Alzheimer's disease


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[Open Access](#) • Published: November 04, 2023 •

DOI: <https://doi.org/10.1016/j.celrep.2023.113392> •  Check for updates






  
Gene Expression Omnibus

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Scope: Self Format: HTML Amount: Quick GEO accession: GSE185642 

Series **GSE185642** [Query DataSets for GSE185642](#)

StatusPublic on Oct 31, 2023

TitleIntegrative multi-omic profiling of adult mouse brain endothelial cells and potential implications in Alzheimer's disease

Organism[Mus musculus](#)

Experiment typeExpression profiling by high throughput sequencing

SummaryThe blood-brain barrier (BBB) is primarily manifested by a variety of physiological properties of brain endothelial cells (ECs), but the molecular foundation for these properties remains incompletely clear. Here, we generate a comprehensive molecular atlas of adult brain ECs using acutely purified mouse ECs and integrated multi-omics. Using RNA-seq and proteomics, we identify the transcripts and proteins selectively enriched in brain ECs and demonstrate that they are partially correlated. Using single-cell RNA-seq, we dissect the molecular basis of functional heterogeneity of brain ECs. Using integrative epigenomics and transcriptomics, we determine that TCF/LEF, SOX, and ETS families are top-ranked transcription factors regulating the BBB. We then validate the identified brain EC-enriched proteins and transcription factors in normal mouse and human brain tissue, and assess their expression changes in mice with Alzheimer's disease. Overall, we present a valuable resource with broad implications for the BBB regulation and treatment of neurological disorders.

Overall designBulk-RNA-seq and ATAC-seq were performed on mouse brain, lung and liver endothelial cells. Single-cell RNA-seq was performed on adult mouse brain endothelial cells.

Web link<https://pubmed.ncbi.nlm.nih.gov/37925638/>

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CountryChina

Platforms (3)[GPL17021](#) Illumina HiSeq 2500 (Mus musculus)  
[GPL21103](#) Illumina HiSeq 4000 (Mus musculus)  
[GPL24247](#) Illumina NovaSeq 6000 (Mus musculus)

Samples (21)  
[Less...](#)

[GSM5621066](#) BR1-EC\_bRNA  
[GSM5621067](#) BR2-EC\_bRNA  
[GSM5621068](#) BR3-EC\_bRNA  
[GSM5621069](#) LG1-EC\_bRNA  
[GSM5621070](#) LG2-EC\_bRNA  
[GSM5621071](#) LG3-EC\_bRNA  
[GSM5621072](#) LV1-EC\_bRNA  
[GSM5621073](#) LV2-EC\_bRNA

# nf-core/fetchngs

[Edit](#)

Pipeline to fetch metadata and raw FastQ files from public databases

[ddbj](#) [download](#) [ena](#) [fastq](#) [geo](#) [sra](#) [synapse](#)

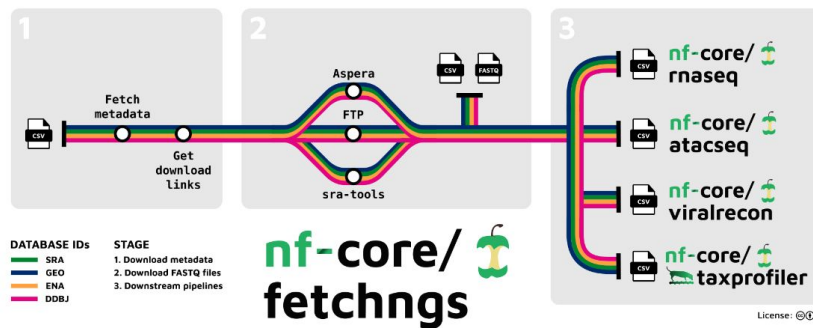
Launch version 1.12.0

<https://github.com/nf-core/fetchngs>

[Introduction](#)[Usage](#)[Parameters](#)[Output](#)[Results](#)[Releases](#)[1.12.0](#)

## Introduction

**nf-core/fetchngs** is a bioinformatics pipeline to fetch metadata and raw FastQ files from both public databases. At present, the pipeline supports SRA / ENA / DDBJ / GEO ids (see [usage docs](#)).



## Usage

### Note

If you are new to Nextflow and nf-core, please refer to [this page](#) on how to set-up Nextflow. Make sure to [test your setup](#) with

>\_ run with

nf-core launch nf-core/fetchngs

nf-core Nextflow Sequera Platform

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open issues open PRs

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last release last update

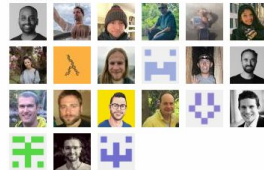
22 days ago 22 days ago

get help

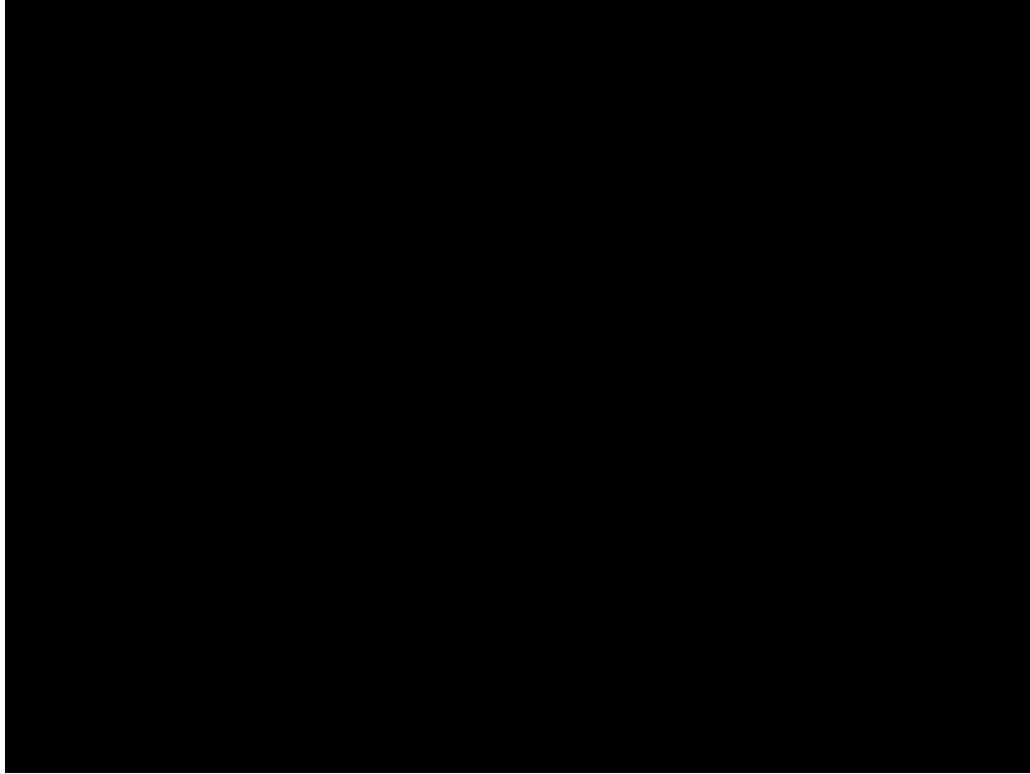
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contributors



VSCode alt+cmd multi-line editing



```
nextflow run nf-core/fetchngs -c KCL-CREATE.config \  
--input ids.csv --profile singularity --outdir raw-data \  
--nf_core_pipeline rnaseq atacseq
```

Take a few minutes to look at the MultiQC reports for the RNA-Seq and ATAC-Seq Nextflow runs

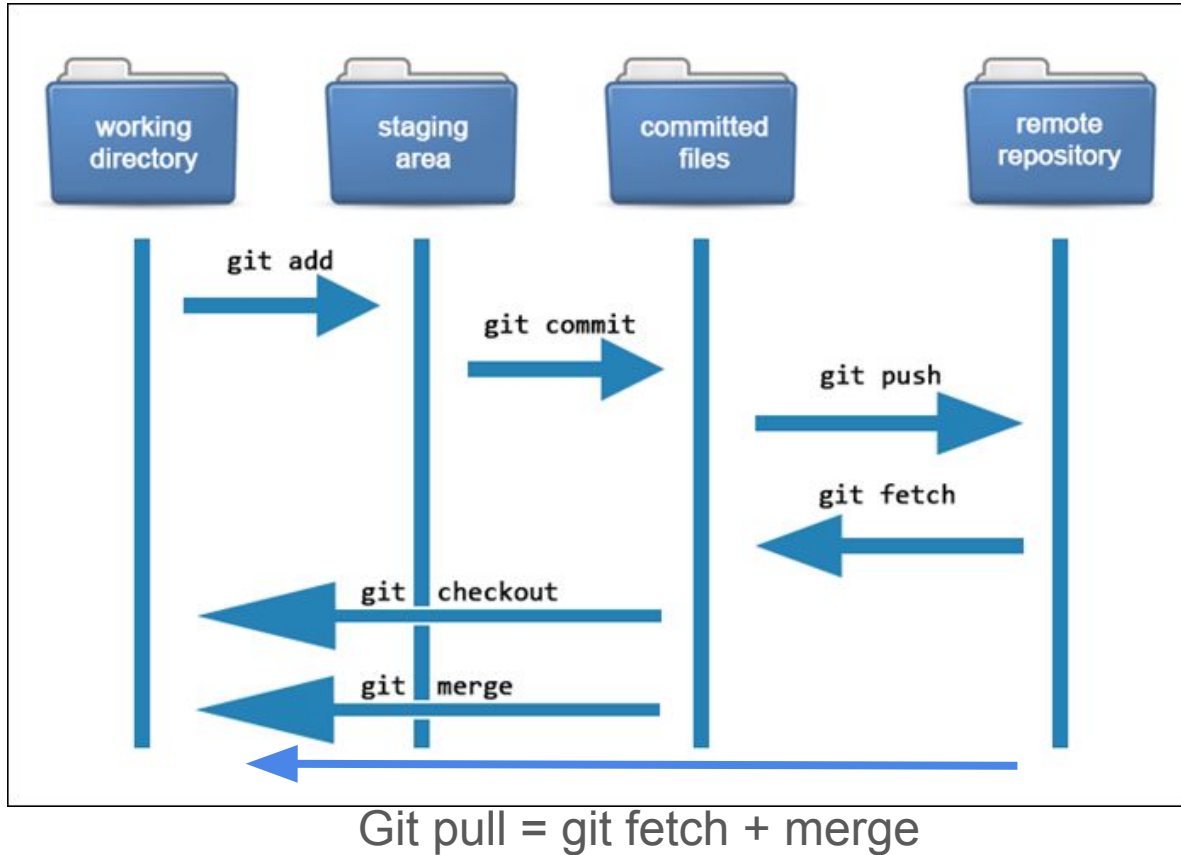
What can you say about the quality of the data?

Does anything worry you about this data?

Do you think it was a good idea to re-process the data from scratch rather than taking processed peaks/counts from the manuscript?



# Quick intro to git



## QR code to GitHub repo (just in case!)

- You should have a direct link to the repo in your handbooks

