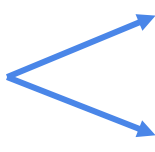


Cellranger Workflow

Files and requirements - What and where to get them?

  fasta files [Gallus_GRCg7b.dna.toplevel.fa]
gtf files [Gallus_GRCg7b.110.fa]

  application [cellranger-arc]

  fastq files [raw data]



 terminal [powerful computer]

File Requirements:

- Genome
- GTF

I have used the release **110** from Ensembl (**bGalGal1.mat.broiler.GRCg7b**)

Archive!Ensembl BioMart | Downloads | Help & Docs | Blog Login/Register

Search all species...

Chicken (bGalGal1.mat.broiler.GRCg7b) ▼

Search Chicken (Gallus gallus)

Search all categories ▼ Search... Go

e.g. [ESRRB](#) or [5:38111022-38265293](#) or [rs13582785](#) or [sphingolipid](#)

Genome assembly: bGalGal1.mat.broiler.GRCg7b (GCA_016699485.1)

[More information and statistics](#)

[Download DNA sequence \(FASTA\)](#)

[Display your data in Ensembl](#)

Other reference assemblies

GRCg6a (Ensembl release 106) Go

Other breeds

This species has data on 2 additional breeds. [View list of breeds](#)

Gene annotation

What can I find? Protein-coding and non-coding genes, splice variants, cDNA and protein sequences, non-coding RNAs.

[More about this genebuild](#)

[Download FASTA files for genes, cDNAs, ncRNA, proteins](#)

[Download GTF or GFF3 files for genes, cDNAs, ncRNA, proteins](#)

[Pax6](#) [Irf5](#) [Fgf2](#) [BrcA2](#) [Dmd](#) [ssh](#)

Example gene

Example transcript

Variation

What can I find? Short sequence variants; disease and other phenotypes

[More about variation in Ensembl](#)

[Download all variants \(GVF\)](#)

ATCGAGCT
ATCCAGCT
ATCGAGAT

Example variant

Example phenotype

Comparative genomics

What can I find? Homologues, gene trees, and whole genome alignments across multiple species.

[More about comparative analysis](#)

[Download alignments \(EMF\)](#)

Example gene tree

Regulation

What can I find? Microarray annotations.

[More about the Ensembl microarray annotation strategy](#)

Ensembl release 110 - July 2023 © EMBL-EBI

File Requirements:

- cellranger-arc



[Products](#)
[Resources](#)
[Support Hub](#)
[Company](#)

[Support home](#)
>
[Cell Ranger ARC](#)
>
[Tutorials](#)
>
[Cell Ranger ARC Installation](#)

Cell Ranger ARC

Overview

Getting Started

Download Center

Analysis

Inputs

Running Pipelines

Outputs

Tutorials

Algorithms

Advanced

Troubleshooting

Release Notes

Q&A

Datasets

Loupe Browser

Cell Ranger ARC Installation

Cell Ranger ARC is delivered as a single, self-contained tar file that can be unpacked anywhere on your system. It bundles all of its required software dependencies, which are pre-compiled to run on a [wide range](#) of Linux distributions. For convenience, the reference data package required for Cell Ranger ARC is provided as a separate download.



Alternatively, you can skip Cell Ranger ARC download and installation and use 10x Genomics Cloud Analysis, our recommended method for running 10x Genomics single cell pipelines for most new customers. [Sign up for a free account](#) or [view tutorials and learn more](#).

Download and install

Step 1 – Download and unpack the **cellranger-arc-2.1.0.tar.gz** tar file in any location. In this example we use `/opt`.

Copy

```

cd /opt
[download file from downloads page]
tar -xzf cellranger-arc-2.1.0.tar.gz

```

This unpacks Cell Ranger ARC, its dependencies, and the `cellranger-arc` script into a new directory called `cellranger-arc-2.1.0`.

Step 2 – Download and unpack any of the **reference data files** in a convenient location:

cellranger processing

File Requirements:

- raw data fastq files

Name ▾	Size	File Ty...
 scRNA_E5_PBS-SI_TT_D10_235GF3LT3_S3_L001_R2_001.fastq.gz	18.46 GB	GZ File
 scRNA_E5_PBS-SI_TT_D10_235GF3LT3_S3_L001_R1_001.fastq.gz	24.47 GB	GZ File
 scRNA_E5_PBS-SI_TT_D10_235GF3LT3_S3_L001_I2_001.fastq.gz	1.71 GB	GZ File
 scRNA_E5_PBS-SI_TT_D10_235GF3LT3_S3_L001_I1_001.fastq.gz	1.82 GB	GZ File
 MD5.txt	364 Bytes	TXT File

Name ▾	Size	File Ty...
 scATAC_E5_PBS-SI_3A_G11_235G7CLT3_S3_L001_R3_001.fastq.gz	16.74 GB	GZ File
 scATAC_E5_PBS-SI_3A_G11_235G7CLT3_S3_L001_R2_001.fastq.gz	4.22 GB	GZ File
 scATAC_E5_PBS-SI_3A_G11_235G7CLT3_S3_L001_R1_001.fastq.gz	17.09 GB	GZ File
 scATAC_E5_PBS-SI_3A_G11_235G7CLT3_S3_L001_I1_001.fastq.gz	1.7 GB	GZ File
 MD5.txt	368 Bytes	TXT File



Terminal

File Requirements:

- cellranger-arc binary
- raw data fastq files
- fasta files
- gtf files

> **cellranger-arc**[mkref] + **fasta files** + **gtf files** = **cellranger reference**

> **cellranger-arc**[counts] + **cellranger reference** + **fastq files** = **filtered h5 file**



Step 1: cellranger Reference

Make Reference file input for Chicken Genome

```
{  
  organism: "chicken"  
  genome: ["GRCg7b"]  
  input_fasta: ["/Gallus_gallus.bGalGal1.mat.broiler.GRCg7b.dna.toplevel.fa"]  
  input_gtf: ["/Gallus_gallus.bGalGal1.mat.broiler.GRCg7b.110.gtf"]  
}
```

txt.file

Run cellranger command to create reference using the file input

```
./cellranger-arc-2.0.2/cellranger-arc mkref \  
--config=1Pre-ref.config
```

code

Step 2: Cellranger count

Library csv input for Chicken Genome

```
$ Library_4FGF.csv
fastqs,sample,library_type
./FGF_Samples/ATAC_fastq,E4_FGF,Chromatin Accessibility
./FGF_Samples/RNA_fastq,E4_FGF,Gene Expression

$ Library_5FGF.csv
./FGF_Samples/ATAC_fastq,E5_FGF,Chromatin Accessibility
./FGF_Samples/RNA_fastq,E5_FGF,Gene Expression
```

csv.files

cellranger-arc count for Chicken Genome

```
#!/bin/bash
# File: Count.sh
list=(4FGF 5FGF)
for i in ${list[@]}
do
./cellranger-arc-2.0.2/cellranger-arc count --id=Multiomix_E${i} \
      --reference=./GRCg7b \
      --libraries=./Library_${i}.csv \
      --localcores=30 \
      --localmem=64
echo "Finish RNA-ATAC_${i}"
done
```

Code: bash Count.sh

cellranger processing