**Smart-seq2 Single Nucleus Multi Sample Pipeline**

**RRID:** SCR_021312  
**Type:** Tool

**Proper Citation**

Smart-seq2 Single Nucleus Multi Sample Pipeline (RRID:SCR_021312)

**Resource Information**

**URL:**  
https://github.com/broadinstitute/warp/tree/master/pipelines/skylab/smartseq2_single_nucleus_multisample

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**Description:** Software pipeline for single-nucleus RNAseq data generated by Smart-seq2 assays. Used to simultaneously process multiple libraries of single nuclei Smart-seq2 and Smart-seq4 data. For each library (nucleus), the pipeline trims paired FASTQ files, aligns trimmed reads to the genome, counts intronic and exonic reads, and calculates quality control metrics. Counts and metrics for all libraries are combined into merged Loom formatted count matrix.

**Resource Type:** Resource, software resource, software application, data processing software, software toolkit

**Keywords:** snRNAseq data, Smart-seq2 assays, single nucleus, multi sample, WARP repository

**Parent Organization:** Allen Institute, Broad Institute, University of California at San Diego; California; USA

**Related resources:** BICCN

**Availability:** Free, Freely available

**Website Status:** Last checked up

**Resource Name:** Smart-seq2 Single Nucleus Multi Sample Pipeline
Resource ID: SCR_021312

Alternate URLs: https://broadinstitute.github.io/warp/docs/Pipelines/Smart-seq2_Single_Nucleus_Multi_Sample_Pipeline/README, https://app.terra.bio/#workspaces/warp-pipelines/Smart-seq2_Single_Nucleus_Muti-Sample

Ratings and Alerts

No rating or validation information has been found for Smart-seq2 Single Nucleus Multi Sample Pipeline.

No alerts have been found for Smart-seq2 Single Nucleus Multi Sample Pipeline.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.