

## Experimental Metadata Specifications:

### ATAC-seq Epigenetic Profiling Assay

**Importance** 1: Required, 2: Required if available, 3: Optional

LINCS Field Name	Definition	Importance
ATACseq_Assay_Date	Date the sequencing was performed	1
ATACseq_Instrument	Name of the high-throughput sequencing system used	1
ATACseq_Software_Version	Software version of the instrument	1
ATACseq_Read_Length	Length of the read that the sequencer produces (the number of base pairs that can be read at one time)	1
ATACseq_Single_Paired	Whether one or both ends of the nucleotide fragment will be sequenced	1
ATACseq_Data_Processing_Pipeline	Link to the step by step protocol by which sequencing data was analyzed	1
ATACseq_Strand_Specificity	Describes the type of DNA-sequencing protocol that was used (stranded vs. non-stranded)	1
ATACseq_Starting_Nuclei	Number of nuclei that were used	1
ATACseq_Lysis_Method	Method used for the lysis of the cells	1
ATACseq_Sample_Preparation	Step by step experimental protocol	1
ATACseq_Library_Prep_Kit	Kit used in the experiment	2
ATACseq_Library_Size_Range	Base pair size ranged of library utilized	1
ATACseq_Total_Reads	Total number of sequencing reads recorded	2
ATACseq_Peak_Calling_Control	Controls used for the peak calling (e.g. inputs, IgG)	2
ATACseq_Nucleic_Acid_Type	Nucleic acid utilized for ATACseq experiment (e.g. DNA)	1
ATACseq_Biosample_Summary	Brief summary of the samples that were processed (organism, age, phenotype, etc.)	1