Experimental Metadata Specifications:

RNA-seq Gene Expression Profiling Assay

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

LINCS Field Name	Description	importance
RNAseq_Assay_Date	Date the sequencing was performed	1
RNAseq_Instrument	Name of the high-throughput sequencing system used	1
RNAseq_Software_Version	Software version of the instrument	1
RNAseq_Single_Paired	Whether one or both ends of the nucleotide fragment will be sequenced	1
RNAseq_Read_Length_1	Number of base pairs sequenced (if paired-end, depth of the first strand)	1
RNAseq_Read_Length_2	Number of base pairs sequenced from the second strand (only for paired-end reading)	1
RNAseq_Strand_Specificity	Describes the type of RNA-Seq protocol that was used (stranded vs. non-stranded)	1
RNAseq_Library_Starting_Quantity	Amount of used RNA	1
RNAseq_RNA_Integrity_Number	Minimum RIN value of the starting RNA	1
RNAseq_Lysis_Method	Method used for the lysis of the cells	1
RNAseq_Extraction_Method	RNA extraction / isolation method that was used	1
RNAseq_Fragmentation_Method	Method used to decrease the size of the nucleic acid	1
RNAseq_Size_Selection_Method	Method used to remove unwanted lengths of nucleic acid fragments	1
RNAseq_Size_Range	Size selection filter used for library construction	1
RNAseq_Spike_in_Controls	Spike-in controls that were used	1
RNAseq_Spike_in_Source	Source of the spike-ins (home-made or commercial or NIST)	1
RNAseq_Spike_in_Concentration	Concentration of each of the spike-ins in the pool used	1
RNAseq_Spike-in_Time	The time when the spike-in was done	2
RNAseq_Mean_Sequencing_Depth	Mean sequencing depth	1
RNAseq_Sequencing_Cycles	Number of sequencing cycles performed	1
RNAseq_Reference_Genome	Reference genome version used during alignment	1
RNAseq_Trim_Metric	Phred score threshold necessary for the removal of low quantity reads	1
RNAseq_Biosample_Type	Biosample type (cell line, primary cell, etc.)	1
RNAseq_Biosample_Summary	A brief summary of the sample that were processed (organism, age, phenotype, etc.)	1
RNAseq_Associated_SOPs	List and links for detailed SOPs that are necessary to reproduce the data	2
RNAseq_Replication_Type	Sample replication type (biological, isogenic, anisogenic, technical, etc.)	1
RNAseq_Replication_Count	Number of sample replicates	1
RNAseq_Pellet_Merge_Method	Method to merge pellets	2
RNAseq_Library_Prep_Kit	Kit used for the NGS library preparation	1
RNAseq_Library_Date_Extracted	Date of library extraction	2
RNAseq_Library_Indexing_Basepairing	Indexing basepairing as needed for de-multiplexing samples	2
RNAseq_Barcode	Barcode assigned to assay plate for multiplex sequencing	3
RNAseq_cDNA_Preparation_Method	Preparation method for the cDNA	1
RNAseq_PCR_Cycle_Number	Number of PCR amplification cycles to make the cDNA	2
RNAseq_Sequencing_Facility	Facility that performed sequencing	1
RNAseq_Sequencing_Chemistry_Version	Chemistry version used by the sequencing facility	2
RNAseq_Raw_File_Type	Format of the raw file (e.g. fastq)	1
RNAseq_Raw_File_Replicate_Number	Link to metadata file for experimental design schema	3
RNAseq_Plate_Format	Number of wells present on plate	2
RNAseq_Temperature	System temperature at which plate was examined, in Celsius	2