

Field group	User-friendly Field Name	Computer Readable Name	Description	Allowed value type	REQUIRED	Examples	Comments	
<h2>Project</h2>								
Project	Label	project_label	A unique label for the project.	Text	REQUIRED	kentBrainOrganoids		
Project	Title	project_title	A summary of the project in a sentence. Less than 30 words.	Text	REQUIRED			
Project	Lab	project_lab	Name of lab within institute where data was generated.	ID	REQUIRED	Kent		
Project	Institution	project_institution	Name of primary institute where data was generated	ID	OPTIONAL	NIH		
Project	Contact	project_contact	An email address for the project contact.	ID	REQUIRED	jane@institution.org		
Project	Submission Date	project_submission_date	Date of first submission of data set.	Date	OPTIONAL	12 May 2017		
Project	PMID	project_pubmed_id	The PubMed ID of the publication associated with this project.	ID	OPTIONAL			
Project	GEO Series Accession	project_geo_series_accession	An NCBI GEO series accession.	ID	OPTIONAL	GSE10001	Accession must start with GSE.	
Project	Supplementary Links	project_supplementary_links	External link(s) pointing to code, supplementary data files, or analysis files associated with the project which	Text	OPTIONAL	http://celtag.org/		
Project	Access	project_access	Controls who can access data under this project.	group, user, or Text	REQUIRED	group, user, or all		
Project	Publication	project_publication	External link(s) pointing to code, supplementary data files, or analysis files associated with the project which	Text	OPTIONAL	http://celtag.org/		
<h2>Sample</h2>								
Biosample	Species	donor_species	Organism of origin; a controlled vocabulary describing the organism from which the primary cell was derive Homo sapiens	REQUIRED	Homo sapiens, Mus musculus	http://purl.obolibrary.org/obo/NCBITaxon_2759		
Biosample	Strain	donor_strain	For nonhuman donors, strain within species.	C57BL/6, BALB/c	REQUIRED	C57BL/6, CD1	http://purl.obolibrary.org/obo/NCBITaxon_10090	
Biosample	NCBI Taxon ID	donor_ncbi_taxonomy_id	A taxonomy ID (taxonID) from NCBI. Multiple IDs can be provided for multi-species samples.	9606, 10090	CV	OPTIONAL	https://www.ncbi.nlm.nih.gov/taxonomy	
Biosample	ID	donor_id	Unique identifier of the organism as the source of the Biosample. If Biosample Source is a human subject pa	ID	REQUIRED	Participant2345		
Biosample	Parents	donor_parents	Biological parents of this donor. Enter the ID of the parent.	ID	OPTIONAL	Participant1, Participant2		
Biosample	Siblings	donor_siblings	A donor that has at least one parent in common. Enter the ID of the sibling.	ID	OPTIONAL	Participant2345		
Biosample	Twin	donor_twin	A human donor that is a twin sibling of this human donor.	ID	OPTIONAL	Participant2345		
Biosample	Twin Type	donor_twin_type	The type of the twin sibling of this donor (dizygotic or monozygotic)	identical_twin, CV	OPTIONAL	identical_twin, fraternal_twin	http://purl.obolibrary.org/obo/NCIT_C73427	
Biosample	Sex	donor_sex	Biological sex of the individual organism from which the initial Biosample was obtained. An organismal qua male, female, CV	REQUIRED	male, female			
Biosample	Ethnicity	donor_ethnicity	Ethnicity of the human donor.	CV	OPTIONAL	Asian, African American	http://purl.obolibrary.org/obo/HANCESTRO_00004	
Biosample	Age	donor_age	Age value of the individual organism from which the initial biosample was obtained. Span of time value bets Enter either a Num	REQUIRED	13.5			
Biosample	Age Unit	donor_age_unit	Age unit of the individual organism from which the initial Biosample was obtained. Span of time unit between entry either a Num	REQUIRED	years, months, embryonic day	http://purl.obolibrary.org/obo/IUO_0000003		
Biosample	Developmental Stage	donor_developmental_stage	The name of the development stage of the donor.	adult, embryo	CV	REQUIRED	adult, embryo, fetus	http://www.ebi.ac.uk/efo/EFO_0000399
Biosample	Health Status	donor_health_status	A description of whether the donor appeared healthy, sick or deceased at the time of sampling. If sick or dey healthy, sick or Text	OPTIONAL	Heart Failure, Epilepsy			
Biosample	Medical History	donor_medical_history	Information about the alcohol, medication, smoking, nutritional state and treatment history of a donor, if av	Text	OPTIONAL	3-6 alcohol.units/day;1 drink		
Biosample	Disease	donor_disease	Disease associated with donor.	Text	REQUIRED	Glioblastoma	http://purl.obolibrary.org/obo/MONDO_0000001	
Biosample	Organ	donor_organ	Controlled term describing the organ from which the Biosample was derived.	CV	REQUIRED	Brain	http://purl.obolibrary.org/obo/UBERON_00000042	
Biosample	Organ Part	donor_organ_part	Controlled term describing the organ part from which the Biosample was derived.	CV	REQUIRED	Hippocampus	http://purl.obolibrary.org/obo/UBERON_00000044	
Biosample	Genotype	donor_genotype	Genotype of donor including strain, cross, and genetic modification information, if applicable.	Text	OPTIONAL	DRB1 0401 protective allele; H		
Biosample	Body Mass Index	donor_body_mass_index	The body mass index of the human donor.	Num	OPTIONAL	18.5		
Biosample	Type	biosample_type	Type of biosample used in experiment.	cell_line, whole_cv	REQUIRED	primary		
Biosample	Biosample ID	biosample_id	Unique identifier of the initial Biosample collected from the Biosample source.	ID	REQUIRED	Blood2345		
Biosample	Description	biosample_description	A general description of the biosample.	Text	OPTIONAL	peripheral blood from patient		
Biosample	Tissue	biosample_tissue	Tissue or bodily fluid type derived from the organ.	CV	REQUIRED	mammary gland fat	http://purl.obolibrary.org/obo/UBERON_0000472	
Biosample	Disease	biosample_disease	Short description of known disease(s) of the biosample.	Text	REQUIRED	Glioblastoma	http://purl.obolibrary.org/obo/MONDO_0000001	
Biosample	Collection Method	biosample_collection_method	Method used to collect the biosample.	biopsy, bone_f	Text	OPTIONAL	blood draw	http://purl.obolibrary.org/obo/OBI_0600005
Biosample	Repository	biosample_repository	Name of repository where a Biosample sample has been deposited.	Text	OPTIONAL	BEI		
Biosample	Repository ID	biosample_repository_id	Unique identifier assigned by sample repository to identify the Biosample sample.	ID	OPTIONAL	Participant2345		
Biosample	Collector's Name	biosample_collectors_name	Name of the person collecting the Biosample and Biosample collection metadata	Text	OPTIONAL	Jane Doe		
Biosample	Collector's Institution	biosample_collectors_institution	Institutional affiliation of the person collecting the Biosample and Biosample collection metadata	ID	OPTIONAL	NIH		
Biosample	Collector's Email	biosample_collectors_email	Preferred email address of the person collecting the Biosample and Biosample collection metadata	Text	OPTIONAL	jane@institution.org		
Biosample	Collection Date	biosample_date	Date when the biosample was collected from the donor at the biosample repository.	Date	OPTIONAL	12 May 2018		
Biosample	Provider	biosample_provider	Center that provided biomaterial for the study	ID	REQUIRED	Stanford Blood Bank		
Biosample	Storage Method	biosample_storage_method	The method by which a biosample was stored after preservation or before another protocol was used.	Text	OPTIONAL	frozen in liquid nitrogen; fresh		
Cell Line	Cell Line ID	cell_line_id	Lab internal ID; this is a batch independent ID	ID	REQUIRED	cellLine234		
Cell Line	Name	cell_line_name	Name of cell line if any (before differentiation protocols if any)	Text	REQUIRED	H9, C12A		
Cell Line	Provider	cell_line_provider	Name of vendor or lab (provider) that supplied the cell line. If purchased, format as: "retail name, manufacturer, catalog number, lot numbe	Text	REQUIRED		Format as: "retail name, manufacturer, catalog number, lot numbe	
Cell Line	Publication	cell_line_publication	List of references (with PMID)s of relevance to cell line derivation, etc	Text	OPTIONAL			
Cell Line	Date Established	cell_line_date_established	When the cell line was established.	Date	OPTIONAL	03 Jun 2007		
Cell Line	Disease	cell_line_disease	Short description of any disease association to the cell line.	Text	REQUIRED	breast cancer, colon cancer, n	http://purl.obolibrary.org/obo/MONDO_0000001	
Cell Line	Source	cell_line_source	The source of the cell line.	Text	OPTIONAL	adherent, suspension	Must be one of primary, immortalized, stem cell-derived, or synth	
Cell Line	Culture Properties	cell_line_culture_properties	A controlled vocabulary describing the culture properties of the cell line (e.g. adherent, suspension)	Adherent, Cell	REQUIRED	adherent, suspension	http://purl.obolibrary.org/obo/NCIT_C19315	
Cell Line	Culture Media	cell_line_culture_media	The solid, liquid, or semi-solid medium used to support the growth of the cell lines.	Text	OPTIONAL	human placental cord serum		
Cell Line	Karyotype	cell_line_karyotype	The karyotype of the cell line.	Text	OPTIONAL	46XY		
Cell Line	Pair	cell_line_pair	For paired cell lines, 'T' or '2' to indicate which of pair.	1 or 2	CV	OPTIONAL		
Cell Line	Storage Method	cell_line_storage_method	The method by which a cell line was stored after preservation or before another protocol was used.	Text	OPTIONAL	frozen in liquid nitrogen; fresh		
Cell Line	Induced Pluripotent Cell Culture	induced_pluripotent_cell_culture_id	Unique identifier of the induced pluripotent stem cell culture or cell line after reprogramming reagents and	ID	REQUIRED	iPSC234		
Cell Line	Differentiated Cell Culture ID	differentiated_cell_culture_id	Unique identifier of the cells in culture or cell line after differentiation reagents and methods are applied.	ID	REQUIRED	diffCardioCell23		
Cell Line	Genetically Modified Cell Culture	genetically_modified_cell_culture_id	Unique identifier of the cells in culture or cell line after genetic modification reagents and methods are appl	ID	REQUIRED	cd47KO23		
Sample	ID	experiment_sample_id	Unique identifier that connects sample to the sequence file. ID must be identical to file_id value.	ID	REQUIRED	sample232		
Cell	Type	cell_type	A controlled vocabulary describing the cell type for which a cell line was derived; e.g. epithelial	primary, immrc	REQUIRED			
Cell	Passage Number	cell_passage_number	The number of times, if any, the cells have been re-plated and allowed to grow back to confluence or to sor	Num	OPTIONAL	3		
Cell	Morphology	cell_morphology	Features relating to the morphology of the cells.	Text	OPTIONAL	adherent cells; form single lay		
Cell	Viability	cell_viability	Percent of cells determined to be viable.	Num	OPTIONAL	98		
Cell	Estimated Count	cell_estimated_count	1 for single cell biosamples, otherwise, total estimated number of cells in biosample.	Num	REQUIRED	4500		
Organoid	Organoid ID	organoid_id	Unique identifier of the organoid culture or line after differentiation reagents and methods are applied.	ID	REQUIRED	organoid23		
Organoid	Organoid Age	organoid_age	Age of the organoid starting from the day embryoid body formation was induced.	Num	REQUIRED	6, 22, 13		

Field group	User-friendly Field Name	Description	Allowed value type	Syntax	REQUIRED	Examples	Comments
Organoid	Organoid_Age_Unit	Age unit of the organoid starting from the day embryoid body formation was induced.	day, minute, n CV	REQUIRED	week, day, hour, year	http://purl.obolibrary.org/obo/UO_0000003	
Organoid	OrganoidFormationMethod	Method used to induce organoid formation.	Text	OPTIONAL	rocking, liquid suspension, serial dilution		
Organoid	OrganoidMorphology	General description of the organoid morphology.	Text	OPTIONAL	epithelial monolayer with bud		
Organoid	OrganoidCultureProperties	Culture properties in which organoid are differentiated.	Text	OPTIONAL	gel matrix, suspension, adherent	http://purl.obolibrary.org/obo/NCIT_C19315	
Organoid	OrganoidCultureMedia	Culture media used to induce a specific differentiation response in organoids.	Text	OPTIONAL	human placental cord serum		
Organoid	OrganoidCellOrigin	organoid_cell_origin	Name of origin cell type that was used to create the organoids.	CV	REQUIRED	H9, ipsc634629	
Organoid	OrganoidModelOrgan	organoid_model_organ	Organ that this organoid is a model system for.	CV	REQUIRED	brain, lung, heart	http://purl.obolibrary.org/obo/UBERON_0000062
Organoid	OrganoidModelOrganPart	organoid_model_organ_part	Organ part that this organoid is a model system for.	CV	REQUIRED	hippocampus	http://purl.obolibrary.org/obo/UBERON_0000064
Organoid	OrganoidSize	organoid_size	Size of the organoid in Organoid size unit. Enter a single value or a range. Average value is acceptable.	Num	OPTIONAL	2	
Organoid	OrganoidSizeUnit	organoid_size_unit	The unit in which the Organoid size is expressed.	centimeter, m CV	OPTIONAL	centimeter	http://purl.obolibrary.org/obo/UO_0000001
Sample	Time	sample_time	For time series experiments, measurement time.	Num	OPTIONAL	5	
Sample	TimeUnit	sample_time_unit	Unit that time is expressed in.	day, minute, n CV	OPTIONAL	day, minute, month, second, week	http://purl.obolibrary.org/obo/UO_0000003
Sample	TimeRelevance	sample_time_relevance	Relevance of time point in experiment.	Text	OPTIONAL	mesoderm formation	

IPSC Induction Protocol

Field group	User-friendly Field Name	Description	Allowed value type	Syntax	REQUIRED	Examples	Comments
IPSC Indu	IPSC Induction Protocol Name	ipsc_induction_protocol_name	Name of the protocol file which captures the details of how the cellular transformation was performed.	Text	REQUIRED	ThermoFisher Scientific: Gene	
IPSC Indu	IPSC Induction Method	ipsc_induction_method	Induction method applied to primary cell culture to induce pluripotent stem cell generation.	lentivirus, sendai	REQUIRED	Lentivirus transfection, Sendai	
IPSC Indu	IPSC Cell Origin	ipsc_cell_origin	Origin cell type where the IPSC cell came from, for example "fibroblast" or "PBMC".	CV	REQUIRED	fibroblast, PBMC	http://purl.obolibrary.org/obo/CL_0000003
Cell line	Induced Pluripotent Cell Culture	induced_pluripotent_cell_culture_id	Unique identifier of the induced pluripotent stem cell culture or cell line after reprogramming reagents and	ID	REQUIRED	IPSC2345	
IPSC Indu	Factors	ipsc_induction_factors	Transcription factors used to induce pluripotency.	Oct3/4, Sox2, Text	OPTIONAL	POU5f, SOX2, KLF4, MYC	
IPSC Indu	Reagents	ipsc_induction_reagents	List of reprogramming reagents added to primary cell culture.	Text	OPTIONAL	"Episomal iPSC Reprogramming"	Format as: "retail name, manufacturer, catalog number, lot number
IPSC Indu	Kit	ipsc_induction_kit	Kit used to induce pluripotent stem cell generation.	Text	OPTIONAL	"CytoTune iPS 2.0 Sendai Repi"	Format as: "retail name, manufacturer, catalog number, lot number
IPSC Indu	Kit Titer	ipsc_induction_kit_titer	Appropriate titer and volume recommendations for induction found in each kit's Certificate of Analysis.	Num	OPTIONAL	3.0x10^-7	
IPSC Indu	Pluripotency Vector Removed	pluripotency_vector_removed	Whether a viral vector was removed after induction. Must be one of: yes, no, unknown.	Must be one c CV	OPTIONAL	yes	Must be one of: yes, no, unknown.
IPSC Indu	Pluripotency Validation Method	pluripotency_validation_method	Description of how pluripotency was validated in induced pluripotent stem cells.	Teratoma form	OPTIONAL	Teratoma formation; PluriTest	
IPSC Indu	Pluripotency Validation Results	pluripotency_validation_results	Percent of iPSCs that passed the pluripotency validation test.	Text	OPTIONAL	9.6% pluripotent, pass	
IPSC Indu	Prepared In-House	prepared_in_house	Whether the induced pluripotent stem cell was prepared in-house. Must be one of: yes, no.	Must be one c CV	OPTIONAL	yes	Must be one of: yes, no, unknown.

Differentiation Protocol

Field group	User-friendly Field Name	Description	Allowed value type	Syntax	REQUIRED	Examples	Comments
Differenti	Differentiation Protocol Name	differentiation_protocol_name	Name of the protocol file which captures the details of how differentiation of cells were performed.	Text	REQUIRED	Abcam: Human embryonic ste	
Differenti	Method	differentiation_method	Differentiation method applied to input cell culture to induce a specific differentiation response.	Text	REQUIRED	Embryoid body formation, dir	
Cell Line	Differentiated Cell Culture ID	differentiated_cell_culture_id	Unique identifier of the differentiated cell culture after differentiation reagents and methods are applied.	ID	REQUIRED	DifCell123	
Differenti	Differentiated Cell Type	differentiated_cell_type	Cell type after differentiation process.	CV	REQUIRED	motor neuron	http://purl.obolibrary.org/obo/CL_0000000
Differenti	Differentiated Cell Model Organ	differentiated_cell_model_organ	Organ for which this cell is a model.	CV	REQUIRED	Brain	http://purl.obolibrary.org/obo/UBERON_0000062
Differenti	Differentiated Cell Model Organ Part	differentiated_cell_model_organ_part	Organ part for which this cell is a model.	CV	REQUIRED	Hippocampus	http://purl.obolibrary.org/obo/UBERON_0000064
Differenti	Small Molecule	differentiation_small_molecule	Small molecule compounds added to stem cell culture to induce a specific differentiation response.	Text	OPTIONAL	Ascl1 (mouse), nuclear receptor	Format as: "retail name, manufacturer, catalog number, lot number
Differenti	Target Pathway	differentiation_target_pathway	Targeted pathway for specific differentiation response.	Text	OPTIONAL	Wnt pathway	http://purl.obolibrary.org/obo/NCIT_C1712
Differenti	Input Cell Type	differentiation_input_cell_type	Cell type before differentiation protocol is followed.	cell_line_name	OPTIONAL	human embryonic stem cell	http://purl.obolibrary.org/obo/CL_0000003
Differenti	Culture Properties	differentiation_culture_properties	Cell culture properties in which stem cells are differentiated.	Text	OPTIONAL	scaffold, monolayer, susensi	http://purl.obolibrary.org/obo/NCIT_C19315
Differenti	Growth Factor	differentiation_growth_factors	List of growth factor added to stem cell culture to induce a specific differentiation response.	Text	OPTIONAL	FLT3 Ligand CTS™ Recombini	http://purl.obolibrary.org/obo/NCIT_C20424
Differenti	Culture Media	differentiation_culture_media	Culture media used to induce a specific differentiation response.	Text	OPTIONAL	neurobasal media, StemPro-3	

Genetic Modification Protocol

Field group	User-friendly Field Name	Description	Allowed value type	Syntax	REQUIRED	Examples	Comments
Genetic N	Protocol Name	genetic_modification_protocol_name	Name of the protocol file which captures the details of how genetic modification of cells was performed.	Text	REQUIRED	Sigma Aldrich CRISPR Cas9 Ge	
Genetic N	Method	genetic_modification_method	Genetic modification method applied to a cell culture to induce a targeted genetic alteration.	Deletion, dupl	REQUIRED	CRISPR-Cas9-mediated editin	http://www.ebi.ac.uk/efo/EFO_0000510
Cell Line	Genetically Modified Cell Culture	genetically_modified_cell_culture_id	Unique identifier of the genetically modified cell culture after genetic modification reagents and method	ID	REQUIRED	GMCel_p53_1571	
Genetic N	Reagents	genetic_modification_reagents	List of genetic modification reagents added to a cell culture to induce the desired genetic change.	Text	OPTIONAL	"ThermoFisher Scientific, True"	Format as: "retail name, manufacturer, catalog number, lot number
Genetic N	Knockout	genetic_modification Knockout	Name of the gene that underwent a genetic knockout.	Text	OPTIONAL	PD-1	
Genetic N	Knockin	genetic_modification Knockin	Name of the gene that underwent a genetic knockin.	Text	OPTIONAL	R274H mutation of AKT2	
Genetic N	CRISPR Enzyme Used	genetic_modification_crispr_enzyme_used	Name of CRISPR Enzyme used to perform genetic modification.	Text	OPTIONAL	spCas9, cpf1	
Genetic N	CRISPR Target Gene	genetic_modification_crispr_target_gene	Gene targeted by the CRISPR guide sequence	Text	OPTIONAL	AAVS1	https://www.addgene.org/crispr/reference/gma-sequence/
Genetic N	CRISPR Guide Sequence	genetic_modification_crispr_guide_sequence	The exact CRISPR guide sequence, including the PAM sequence, so 20 base pairs of DNA + 3 base pairs for t	Text	OPTIONAL	ACAGTGCCCCCACTAGGGAC	https://www.addgene.org/crispr/reference/gma-sequence/
Genetic N	Cloning Plasmid	genetic_modification_cloning_plasmid	The name of the plasmid into which the guide sequence was cloned.	Text	OPTIONAL	pBR322 Plasmid	
Genetic N	Plasmid Delivery Method	genetic_modification_plasmid_delivery	Method used to deliver the plasmid into the cell.	Transfection, r	OPTIONAL	gene gun, electroporation, len	
Genetic N	Validation Method	genetic_modification_validation_method	Method used to validate genetic modification.	Text	OPTIONAL	PCR, T7 Endonuclease, NGS S	
Genetic N	Validation Result	genetic_modification_validation_result	Percentage of the tested cells had the genome editing event.	Text	OPTIONAL	90	

Sequencing Protocol

Field group	User-friendly Field Name	Description	Allowed value type	Syntax	REQUIRED	Examples	Comments
Sequenzi	Protocol Name	sequencing_protocol_name	Name of the protocol file which captures the details of how the sequencing assay was performed.	Text	REQUIRED	AssayProtocol12345	
Sequenzi	Method	sequencing_method	The name of the sequencing assay method applied to input material.	CV	REQUIRED	large-whole genome sequenci	
Sequenzi	Instrument	sequencing_instrument	Name of sequencing instrument used for experiment	CV	REQUIRED	Illumina HiSeq 2500	http://www.ebi.ac.uk/efo/EFO_0003739
Sequenzi	Input Material	sequencing_input_material	The input material used in the assay after biomaterial transformations.	Text	REQUIRED	RNA Poly(A) library, Small RN	
Sequenzi	Barcode	sequencing_barcode	The sequence of the barcode used to identify the sample when samples are barcoded and pooled for sequ	Text	REQUIRED	yes	
Sequenzi	Paired End	sequencing_paired_end	Was a paired-end sequencing strategy used? Must be either yes or no.	yes or no	CV	REQUIRED	yes
Sequenzi	Ratio 260 280	sequencing_ratio_260_280	DNA quality metric - ratio of light absorbance at 260 nm vs 280 nm.	Num	OPTIONAL		

Field group	User-friendly Field Name	Description	Allowed value type	REQUIRED	Examples	Comments
SequenCI DNA Concentration	sequencing_dna_concentration	Concentration of DNA sent to be sequenced in nanograms per microliter (ng/uL)	Num	OPTIONAL		
SequenCI Average Insert Size	sequencing_average_insert_size	Average size of inserted DNA in sequencing library.	Num	OPTIONAL		
SequenCI Lane	sequencing_lane	Which lane on sequencing machine sample was run on	Num	OPTIONAL	8	
SequenCI Pooled Channel	sequencing_pooled_channel	The number of channels pooled within a sequencing lane.	Num	OPTIONAL	2	
SequenCI Index (i7) Adapters	sequencing_index_1_i7_sequence	Illumina adapter i7 sequence	Text	OPTIONAL		
SequenCI Index (i5) Adapters	sequencing_index_2_i5_sequence	Illumina adapter i5 sequence	Text	OPTIONAL		
SequenCI Index i7 name	sequencing_index_i7_name	Name of i7 index adapter	Text	OPTIONAL		
SequenCI Index i5 name	sequencing_index_i5_name	Name of i5 index adapter	Text	OPTIONAL		

Library Preparation Protocol

Field group	User-friendly Field Name	Computer Readable Name	Description	Allowed value type	Syntax	REQUIRED	Examples	Comments
Library Pr	Library Preparation Protocol	library_preparation_protocol_name	Name of the protocol file which captures the details of how the sequencing library preparation was performed.	ID	REQUIRED	Standard 10x Genomics single		
Library Pr	Construction Platform	library_preparation_construction_platform	The device used to construct the library. Use in cases of automated/proprietary library preparation.	CV	REQUIRED	Fluidigm, 10X		
Library Pr	Library Construction Method	library_preparation_construction_method	The name of a library construction method being used.	CV	REQUIRED	10X v2 sequencing; Smart-seq		
Library Pr	Library Construction Kit	library_preparation_construction_kit	Name of library preparation construction kit used.	Text	OPTIONAL	10X V2 Single Cell RNA Sequencer Format as: "retail name, manufacturer, catalog number, lot number		
Library Pr	End Bias	library_preparation_end_bias	The type of tag or end bias the library has.	Text	Should be one Text	3 prime tag,		
Library Pr	Primer	library_preparation_primer	Primer used for cDNA synthesis from RNA.	Text	Should be one Text	poly-dT		
Library Pr	Strand	library_preparation_strand	Library strandedness.	Text	first, second, t	REQUIRED	first	
Library Pr	Input Nucleic Acid Molecule	library_preparation_input_nucleic_acid_m	Starting nucleic acid molecule isolated for sequencing.	DNA, mRNA, Text	REQUIRED			
Library Pr	Nucleic Acid Source	library_preparation_nucleic_acid_source	Source cells or organelles from which nucleic acid molecules were collected.	Text	single cell, bulk	REQUIRED		
Library Pr	Nucleic Acid Conversion Kit	library_preparation_nucleic_acid_convertis	Name of kit used to convert RNA to DNA for sequencing.	Text	OPTIONAL			
Library Pr	Amplification Method	library_preparation_amplification_method	The method used to amplify a cDNA library prior to sequencing.	Text	OPTIONAL	PCR		
Library Pr	Size Range	library_preparation_size_range	The measured size range of the purified nucleic acid, in bp.	Num	OPTIONAL			
Library Pr	Spike-in Dilution	library_preparation_spike_in_dilution	Dilution of spike-in.	Num	OPTIONAL	100		
Library Pr	Plate ID	library_preparation_plate_id	The plate the single cell sample comes from.	ID	REQUIRED	Plate_345		
Library Pr	Plate Location	library_preparation_plate_location	The location (such as A1) of the single cell sample on the plate.	ID	REQUIRED	A12		
Library Pr	Droplet Uniformity	drop_uniformity	Whether drop uniformity was achieved as a result of visual inspection of emulsion after a 10x run.	yes, no, no	Text	OPTIONAL		
Library Pr	Barcode Read	library_preparation_barcode_read	The read that the barcode is found in.	Text	Should be one Text	Read 1		
Library Pr	Barcode Offset	library_preparation_barcode_offset	0-based offset of start of barcode in read. 0 for beginning of read.	Num	OPTIONAL	0		
Library Pr	Barcode length	library_preparation_barcode_length	Length of barcode in nucleotides.	Num	OPTIONAL	16		
Library Pr	Umi Barcode Read	library_preparation_umi_barcode_read	Information about unique molecular identifier (UMI) barcodes.	Text	OPTIONAL	Read 1		
Library Pr	Umi Barcode Offset	library_preparation_umi_barcode_offset	0-based offset of start of barcode in read. 0 for beginning of read.	Num	OPTIONAL	0		
Library Pr	Umi Barcode Length	library_preparation_umi_barcode_length	Length of barcode in nucleotides.	Num	OPTIONAL	16		
Library Pr	RNA Integrity Number	library_preparation_rin	The RNA integrity number (RIN) value.	Num	OPTIONAL			

Dissociation Protocol

Field group	User-friendly Field Name	Computer Readable Name	Description	Allowed value type	Syntax	REQUIRED	Examples	Comments
Dissociate	Protocol Name	dissociation_protocol_name	Name of the protocol file which captures the details of how the dissociation of cells was performed.	ID	REQUIRED	Primary Cell Dissociation Prot		
Dissociate	Method	dissociation_method	How cells or organelles were dissociated.	Enzymatic diss: CV	REQUIRED	Enzymatic dissociation, mech: http://www.ebi.ac.uk/efo/EFO_0009029		
Dissociate	Reagents	dissociation_reagents	A list of purchased reagents used in dissociation protocol. Format as: "retail name, manufacturer, catalog number, lot number	Text	OPTIONAL			Format as: "retail name, manufacturer, catalog number, lot number
Dissociate	Kit	dissociation_kit	Name of kit used in dissociation protocol. Format as: "retail name, manufacturer, catalog number, lot number	Text	OPTIONAL	"miltenyi biotec, Adult Brain D	Format as: "retail name, manufacturer, catalog number, lot number	Format as: "retail name, manufacturer, catalog number, lot number

Enrichment Protocol

Field group	User-friendly Field Name	Computer Readable Name	Description	Allowed value type	Syntax	REQUIRED	Examples	Comments
Enrichme	Enrichment Protocol Name	enrichment_protocol_name	Name of the protocol file which captures the details of how target enrichment was performed.	ID	REQUIRED	EasySep™ Human B Cell Enrich		
Enrichme	Enrichment Method	enrichment_method	The name of the enrichment method of applied to input material.	Cell size select: CV	REQUIRED	FACS, IMAC column bead enri		
Enrichme	Analyte	enrichment_analyte	Cell surface target that is specifically bound by the analyte detector.	Text	OPTIONAL	CD25		
Enrichme	Analyte Detector	enrichment_analyte_detector	The fluorescence reagent specifically binds to the analyte to make it detectable.	Text	OPTIONAL	anti-CD25		
Enrichme	Analyte Reporter	enrichment_analyte_reporter	The fluorescence reagent that is used to generate the measured signal.	Text	OPTIONAL	FITC		
Enrichme	Markers	enrichment_markers	A list of markers used to enrich for or against certain cells.	Text	OPTIONAL	CD11b+CD47+		
Enrichme	Min Size Selected	enrichment_min_size_selected	Minimum cell or organelle size passing selection, in microns.	Num	OPTIONAL	40		
Enrichme	Max Size Selected	enrichment_max_size_selected	Maximum cell or organelle size passing selection, in microns.	Num	OPTIONAL	70		
Enrichme	Instrument	enrichment_instrument	Name of instrument used for enrichment.	Text	OPTIONAL	FACS Aria		
Enrichme	kit	enrichment_kit	Name of kit used to enrich for cell types.	Text	OPTIONAL	"miltenyi biotec, CD8a+ T Cell		
Enrichme	reagents	enrichment_reagents	A fluorescence reagent is a chemical substance used in the detection of an analyte.	Text	OPTIONAL	anti-CD25-FITC	Format as: "retail name, manufacturer, catalog number, lot number	Format as: "retail name, manufacturer, catalog number, lot number
Enrichme	Immunoprecipitation Target	immunoprecipitation_target	Molecular target of the immunoprecipitating reagent.	Text	OPTIONAL	histone H3 acetylated at posit		
Enrichme	Immunoprecipitation Reagent	immunoprecipitation_reagent	Reagent, often a specific antibody preparation, used to immunoprecipitate a specific chromatin target mole	Text	OPTIONAL	antibody 12345 to histone H3	Format as: "retail name, manufacturer, catalog number, lot number	Format as: "retail name, manufacturer, catalog number, lot number

Experimental Design

Field group	User-friendly Field Name	Computer Readable Name	Description	Allowed value type	Syntax	REQUIRED	Examples	Comments
Experime	Characteristic Being Measured	experimental_design_characteristic_being	The characteristics being measured shall be provided whenever there is ambiguity about the analyte being measured.	Text	OPTIONAL	protein expression level, cell		
Experime	Variables	experimental_design_variable	Variables are attribute(s) that differ between samples within an experiment due to pre-existing differences	Text	OPTIONAL	e.g., smoker vs. nonsmoker, IL		
Experime	Enriched_In	experimental_design_enriched_in	Genomic regions where the expectation is the data will be concentrated as defined in the enrichment table, open, exon, in CV	Text	OPTIONAL	open, exon, intron, genome		
Experime	Control	experimental_design_control	If this is an experimental control, what type of control.	Text	OPTIONAL			
Experime	Control Type	experimental_design_control_type	Typically either "input" or "mock IP" for ChIP-seq experiment	input, mock IP	CV	OPTIONAL	input, mock IP	
Experime	Control Association	experimental_design_control_association	Used to link together experiments and their controls	Text	OPTIONAL			
Experime	Target Epitope	experimental_design_target_epitope	Name of part of gene or other molecule that antibody reacts with. Protein modification for histone ChIP-seq	Text	OPTIONAL			

Field group	User-friendly Field Name	Description	Allowed value type	REQUIRED	Examples	Comments
Experiment	experimental_design_target_gene	Name of gene that assay is targeting. Factor name that antibody is targeting for transcription factor ChIP-seq	Text	OPTIONAL		
Experiment	experimental_design_treatment	Name of treatment tested in experiment.	Text	OPTIONAL		
Experiment	experimental_design_comments	Comments or notes from data generators about their experiment.	Text	OPTIONAL	low cell count	

Data Files

Field group	Field Name	Description	Allowed value	Syntax	REQUIRED	Examples	Comments
File	Input Data	input_data	File link to primary data generated from the assay run	Text	OPTIONAL	SR0001203_filt.fastq.gz	
File	Output Data	output_data	The link to the mapped data after quality control process	Text	OPTIONAL	SR0001.bam	output of .bam or .sam file format
File	Reference Data	reference_data	The link or pointer to the reference data file. This includes any versioning source information	Text	OPTIONAL	NCBI Reference Sequence	NC If reference data is genomic sequence data, then use NCBI RefSeq
File	Format	file_format	The format of the data file.	Text	REQUIRED	fastq, fcs, bcl	
File	checksum	file_checksum	MDS checksum of the data file.	Text	OPTIONAL		
File	Read Index	file_read_index	Whether the read file contains the read1, read2, index1 or index2 part of the sequencing read.	read1, read2, i	Text	REQUIRED	read1
File	Lane Index	file_lane_index	The index of the lane that this file was sequenced from.	Num	REQUIRED	1	
File	ID	file_id	Unique identifier that connects the sequence and analysis files to the sample. ID must be identical to 'sample_id'.	ID	REQUIRED	seqSample123	
File	Name	file_name	The filename of the data file.	Text	REQUIRED	example.fastq.gz	
Process	Data Processing Method/Algorithm	data_processing_method_algorithm	The purpose of each performed transformation shall be specified	Text	REQUIRED	calculation of signal intensity	
Process	Data Processing Description	data_processing_description	This will be the exact mathematical formulas/algorithms of each data transformation involved in the data processing.	Text	REQUIRED	align.py	
Process	Data Processing Software	data_processing_software		Text	REQUIRED	Tophat	
Process	Data Processing Protocol Name	data_processing_protocol_name	A unique identifier for the protocol which was executed to process the data method used	ID	REQUIRED	DataProtocol12345	
Process	Data Processor Name	data_processor_name	Name of the person processing the data collection	Text	OPTIONAL	Spyros A	
Process	Data Processor Institution	data_processor_institution	Institutional affiliation of the person processing the data and metadata	Text	OPTIONAL	Stanford University	
Process	UCSC DB	ucsc_db	UCSC assembly database identifier for reference genome used in mapping.	hg19, hg38, mm10	CV	REQUIRED	hg19, hg38, mm10, mm9
Process	Data File Creation Method	data_file_creation_method	Method used for the generation of data files from bcl files.	Text	REQUIRED	Cellranger	
Process	Data File Creation Method Version	data_file_creation_method_version	Version of the program used for data generation.	Text	REQUIRED	2.1; v2.20	