

[1] The name of the file.

[2] Indicates which milestone report you're annotating data files for. Currently only required for projects funded by NTAP, GFF, and NFRI. An example: if submitting a 6-month milestone report for NTAP, reportMilestone=1.

[3] Defined format of the data file, typically corresponding to extension, but sometimes indicating more general group of files produced by the same tool or software

[4] The type of resource being stored and annotated

[5] Types of input/output data in bioinformatics pipelines

[6] Further qualification of dataType, which may be used to indicate the state of processing of the data, aggregation of the data, or presence of metadata.

[7] Metadata describing properties of an assay conducted in the study.

[8] A unique identifier (non-PII) that represents the individual from which the data came. This could be a patient or animal ID.

[9] Phenotypic expression of chromosomal makeup that defines a study subject as male, female, or other.

[10] The name of a species (typically a taxonomic group) of organism.

[11] A group of presumed common ancestry with clear-cut physiological but usually not morphological distinctions such as an animal model or cell line. EXAMPLE(S): HEK293T (cell line), Minnesota5 (swine strain), DXL (poultry strain), RB51 (vaccine strain of Brucella abortus)

[12] Listing of the genetic changes made deliberately in order to generate the animal model.

[13] Specific way in which a single gene was perturbed in a sample

[14] Technology used to perform gene perturbation

[15] The HUGO gene symbol for the gene that is perturbed.

[16] A diagnosis is the result of a medical investigation to identify a disorder from its signs and symptoms.

[17] A unique identifier (non-PII) that represents the specimen (sample) from which the data came. e.g. an ID that indicates a specific tumor specimen.

[18] A unique macroscopic (gross) anatomic structure that performs specific functions. It is composed of various tissues. An organ is part of an anatomic system or a body region.

[19] A tissue is a morphologically maximal collection of cells that together perform physiological function.

[20] Genotype of NF1 gene, if known

[21] Genotype of NF2 gene, if known

[22] Boolean flag indicating whether or not sample source is a cell line. (Note: TRUE = Yes; FALSE = No)

[23] Boolean flag indicating whether or not cellType is primary (Note: TRUE = Yes; FALSE = No)

[24] The type of cells that carcinoma arises from.

[25] The HUGO gene symbol that represents the target analyte assayed.

[26] A free-text description of the experimental condition (e.g. 5 mM doxorubicin).

[27] The numeric value indicating the time elapsed from the beginning of the experiment at which the specimen was collected. Use in tandem with timePointUnit

[28] For timed experiments this represents the unit of time measured

[29] HiSeq3000, HiSeq2500, HiSeq4000, NextSeq500, HiSeq2000, MiSeq, Zeiss LSM 980, Affy5.0, Affy6.0, PacBioRSII, GAIIX, Illumina_HumanOmni1-Quadv1.0, Illumina_1M, Illumina_h650, Illumina_Omni2pt5M, Illumina_Omni5M, Illumina MouseWG-6 v2.0 expression beadchip, Perlegen300Karray, Agilent44Karray, IlluminaWholeGenomeDASL, IlluminaHumanHap300, NanostringnCounter, LTQOrbitrapXL, IlluminaHumanMethylation450, Illumina Infinium MethylationEPIC BeadChip, AffymetrixU133AB, Affymetrix Human Gene 1.0 ST Array, AffymetrixU133Plus2, HiSeqX, Bionano Irys, Infinium HumanOmniExpressExome, NextSeq 550, NextSeq 1000, NextSeq 2000, PacBio Sequel IIe System, PacBio Sequel II System, NanostringGeoMx, LI-COR Odyssey CLx, Spectramax M Series

[30] Database or repository to which individual ID maps

[31] Boolean flag indicating whether or not a file has data for multiple individuals (Note: TRUE = Yes; FALSE = No)

[32] Boolean flag indicating whether or not a file has data for multiple specimens (Note: TRUE = Yes; FALSE = No)