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- [2] The name of the file.
- [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] Links an entity to data types that the entity represents/contains. This is closely tied to the assay property. For example, a file of dataType `genomicVariants` might have an assay value of `whole genome sequencing`.
- [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] The technology used to generate the data in this file.
- [8] A unique identifier (non-PII) that represents the individual from which the data came. This could be a patient or animal ID.
- [9] The name of a species (typically a taxonomic group) of organism.
- [10] Phenotypic expression of chromosomal makeup that defines a study subject as male, female, or other.
- [11] A numeric value representing age of the individual. Use with `ageUnit`.
- [12] A time unit that can be used with a given age value, e.g. years.
- [13] Diagnosis for the individual given signs and symptoms. Use the most specific diagnosis term that applies.
- [14] Genotype of NF1 gene in the biospecimen from which the data were derived, if known.
- [15] Genotype of NF2 gene in the biospecimen from which the data were derived, if known
- [16] The type of tumor that the biospecimen used to generate the data were collected from.
- [17] HEK293 (cell line), Minnesota5 (swine strain), DXL (poultry strain), RB51 (vaccine strain of Brucella abortus)
- [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] Brief free-text comments that may also be important to understanding the resource.
- [20] A unique identifier (non-PII) that represents the parent specimen (sample) from which the data came from, e.g. the single parent tumor that was subsectioned into several samples. The parentSpecimenID can be the same as specimenID when there is no subsectioning.
- [21] A unique identifier (non-PII) that represents the subspecimen (subsample) from which the data came, e.g. an ID that distinguishes between different parts of the same parent tumor specimen.
- [22] A unique identifier (non-PII) that represents the aliquots used for e.g. replicate runs. This is linked to

the specimenID.

[23] A sequencing platform, microscope, spectroscope/plate reader, or other platform for collecting data.

[24] Source of the extracted nucleic acid used in the experiment

[25] Term that represents preservation of the sample before usage in, e.g. sequencing

[26] The type of a material sample taken from a biological entity for testing, diagnostic, propagation, treatment or research purposes. This includes particular types of cellular molecules, cells, tissues, organs, body fluids, embryos, and body excretory substances.

[27] Sequencing run type.

[28] Strandedness of paired-end RNA-Sequencing data. This is an important parameter for RNA-seq analysis.

[29] The general strategy by which the library was prepared

[30] Method by which library was prepared

[31] The read of origin, Read 1 or Read 2

[32] Number of base pairs (bp) sequenced for a read

[33] If available, the coverage statistic as output from bedtools coverage or samtools stats.

[34] The targeted read depth prior to sequencing.

[35] Batch identifier, can be used in any context where added batch information is helpful, such as different sequencing runs or collection times.

[36] A unique identifier for the kit used to construct a genomic library using target capture-based techniques, which should be composed of the vendor name, kit name and kit version.

[37] Please enter applicable comma-separated items selected from the set of allowable terms for this attribute. See our data standards for allowable terms

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