

Component	Reference	Resource	Type	Category	Sub-Category	Item	Year	Value	Unit	Notes	Source	Link	Quality	Length	Quality	Duplicate	Percent	Coverage	Percent	Coverage	Depth	Reads	Flow	Link	Assay	Screen
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- [1] Type of metadata template; provide the same one for all items/rows.
- [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] Version of genome reference used for alignment in processing workflow
- [21] Link to genome reference data file used for alignment in processing workflow
- [22] Average insert size as reported by samtools
- [23] Average read length collected from samtools
- [24] Average base quality collected from samtools

- [25] Pairs on different chromosomes collected from samtools
- [26] Percent of duplicated reads collected from samtools
- [27] Percent of mapped reads collected from samtools
- [28] Mean coverage for whole genome sequencing, or mean target coverage for whole exome and targeted sequencing, collected from Picard Tools
- [29] Proportion of all reference bases for whole genome sequencing, or targeted bases for whole exome and targeted sequencing, that achieves 10X or greater coverage from Picard Tools
- [30] Proportion of all reference bases for whole genome sequencing, or targeted bases for whole exome and targeted sequencing, that achieves 30X or greater coverage from Picard Tools
- [31] If available, the coverage statistic as output from bedtools coverage or samtools stats.
- [32] If available, the total number of reads collected from samtools.
- [33] Name and version of the workflow used to generate/analyze the data
- [34] Workflow URL reference
- [35] URI to supplemental asset(s), e.g. QC reports or other auxiliary files to support the processing, analysis, or interpretation of the current entity.
- [36] 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.
- [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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