bdg.avdl

Fragment — Sequenced fragment of one or more reads
- readName
- instrument
- runId
- fragmentSize
- alignments

AlignmentRecord — Genomic read description
- readInFragment
- contigName
- start
- oldPosition
- end
- mapq
- readName
- sequence
- qual
- cigar
- oldCigar
- basesTrimmedFromStart
- basesTrimmedFromEnd
- readPaired
- properPair
- readMapped
- mateMapped
- failedVendorQualityChecks
- duplicateRead
- readNegativeStrand
- mateNegativeStrand
- primaryAlignment
- secondaryAlignment
- supplementaryAlignment
- mismatchingPositions
- origQual
- attributes
- recordGroupName
- recordGroupSample
- mateAlignmentStart
- mateContigName
- inferredInsertSize

GenotypeType

RecordGroup
- name
- sample
- sequencingCenter
- description
- runDateEpoch
- flowOrder
- keySequence
- library
- predictedMedianInsertSize
- platform
- platformUnit
- processingSteps

ProcessingStep — Computational lineage
- id
- programName
- commandLine
- previousId
- description
- version

Sample
- sampleId
- name
- attributes
- processingSteps

Sequence
- name
- description
- alphabet
- sequence
- length
- attributes

Alphabet

QualityScoreVariant

Read
- name
- description
- alphabet
- length
- sequence
- qualityScores

Slice
- name
- description
- alphabet
- sequence
- start
- end
- strand
- length
- totalLength
- index
- slices
- attributes

NucleotideContigFragment — A fragment of a contig
- contigName
- start
- end
- contigLength
- description
- length
- sequence
- index
- fragments

Variant — A genomic sequence change
- contigName
- start
- end
- names
- splitFromMultiAllelic
- referenceAllele
- alternateAllele
- quality
- filtersApplied
- filtersPassed
- filtersFailed
- annotation

VariantAnnotation — Statistical/effect annotations on a variant
- ancestralAllele
- alleleCount
- readDepth
- forwardReadDepth
- reverseReadDepth
- referenceReadDepth
- referenceForwardReadDepth
- referenceReverseReadDepth
- alleleFrequency
- cigar
- dbSnp
- hapMap2
- hapMap3
- validated
- thousandGenomes
- somatic
- transcriptEffects
- attributes

TranscriptEffect — The effect of a coding variant
- alternateAllele
- effects
- geneName
- geneId
- featureType
- featureId
- biotype
- rank
- total
- genomicHgvs
- transcriptHgvs
- proteinHgvs
- cdnaPosition
- cdnaLength
- cdsPosition
- cdsLength
- proteinPosition
- proteinLength
- distance
- messages

VariantAnnotationMessage

VariantCallingAnnotations — Statistics about a genotype call
- filtersApplied
- filtersPassed
- filtersFailed
- downsampled
- baseQRankSum
- fisherStrandBiasPValue
- rmsMapQ
- mapoReads
- mqRankSum
- readPositionRankSum
- genotypePriors
- genotypePosteriors
- vqslod
- culprit
- attributes

Genotype — Genotype call
- variant
- contigName
- start
- end
- variantCallingAnnotations
- sampleId
- sampleDescription
- processingDescription
- alleles
- expectedAlleleDosage
- referenceReadDepth
- alternateReadDepth
- readDepth
- minReadDepth
- genotypeQuality
- genotypeLikelihoods
- nonReferenceLikelihoods
- strandBiasComponents
- splitFromMultiAllelic
- phased
- phaseSetId
- phaseQuality

GenotypeAllele

Strand

Contig — Genomic reference metadata
- contigName
- contigLength
- contigMD5
- referenceURL
- assembly
- species
- referenceIndex

Dbxref — Feature cross reference
- db
- accession

Feature — Generic genomic feature
- featureId
- name
- source
- featureType
- contigName
- start
- end
- strand
- gap
- derivesFrom
- notes
- dbxrefs
- parentIds
- target
- geneId
- transcriptId
- exonId
- aliases
- phase
- frame
- score
- attributes
- ontologyTerms
- circular

OntologyTerm — A term describing a feature
- db
- accession