

Clinical Quality Control Data Model Schema

quality Enum	Quality control result.			
	HIGH	QC passed.		
	MEDIUM	Uncertainty.		
	LOW	QC failed.		
	UNKNOWN	QC not assessed.		
variant VariantQc	Quality control on variant data.			
	stats List<SampleVariantStats>	Sample variant stats. See sample variant stats data model .		
	files List<File>	List of files related to this sampleId the variant data, e.g.: images.		
alignment AlignmentQc	Quality control on variant data.			
	stats List<AlignmentStats>	Alignment stats for each alignment file (BAM). See alignment stats data model schema .		
	files List<File>	List of files related to the variant data, , e.g.: images.		
	geneCoverageStats List<GeneCoverageStats>	Gene coverage stats for each alignment file (BAM).		
		fileId String	File ID.	
		sampleId String	Sample ID.	
		gene String	Gene name.	
		stats List<TranscriptCoverageStats>	id String	Transcript ID.
			name String	Transcript name.
			biotype String	Transcript biotype.
			chromosome String	Chromosome where the transcript is located.
			start int	Position where the transcript starts.
			end int	Position where the transcript ends.

length <i>int</i>	The transcript length as the sum of the lengths of its exons.														
depths <i>Double[10]</i>	% coverage for 1x, 5x, 10x, 15x, 20x, 25x, 30x, 40x, 50x, 60x, 75x and 100x														
lowCoverageThreshold <i>int</i>	Regions under this coverage depth threshold will be reported in the list <code>lowCoverageRegions</code> . Default value: 30.														
lowCoverageRegionStats <i>List<LowCoverageRegionStats></i>	Statistics for regions whose coverage depth is under the value <i>lowCoverageThreshold</i> . <table><tr><td>chromosome <i>String</i></td><td>Chromosome.</td></tr><tr><td>start <i>int</i></td><td>Region start position.</td></tr><tr><td>end <i>int</i></td><td>Region end position</td></tr><tr><td>depthAvg <i>double</i></td><td>Average depth.</td></tr><tr><td>depthMin <i>int</i></td><td>Minimum depth.</td></tr></table>	chromosome <i>String</i>	Chromosome.	start <i>int</i>	Region start position.	end <i>int</i>	Region end position	depthAvg <i>double</i>	Average depth.	depthMin <i>int</i>	Minimum depth.				
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end <i>int</i>	Region end position														
depthAvg <i>double</i>	Average depth.														
depthMin <i>int</i>	Minimum depth.														
exonStats <i>List<ExonCoverageStats></i>	Statistics for each exon in the transcript. <table><tr><td>id <i>String</i></td><td>Exon ID.</td></tr><tr><td>chromosome <i>String</i></td><td>Chromosome.</td></tr><tr><td>start <i>int</i></td><td>Region start position.</td></tr><tr><td>end <i>int</i></td><td>Region end position</td></tr><tr><td>depthAvg <i>double</i></td><td>Average depth.</td></tr><tr><td>depthMin <i>int</i></td><td>Minimum depth.</td></tr><tr><td>depthMax <i>int</i></td><td>Maximum depth.</td></tr></table>	id <i>String</i>	Exon ID.	chromosome <i>String</i>	Chromosome.	start <i>int</i>	Region start position.	end <i>int</i>	Region end position	depthAvg <i>double</i>	Average depth.	depthMin <i>int</i>	Minimum depth.	depthMax <i>int</i>	Maximum depth.
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analyst Analyst	Analyst carrying out the QC.									
	<table><tr><td>name <i>String</i></td><td>Name.</td></tr><tr><td>email <i>String</i></td><td>E-mail.</td></tr><tr><td>company <i>String</i></td><td>Company.</td></tr></table>	name <i>String</i>	Name.	email <i>String</i>	E-mail.	company <i>String</i>	Company.			
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