

Clinical Quality Control Data Model Schema

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