

Alignment Stats Data Model Schema

fileId <i>String</i>	File ID.
sampleId <i>String</i>	Sample ID.
rawTotalSequences <i>int</i>	Total number of raw sequences.
filteredSequences <i>int</i>	Number of filtered sequences.
sequences <i>int</i>	Number of sequences.
isSorted <i>int</i>	If 1 then file is sorted.
firstFragments <i>int</i>	Number of 1st fragments.
lastFragments <i>int</i>	Number of last fragments.
readsMapped <i>int</i>	Number of reads mapped.
readsMappedAndPaired <i>int</i>	Number of reads mapped and paired (paired-end technology bit set + both mates mapped).
readsUnmapped <i>int</i>	Number of reads unmapped.
readsProperlyPaired <i>int</i>	Number of reads properly paired (proper-pair bit set).
readsPaired <i>int</i>	Number of reads paired (paired-end technology bit set).
readsDuplicated <i>int</i>	Number of reads duplicated (PCR or optical duplicate bit set).
readsMq0 <i>int</i>	Number of reads mapped and MQ=0.
readsQcFailed <i>int</i>	Number of reads whose QC failed.
nonPrimaryAlignments <i>int</i>	Number of non-primary alignments.
totalLength <i>int</i>	Total length (ignores clipping).
basesMapped <i>int</i>	Number of bases mapped (ignores clipping)

basesMappedCigar <i>int</i>	Number of bases mapped taking into account the CIGAR codes (more accurate).
basesTrimmed <i>int</i>	Number of bases trimmed.
basesDuplicated <i>int</i>	Number of bases duplicated.
mismatches <i>int</i>	Number of mismatches (from NM fields).
errorRate <i>Double</i>	Error rate, i.e.: mismatches / bases mapped (cigar)
averageLength <i>Double</i>	Average read length.
maximumLength <i>int</i>	Maximum read length.
averageQuality <i>Double</i>	Average quality.
insertSizeAverage <i>Double</i>	Insert size average.
insertSizeStandardDeviation <i>Double</i>	Standard deviation of the insert size.
inwardOrientedPairs <i>int</i>	Number of inward oriented pairs.
outwardOrientedPairs <i>int</i>	Number of outward oriented pairs.
pairsWithOtherOrientation <i>int</i>	Number of pairs with other orientation.
pairsOnDifferentChromosomes <i>int</i>	Number of pairs on different chromosomes.