

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 04:56:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173903.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10173903 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173903_1.fastq.gz SRR10173903_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 04:56:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173903.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,807,734
Mapped reads	3,702,622 / 97.24%
Unmapped reads	105,112 / 2.76%
Mapped paired reads	3,702,622 / 97.24%
Mapped reads, first in pair	1,853,694 / 48.68%
Mapped reads, second in pair	1,848,928 / 48.56%
Mapped reads, both in pair	3,633,594 / 95.43%
Mapped reads, singletons	69,028 / 1.81%
Secondary alignments	0
Supplementary alignments	383,707 / 10.08%
Read min/max/mean length	30 / 133 / 128.41
Duplicated reads (estimated)	2,928,595 / 76.91%
Duplication rate	65.05%
Clipped reads	1,519,978 / 39.92%

2.2. ACGT Content

Number/percentage of A's	131,816,885 / 30.11%
Number/percentage of C's	85,616,945 / 19.55%
Number/percentage of T's	131,563,708 / 30.05%
Number/percentage of G's	88,825,333 / 20.29%
Number/percentage of N's	5,419 / 0%

GC Percentage	39.84%
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2.3. Coverage

Mean	0.1415
Standard Deviation	2.1263

2.4. Mapping Quality

Mean Mapping Quality	52.71
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2.5. Insert size

Mean	888,855.97
Standard Deviation	8,772,567
P25/Median/P75	146 / 203 / 290

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	4,543,899
Insertions	44,902
Mapped reads with at least one insertion	1.18%
Deletions	108,550
Mapped reads with at least one deletion	2.86%
Homopolymer indels	42.16%

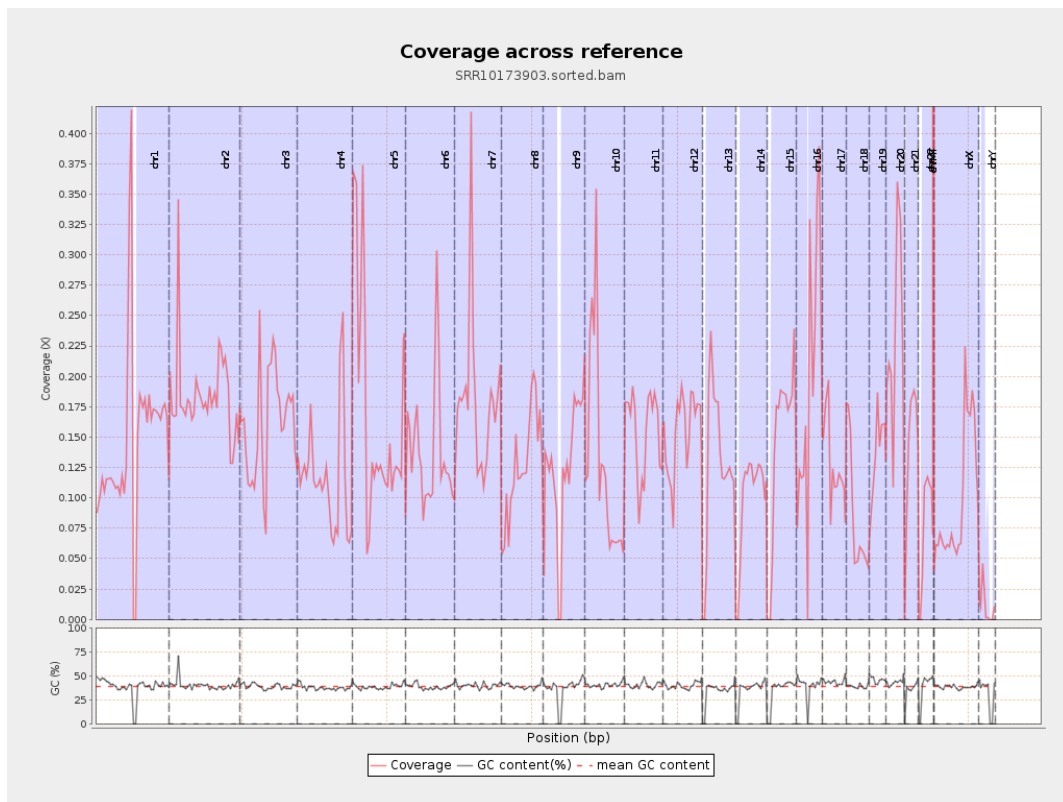
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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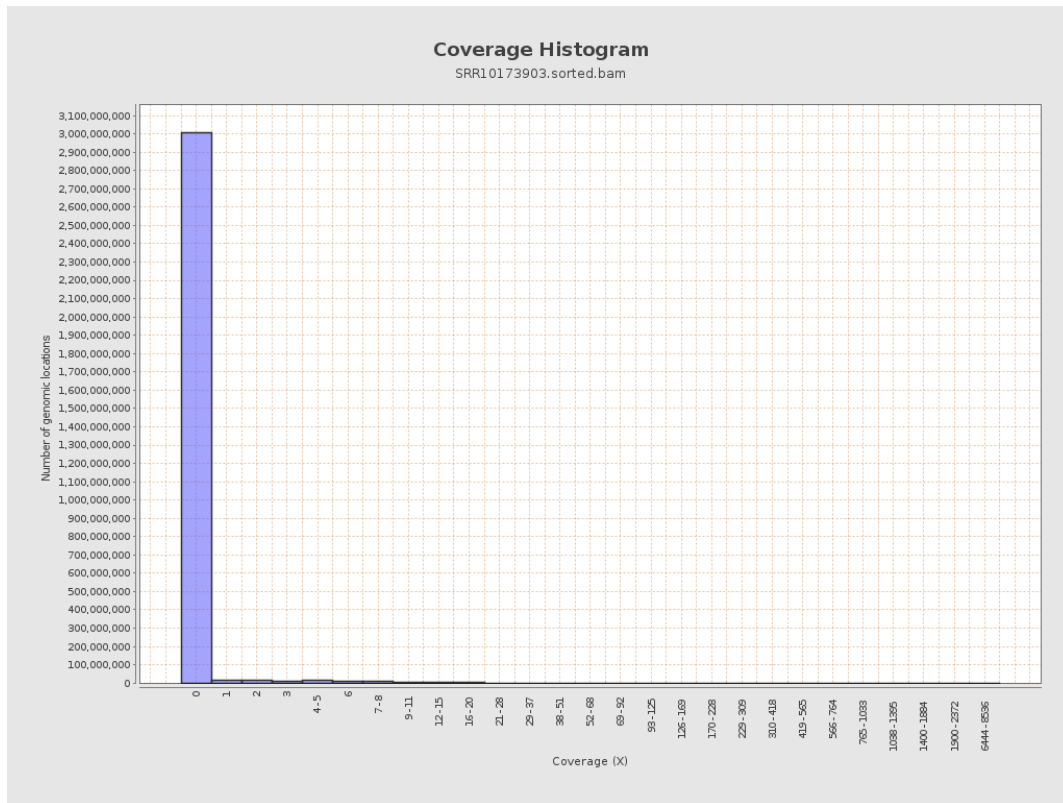
		bases	coverage	deviation
chr1	249250621	36626324	0.1469	1.7404
chr2	243199373	44695958	0.1838	6.0266
chr3	198022430	31978263	0.1615	1.1921
chr4	191154276	21904396	0.1146	1.1582
chr5	180915260	30559707	0.1689	1.2155
chr6	171115067	23813146	0.1392	1.1309
chr7	159138663	28468984	0.1789	1.7984
chr8	146364022	18746642	0.1281	1.2534
chr9	141213431	17759894	0.1258	1.1791
chr10	135534747	17600816	0.1299	2.0667
chr11	135006516	20803508	0.1541	1.1734
chr12	133851895	20624880	0.1541	1.164
chr13	115169878	14570667	0.1265	1.0635
chr14	107349540	10565720	0.0984	0.9276
chr15	102531392	14798838	0.1443	1.1129
chr16	90354753	17742417	0.1964	1.6724
chr17	81195210	10220735	0.1259	1.1032
chr18	78077248	6578501	0.0843	1.4595
chr19	59128983	8074826	0.1366	1.6733
chr20	63025520	14611827	0.2318	1.4149
chr21	48129895	6763540	0.1405	1.1347
chr22	51304566	3860758	0.0753	0.7713
chrMT	16571	942234	56.8604	47.7396
chrX	155270560	15170720	0.0977	0.9244

chrY	59373566	609856	0.0103	0.537
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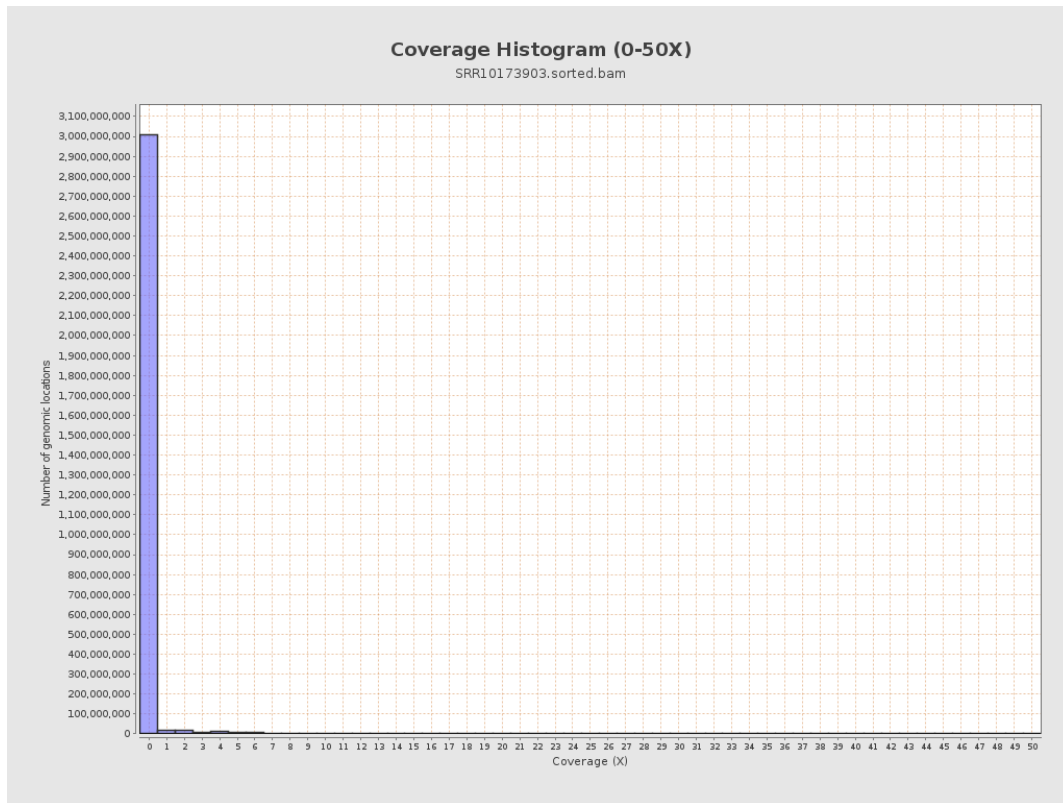
3. Results : Coverage across reference



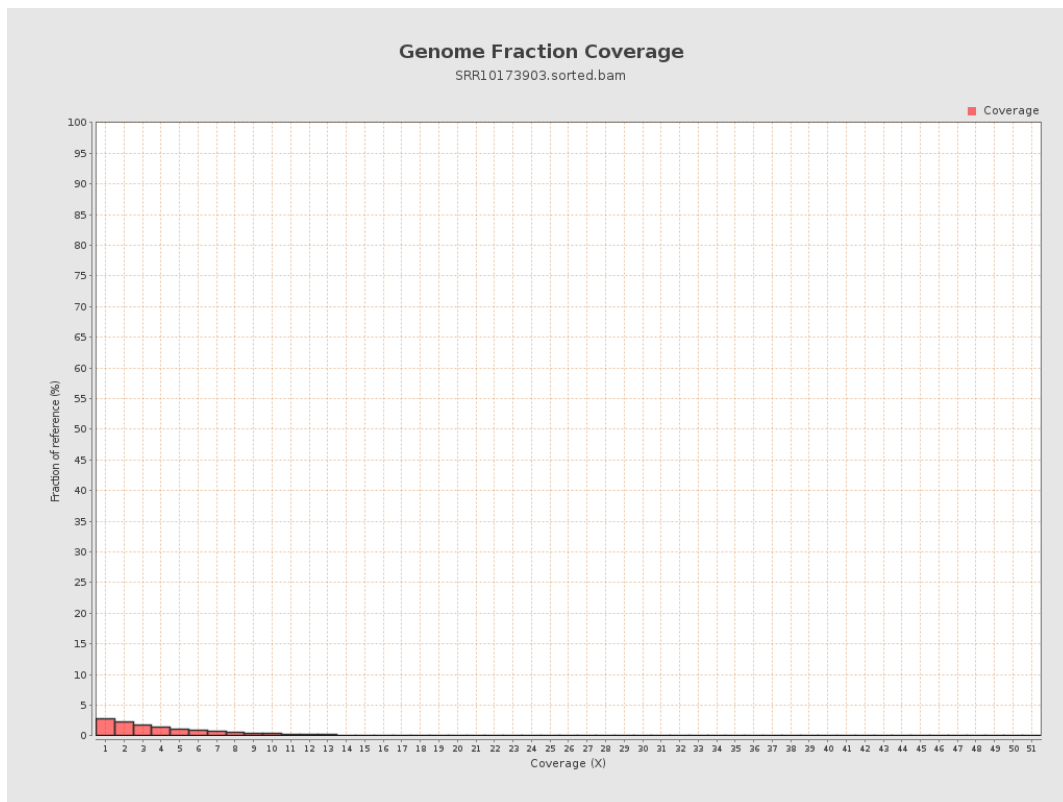
4. Results : Coverage Histogram



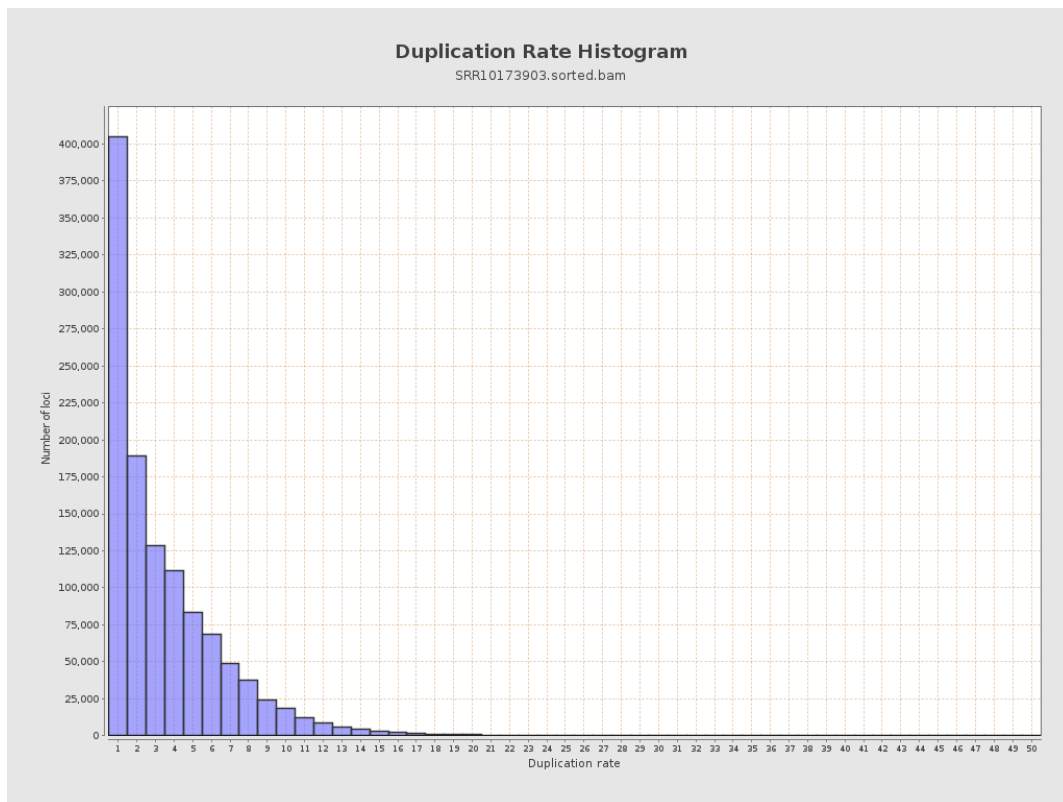
5. Results : Coverage Histogram (0-50X)



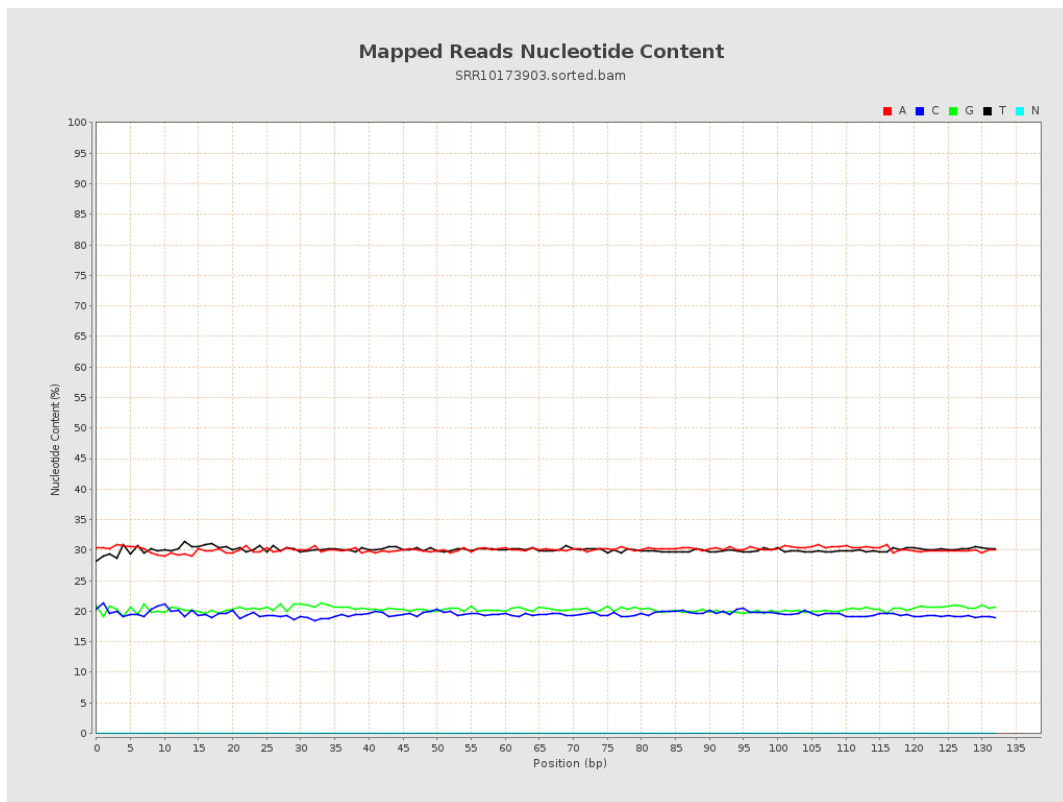
6. Results : Genome Fraction Coverage



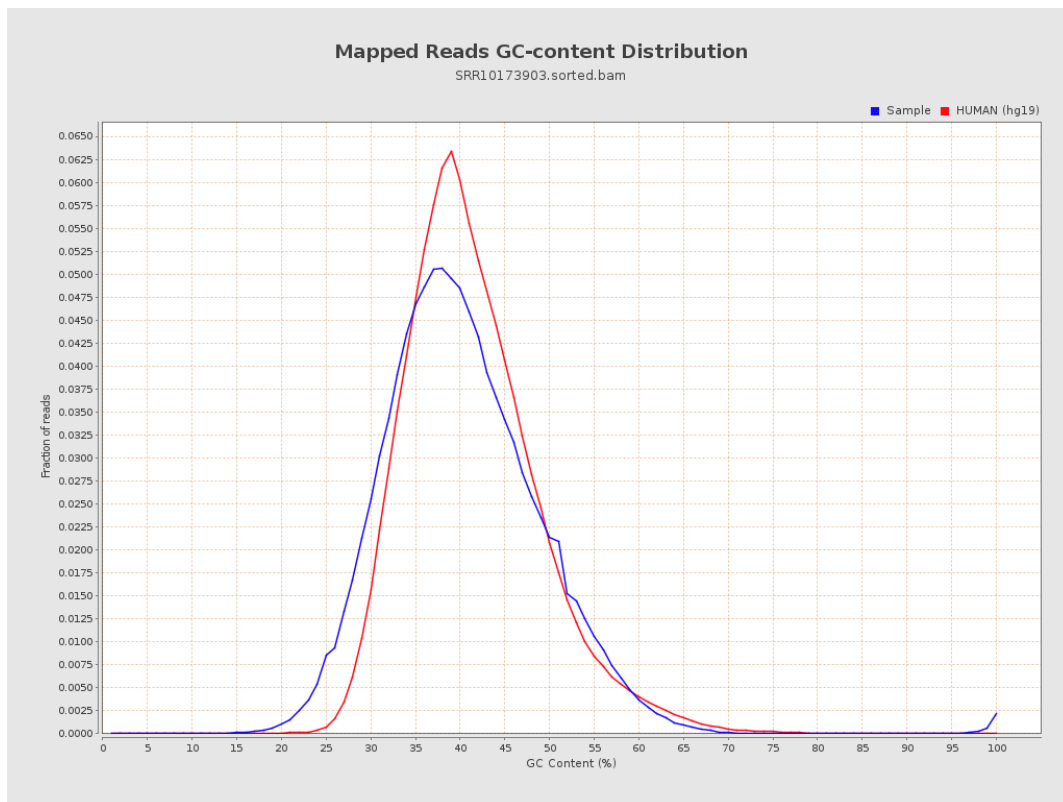
7. Results : Duplication Rate Histogram



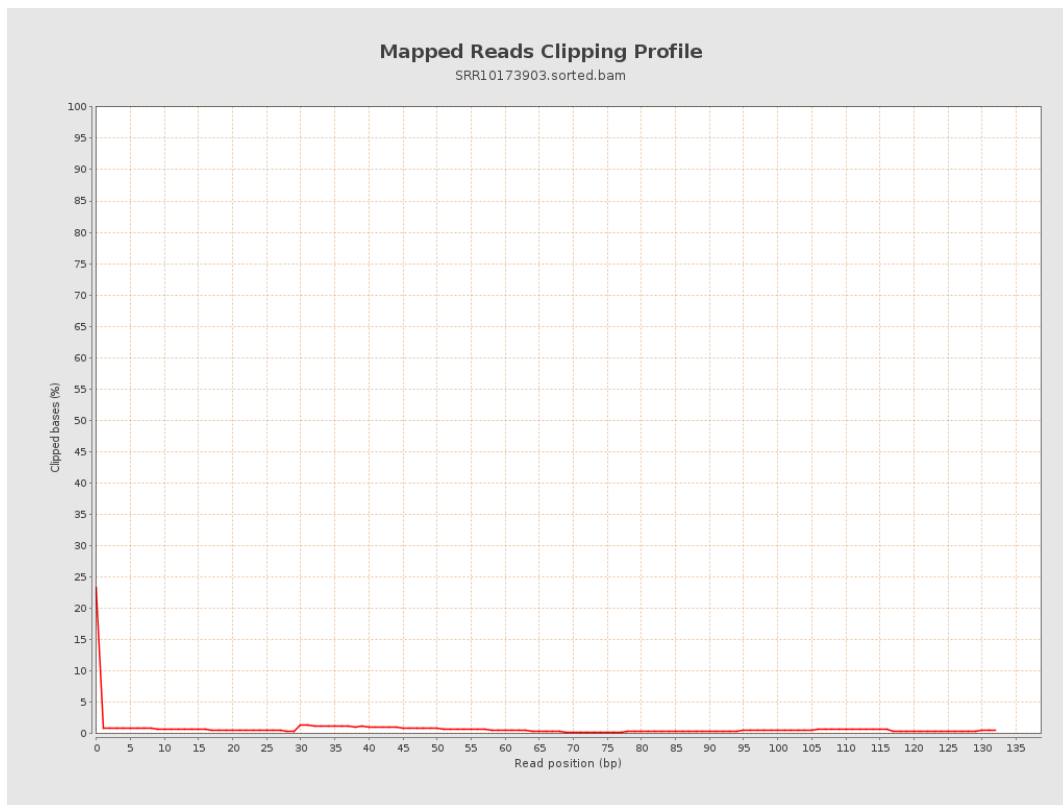
8. Results : Mapped Reads Nucleotide Content



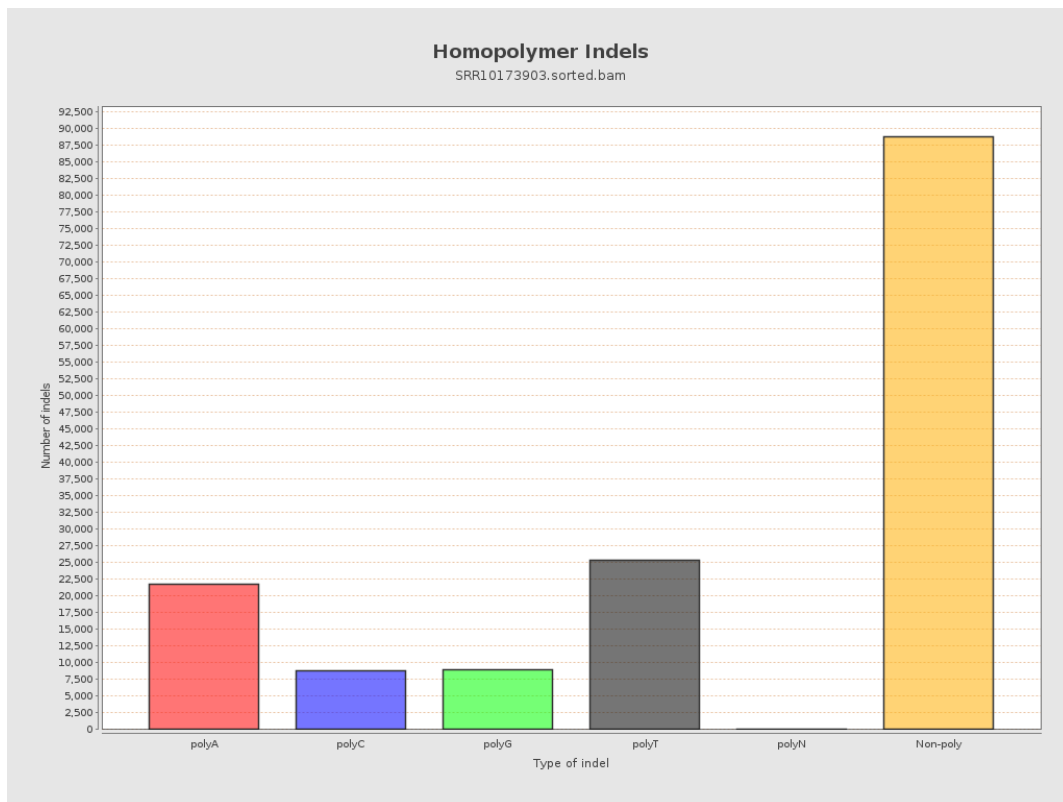
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



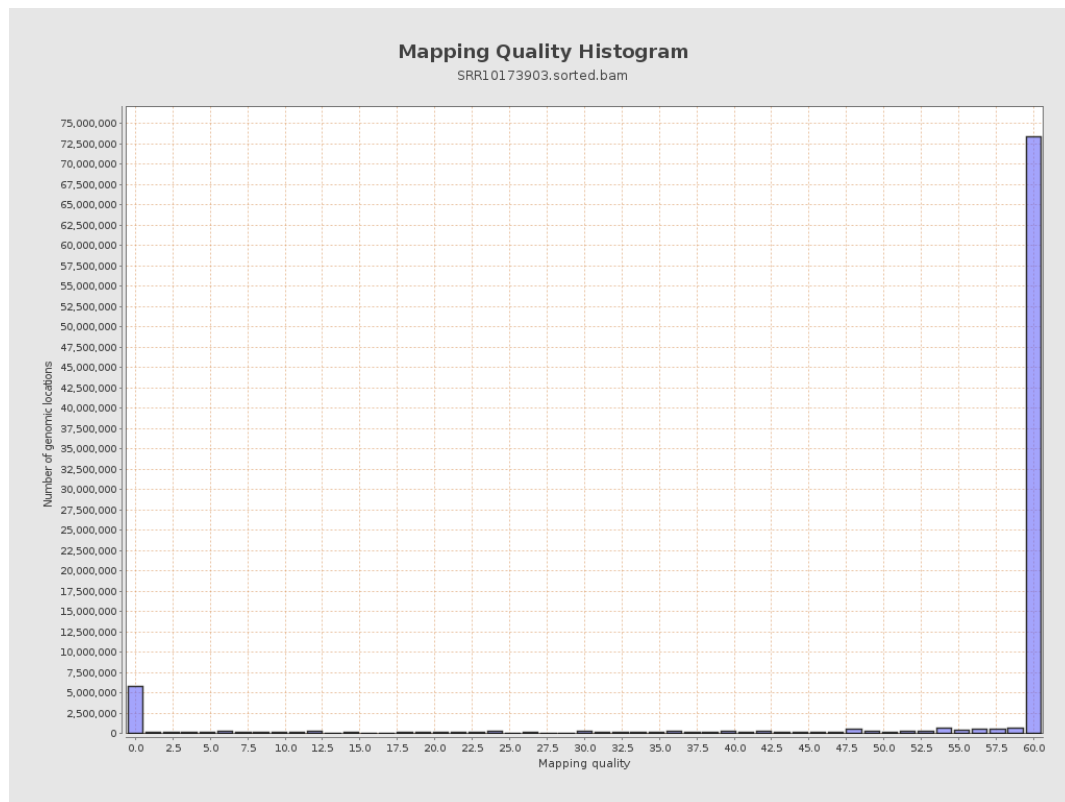
11. Results : Homopolymer Indels



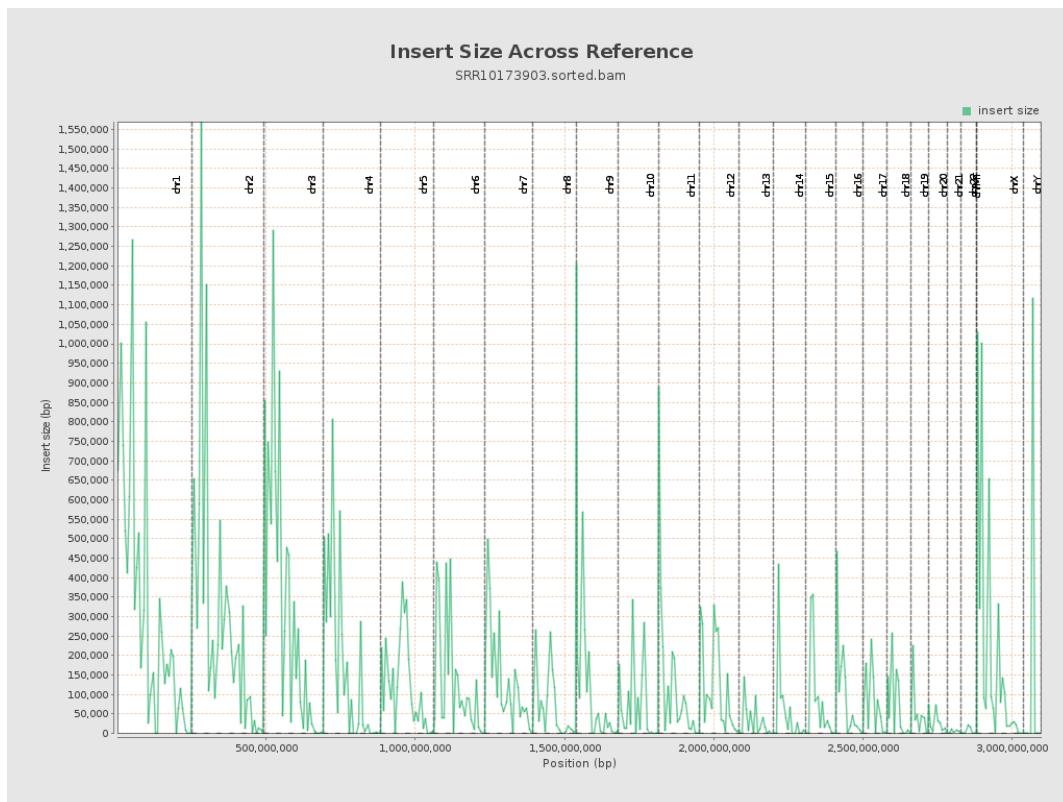
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

