

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 05:00:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173904.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_SRR10173904 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173904_1.fastq.gz SRR10173904_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 05:00:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173904.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,275,998
Mapped reads	1,246,751 / 97.71%
Unmapped reads	29,247 / 2.29%
Mapped paired reads	1,246,751 / 97.71%
Mapped reads, first in pair	623,716 / 48.88%
Mapped reads, second in pair	623,035 / 48.83%
Mapped reads, both in pair	1,227,618 / 96.21%
Mapped reads, singletons	19,133 / 1.5%
Secondary alignments	0
Supplementary alignments	118,123 / 9.26%
Read min/max/mean length	30 / 133 / 128.13
Duplicated reads (estimated)	952,596 / 74.65%
Duplication rate	64.04%
Clipped reads	463,715 / 36.34%

2.2. ACGT Content

Number/percentage of A's	44,454,171 / 29.99%
Number/percentage of C's	29,222,422 / 19.71%
Number/percentage of T's	44,331,671 / 29.9%
Number/percentage of G's	30,238,986 / 20.4%
Number/percentage of N's	1,643 / 0%

GC Percentage	40.11%
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2.3. Coverage

Mean	0.0479
Standard Deviation	0.8601

2.4. Mapping Quality

Mean Mapping Quality	53.12
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2.5. Insert size

Mean	1,133,612.45
Standard Deviation	9,603,805.39
P25/Median/P75	151 / 210 / 294

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	1,534,317
Insertions	16,699
Mapped reads with at least one insertion	1.29%
Deletions	35,573
Mapped reads with at least one deletion	2.79%
Homopolymer indels	42.95%

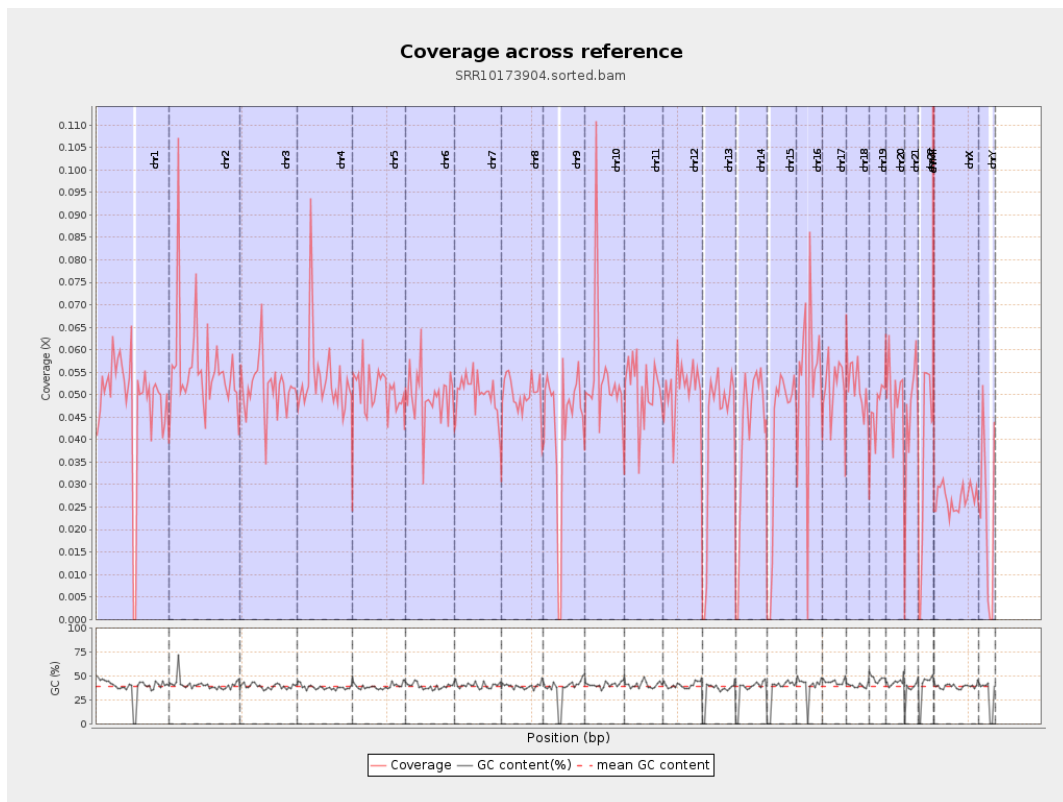
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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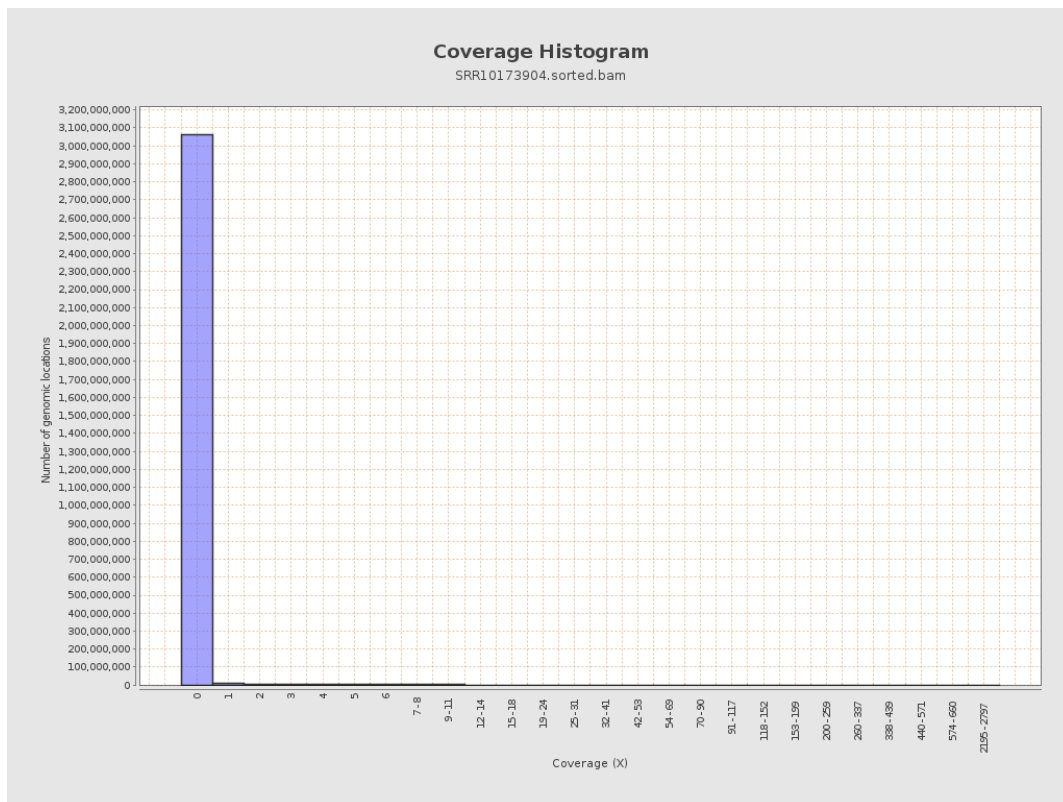
		bases	coverage	deviation
chr1	249250621	12057582	0.0484	0.7062
chr2	243199373	13613769	0.056	2.0602
chr3	198022430	10221705	0.0516	0.6455
chr4	191154276	10153022	0.0531	0.7194
chr5	180915260	9213406	0.0509	0.6396
chr6	171115067	8490058	0.0496	0.6487
chr7	159138663	8014851	0.0504	0.6897
chr8	146364022	7327882	0.0501	0.7407
chr9	141213431	6150354	0.0436	0.6682
chr10	135534747	7299583	0.0539	0.8317
chr11	135006516	6884663	0.051	0.6344
chr12	133851895	6852148	0.0512	0.6316
chr13	115169878	4813895	0.0418	0.5754
chr14	107349540	4449266	0.0414	0.5749
chr15	102531392	4165062	0.0406	0.5605
chr16	90354753	4860705	0.0538	0.7288
chr17	81195210	4150111	0.0511	0.6708
chr18	78077248	4057695	0.052	0.8784
chr19	59128983	2778019	0.047	0.6549
chr20	63025520	3119938	0.0495	0.6145
chr21	48129895	2142110	0.0445	0.641
chr22	51304566	1835111	0.0358	0.5163
chrMT	16571	208347	12.573	15.6848
chrX	155270560	4186295	0.027	0.4616

chrY	59373566	1292041	0.0218	0.4599
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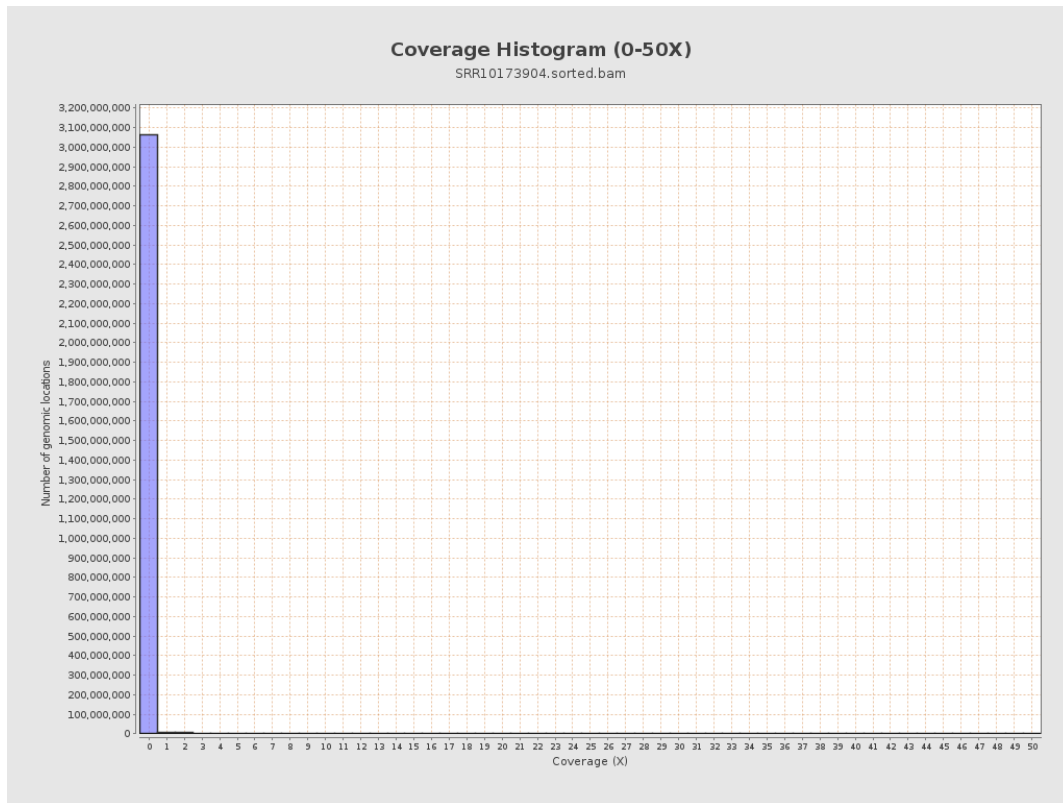
3. Results : Coverage across reference



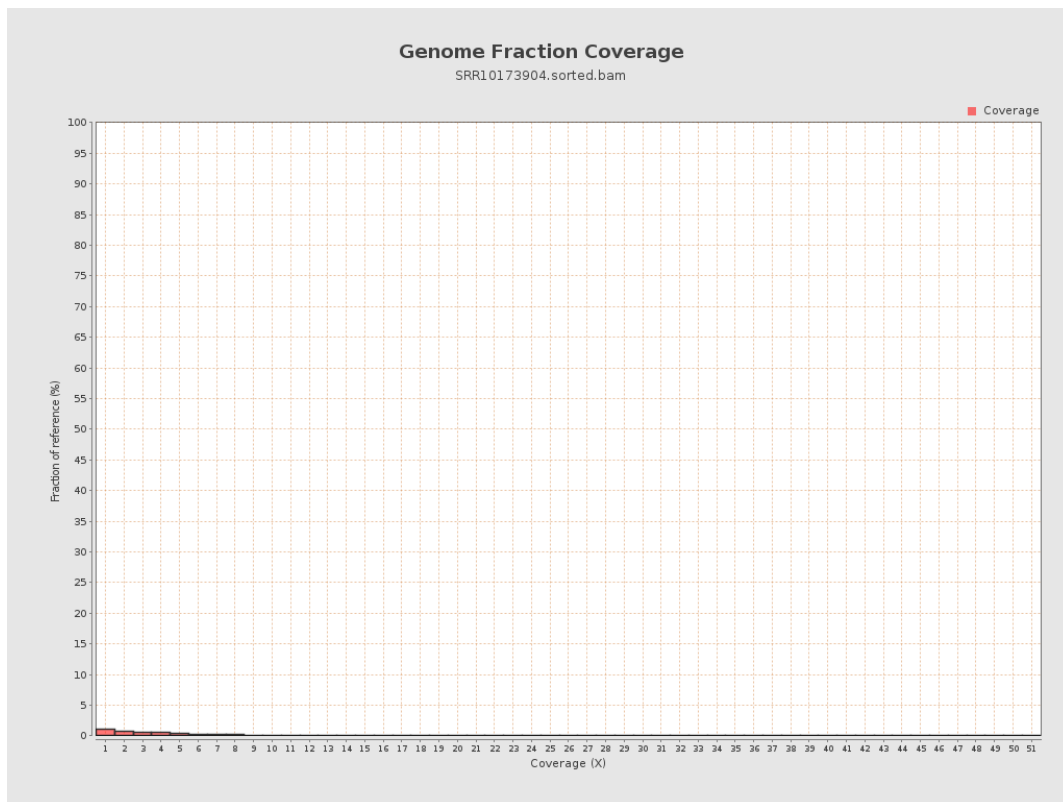
4. Results : Coverage Histogram



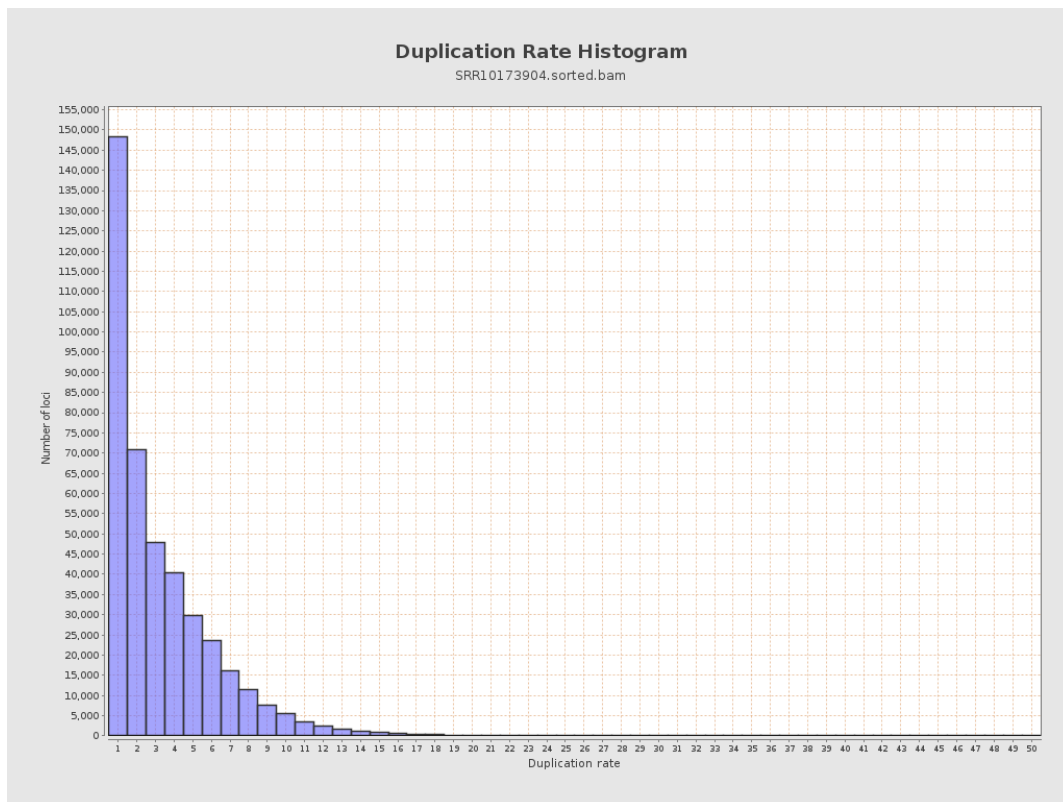
5. Results : Coverage Histogram (0-50X)



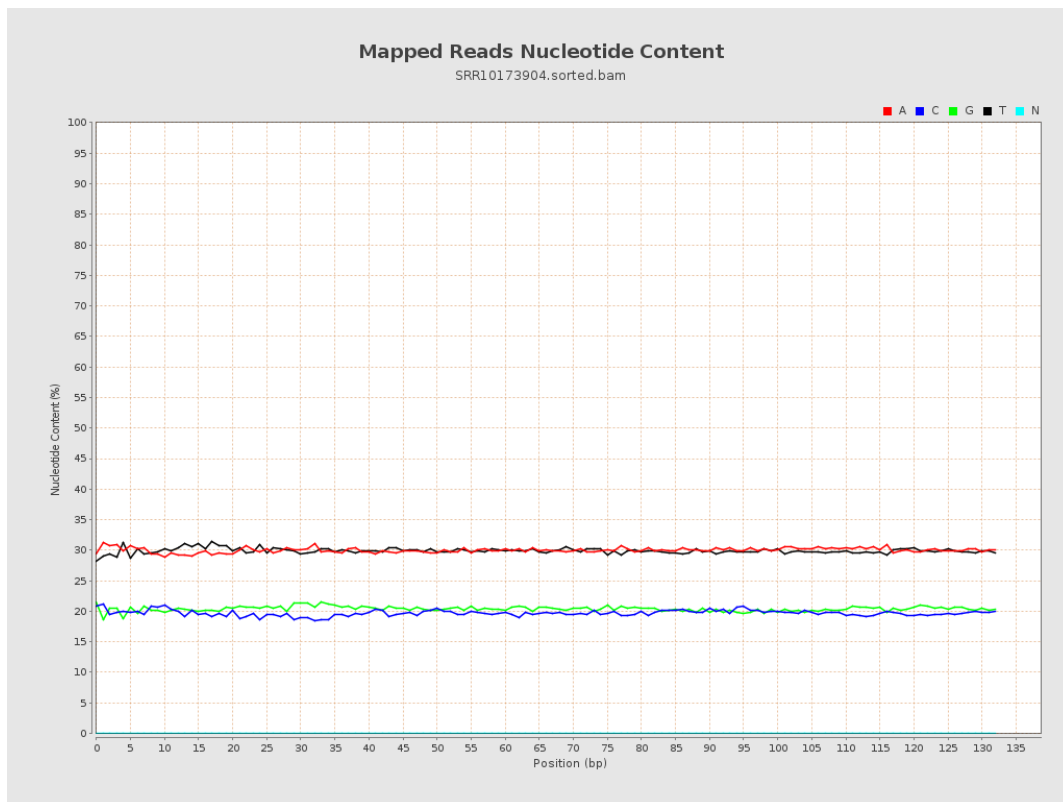
6. Results : Genome Fraction Coverage



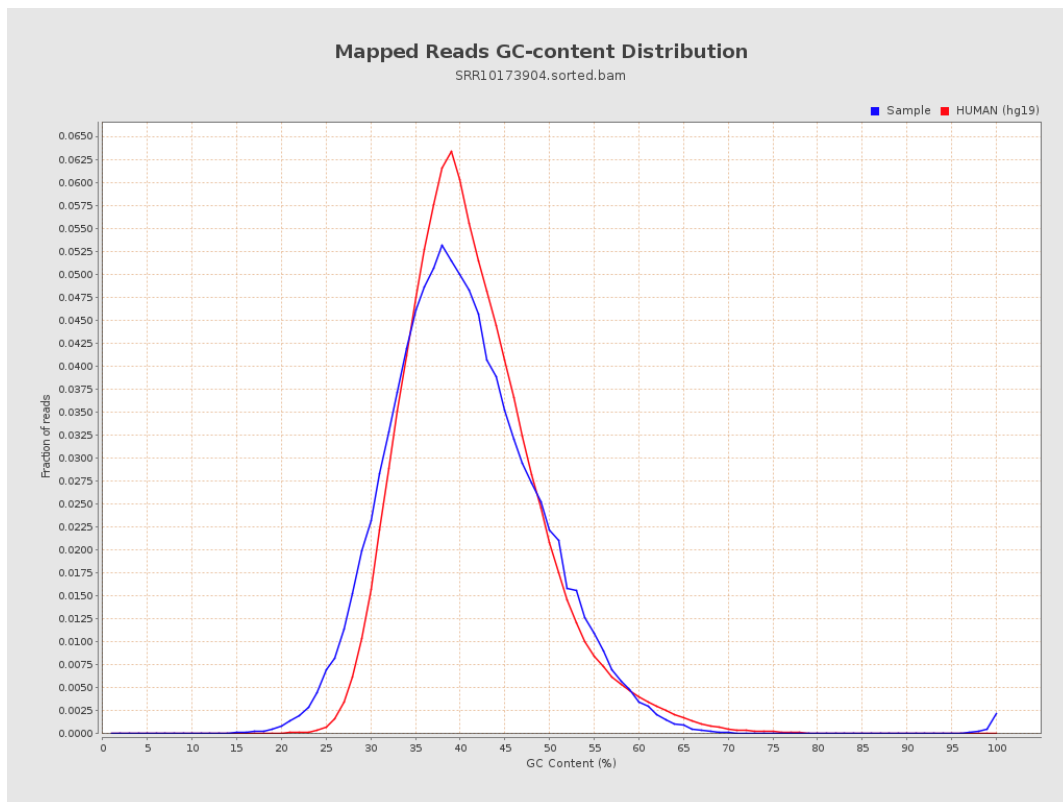
7. Results : Duplication Rate Histogram



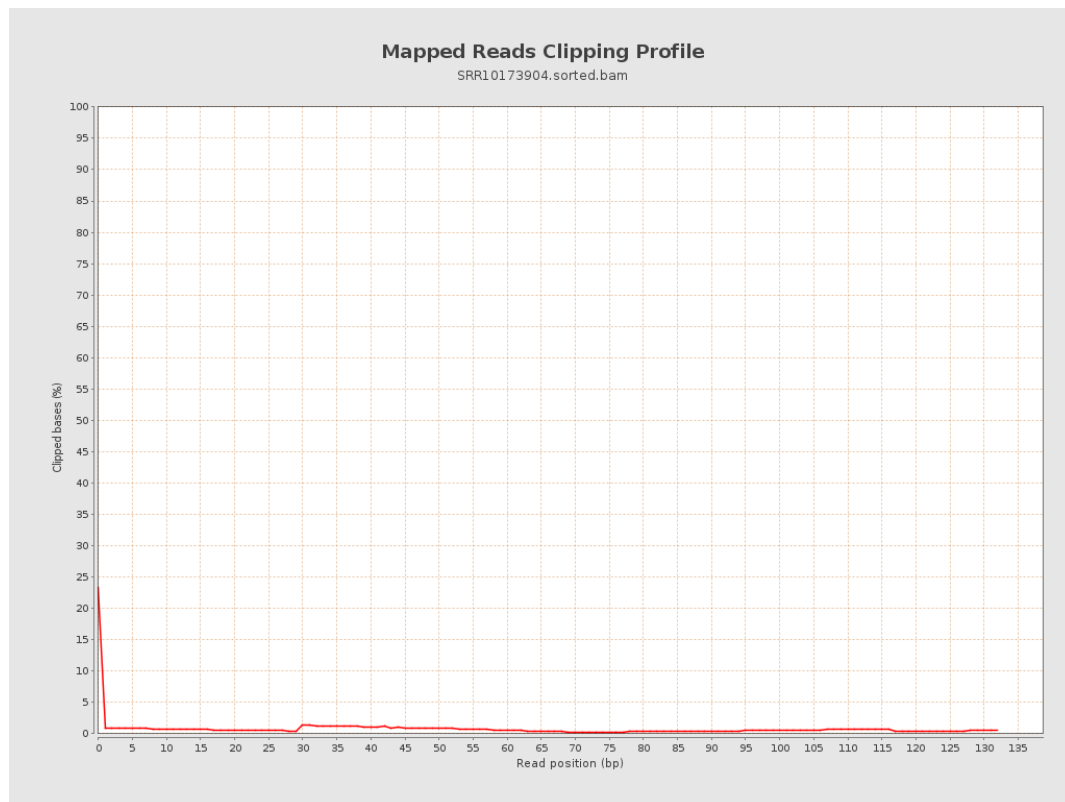
8. Results : Mapped Reads Nucleotide Content



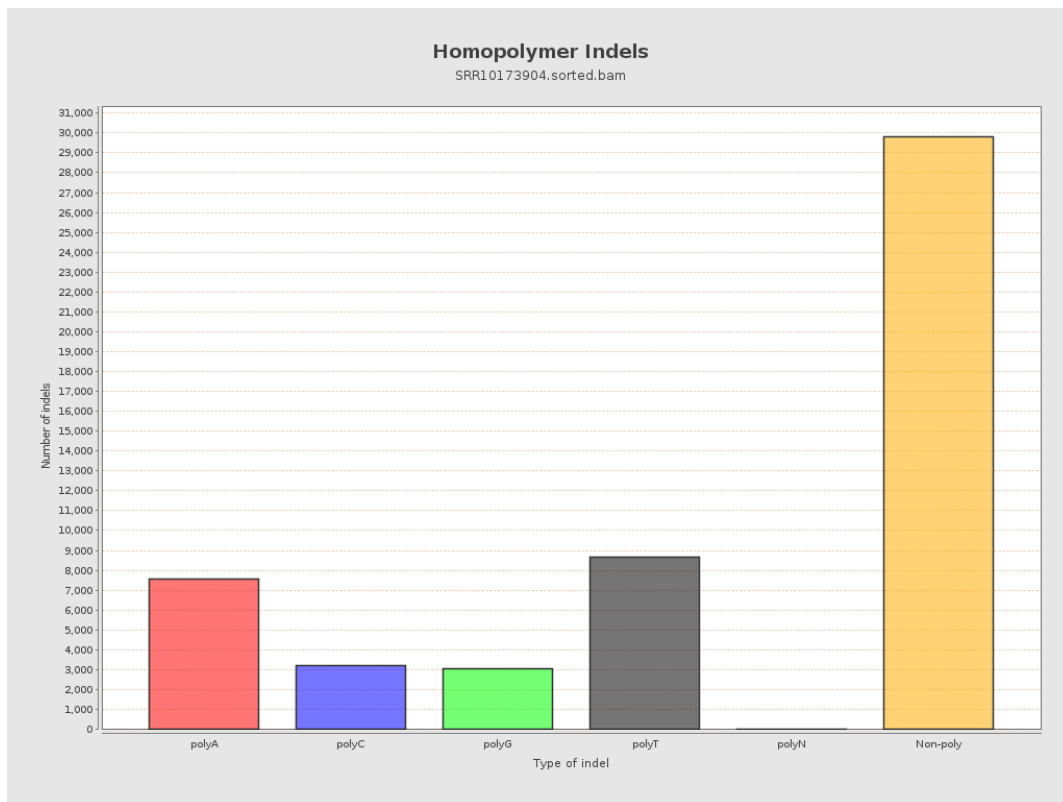
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



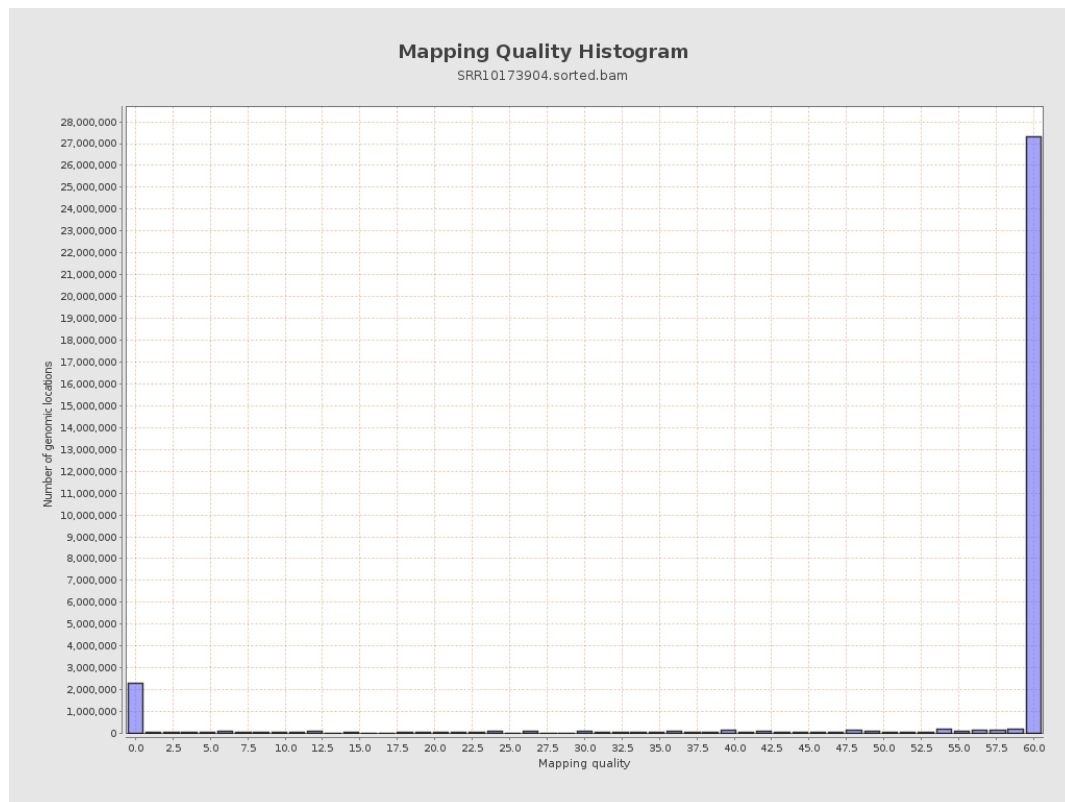
11. Results : Homopolymer Indels



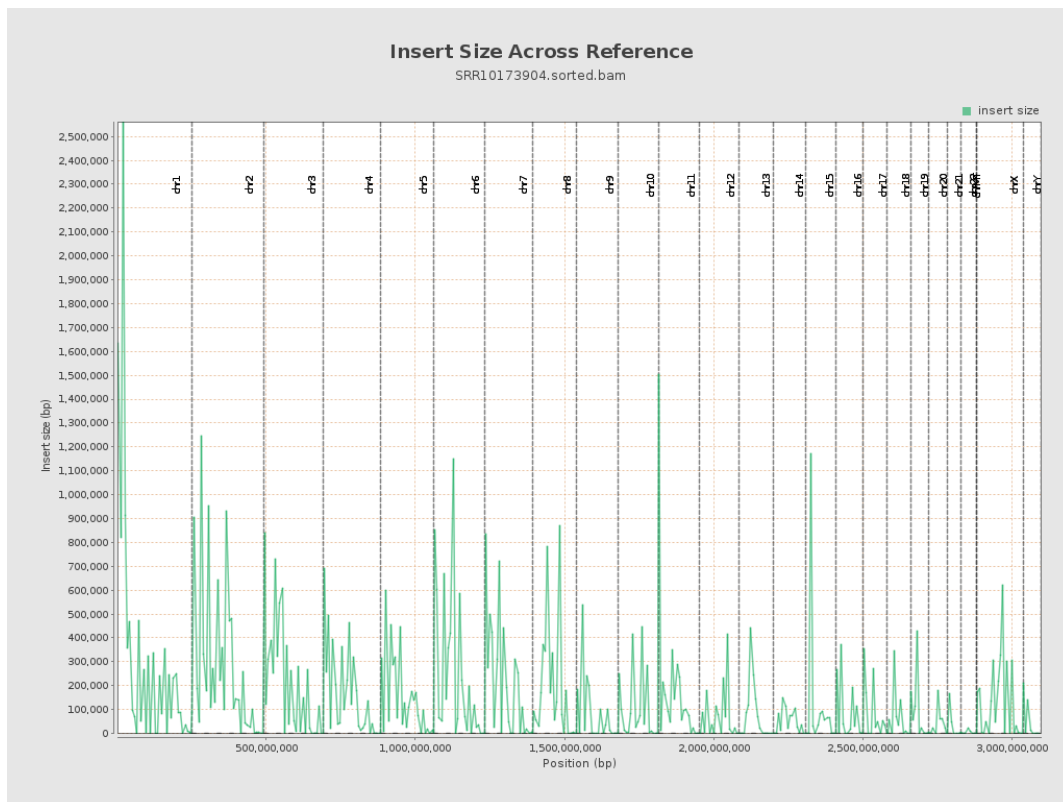
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

