

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 12:28:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173956.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_SRR10173956 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173956_1.fastq.gz SRR10173956_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 12:28:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173956.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,024,502
Mapped reads	3,919,200 / 97.38%
Unmapped reads	105,302 / 2.62%
Mapped paired reads	3,919,200 / 97.38%
Mapped reads, first in pair	1,963,271 / 48.78%
Mapped reads, second in pair	1,955,929 / 48.6%
Mapped reads, both in pair	3,851,442 / 95.7%
Mapped reads, singletons	67,758 / 1.68%
Secondary alignments	0
Supplementary alignments	510,589 / 12.69%
Read min/max/mean length	30 / 133 / 126.02
Duplicated reads (estimated)	3,110,487 / 77.29%
Duplication rate	64.28%
Clipped reads	2,001,544 / 49.73%

2.2. ACGT Content

Number/percentage of A's	132,258,755 / 29.69%
Number/percentage of C's	89,119,942 / 20.01%
Number/percentage of T's	131,132,527 / 29.44%
Number/percentage of G's	92,880,589 / 20.85%
Number/percentage of N's	3,546 / 0%

GC Percentage	40.86%
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2.3. Coverage

Mean	0.144
Standard Deviation	2.791

2.4. Mapping Quality

Mean Mapping Quality	52.48
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2.5. Insert size

Mean	1,099,087.92
Standard Deviation	9,754,363.75
P25/Median/P75	109 / 162 / 252

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	3,979,127
Insertions	50,338
Mapped reads with at least one insertion	1.23%
Deletions	125,156
Mapped reads with at least one deletion	3.11%
Homopolymer indels	40.84%

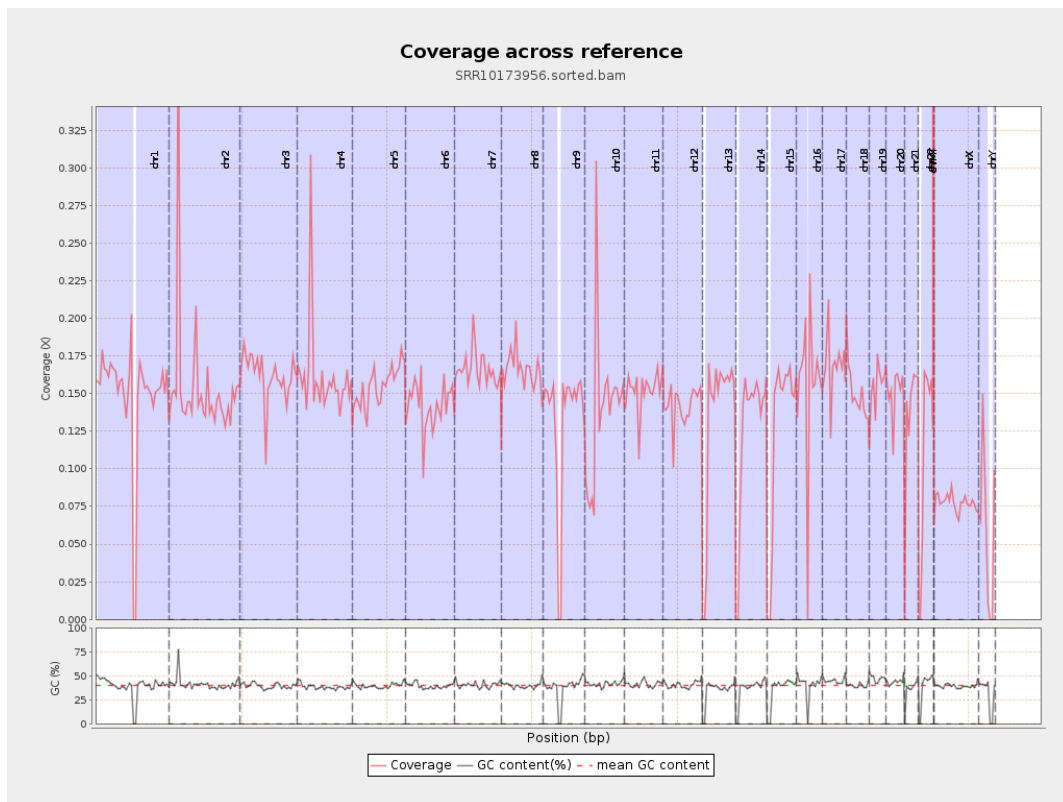
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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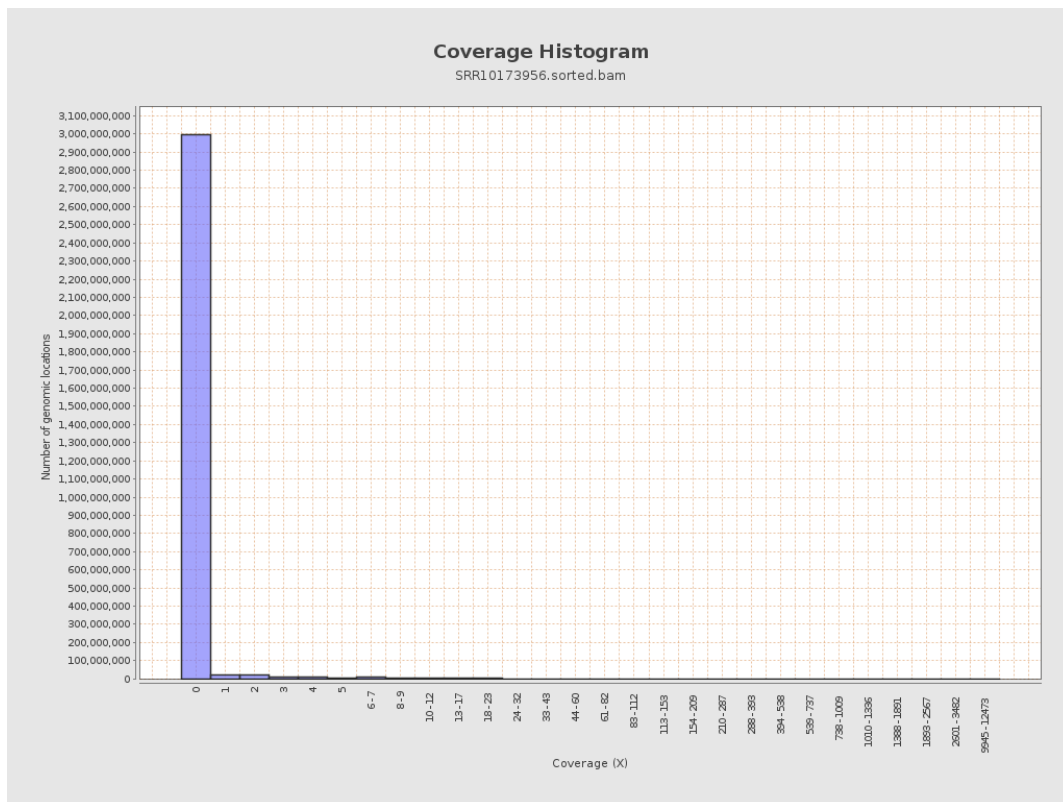
		bases	coverage	deviation
chr1	249250621	37158145	0.1491	1.738
chr2	243199373	37629228	0.1547	8.7357
chr3	198022430	32003076	0.1616	1.1889
chr4	191154276	30660340	0.1604	1.5727
chr5	180915260	28087283	0.1553	1.1728
chr6	171115067	24271069	0.1418	1.2173
chr7	159138663	26527618	0.1667	1.607
chr8	146364022	24244770	0.1656	1.8567
chr9	141213431	18566634	0.1315	1.3754
chr10	135534747	18560554	0.1369	1.8468
chr11	135006516	20519583	0.152	1.1702
chr12	133851895	18971778	0.1417	1.1458
chr13	115169878	15298430	0.1328	1.0874
chr14	107349540	13360723	0.1245	1.0491
chr15	102531392	12991690	0.1267	1.0603
chr16	90354753	14147913	0.1566	1.3783
chr17	81195210	13638836	0.168	1.2758
chr18	78077248	11705290	0.1499	1.7354
chr19	59128983	9218095	0.1559	1.3767
chr20	63025520	9468959	0.1502	1.1646
chr21	48129895	6524543	0.1356	1.2807
chr22	51304566	5582460	0.1088	1.0481
chrMT	16571	1137968	68.6723	58.4764
chrX	155270560	12026634	0.0775	0.8143

chrY	59373566	3395434	0.0572	1.0222
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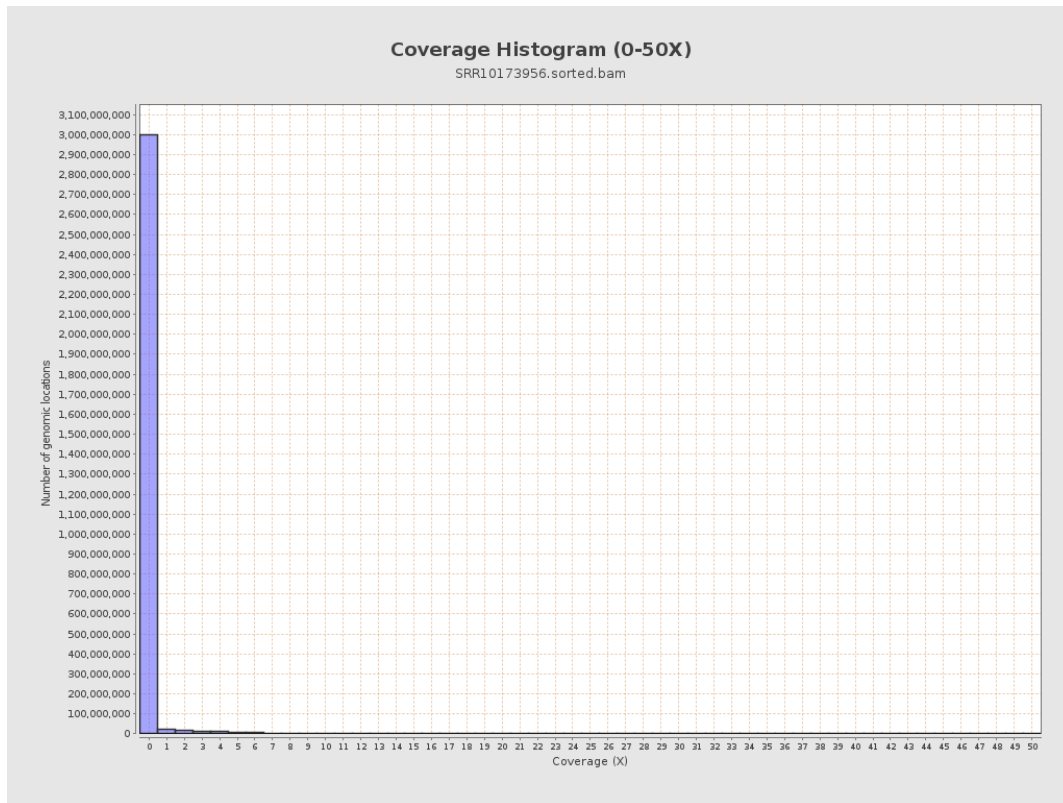
3. Results : Coverage across reference



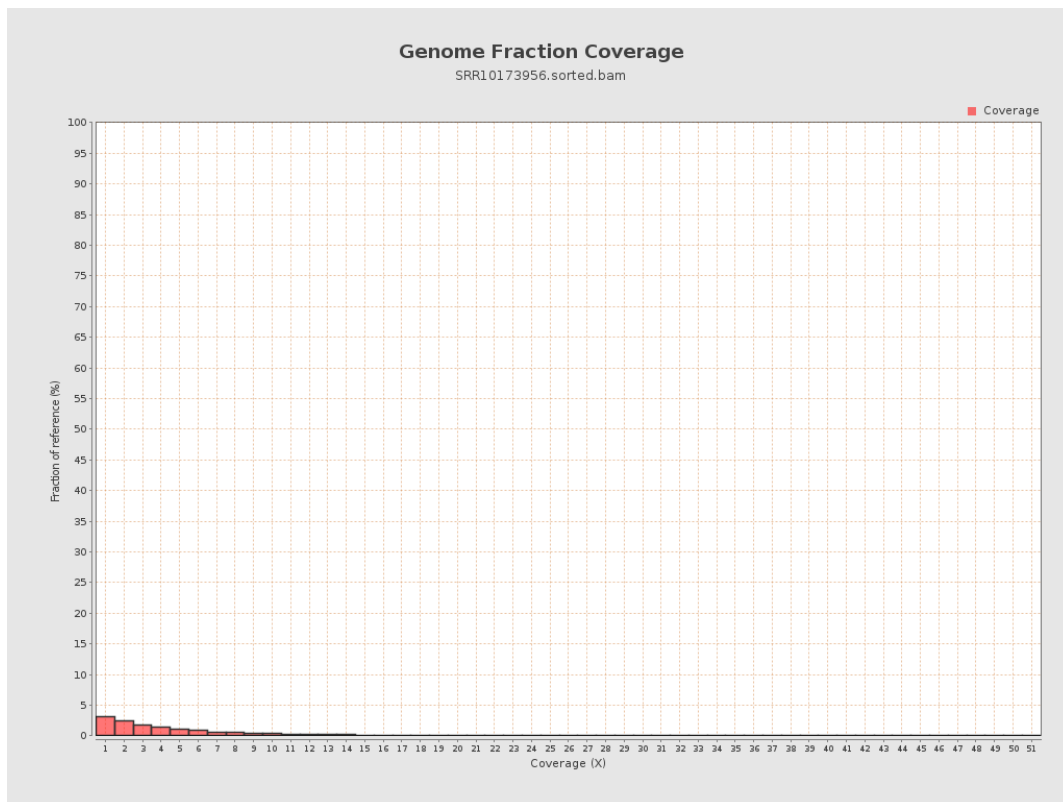
4. Results : Coverage Histogram



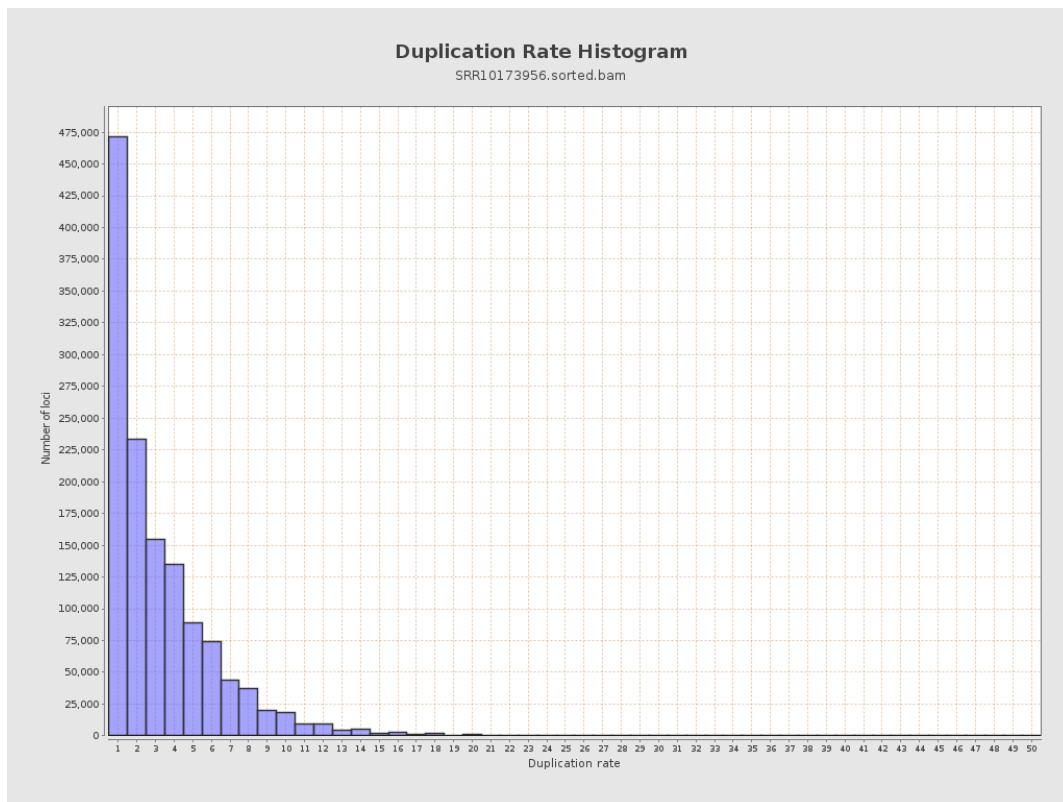
5. Results : Coverage Histogram (0-50X)



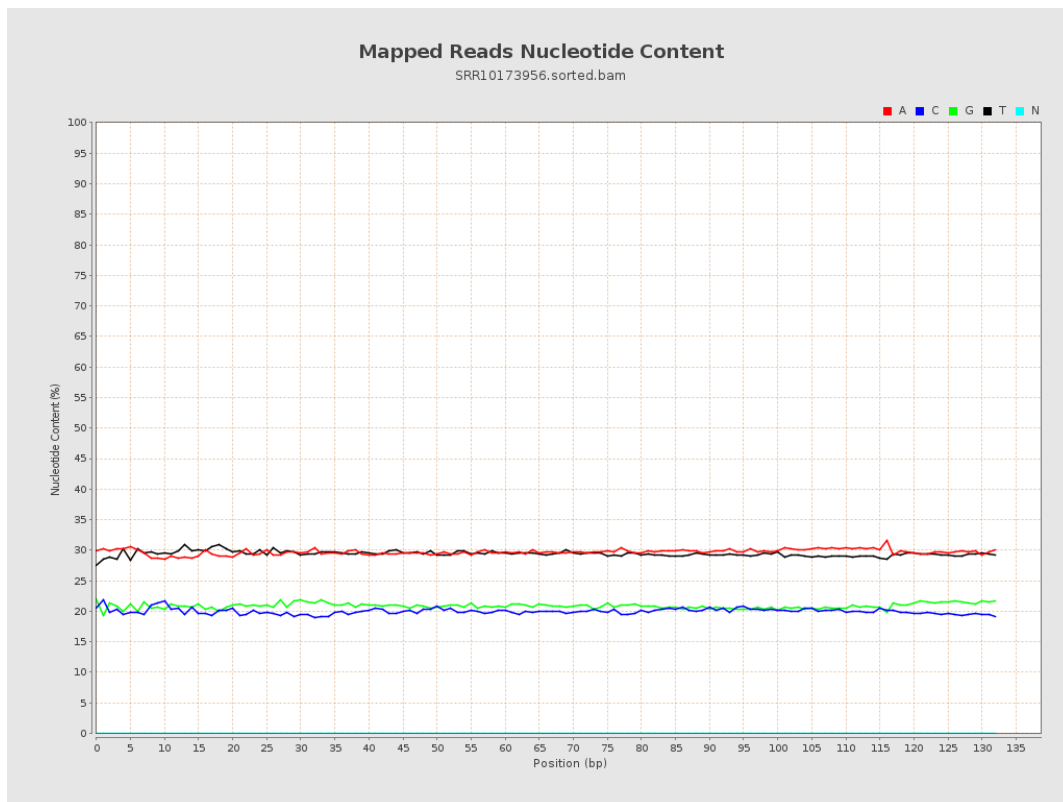
6. Results : Genome Fraction Coverage



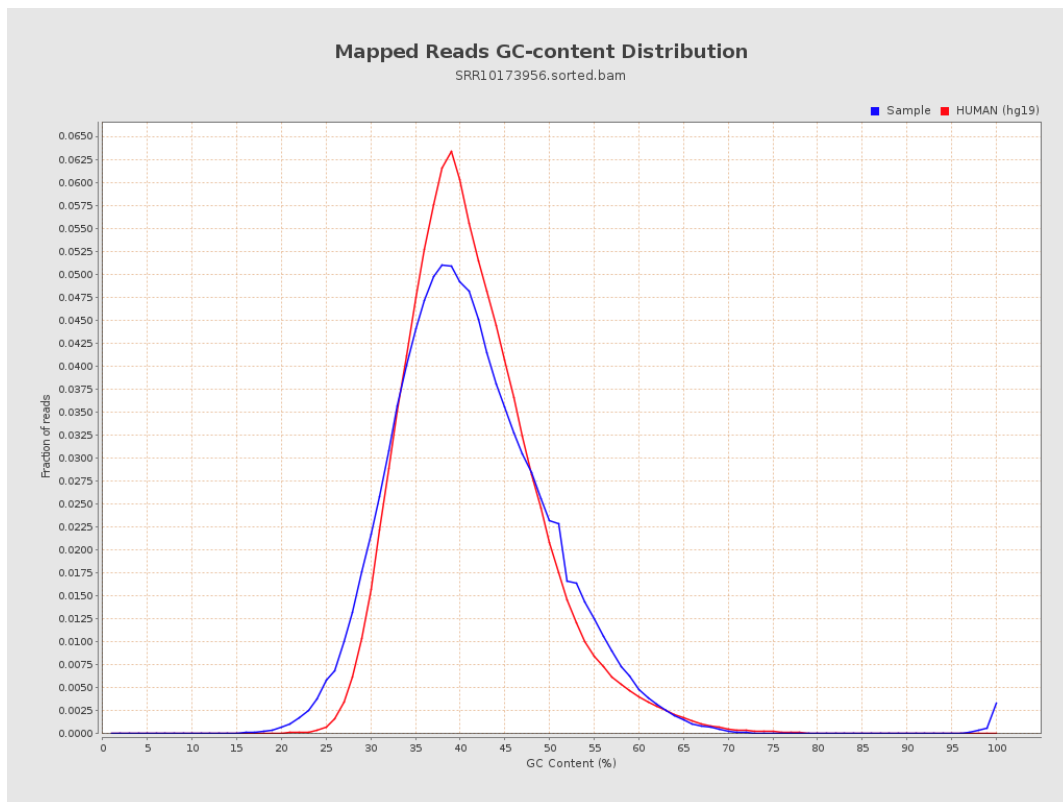
7. Results : Duplication Rate Histogram



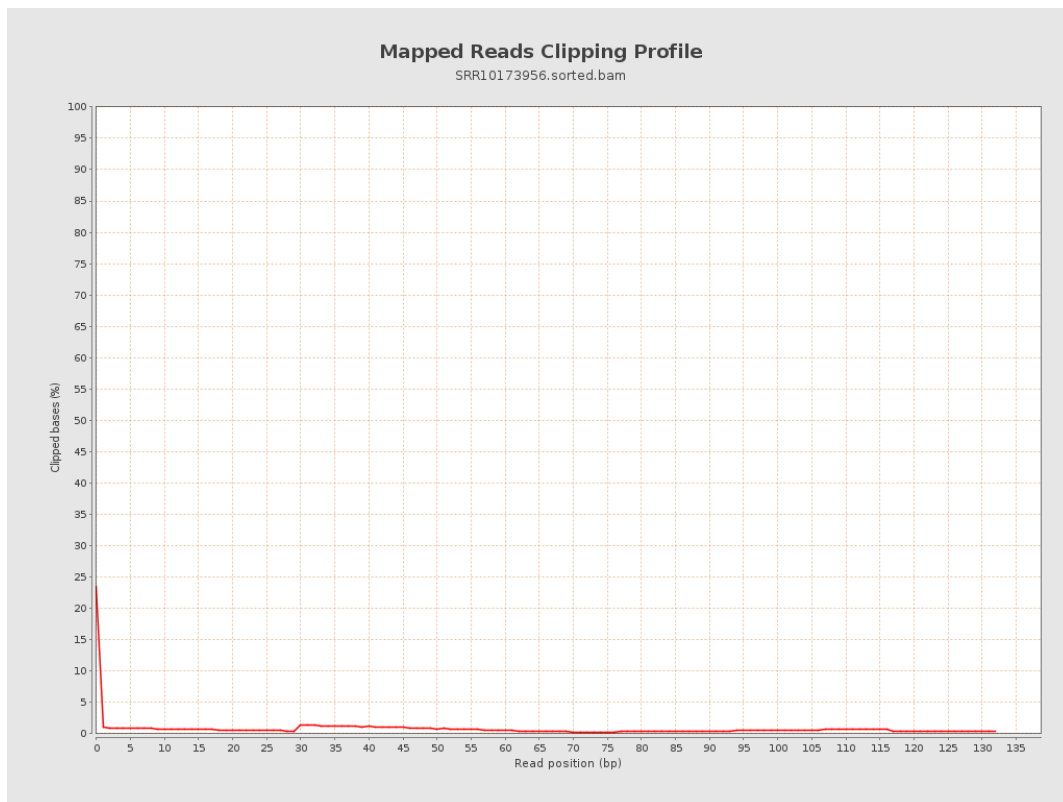
8. Results : Mapped Reads Nucleotide Content



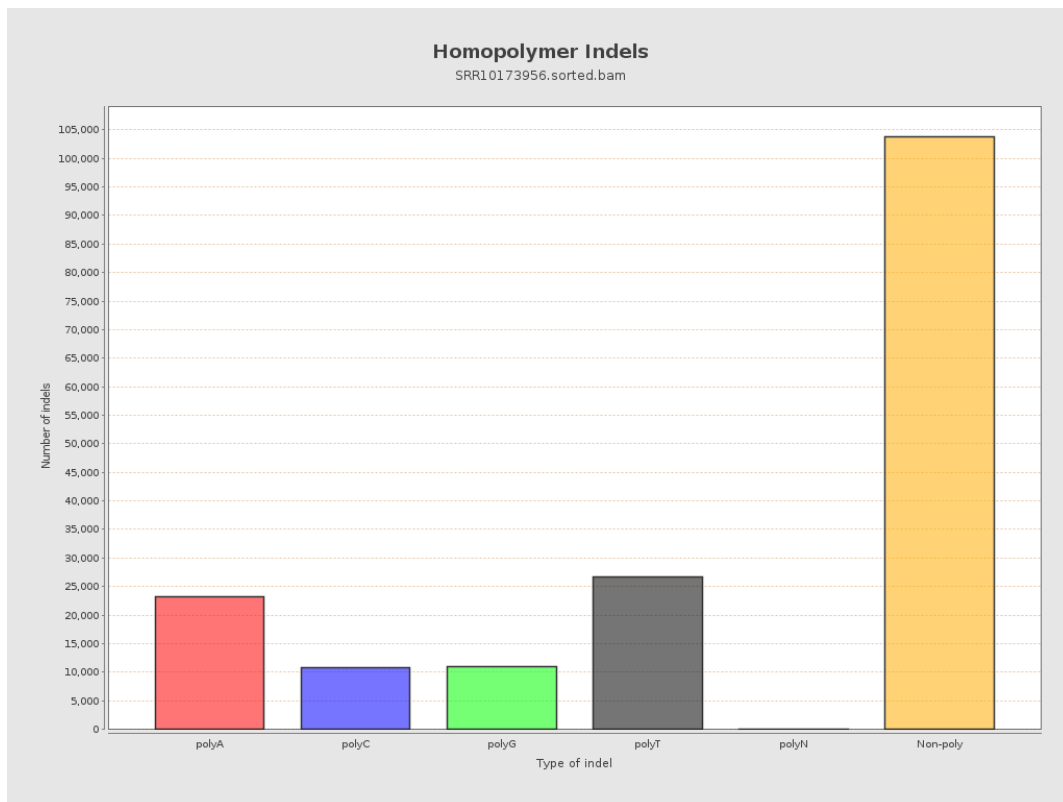
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



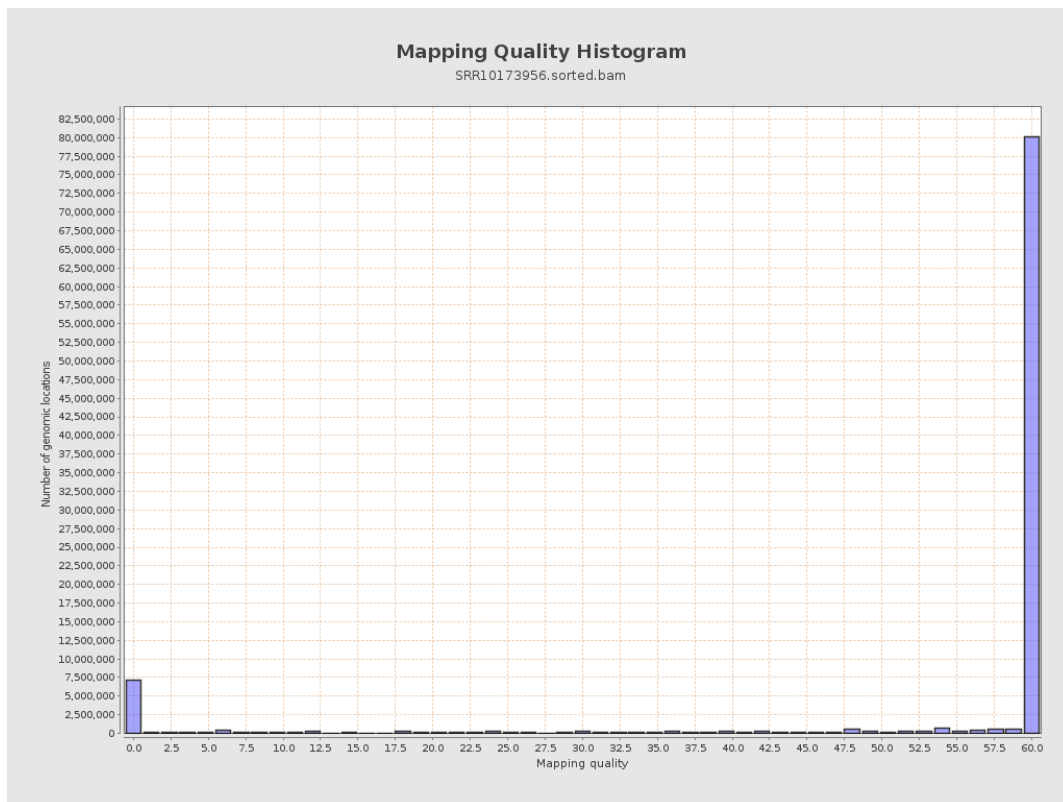
11. Results : Homopolymer Indels



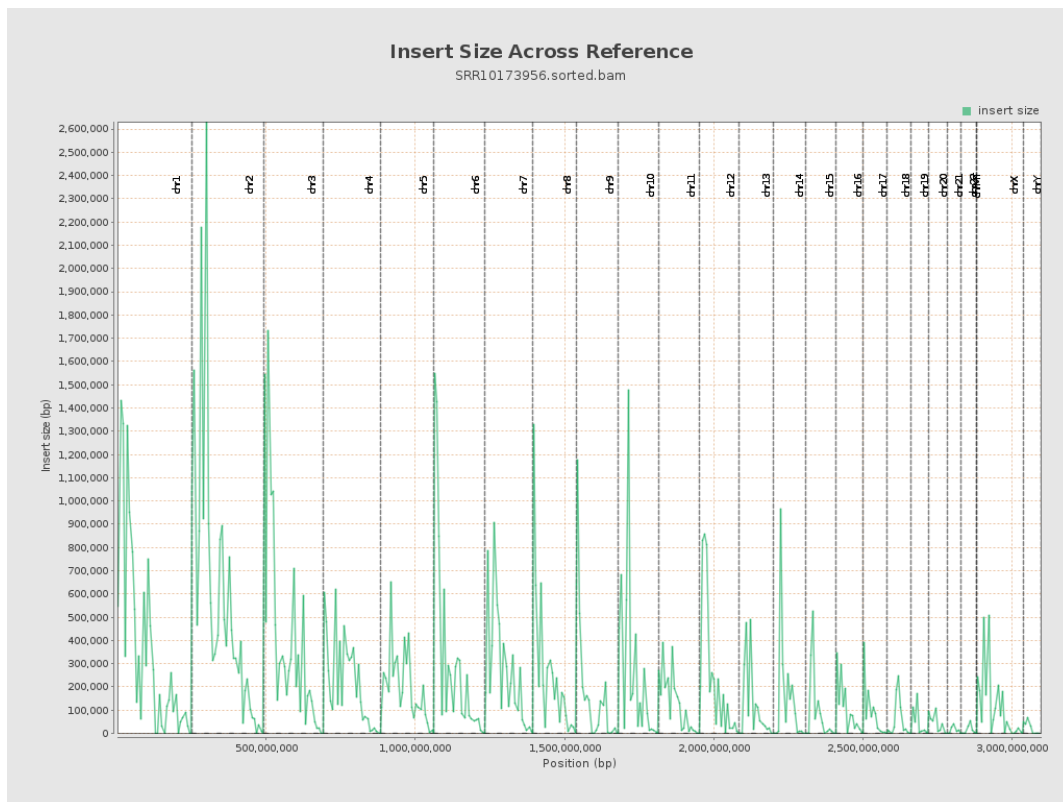
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

