

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 09:57:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124956.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_SRR3124956 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124956_1.fastq.gz SRR3124956_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 09:57:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124956.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,035,486
Mapped reads	5,501,826 / 91.16%
Unmapped reads	533,660 / 8.84%
Mapped paired reads	5,501,826 / 91.16%
Mapped reads, first in pair	2,834,041 / 46.96%
Mapped reads, second in pair	2,667,785 / 44.2%
Mapped reads, both in pair	5,263,226 / 87.2%
Mapped reads, singletons	238,600 / 3.95%
Secondary alignments	0
Supplementary alignments	7,675 / 0.13%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	448,257 / 7.43%
Duplication rate	4.77%
Clipped reads	2,572,658 / 42.63%

2.2. ACGT Content

Number/percentage of A's	95,226,932 / 27.97%
Number/percentage of C's	59,304,376 / 17.42%
Number/percentage of T's	104,598,893 / 30.72%
Number/percentage of G's	81,376,976 / 23.9%
Number/percentage of N's	2,691 / 0%

GC Percentage	41.31%
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2.3. Coverage

Mean	0.11
Standard Deviation	1.627

2.4. Mapping Quality

Mean Mapping Quality	51.61
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2.5. Insert size

Mean	26,222.36
Standard Deviation	1,485,337.05
P25/Median/P75	146 / 197 / 272

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	2,102,225
Insertions	36,616
Mapped reads with at least one insertion	0.66%
Deletions	89,134
Mapped reads with at least one deletion	1.6%
Homopolymer indels	48.98%

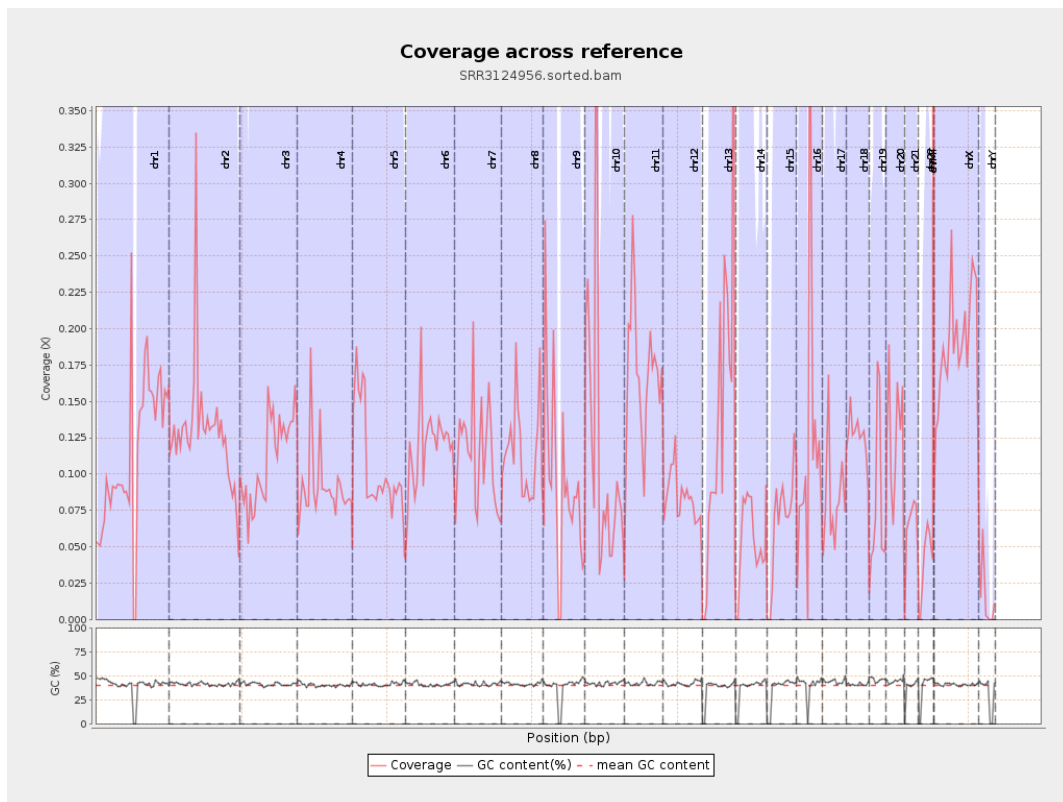
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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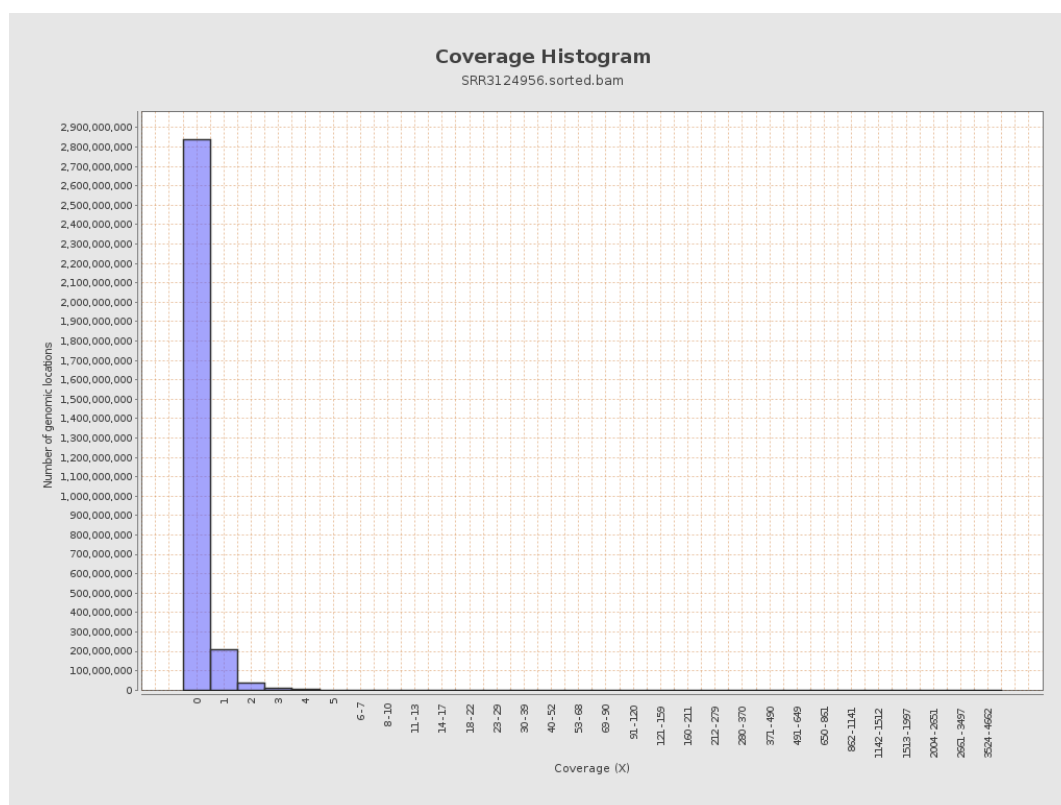
		bases	coverage	deviation
chr1	249250621	28418850	0.114	1.7106
chr2	243199373	31301575	0.1287	2.4538
chr3	198022430	21824364	0.1102	0.4395
chr4	191154276	17314972	0.0906	2.7827
chr5	180915260	19046149	0.1053	1.1193
chr6	171115067	20325216	0.1188	0.9427
chr7	159138663	18226467	0.1145	1.4998
chr8	146364022	16897785	0.1155	0.6668
chr9	141213431	13339898	0.0945	2.3913
chr10	135534747	15665901	0.1156	3.2541
chr11	135006516	22648328	0.1678	1.488
chr12	133851895	11209133	0.0837	0.3684
chr13	115169878	16516586	0.1434	0.559
chr14	107349540	5668481	0.0528	0.4185
chr15	102531392	6904804	0.0673	0.3243
chr16	90354753	10543782	0.1167	2.2667
chr17	81195210	6581352	0.0811	1.0129
chr18	78077248	9910699	0.1269	1.6861
chr19	59128983	4834728	0.0818	1.2706
chr20	63025520	7889887	0.1252	0.4666
chr21	48129895	2992835	0.0622	0.417
chr22	51304566	1984006	0.0387	0.233
chrMT	16571	270140	16.302	11.7126
chrX	155270560	29455666	0.1897	0.8895

chrY	59373566	871229	0.0147	0.744
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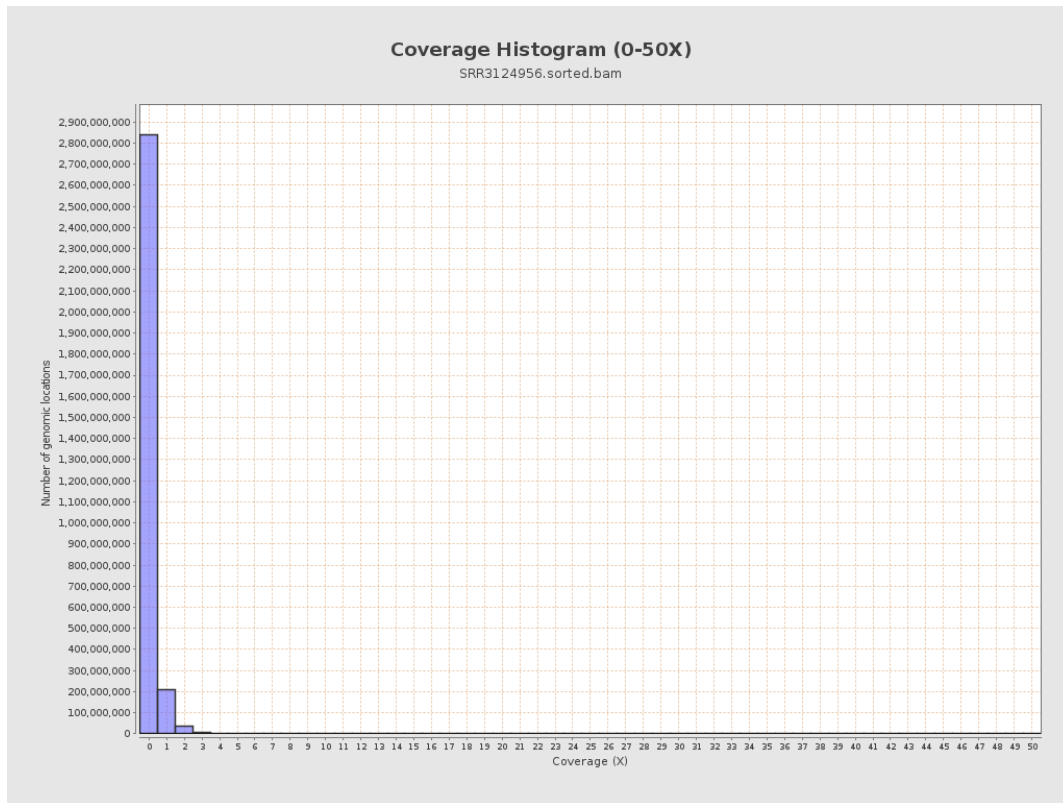
3. Results : Coverage across reference



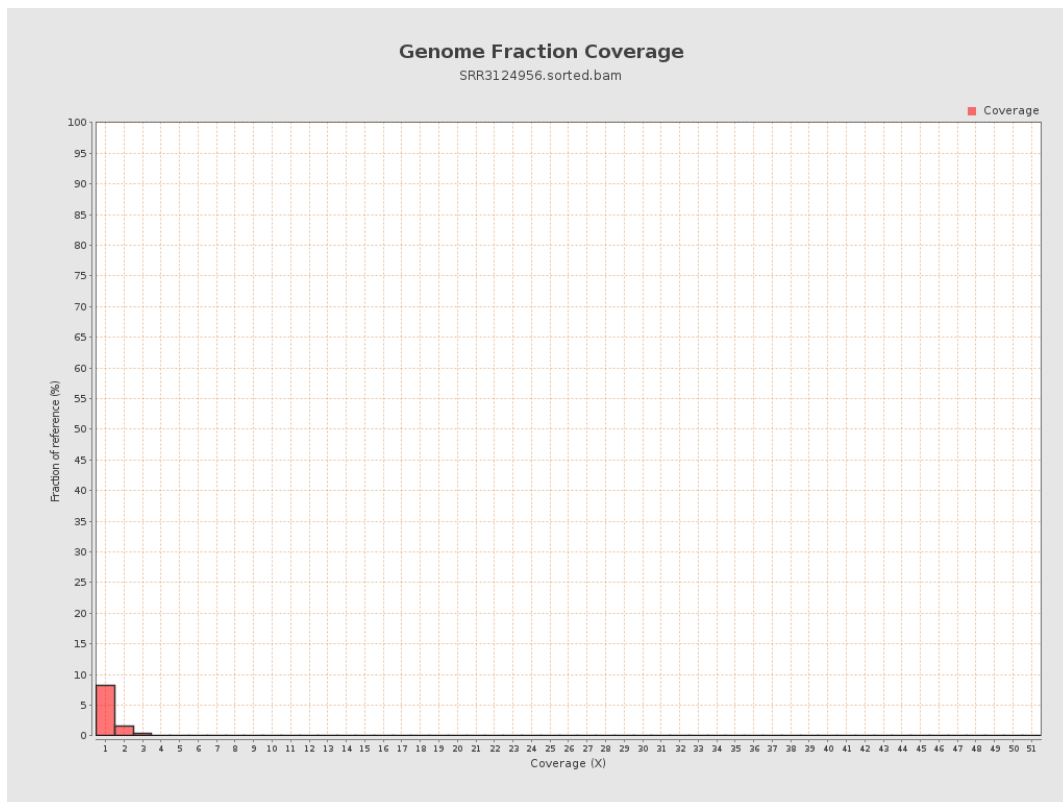
4. Results : Coverage Histogram



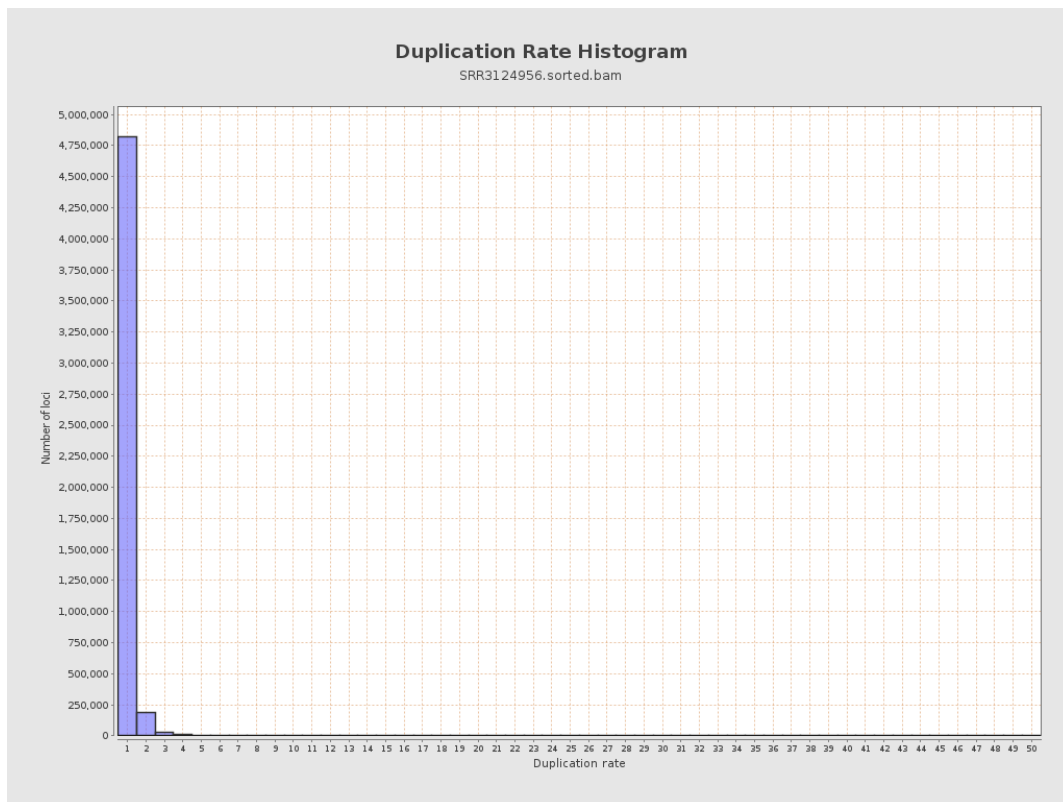
5. Results : Coverage Histogram (0-50X)



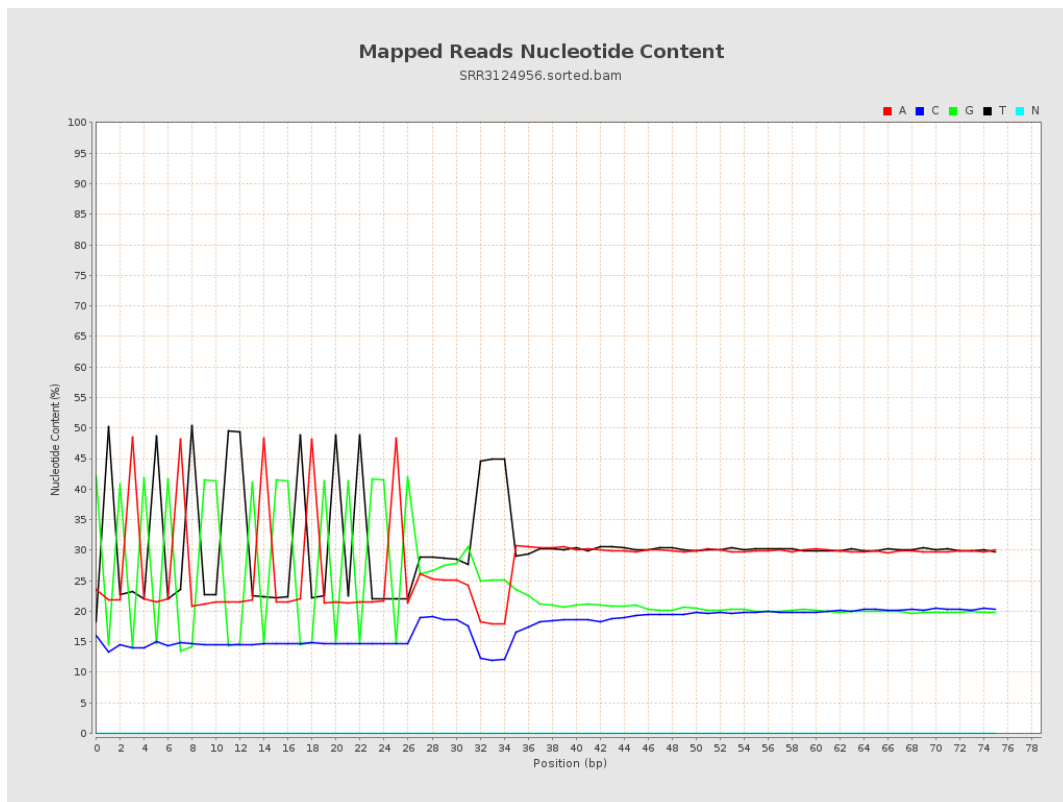
6. Results : Genome Fraction Coverage



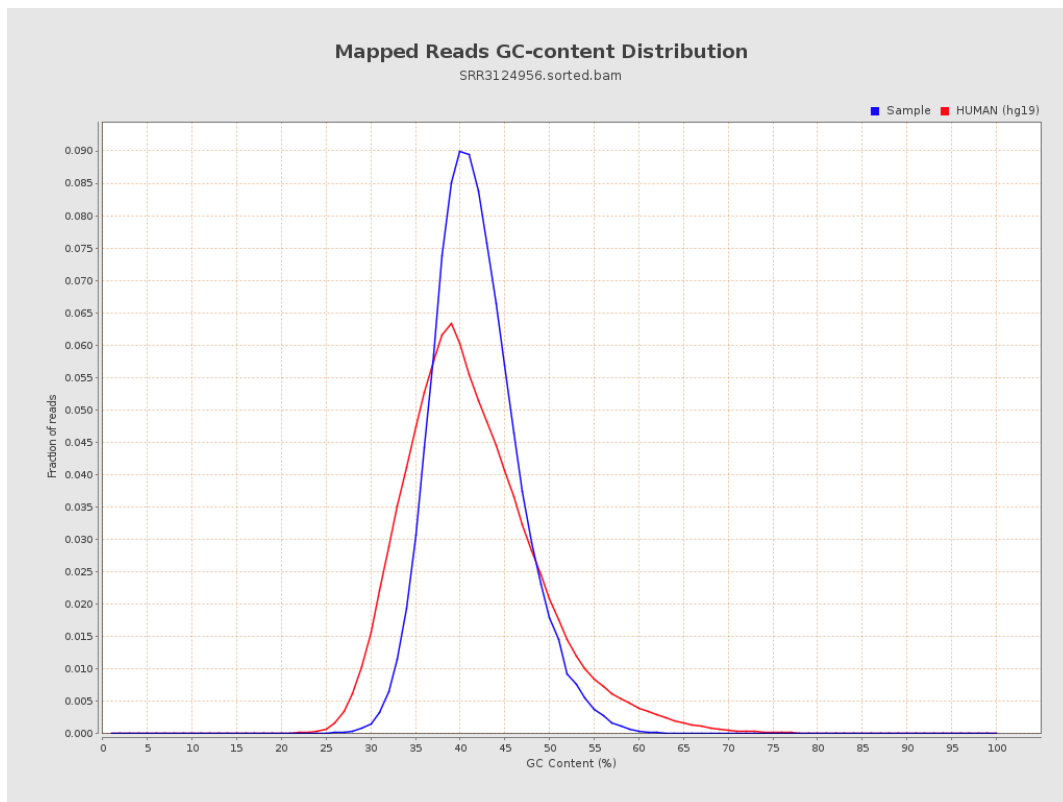
7. Results : Duplication Rate Histogram



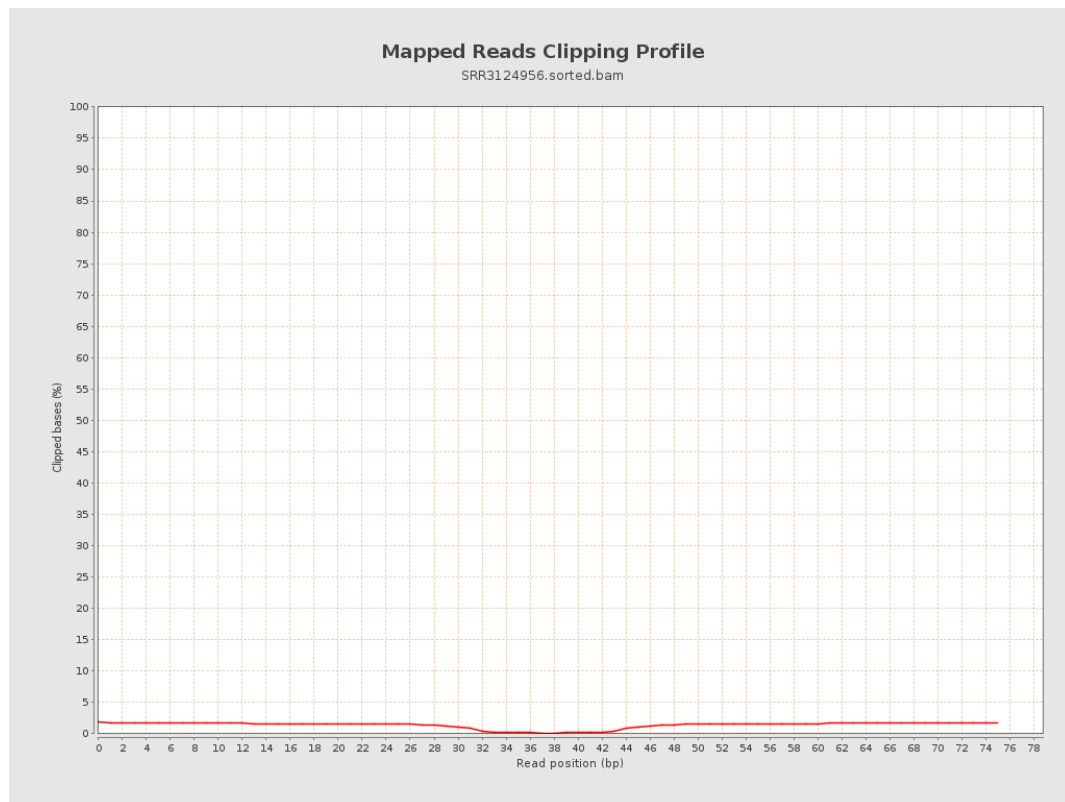
8. Results : Mapped Reads Nucleotide Content



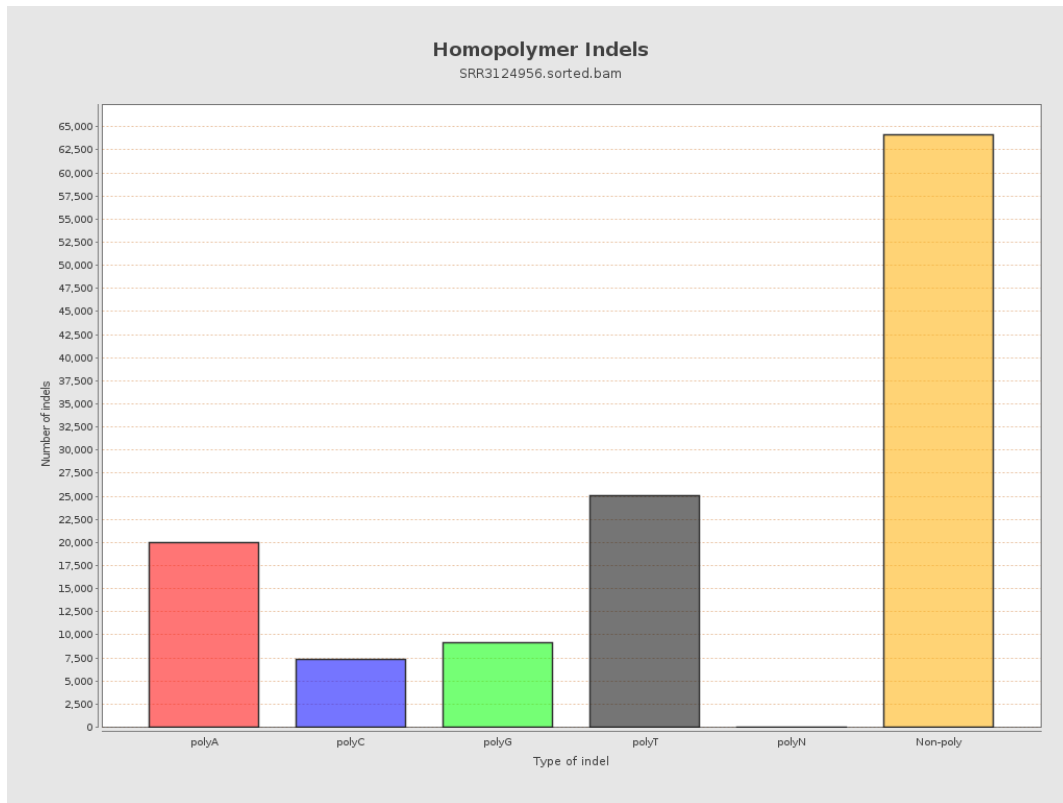
9. Results : Mapped Reads GC-content Distribution



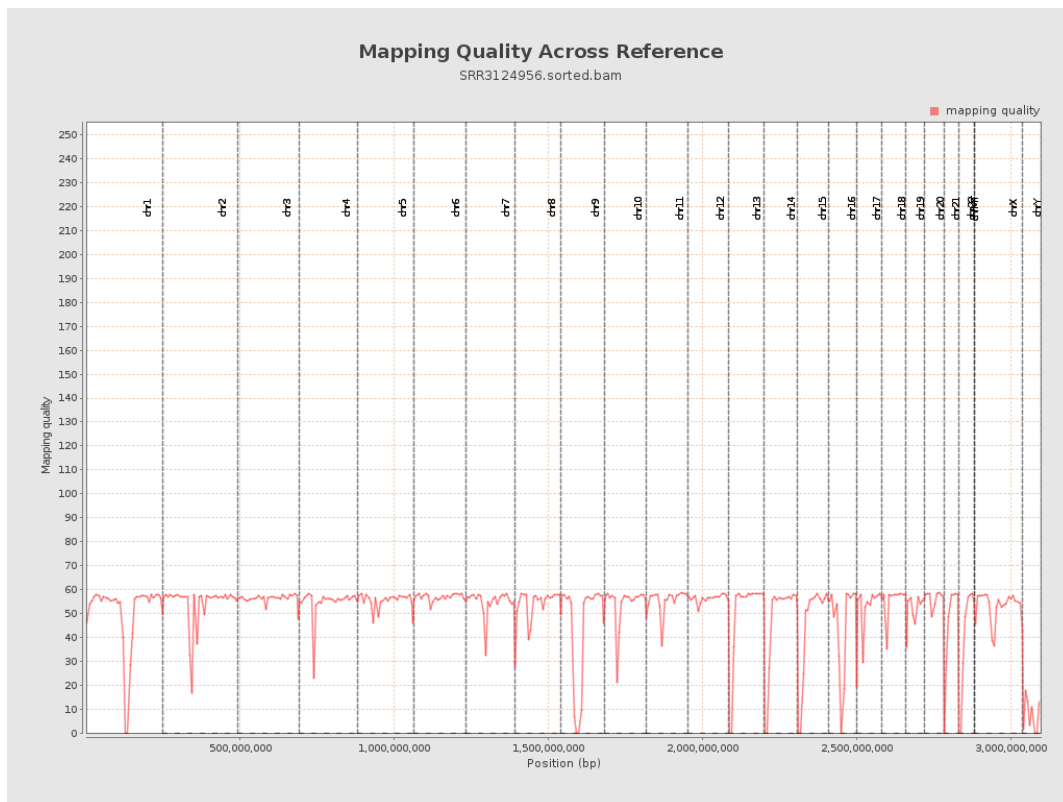
10. Results : Mapped Reads Clipping Profile



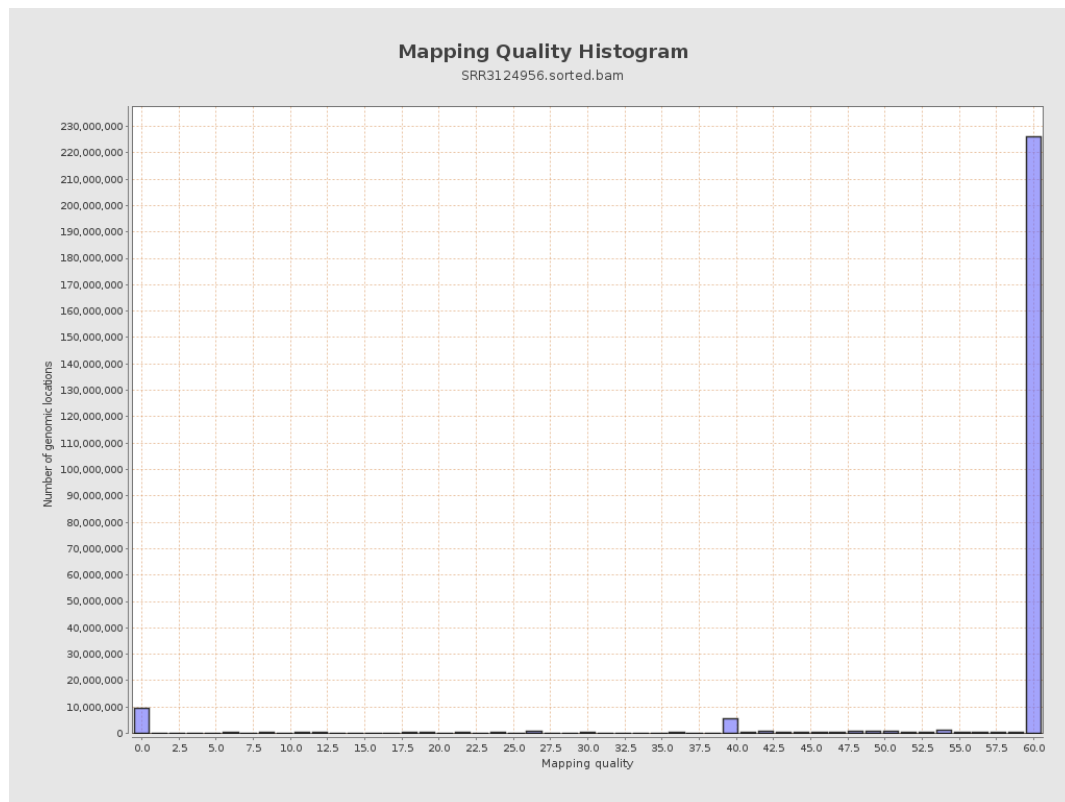
11. Results : Homopolymer Indels



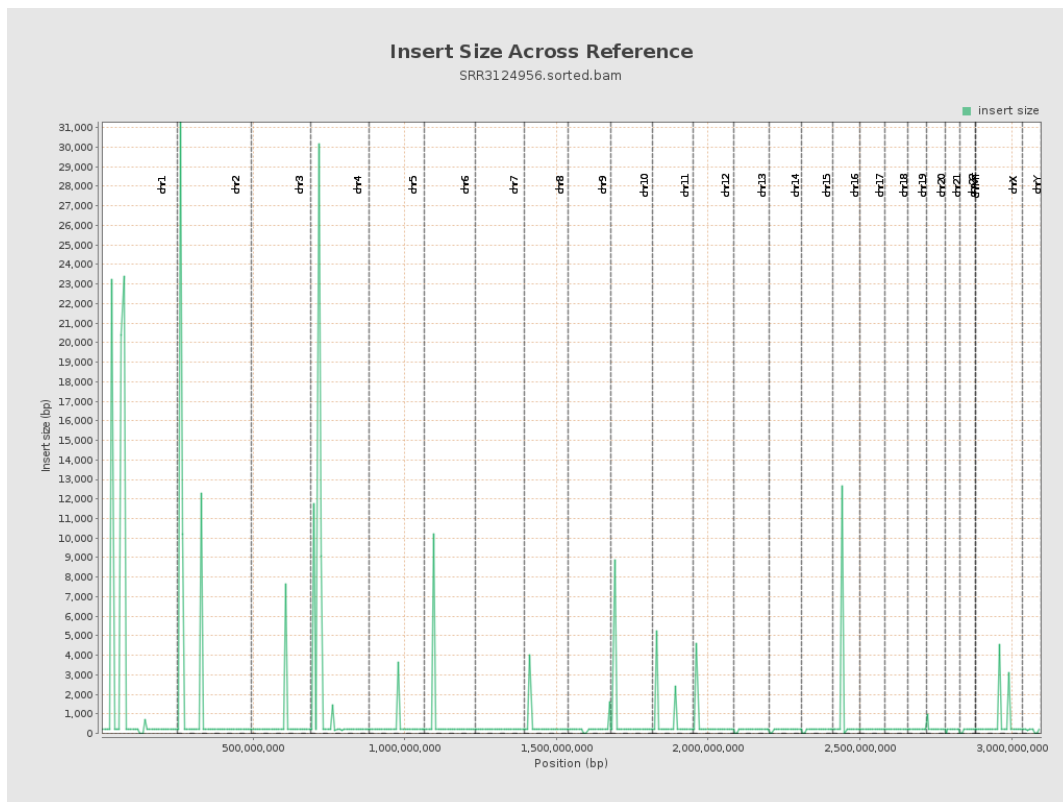
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

