

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 10:35:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472564.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_SRR3472564 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472564_1.fastq.gz SRR3472564_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 10:35:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472564.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	226,744
Mapped reads	194,730 / 85.88%
Unmapped reads	32,014 / 14.12%
Mapped paired reads	194,730 / 85.88%
Mapped reads, first in pair	99,668 / 43.96%
Mapped reads, second in pair	95,062 / 41.92%
Mapped reads, both in pair	189,386 / 83.52%
Mapped reads, singletons	5,344 / 2.36%
Secondary alignments	0
Supplementary alignments	864 / 0.38%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	24,672 / 10.88%
Duplication rate	12.5%
Clipped reads	17,652 / 7.78%

2.2. ACGT Content

Number/percentage of A's	5,298,822 / 27.74%
Number/percentage of C's	4,287,282 / 22.45%
Number/percentage of T's	5,249,954 / 27.49%
Number/percentage of G's	4,260,742 / 22.31%
Number/percentage of N's	2,702 / 0.01%

GC Percentage	44.76%
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2.3. Coverage

Mean	0.0062
Standard Deviation	0.1599

2.4. Mapping Quality

Mean Mapping Quality	54.32
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2.5. Insert size

Mean	29,412.34
Standard Deviation	1,628,132.89
P25/Median/P75	167 / 233 / 316

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	119,707
Insertions	1,117
Mapped reads with at least one insertion	0.56%
Deletions	982
Mapped reads with at least one deletion	0.5%
Homopolymer indels	44.88%

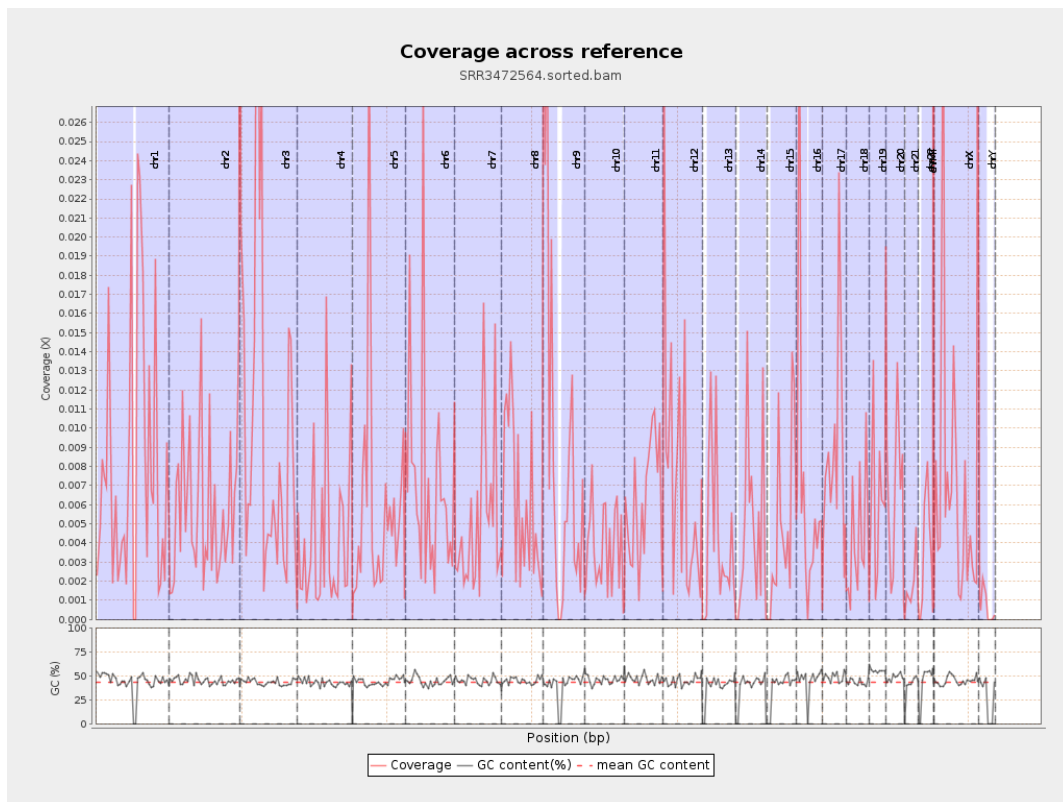
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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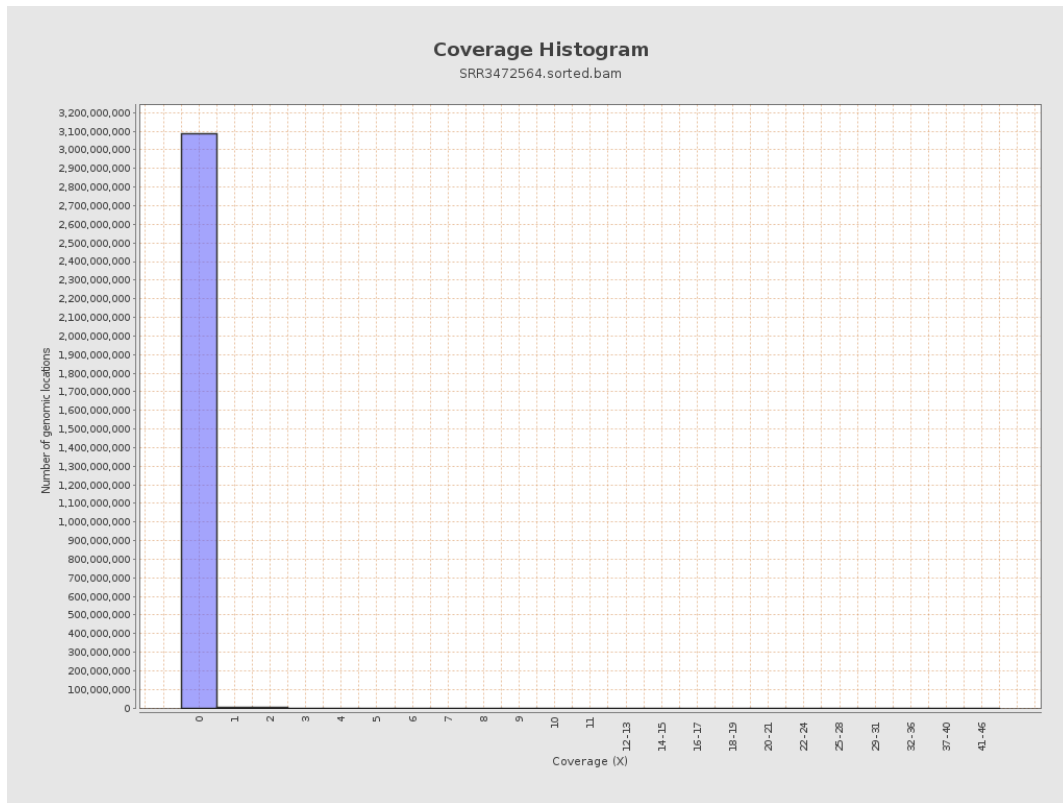
		bases	coverage	deviation
chr1	249250621	1982953	0.008	0.2077
chr2	243199373	1385053	0.0057	0.1582
chr3	198022430	2167302	0.0109	0.2023
chr4	191154276	780771	0.0041	0.1309
chr5	180915260	1037699	0.0057	0.1488
chr6	171115067	1242563	0.0073	0.1649
chr7	159138663	816518	0.0051	0.1374
chr8	146364022	881795	0.006	0.155
chr9	141213431	1162213	0.0082	0.1806
chr10	135534747	522468	0.0039	0.1317
chr11	135006516	838806	0.0062	0.1617
chr12	133851895	1006172	0.0075	0.1849
chr13	115169878	466362	0.004	0.1275
chr14	107349540	514917	0.0048	0.1513
chr15	102531392	499240	0.0049	0.1392
chr16	90354753	626259	0.0069	0.1677
chr17	81195210	690304	0.0085	0.1742
chr18	78077248	334293	0.0043	0.1387
chr19	59128983	387280	0.0065	0.157
chr20	63025520	402520	0.0064	0.1617
chr21	48129895	85000	0.0018	0.0718
chr22	51304566	179664	0.0035	0.1
chrMT	16571	2166	0.1307	0.4633
chrX	155270560	1051889	0.0068	0.1585

chrY	59373566	37518	0.0006	0.037
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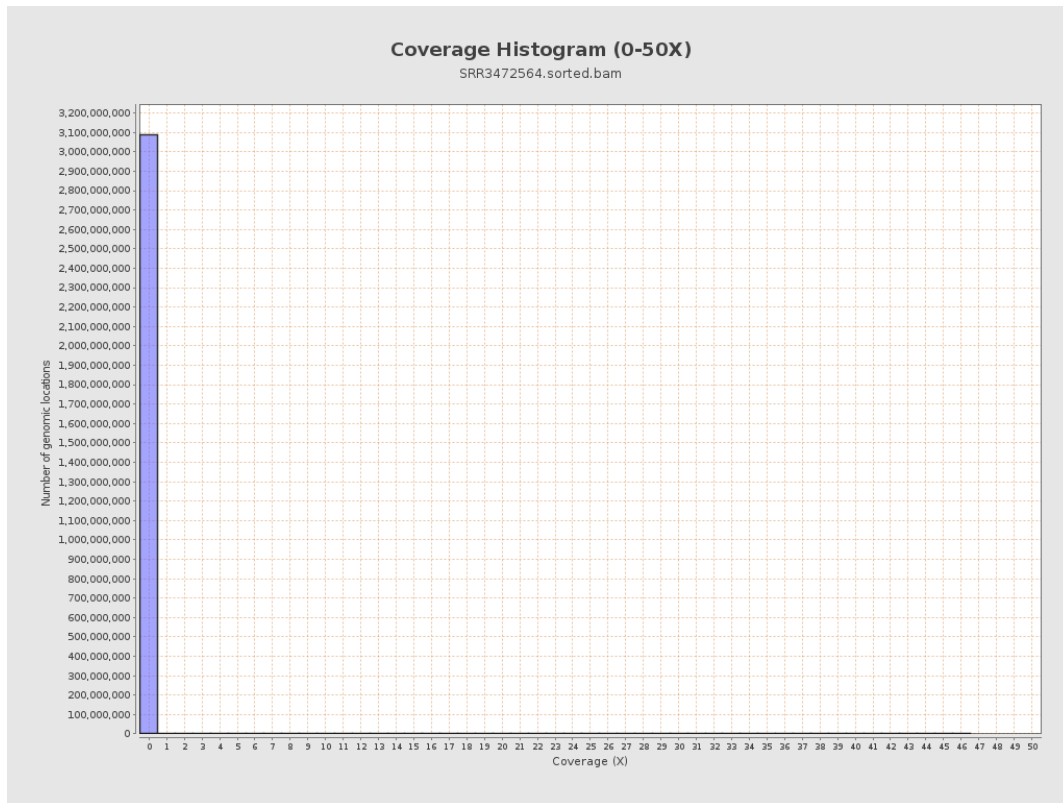
3. Results : Coverage across reference



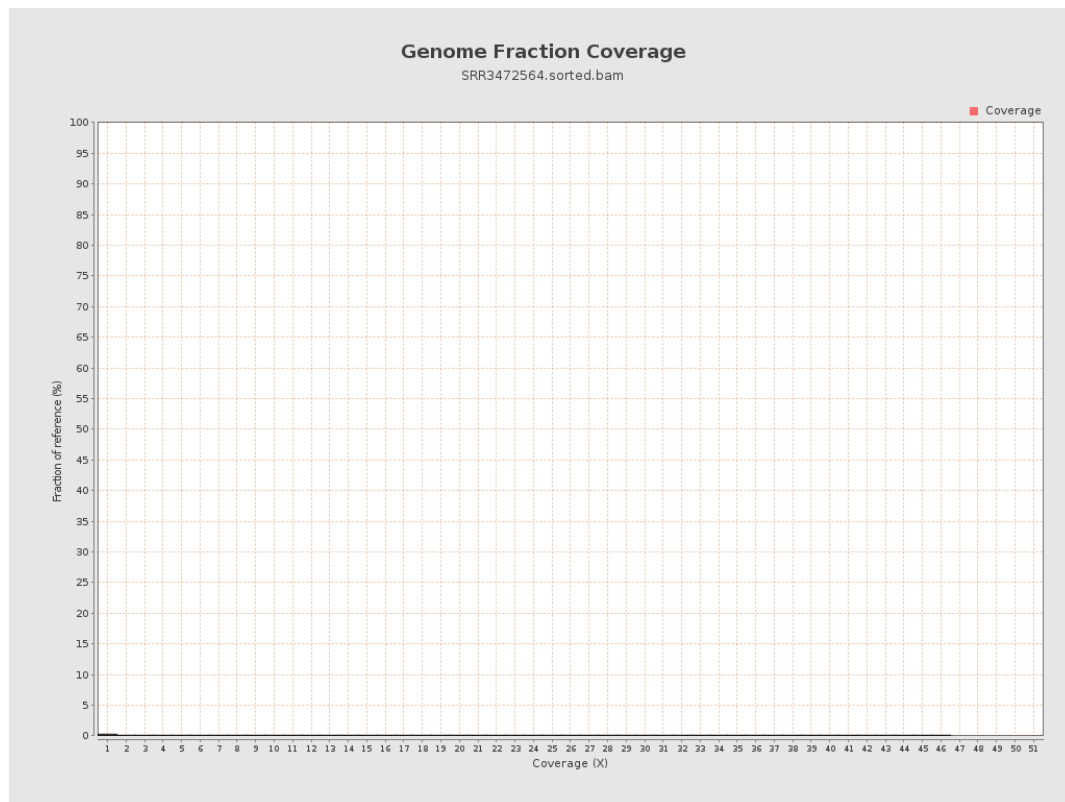
4. Results : Coverage Histogram



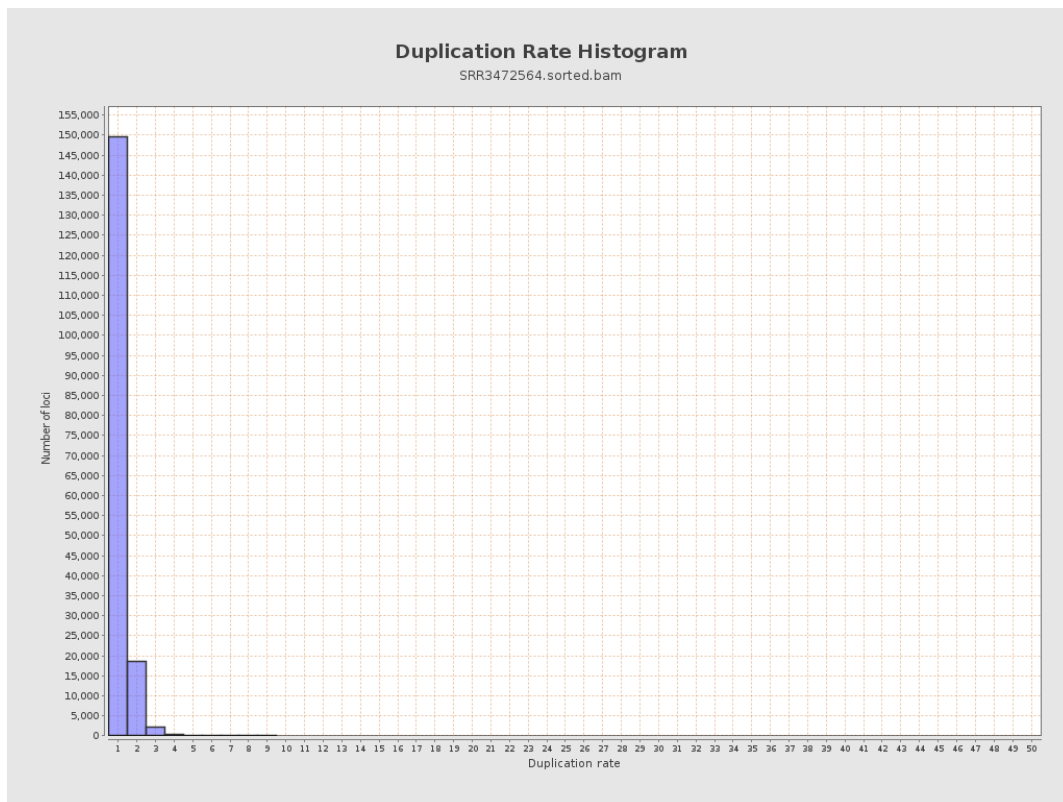
5. Results : Coverage Histogram (0-50X)



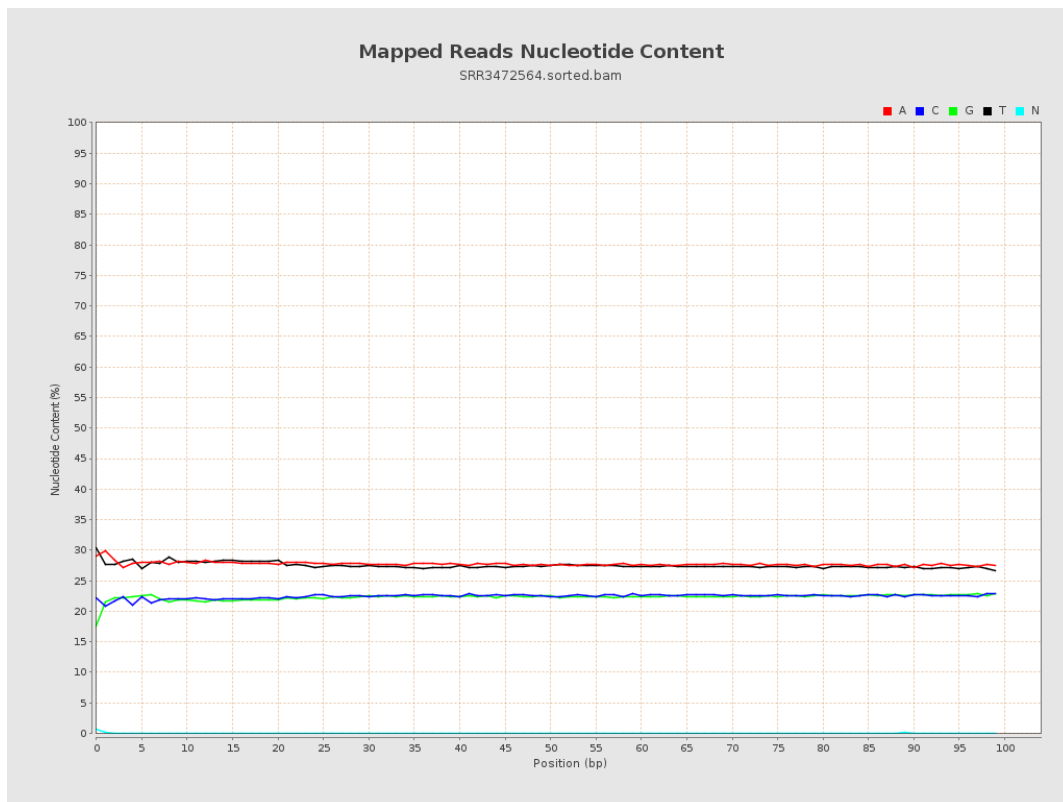
6. Results : Genome Fraction Coverage



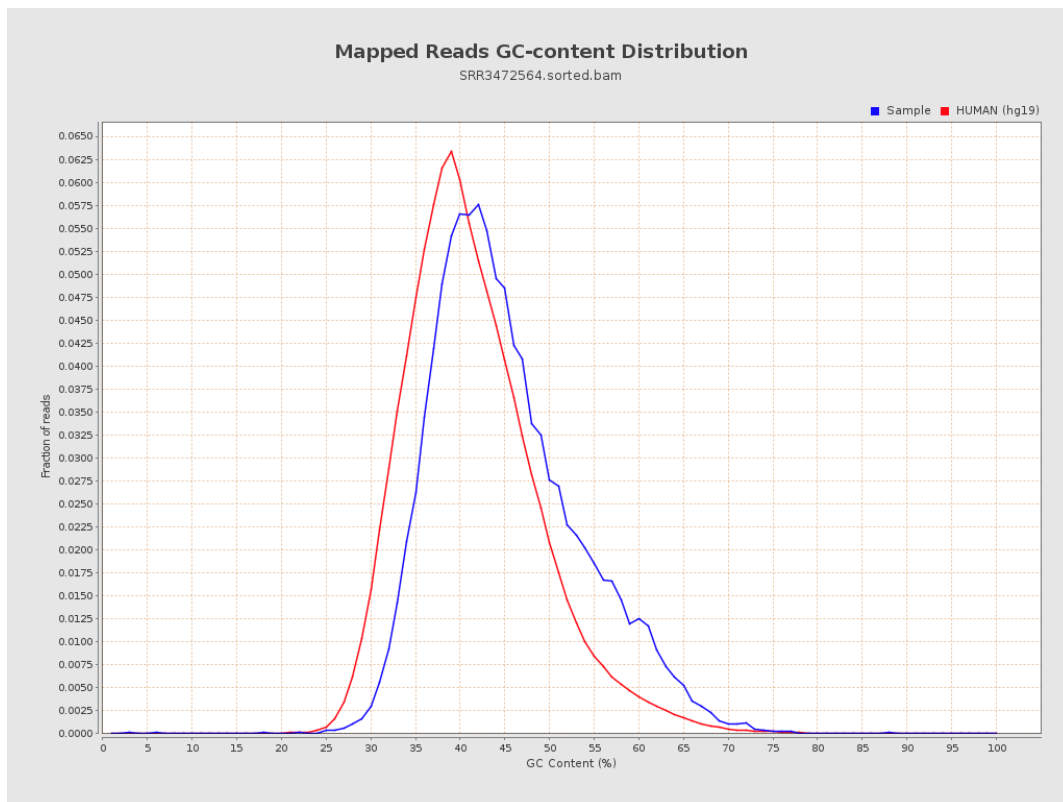
7. Results : Duplication Rate Histogram



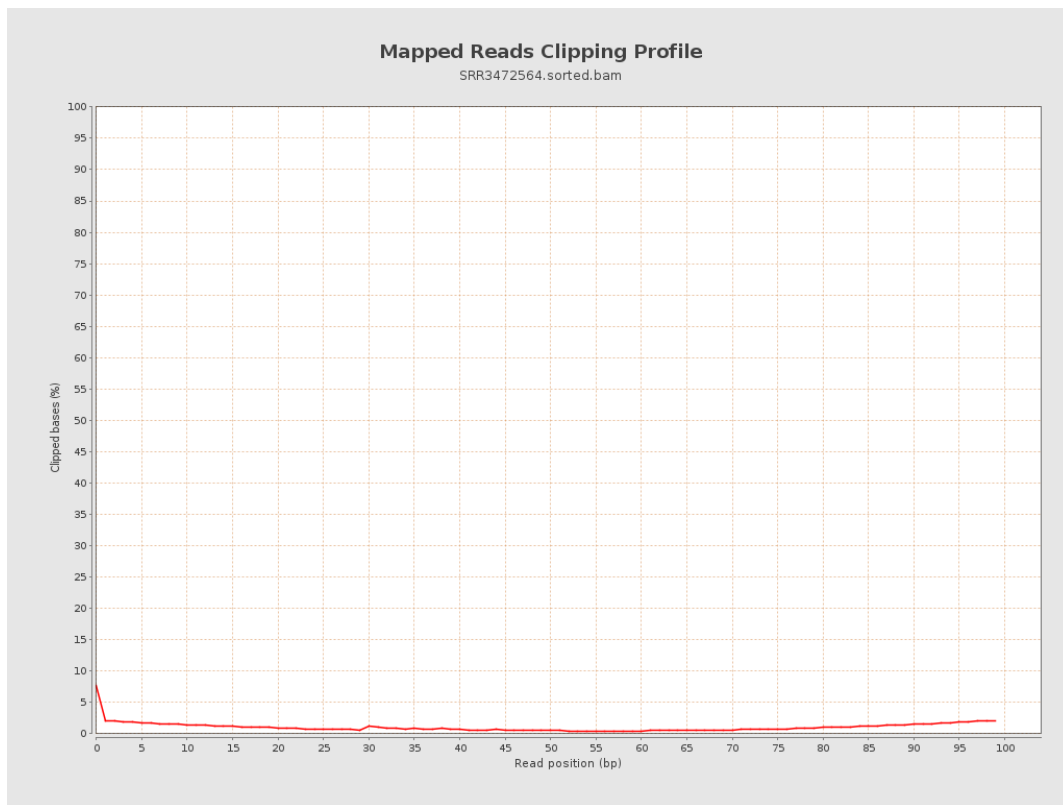
8. Results : Mapped Reads Nucleotide Content



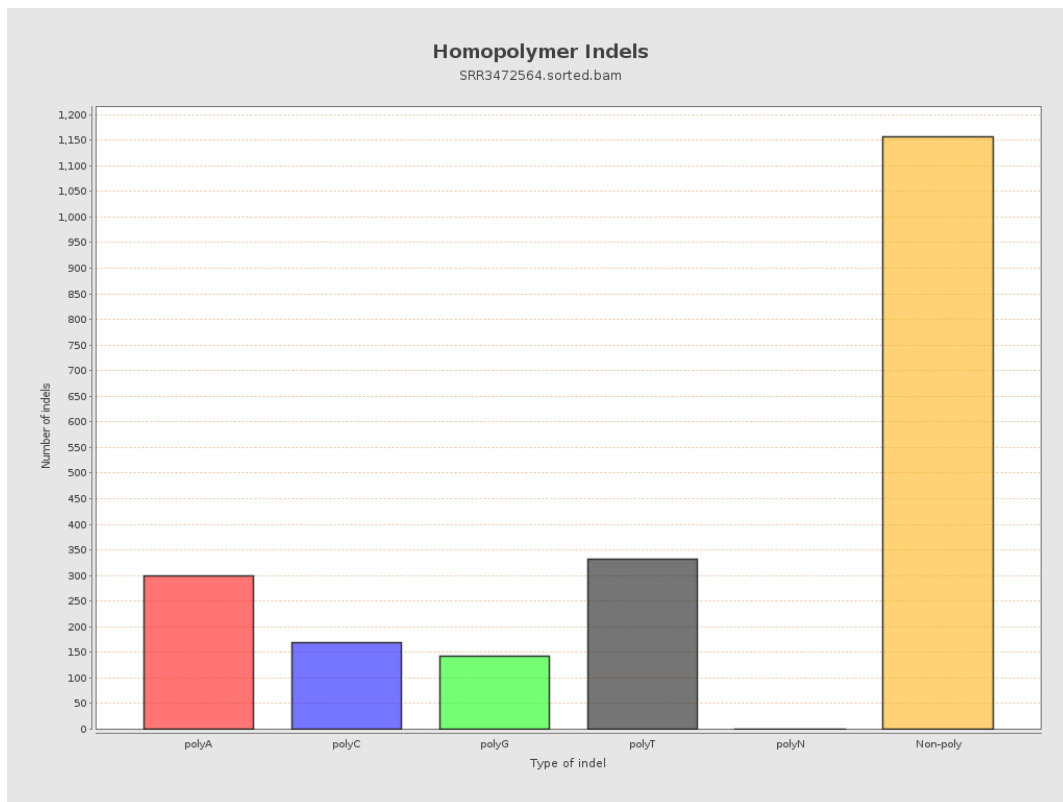
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



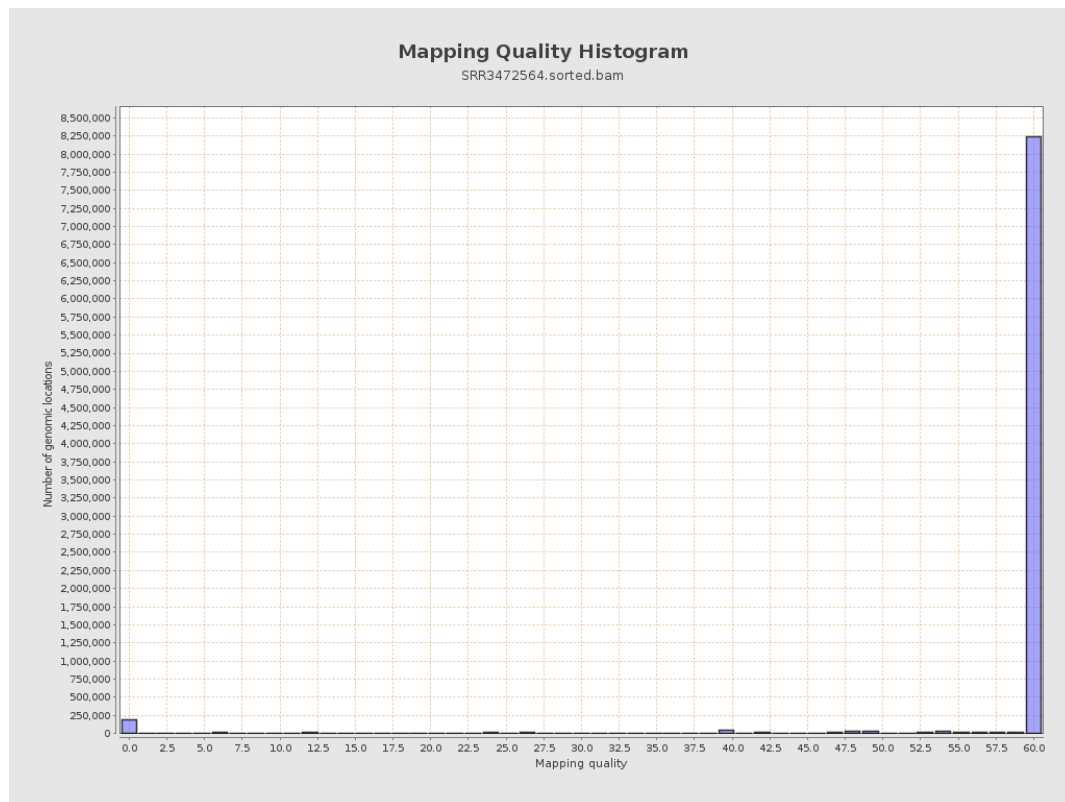
11. Results : Homopolymer Indels



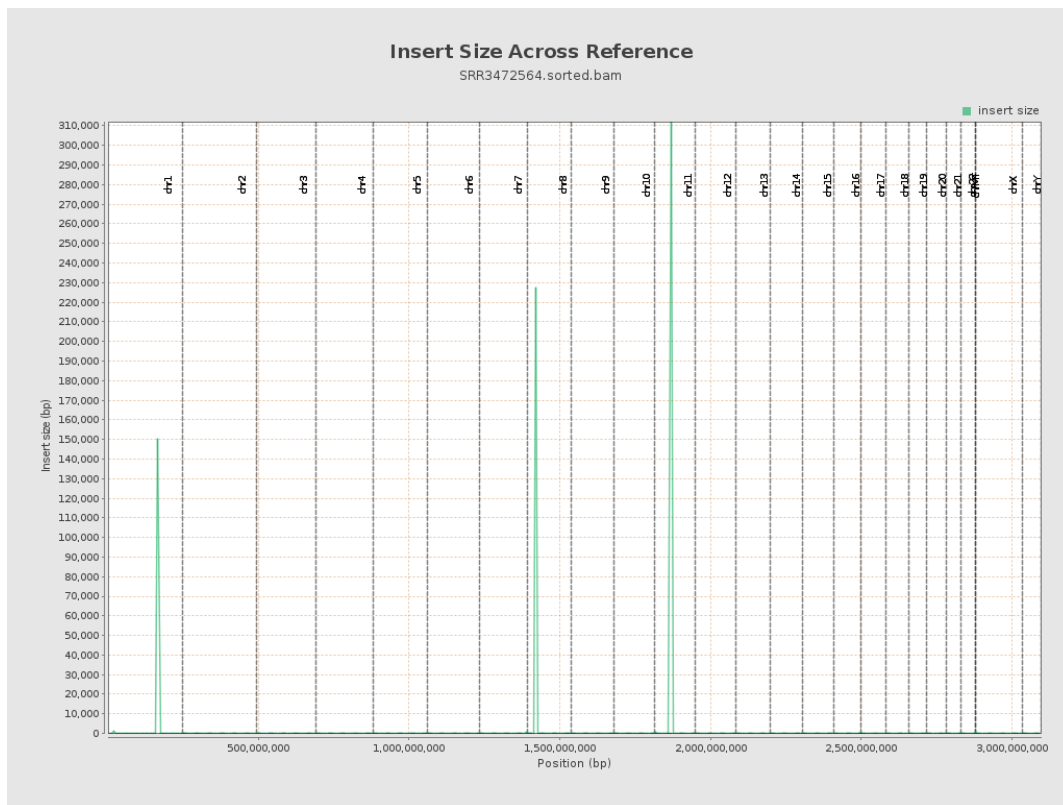
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

