

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:20:15

1. Input data & parameters

1.1. QualiMap command line

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qualimap bamqc -bam SRR3472510.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_SRR3472510 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472510_1.fastq.gz SRR3472510_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:20:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472510.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,291,552
Mapped reads	16,054,961 / 98.55%
Unmapped reads	236,591 / 1.45%
Mapped paired reads	16,054,961 / 98.55%
Mapped reads, first in pair	8,062,422 / 49.49%
Mapped reads, second in pair	7,992,539 / 49.06%
Mapped reads, both in pair	15,929,922 / 97.78%
Mapped reads, singletons	125,039 / 0.77%
Secondary alignments	0
Supplementary alignments	69,238 / 0.42%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	10,453,581 / 64.17%
Duplication rate	44.58%
Clipped reads	1,276,330 / 7.83%

2.2. ACGT Content

Number/percentage of A's	444,430,143 / 28.12%
Number/percentage of C's	348,386,733 / 22.04%
Number/percentage of T's	440,599,768 / 27.88%
Number/percentage of G's	346,839,948 / 21.94%
Number/percentage of N's	243,298 / 0.02%

GC Percentage	43.99%
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2.3. Coverage

Mean	0.5106
Standard Deviation	21.9401

2.4. Mapping Quality

Mean Mapping Quality	54.89
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2.5. Insert size

Mean	32,090.95
Standard Deviation	1,826,662.68
P25/Median/P75	178 / 252 / 344

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	10,009,290
Insertions	97,153
Mapped reads with at least one insertion	0.6%
Deletions	83,421
Mapped reads with at least one deletion	0.51%
Homopolymer indels	46.14%

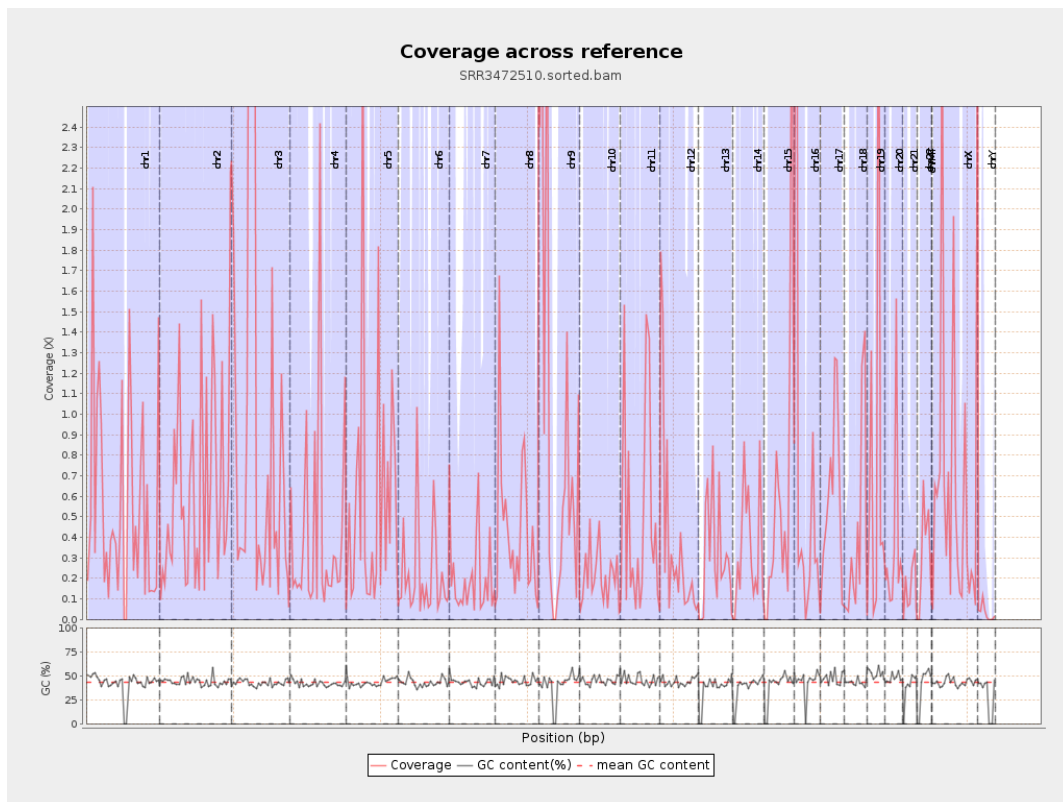
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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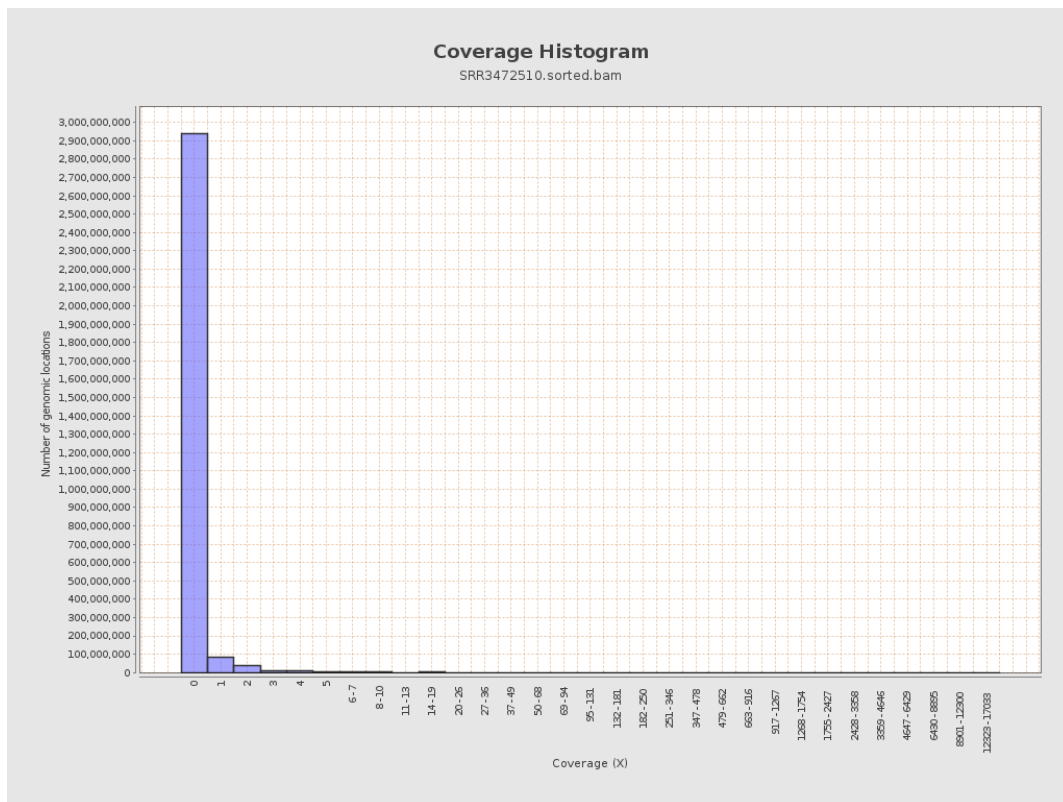
		bases	coverage	deviation
chr1	249250621	140192822	0.5625	20.4234
chr2	243199373	150675537	0.6196	24.5737
chr3	198022430	214046248	1.0809	33.0802
chr4	191154276	76404247	0.3997	16.3623
chr5	180915260	107941795	0.5966	22.065
chr6	171115067	36339882	0.2124	7.8749
chr7	159138663	32279987	0.2028	7.4502
chr8	146364022	65027086	0.4443	26.0206
chr9	141213431	128149907	0.9075	29.3484
chr10	135534747	28860892	0.2129	9.3823
chr11	135006516	65273280	0.4835	20.8457
chr12	133851895	50442062	0.3768	17.4147
chr13	115169878	36391735	0.316	13.3775
chr14	107349540	36005125	0.3354	11.7568
chr15	102531392	70943815	0.6919	35.5312
chr16	90354753	63405808	0.7017	25.2773
chr17	81195210	47475591	0.5847	16.0971
chr18	78077248	32190709	0.4123	21.0939
chr19	59128983	49860853	0.8433	48.6831
chr20	63025520	23298358	0.3697	23.21
chr21	48129895	7591868	0.1577	7.6703
chr22	51304566	16074716	0.3133	8.8771
chrMT	16571	5383	0.3248	0.8704
chrX	155270560	99874494	0.6432	21.5895

chrY	59373566	1944499	0.0328	1.248
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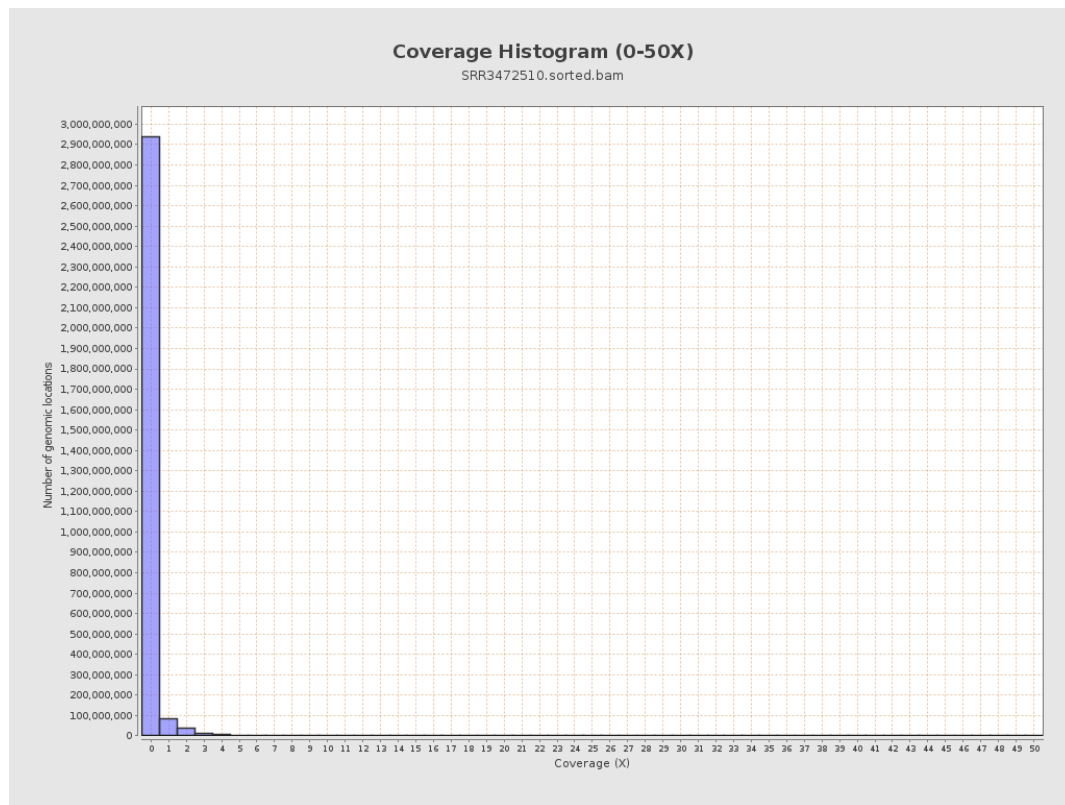
3. Results : Coverage across reference



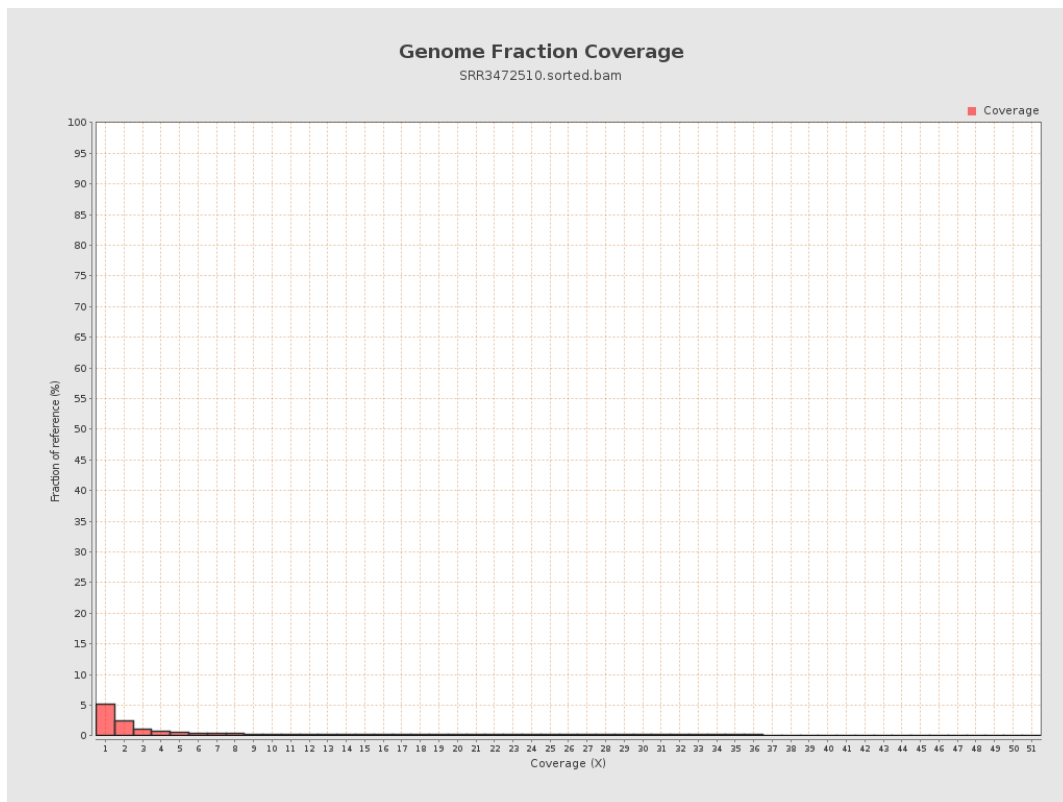
4. Results : Coverage Histogram



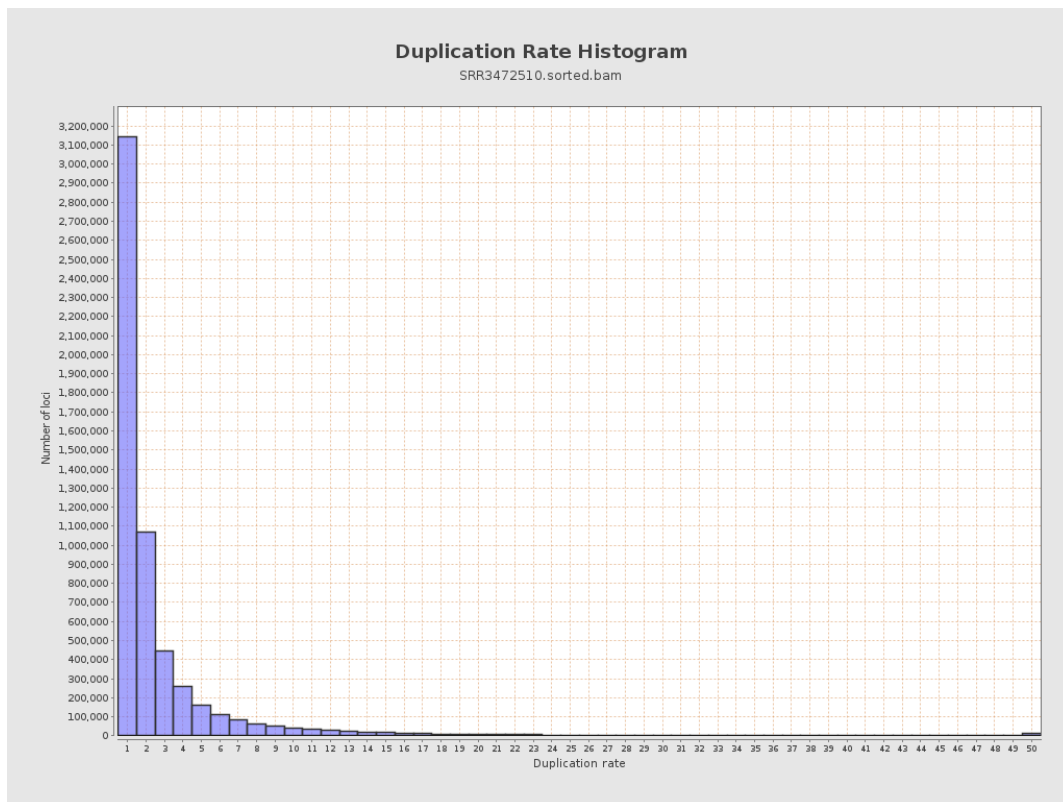
5. Results : Coverage Histogram (0-50X)



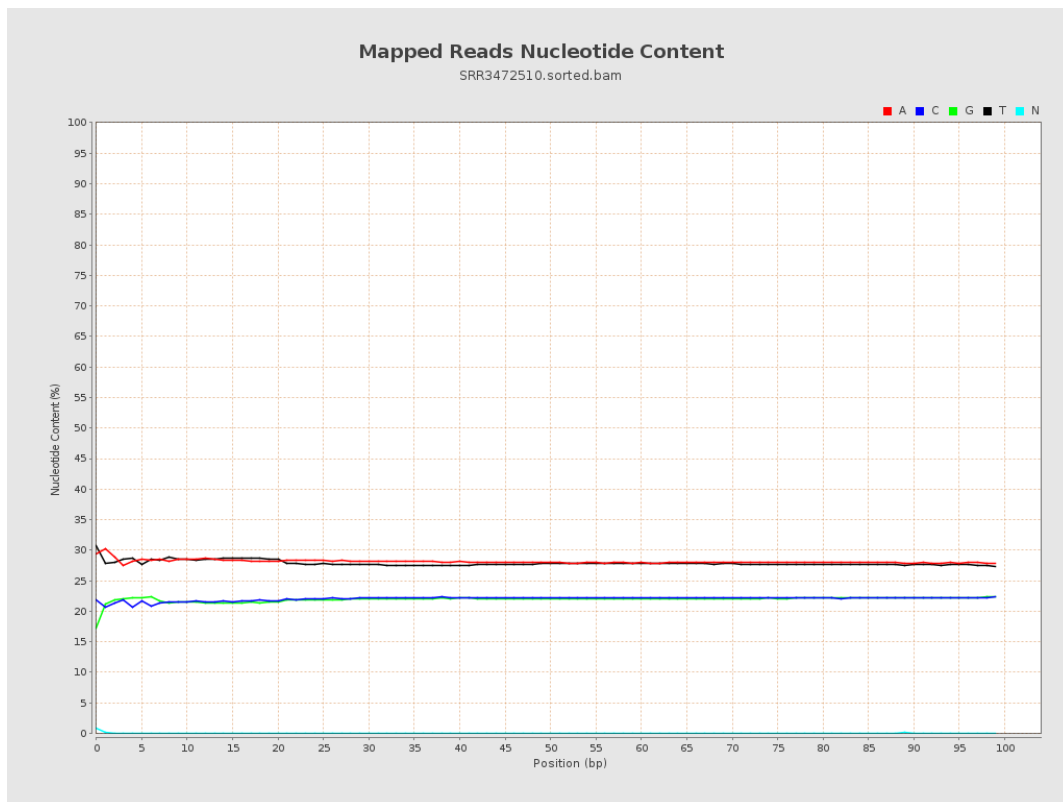
6. Results : Genome Fraction Coverage



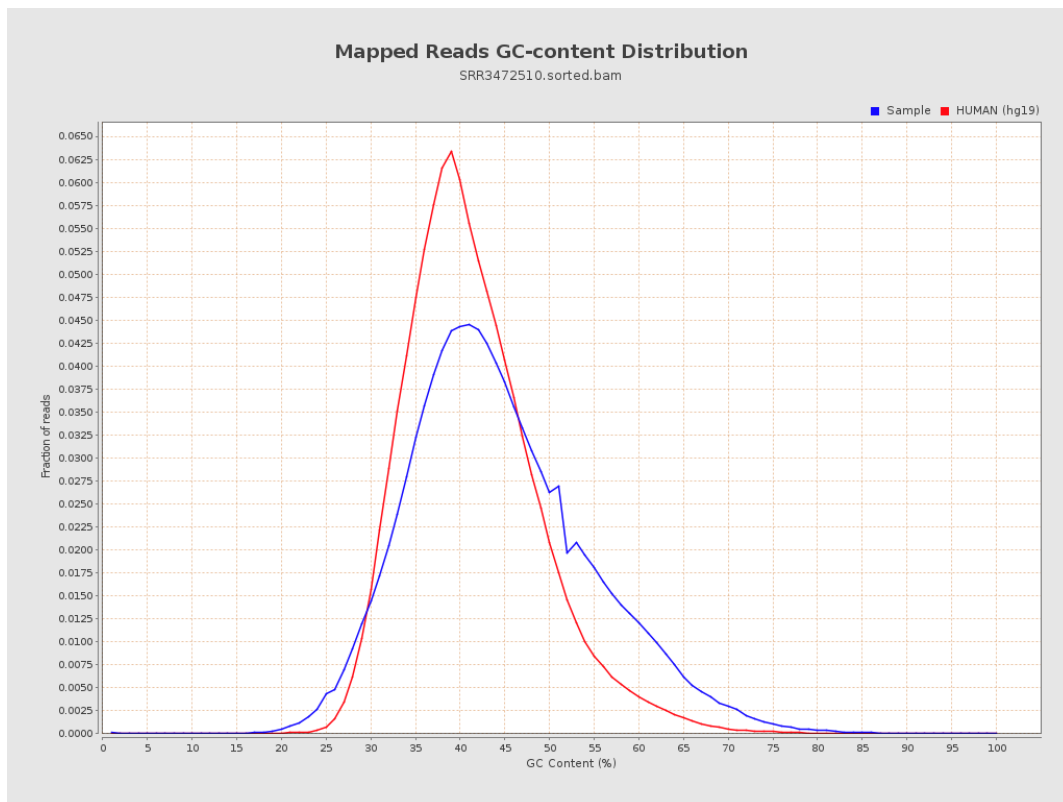
7. Results : Duplication Rate Histogram



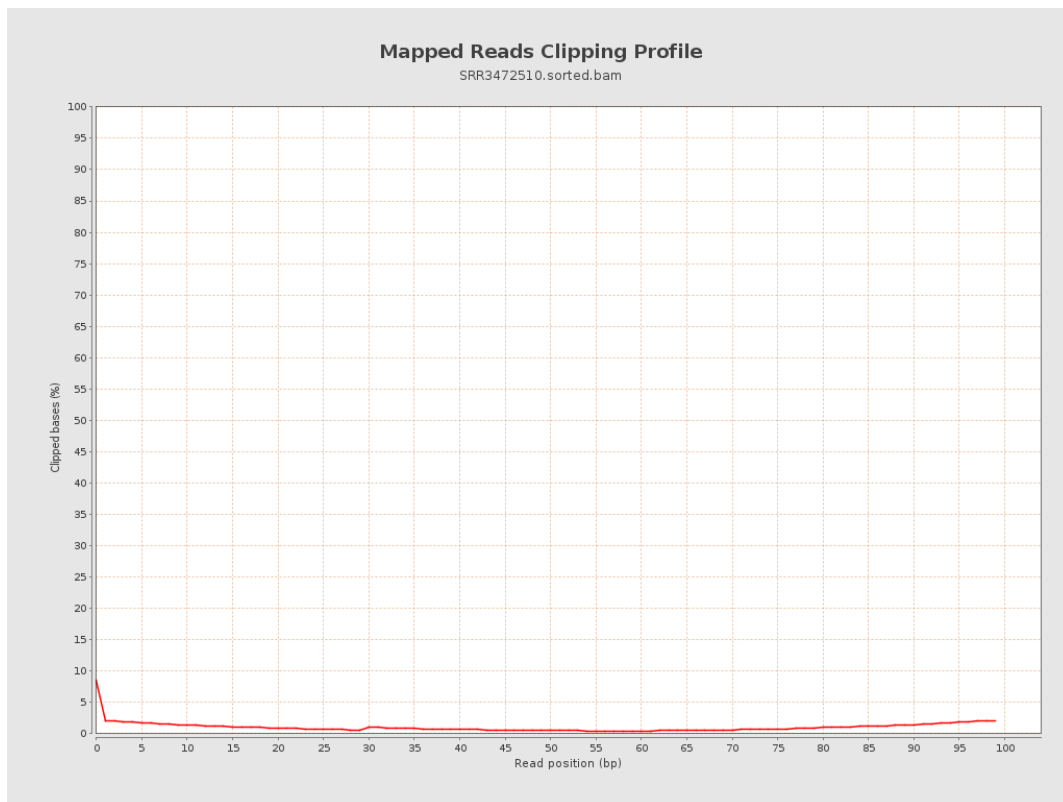
8. Results : Mapped Reads Nucleotide Content



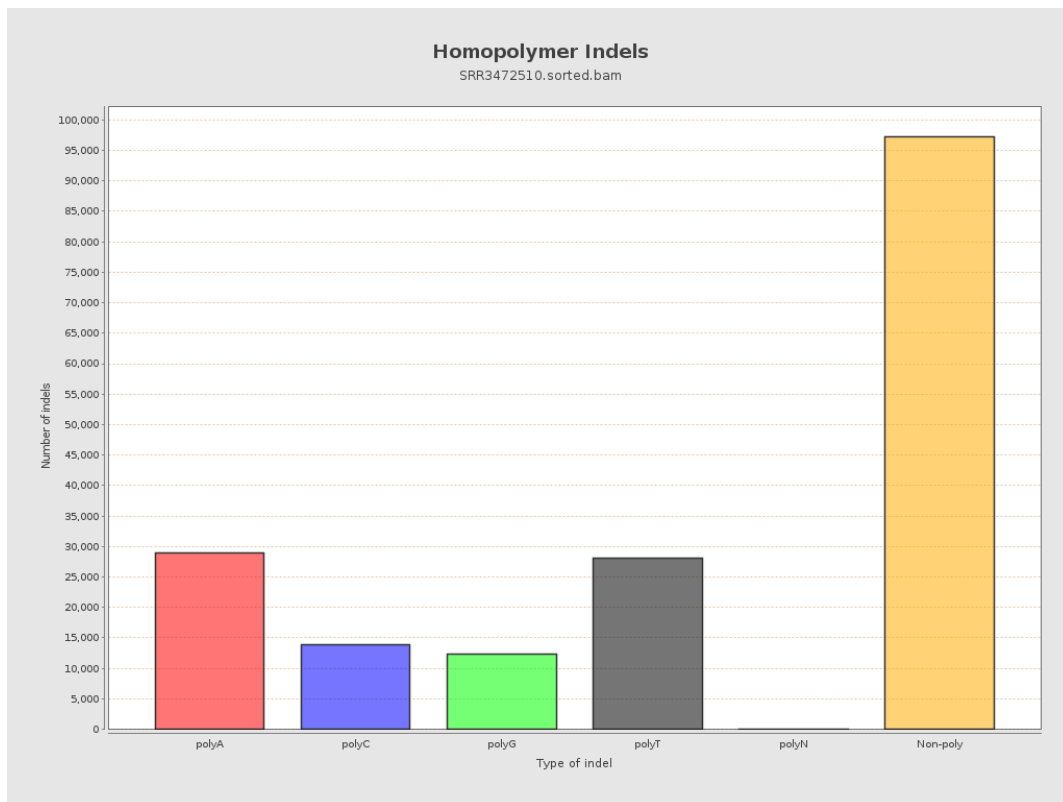
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



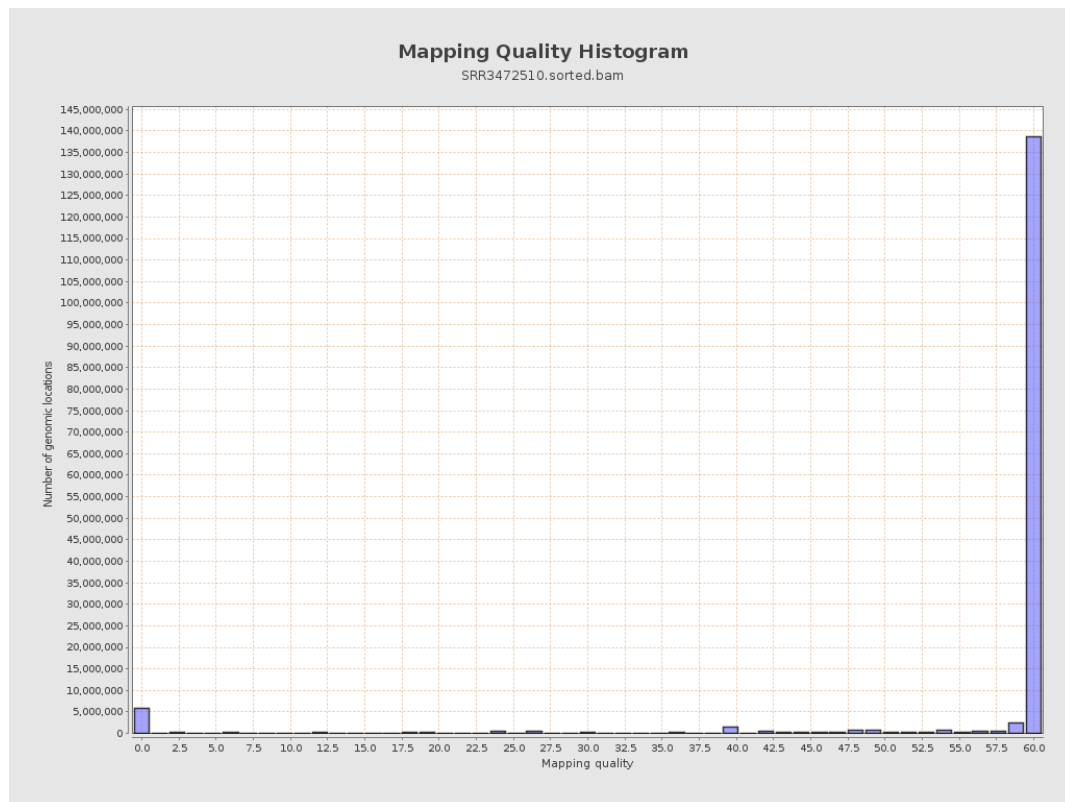
11. Results : Homopolymer Indels



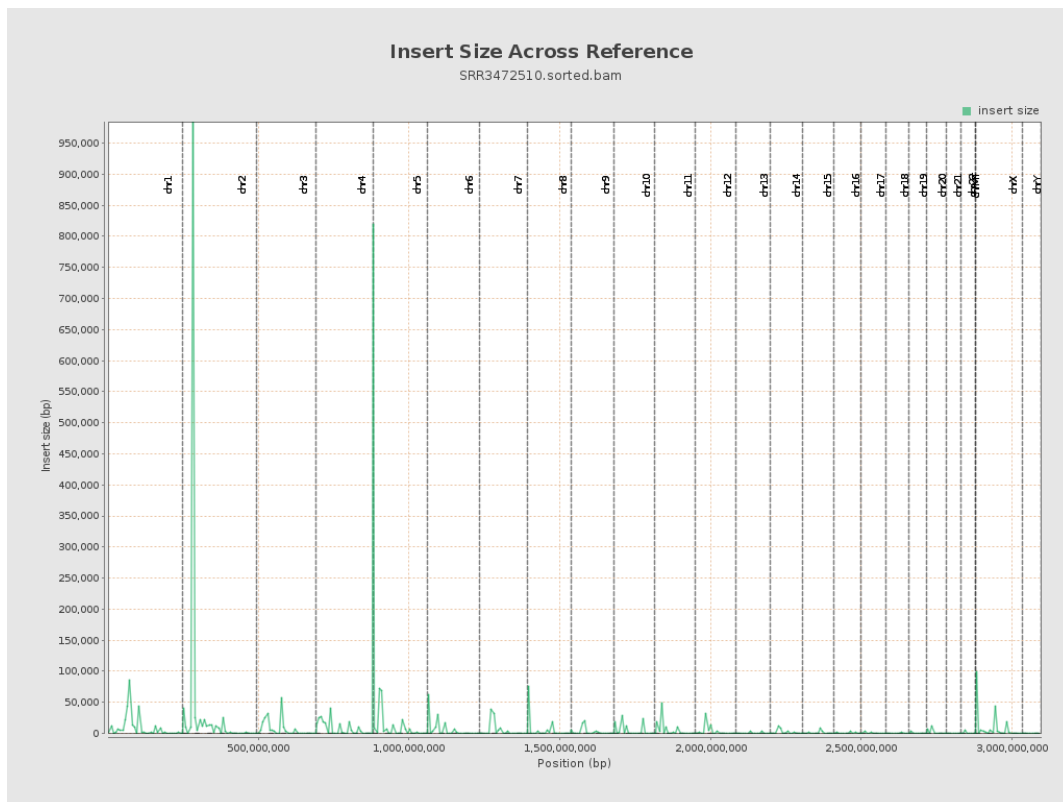
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

