

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 01:44:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472460.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_SRR3472460 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472460_1.fastq.gz SRR3472460_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 01:44:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472460.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,783,850
Mapped reads	16,635,932 / 99.12%
Unmapped reads	147,918 / 0.88%
Mapped paired reads	16,635,932 / 99.12%
Mapped reads, first in pair	8,339,957 / 49.69%
Mapped reads, second in pair	8,295,975 / 49.43%
Mapped reads, both in pair	16,547,494 / 98.59%
Mapped reads, singletons	88,438 / 0.53%
Secondary alignments	0
Supplementary alignments	58,108 / 0.35%
Read min/max/mean length	30 / 100 / 99.34
Duplicated reads (estimated)	9,573,451 / 57.04%
Duplication rate	46.61%
Clipped reads	1,065,850 / 6.35%

2.2. ACGT Content

Number/percentage of A's	452,204,802 / 27.7%
Number/percentage of C's	365,163,986 / 22.37%
Number/percentage of T's	453,530,424 / 27.78%
Number/percentage of G's	361,350,300 / 22.14%
Number/percentage of N's	196,794 / 0.01%

GC Percentage	44.5%
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2.3. Coverage

Mean	0.5274
Standard Deviation	13.2393

2.4. Mapping Quality

Mean Mapping Quality	55.08
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2.5. Insert size

Mean	19,668.1
Standard Deviation	1,381,776.49
P25/Median/P75	154 / 210 / 279

2.6. Mismatches and indels

General error rate	0.55%
Mismatches	8,784,200
Insertions	105,787
Mapped reads with at least one insertion	0.63%
Deletions	81,860
Mapped reads with at least one deletion	0.48%
Homopolymer indels	47.24%

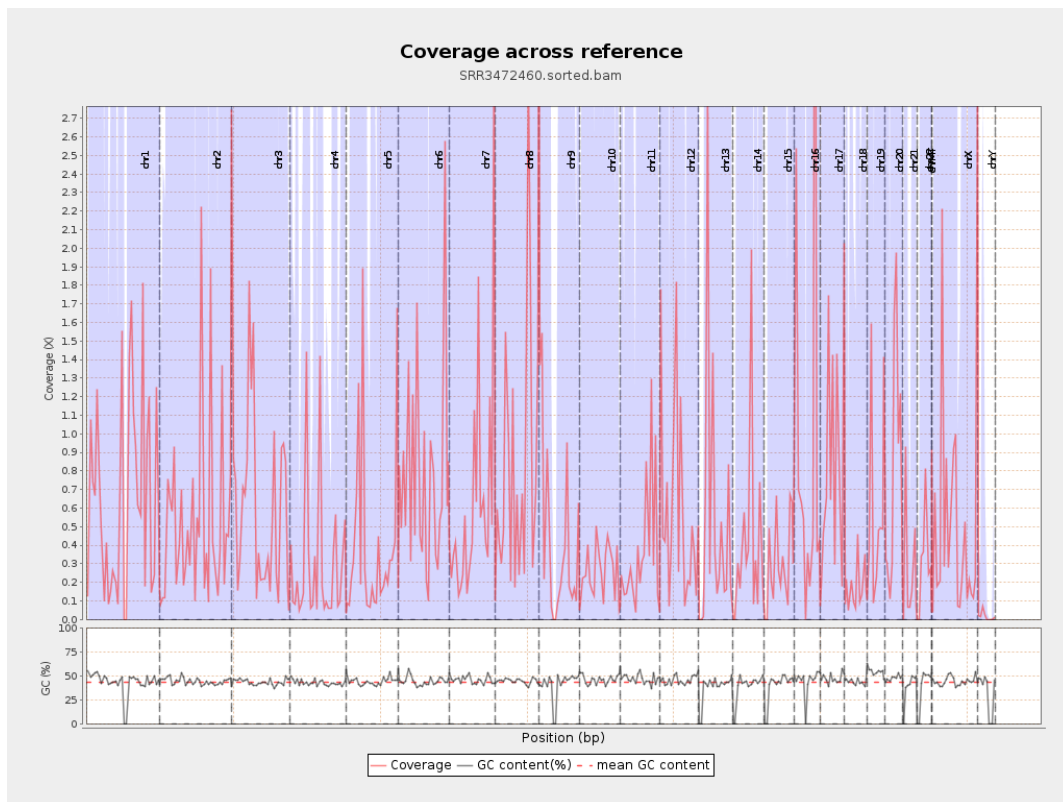
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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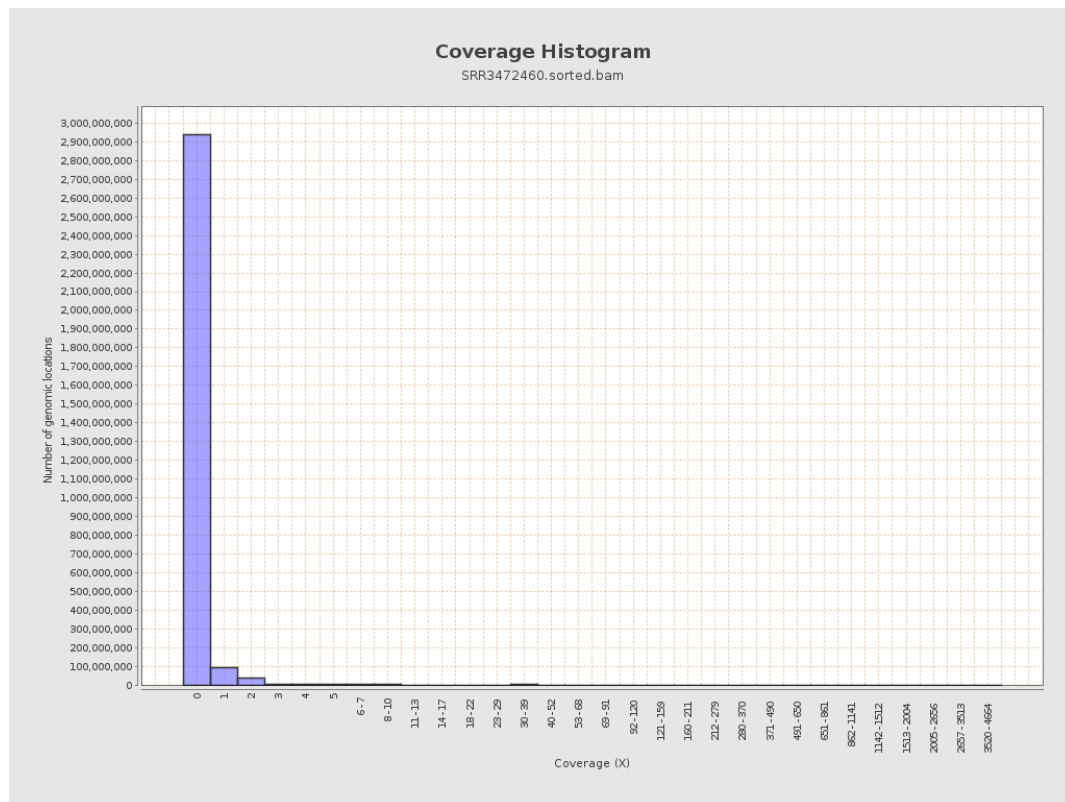
		bases	coverage	deviation
chr1	249250621	166365187	0.6675	15.2393
chr2	243199373	127706015	0.5251	13.0326
chr3	198022430	126439172	0.6385	11.2307
chr4	191154276	54715709	0.2862	10.2113
chr5	180915260	73265528	0.405	12.2407
chr6	171115067	129631392	0.7576	15.2265
chr7	159138663	103893997	0.6529	16.5807
chr8	146364022	125075593	0.8546	19.0626
chr9	141213431	63176809	0.4474	9.5199
chr10	135534747	35533155	0.2622	7.0481
chr11	135006516	49457175	0.3663	9.643
chr12	133851895	80883029	0.6043	12.2328
chr13	115169878	61492509	0.5339	17.0103
chr14	107349540	42619869	0.397	9.7518
chr15	102531392	30902208	0.3014	7.6772
chr16	90354753	88304392	0.9773	22.8514
chr17	81195210	67528650	0.8317	16.0926
chr18	78077248	14027769	0.1797	4.6288
chr19	59128983	32273003	0.5458	9.9807
chr20	63025520	52748047	0.8369	20.6728
chr21	48129895	13559762	0.2817	14.1025
chr22	51304566	15859692	0.3091	8.4568
chrMT	16571	15121	0.9125	1.1496
chrX	155270560	76073429	0.4899	10.4499

chrY	59373566	1089818	0.0184	1.0774
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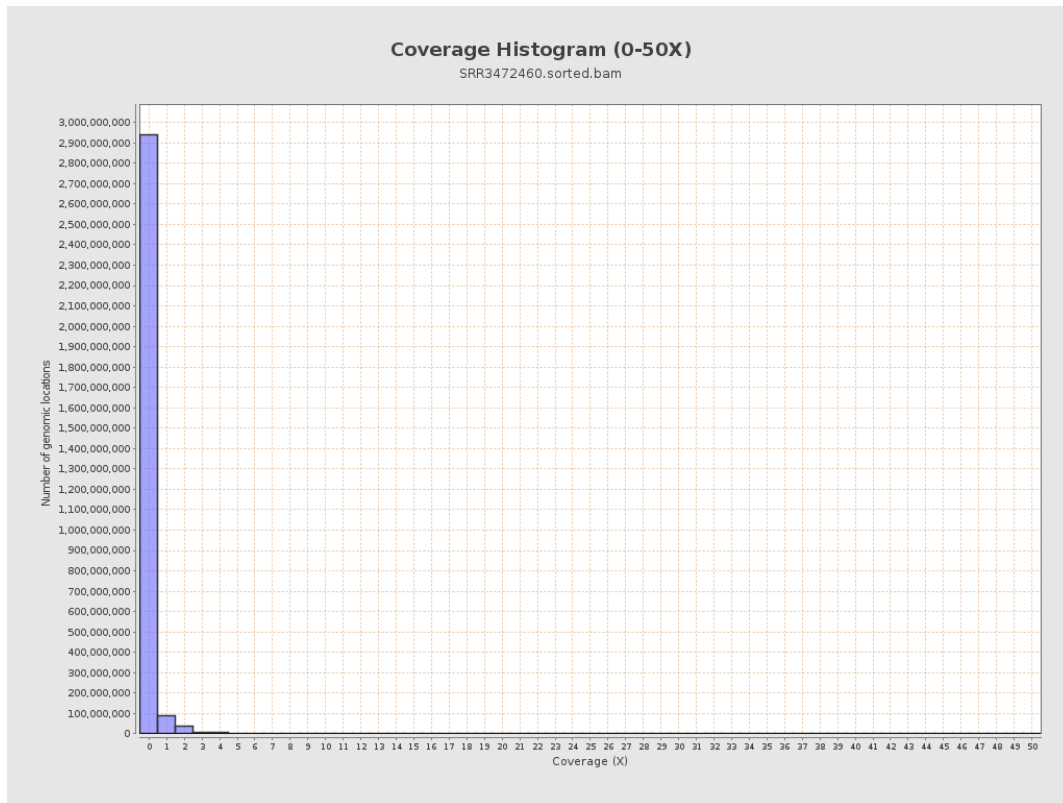
3. Results : Coverage across reference



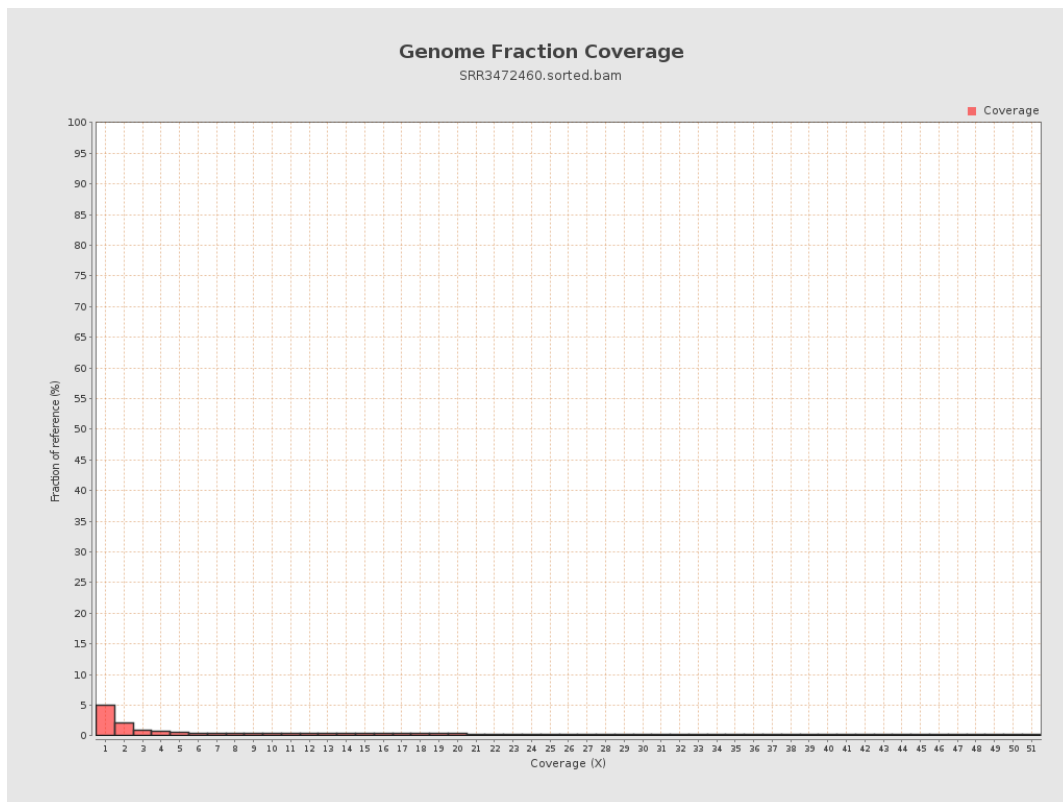
4. Results : Coverage Histogram



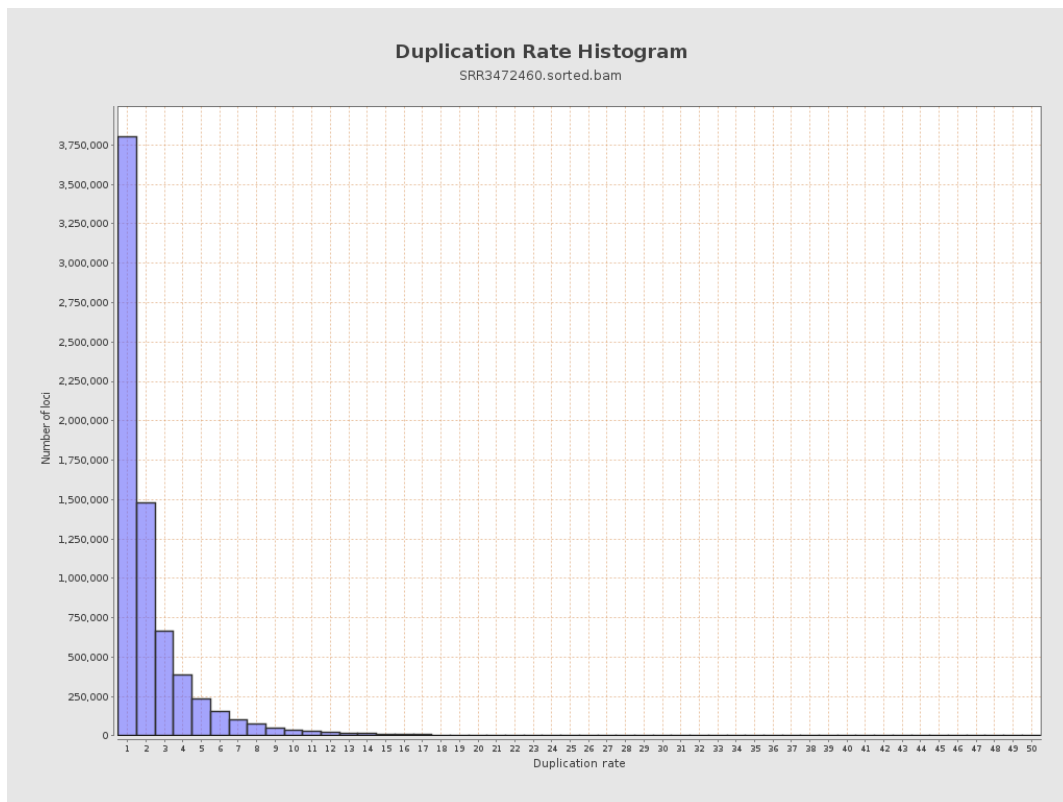
5. Results : Coverage Histogram (0-50X)



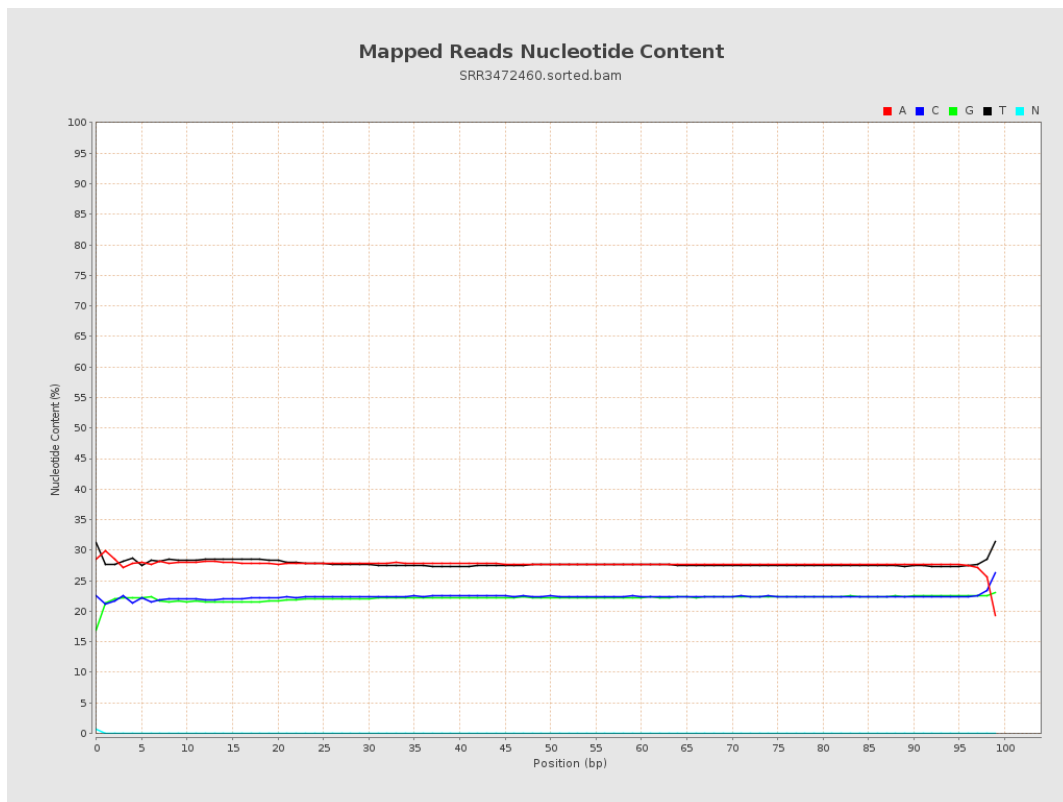
6. Results : Genome Fraction Coverage



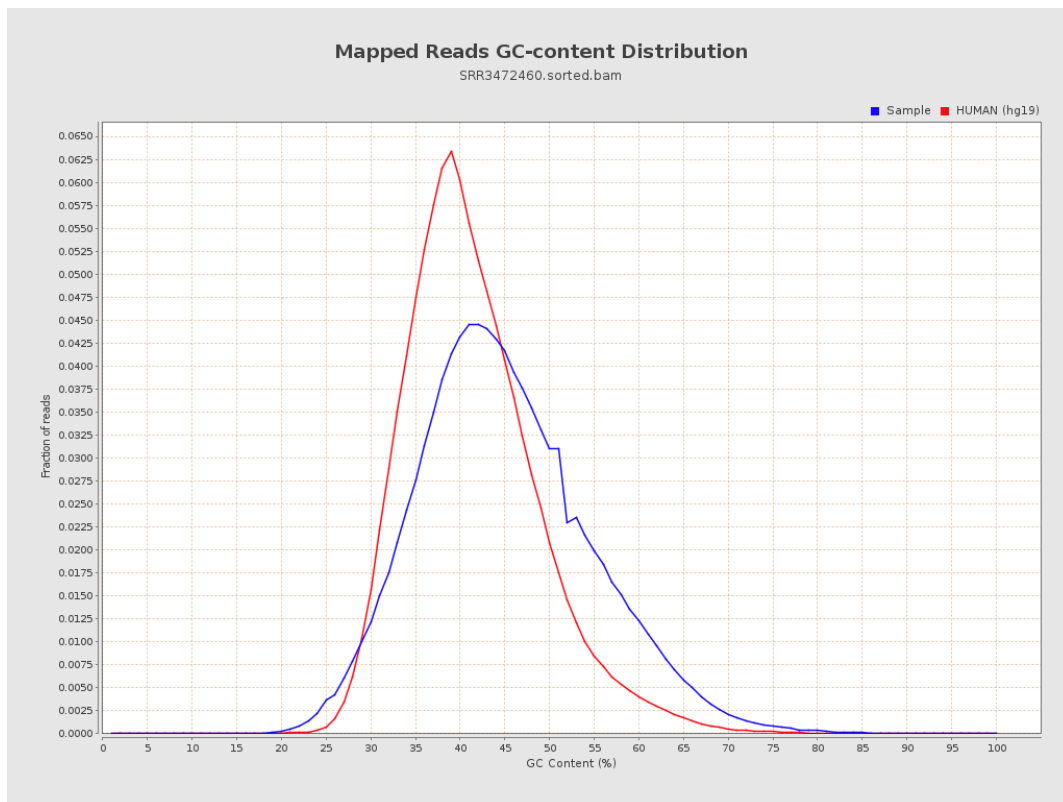
7. Results : Duplication Rate Histogram



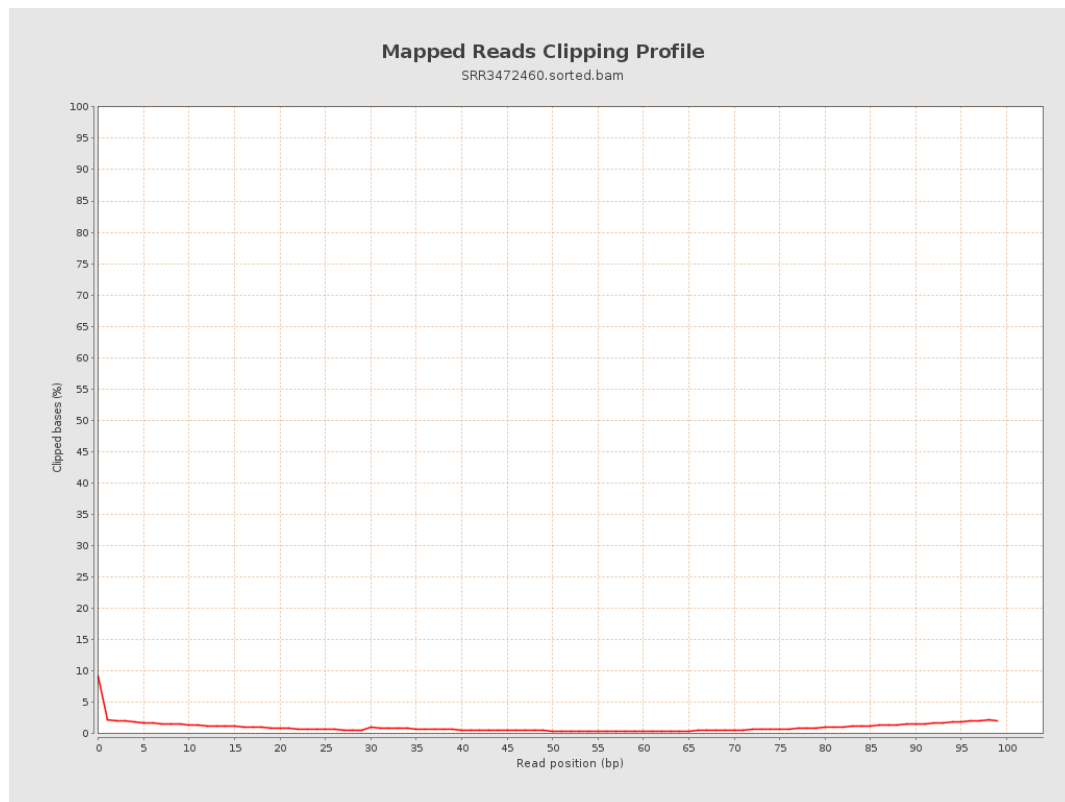
8. Results : Mapped Reads Nucleotide Content



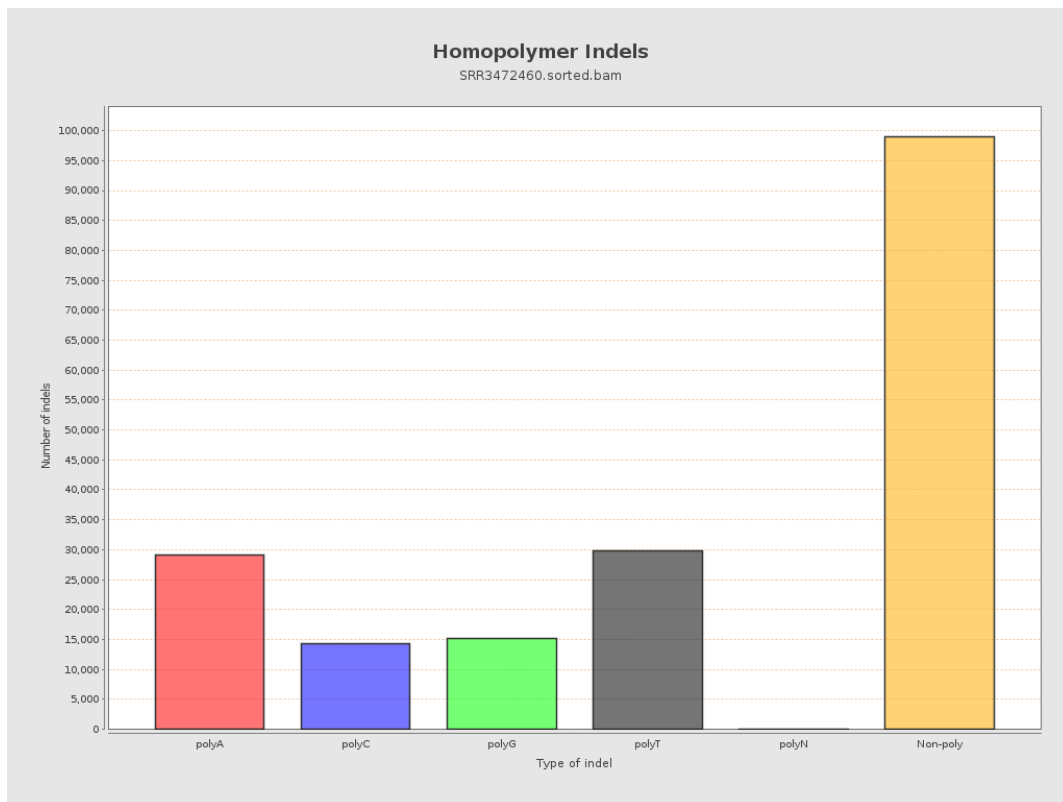
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



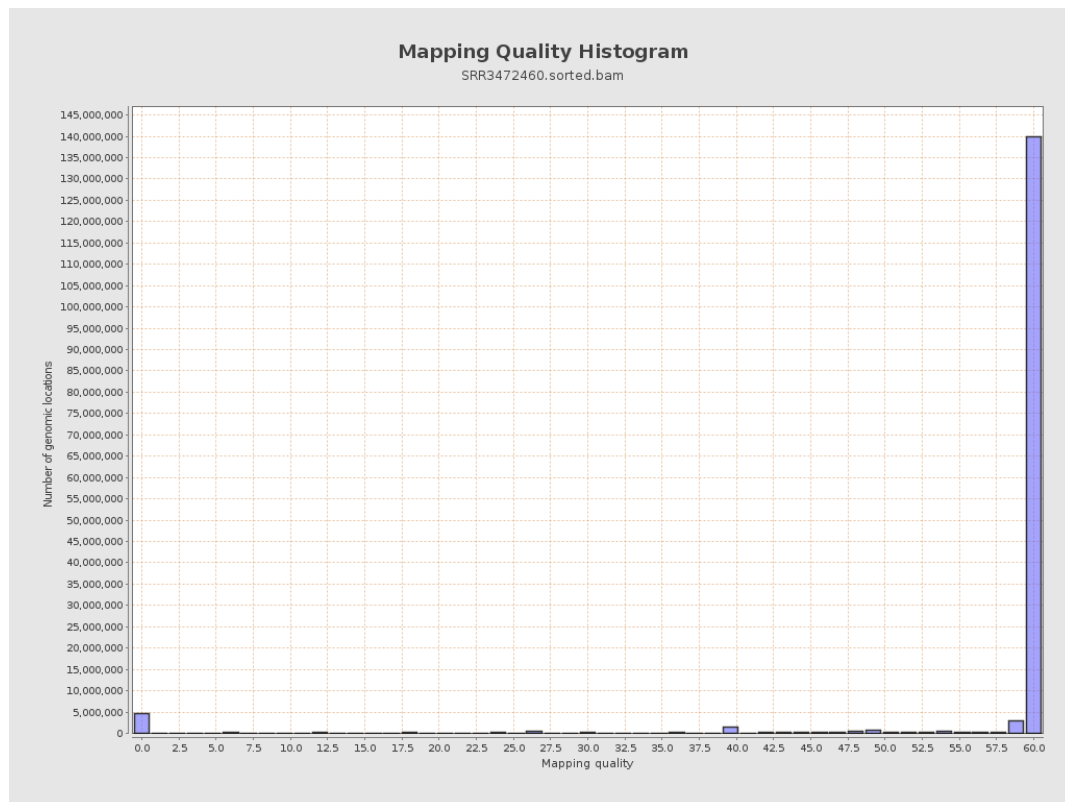
11. Results : Homopolymer Indels



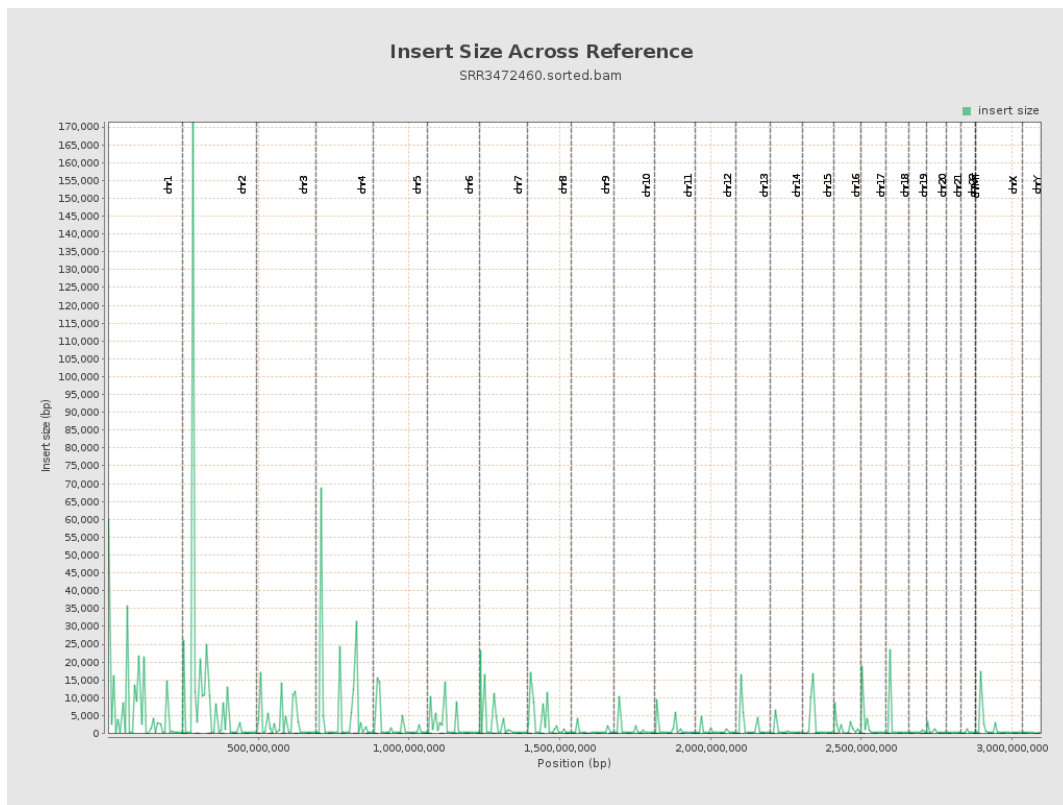
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

