

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:15:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472484.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_SRR3472484 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472484_1.fastq.gz SRR3472484_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:15:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472484.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	35,016,806
Mapped reads	34,539,386 / 98.64%
Unmapped reads	477,420 / 1.36%
Mapped paired reads	34,539,386 / 98.64%
Mapped reads, first in pair	17,321,793 / 49.47%
Mapped reads, second in pair	17,217,593 / 49.17%
Mapped reads, both in pair	34,309,378 / 97.98%
Mapped reads, singletons	230,008 / 0.66%
Secondary alignments	0
Supplementary alignments	128,314 / 0.37%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	23,154,820 / 66.12%
Duplication rate	47.37%
Clipped reads	3,089,489 / 8.82%

2.2. ACGT Content

Number/percentage of A's	944,395,399 / 27.85%
Number/percentage of C's	756,181,002 / 22.3%
Number/percentage of T's	937,523,175 / 27.65%
Number/percentage of G's	752,300,822 / 22.19%
Number/percentage of N's	526,459 / 0.02%

GC Percentage	44.49%
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2.3. Coverage

Mean	1.0955
Standard Deviation	29.7868

2.4. Mapping Quality

Mean Mapping Quality	55.16
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2.5. Insert size

Mean	27,163.07
Standard Deviation	1,619,786.82
P25/Median/P75	166 / 234 / 316

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	20,175,536
Insertions	182,108
Mapped reads with at least one insertion	0.52%
Deletions	183,663
Mapped reads with at least one deletion	0.53%
Homopolymer indels	45.51%

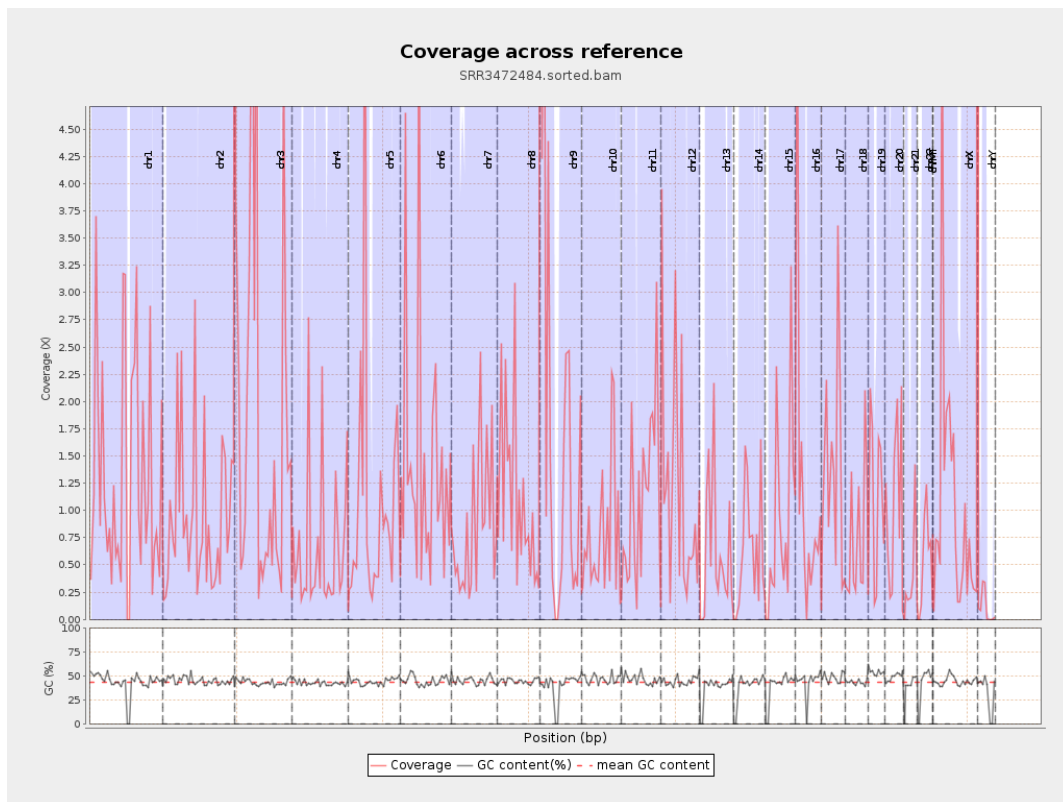
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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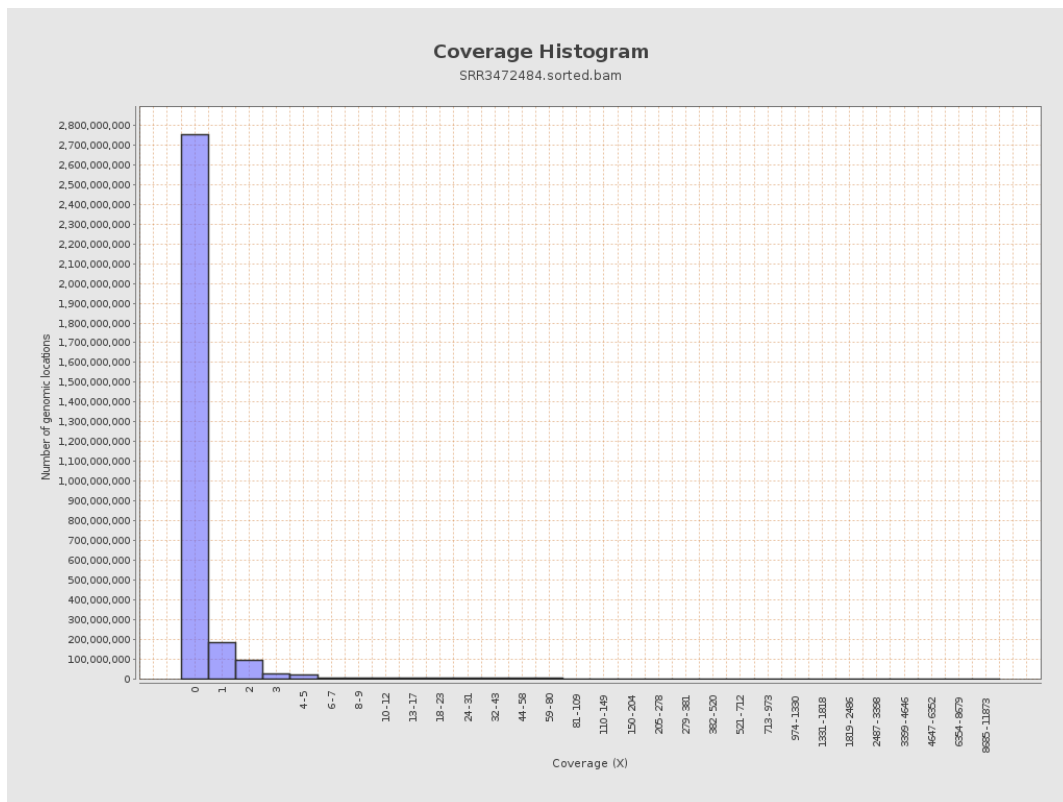
		bases	coverage	deviation
chr1	249250621	329534215	1.3221	37.0801
chr2	243199373	229300633	0.9429	27.1787
chr3	198022430	396942437	2.0045	40.239
chr4	191154276	128444661	0.6719	19.5919
chr5	180915260	196512840	1.0862	29.6725
chr6	171115067	248812534	1.4541	36.6067
chr7	159138663	136531333	0.8579	22.2079
chr8	146364022	158349410	1.0819	28.1648
chr9	141213431	239130708	1.6934	36.3872
chr10	135534747	108616242	0.8014	25.2044
chr11	135006516	149720843	1.109	32.8586
chr12	133851895	164564238	1.2295	31.9499
chr13	115169878	69681458	0.605	18.7287
chr14	107349540	69759499	0.6498	18.0459
chr15	102531392	88559651	0.8637	26.8432
chr16	90354753	106790160	1.1819	26.8069
chr17	81195210	117015420	1.4412	28.73
chr18	78077248	57578623	0.7375	20.8844
chr19	59128983	66129207	1.1184	31.0257
chr20	63025520	64748166	1.0273	25.2516
chr21	48129895	19339188	0.4018	13.8578
chr22	51304566	28905245	0.5634	15.4722
chrMT	16571	12998	0.7844	1.7999
chrX	155270560	209715444	1.3506	40.6185

chrY	59373566	6666556	0.1123	4.3489
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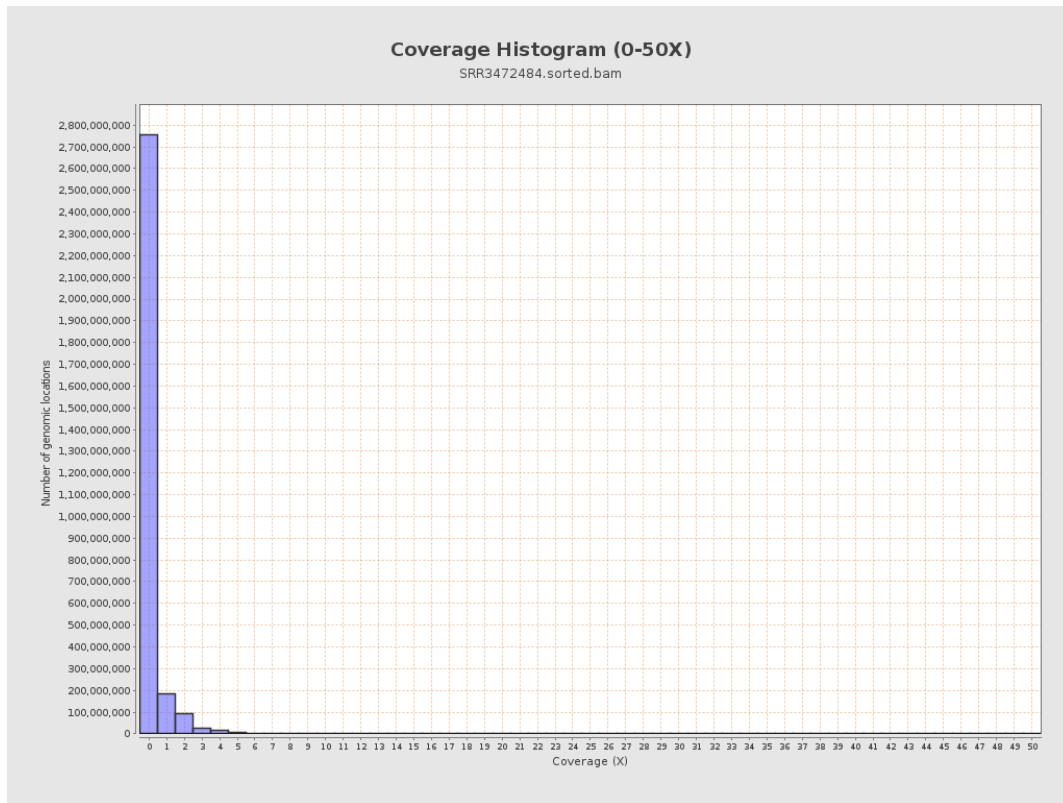
3. Results : Coverage across reference



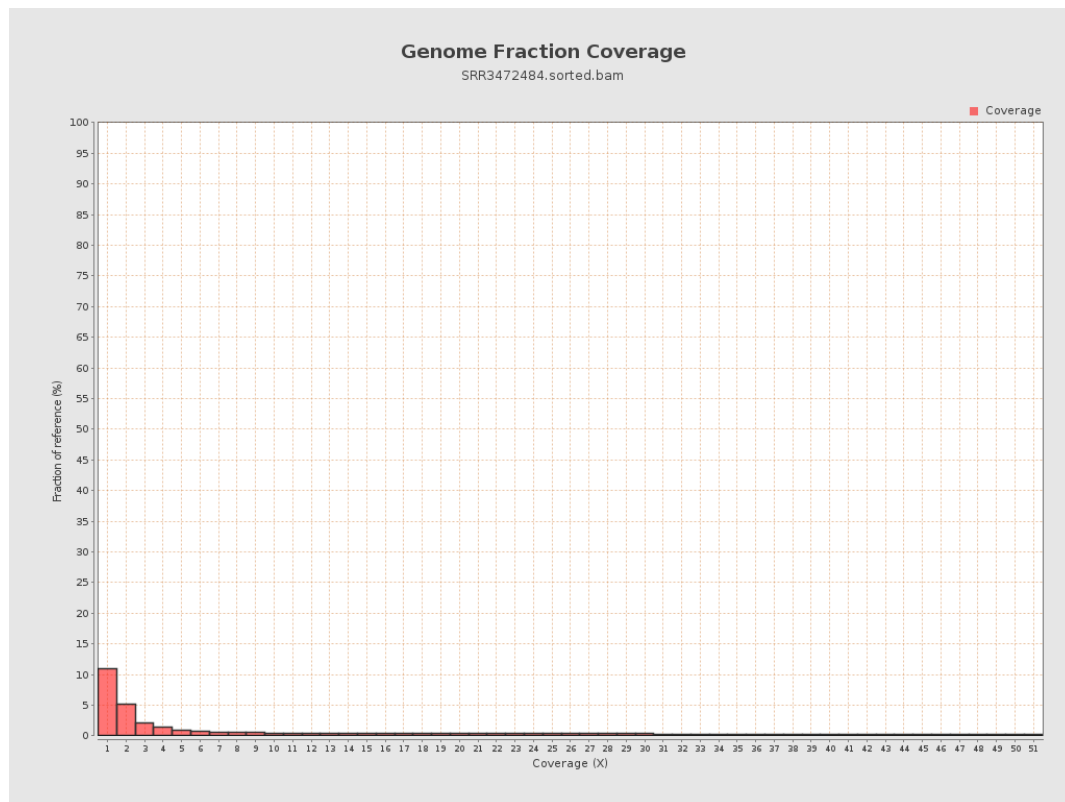
4. Results : Coverage Histogram



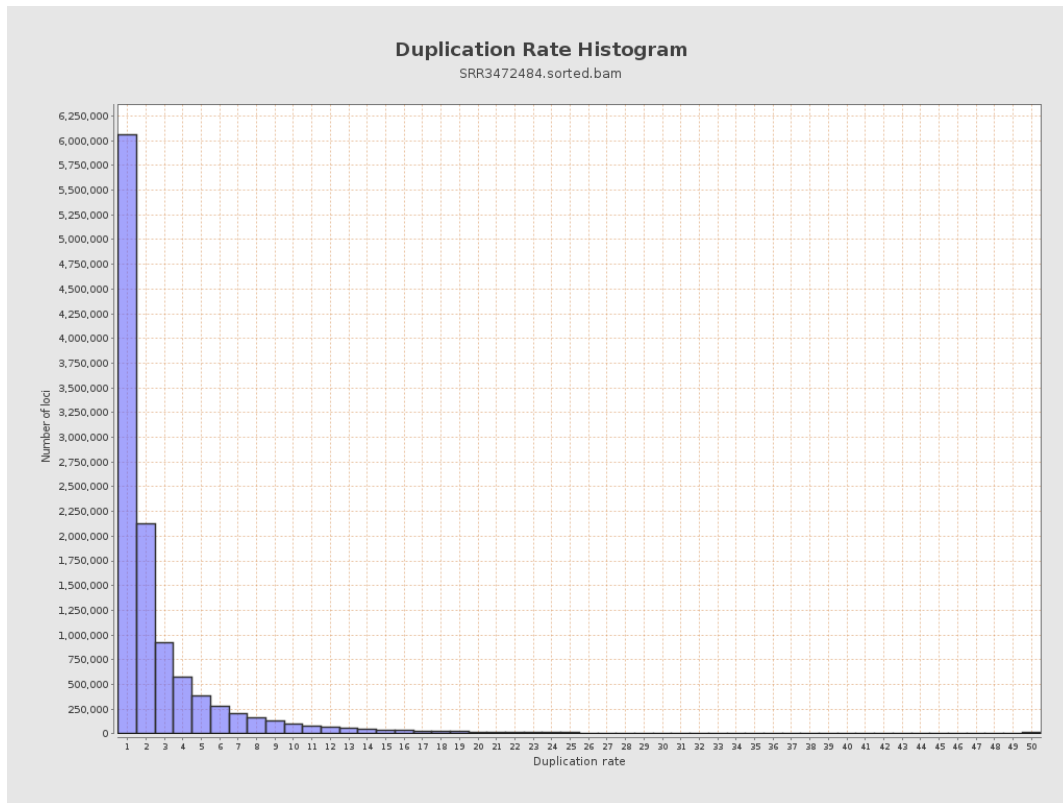
5. Results : Coverage Histogram (0-50X)



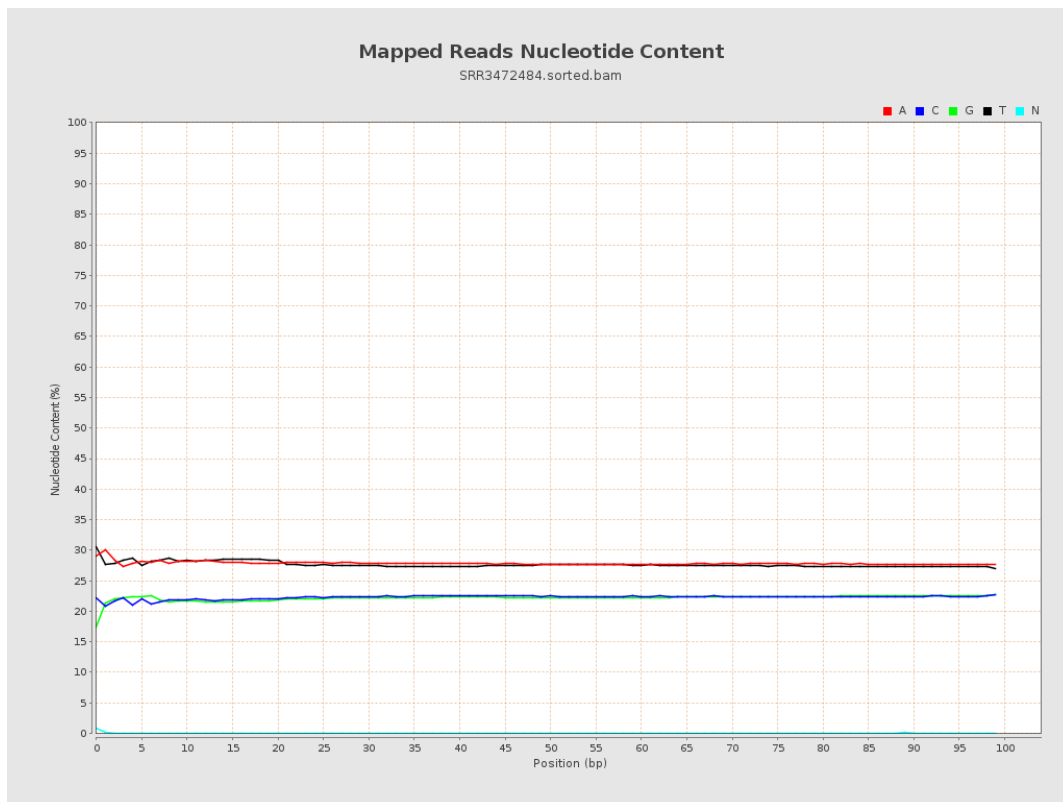
6. Results : Genome Fraction Coverage



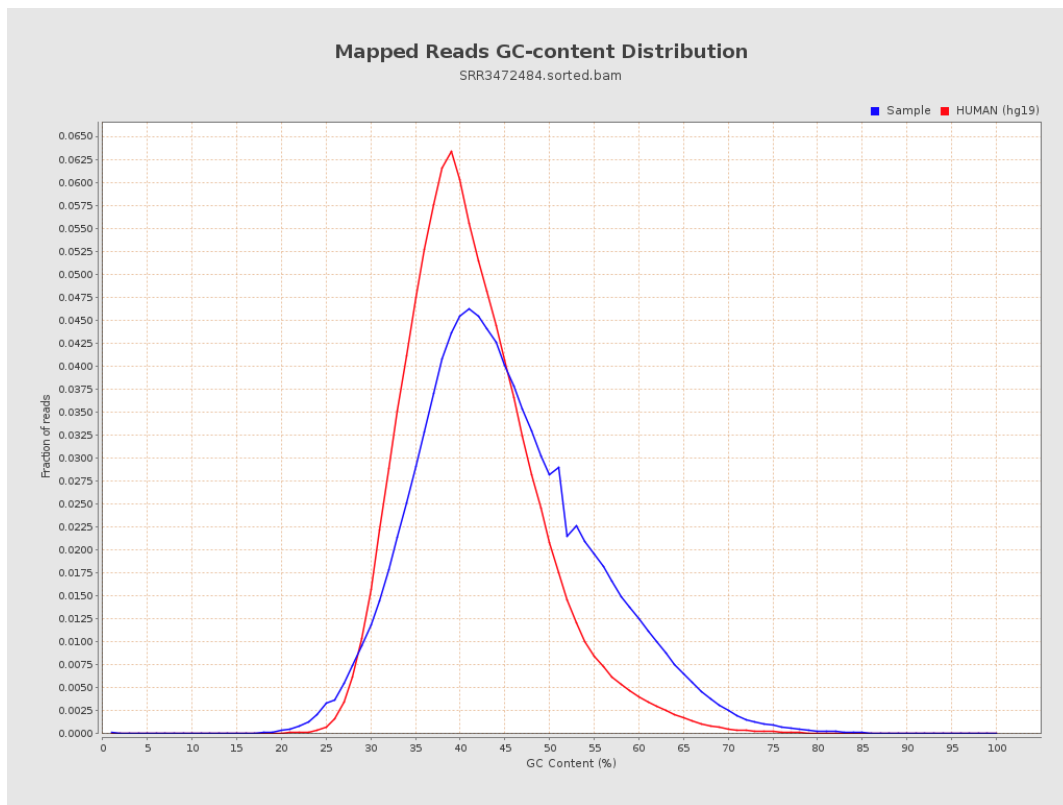
7. Results : Duplication Rate Histogram



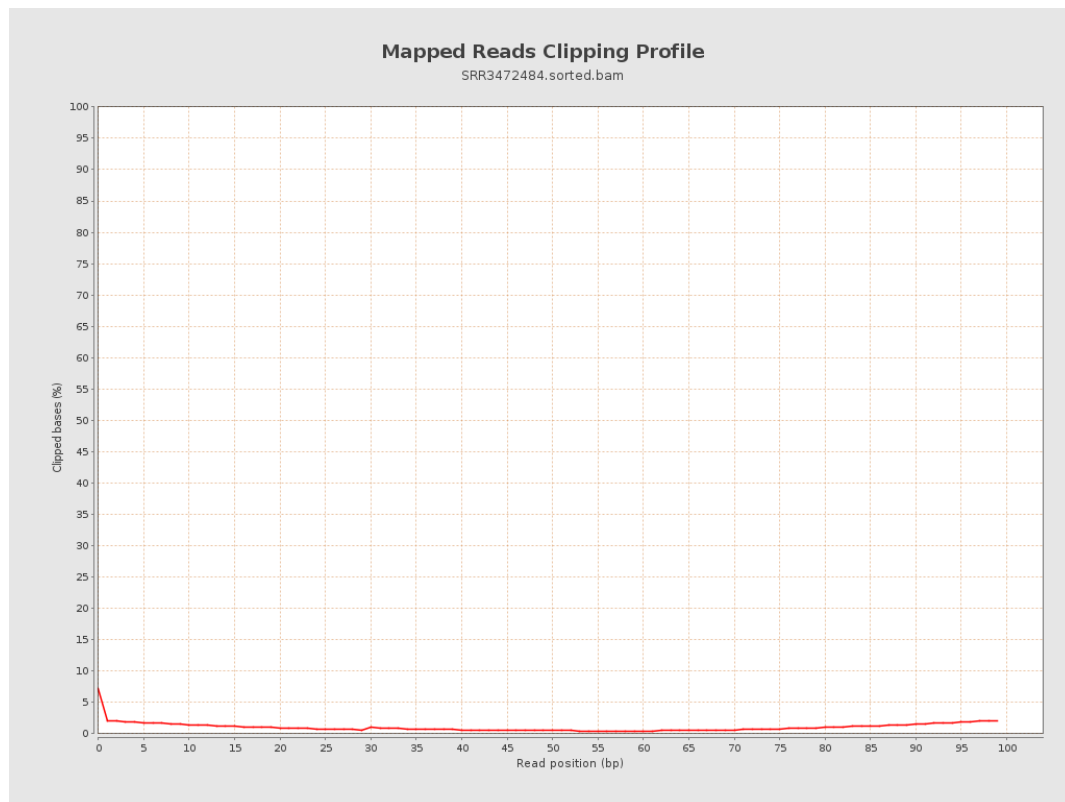
8. Results : Mapped Reads Nucleotide Content



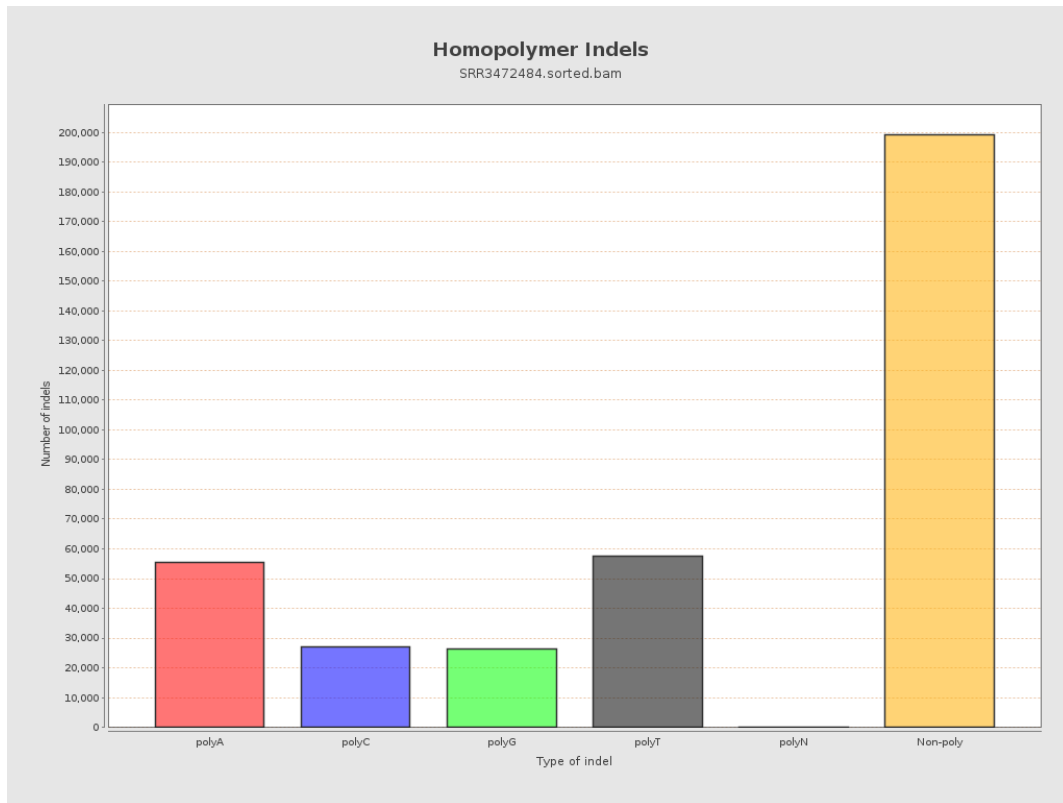
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



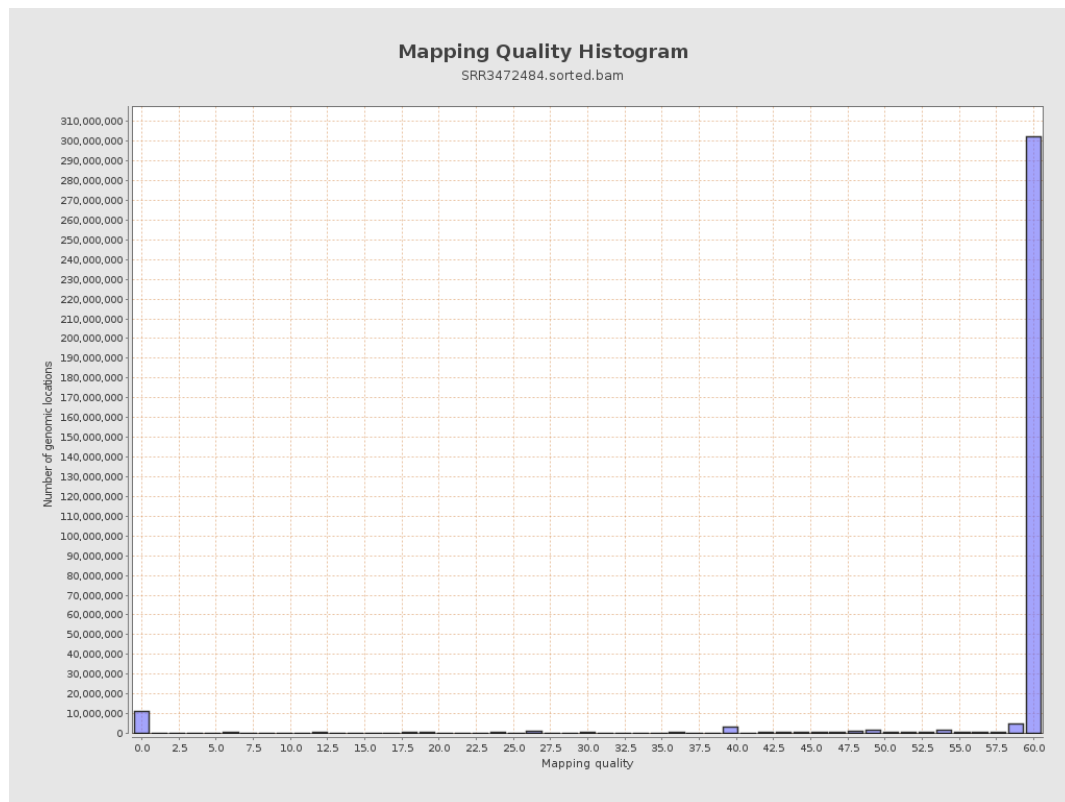
11. Results : Homopolymer Indels



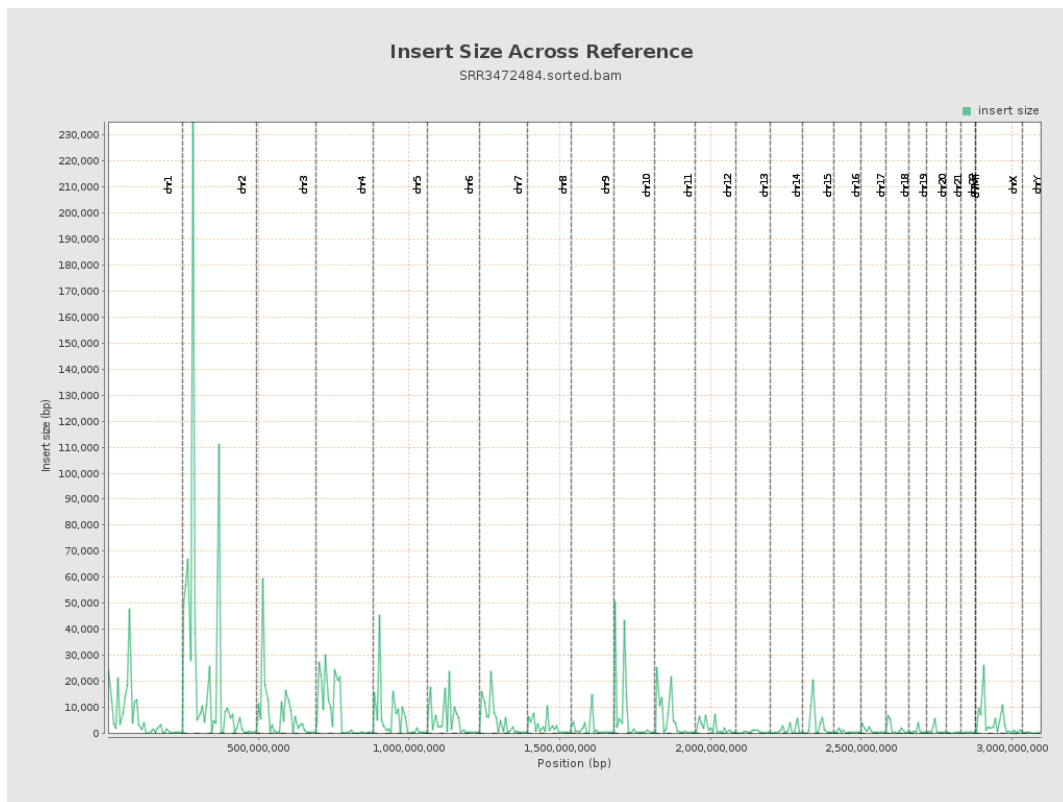
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

