

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 05:56:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472596.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_SRR3472596 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472596_1.fastq.gz SRR3472596_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 05:56:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472596.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,265,656
Mapped reads	9,524,340 / 92.78%
Unmapped reads	741,316 / 7.22%
Mapped paired reads	9,524,340 / 92.78%
Mapped reads, first in pair	4,806,579 / 46.82%
Mapped reads, second in pair	4,717,761 / 45.96%
Mapped reads, both in pair	9,313,966 / 90.73%
Mapped reads, singletons	210,374 / 2.05%
Secondary alignments	0
Supplementary alignments	307,554 / 3%
Read min/max/mean length	30 / 100 / 101.17
Duplicated reads (estimated)	1,490,609 / 14.52%
Duplication rate	13.53%
Clipped reads	7,247,245 / 70.6%

2.2. ACGT Content

Number/percentage of A's	201,015,895 / 25.92%
Number/percentage of C's	154,692,809 / 19.95%
Number/percentage of T's	231,257,276 / 29.82%
Number/percentage of G's	188,040,216 / 24.25%
Number/percentage of N's	488,974 / 0.06%

GC Percentage	44.2%
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2.3. Coverage

Mean	0.2506
Standard Deviation	2.2238

2.4. Mapping Quality

Mean Mapping Quality	50.52
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2.5. Insert size

Mean	243,647.14
Standard Deviation	4,724,679.65
P25/Median/P75	91 / 129 / 176

2.6. Mismatches and indels

General error rate	1.17%
Mismatches	8,926,814
Insertions	72,463
Mapped reads with at least one insertion	0.75%
Deletions	174,837
Mapped reads with at least one deletion	1.8%
Homopolymer indels	42.98%

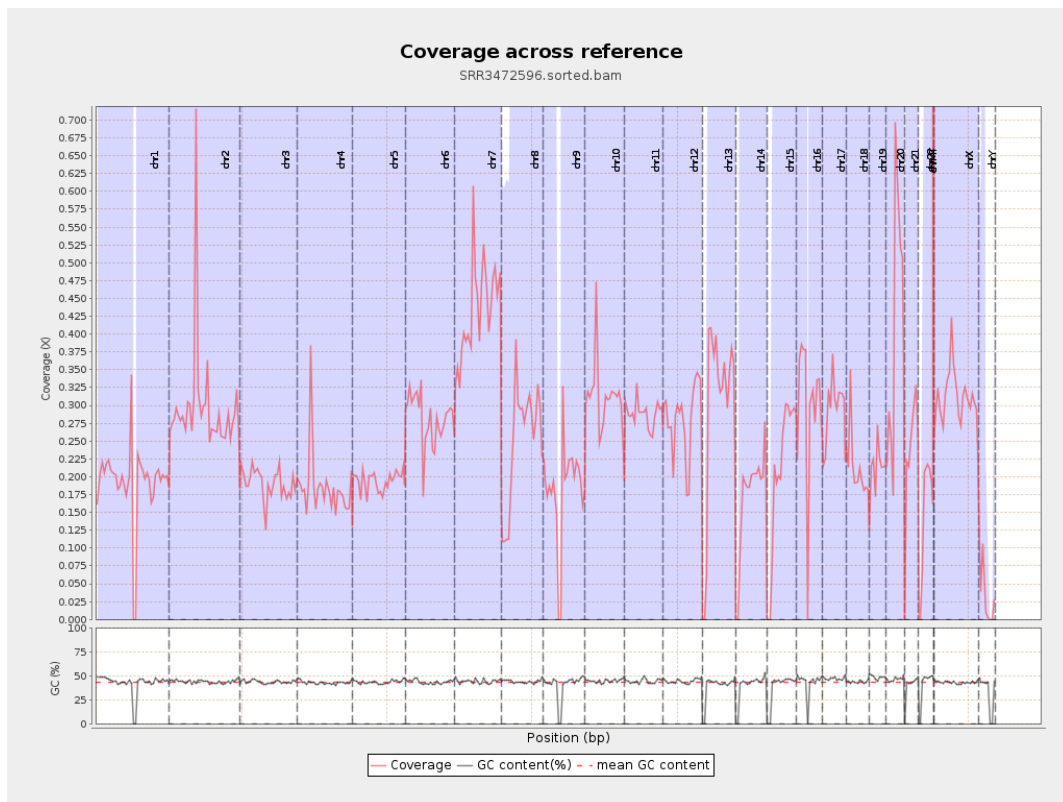
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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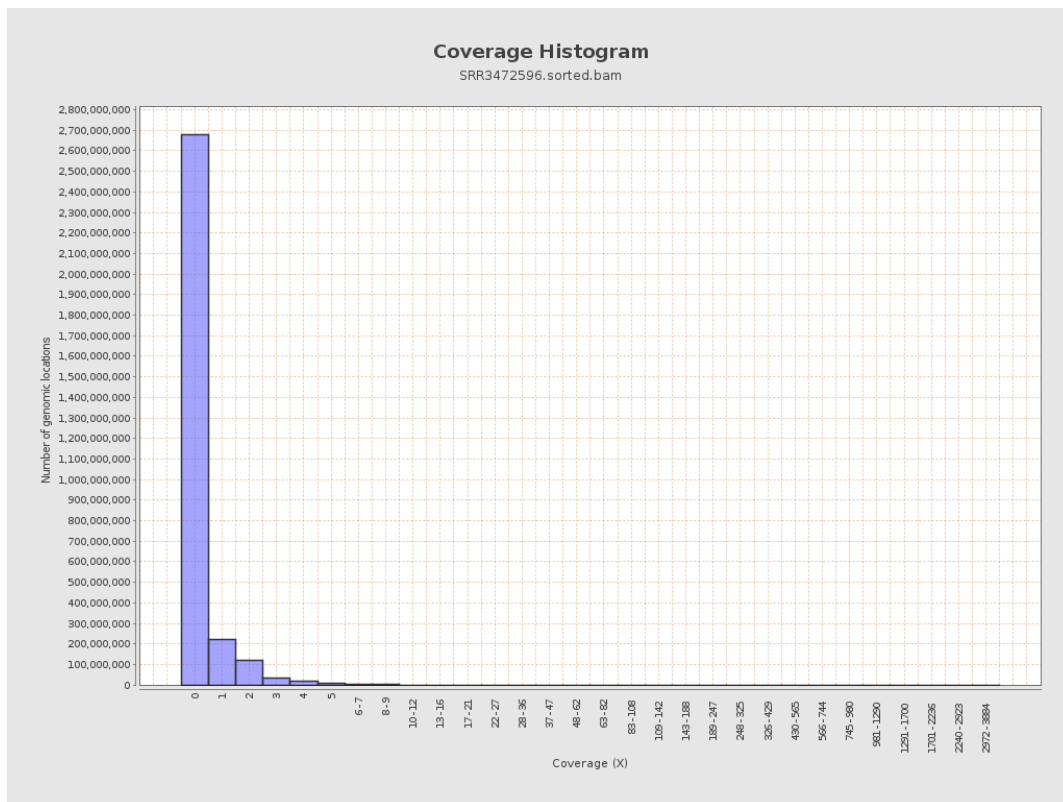
		bases	coverage	deviation
chr1	249250621	47752706	0.1916	2.7799
chr2	243199373	72258030	0.2971	3.3472
chr3	198022430	37718521	0.1905	0.6612
chr4	191154276	35218392	0.1842	1.2163
chr5	180915260	35055501	0.1938	0.7088
chr6	171115067	48185550	0.2816	1.2113
chr7	159138663	69356009	0.4358	4.3985
chr8	146364022	36628168	0.2503	1.8583
chr9	141213431	25464506	0.1803	2.5207
chr10	135534747	42212112	0.3114	2.2395
chr11	135006516	38647652	0.2863	2.2569
chr12	133851895	37372852	0.2792	0.8446
chr13	115169878	34384657	0.2986	0.8841
chr14	107349540	18396065	0.1714	3.6207
chr15	102531392	21194188	0.2067	0.715
chr16	90354753	27143010	0.3004	1.2801
chr17	81195210	23924970	0.2947	1.7607
chr18	78077248	16789709	0.215	4.07
chr19	59128983	12735489	0.2154	2.0092
chr20	63025520	26125033	0.4145	1.2914
chr21	48129895	11433170	0.2375	1.0285
chr22	51304566	7252288	0.1414	0.5938
chrMT	16571	148893	8.9852	6.605
chrX	155270560	48466009	0.3121	1.3261

chrY	59373566	1960997	0.033	0.9543
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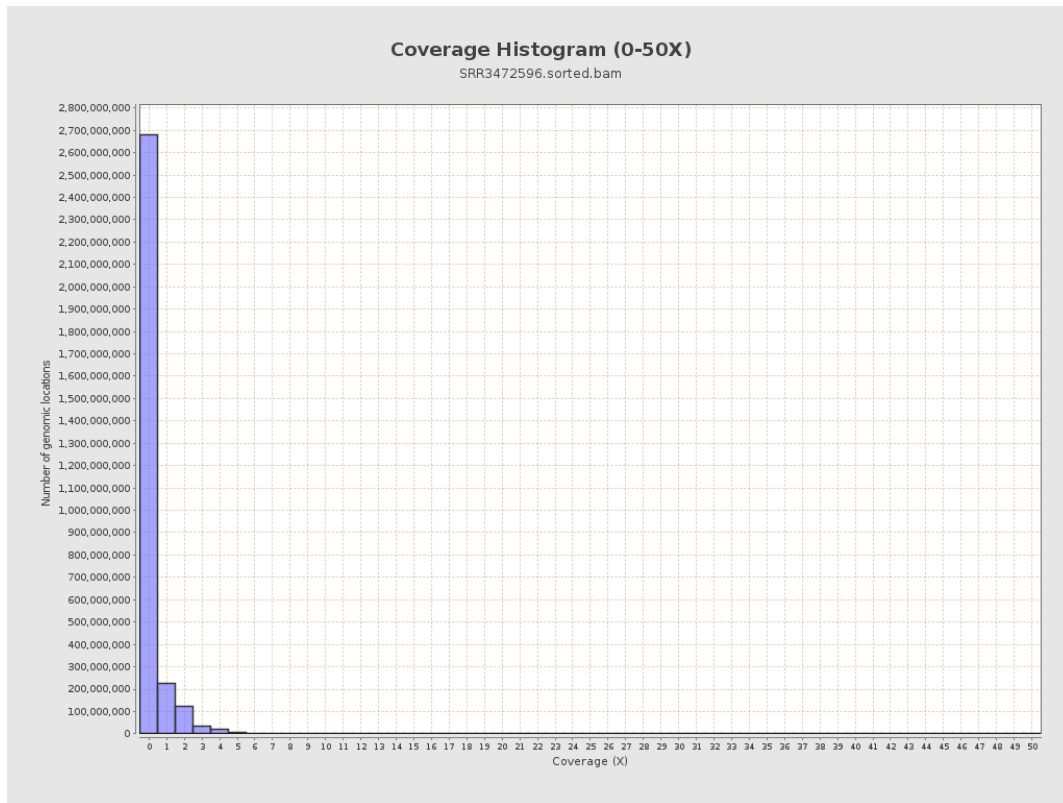
3. Results : Coverage across reference



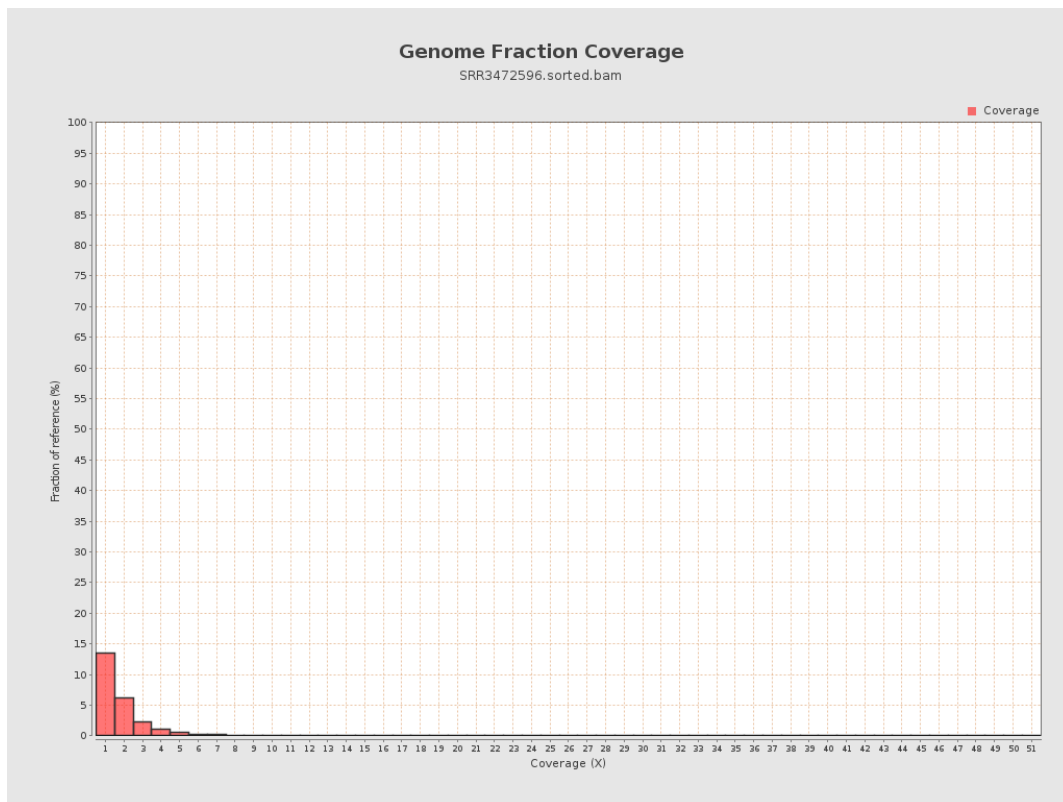
4. Results : Coverage Histogram



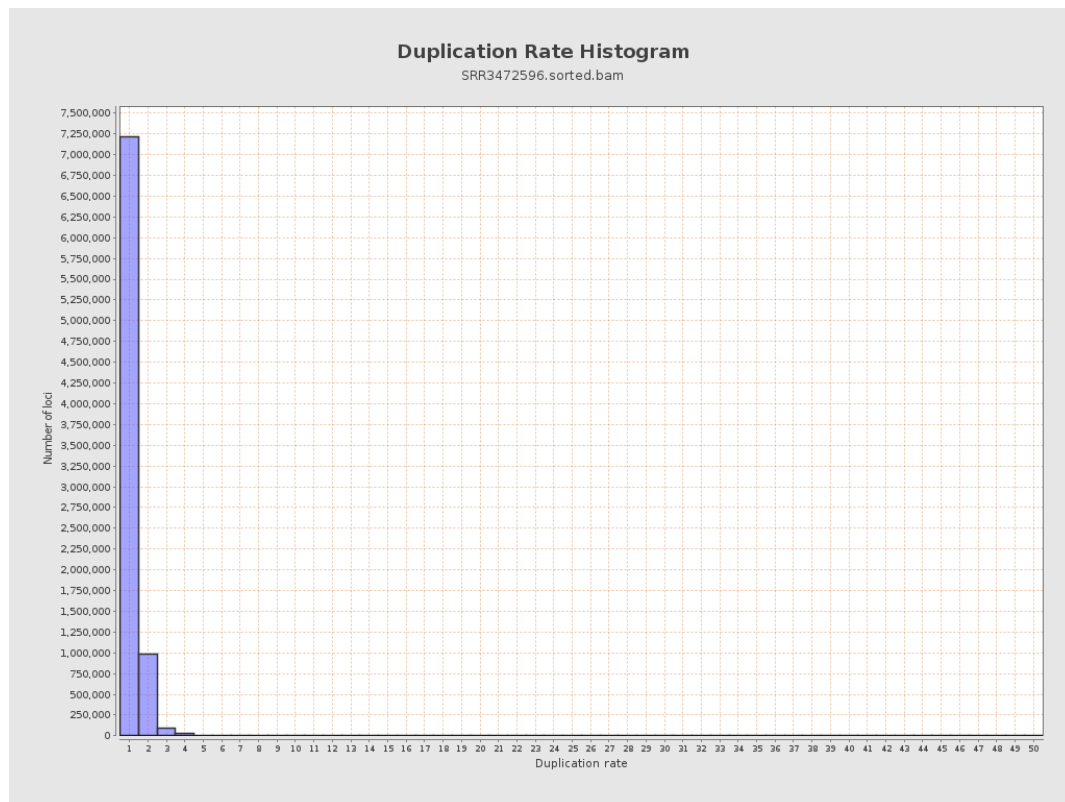
5. Results : Coverage Histogram (0-50X)



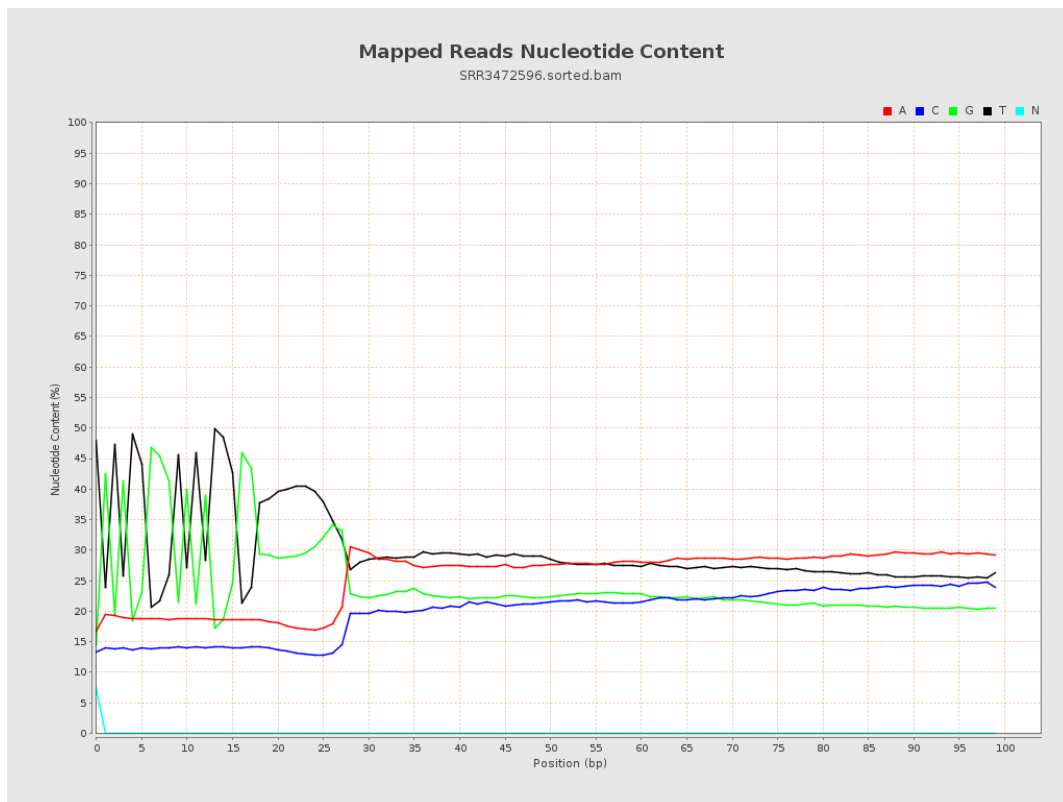
6. Results : Genome Fraction Coverage



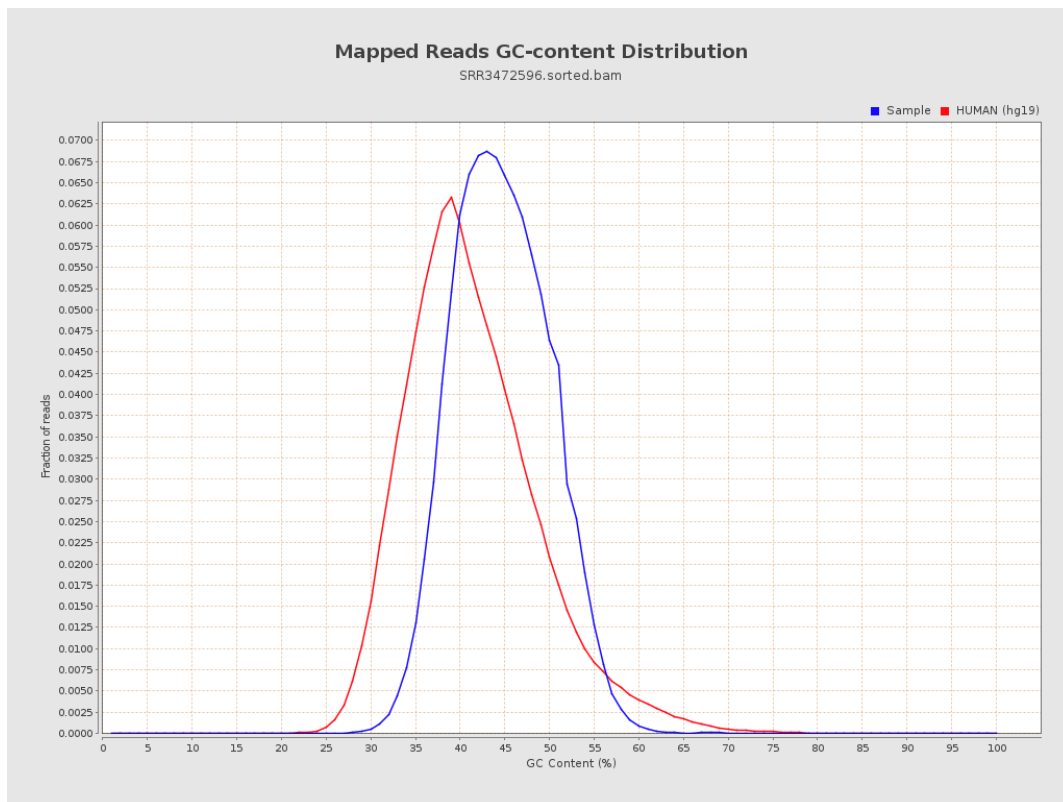
7. Results : Duplication Rate Histogram



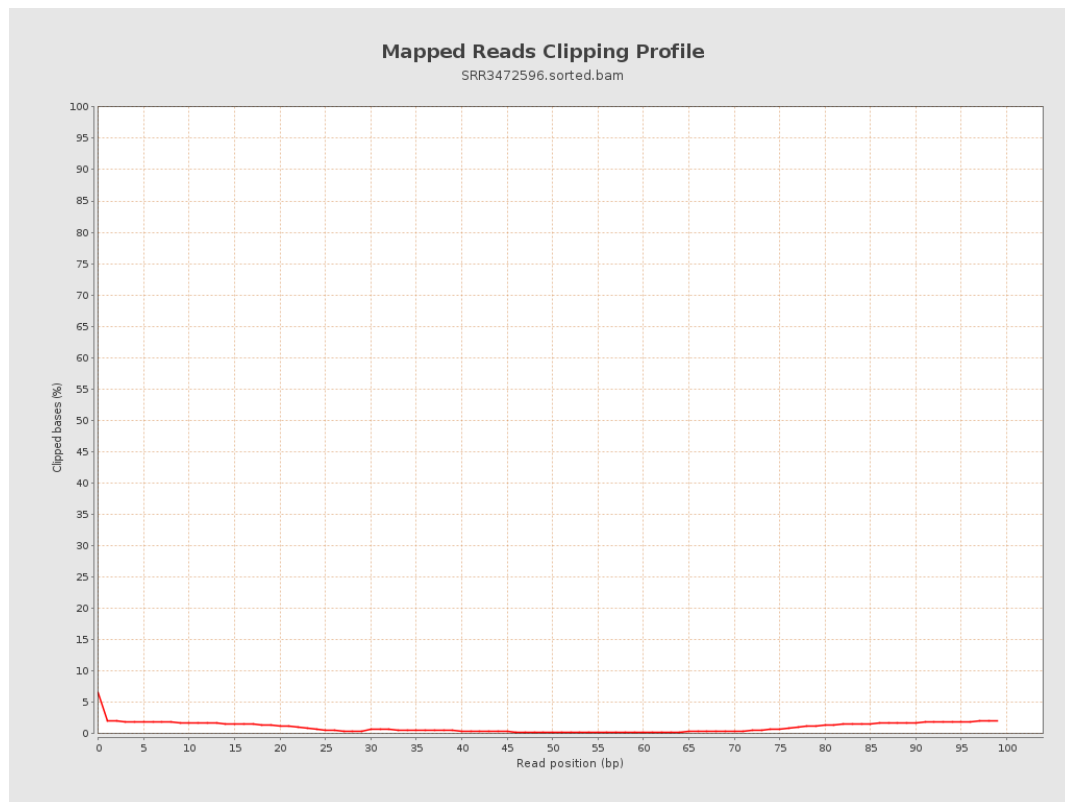
8. Results : Mapped Reads Nucleotide Content



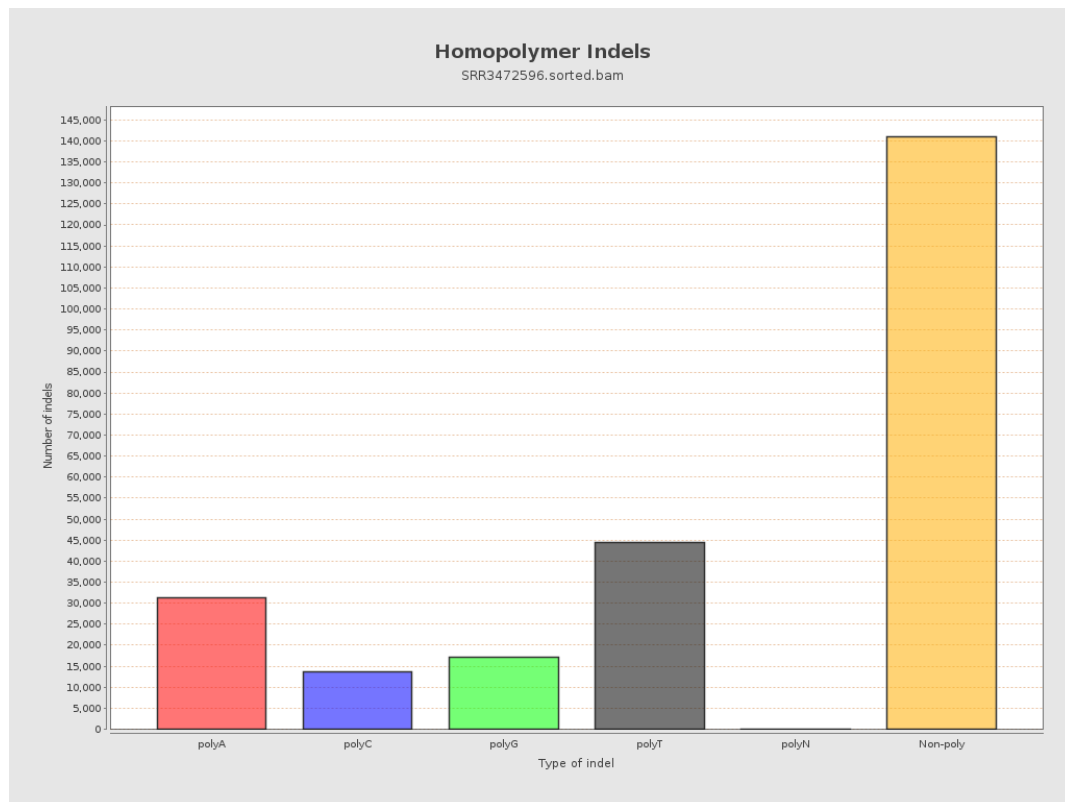
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



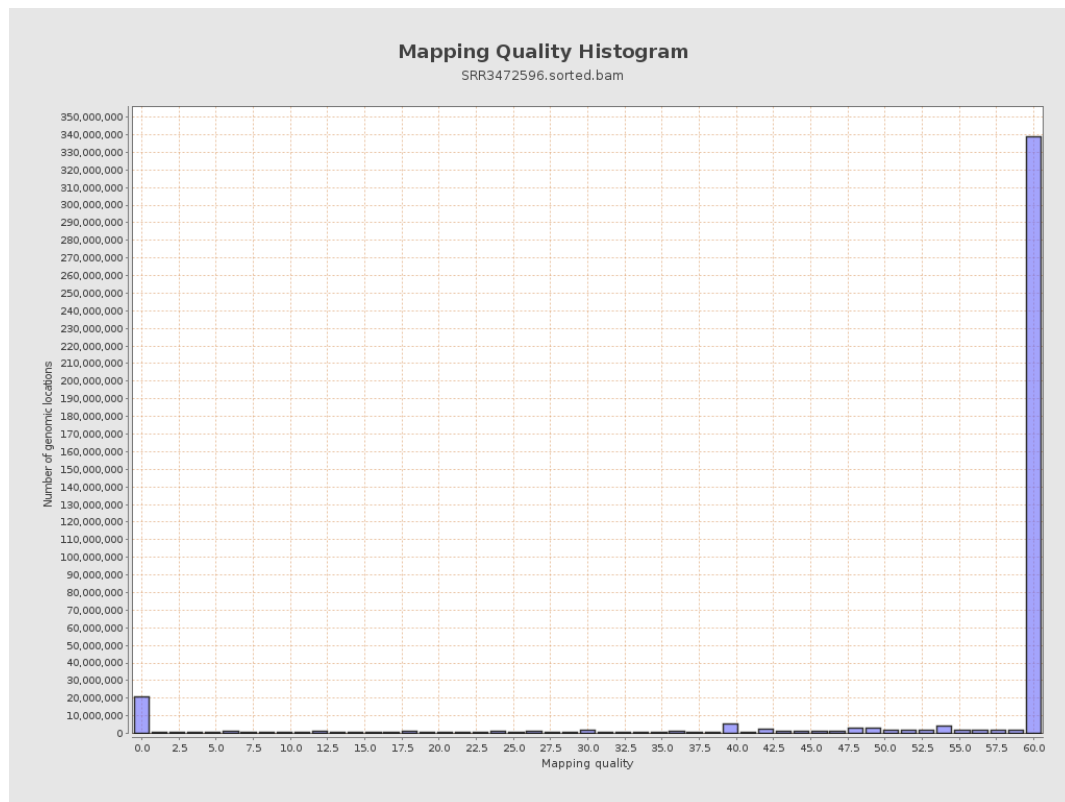
11. Results : Homopolymer Indels



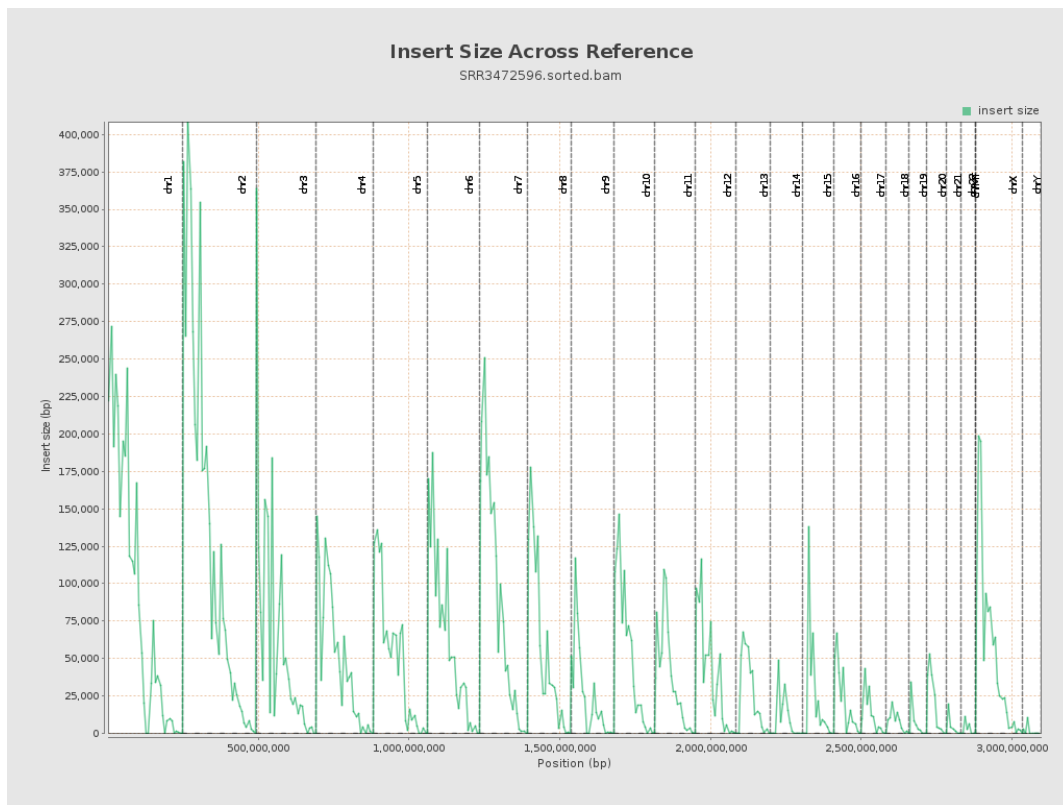
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

