Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:44:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472480.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_SRR3472480 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472480_1.fastq.gz SRR3472480_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:44:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472480.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,526,178
Mapped reads	16,336,611 / 98.85%
Unmapped reads	189,567 / 1.15%
Mapped paired reads	16,336,611 / 98.85%
Mapped reads, first in pair	8,183,941 / 49.52%
Mapped reads, second in pair	8,152,670 / 49.33%
Mapped reads, both in pair	16,249,564 / 98.33%
Mapped reads, singletons	87,047 / 0.53%
Secondary alignments	0
Supplementary alignments	80,121 / 0.48%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	11,202,912 / 67.79%
Duplication rate	44.71%
Clipped reads	1,806,378 / 10.93%

2.2. ACGT Content

Number/percentage of A's	450,081,800 / 28.17%
Number/percentage of C's	351,004,611 / 21.97%
Number/percentage of T's	446,556,427 / 27.95%
Number/percentage of G's	349,888,107 / 21.9%
Number/percentage of N's	254,205 / 0.02%

GC Percentage	43.87%

2.3. Coverage

Mean	0.5162
Standard Deviation	25.6831

2.4. Mapping Quality

Mean Mapping Quality	54.65

2.5. Insert size

Mean	33,396.12
Standard Deviation	1,757,929.34
P25/Median/P75	147 / 206 / 278

2.6. Mismatches and indels

General error rate	0.54%
Mismatches	8,413,490
Insertions	88,184
Mapped reads with at least one insertion	0.54%
Deletions	78,786
Mapped reads with at least one deletion	0.48%
Homopolymer indels	43.01%

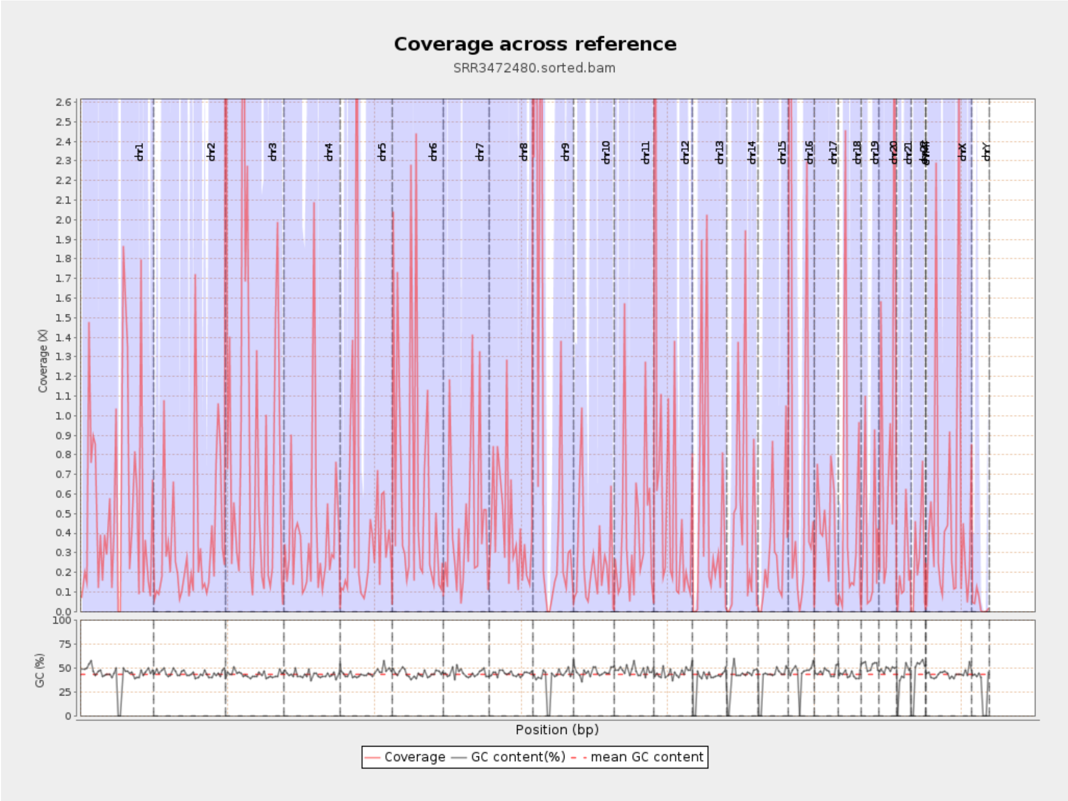
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

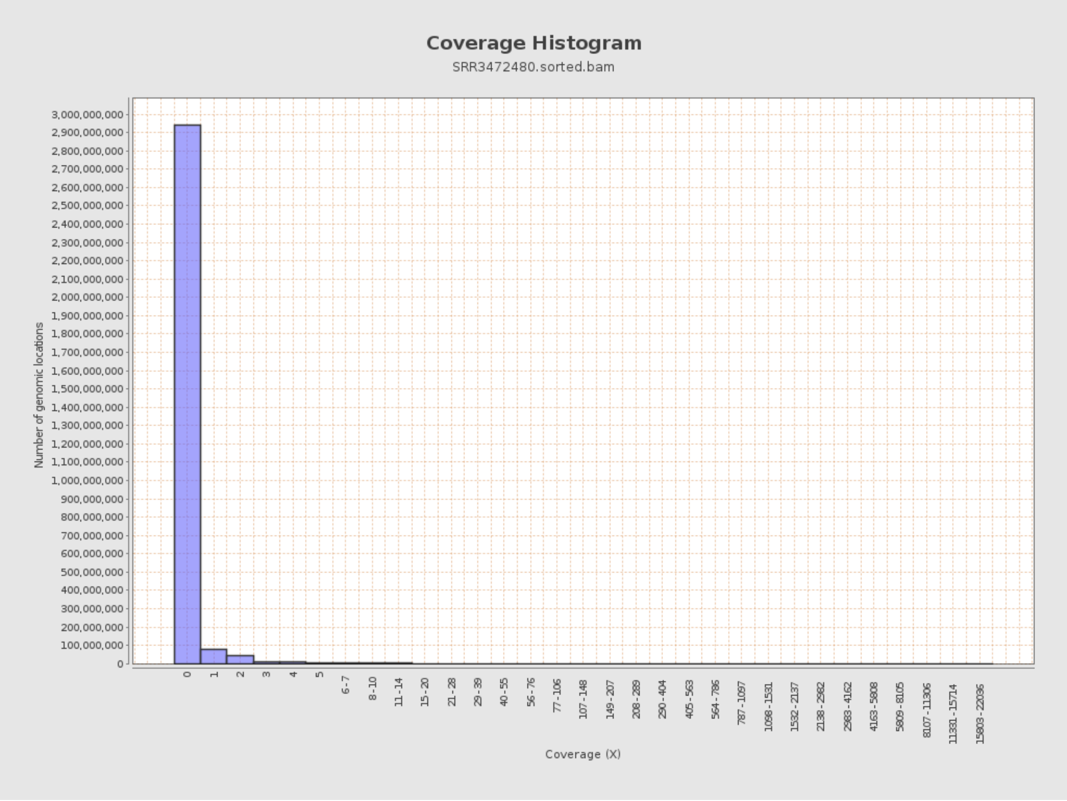
		bases	coverage	deviation
chr1	249250621	139945820	0.5615	23.3052
chr2	243199373	84589644	0.3478	16.0775
chr3	198022430	178477800	0.9013	30.3946
chr4	191154276	74618641	0.3904	19.5884
chr5	180915260	90585682	0.5007	19.2814
chr6	171115067	113182218	0.6614	29.6066
chr7	159138663	71662730	0.4503	22.2718
chr8	146364022	64742379	0.4423	20.8932
chr9	141213431	120586391	0.8539	26.3506
chr10	135534747	37236773	0.2747	16.5799
chr11	135006516	58770801	0.4353	18.0384
chr12	133851895	90460569	0.6758	35.1957
chr13	115169878	56596351	0.4914	30.4951
chr14	107349540	50969735	0.4748	39.3635
chr15	102531392	32227544	0.3143	18.4138
chr16	90354753	78697617	0.871	47.2777
chr17	81195210	32663557	0.4023	16.5777
chr18	78077248	35787141	0.4584	33.6533
chr19	59128983	21950802	0.3712	11.8734
chr20	63025520	59048451	0.9369	42.2104
chr21	48129895	10014798	0.2081	14.4457
chr22	51304566	13454014	0.2622	14.6885
chrMT	16571	4108	0.2479	0.8198
chrX	155270560	79431019	0.5116	27.742

chrY	59373566	2272826	0.0383	1.0862

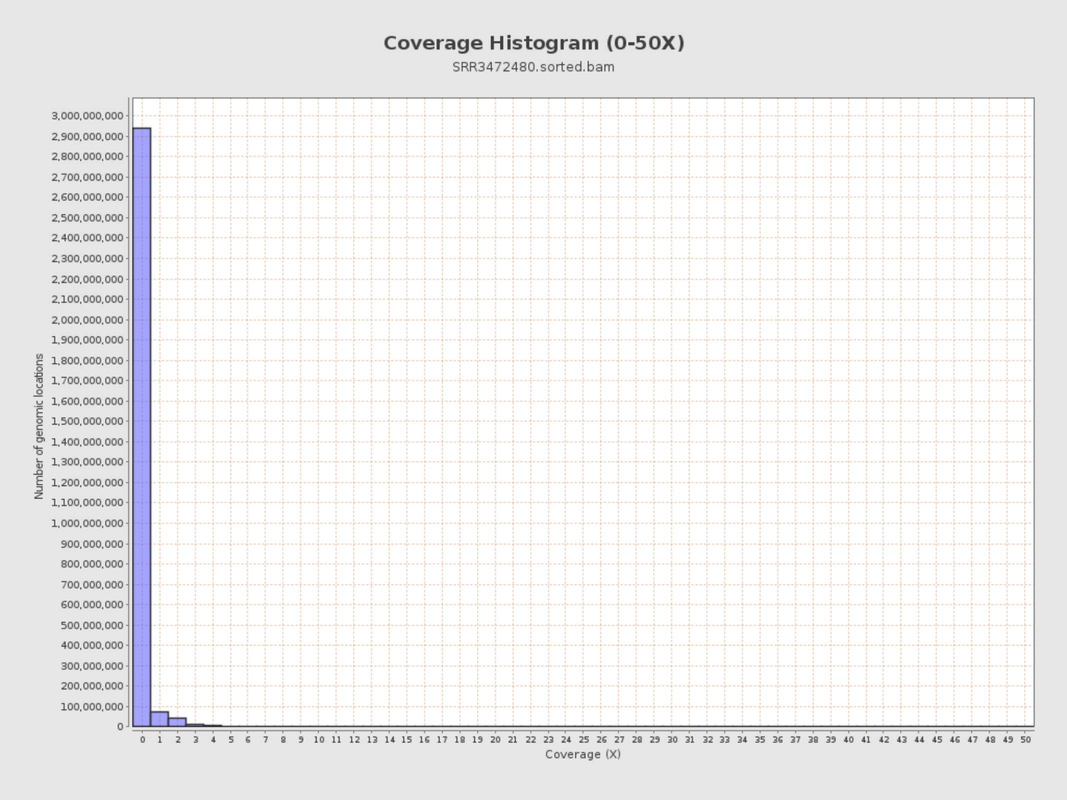
3. Results : Coverage across reference



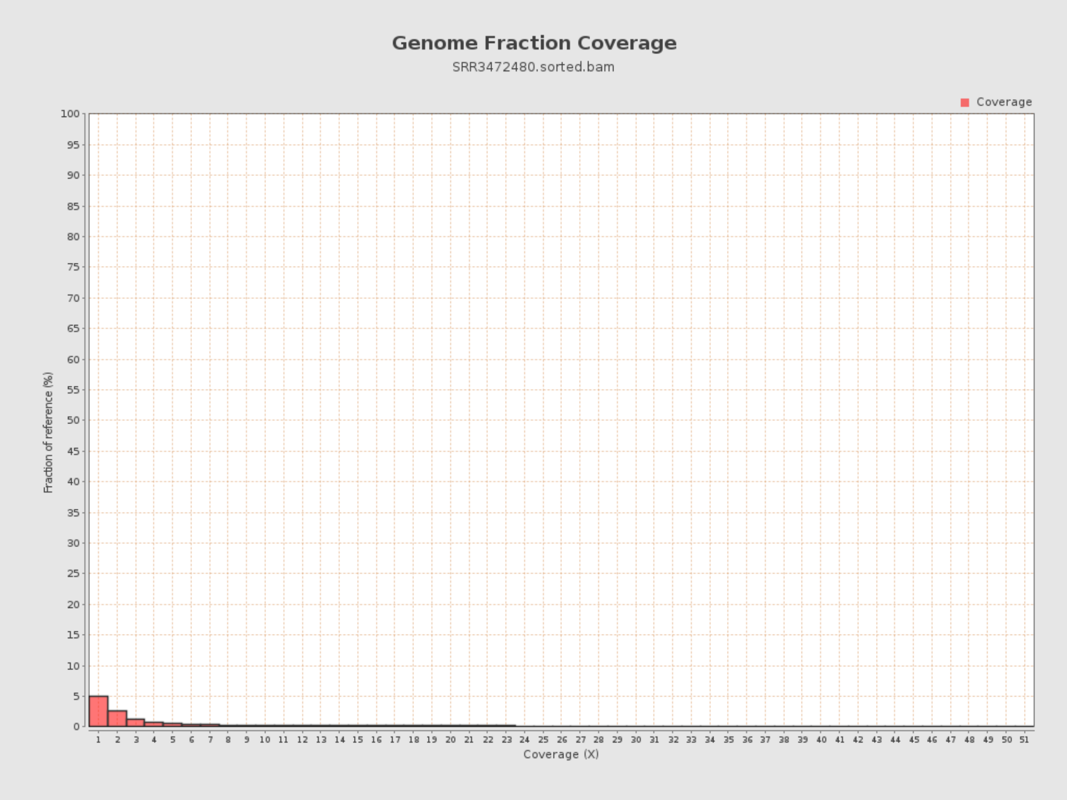
4. Results : Coverage Histogram



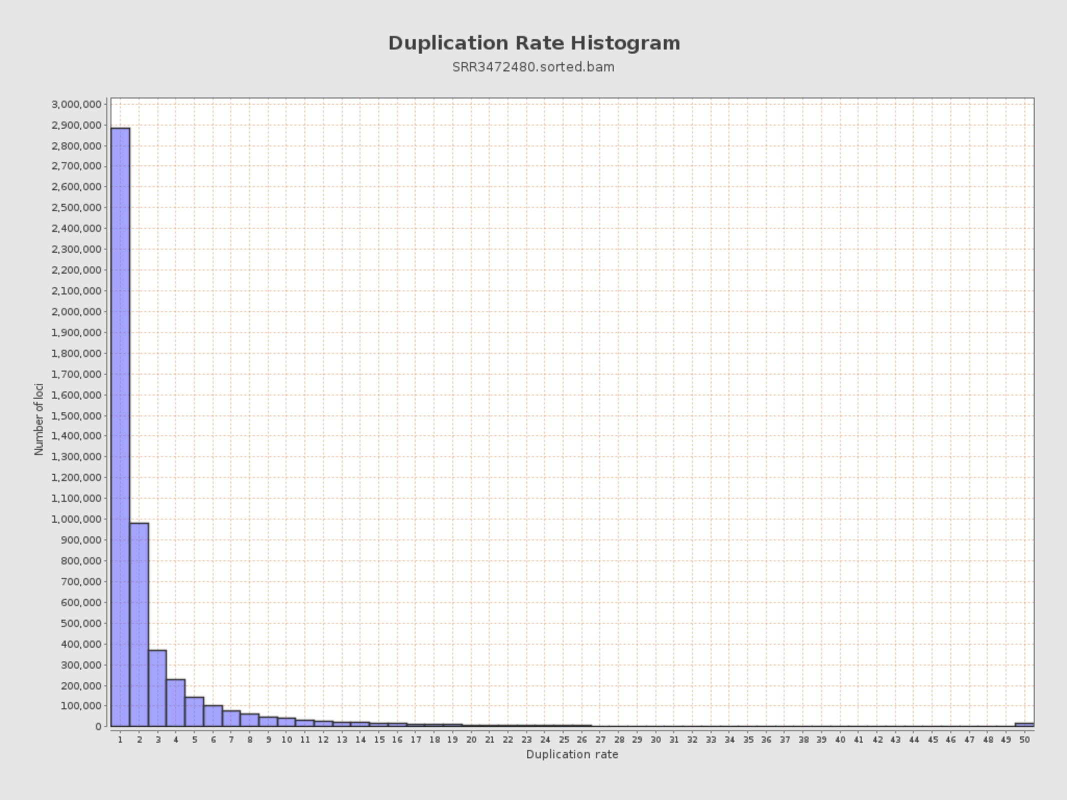
5. Results : Coverage Histogram (0-50X)



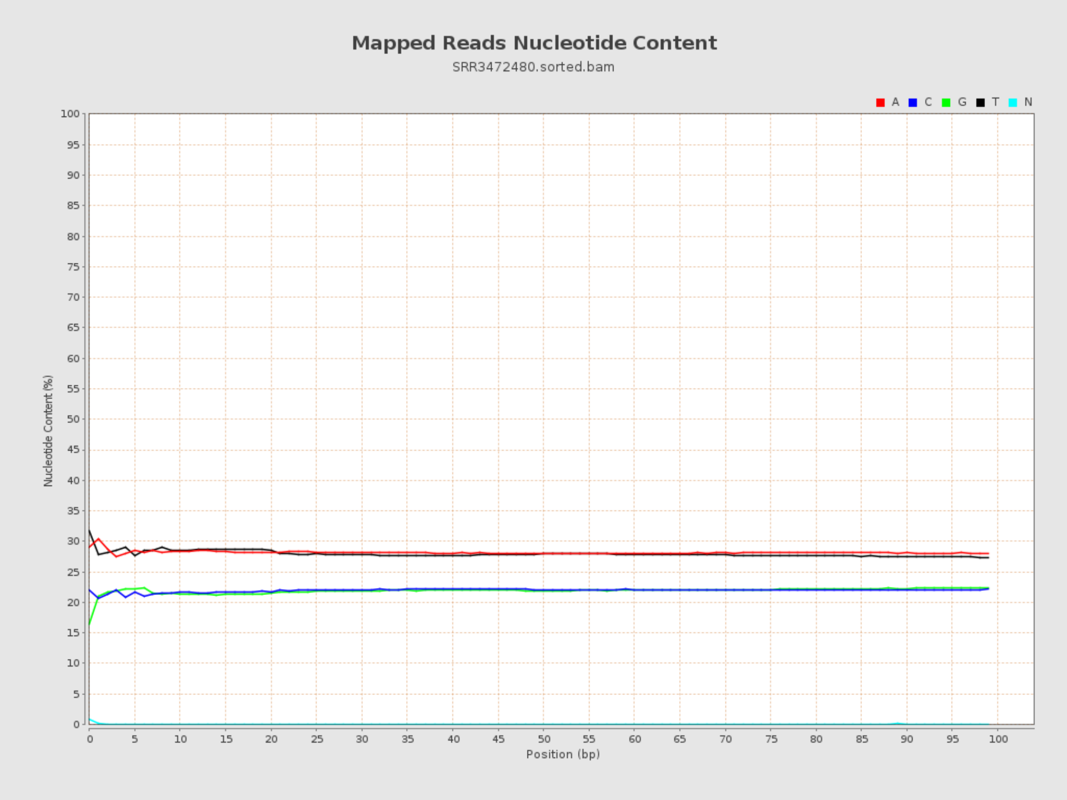
6. Results : Genome Fraction Coverage



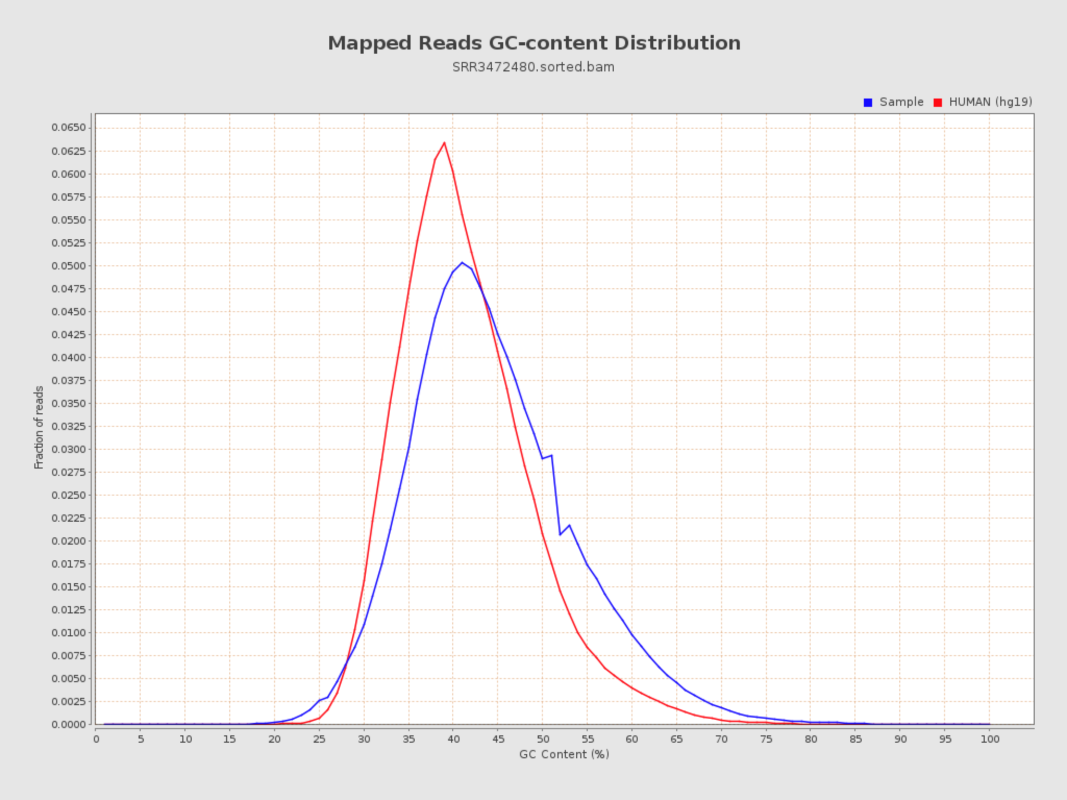
7. Results : Duplication Rate Histogram



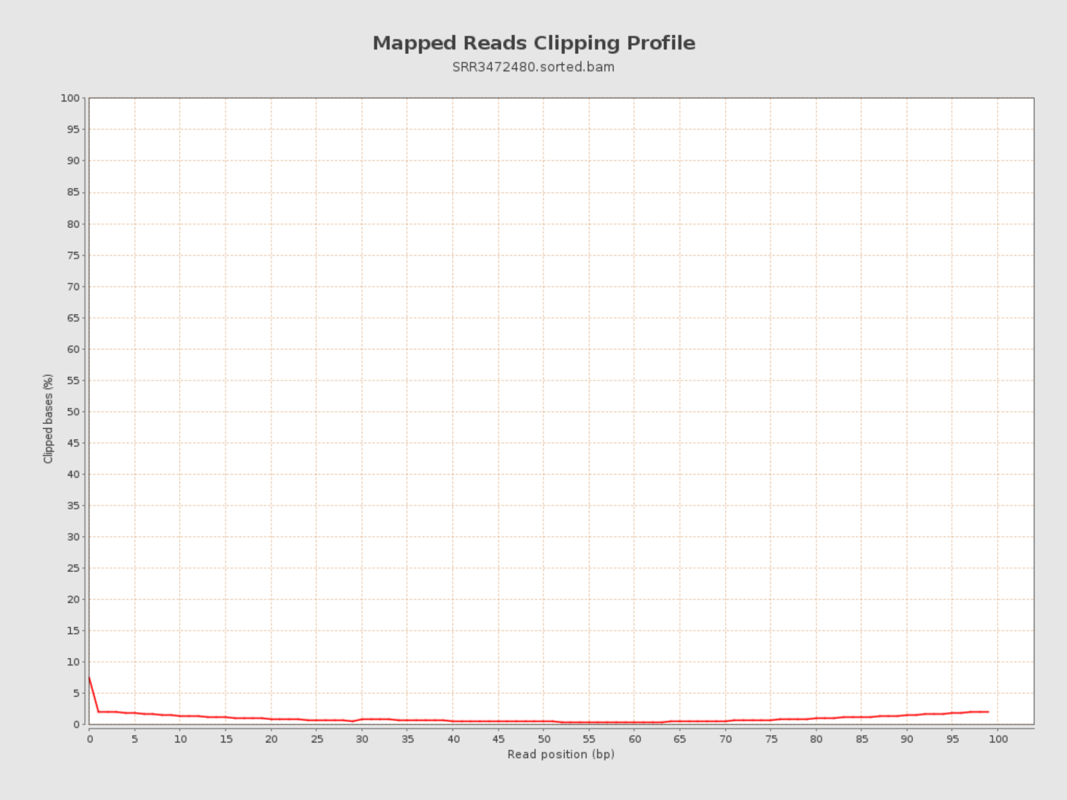
8. Results : Mapped Reads Nucleotide Content



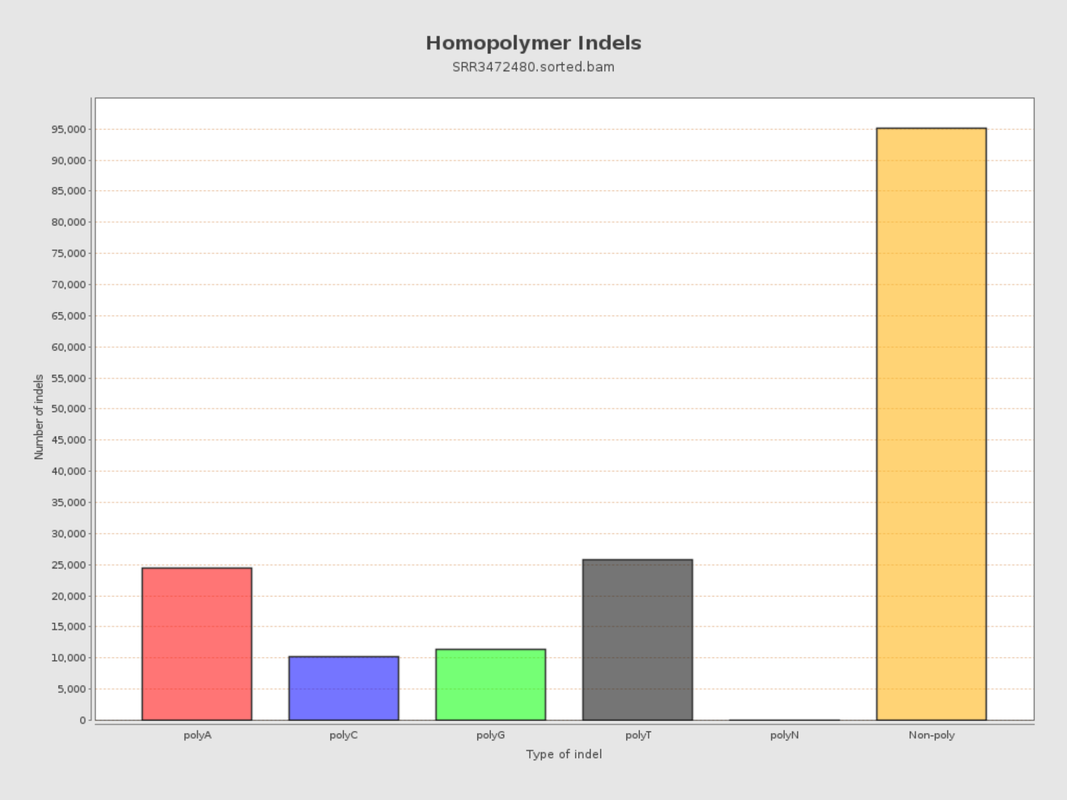
9. Results : Mapped Reads GC-content Distribution



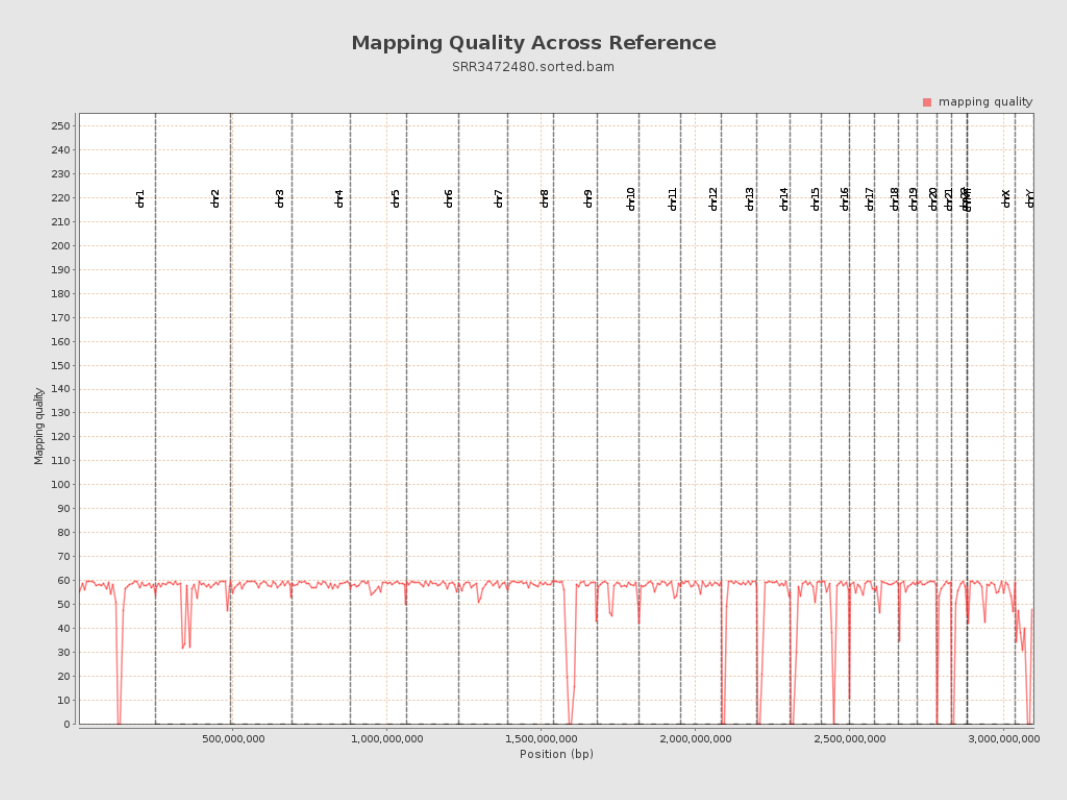
10. Results : Mapped Reads Clipping Profile



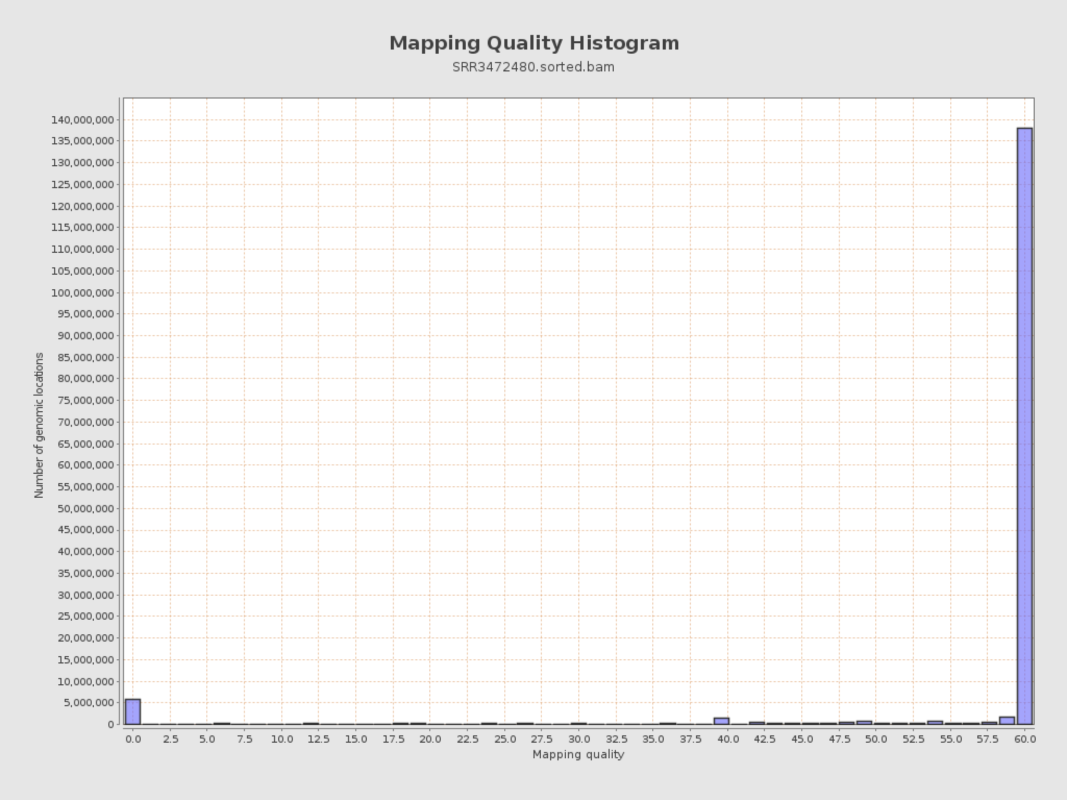
11. Results : Homopolymer Indels



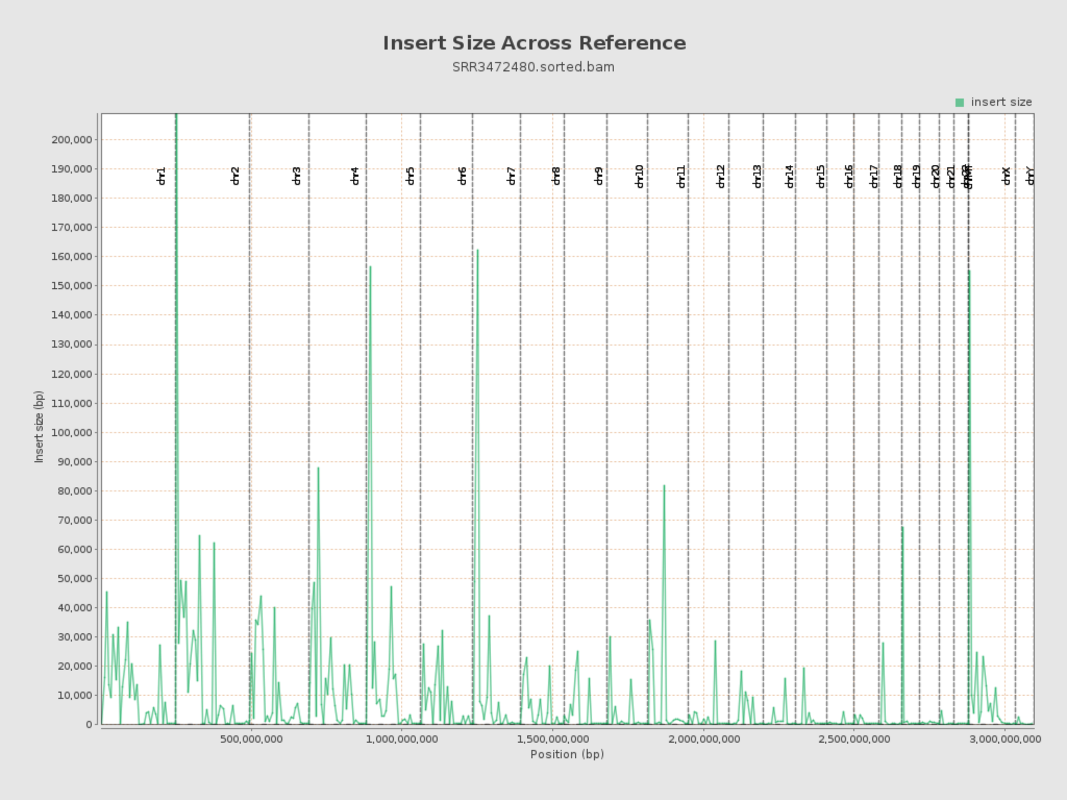
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram