Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:03:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472489.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_SRR3472489 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472489_1.fastq.gz SRR3472489_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:03:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472489.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,585,898
Mapped reads	15,413,989 / 98.9%
Unmapped reads	171,909 / 1.1%
Mapped paired reads	15,413,989 / 98.9%
Mapped reads, first in pair	7,729,426 / 49.59%
Mapped reads, second in pair	7,684,563 / 49.3%
Mapped reads, both in pair	15,322,550 / 98.31%
Mapped reads, singletons	91,439 / 0.59%
Secondary alignments	0
Supplementary alignments	68,262 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	9,821,180 / 63.01%
Duplication rate	45.94%
Clipped reads	1,234,079 / 7.92%

2.2. ACGT Content

Number/percentage of A's	432,192,097 / 28.47%
Number/percentage of C's	328,788,615 / 21.66%
Number/percentage of T's	429,566,595 / 28.29%
Number/percentage of G's	327,438,464 / 21.57%
Number/percentage of N's	237,928 / 0.02%

GC Percentage	43.22%

2.3. Coverage

Mean	0.4905
Standard Deviation	18.263

2.4. Mapping Quality

Mean Mapping Quality	55.01

2.5. Insert size

Mean	31,142.1
Standard Deviation	1,712,690.22
P25/Median/P75	175 / 245 / 331

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	9,193,898
Insertions	86,624
Mapped reads with at least one insertion	0.56%
Deletions	80,305
Mapped reads with at least one deletion	0.51%
Homopolymer indels	44.37%

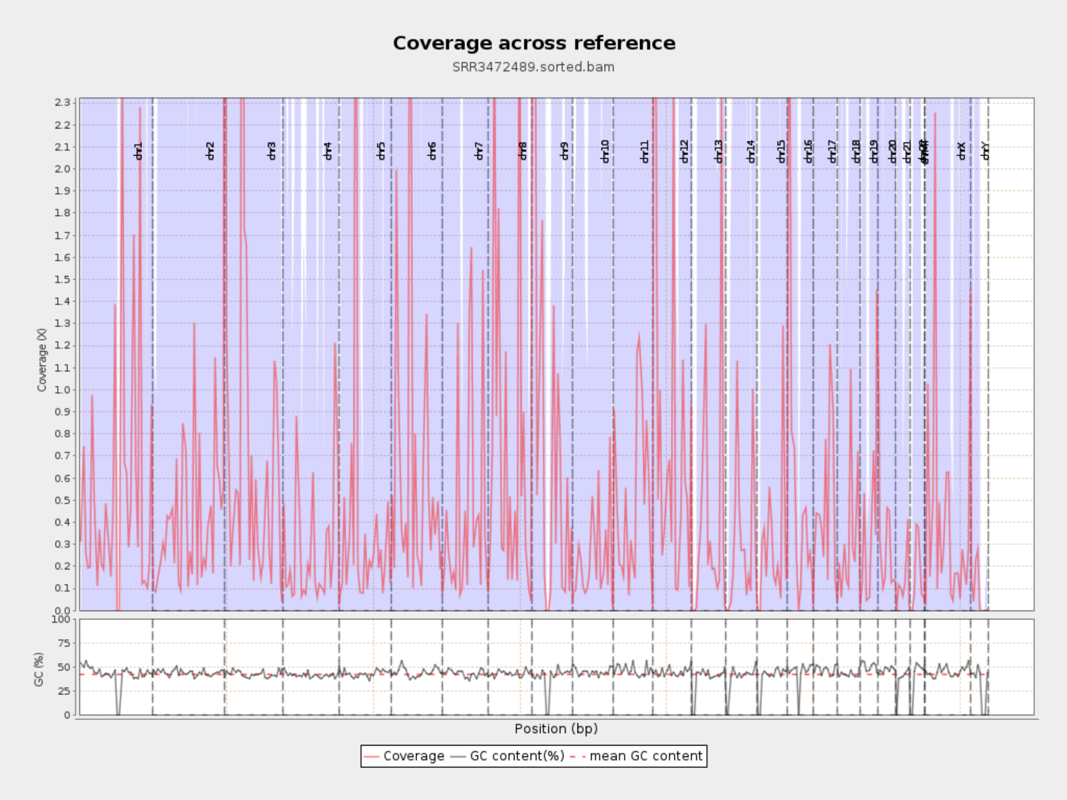
2.7. Chromosome stats

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

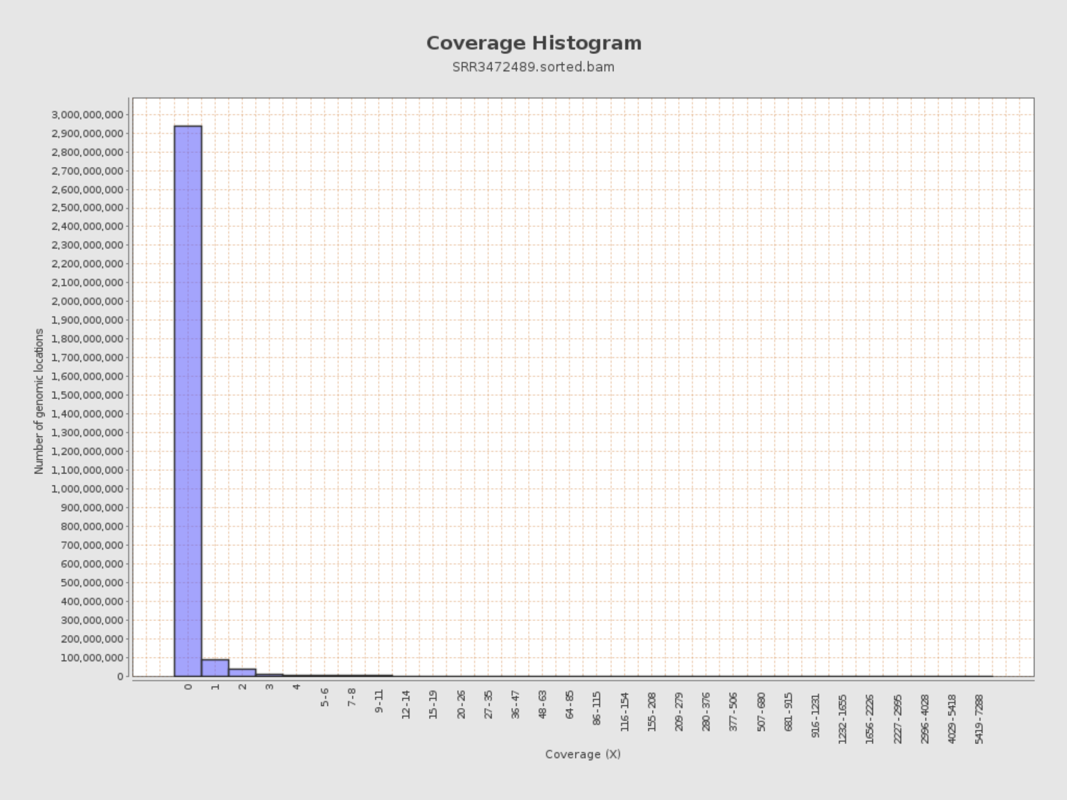
		bases	coverage	deviation
chr1	249250621	137698266	0.5524	20.2461
chr2	243199373	97962700	0.4028	14.8897
chr3	198022430	162551203	0.8209	18.87
chr4	191154276	53477284	0.2798	12.226
chr5	180915260	74560912	0.4121	16.4207
chr6	171115067	112607638	0.6581	22.3842
chr7	159138663	74672844	0.4692	17.9288
chr8	146364022	114358486	0.7813	28.2064
chr9	141213431	117216910	0.8301	23.6884
chr10	135534747	33758438	0.2491	9.5719
chr11	135006516	68301480	0.5059	17.7952
chr12	133851895	118272169	0.8836	31.4308
chr13	115169878	48918695	0.4248	25.0478
chr14	107349540	33209892	0.3094	12.4697
chr15	102531392	31358890	0.3058	11.9428
chr16	90354753	53337806	0.5903	15.1775
chr17	81195210	38112910	0.4694	13.3646
chr18	78077248	26516097	0.3396	18.0221
chr19	59128983	20346887	0.3441	9.2238
chr20	63025520	19481188	0.3091	11.7804
chr21	48129895	6425548	0.1335	4.3931
chr22	51304566	7624218	0.1486	5.0735
chrMT	16571	2808	0.1695	0.5201
chrX	155270560	62646536	0.4035	13.1634

chrY	59373566	5000932	0.0842	4.6572

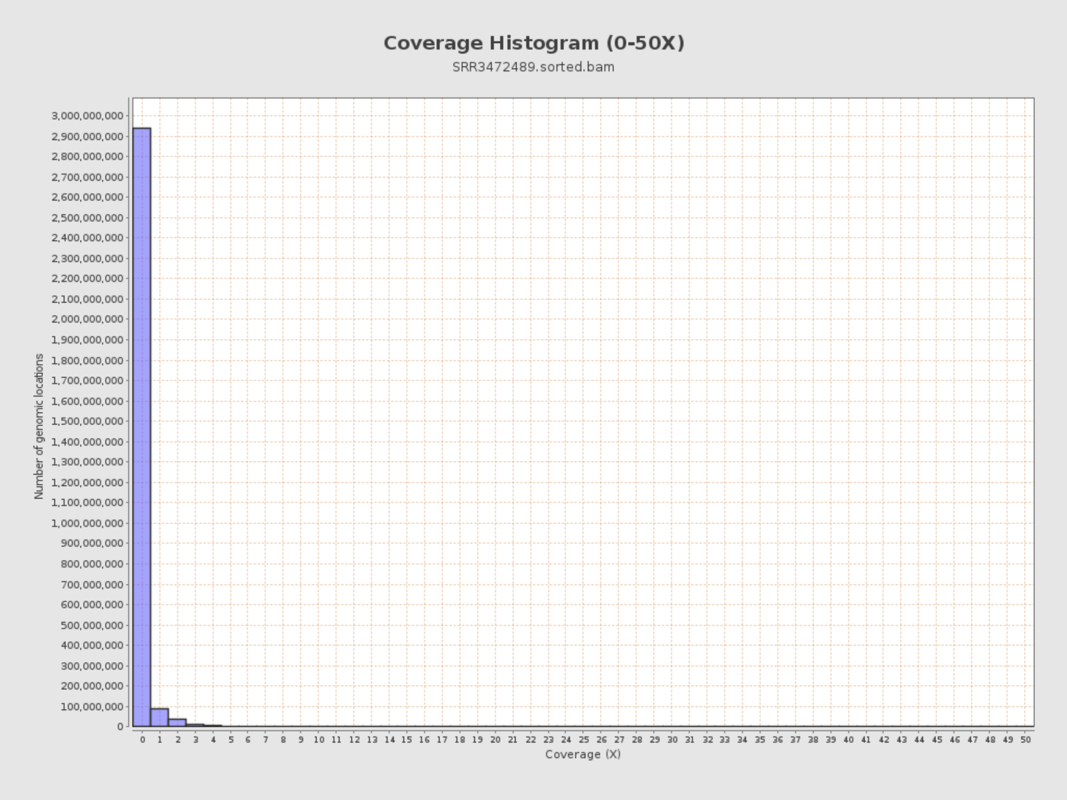
3. Results : Coverage across reference



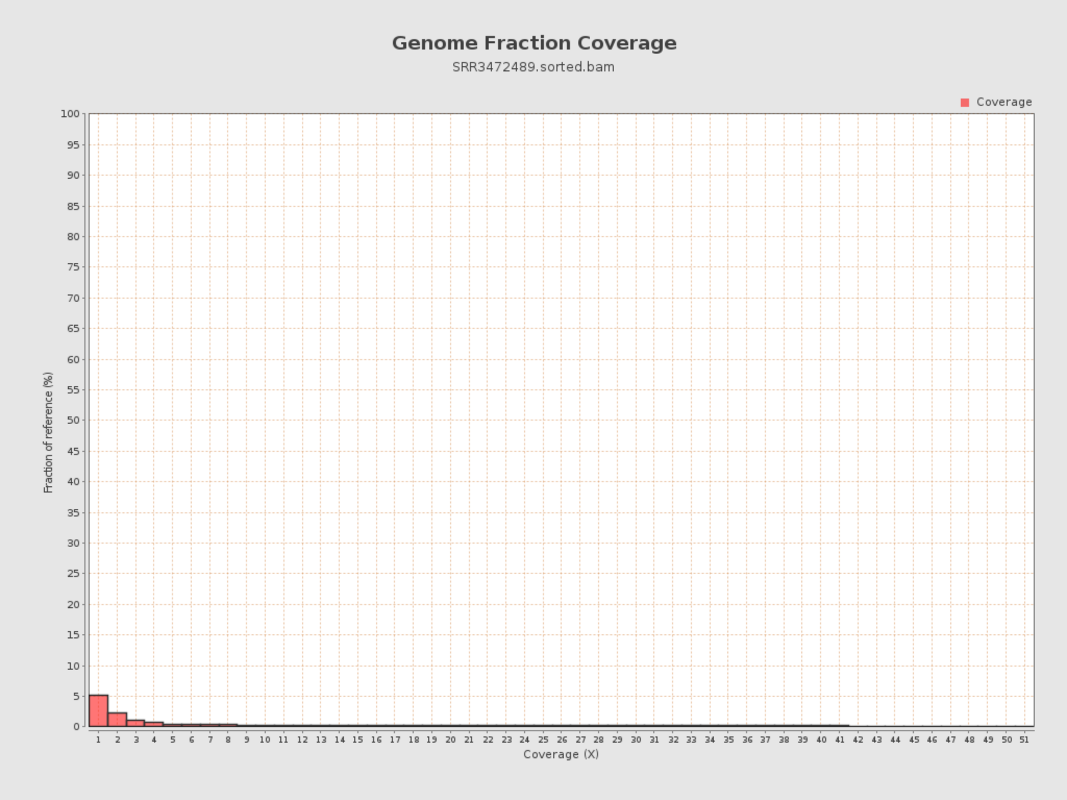
4. Results : Coverage Histogram



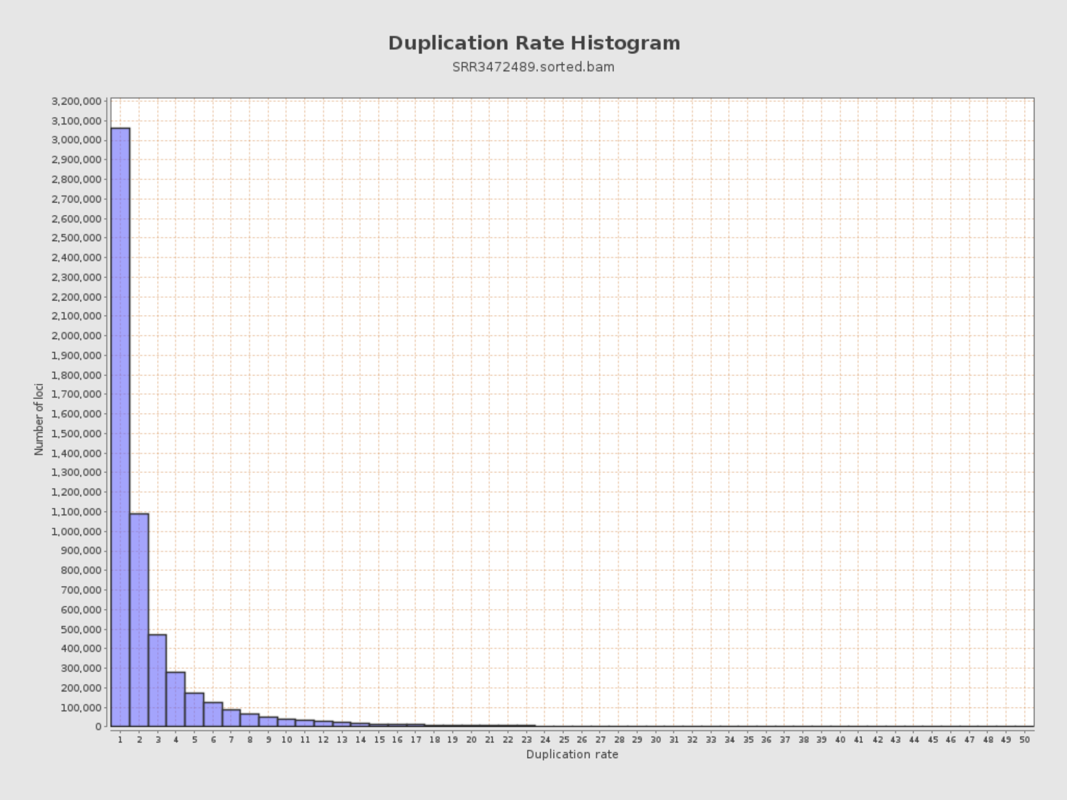
5. Results : Coverage Histogram (0-50X)



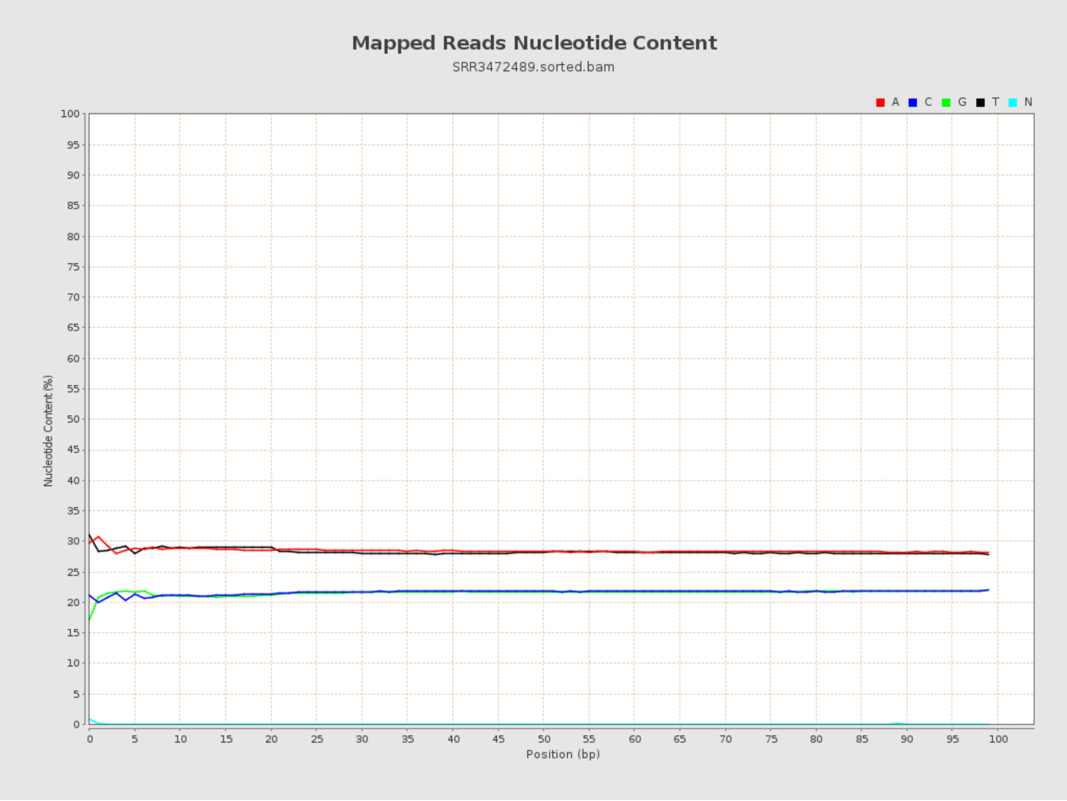
6. Results : Genome Fraction Coverage



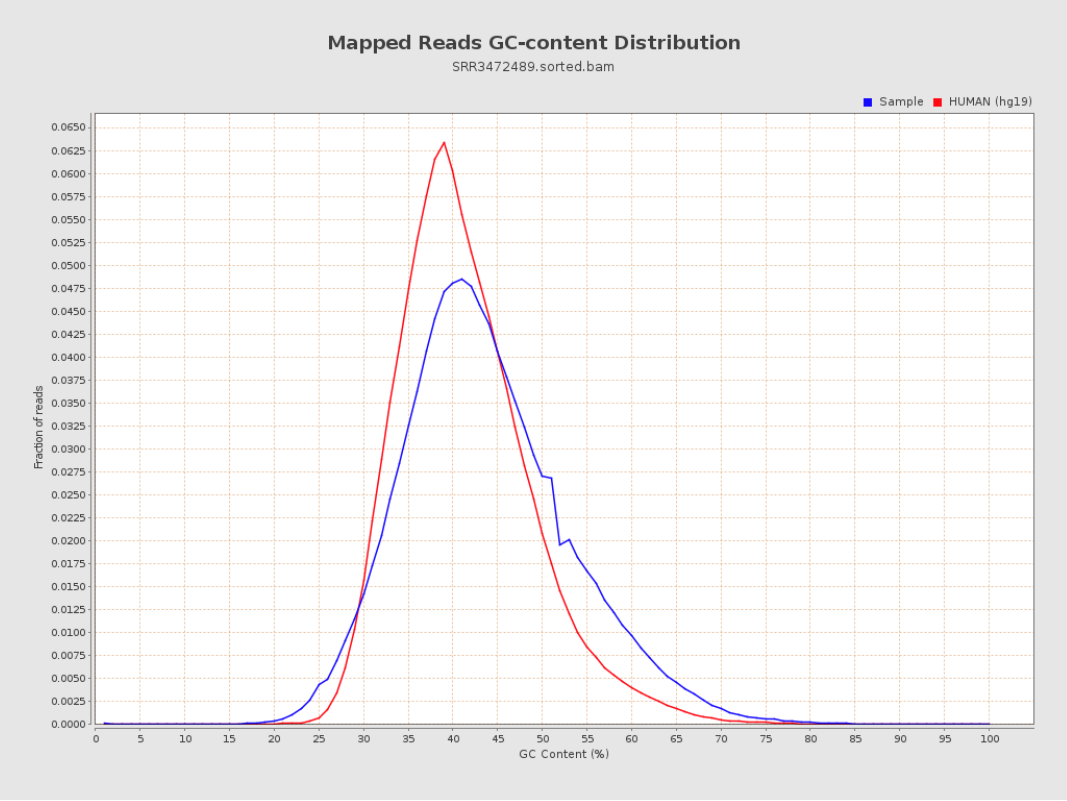
7. Results : Duplication Rate Histogram



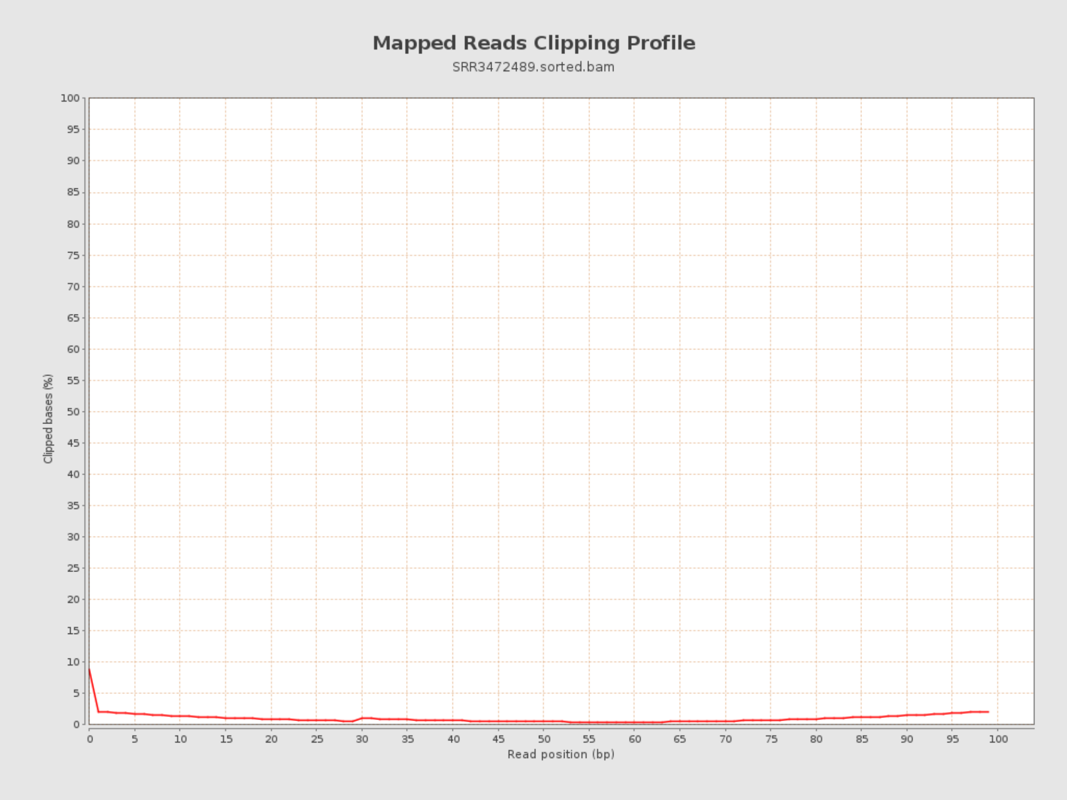
8. Results : Mapped Reads Nucleotide Content



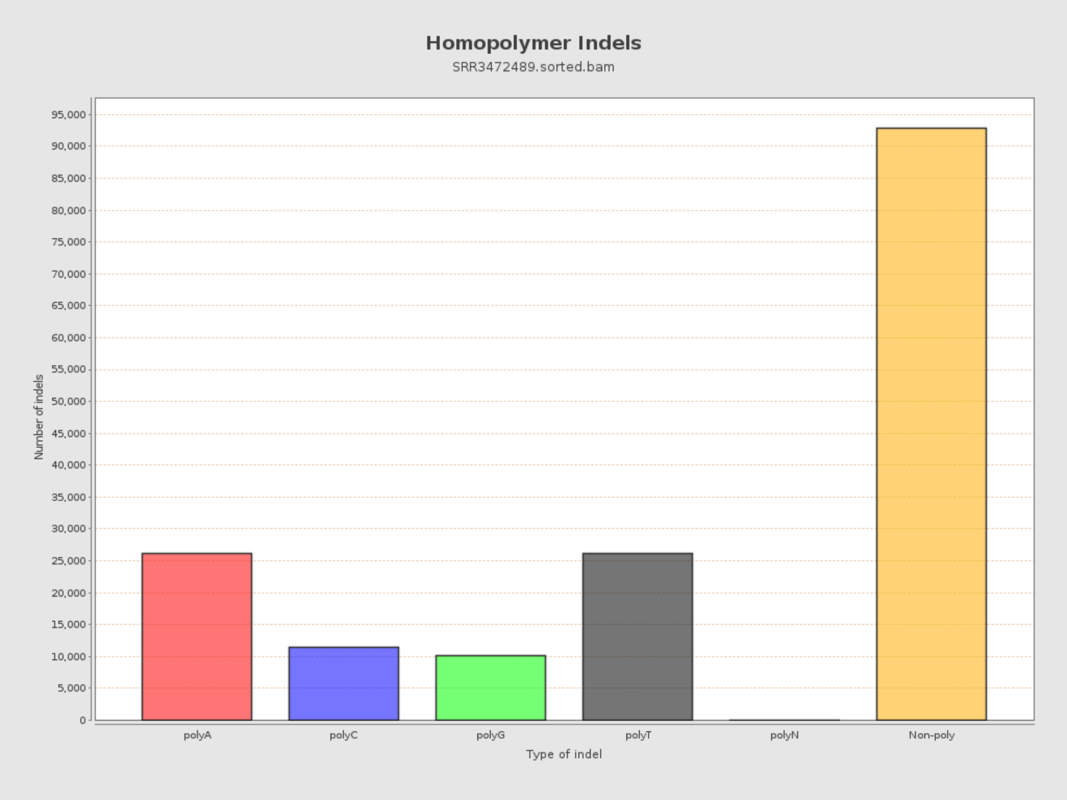
9. Results : Mapped Reads GC-content Distribution



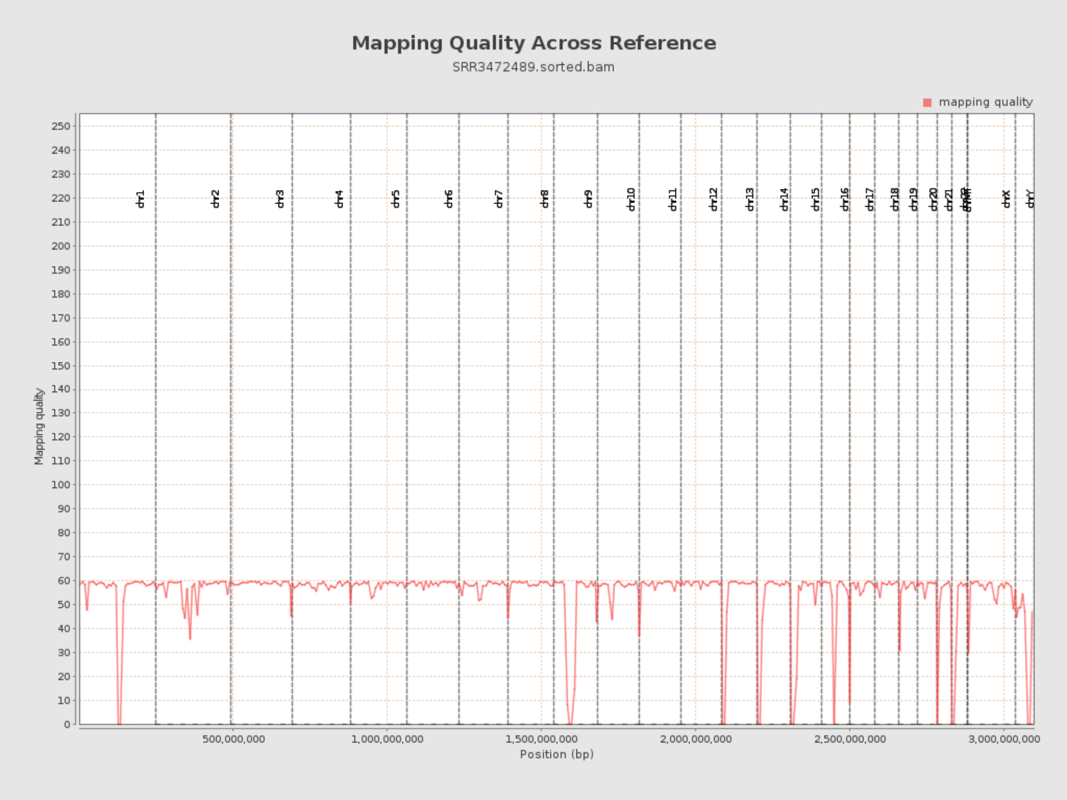
10. Results : Mapped Reads Clipping Profile



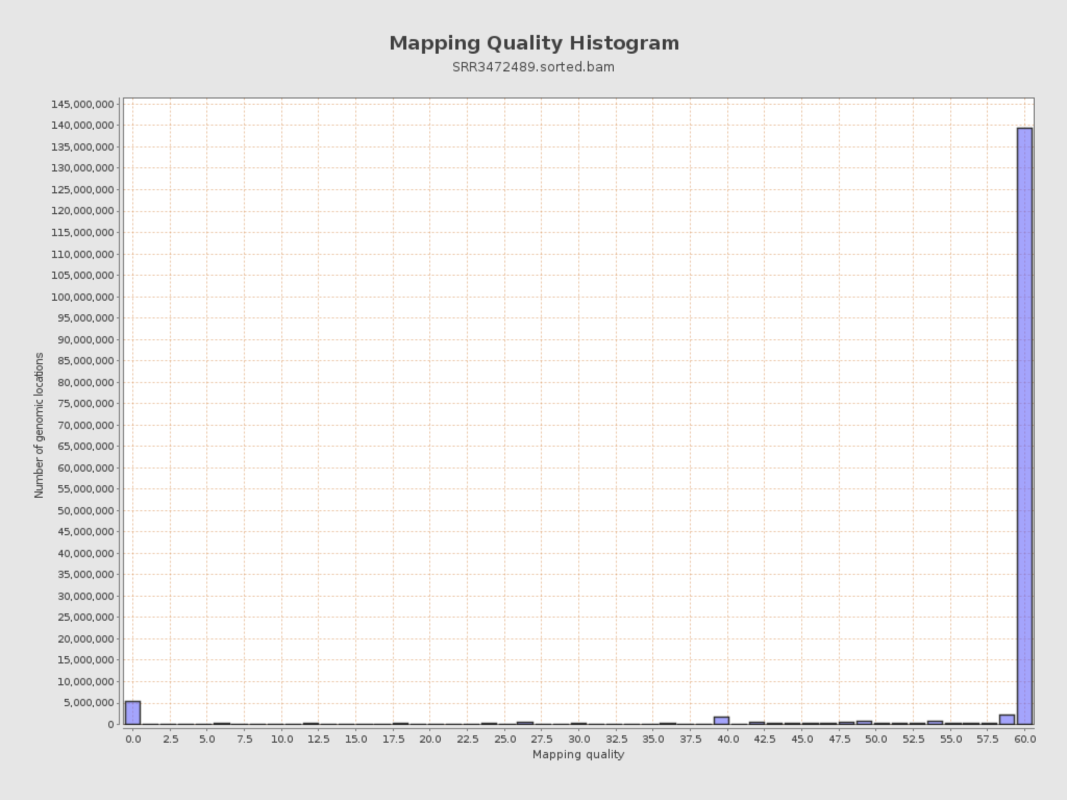
11. Results : Homopolymer Indels



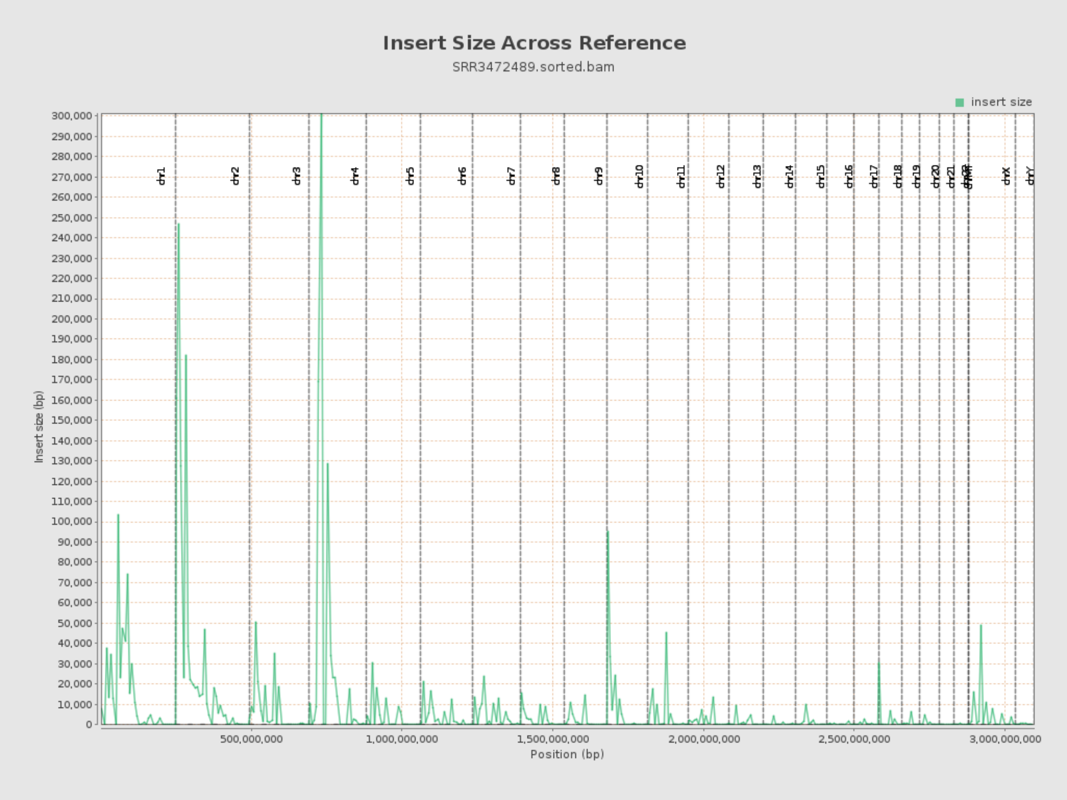
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram