Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 08:47:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472483.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_SRR3472483 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472483_1.fastq.gz SRR3472483_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 08:47:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472483.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,359,664
Mapped reads	17,109,278 / 98.56%
Unmapped reads	250,386 / 1.44%
Mapped paired reads	17,109,278 / 98.56%
Mapped reads, first in pair	8,592,349 / 49.5%
Mapped reads, second in pair	8,516,929 / 49.06%
Mapped reads, both in pair	16,976,064 / 97.79%
Mapped reads, singletons	133,214 / 0.77%
Secondary alignments	0
Supplementary alignments	58,075 / 0.33%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	10,801,656 / 62.22%
Duplication rate	45.18%
Clipped reads	1,590,704 / 9.16%

2.2. ACGT Content

Number/percentage of A's	463,811,525 / 27.64%
Number/percentage of C's	378,132,608 / 22.53%
Number/percentage of T's	460,661,638 / 27.45%
Number/percentage of G's	375,466,256 / 22.37%
Number/percentage of N's	259,514 / 0.02%

GC Percentage	44.9%

2.3. Coverage

Mean	0.5422
Standard Deviation	20.4004

2.4. Mapping Quality

Mean Mapping Quality	54.91

2.5. Insert size

Mean	27,920.26
Standard Deviation	1,626,238.98
P25/Median/P75	160 / 226 / 306

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	10,035,764
Insertions	90,142
Mapped reads with at least one insertion	0.52%
Deletions	91,192
Mapped reads with at least one deletion	0.53%
Homopolymer indels	44.74%

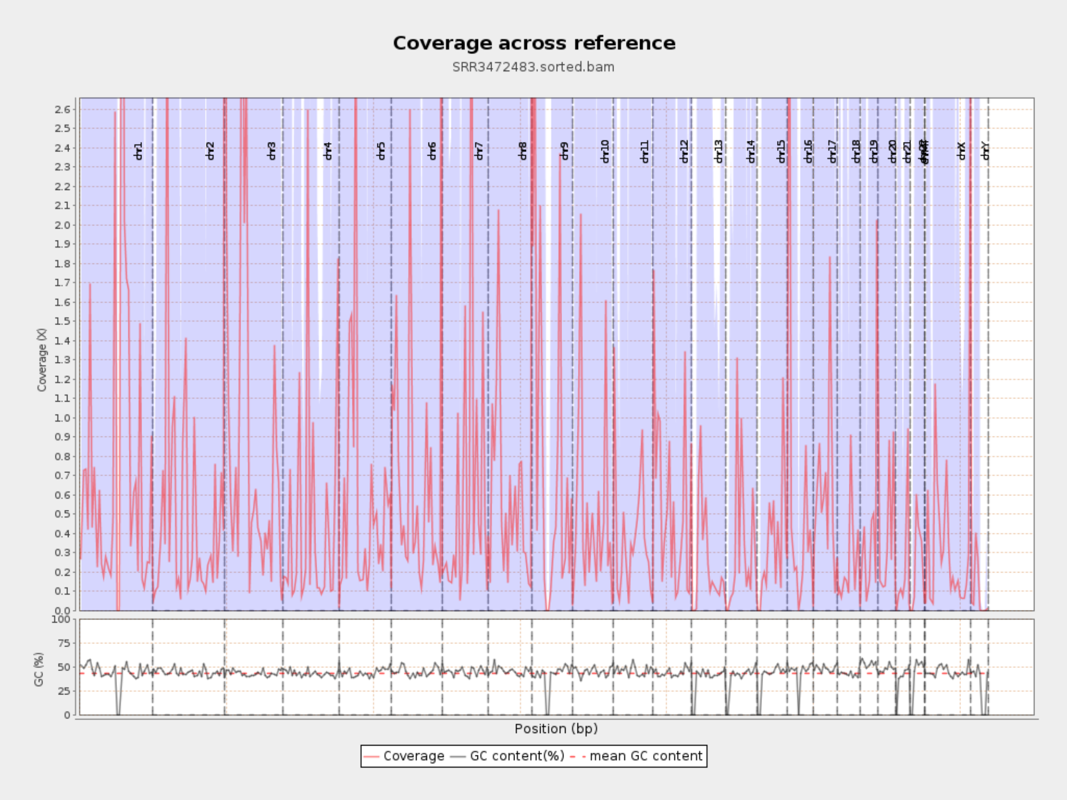
2.7. Chromosome stats

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

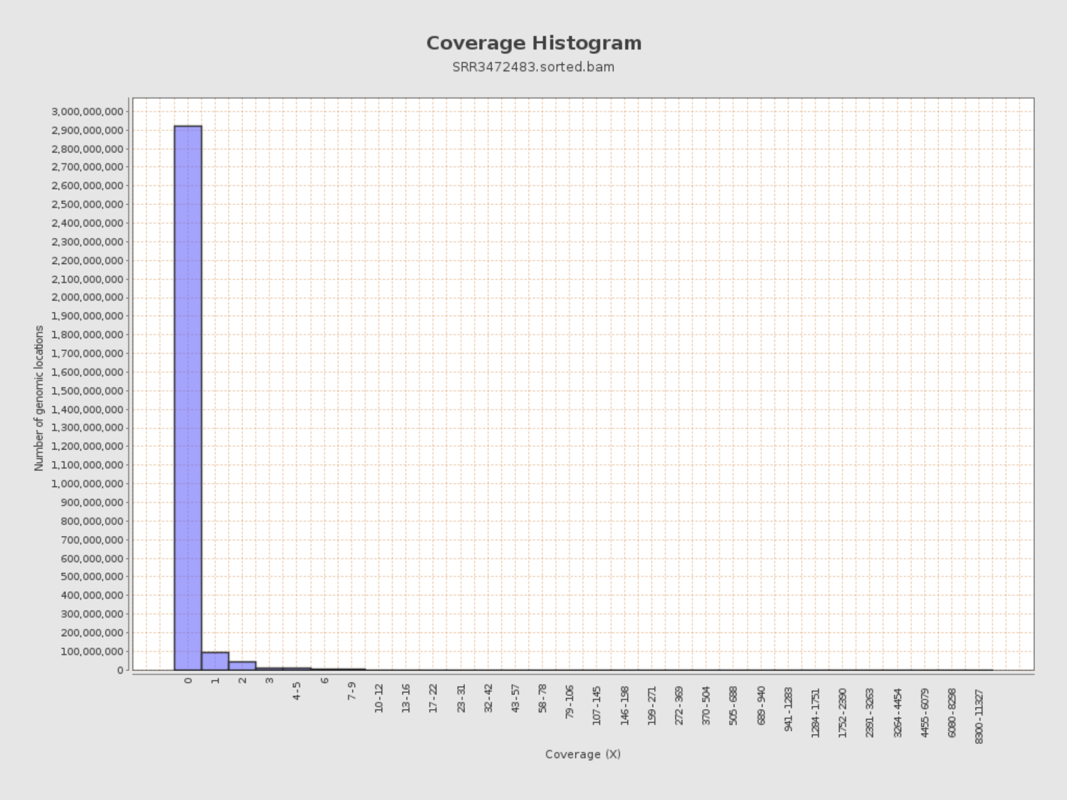
		bases	coverage	deviation
chr1	249250621	198864572	0.7978	32.259
chr2	243199373	120244167	0.4944	29.1798
chr3	198022430	191525803	0.9672	21.3856
chr4	191154276	86834407	0.4543	20.7969
chr5	180915260	108776151	0.6013	18.7568
chr6	171115067	116948828	0.6835	20.7008
chr7	159138663	101691428	0.639	21.1708
chr8	146364022	84805553	0.5794	18.4194
chr9	141213431	118859896	0.8417	21.1124
chr10	135534747	71496961	0.5275	28.3261
chr11	135006516	51391114	0.3807	15.3382
chr12	133851895	75419771	0.5635	19.8876
chr13	115169878	28941093	0.2513	7.8921
chr14	107349540	34541452	0.3218	11.0977
chr15	102531392	36330470	0.3543	12.1849
chr16	90354753	53976079	0.5974	18.6974
chr17	81195210	49190226	0.6058	12.8914
chr18	78077248	20651084	0.2645	9.4384
chr19	59128983	20017394	0.3385	9.8363
chr20	63025520	25814988	0.4096	13.6381
chr21	48129895	10829844	0.225	9.5337
chr22	51304566	12407196	0.2418	9.258
chrMT	16571	1752	0.1057	0.399
chrX	155270560	53222432	0.3428	10.9973

chrY	59373566	5789522	0.0975	5.0666

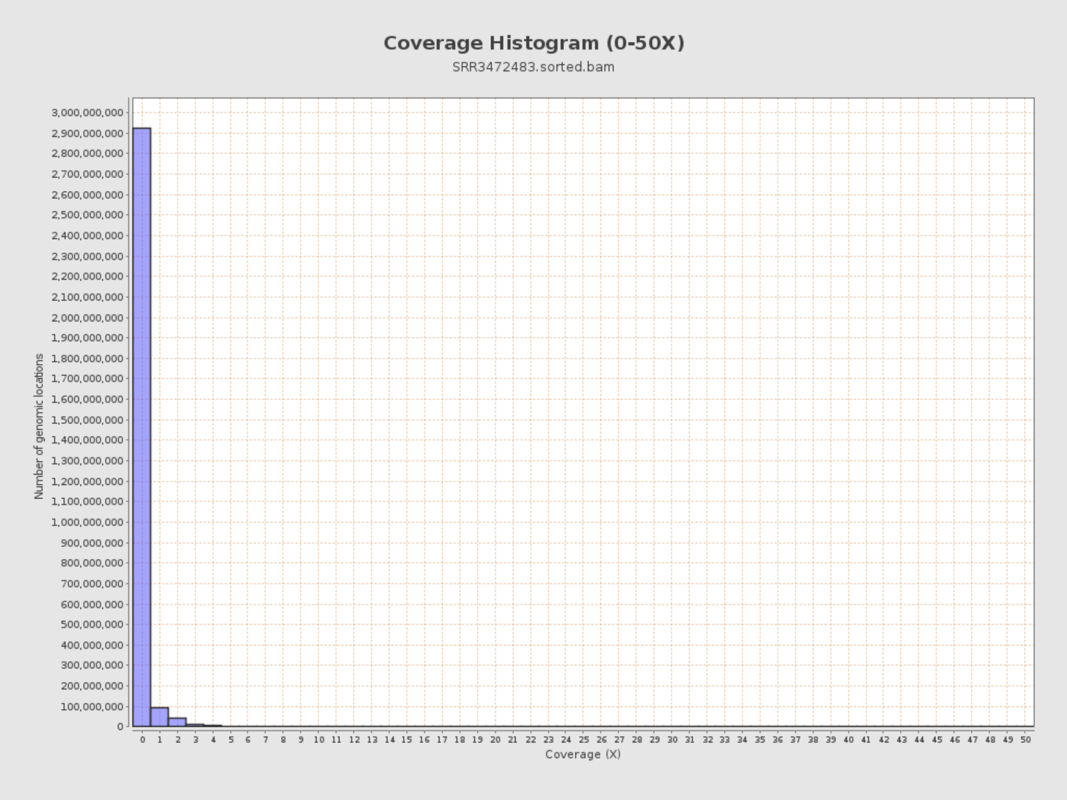
3. Results : Coverage across reference



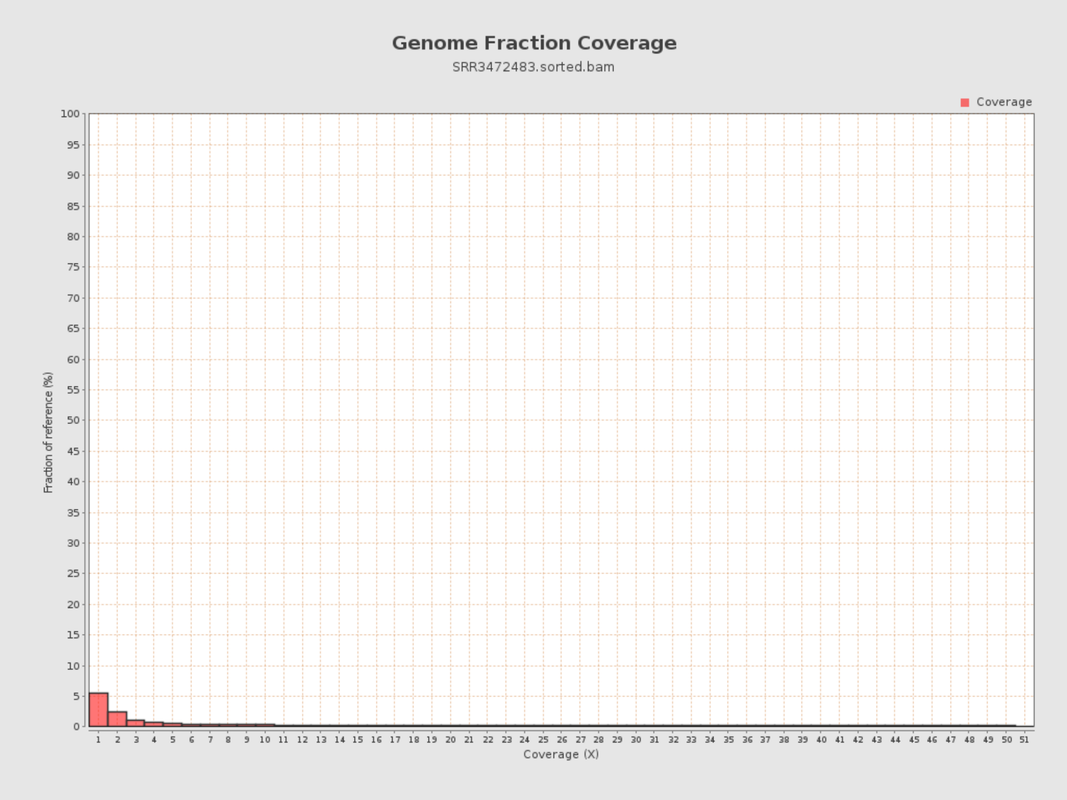
4. Results : Coverage Histogram



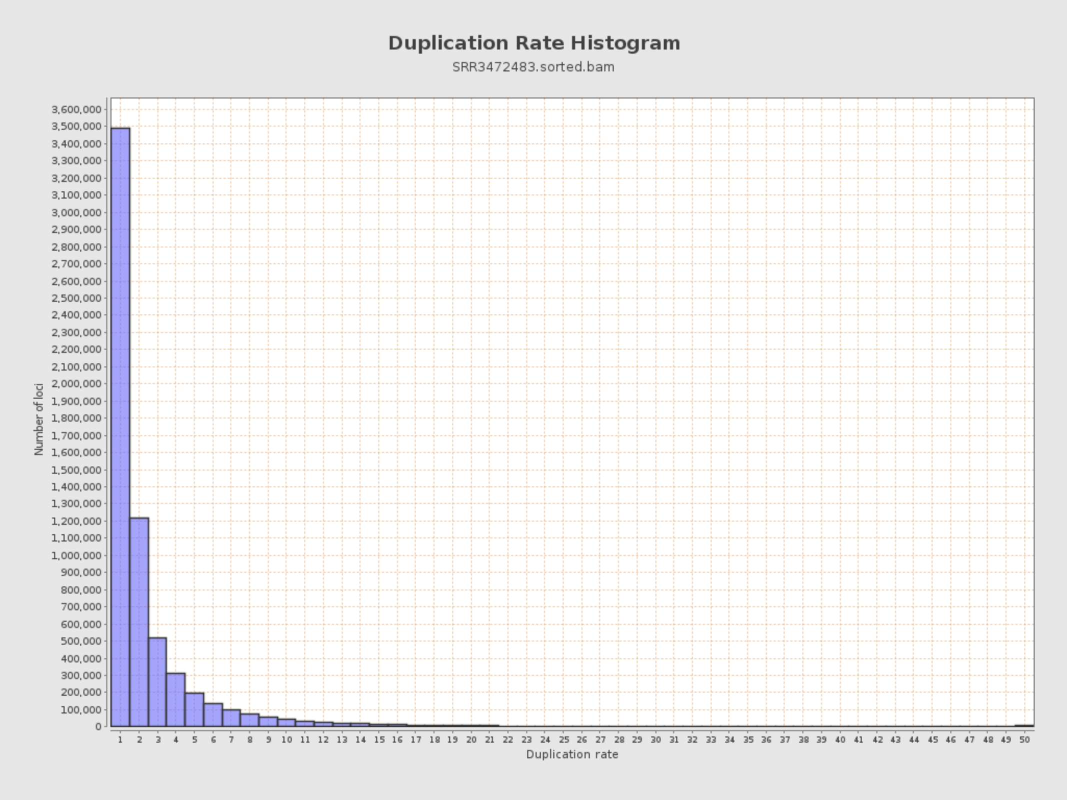
5. Results : Coverage Histogram (0-50X)



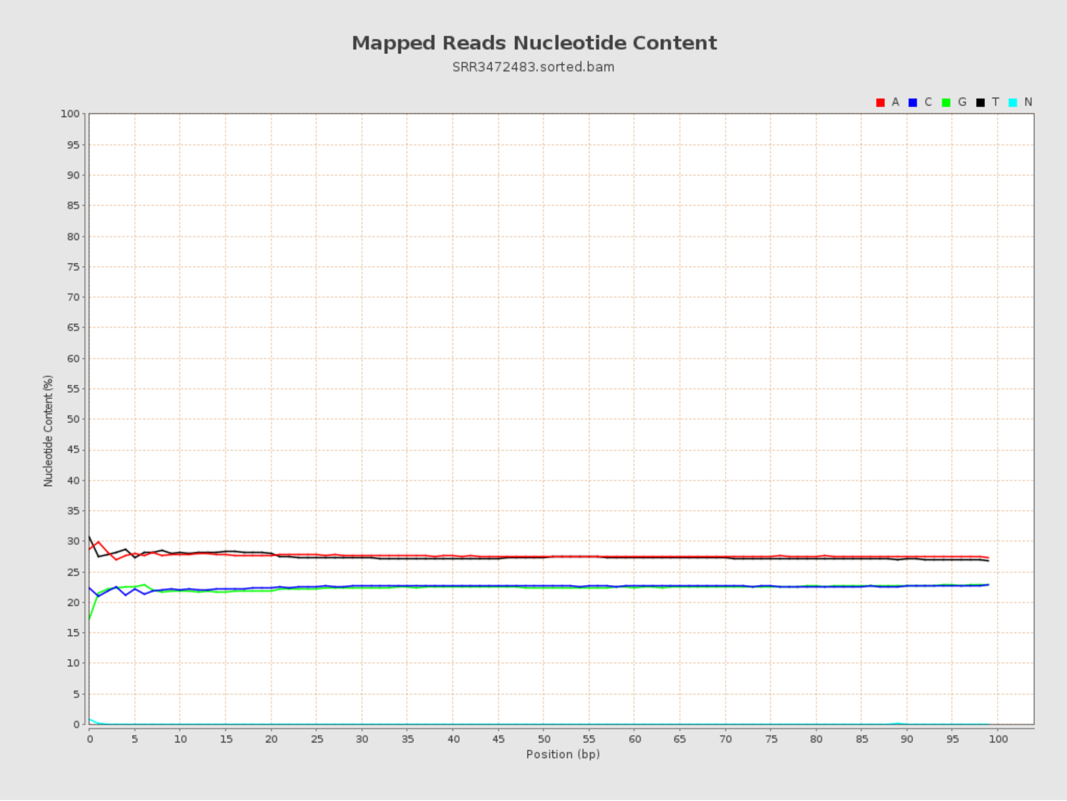
6. Results : Genome Fraction Coverage



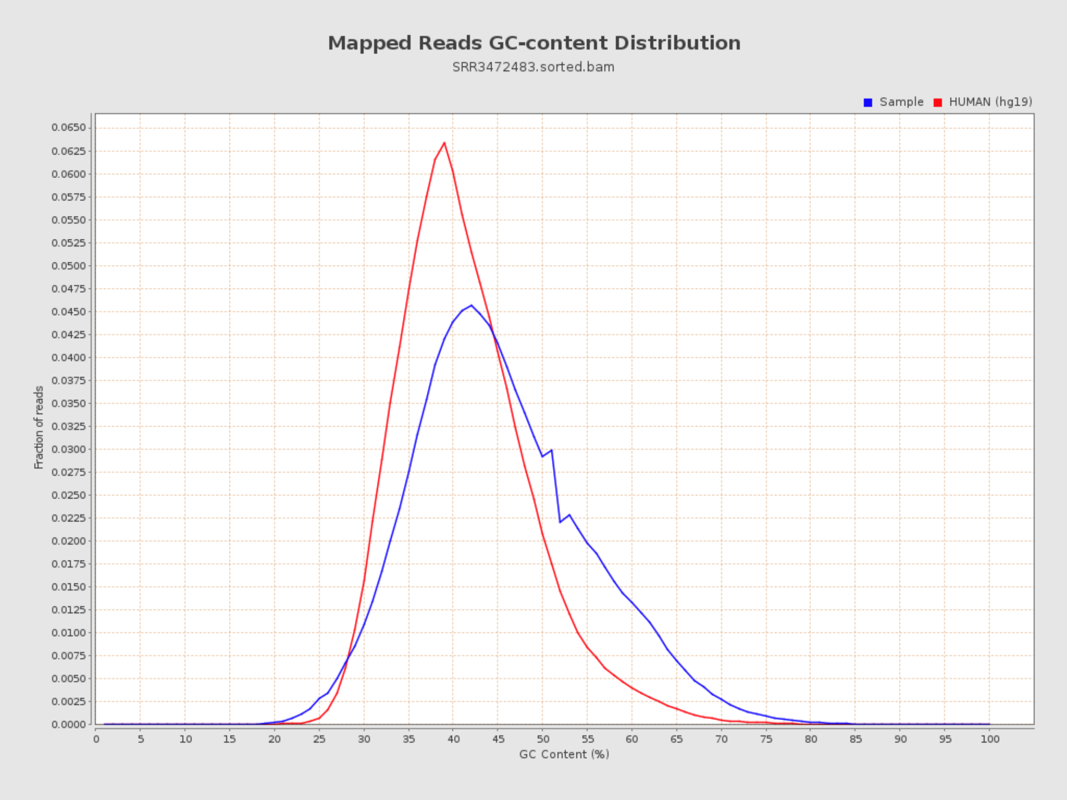
7. Results : Duplication Rate Histogram



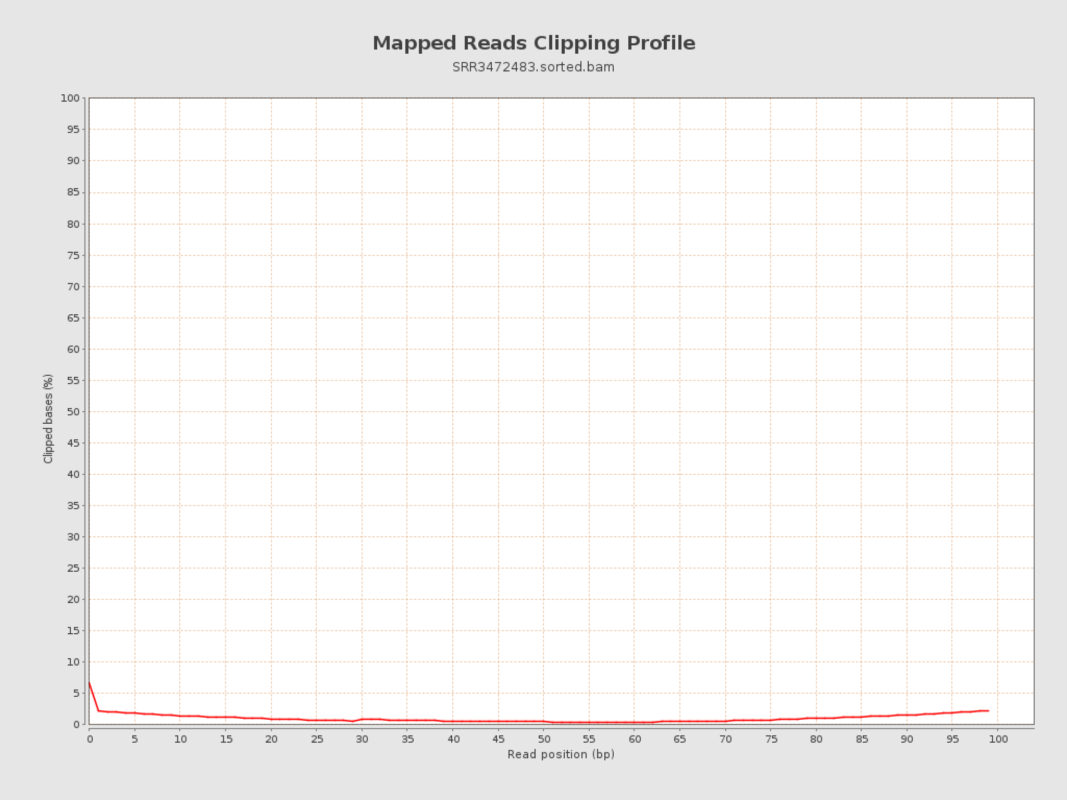
8. Results : Mapped Reads Nucleotide Content



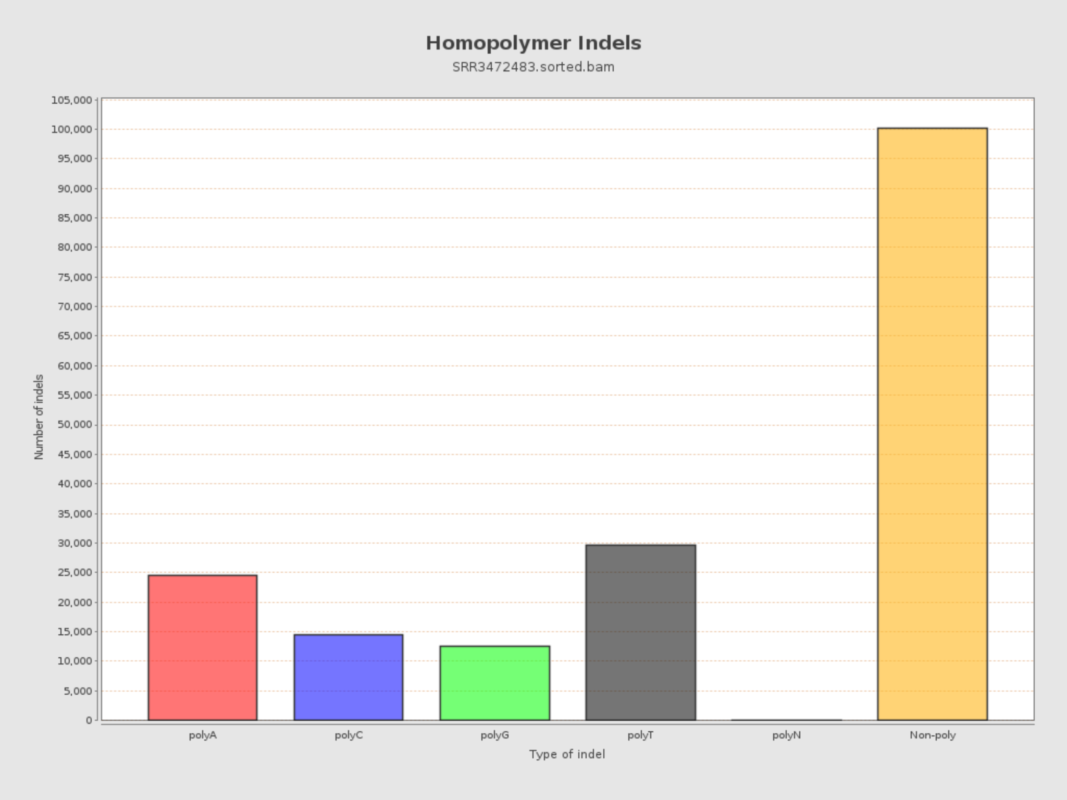
9. Results : Mapped Reads GC-content Distribution



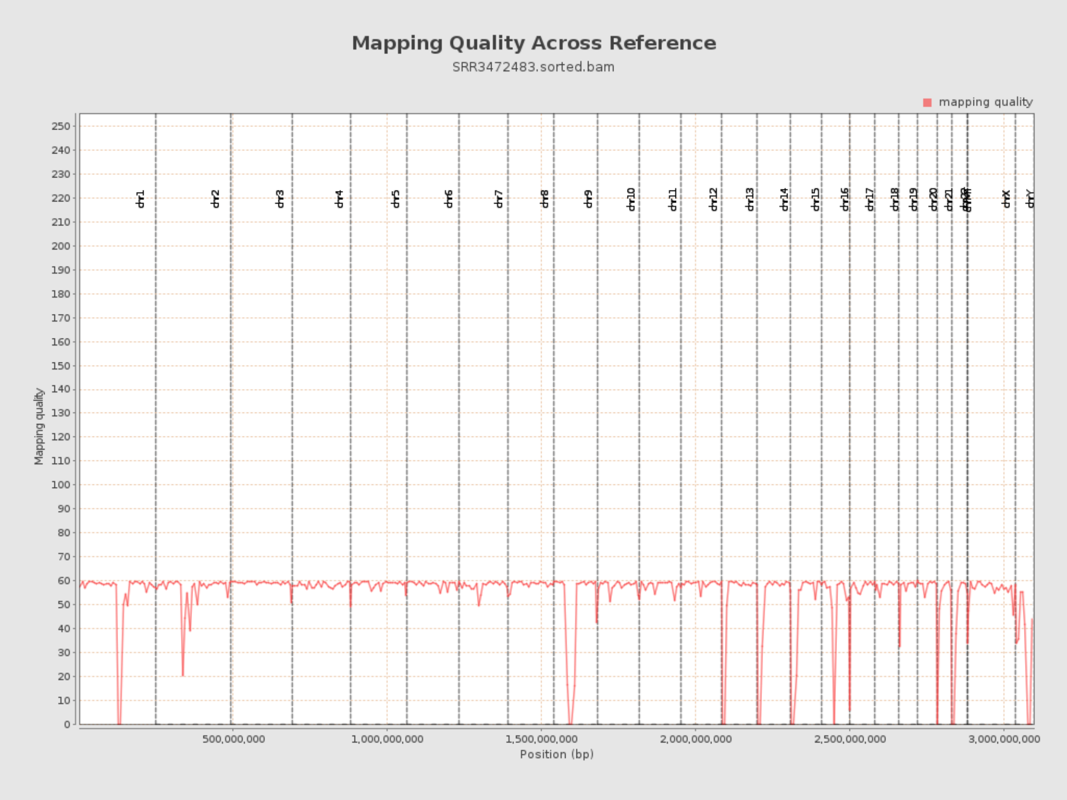
10. Results : Mapped Reads Clipping Profile



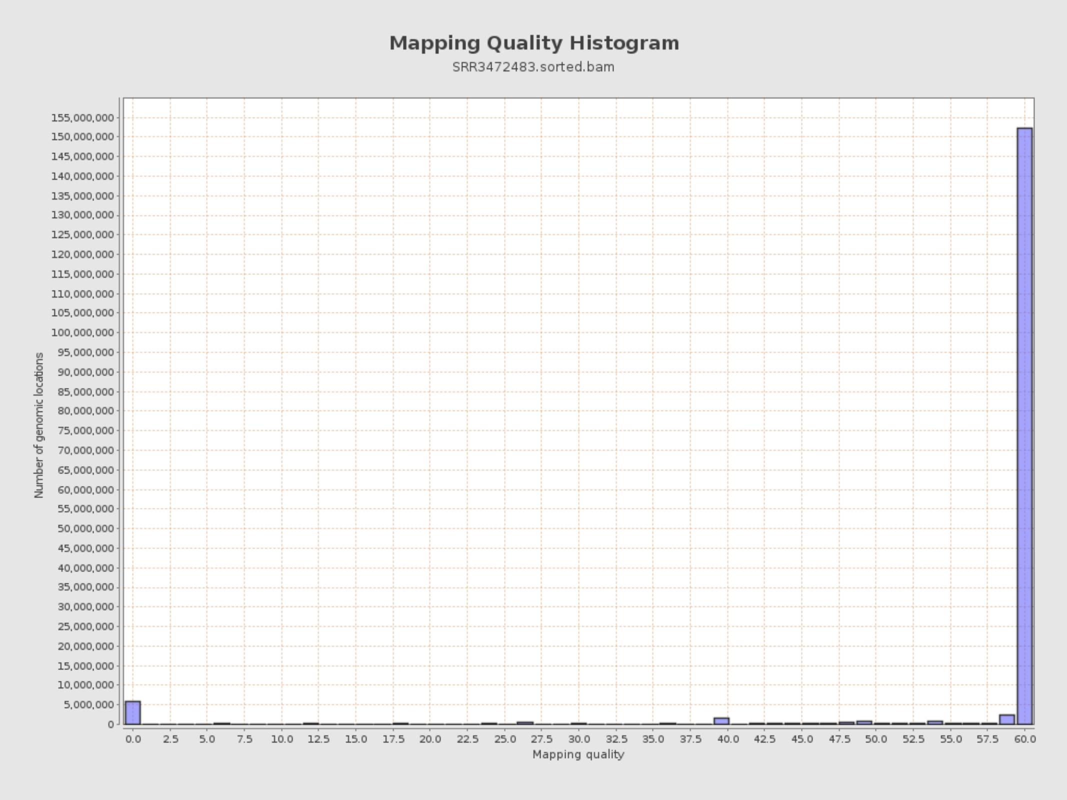
11. Results : Homopolymer Indels



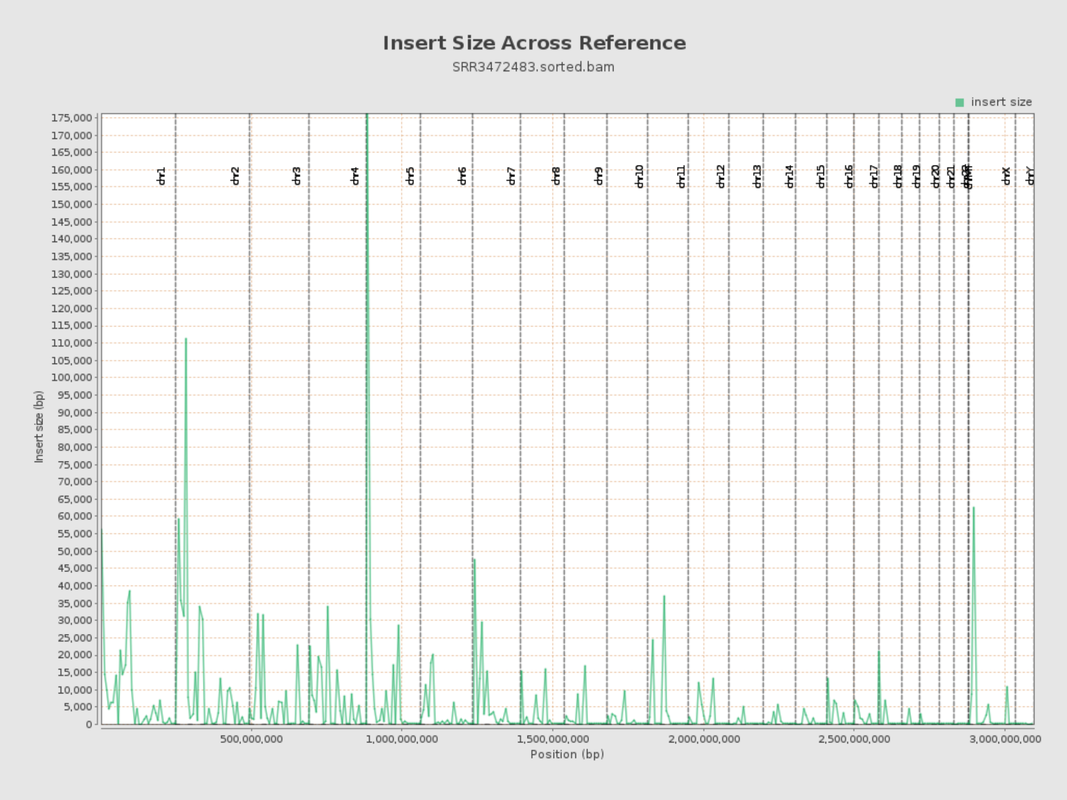
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram