Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:05:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472478.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_SRR3472478 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472478_1.fastq.gz SRR3472478_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:05:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472478.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,015,494
Mapped reads	14,637,987 / 97.49%
Unmapped reads	377,507 / 2.51%
Mapped paired reads	14,637,987 / 97.49%
Mapped reads, first in pair	7,350,866 / 48.96%
Mapped reads, second in pair	7,287,121 / 48.53%
Mapped reads, both in pair	14,528,464 / 96.76%
Mapped reads, singletons	109,523 / 0.73%
Secondary alignments	0
Supplementary alignments	73,959 / 0.49%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	9,509,136 / 63.33%
Duplication rate	43.8%
Clipped reads	1,349,989 / 8.99%

2.2. ACGT Content

Number/percentage of A's	415,570,068 / 28.9%
Number/percentage of C's	304,872,012 / 21.2%
Number/percentage of T's	413,099,300 / 28.73%
Number/percentage of G's	304,143,368 / 21.15%
Number/percentage of N's	221,678 / 0.02%

GC Percentage	42.35%

2.3. Coverage

Mean	0.4645
Standard Deviation	22.4934

2.4. Mapping Quality

Mean Mapping Quality	54.75

2.5. Insert size

Mean	40,634.08
Standard Deviation	1,932,113.94
P25/Median/P75	169 / 239 / 325

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	8,948,924
Insertions	78,476
Mapped reads with at least one insertion	0.53%
Deletions	71,648
Mapped reads with at least one deletion	0.48%
Homopolymer indels	43.4%

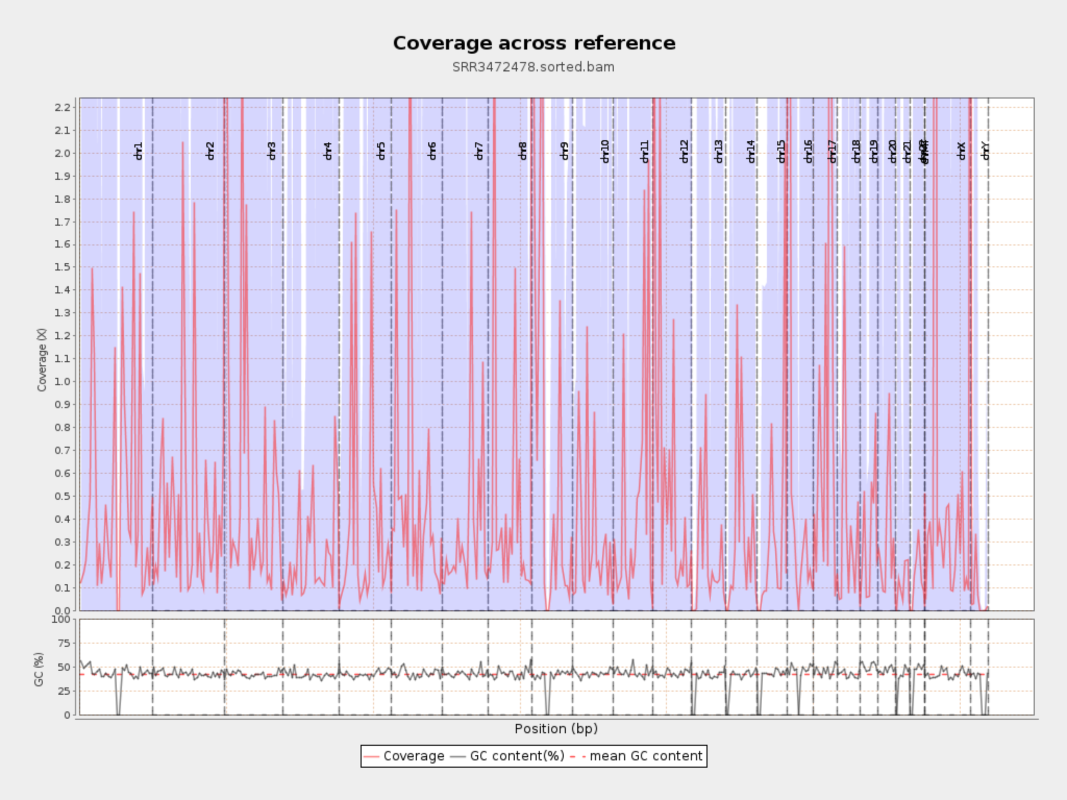
2.7. Chromosome stats

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

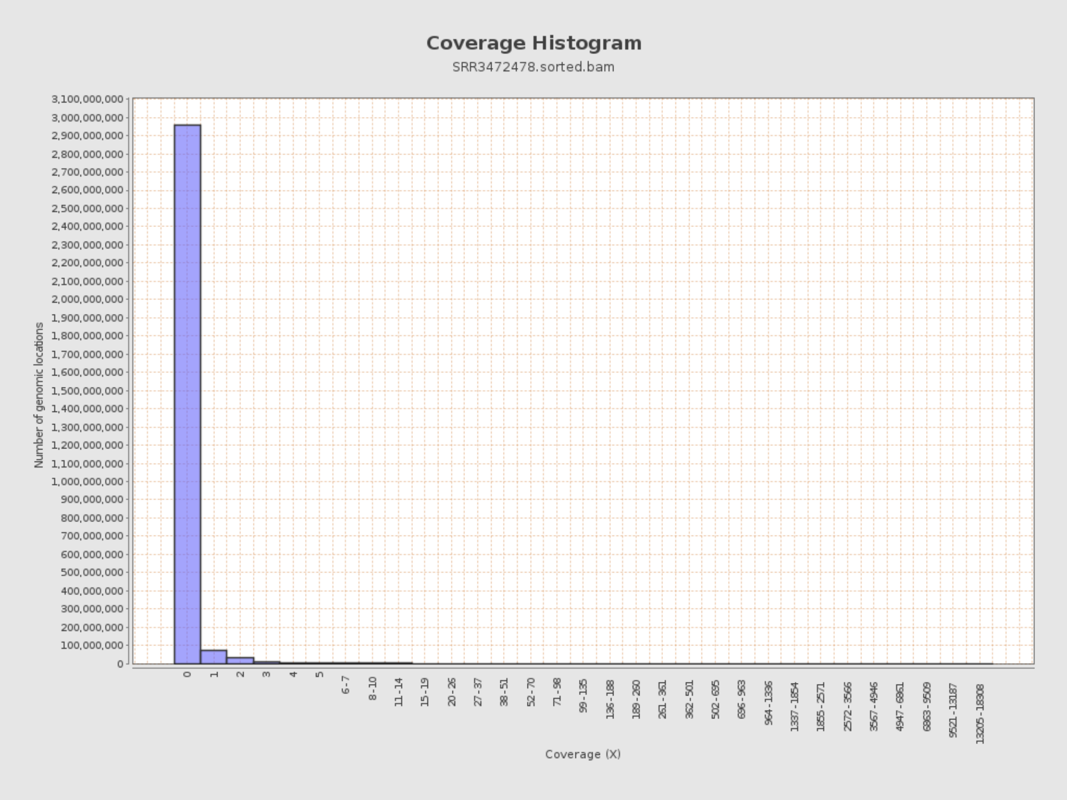
		bases	coverage	deviation
chr1	249250621	121965454	0.4893	18.2835
chr2	243199373	105064373	0.432	29.7087
chr3	198022430	130810190	0.6606	23.3608
chr4	191154276	45896832	0.2401	10.4039
chr5	180915260	71331517	0.3943	16.9395
chr6	171115067	87974255	0.5141	18.3956
chr7	159138663	58835333	0.3697	15.4964
chr8	146364022	68038117	0.4649	24.2956
chr9	141213431	111822153	0.7919	38.139
chr10	135534747	45313583	0.3343	17.107
chr11	135006516	68007834	0.5037	19.1802
chr12	133851895	89363528	0.6676	27.5729
chr13	115169878	27207868	0.2362	9.359
chr14	107349540	35775962	0.3333	14.0263
chr15	102531392	38490662	0.3754	17.4954
chr16	90354753	65272453	0.7224	24.3631
chr17	81195210	75013872	0.9239	41.1821
chr18	78077248	26726318	0.3423	22.1667
chr19	59128983	21679944	0.3667	12.8303
chr20	63025520	20094554	0.3188	10.8232
chr21	48129895	5758386	0.1196	6.0802
chr22	51304566	7344737	0.1432	6.8798
chrMT	16571	8473	0.5113	1.4282
chrX	155270560	106650204	0.6869	35.3305

chrY	59373566	3624863	0.0611	4.2786

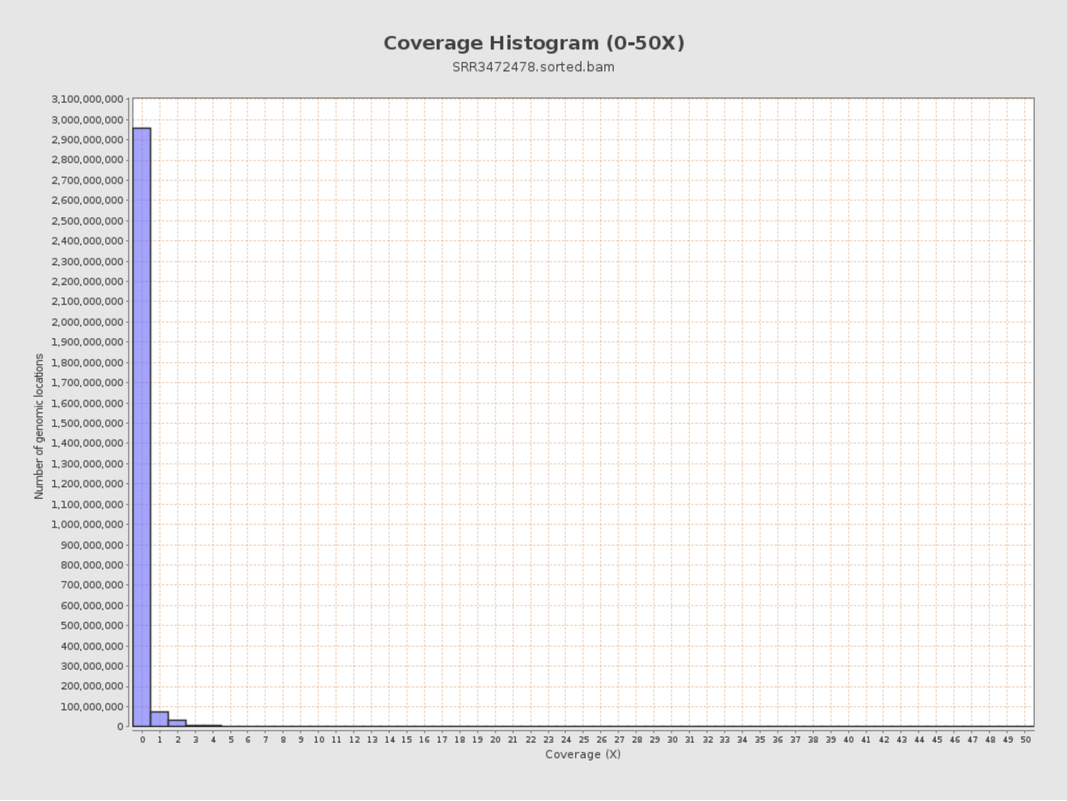
3. Results : Coverage across reference



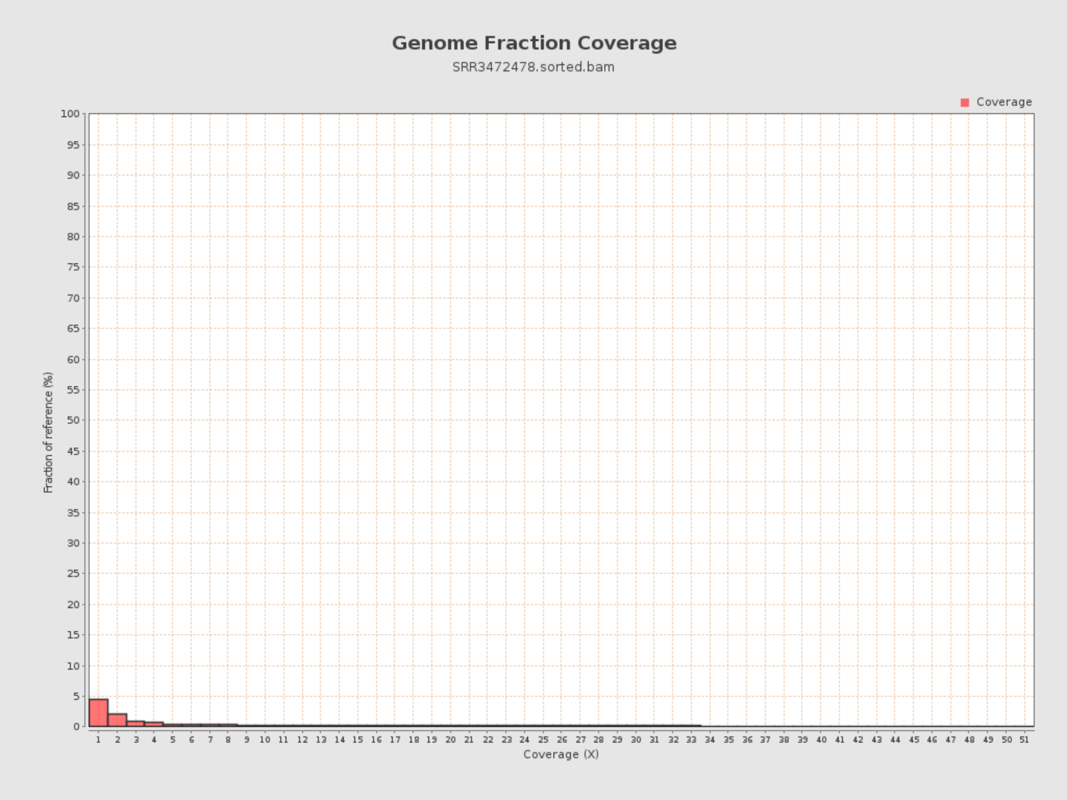
4. Results : Coverage Histogram



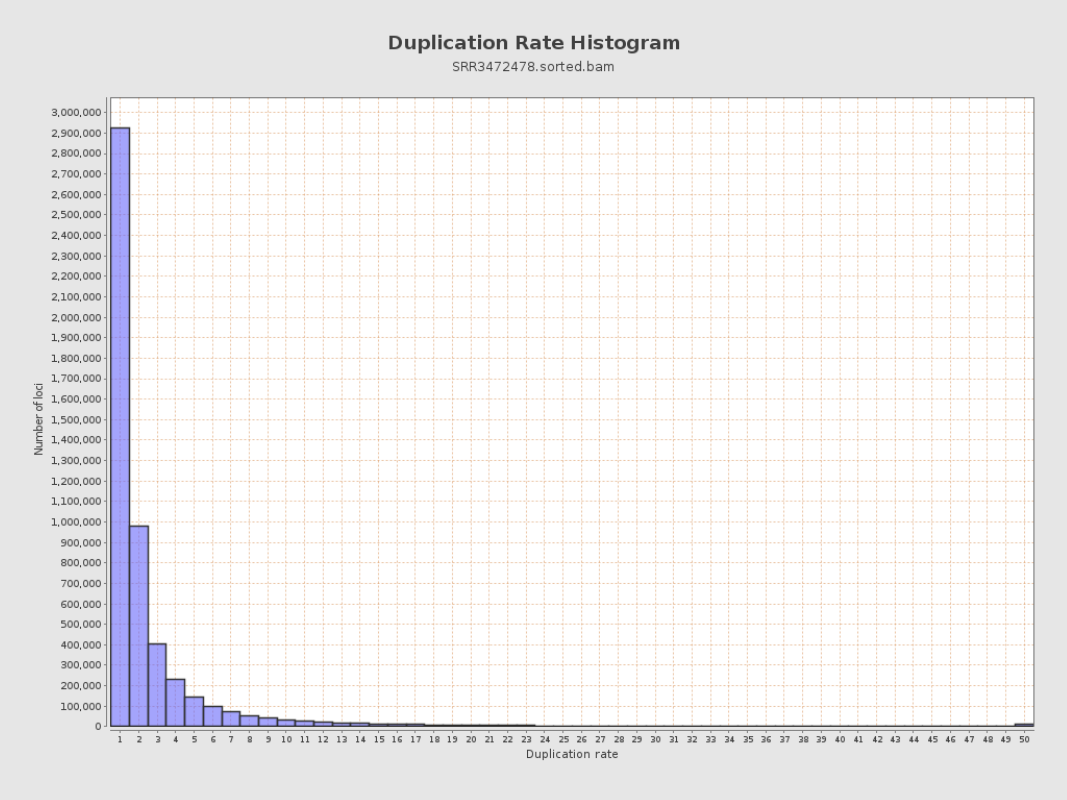
5. Results : Coverage Histogram (0-50X)



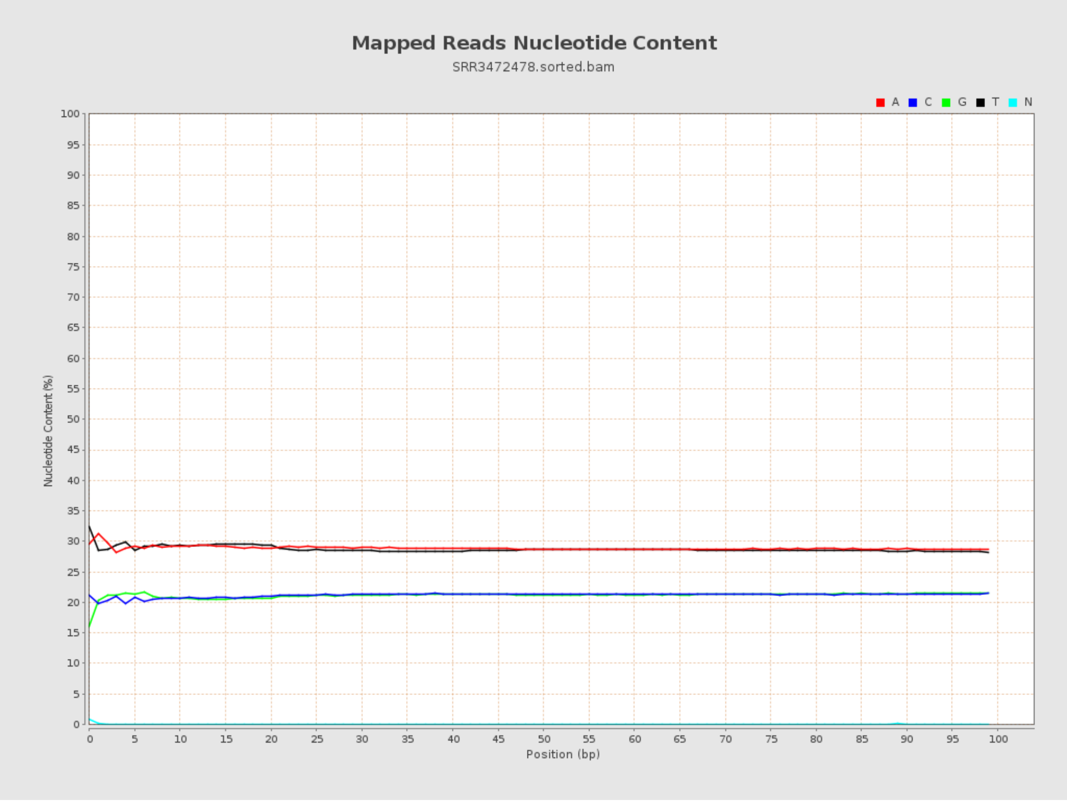
6. Results : Genome Fraction Coverage



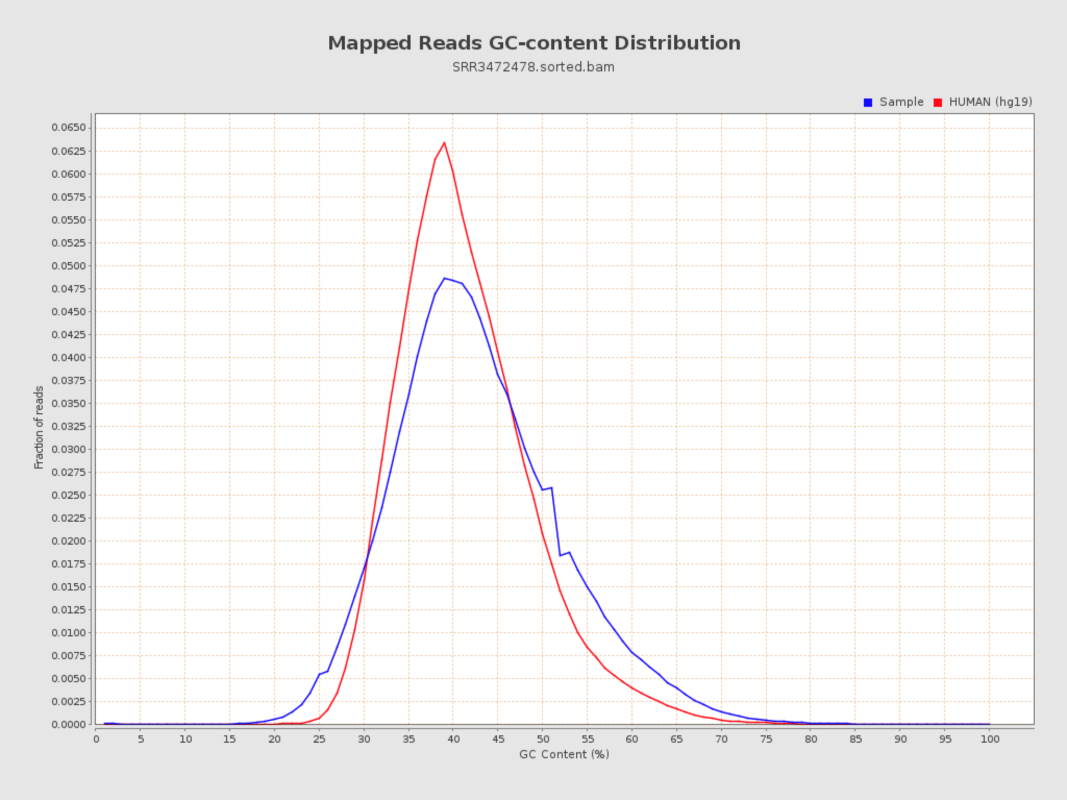
7. Results : Duplication Rate Histogram



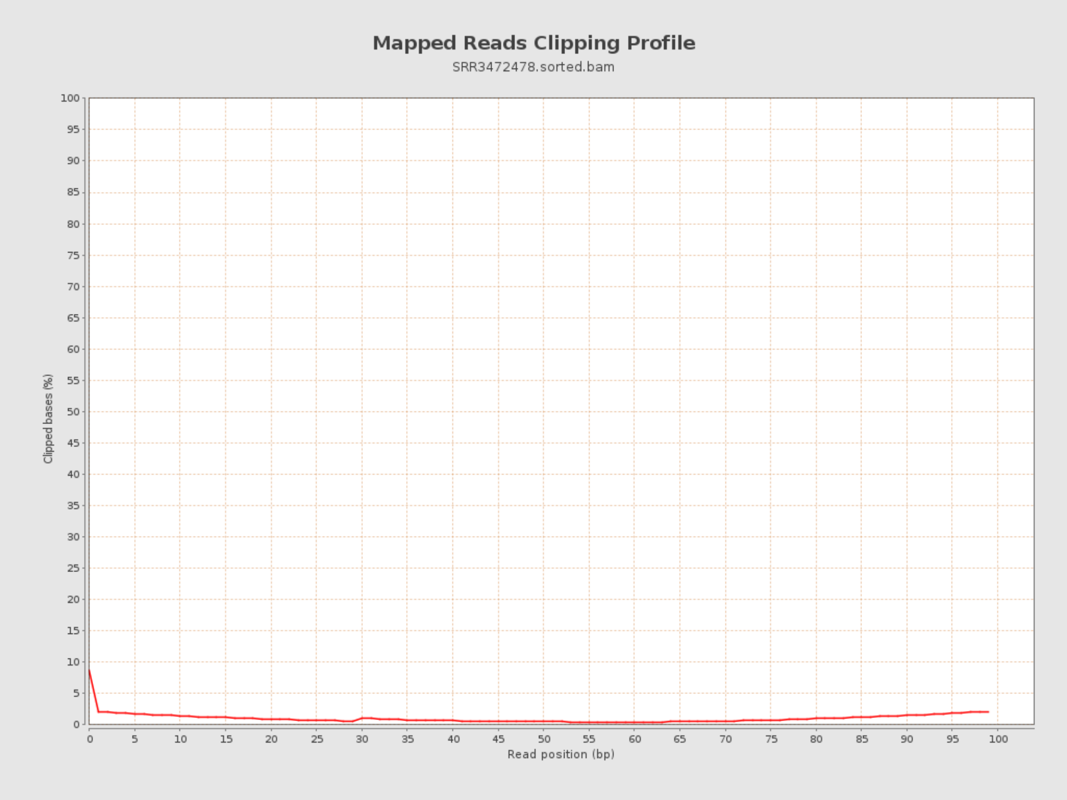
8. Results : Mapped Reads Nucleotide Content



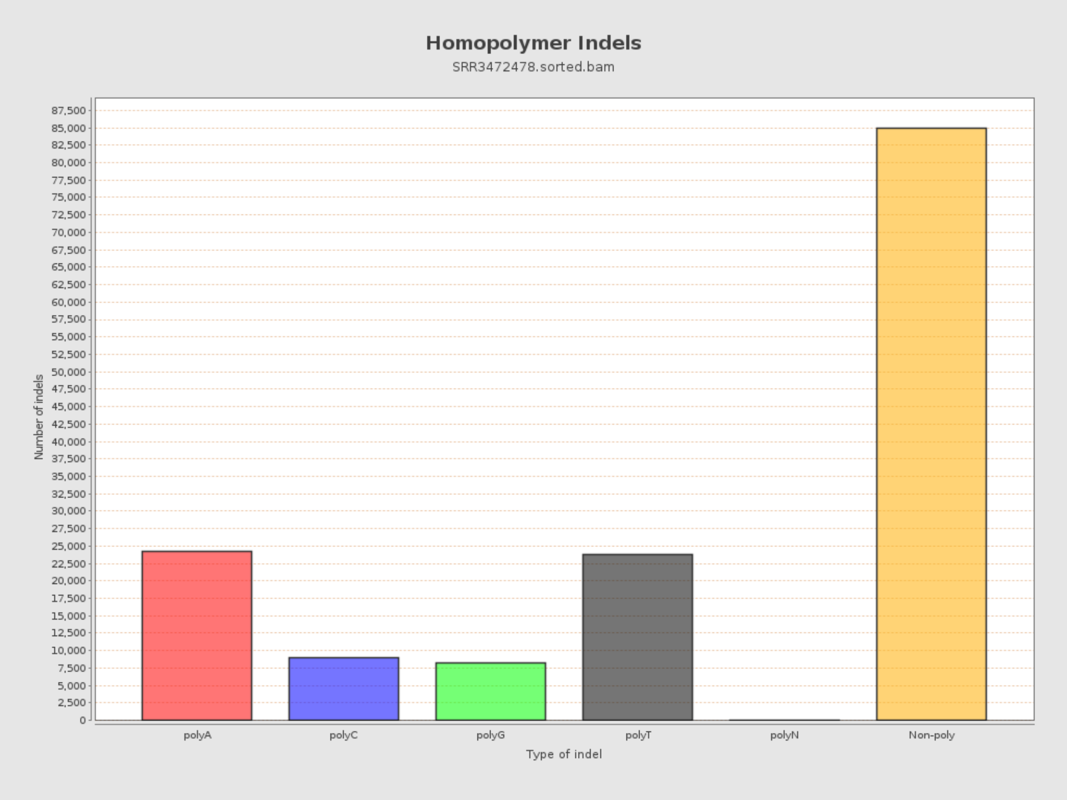
9. Results : Mapped Reads GC-content Distribution



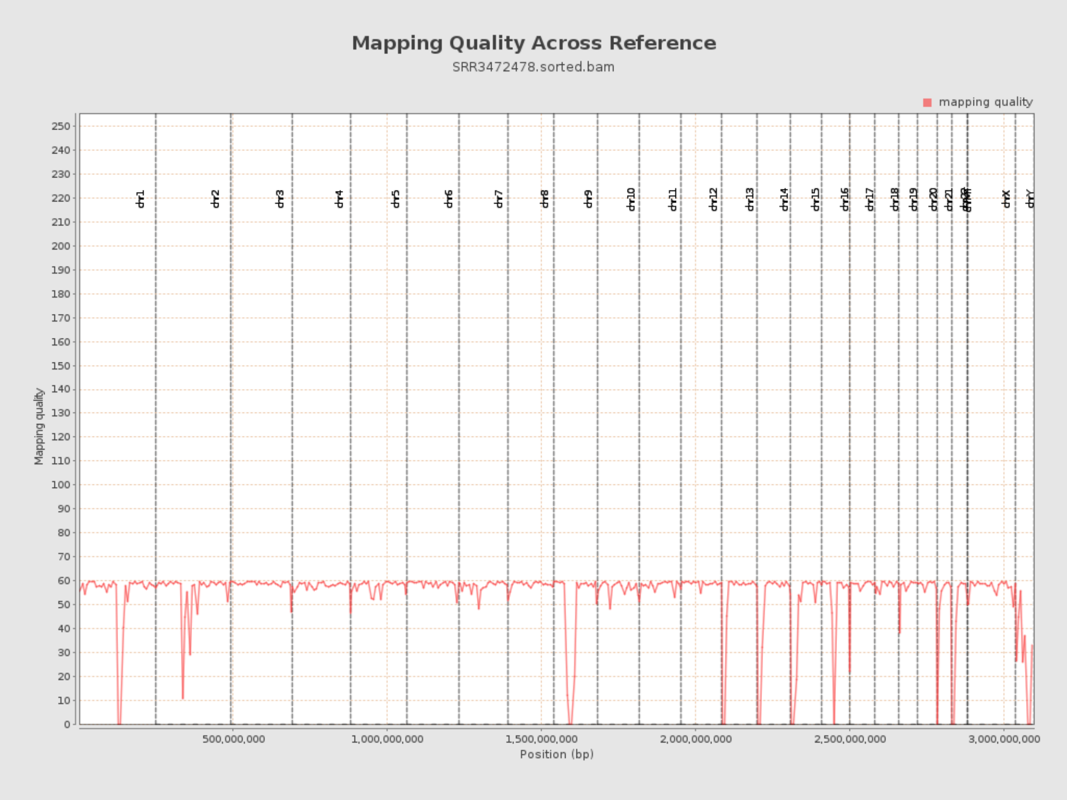
10. Results : Mapped Reads Clipping Profile



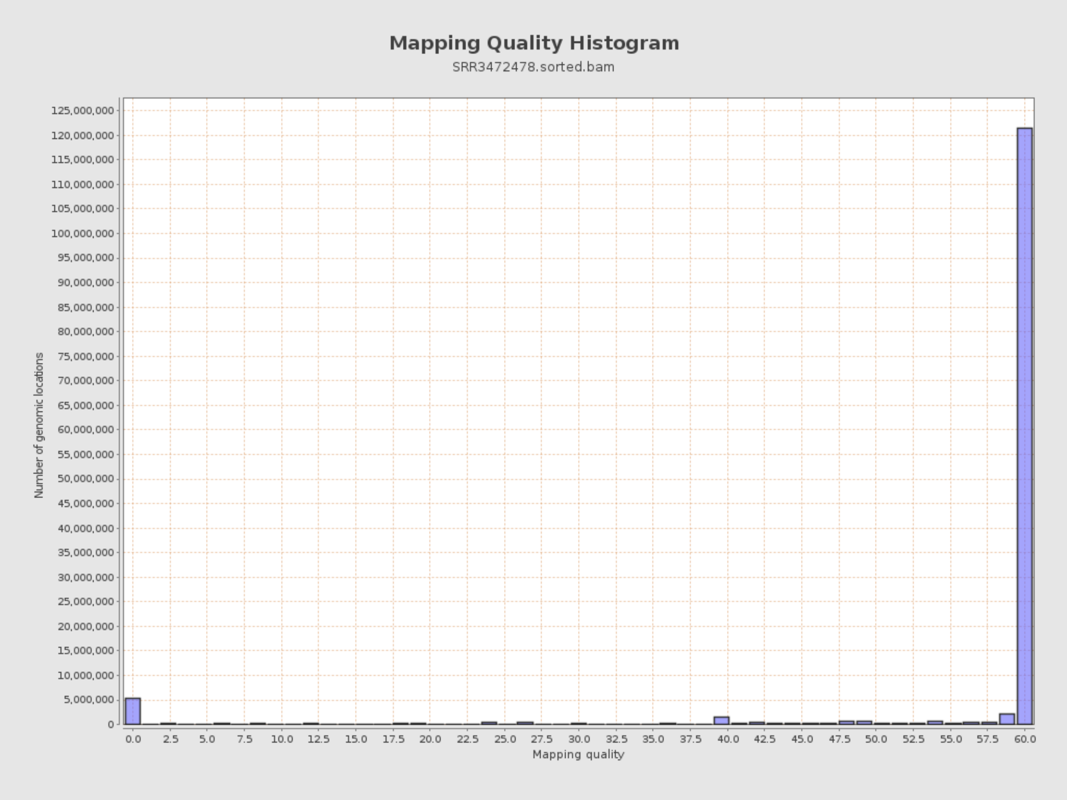
11. Results : Homopolymer Indels



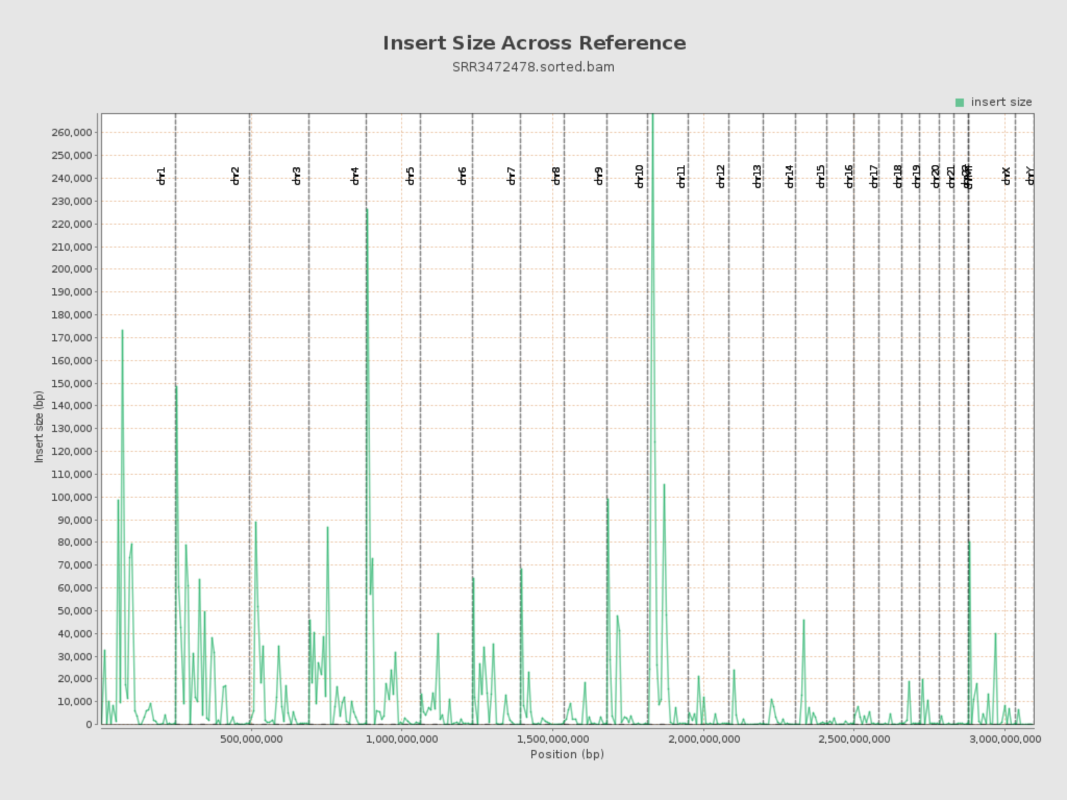
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram