Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:45:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472519.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_SRR3472519 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472519_1.fastq.gz SRR3472519_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:45:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472519.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,208,066
Mapped reads	14,998,638 / 98.62%
Unmapped reads	209,428 / 1.38%
Mapped paired reads	14,998,638 / 98.62%
Mapped reads, first in pair	7,532,661 / 49.53%
Mapped reads, second in pair	7,465,977 / 49.09%
Mapped reads, both in pair	14,885,850 / 97.88%
Mapped reads, singletons	112,788 / 0.74%
Secondary alignments	0
Supplementary alignments	57,537 / 0.38%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	9,120,955 / 59.97%
Duplication rate	45.13%
Clipped reads	1,144,974 / 7.53%

2.2. ACGT Content

Number/percentage of A's	414,496,679 / 28.04%
Number/percentage of C's	326,341,129 / 22.08%
Number/percentage of T's	413,036,012 / 27.94%
Number/percentage of G's	324,151,363 / 21.93%
Number/percentage of N's	226,616 / 0.02%

GC Percentage	44%

2.3. Coverage

Mean	0.4776
Standard Deviation	16.422

2.4. Mapping Quality

Mean Mapping Quality	54.99

2.5. Insert size

Mean	31,556.09
Standard Deviation	1,798,961.03
P25/Median/P75	178 / 248 / 335

2.6. Mismatches and indels

General error rate	0.66%
Mismatches	9,605,902
Insertions	82,553
Mapped reads with at least one insertion	0.54%
Deletions	75,158
Mapped reads with at least one deletion	0.5%
Homopolymer indels	44.03%

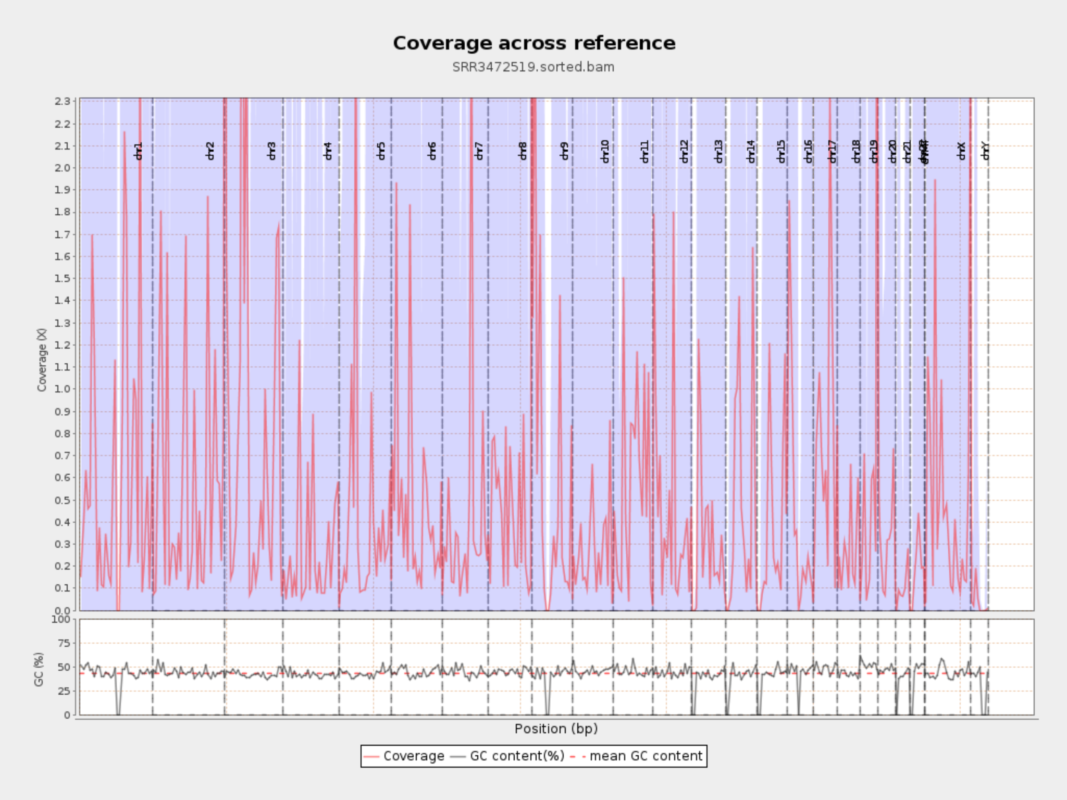
2.7. Chromosome stats

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

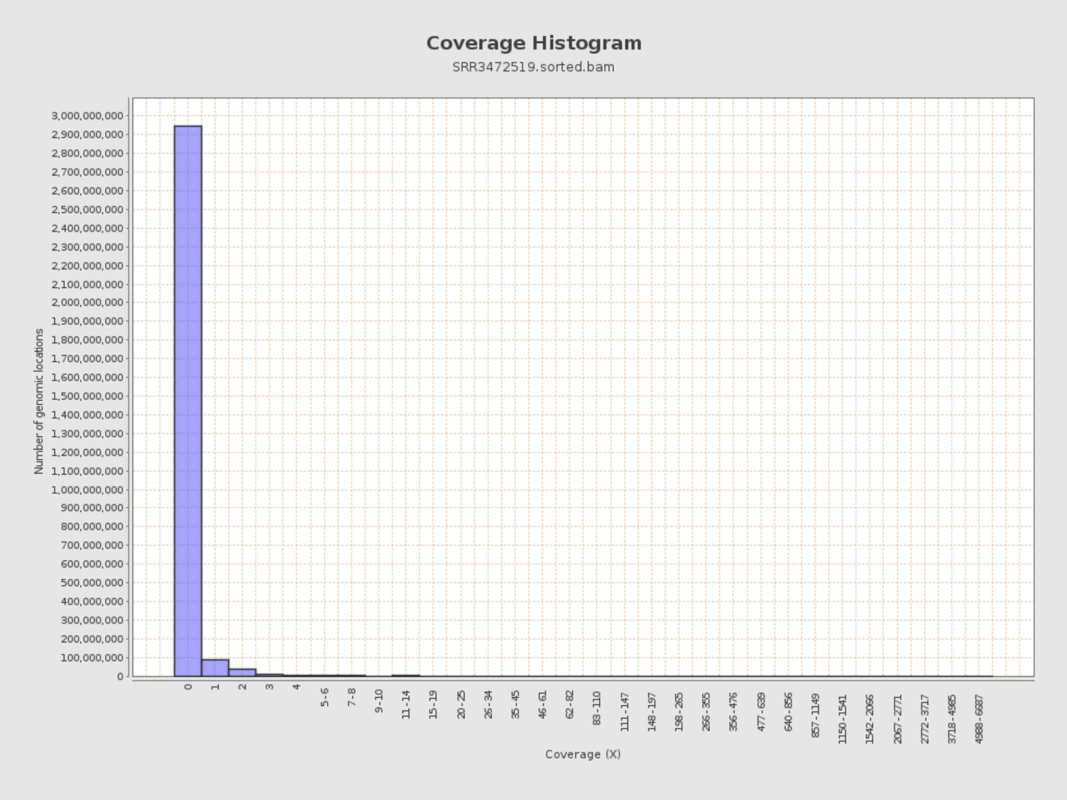
		bases	coverage	deviation
chr1	249250621	154936046	0.6216	19.4509
chr2	243199373	134443994	0.5528	22.1382
chr3	198022430	180859191	0.9133	23.6616
chr4	191154276	51522773	0.2695	11.0026
chr5	180915260	77861588	0.4304	12.8485
chr6	171115067	82886627	0.4844	12.2198
chr7	159138663	66509769	0.4179	16.8906
chr8	146364022	63507969	0.4339	19.2479
chr9	141213431	88413785	0.6261	16.8662
chr10	135534747	37739639	0.2784	9.7081
chr11	135006516	79435789	0.5884	20.1724
chr12	133851895	65490416	0.4893	16.1337
chr13	115169878	37303343	0.3239	11.013
chr14	107349540	51824744	0.4828	20.2067
chr15	102531392	38780852	0.3782	13.4685
chr16	90354753	39472563	0.4369	12.3576
chr17	81195210	62316538	0.7675	17.3945
chr18	78077248	22158925	0.2838	10.0145
chr19	59128983	27593279	0.4667	16.8236
chr20	63025520	20754159	0.3293	9.5767
chr21	48129895	5065366	0.1052	3.236
chr22	51304566	9671139	0.1885	6.347
chrMT	16571	3047	0.1839	0.6724
chrX	155270560	77483971	0.499	16.3754

chrY	59373566	2398681	0.0404	1.6888

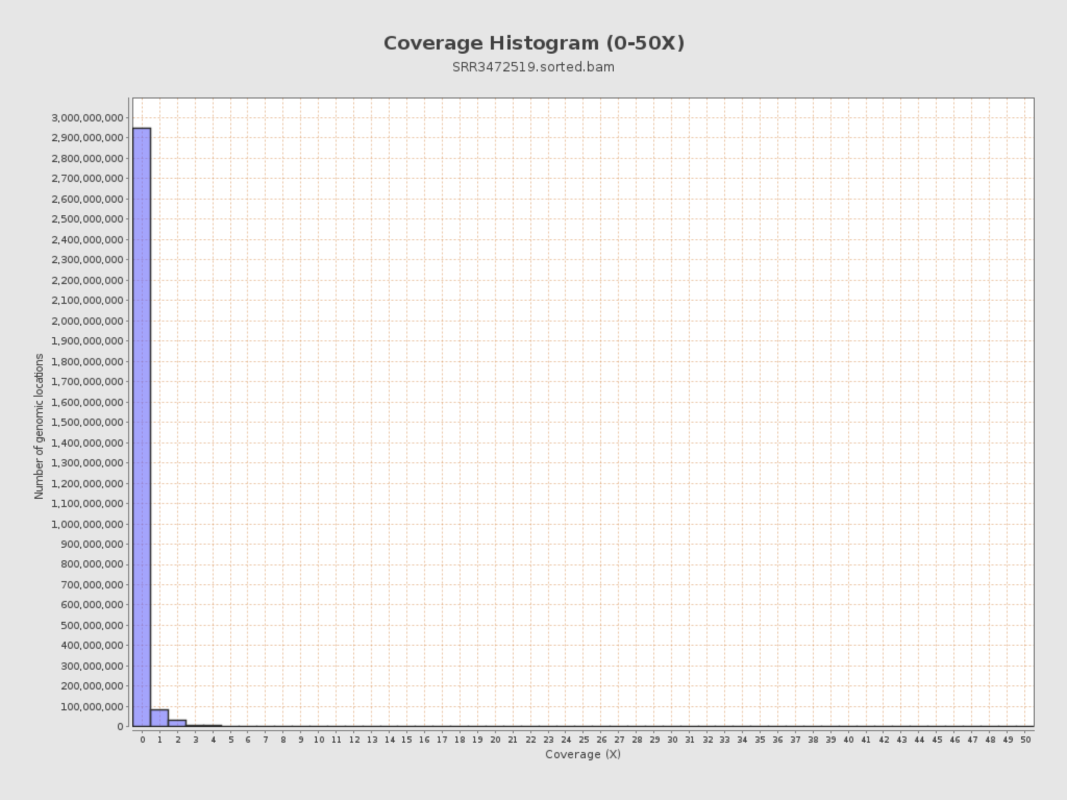
3. Results : Coverage across reference



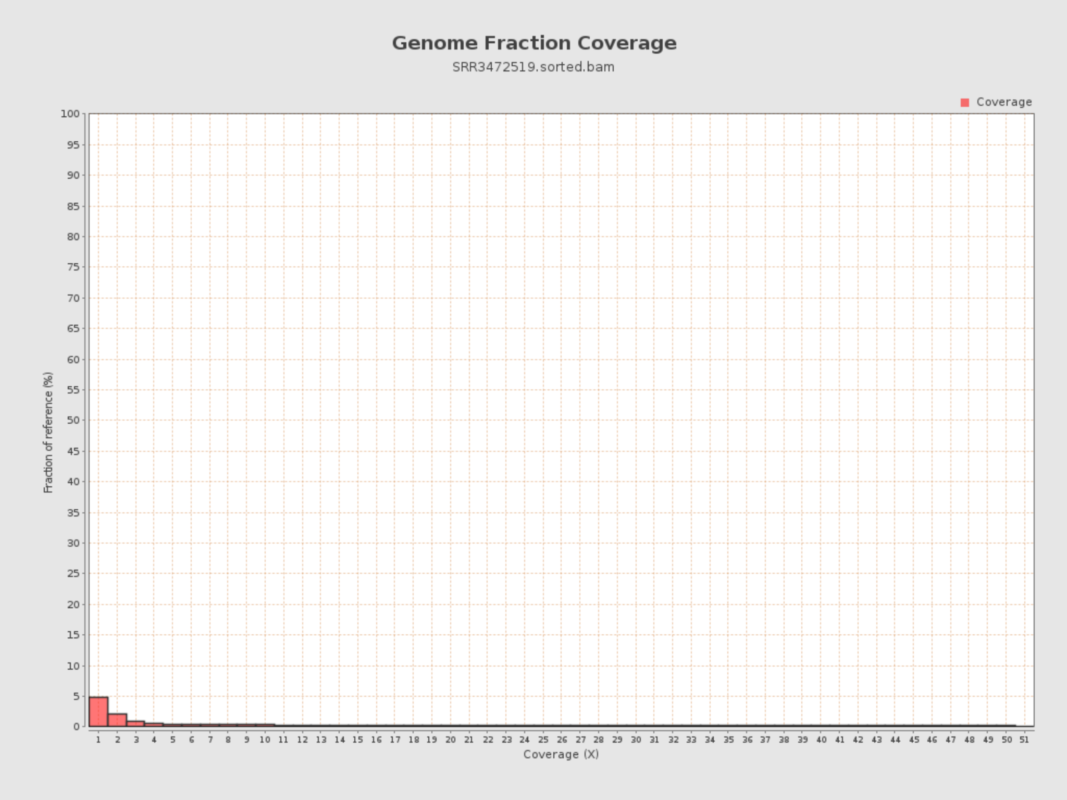
4. Results : Coverage Histogram



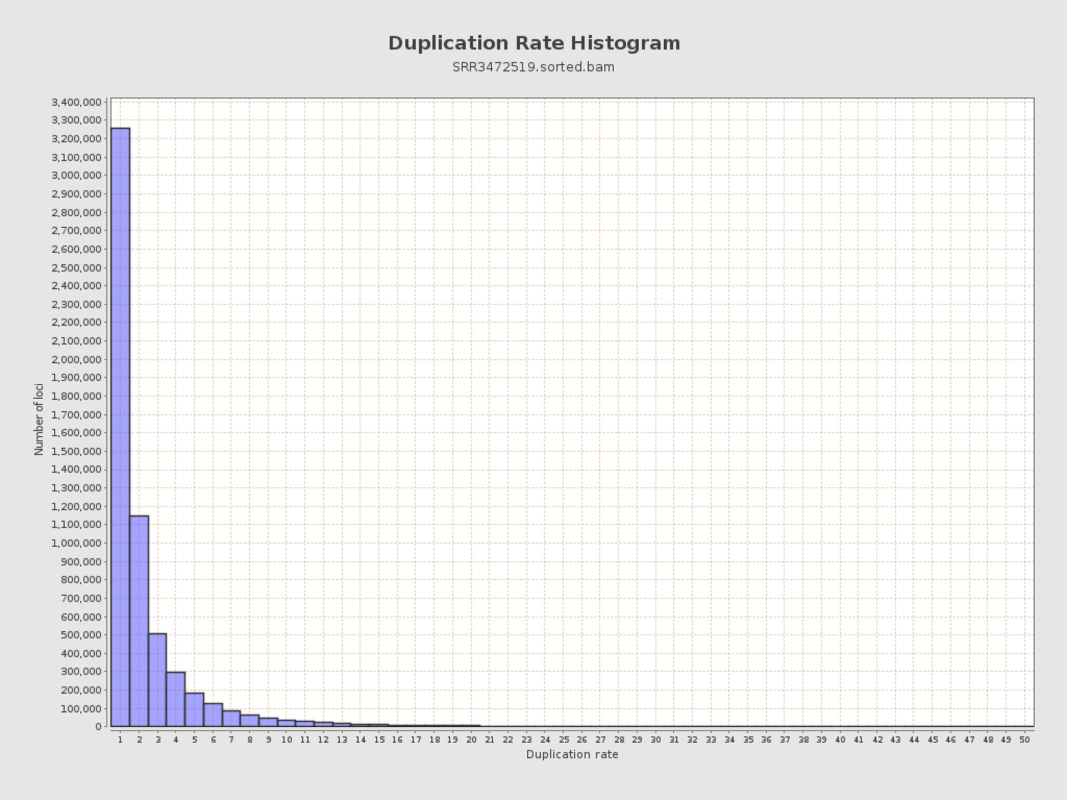
5. Results : Coverage Histogram (0-50X)



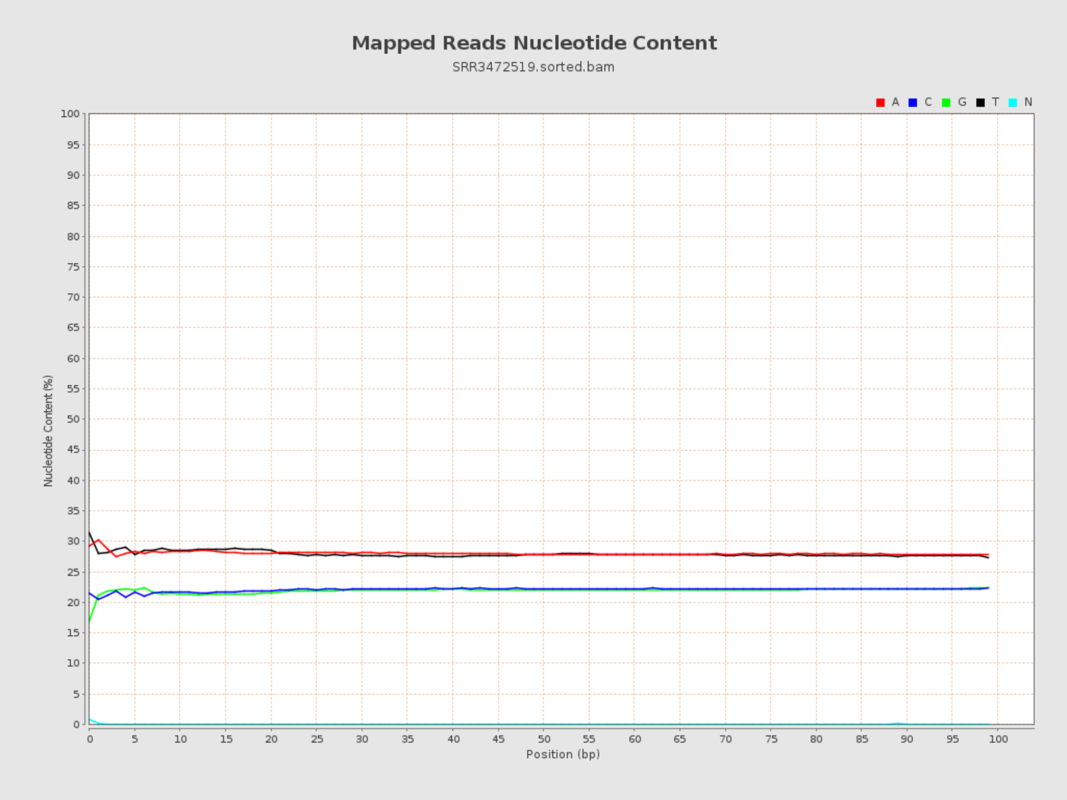
6. Results : Genome Fraction Coverage



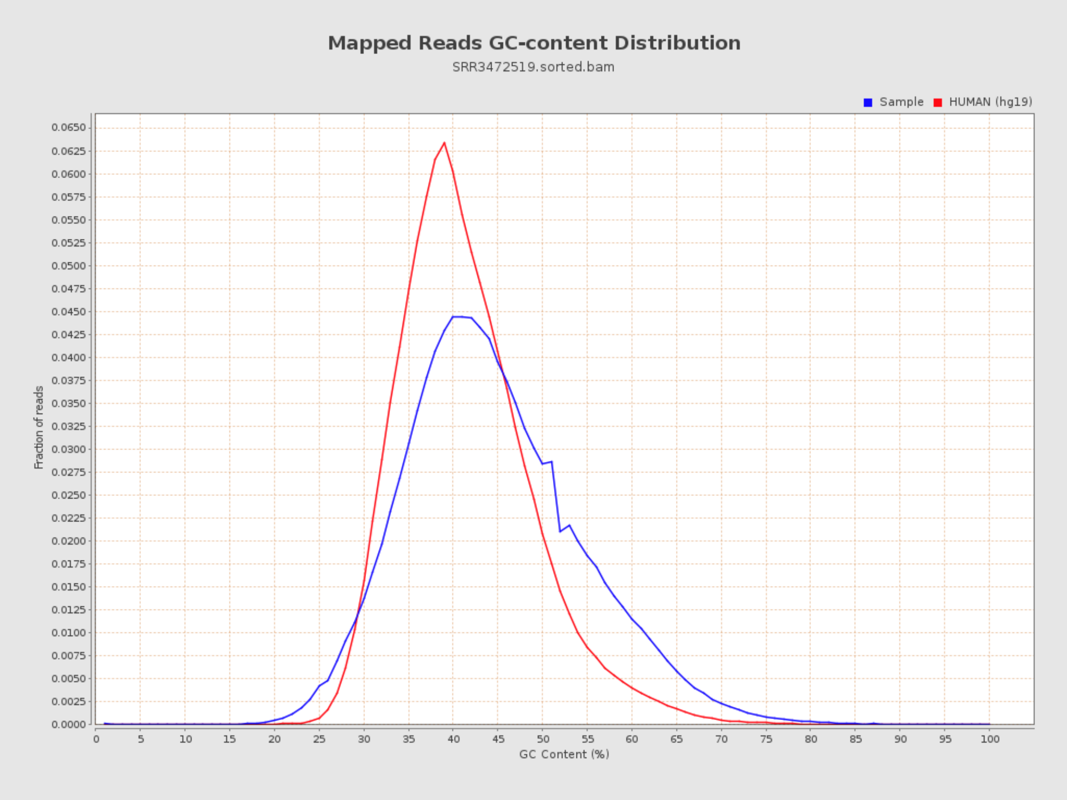
7. Results : Duplication Rate Histogram



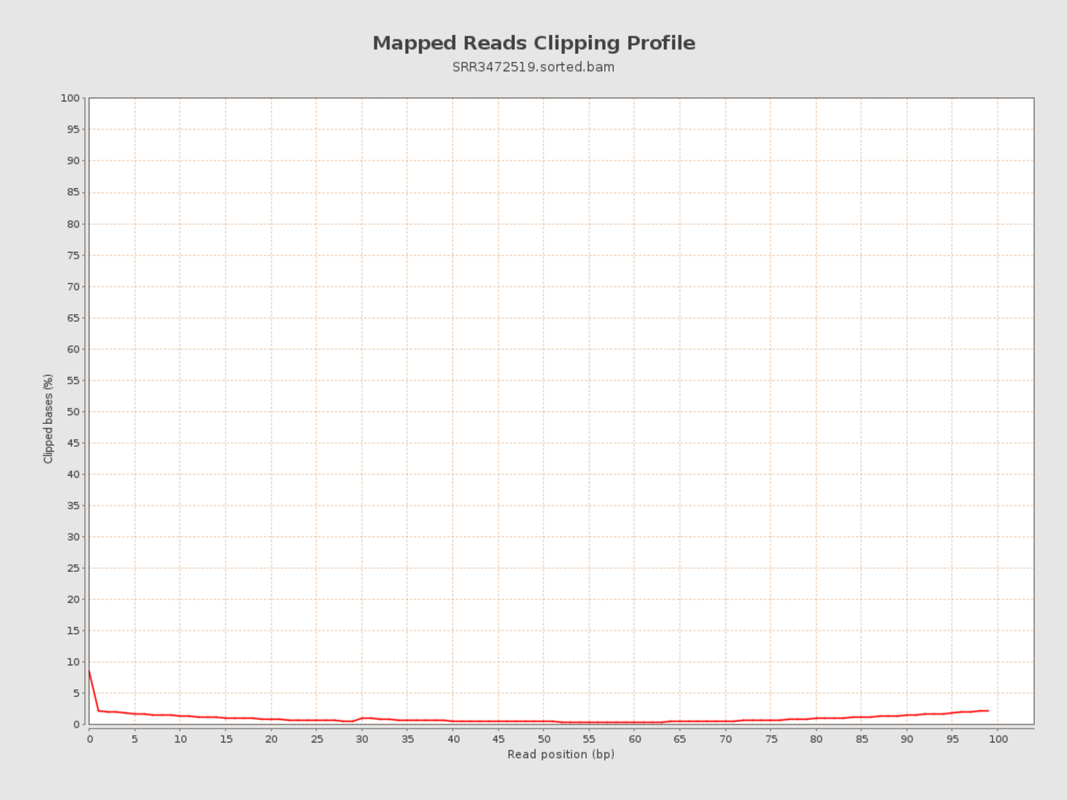
8. Results : Mapped Reads Nucleotide Content



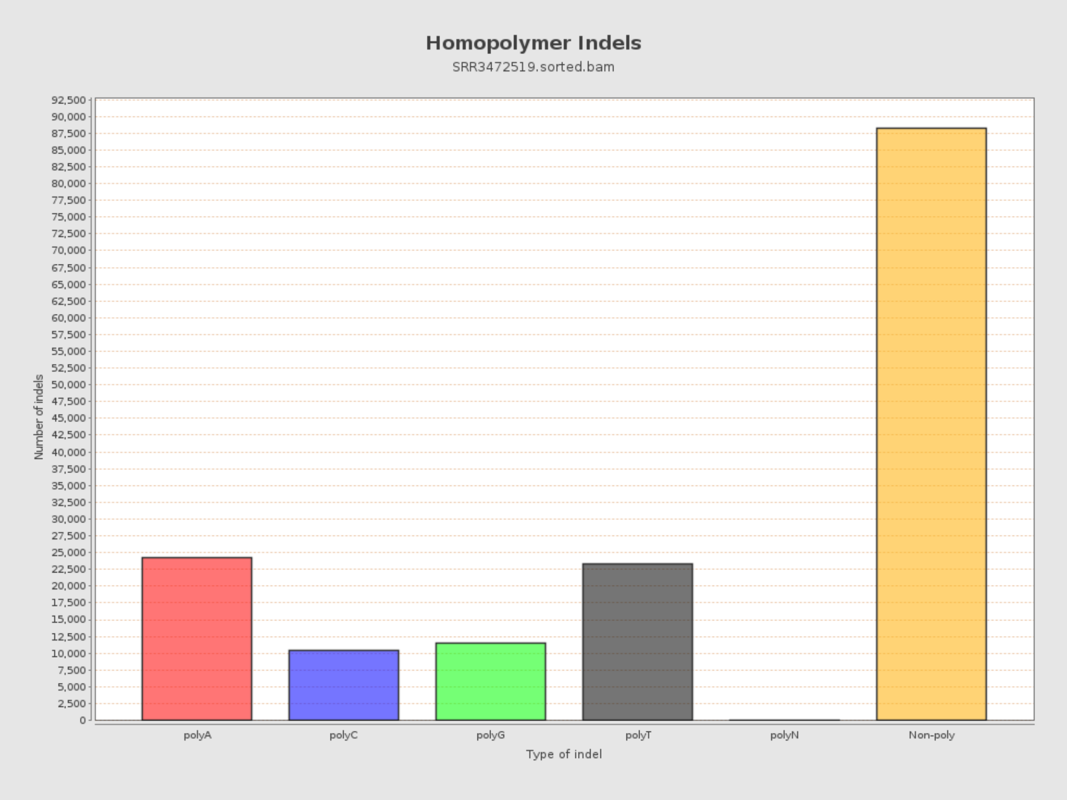
9. Results : Mapped Reads GC-content Distribution



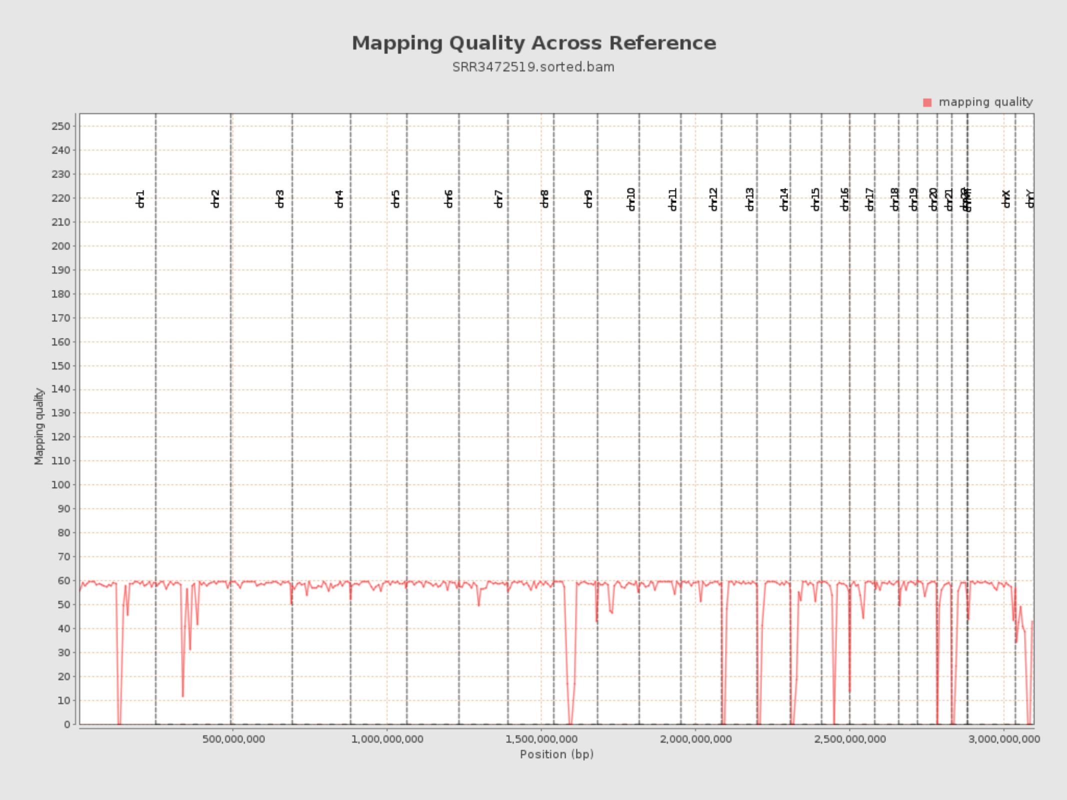
10. Results : Mapped Reads Clipping Profile



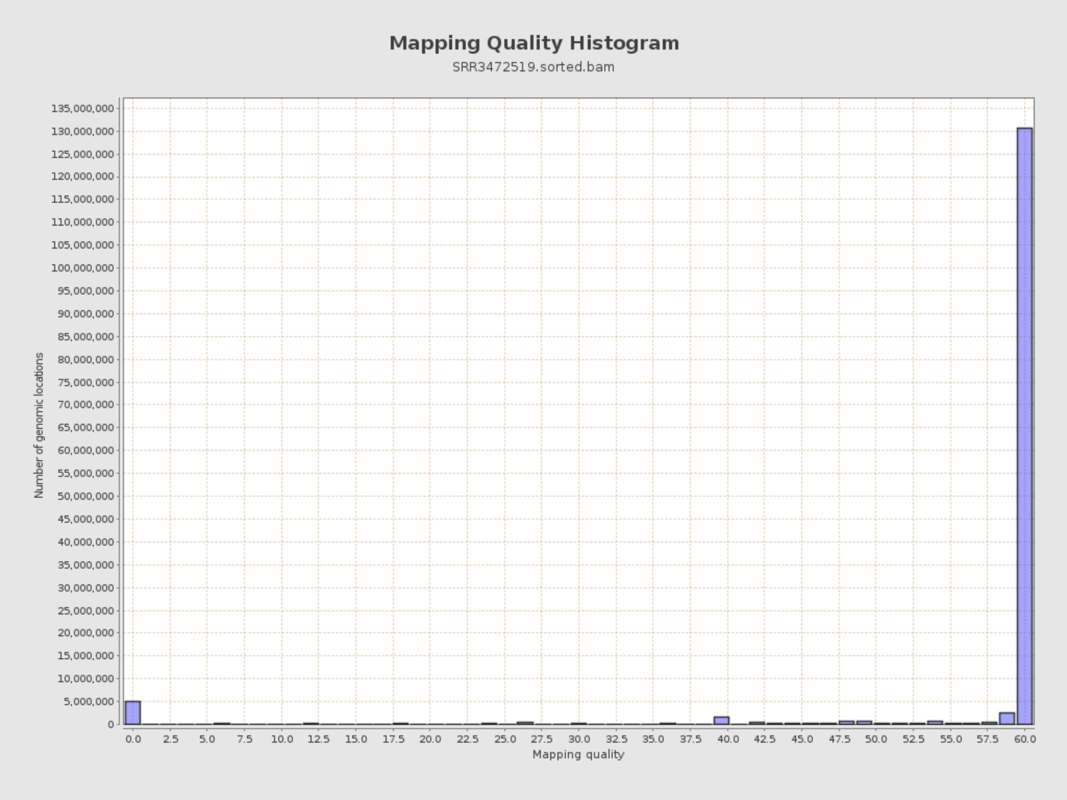
11. Results : Homopolymer Indels



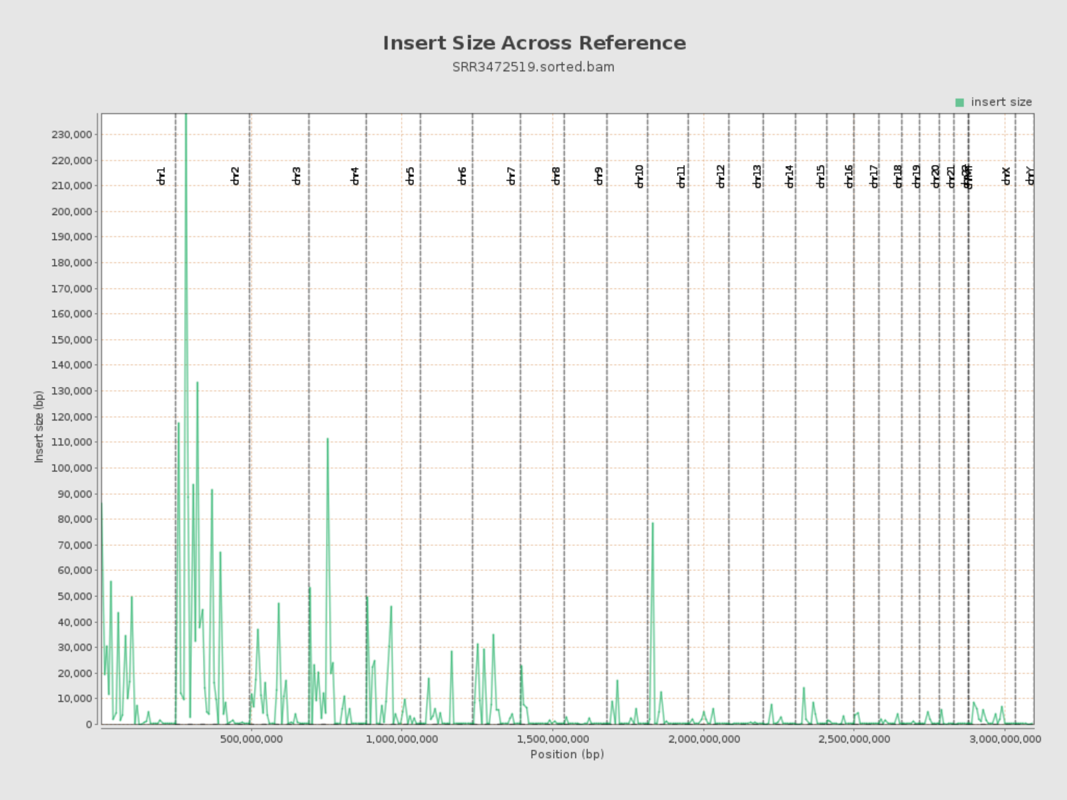
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram