Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:08:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472504.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_SRR3472504 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472504_1.fastq.gz SRR3472504_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:07:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472504.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,344,428
Mapped reads	14,123,617 / 98.46%
Unmapped reads	220,811 / 1.54%
Mapped paired reads	14,123,617 / 98.46%
Mapped reads, first in pair	7,097,043 / 49.48%
Mapped reads, second in pair	7,026,574 / 48.98%
Mapped reads, both in pair	14,008,934 / 97.66%
Mapped reads, singletons	114,683 / 0.8%
Secondary alignments	0
Supplementary alignments	57,225 / 0.4%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	8,501,693 / 59.27%
Duplication rate	44.21%
Clipped reads	1,163,779 / 8.11%

2.2. ACGT Content

Number/percentage of A's	387,413,581 / 27.86%
Number/percentage of C's	310,822,181 / 22.36%
Number/percentage of T's	384,172,325 / 27.63%
Number/percentage of G's	307,779,465 / 22.14%
Number/percentage of N's	203,032 / 0.01%

GC Percentage	44.49%

2.3. Coverage

Mean	0.4492
Standard Deviation	17.5464

2.4. Mapping Quality

Mean Mapping Quality	55.21

2.5. Insert size

Mean	32,169.22
Standard Deviation	1,754,324.8
P25/Median/P75	174 / 243 / 328

2.6. Mismatches and indels

General error rate	0.75%
Mismatches	10,302,695
Insertions	72,580
Mapped reads with at least one insertion	0.51%
Deletions	73,865
Mapped reads with at least one deletion	0.52%
Homopolymer indels	44.03%

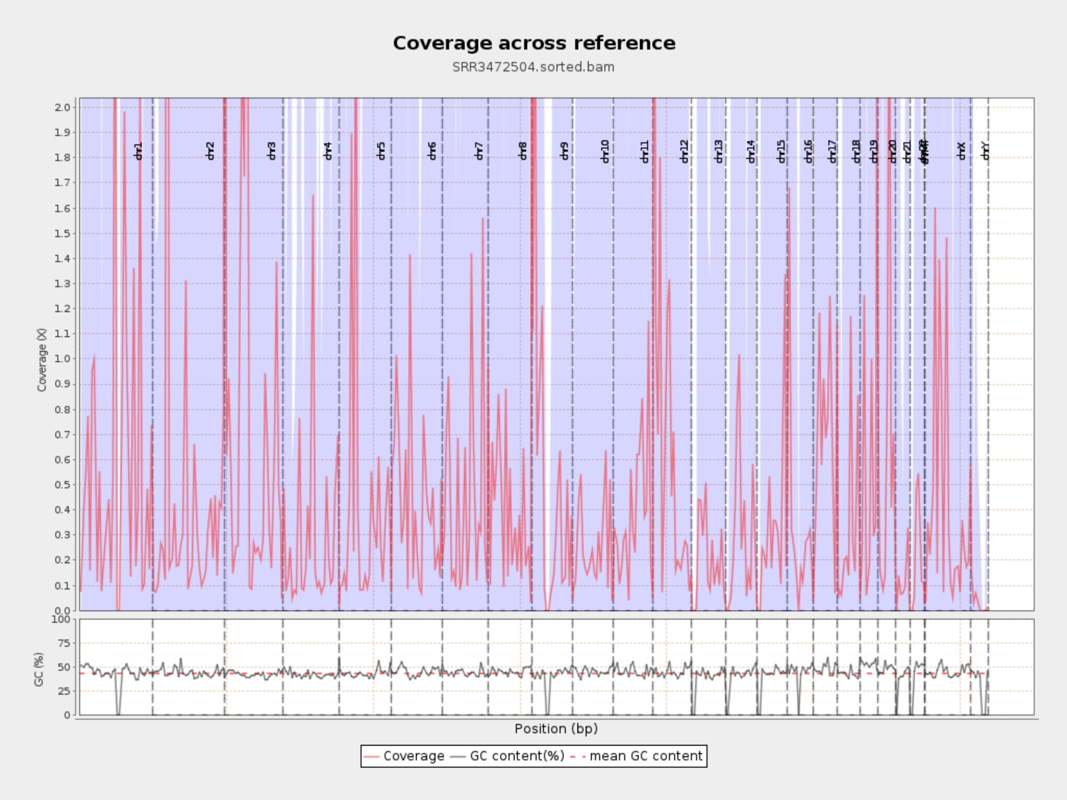
2.7. Chromosome stats

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

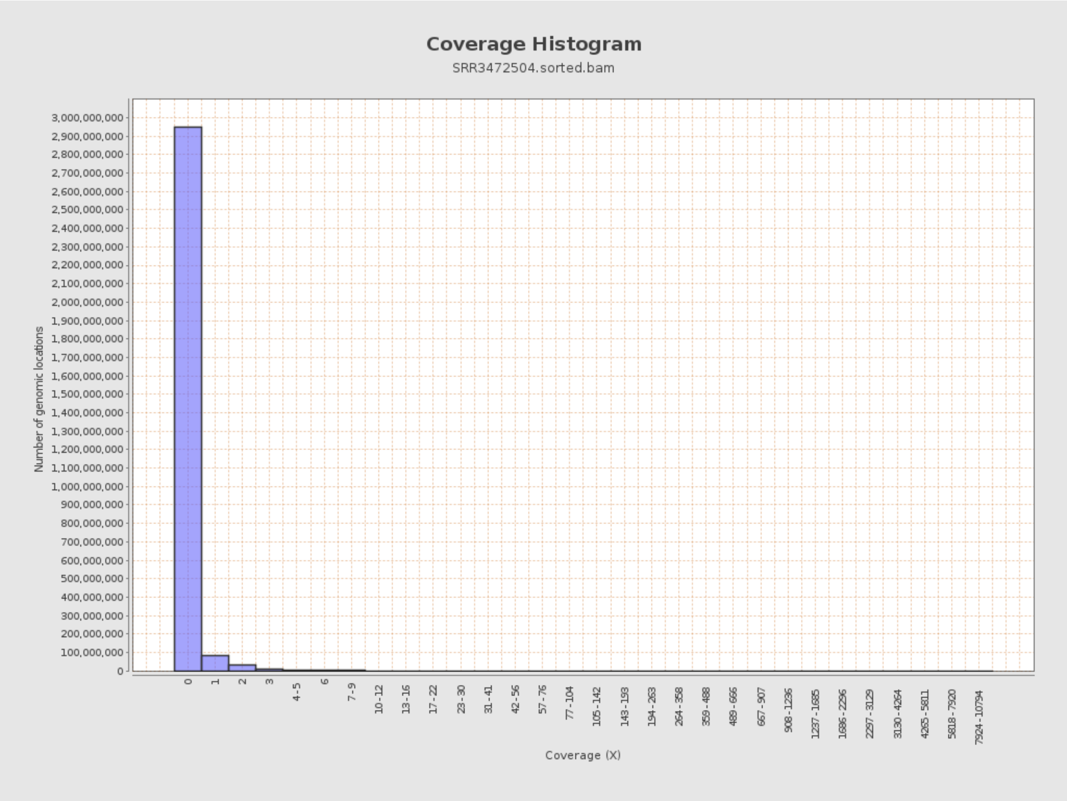
		bases	coverage	deviation
chr1	249250621	152406742	0.6115	20.5162
chr2	243199373	119482319	0.4913	37.1499
chr3	198022430	159816829	0.8071	19.4931
chr4	191154276	54432466	0.2848	10.6502
chr5	180915260	78087838	0.4316	15.7253
chr6	171115067	75250450	0.4398	11.8764
chr7	159138663	70844457	0.4452	16.3559
chr8	146364022	55052977	0.3761	13.7628
chr9	141213431	76872485	0.5444	13.9781
chr10	135534747	35501905	0.2619	9.1514
chr11	135006516	52895302	0.3918	11.543
chr12	133851895	96513587	0.721	20.9036
chr13	115169878	23367283	0.2029	7.7149
chr14	107349540	32554645	0.3033	11.9999
chr15	102531392	36079554	0.3519	11.594
chr16	90354753	30469703	0.3372	7.93
chr17	81195210	55748360	0.6866	15.9845
chr18	78077248	26487368	0.3392	14.4649
chr19	59128983	30682106	0.5189	15.5534
chr20	63025520	42539308	0.675	20.5318
chr21	48129895	5675169	0.1179	5.0054
chr22	51304566	10155472	0.1979	6.6022
chrMT	16571	1799	0.1086	0.46
chrX	155270560	67747007	0.4363	15.4431

chrY	59373566	1893378	0.0319	3.4949

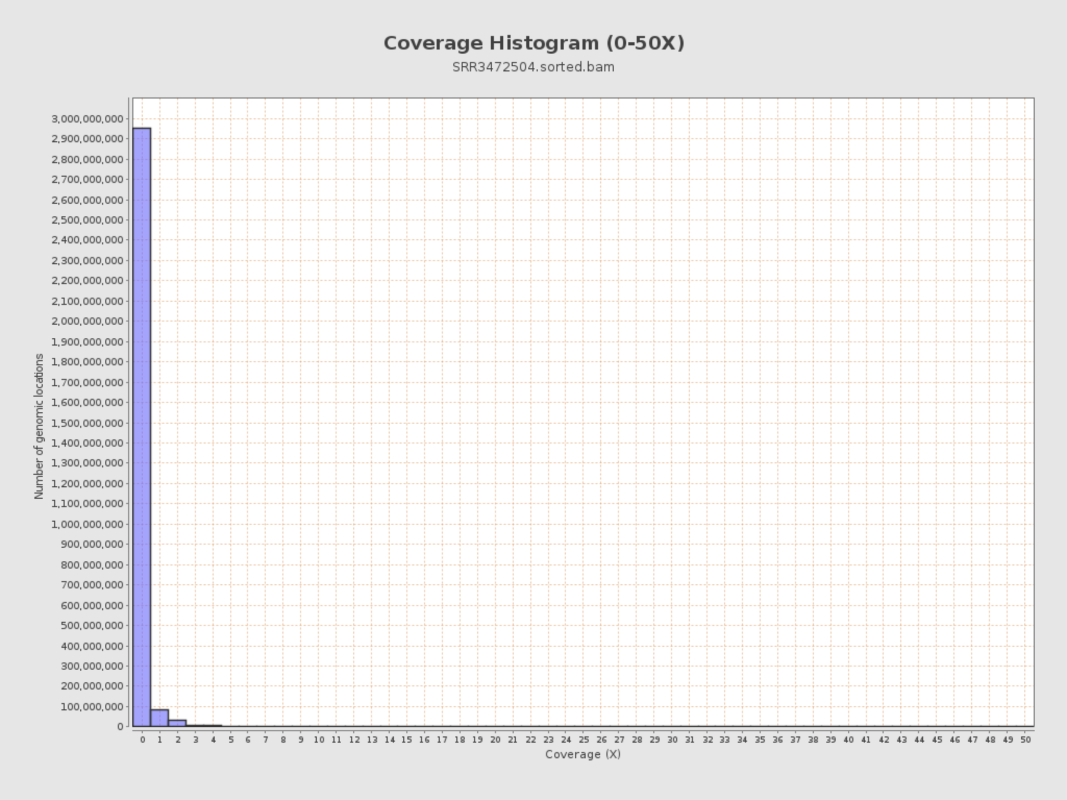
3. Results : Coverage across reference



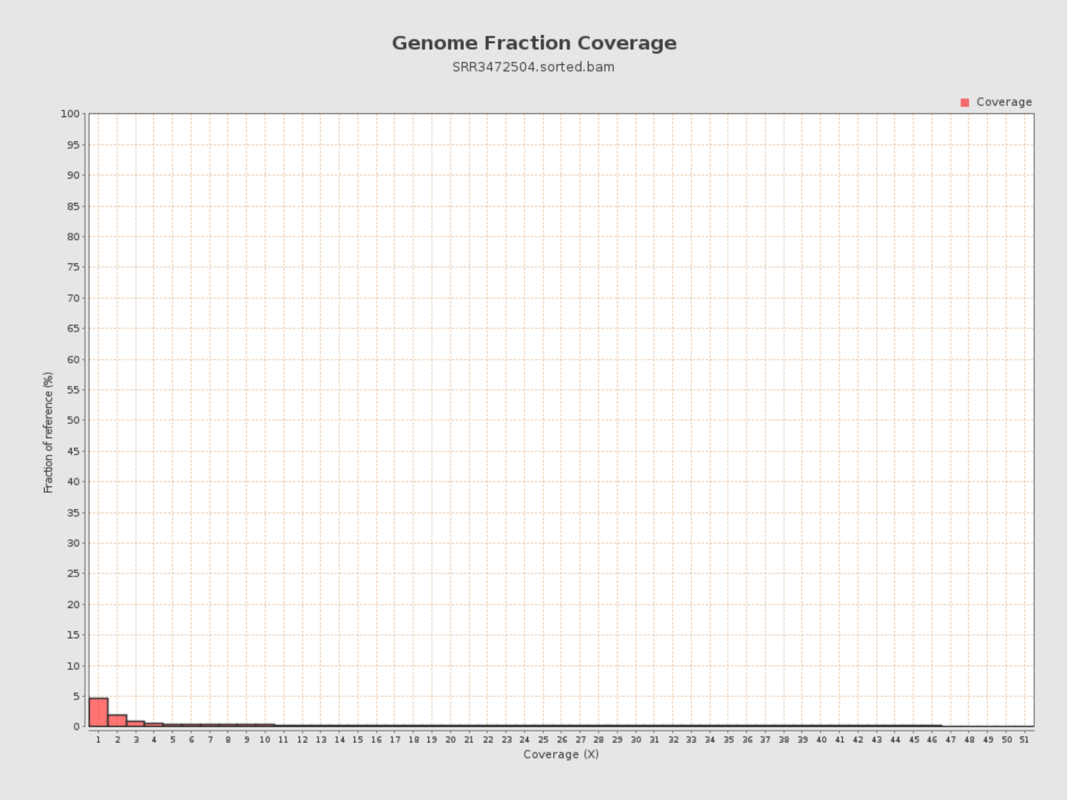
4. Results : Coverage Histogram



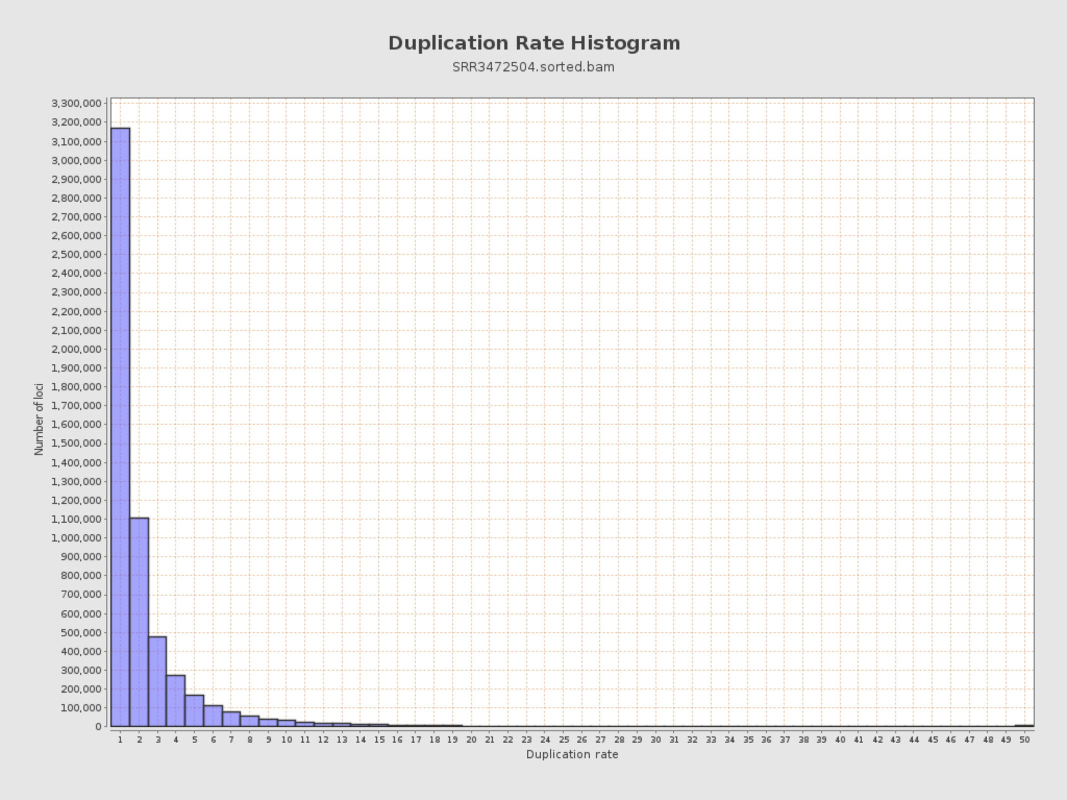
5. Results : Coverage Histogram (0-50X)



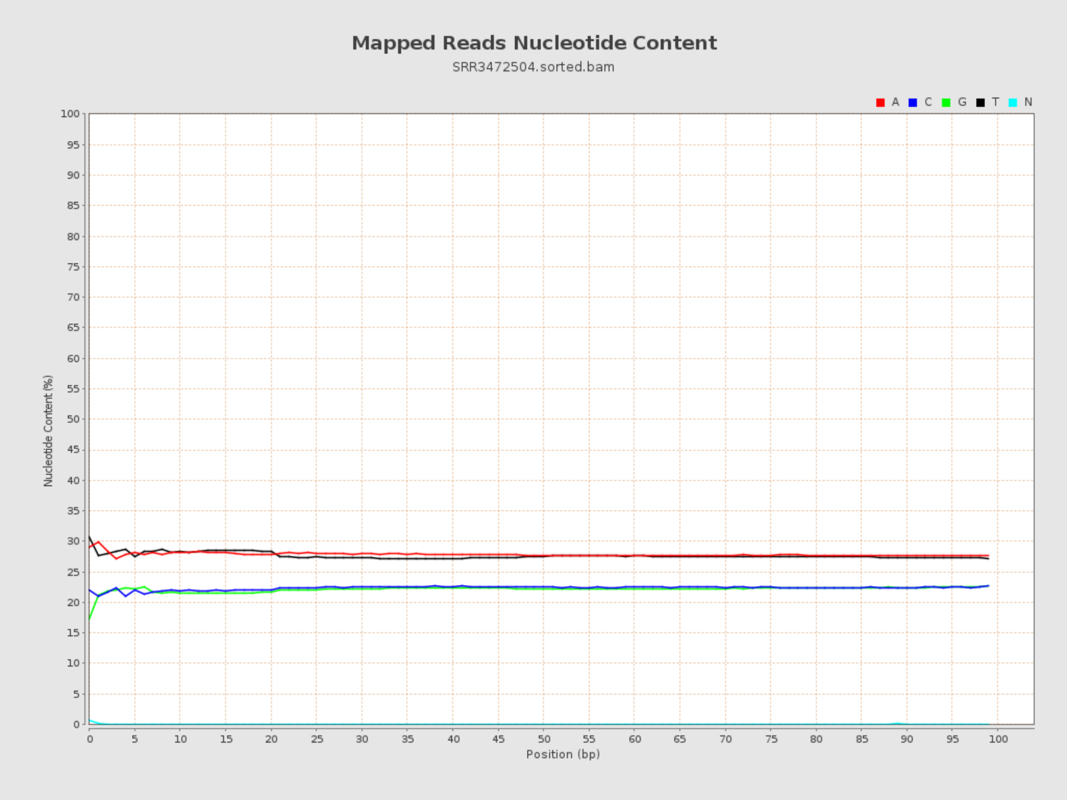
6. Results : Genome Fraction Coverage



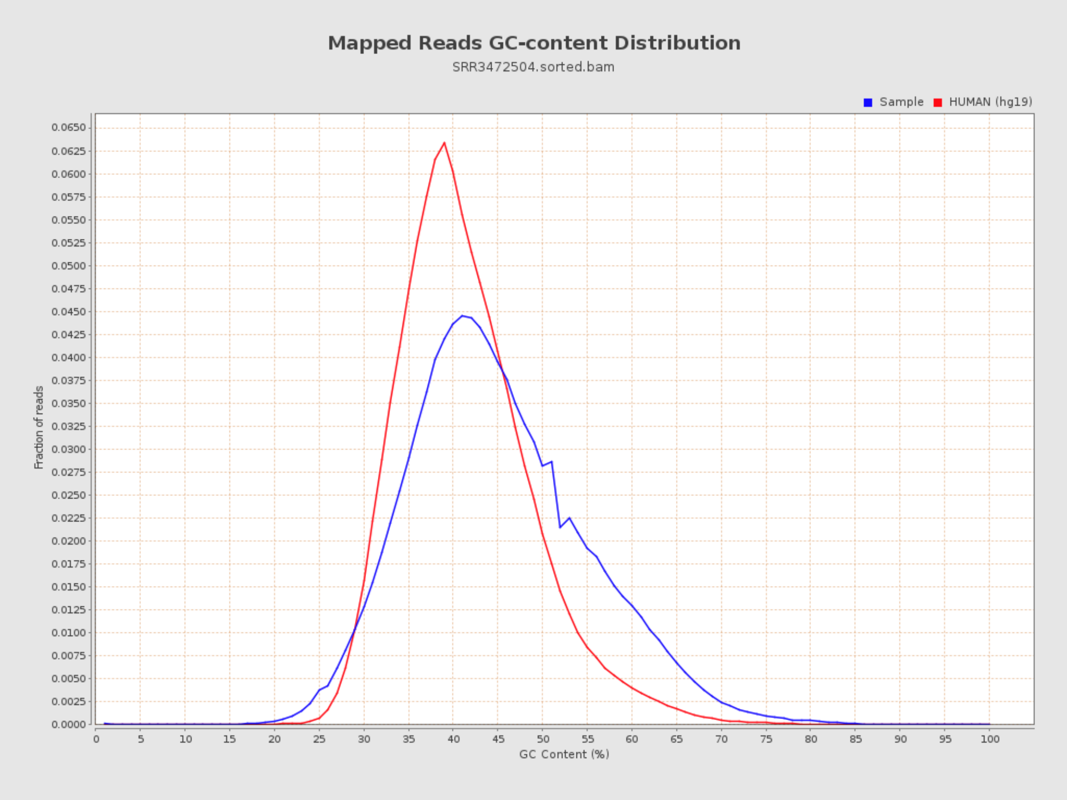
7. Results : Duplication Rate Histogram



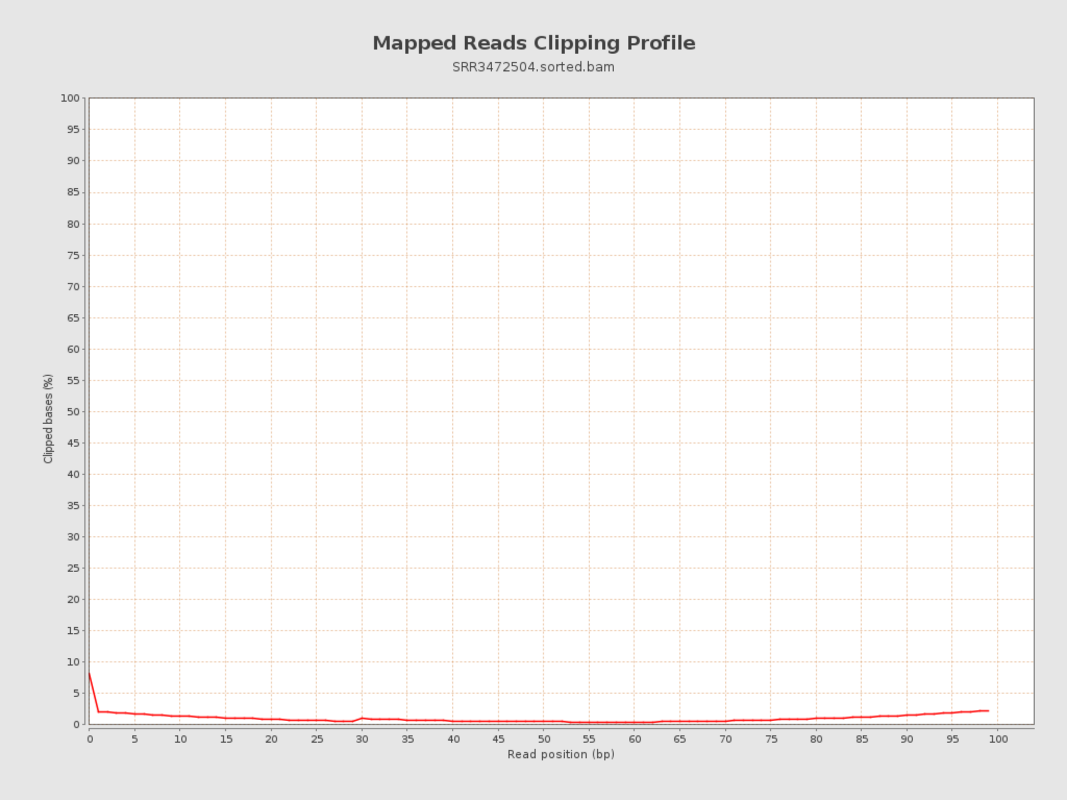
8. Results : Mapped Reads Nucleotide Content



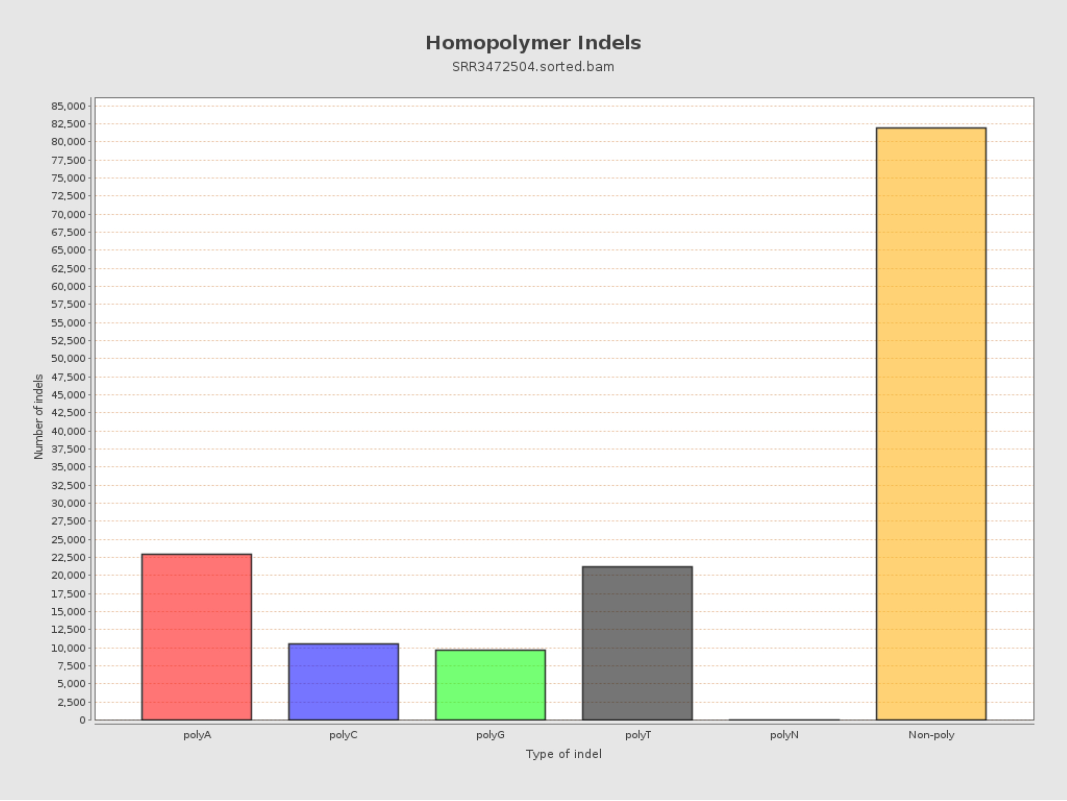
9. Results : Mapped Reads GC-content Distribution



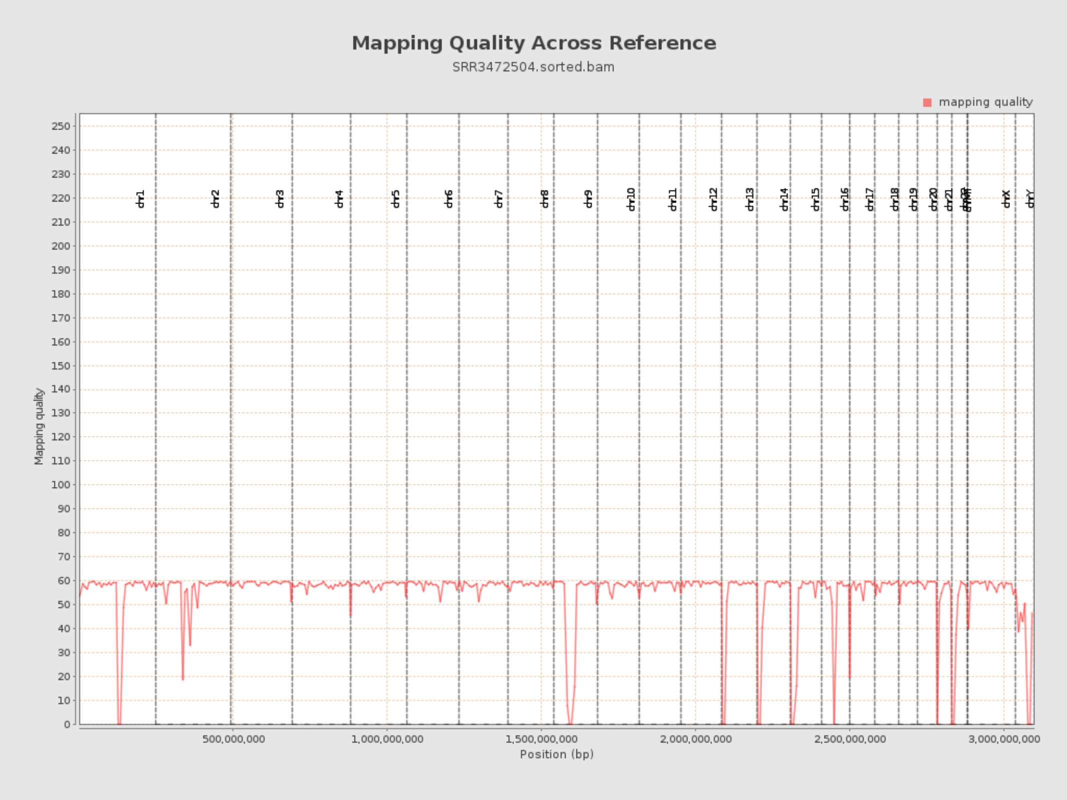
10. Results : Mapped Reads Clipping Profile



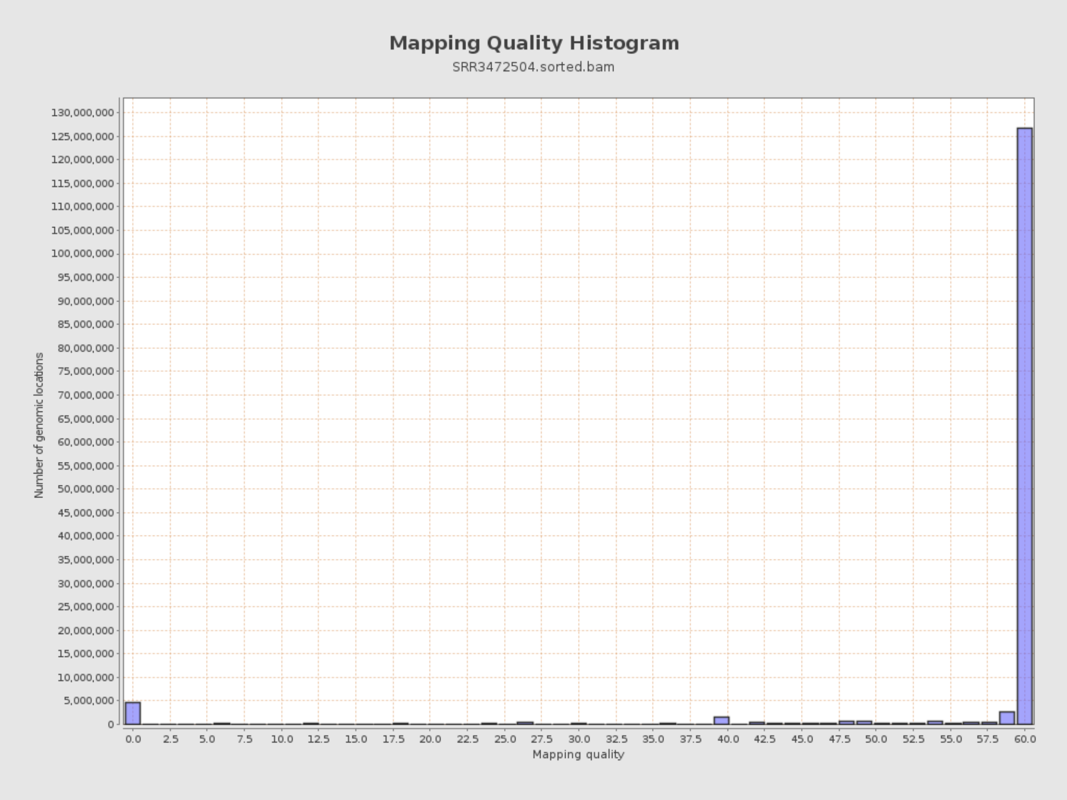
11. Results : Homopolymer Indels



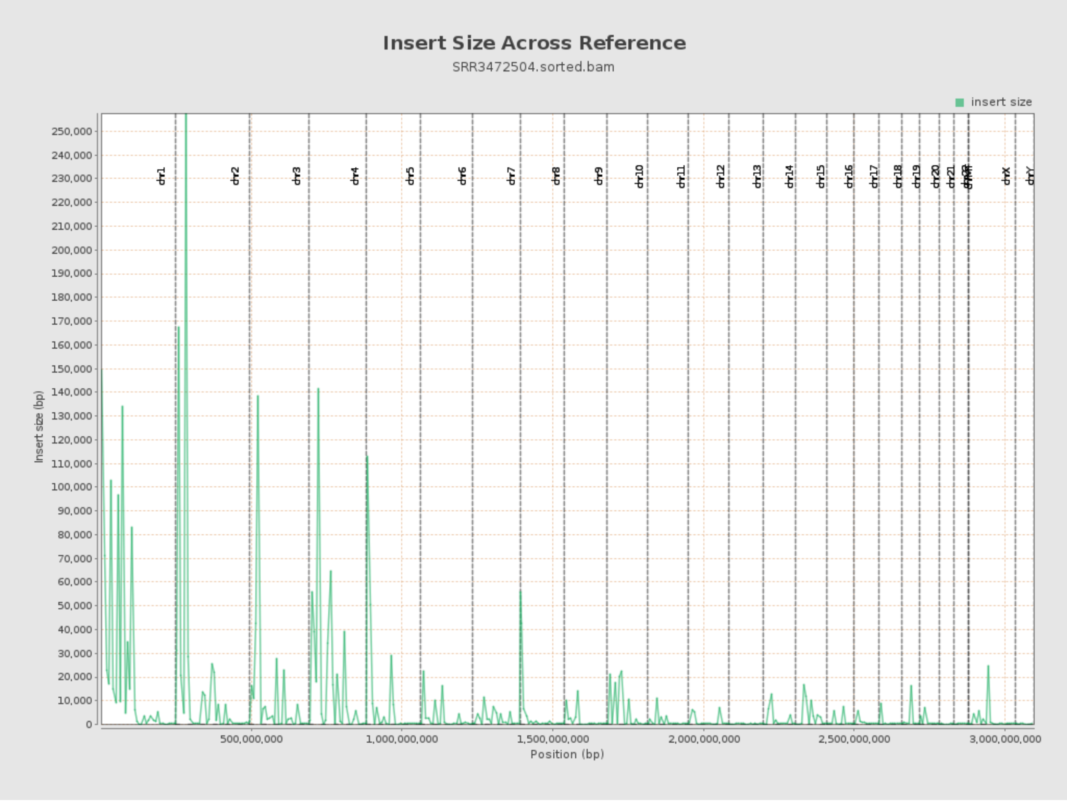
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram