Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:19:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472540.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_SRR3472540 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472540_1.fastq.gz SRR3472540_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:19:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472540.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,204,788
Mapped reads	15,970,720 / 98.56%
Unmapped reads	234,068 / 1.44%
Mapped paired reads	15,970,720 / 98.56%
Mapped reads, first in pair	8,014,113 / 49.46%
Mapped reads, second in pair	7,956,607 / 49.1%
Mapped reads, both in pair	15,866,026 / 97.91%
Mapped reads, singletons	104,694 / 0.65%
Secondary alignments	0
Supplementary alignments	70,412 / 0.43%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	10,005,919 / 61.75%
Duplication rate	44.65%
Clipped reads	1,316,443 / 8.12%

2.2. ACGT Content

Number/percentage of A's	435,841,749 / 27.72%
Number/percentage of C's	352,768,086 / 22.44%
Number/percentage of T's	433,189,397 / 27.55%
Number/percentage of G's	350,088,574 / 22.27%
Number/percentage of N's	242,075 / 0.02%

GC Percentage	44.71%

2.3. Coverage

Mean	0.5079
Standard Deviation	18.2099

2.4. Mapping Quality

Mean Mapping Quality	55.07

2.5. Insert size

Mean	32,763.73
Standard Deviation	1,802,164.54
P25/Median/P75	172 / 239 / 320

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	9,748,326
Insertions	84,222
Mapped reads with at least one insertion	0.52%
Deletions	89,529
Mapped reads with at least one deletion	0.55%
Homopolymer indels	43.19%

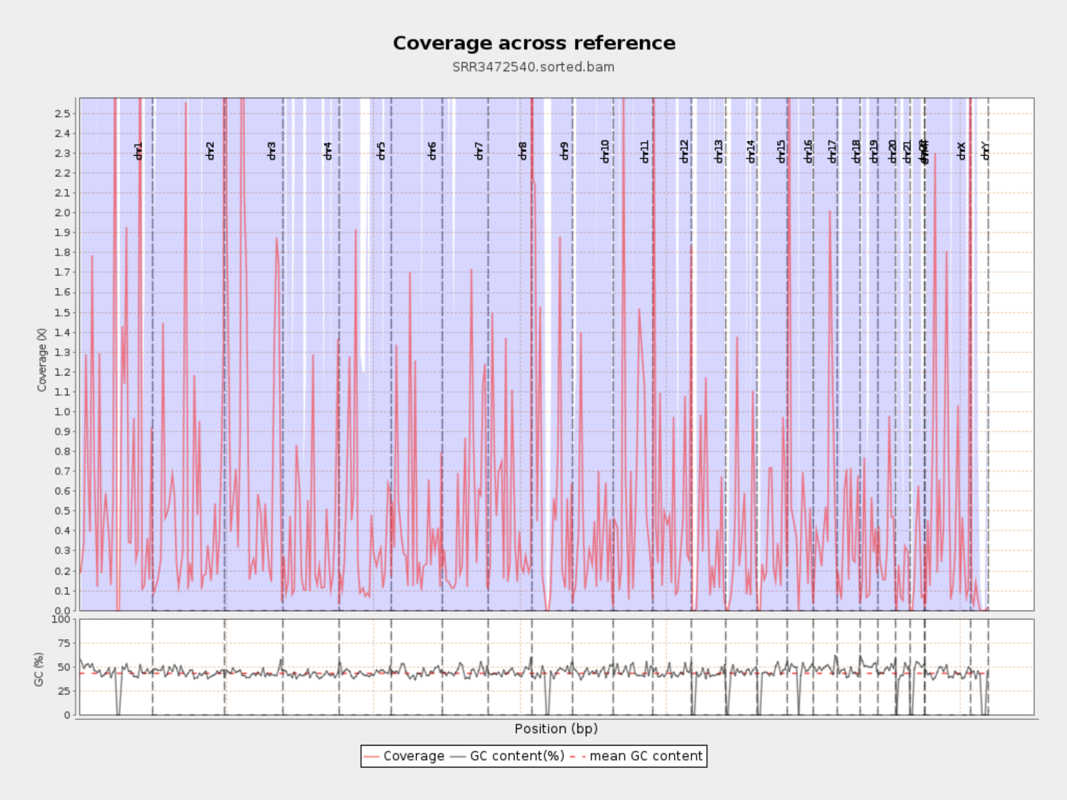
2.7. Chromosome stats

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

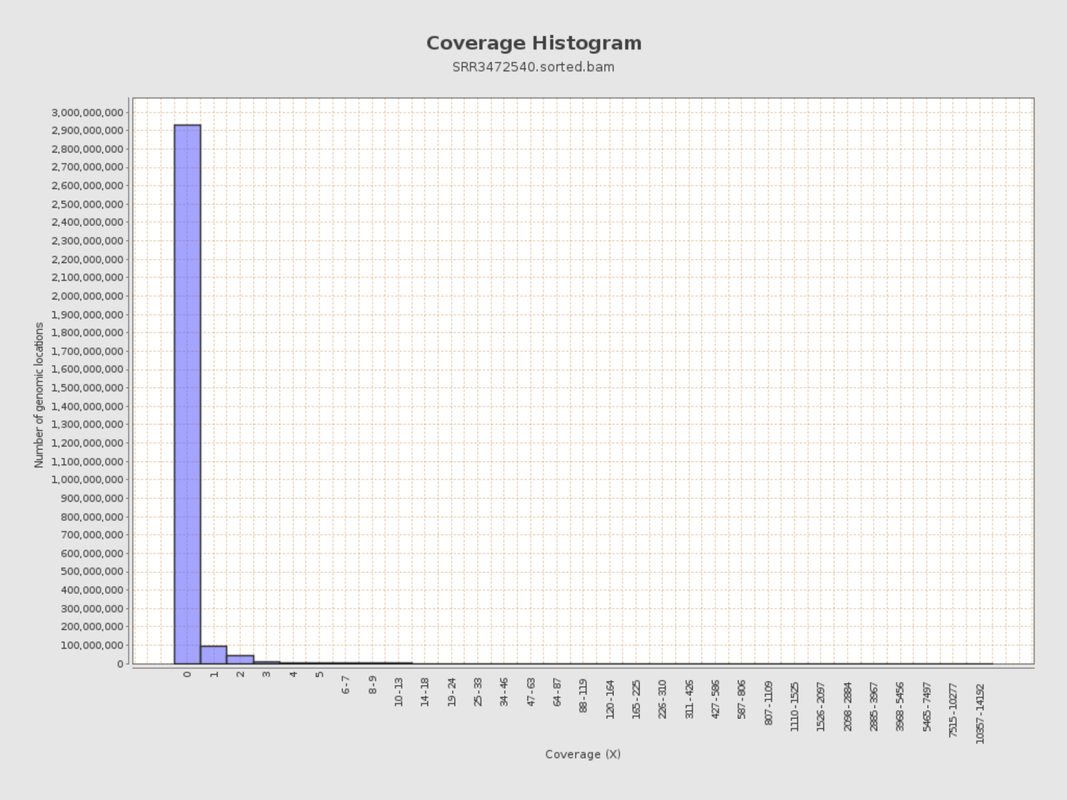
		bases	**coverage**	**deviation**
chr1	249250621	185734010	0.7452	25.7475
chr2	243199373	118114970	0.4857	18.0309
chr3	198022430	195707283	0.9883	24.5689
chr4	191154276	64569970	0.3378	12.356
chr5	180915260	71168824	0.3934	13.2084
chr6	171115067	78374854	0.458	14.2453
chr7	159138663	80703987	0.5071	17.0915
chr8	146364022	72788440	0.4973	19.1131
chr9	141213431	96731300	0.685	19.9576
chr10	135534747	50155215	0.3701	17.3996
chr11	135006516	89446726	0.6625	26.2017
chr12	133851895	79306627	0.5925	19.3851
chr13	115169878	39422487	0.3423	16.0113
chr14	107349540	37825530	0.3524	14.3593
chr15	102531392	35823065	0.3494	10.1522
chr16	90354753	50014170	0.5535	19.8534
chr17	81195210	45687266	0.5627	18.8216
chr18	78077248	29212142	0.3741	13.6924
chr19	59128983	18510137	0.313	10.3297
chr20	63025520	24222210	0.3843	12.2256
chr21	48129895	7627298	0.1585	9.2335
chr22	51304566	10534807	0.2053	8.9694
chrMT	16571	5517	0.3329	1.076
chrX	155270560	88394059	0.5693	19.9047

chrY	59373566	2259277	0.0381	1.6908

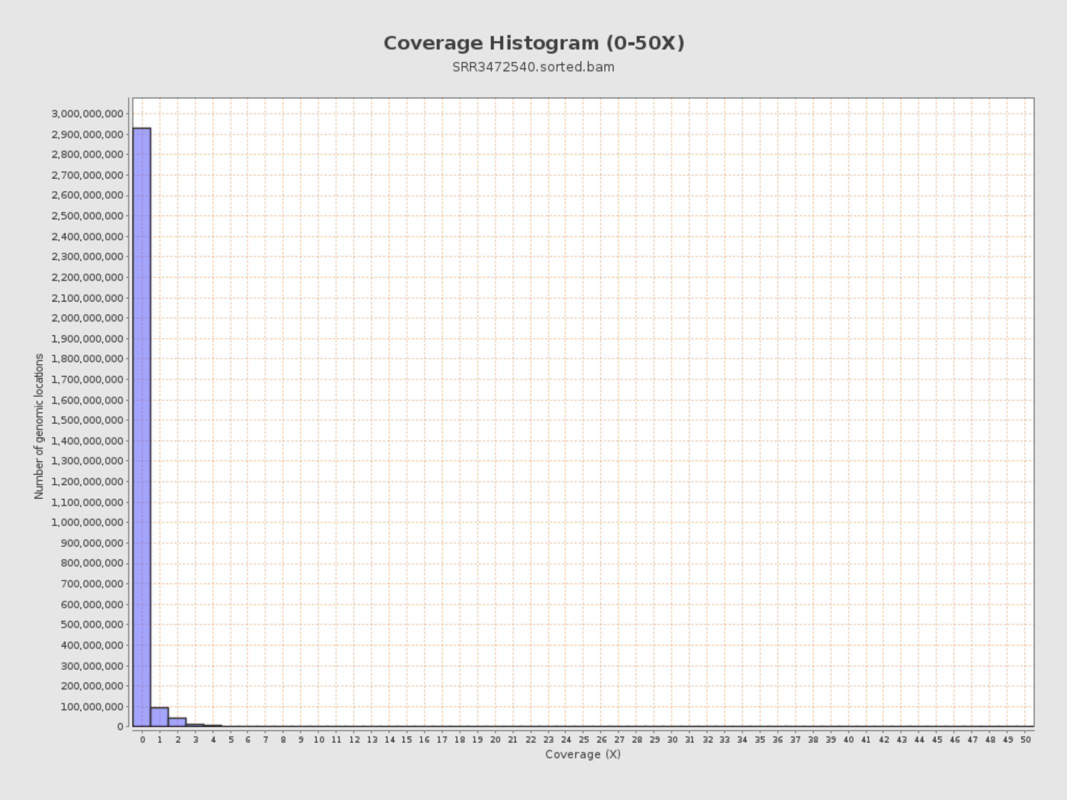
3. Results : Coverage across reference



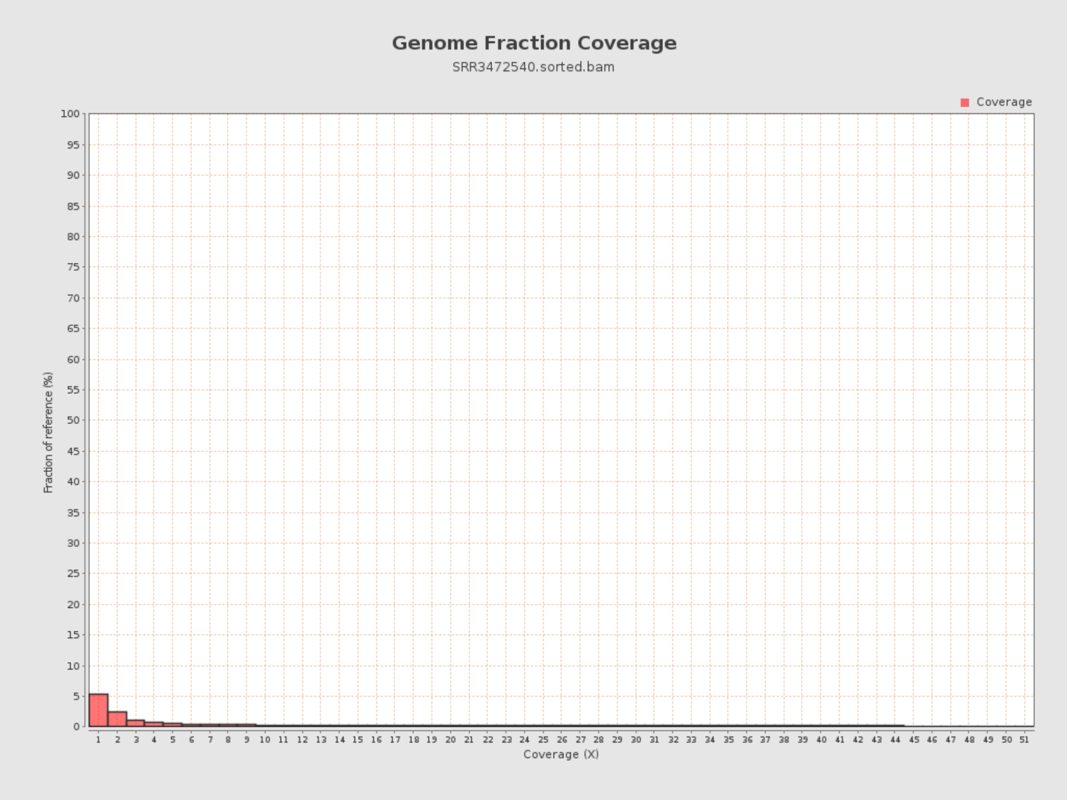
4. Results : Coverage Histogram



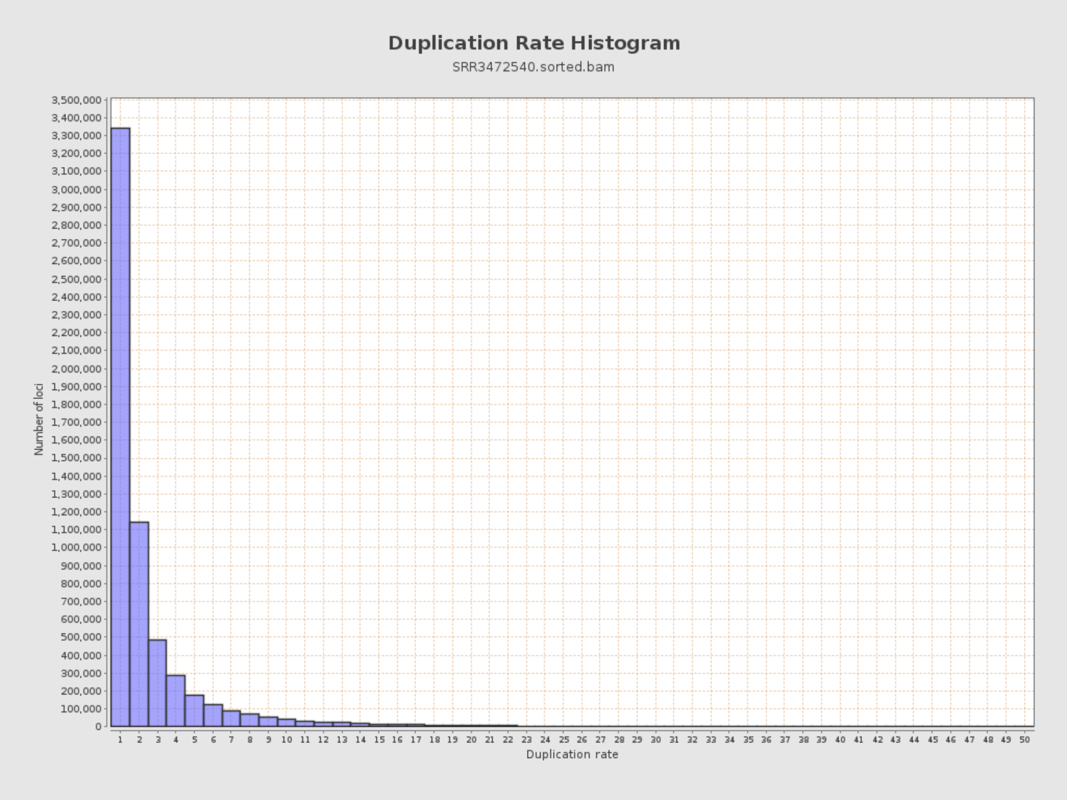
5. Results : Coverage Histogram (0-50X)



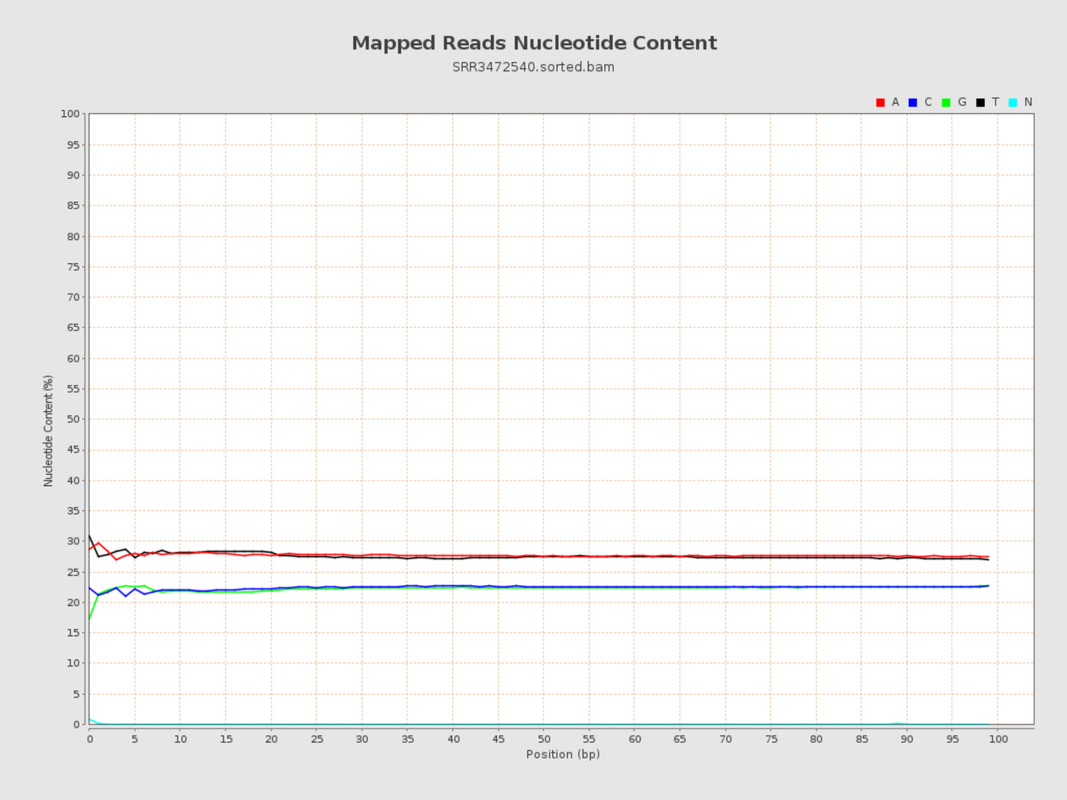
6. Results : Genome Fraction Coverage



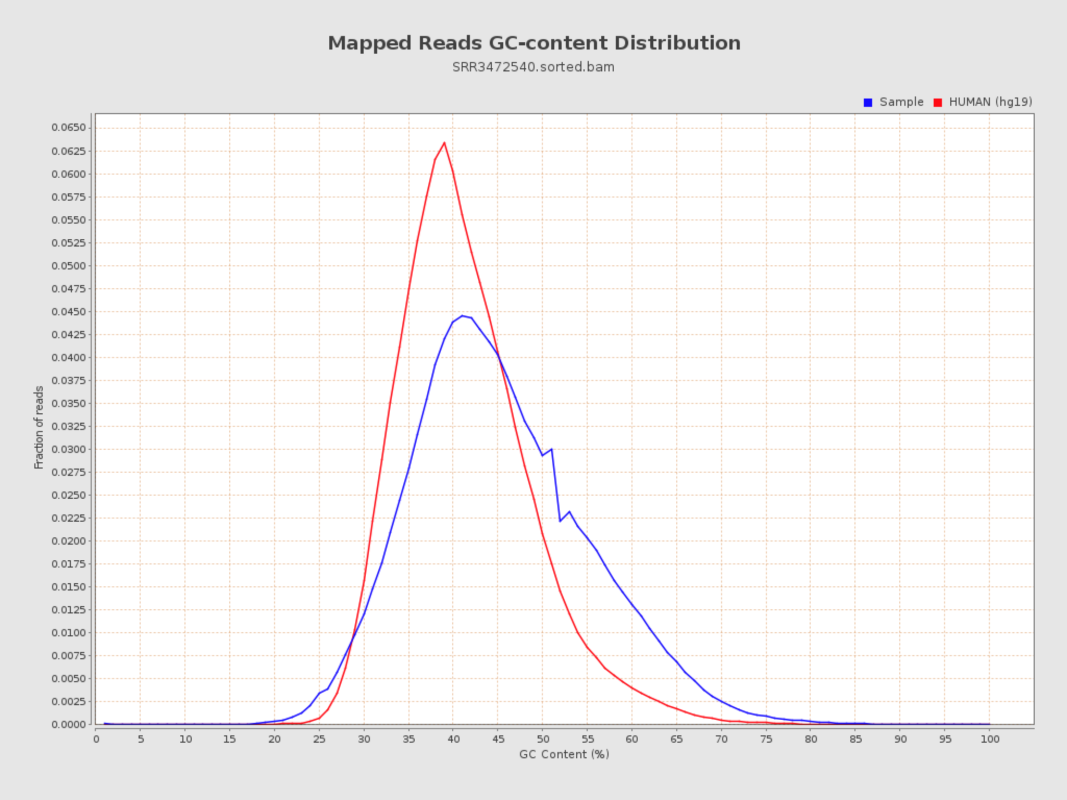
7. Results : Duplication Rate Histogram



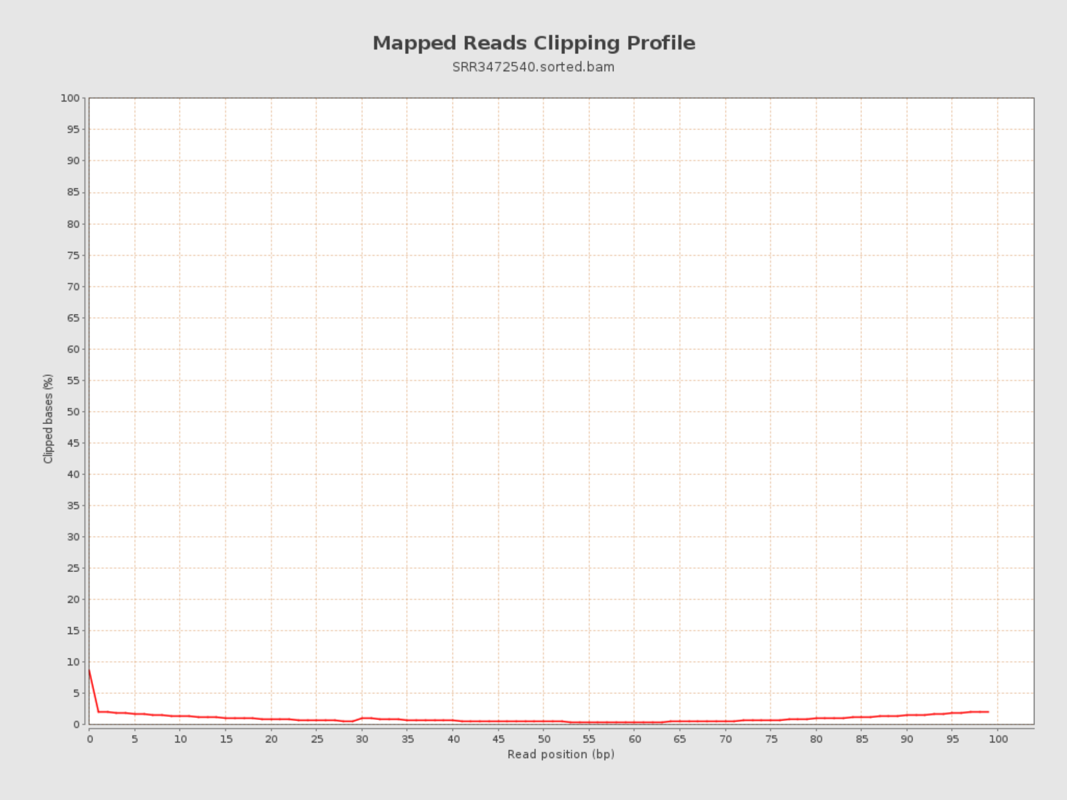
8. Results : Mapped Reads Nucleotide Content



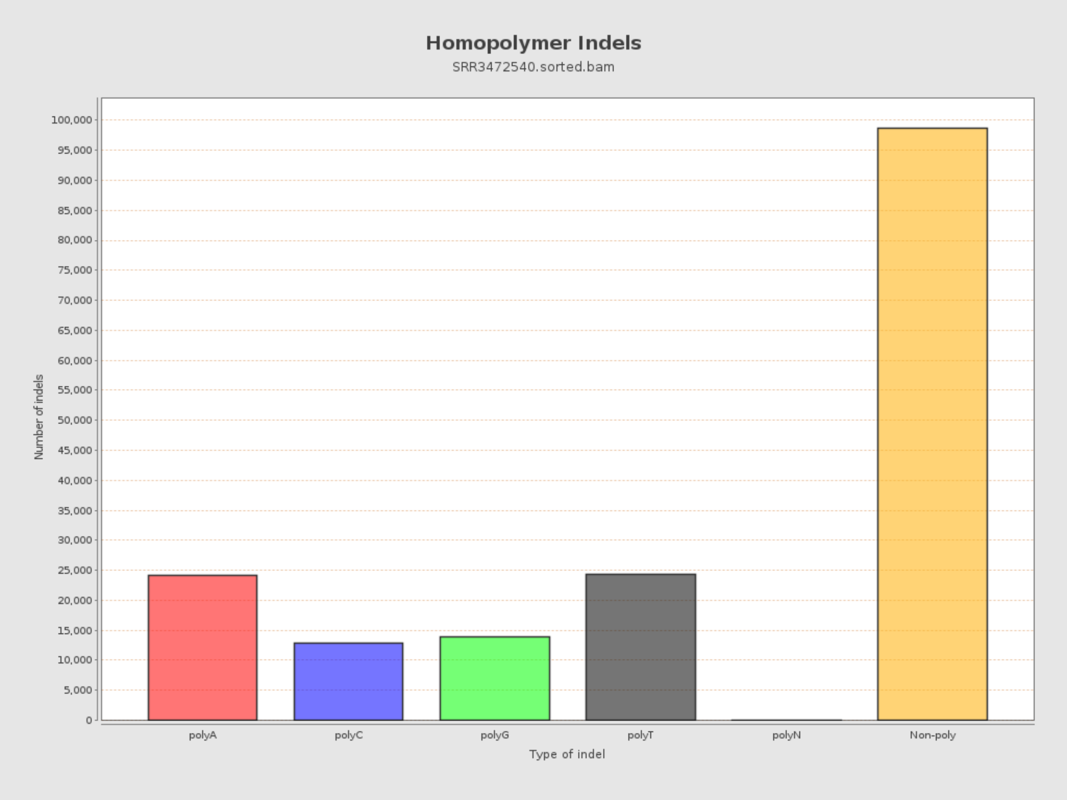
9. Results : Mapped Reads GC-content Distribution



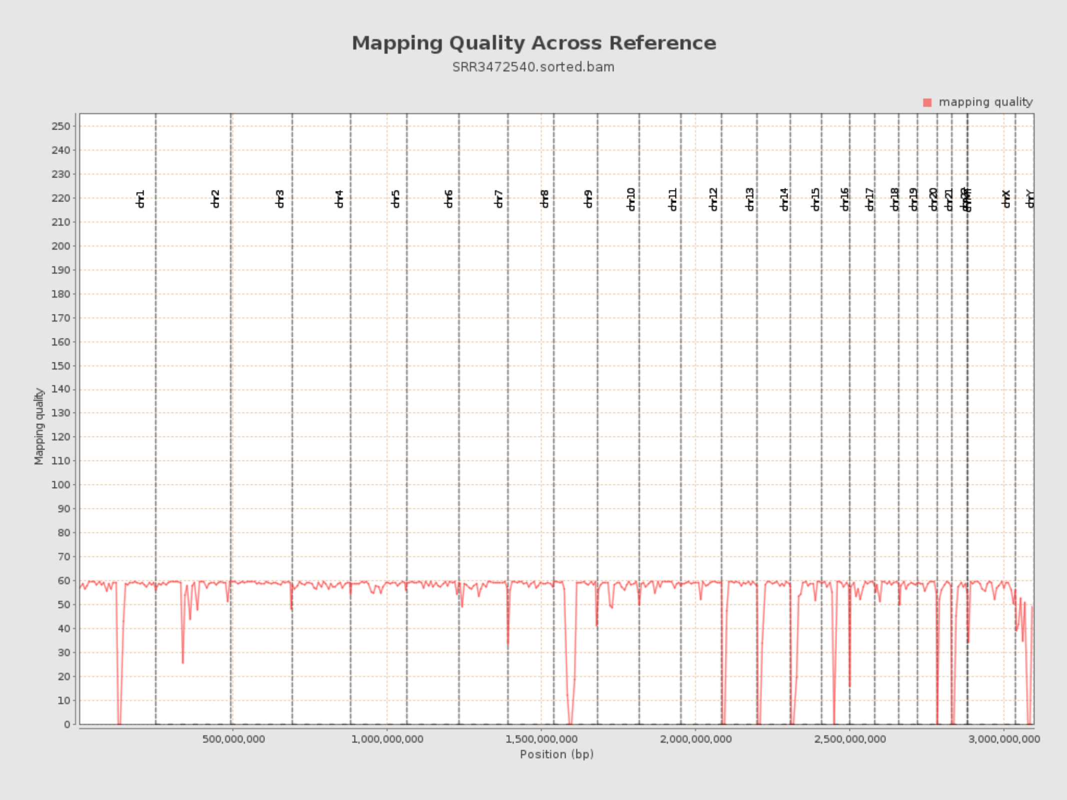
10. Results : Mapped Reads Clipping Profile



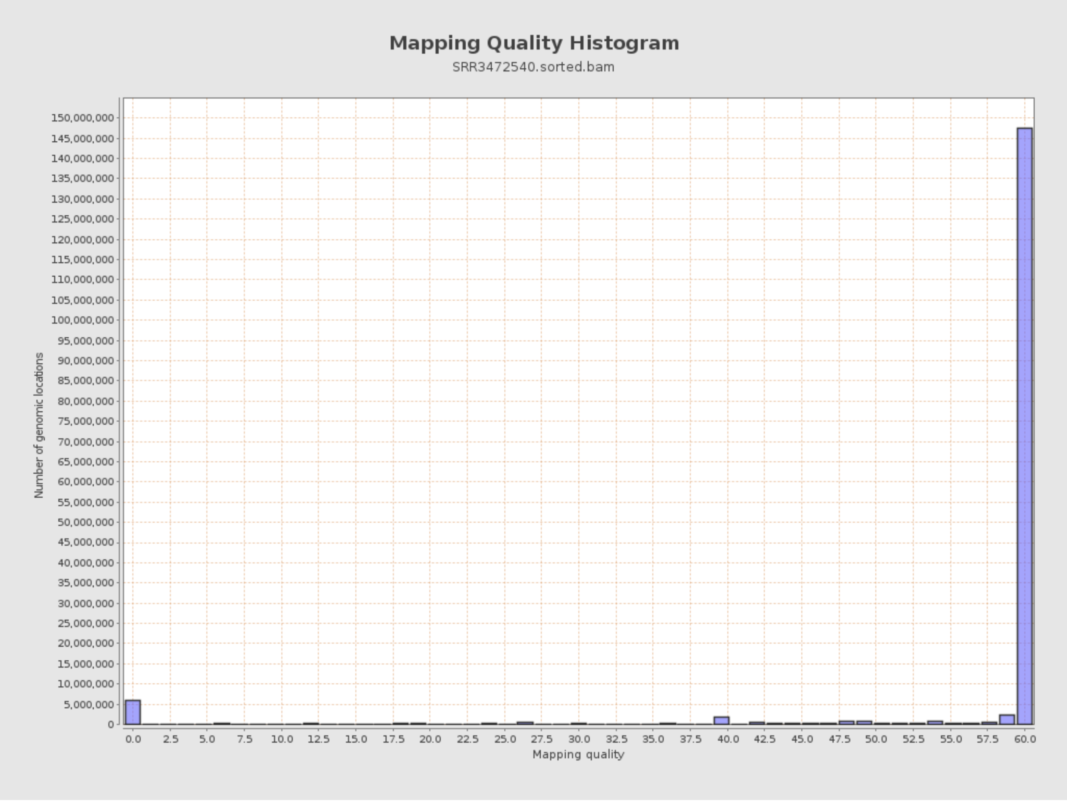
11. Results : Homopolymer Indels



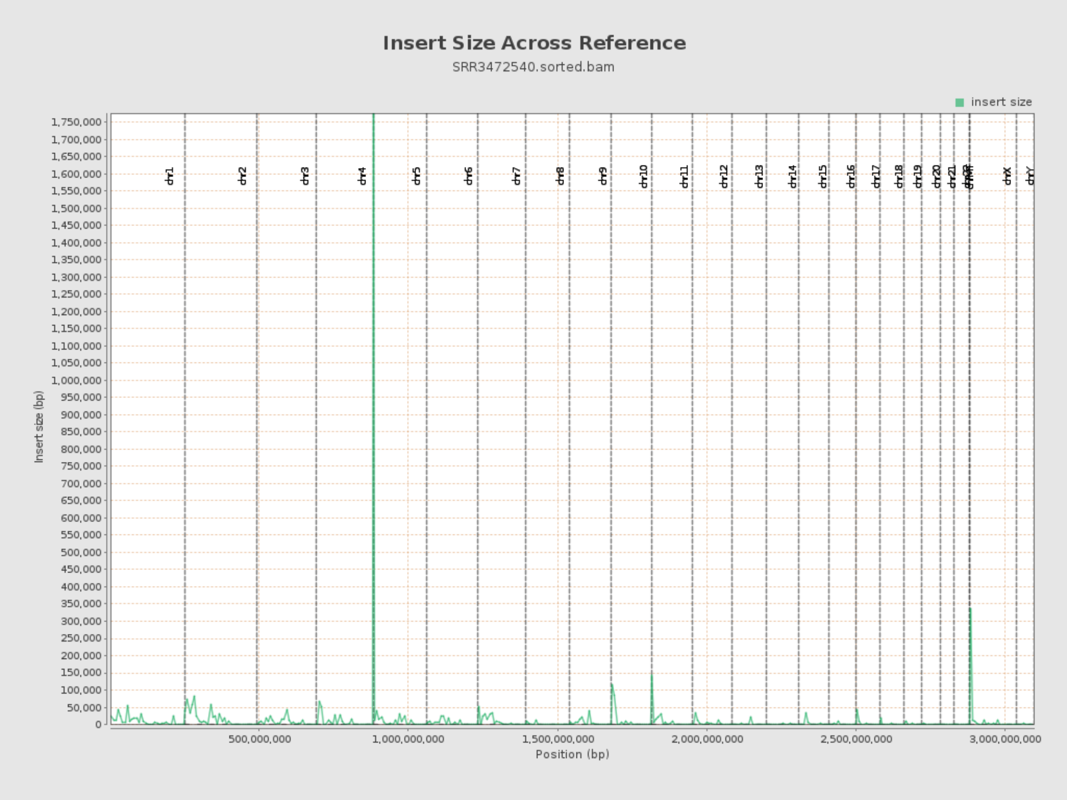
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram