Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 23:24:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472532.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_SRR3472532 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472532_1.fastq.gz SRR3472532_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 23:24:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472532.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,821,760
Mapped reads	19,601,210 / 98.89%
Unmapped reads	220,550 / 1.11%
Mapped paired reads	19,601,210 / 98.89%
Mapped reads, first in pair	9,828,712 / 49.59%
Mapped reads, second in pair	9,772,498 / 49.3%
Mapped reads, both in pair	19,488,998 / 98.32%
Mapped reads, singletons	112,212 / 0.57%
Secondary alignments	0
Supplementary alignments	78,295 / 0.39%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	12,851,430 / 64.83%
Duplication rate	47.12%
Clipped reads	1,573,809 / 7.94%

2.2. ACGT Content

Number/percentage of A's	528,179,359 / 27.37%
Number/percentage of C's	439,648,023 / 22.78%
Number/percentage of T's	526,500,707 / 27.28%
Number/percentage of G's	435,426,413 / 22.56%
Number/percentage of N's	300,127 / 0.02%

GC Percentage	45.34%

2.3. Coverage

Mean	0.6235
Standard Deviation	22.2046

2.4. Mapping Quality

Mean Mapping Quality	54.99

2.5. Insert size

Mean	30,717.86
Standard Deviation	1,730,289.94
P25/Median/P75	172 / 237 / 317

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	11,373,695
Insertions	102,759
Mapped reads with at least one insertion	0.52%
Deletions	96,921
Mapped reads with at least one deletion	0.49%
Homopolymer indels	45.98%

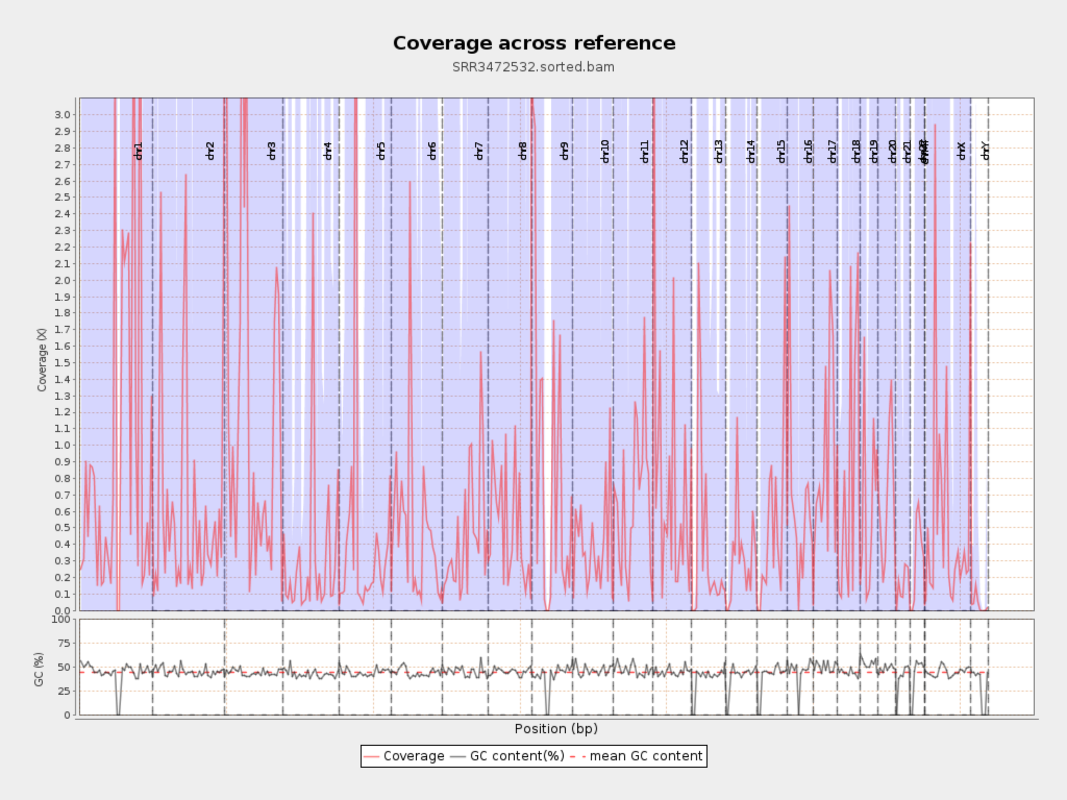
2.7. Chromosome stats

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

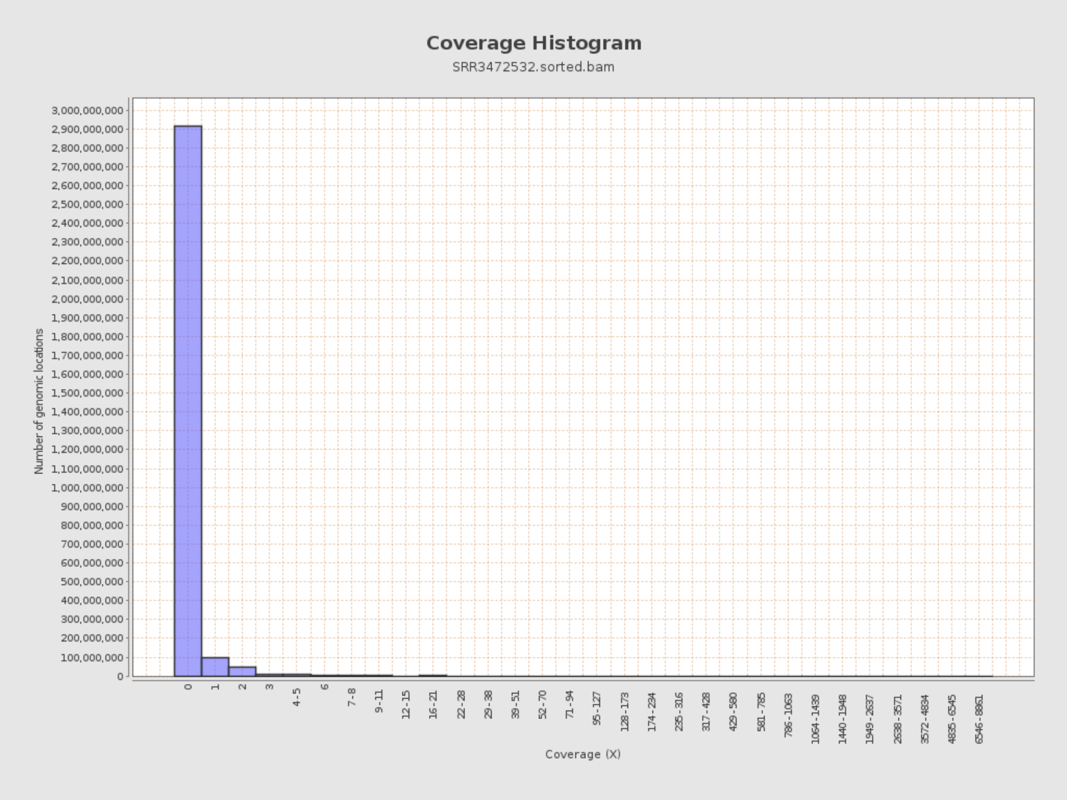
		bases	**coverage**	**deviation**
chr1	249250621	254725680	1.022	38.9695
chr2	243199373	139084278	0.5719	20.4233
chr3	198022430	256332515	1.2945	29.0858
chr4	191154276	57713583	0.3019	16.0845
chr5	180915260	86039726	0.4756	18.4693
chr6	171115067	84585048	0.4943	14.1313
chr7	159138663	73684764	0.463	18.7248
chr8	146364022	74120286	0.5064	16.7735
chr9	141213431	126464543	0.8956	27.7616
chr10	135534747	54536168	0.4024	12.9885
chr11	135006516	92783463	0.6873	23.097
chr12	133851895	110017183	0.8219	26.8342
chr13	115169878	45296940	0.3933	16.3926
chr14	107349540	34144619	0.3181	11.0716
chr15	102531392	56980378	0.5557	21.0969
chr16	90354753	58305095	0.6453	18.0168
chr17	81195210	73246035	0.9021	20.4315
chr18	78077248	60637039	0.7766	33.994
chr19	59128983	37921387	0.6413	17.146
chr20	63025520	43914182	0.6968	23.9192
chr21	48129895	7540671	0.1567	6.7866
chr22	51304566	15876928	0.3095	9.4633
chrMT	16571	1715	0.1035	0.3463
chrX	155270560	84066236	0.5414	14.4998

chrY	59373566	2276347	0.0383	1.1641

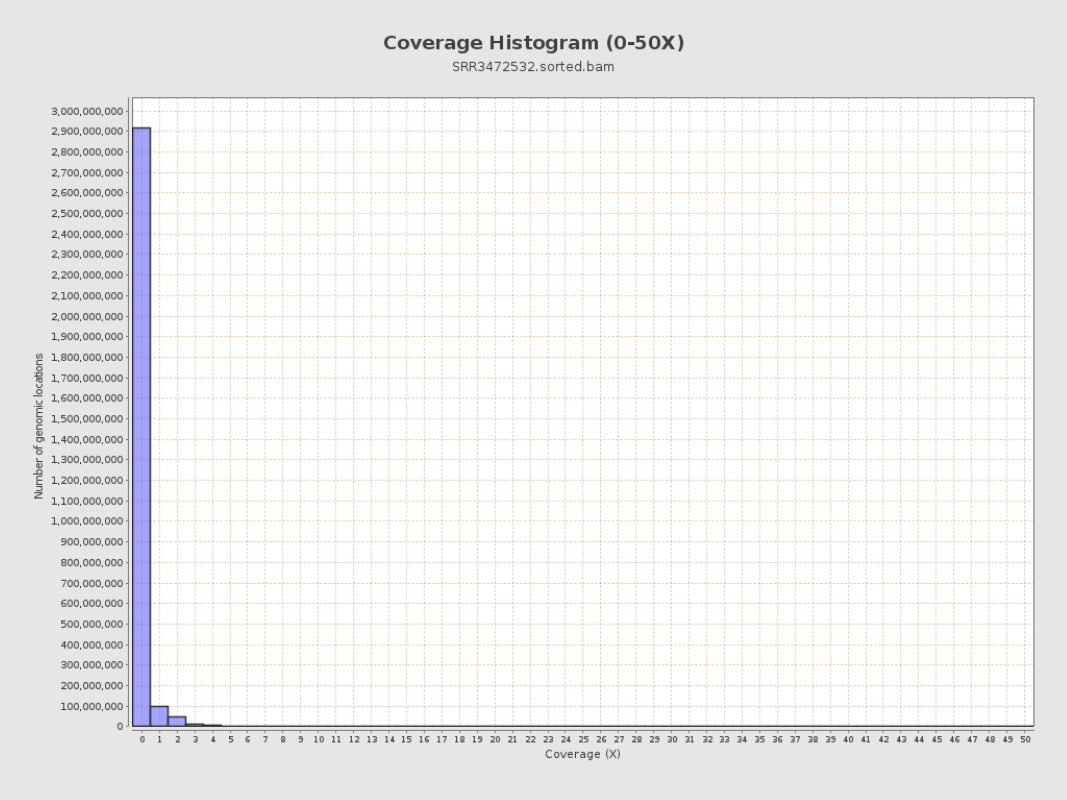
3. Results : Coverage across reference



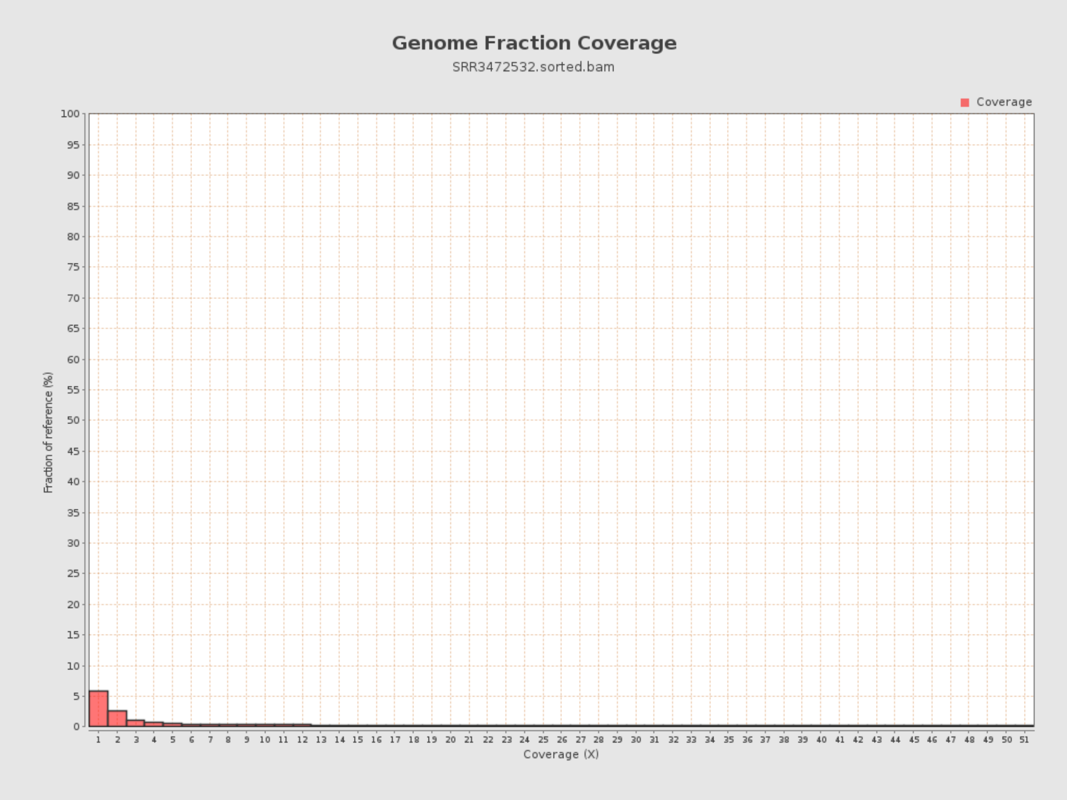
4. Results : Coverage Histogram



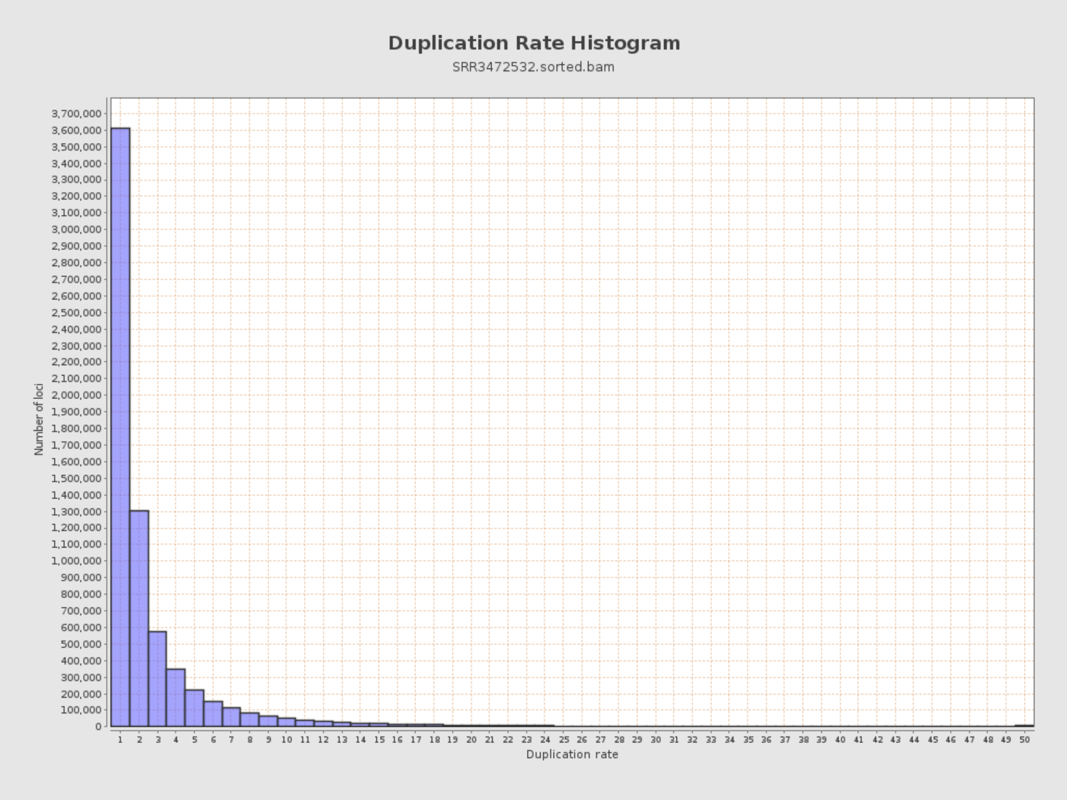
5. Results : Coverage Histogram (0-50X)



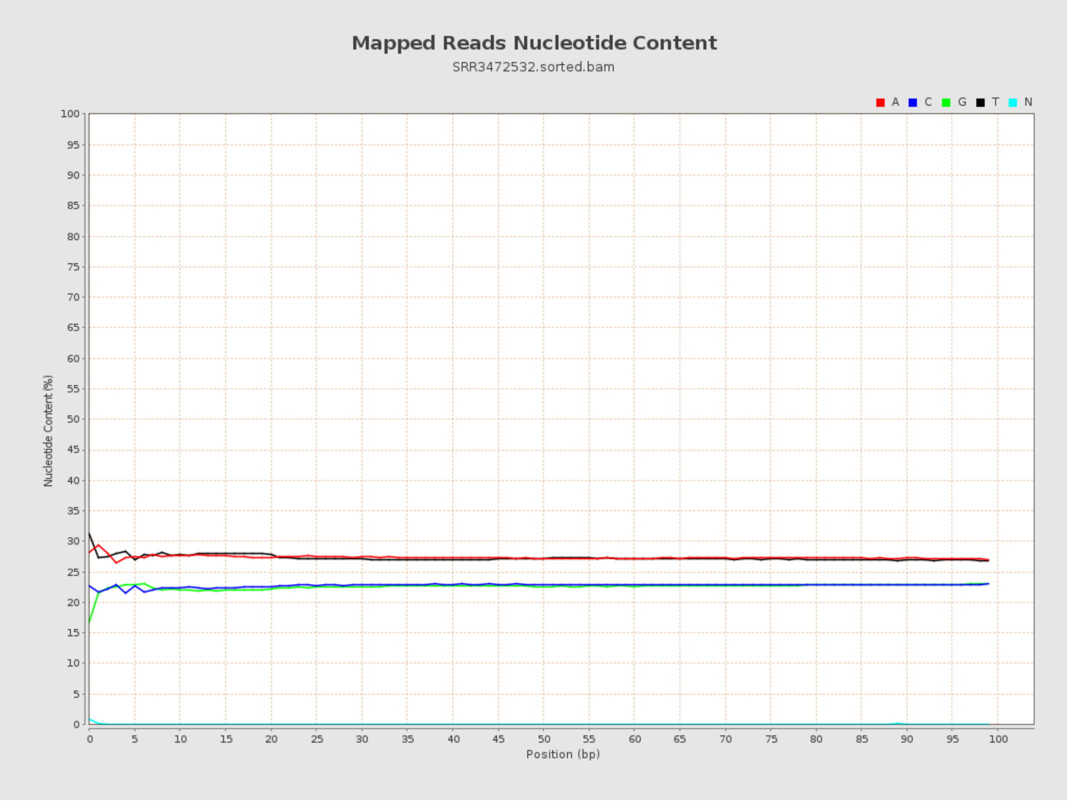
6. Results : Genome Fraction Coverage



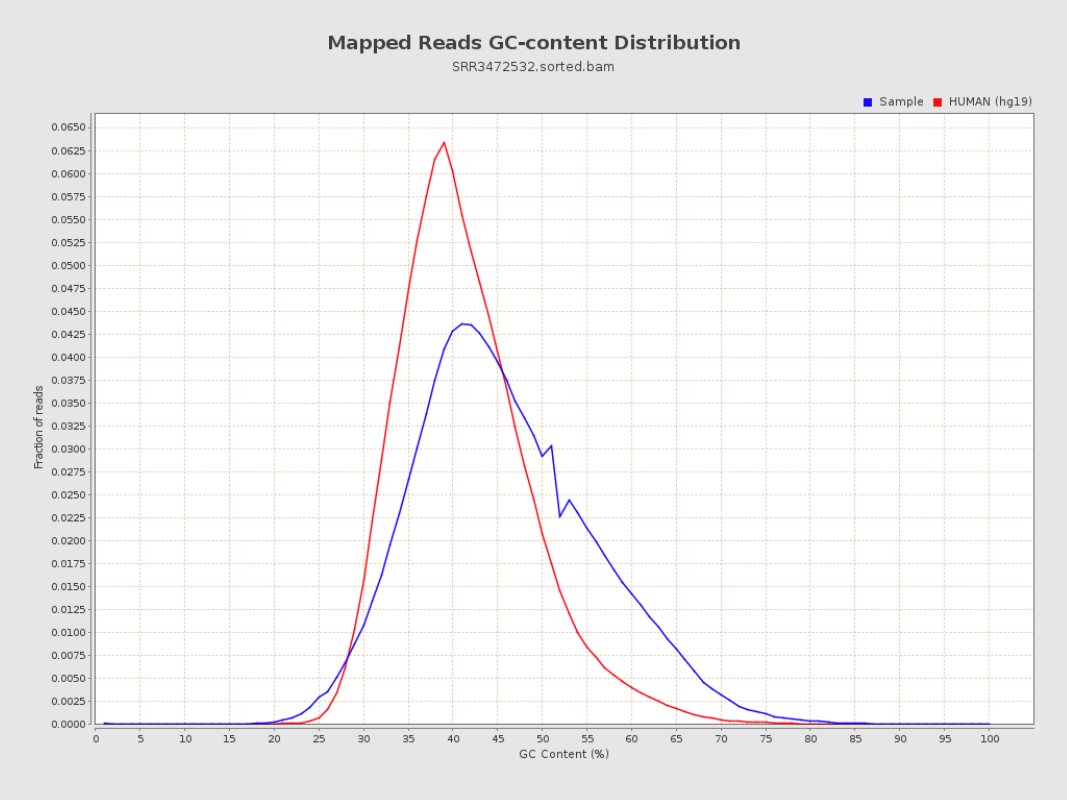
7. Results : Duplication Rate Histogram



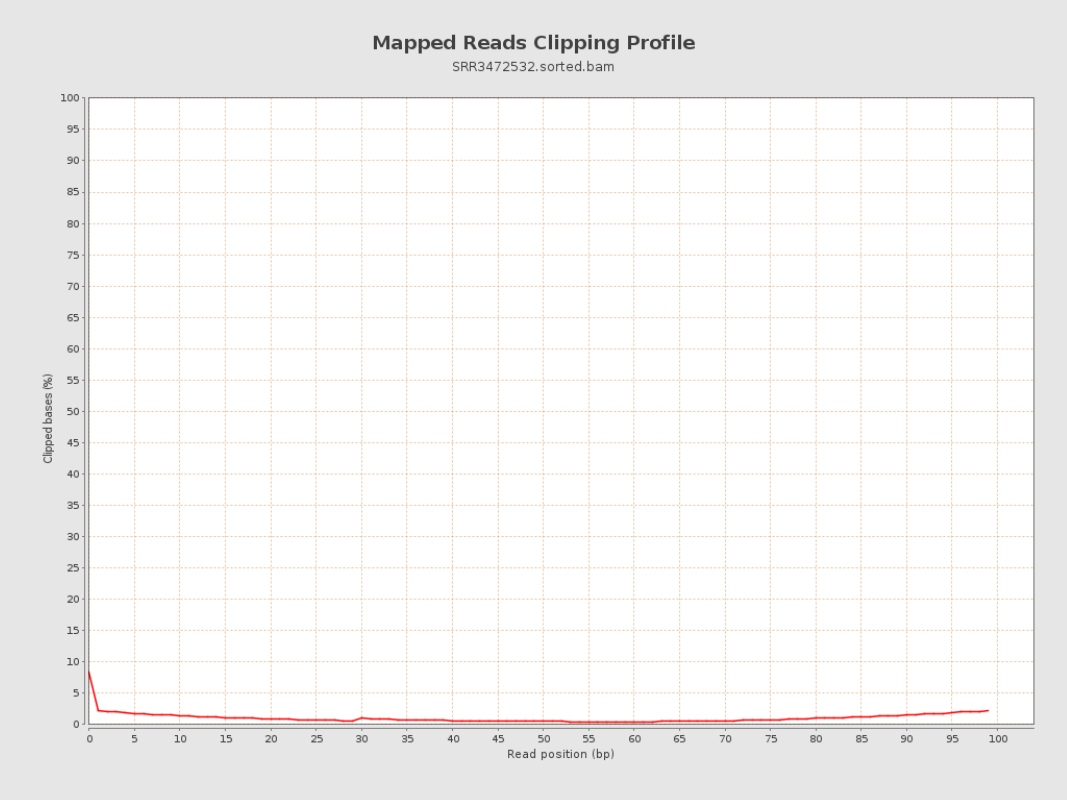
8. Results : Mapped Reads Nucleotide Content



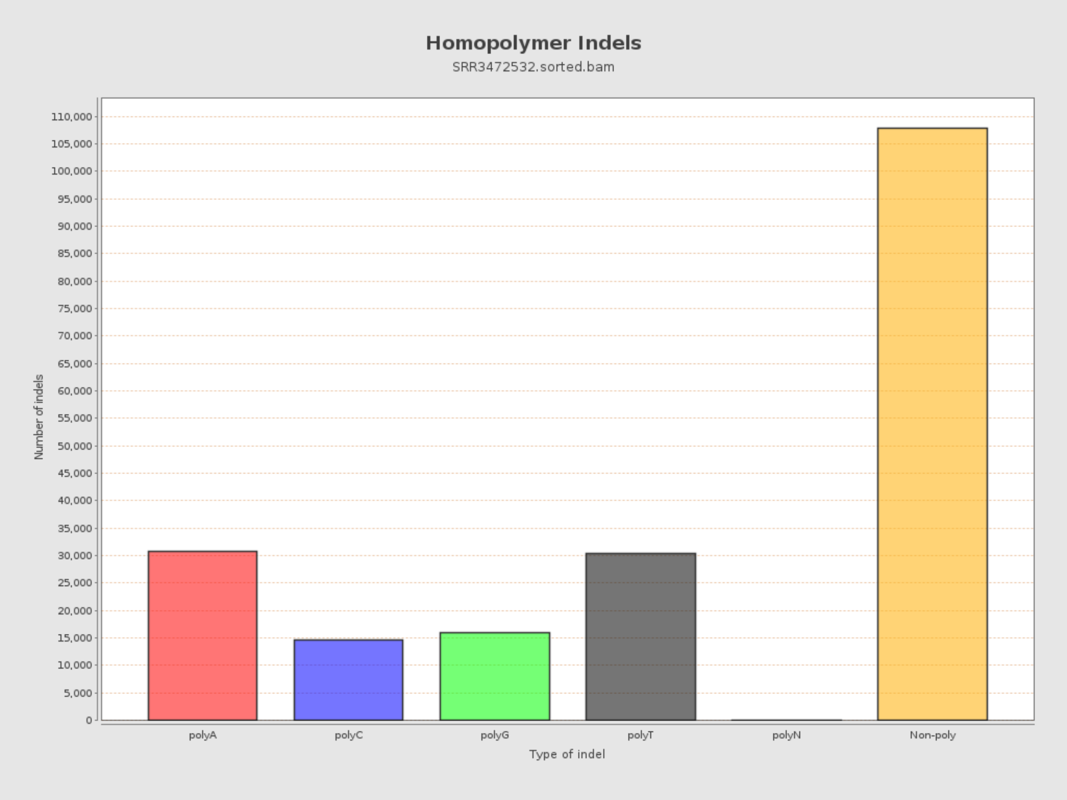
9. Results : Mapped Reads GC-content Distribution



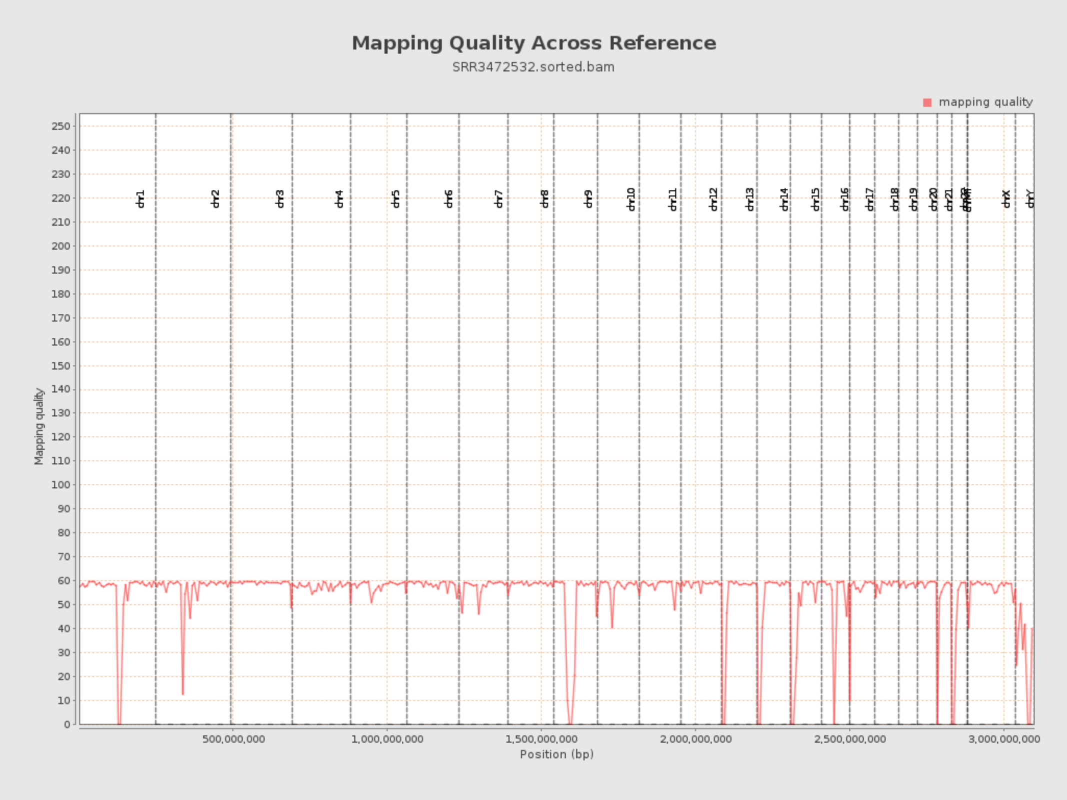
10. Results : Mapped Reads Clipping Profile



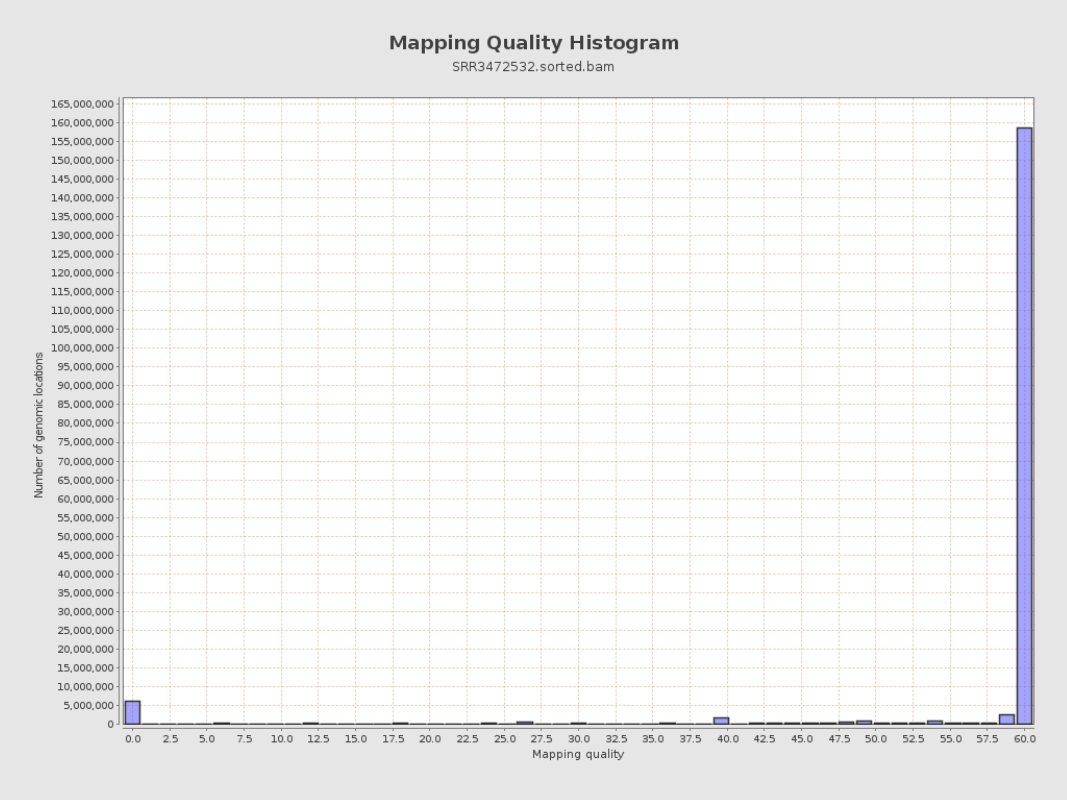
11. Results : Homopolymer Indels



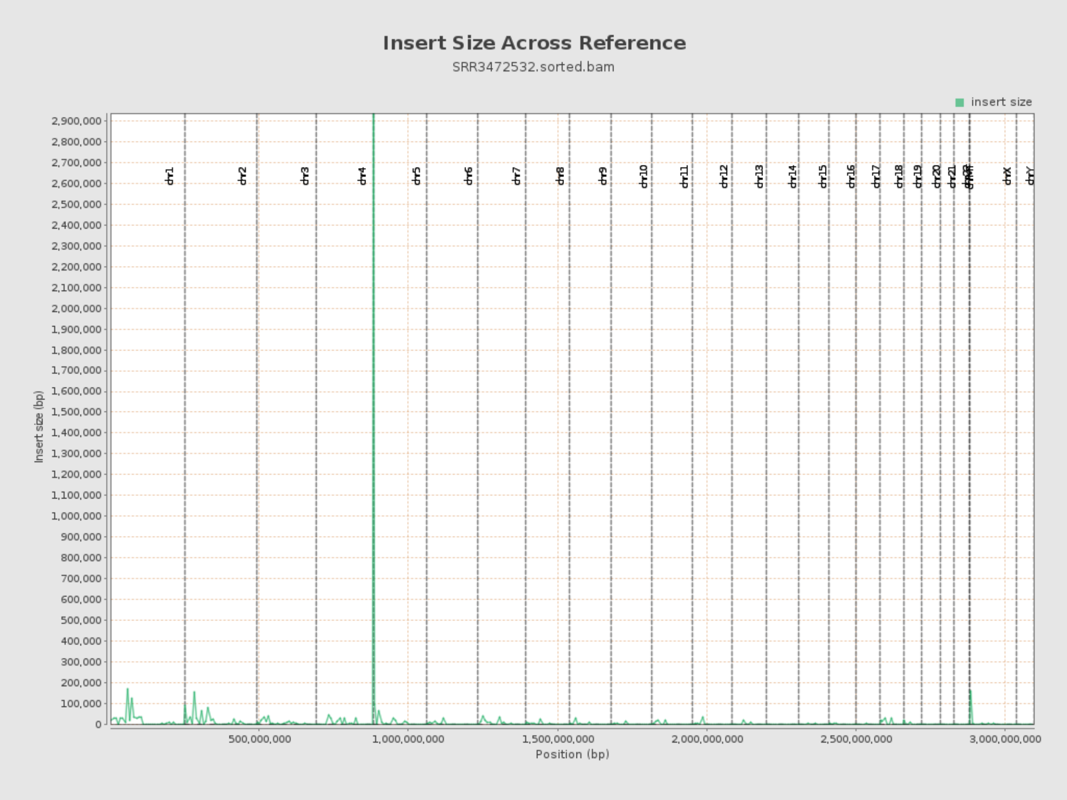
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram