Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:56:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472556.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_SRR3472556 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472556_1.fastq.gz SRR3472556_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:56:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472556.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,719,770
Mapped reads	10,252,335 / 95.64%
Unmapped reads	467,435 / 4.36%
Mapped paired reads	10,252,335 / 95.64%
Mapped reads, first in pair	5,145,152 / 48%
Mapped reads, second in pair	5,107,183 / 47.64%
Mapped reads, both in pair	10,158,218 / 94.76%
Mapped reads, singletons	94,117 / 0.88%
Secondary alignments	0
Supplementary alignments	44,714 / 0.42%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	5,948,383 / 55.49%
Duplication rate	43.98%
Clipped reads	1,079,773 / 10.07%

2.2. ACGT Content

Number/percentage of A's	271,487,260 / 27.1%
Number/percentage of C's	231,499,490 / 23.11%
Number/percentage of T's	268,632,065 / 26.81%
Number/percentage of G's	230,156,583 / 22.97%
Number/percentage of N's	155,837 / 0.02%

GC Percentage	46.08%

2.3. Coverage

Mean	0.3237
Standard Deviation	13.926

2.4. Mapping Quality

Mean Mapping Quality	54.48

2.5. Insert size

Mean	36,439.77
Standard Deviation	1,877,753.85
P25/Median/P75	154 / 217 / 295

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	5,662,925
Insertions	50,777
Mapped reads with at least one insertion	0.49%
Deletions	46,773
Mapped reads with at least one deletion	0.45%
Homopolymer indels	44.25%

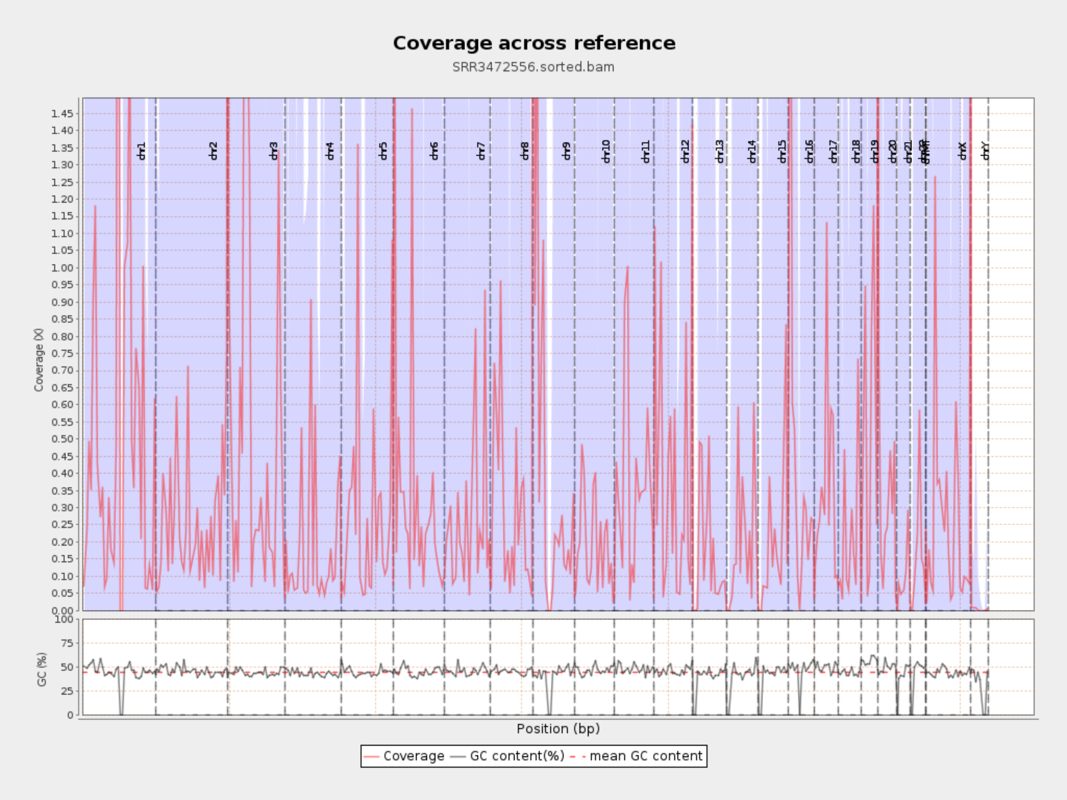
2.7. Chromosome stats

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

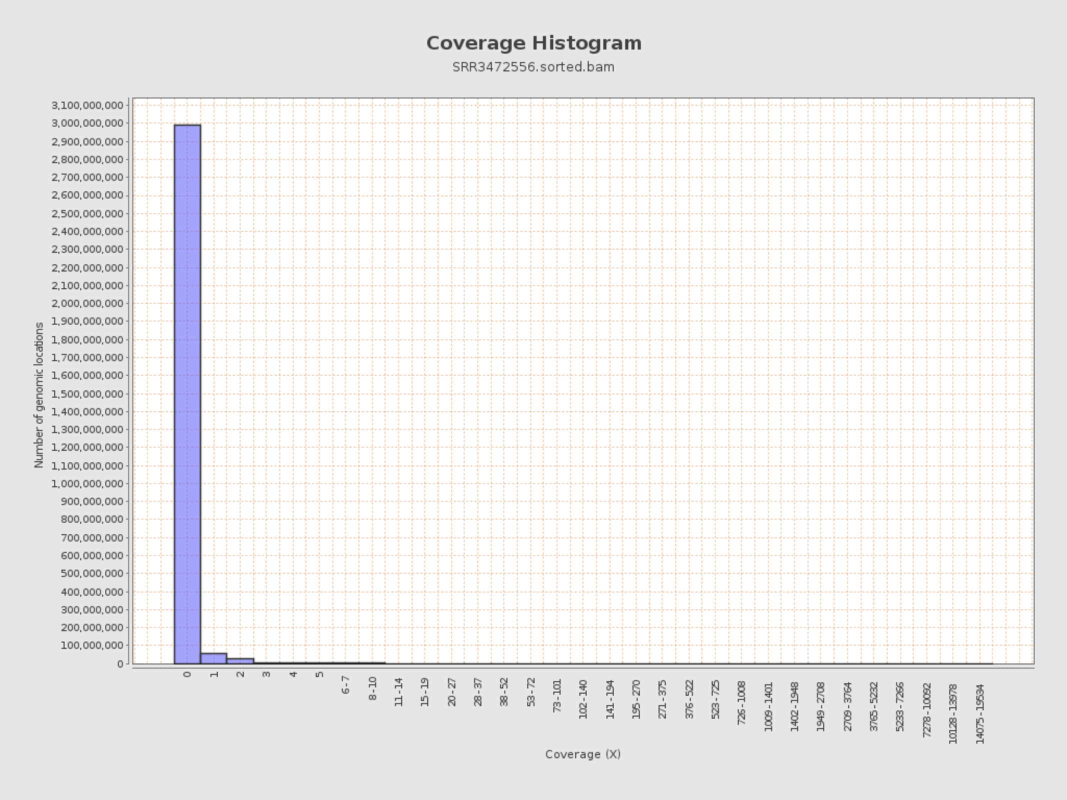
		bases	coverage	deviation
chr1	249250621	136783378	0.5488	31.0039
chr2	243199373	61959548	0.2548	8.1965
chr3	198022430	113581473	0.5736	15.5733
chr4	191154276	35882953	0.1877	11.5278
chr5	180915260	52899791	0.2924	13.7389
chr6	171115067	59356432	0.3469	14.6341
chr7	159138663	43966454	0.2763	8.801
chr8	146364022	43309463	0.2959	9.9312
chr9	141213431	58067991	0.4112	12.6647
chr10	135534747	26986293	0.1991	8.3688
chr11	135006516	49202044	0.3644	16.2619
chr12	133851895	54026671	0.4036	11.6035
chr13	115169878	19101695	0.1659	6.2548
chr14	107349540	22179018	0.2066	7.1428
chr15	102531392	21045452	0.2053	7.183
chr16	90354753	41591608	0.4603	13.666
chr17	81195210	30496844	0.3756	9.5332
chr18	78077248	17428824	0.2232	8.1497
chr19	59128983	35421578	0.5991	18.5753
chr20	63025520	19234432	0.3052	8.534
chr21	48129895	4683894	0.0973	5.3091
chr22	51304566	9077072	0.1769	6.4473
chrMT	16571	4018	0.2425	0.8852
chrX	155270560	45529436	0.2932	9.605

chrY	59373566	228116	0.0038	0.2269

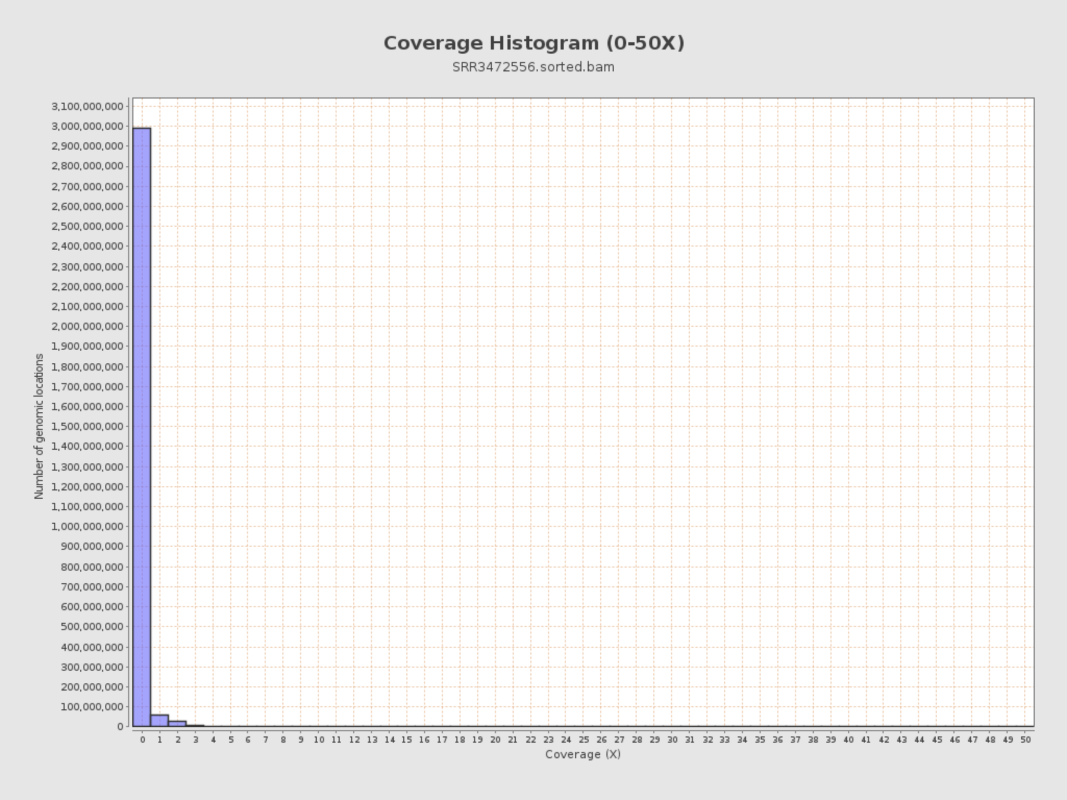
3. Results : Coverage across reference



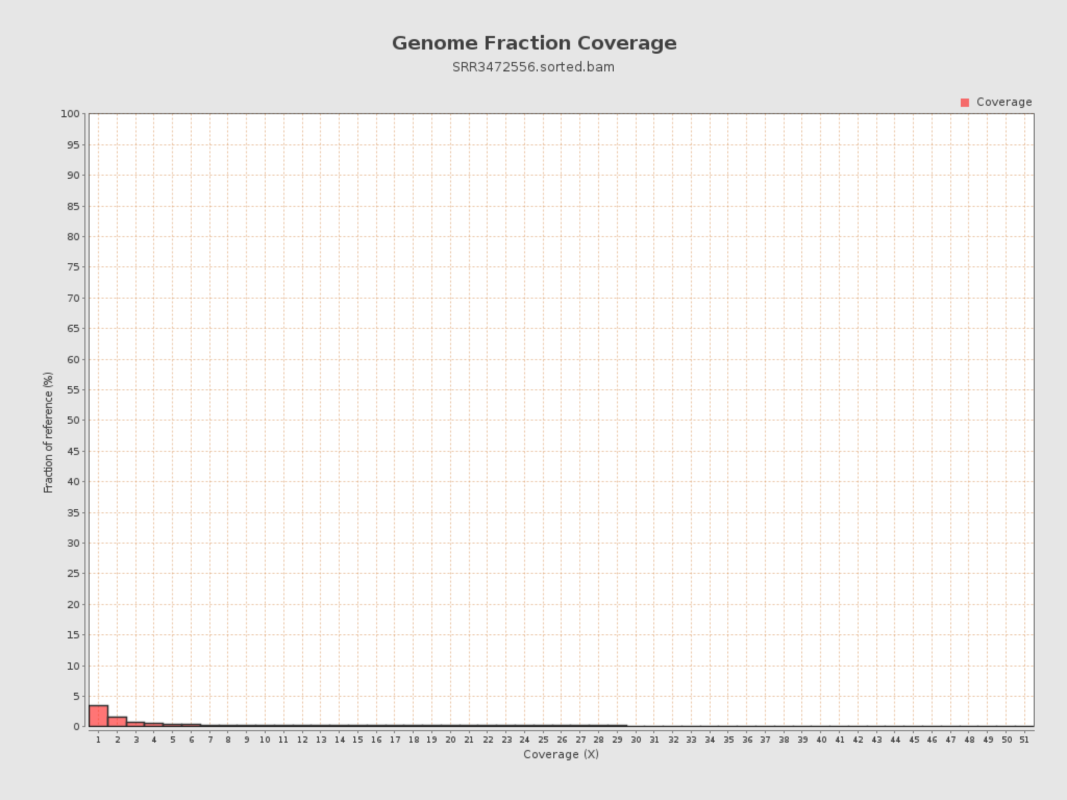
4. Results : Coverage Histogram



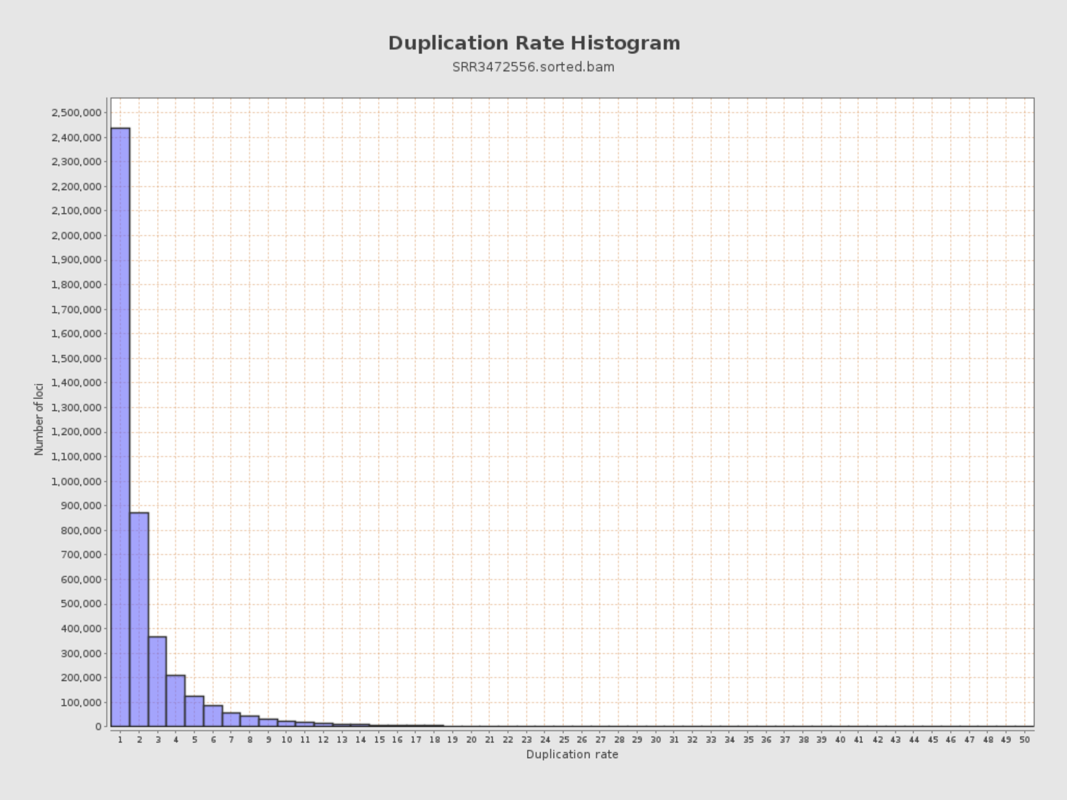
5. Results : Coverage Histogram (0-50X)



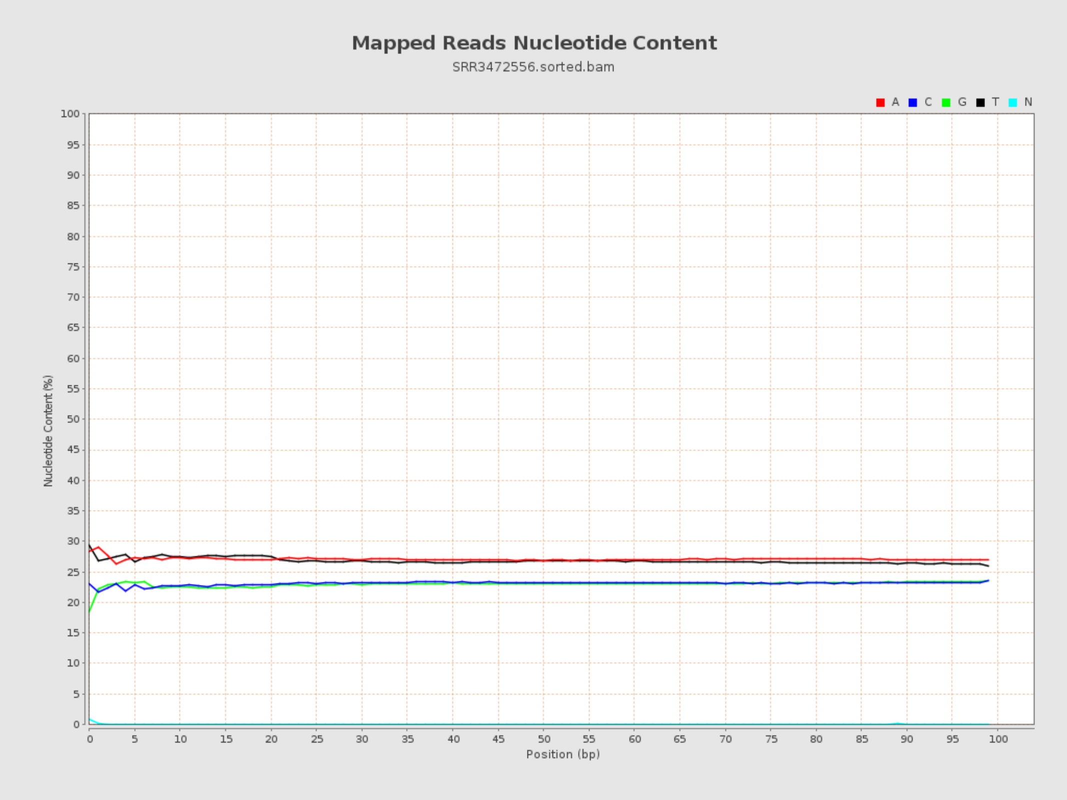
6. Results : Genome Fraction Coverage



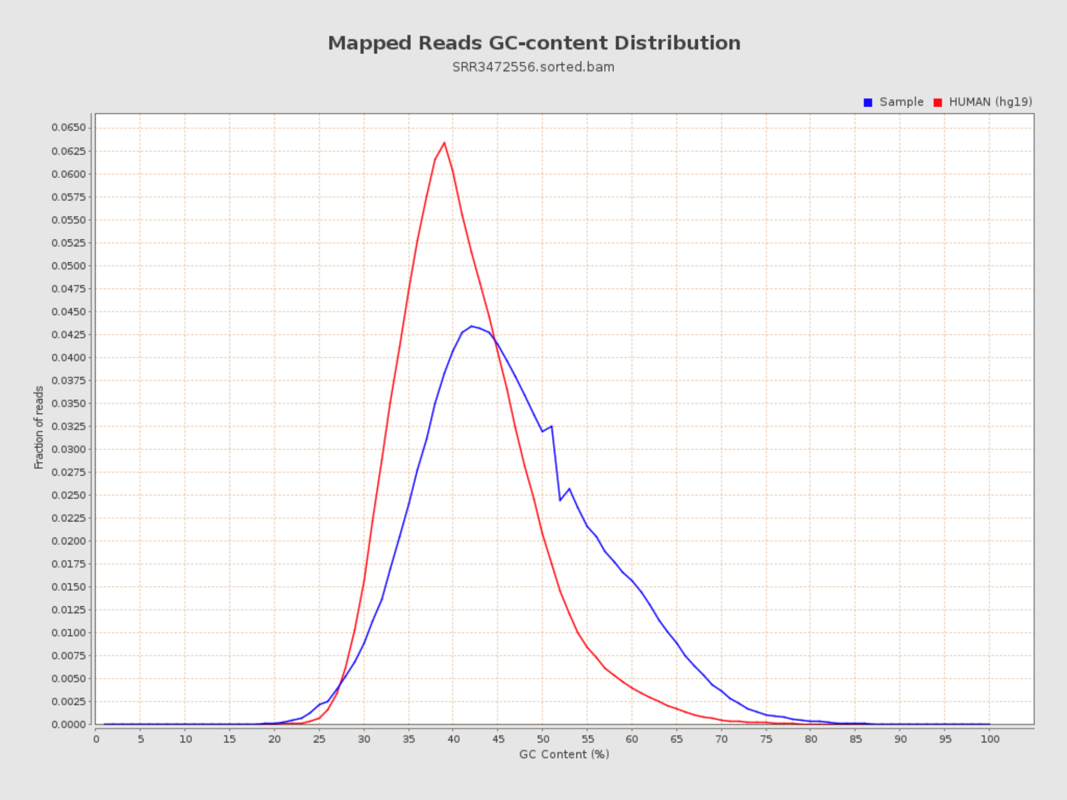
7. Results : Duplication Rate Histogram



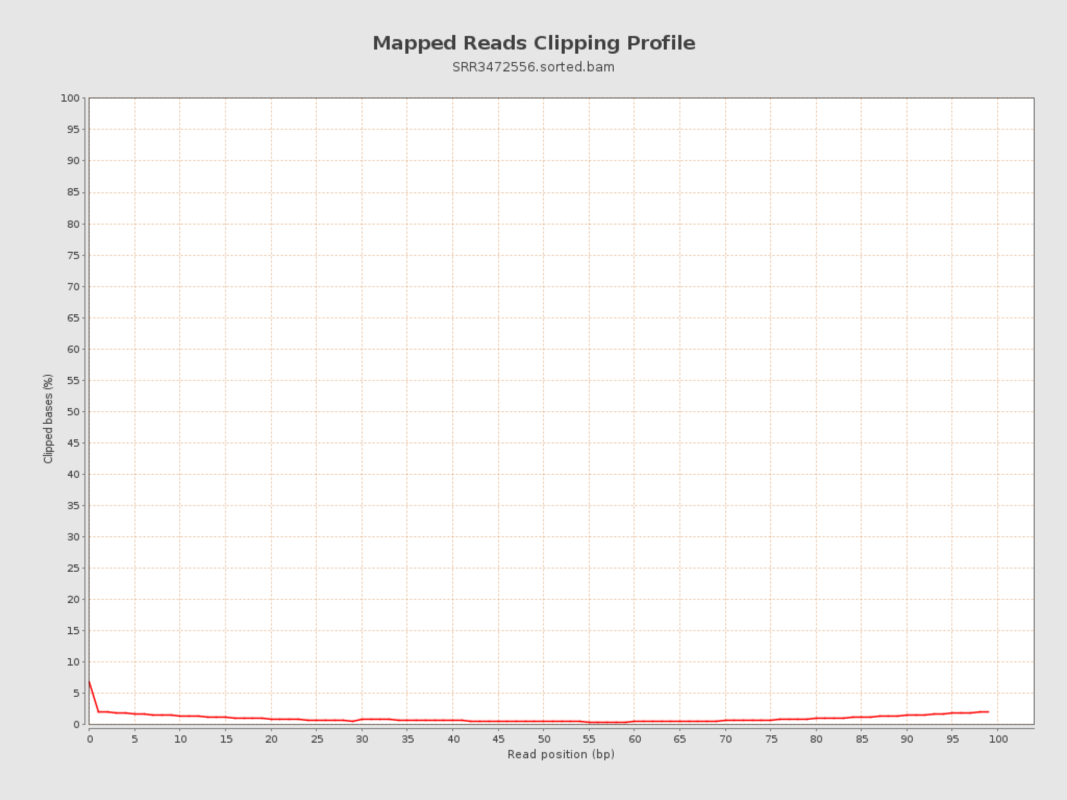
8. Results : Mapped Reads Nucleotide Content



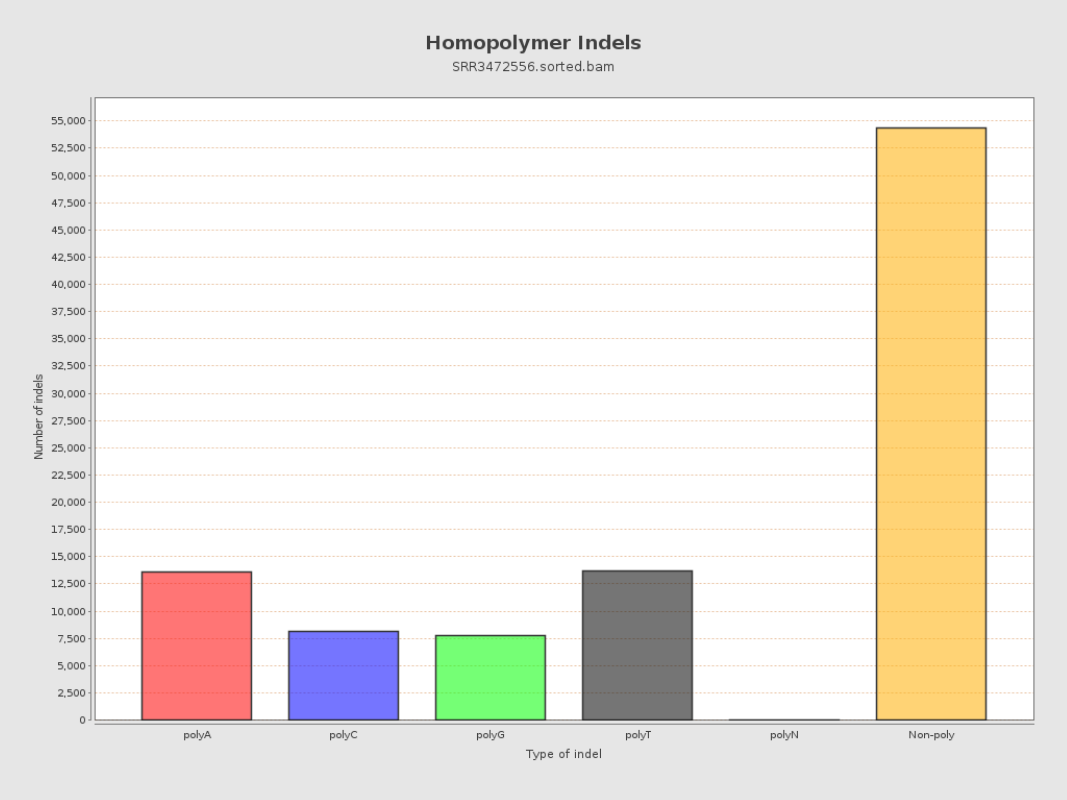
9. Results : Mapped Reads GC-content Distribution



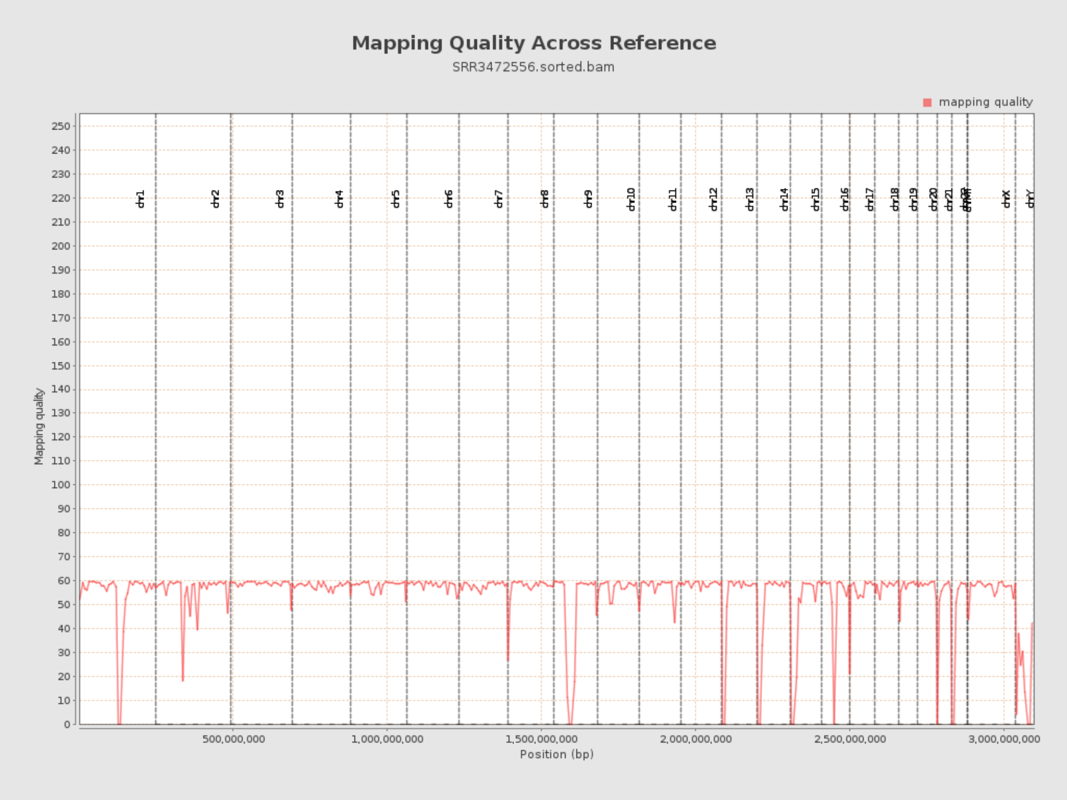
10. Results : Mapped Reads Clipping Profile



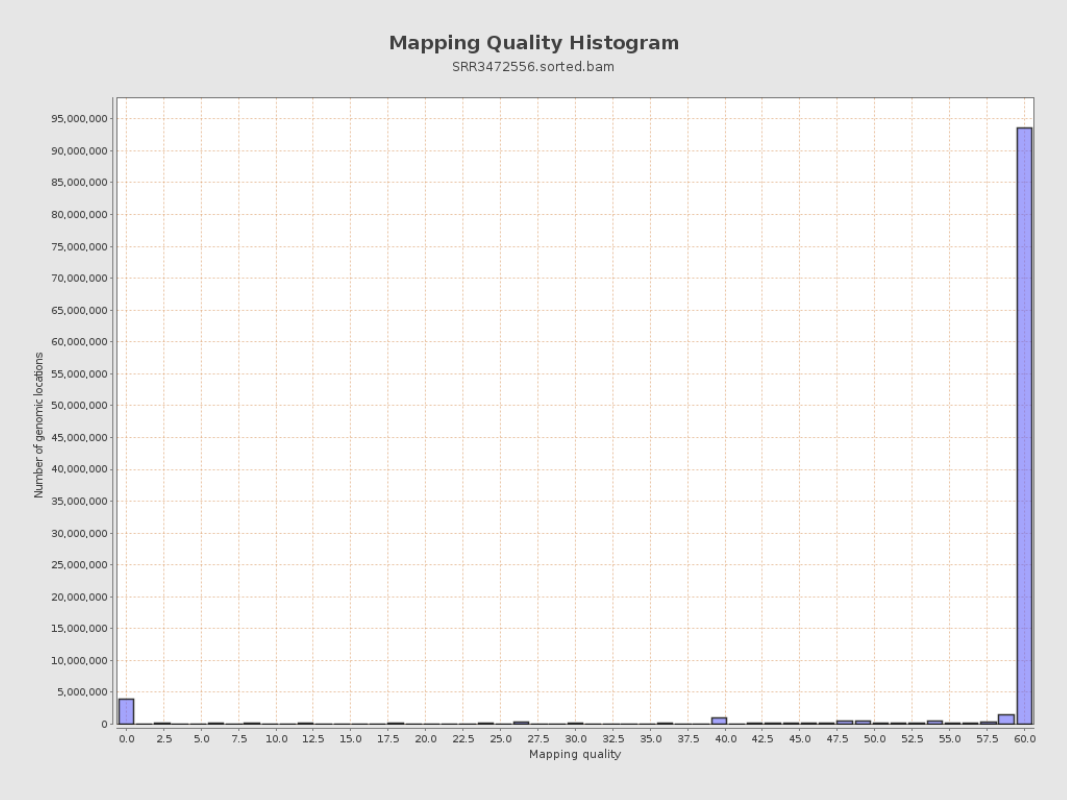
11. Results : Homopolymer Indels



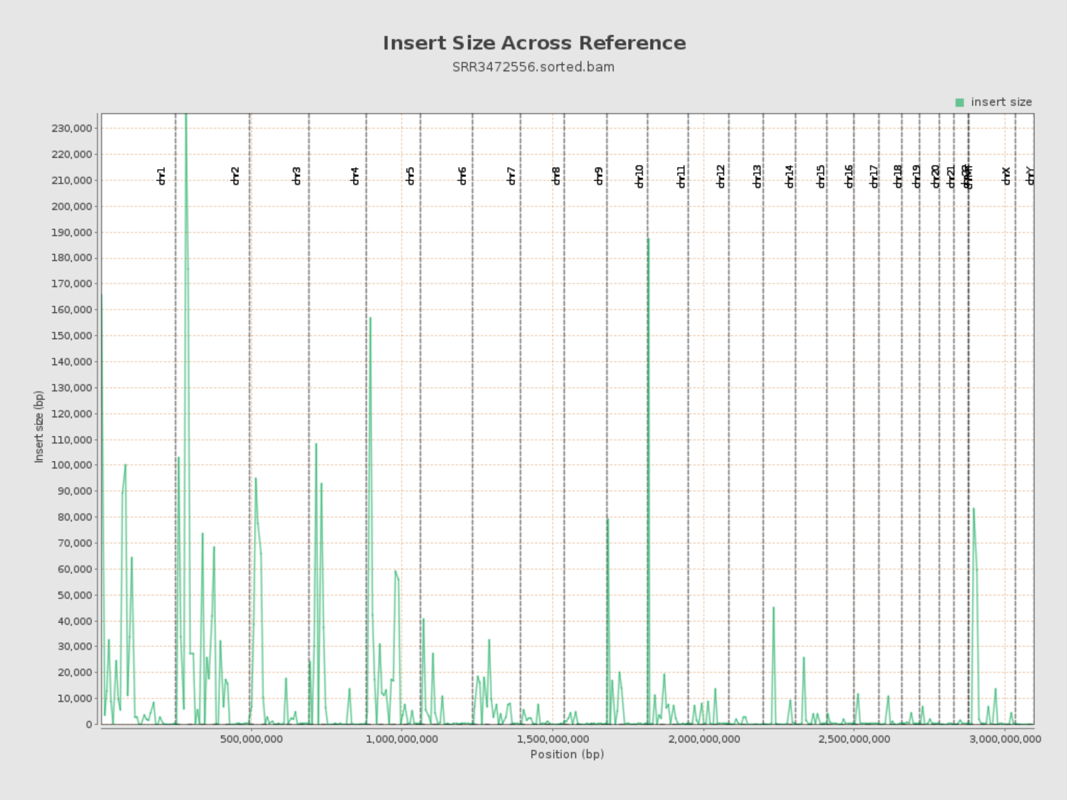
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram