Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 23:47:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472533.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_SRR3472533 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472533_1.fastq.gz SRR3472533_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 23:47:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472533.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,076,474
Mapped reads	21,712,106 / 98.35%
Unmapped reads	364,368 / 1.65%
Mapped paired reads	21,712,106 / 98.35%
Mapped reads, first in pair	10,906,653 / 49.4%
Mapped reads, second in pair	10,805,453 / 48.95%
Mapped reads, both in pair	21,530,020 / 97.52%
Mapped reads, singletons	182,086 / 0.82%
Secondary alignments	0
Supplementary alignments	74,629 / 0.34%
Read min/max/mean length	30 / 100 / 100.14
Duplicated reads (estimated)	14,444,414 / 65.43%
Duplication rate	45.72%
Clipped reads	1,764,316 / 7.99%

2.2. ACGT Content

Number/percentage of A's	593,469,789 / 27.8%
Number/percentage of C's	477,367,188 / 22.36%
Number/percentage of T's	589,681,578 / 27.62%
Number/percentage of G's	473,749,050 / 22.19%
Number/percentage of N's	331,188 / 0.02%

GC Percentage	44.56%

2.3. Coverage

Mean	0.6896
Standard Deviation	26.5462

2.4. Mapping Quality

Mean Mapping Quality	55.1

2.5. Insert size

Mean	24,390.88
Standard Deviation	1,566,793.74
P25/Median/P75	174 / 241 / 322

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	13,271,640
Insertions	114,361
Mapped reads with at least one insertion	0.52%
Deletions	112,948
Mapped reads with at least one deletion	0.51%
Homopolymer indels	45.48%

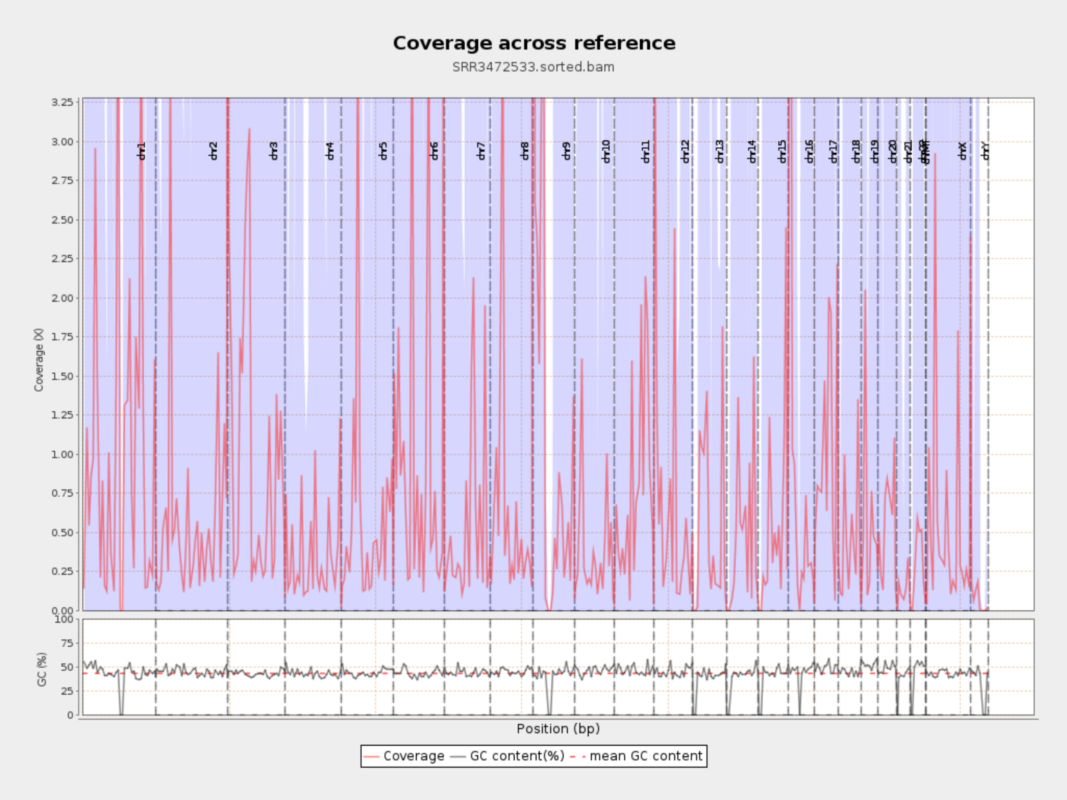
2.7. Chromosome stats

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

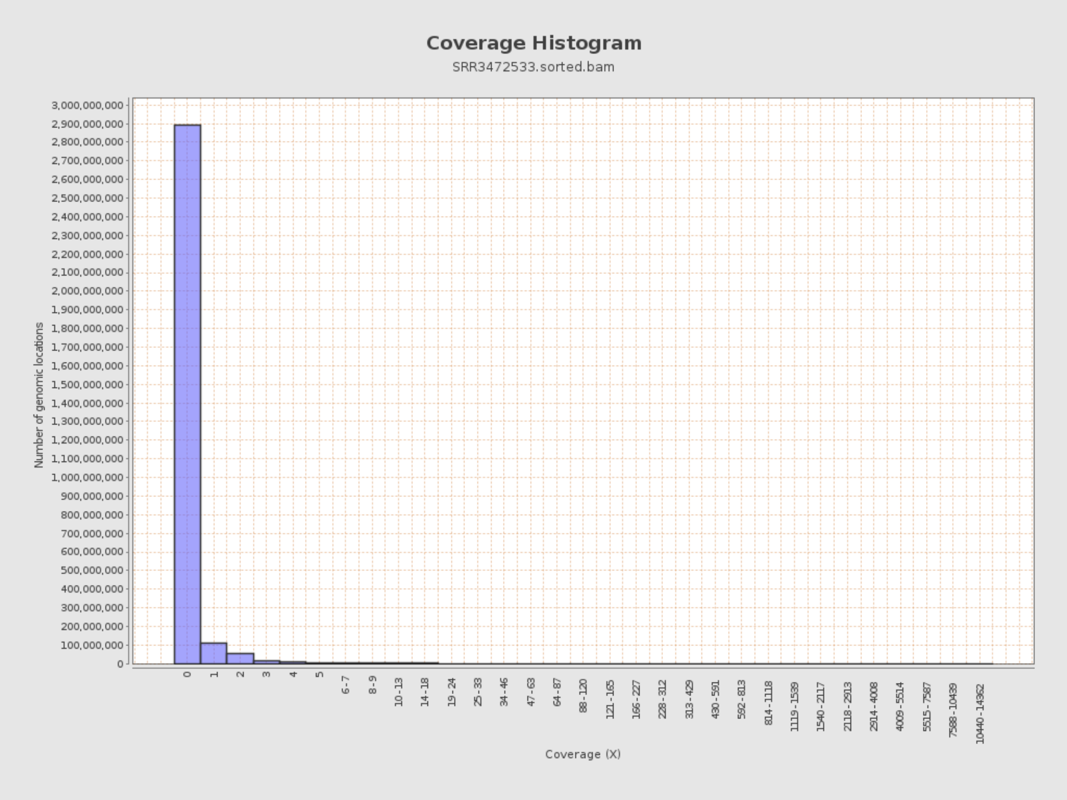
		bases	**coverage**	**deviation**
chr1	249250621	261359932	1.0486	37.8658
chr2	243199373	138081084	0.5678	32.8227
chr3	198022430	208692839	1.0539	24.8985
chr4	191154276	68707832	0.3594	12.4822
chr5	180915260	109610969	0.6059	19.5754
chr6	171115067	169990098	0.9934	33.7308
chr7	159138663	87808393	0.5518	19.6024
chr8	146364022	98143727	0.6705	25.4374
chr9	141213431	165818746	1.1742	42.5862
chr10	135534747	54955164	0.4055	19.8724
chr11	135006516	109123246	0.8083	34.9015
chr12	133851895	98951319	0.7393	24.1923
chr13	115169878	61732954	0.536	25.3481
chr14	107349540	53282710	0.4963	19.5956
chr15	102531392	55984124	0.546	19.1068
chr16	90354753	87957609	0.9735	31.7351
chr17	81195210	82007811	1.01	26.2298
chr18	78077248	35890829	0.4597	19.2051
chr19	59128983	34862613	0.5896	20.5183
chr20	63025520	37053837	0.5879	19.4752
chr21	48129895	6765327	0.1406	5.1789
chr22	51304566	15443412	0.301	9.5777
chrMT	16571	2108	0.1272	0.4555
chrX	155270560	88723325	0.5714	18.4282

chrY	59373566	3921677	0.0661	4.6059

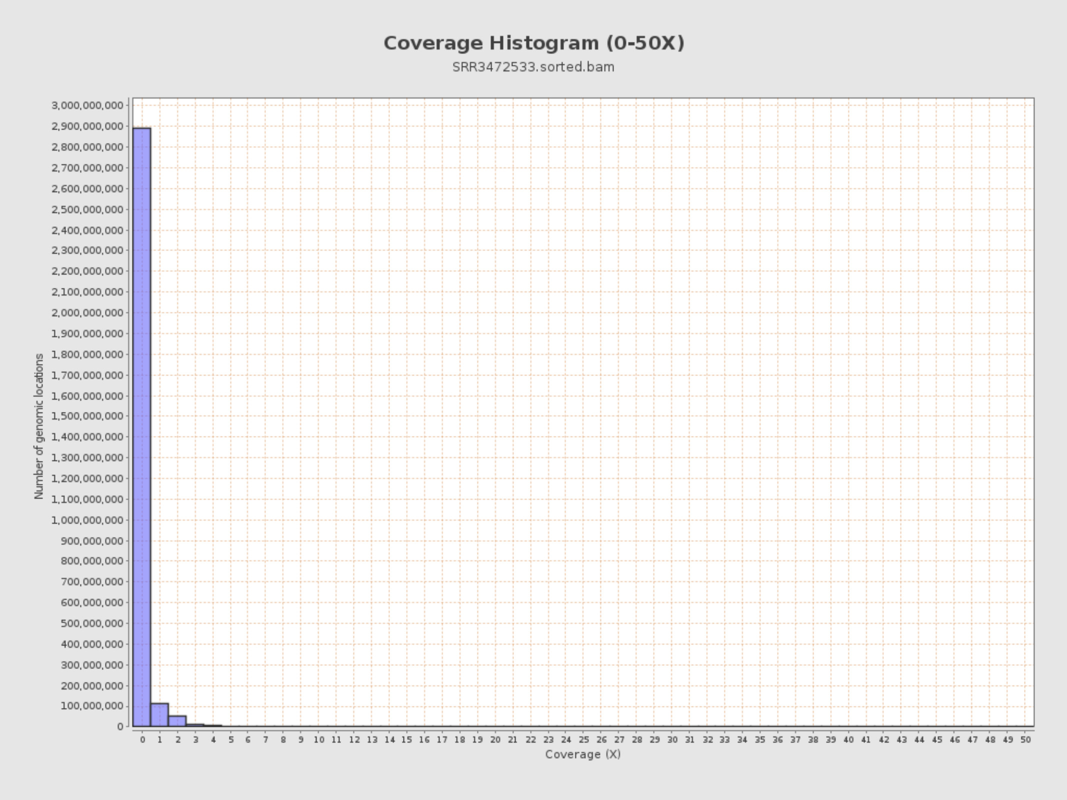
3. Results : Coverage across reference



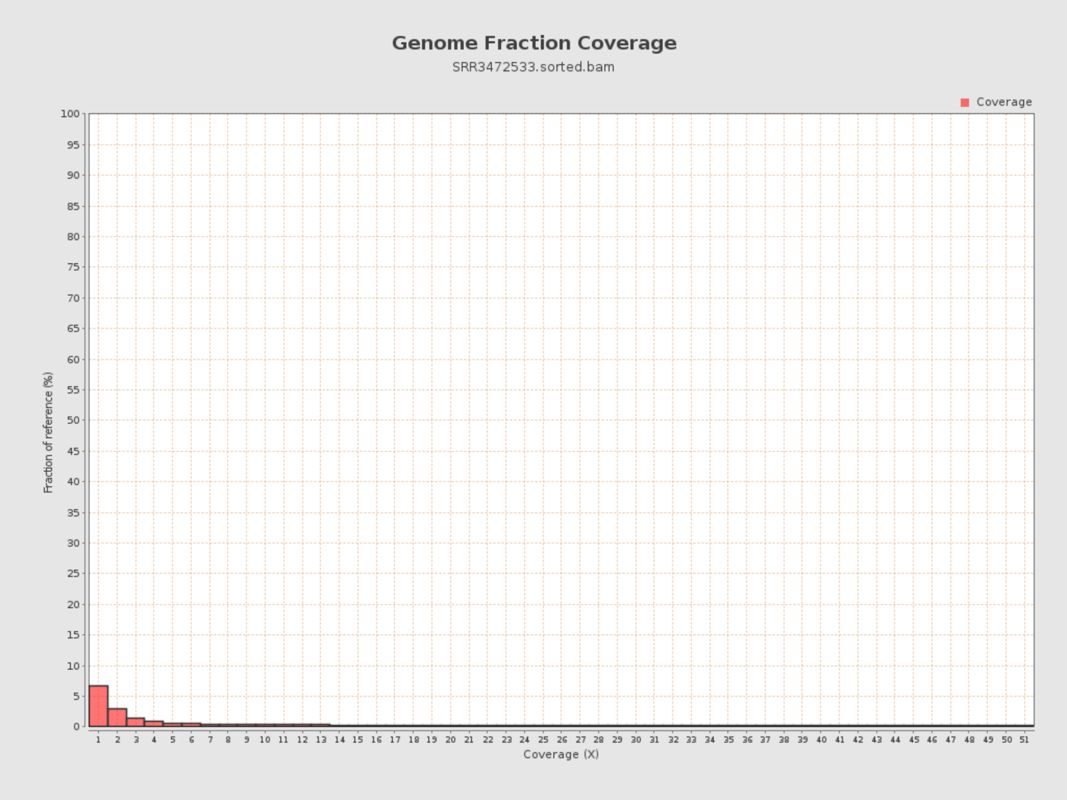
4. Results : Coverage Histogram



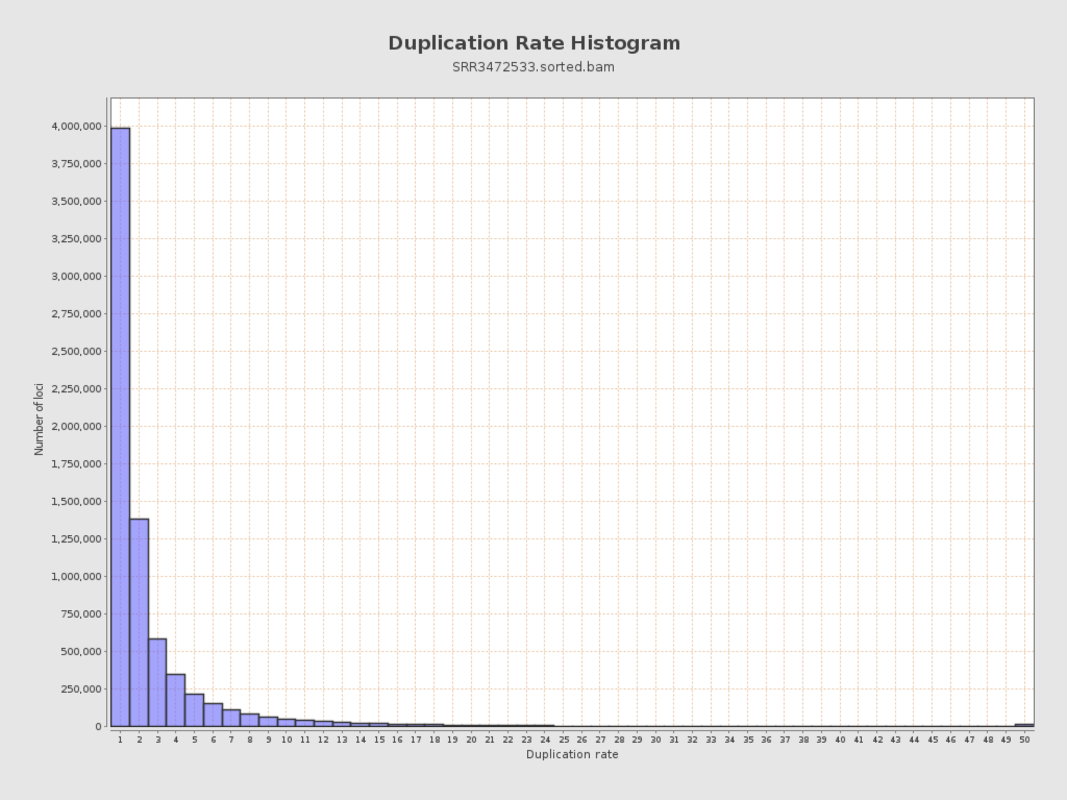
5. Results : Coverage Histogram (0-50X)



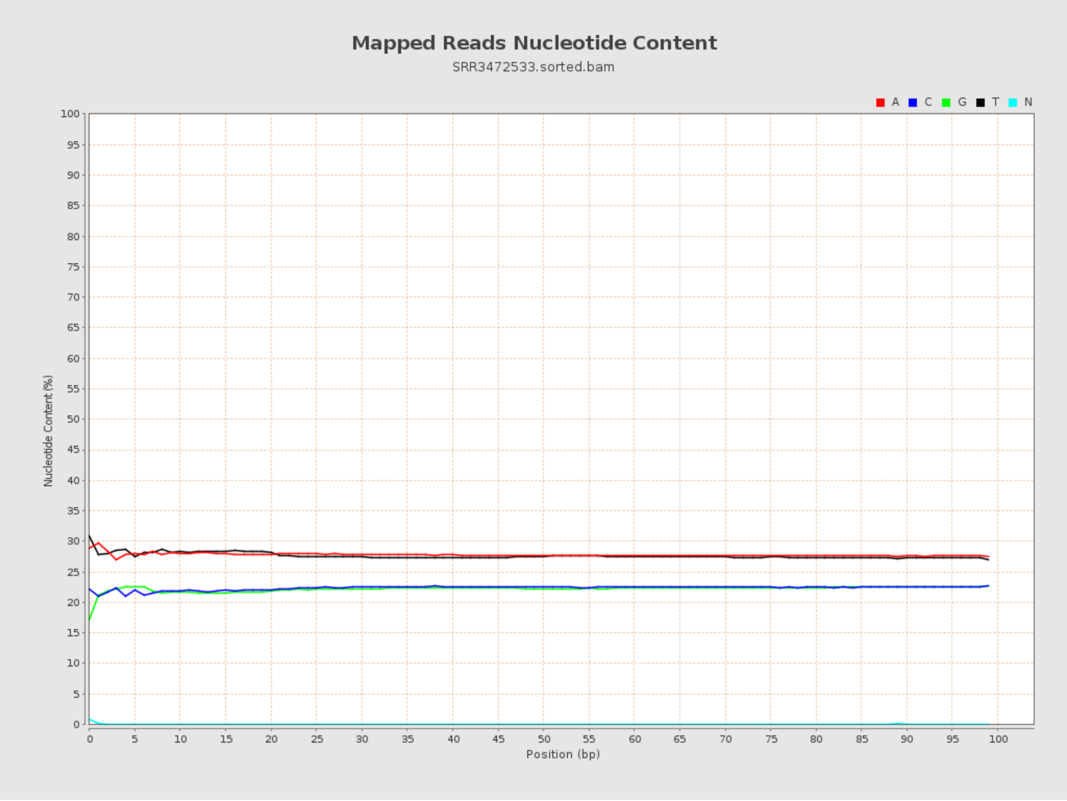
6. Results : Genome Fraction Coverage



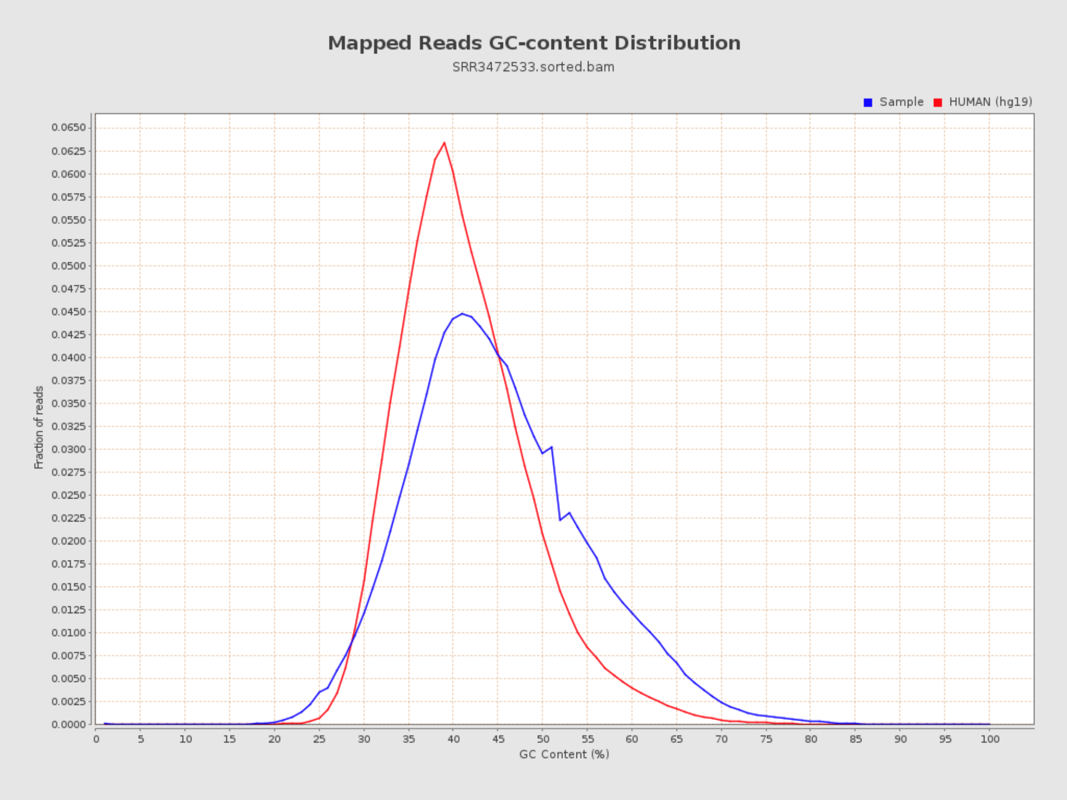
7. Results : Duplication Rate Histogram



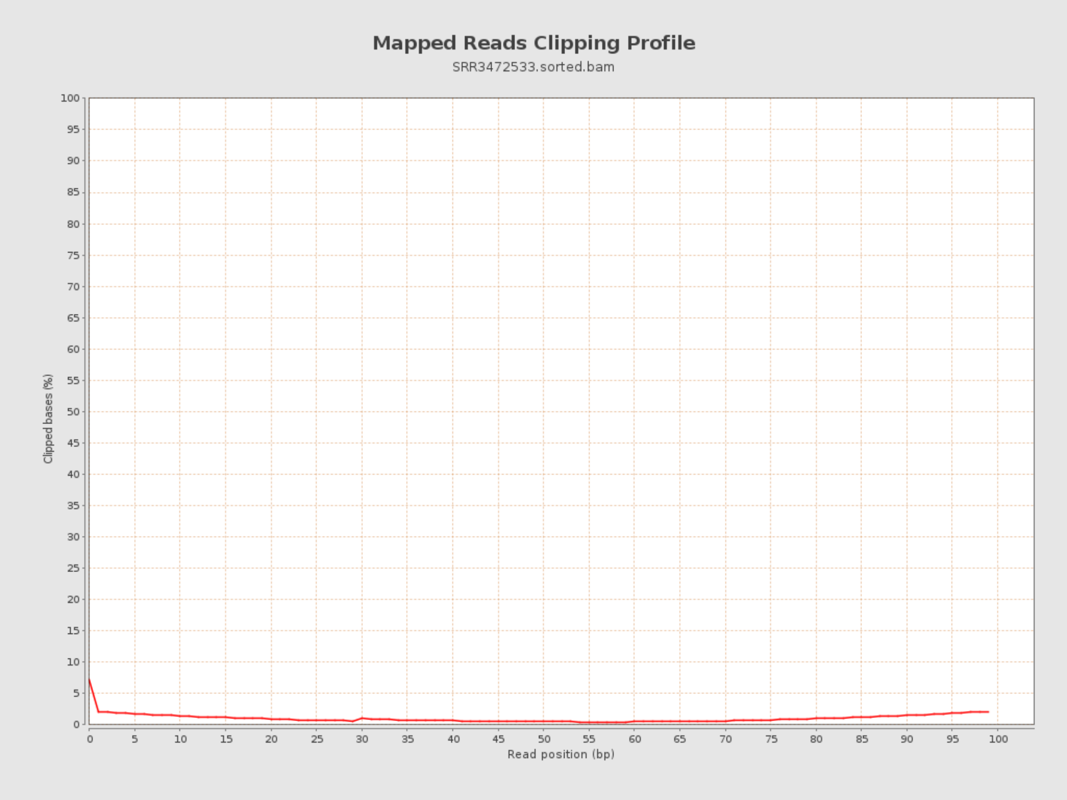
8. Results : Mapped Reads Nucleotide Content



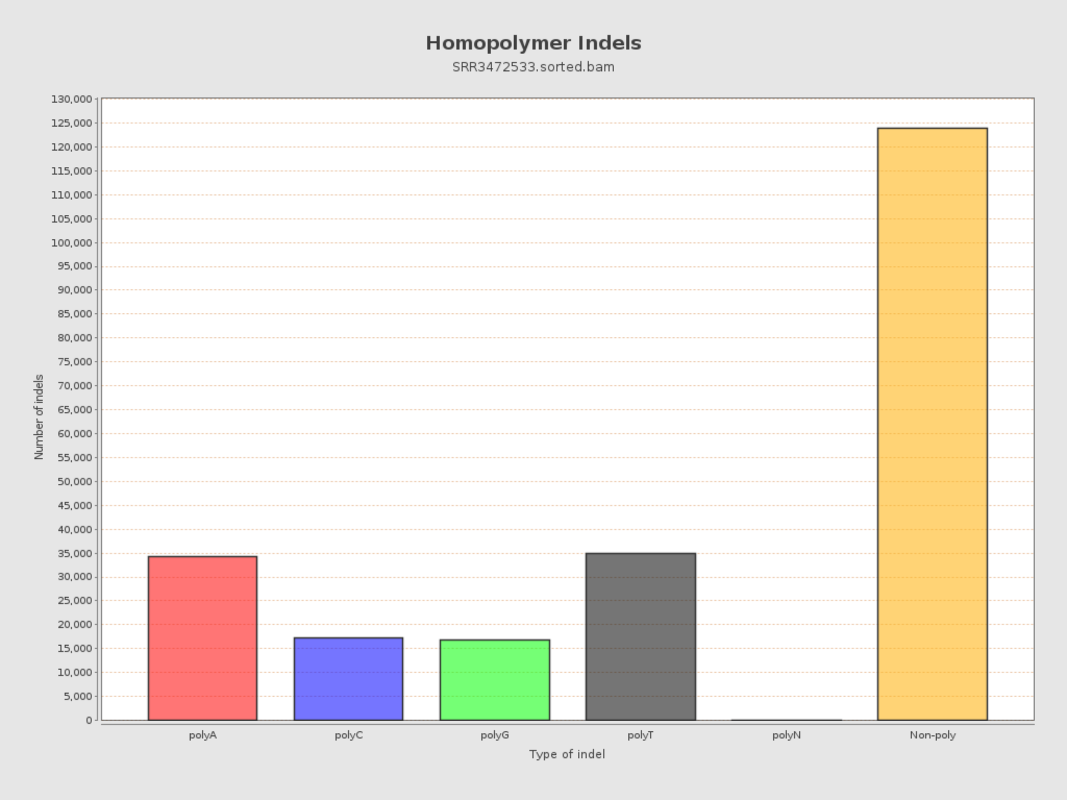
9. Results : Mapped Reads GC-content Distribution



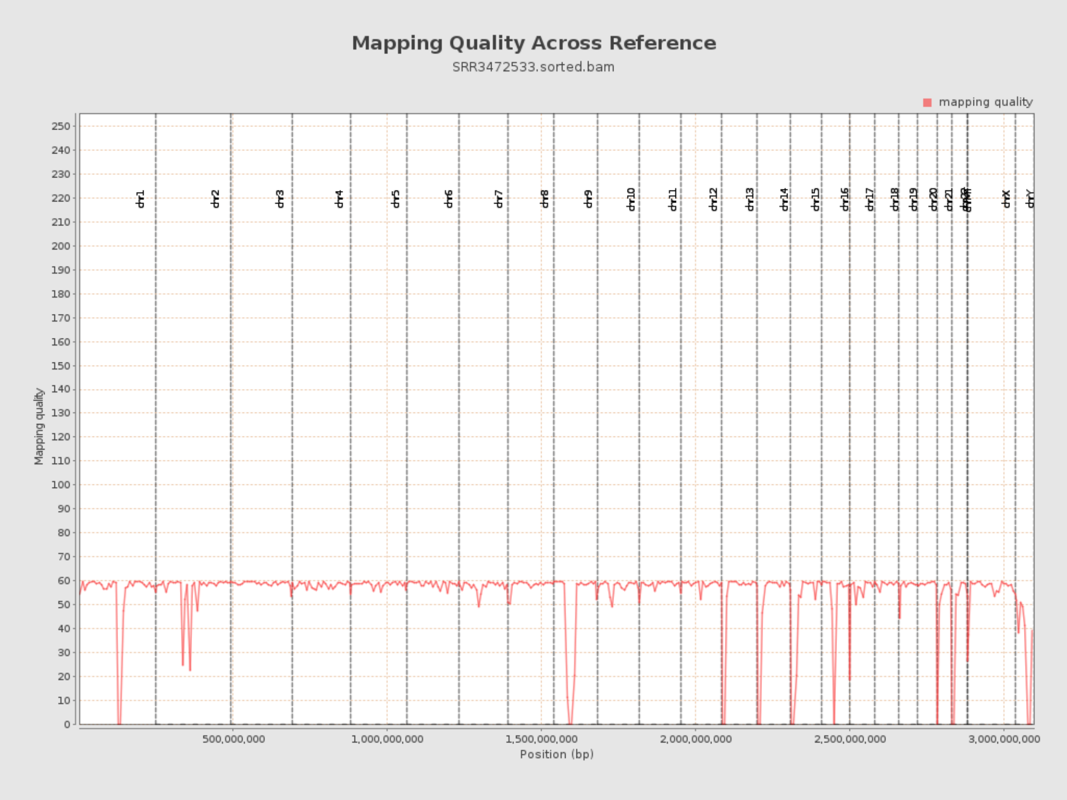
10. Results : Mapped Reads Clipping Profile



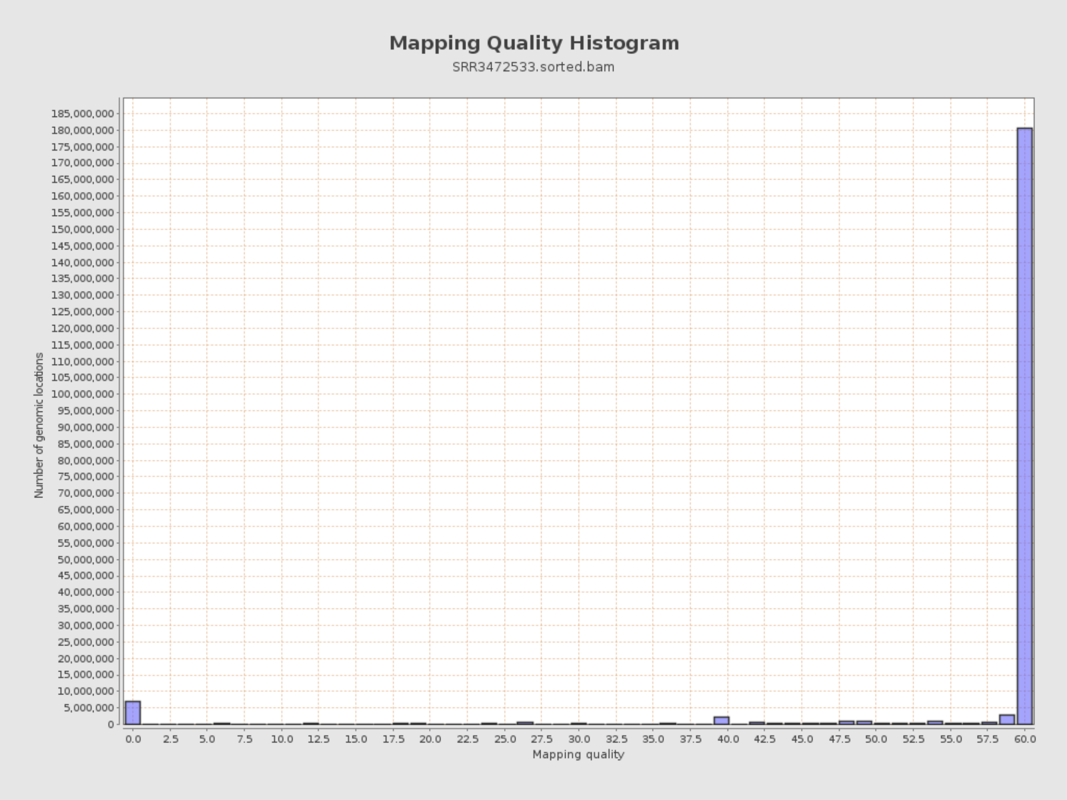
11. Results : Homopolymer Indels



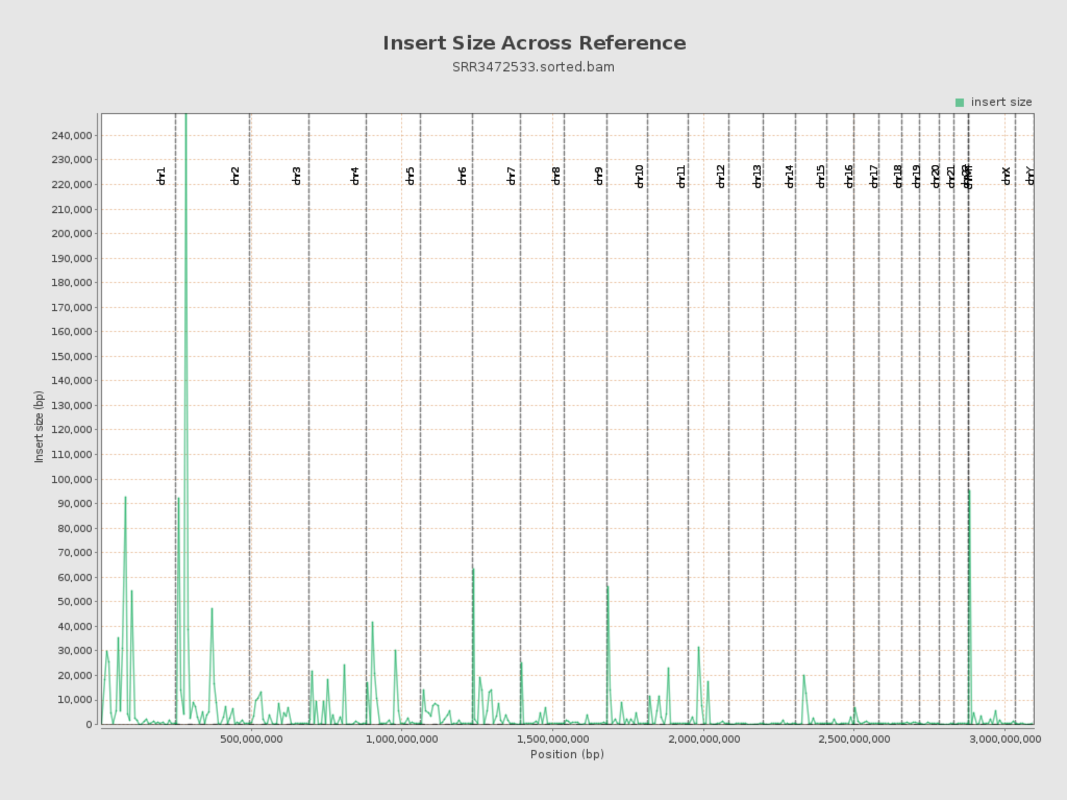
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram