Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 04:46:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472591.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_SRR3472591 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472591_1.fastq.gz SRR3472591_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 04:46:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472591.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,533,068
Mapped reads	5,112,468 / 92.4%
Unmapped reads	420,600 / 7.6%
Mapped paired reads	5,112,468 / 92.4%
Mapped reads, first in pair	2,583,007 / 46.68%
Mapped reads, second in pair	2,529,461 / 45.72%
Mapped reads, both in pair	4,982,604 / 90.05%
Mapped reads, singletons	129,864 / 2.35%
Secondary alignments	0
Supplementary alignments	169,123 / 3.06%
Read min/max/mean length	30 / 100 / 101.19
Duplicated reads (estimated)	649,077 / 11.73%
Duplication rate	11.22%
Clipped reads	3,900,753 / 70.5%

2.2. ACGT Content

Number/percentage of A's	106,669,776 / 25.61%
Number/percentage of C's	83,266,805 / 19.99%
Number/percentage of T's	124,140,012 / 29.8%
Number/percentage of G's	102,221,234 / 24.54%
Number/percentage of N's	257,934 / 0.06%

GC Percentage	44.53%

2.3. Coverage

Mean	0.1346
Standard Deviation	1.1708

2.4. Mapping Quality

Mean Mapping Quality	50.39

2.5. Insert size

Mean	274,322.28
Standard Deviation	5,060,131.57
P25/Median/P75	94 / 133 / 185

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	4,886,687
Insertions	39,611
Mapped reads with at least one insertion	0.76%
Deletions	95,275
Mapped reads with at least one deletion	1.83%
Homopolymer indels	42.47%

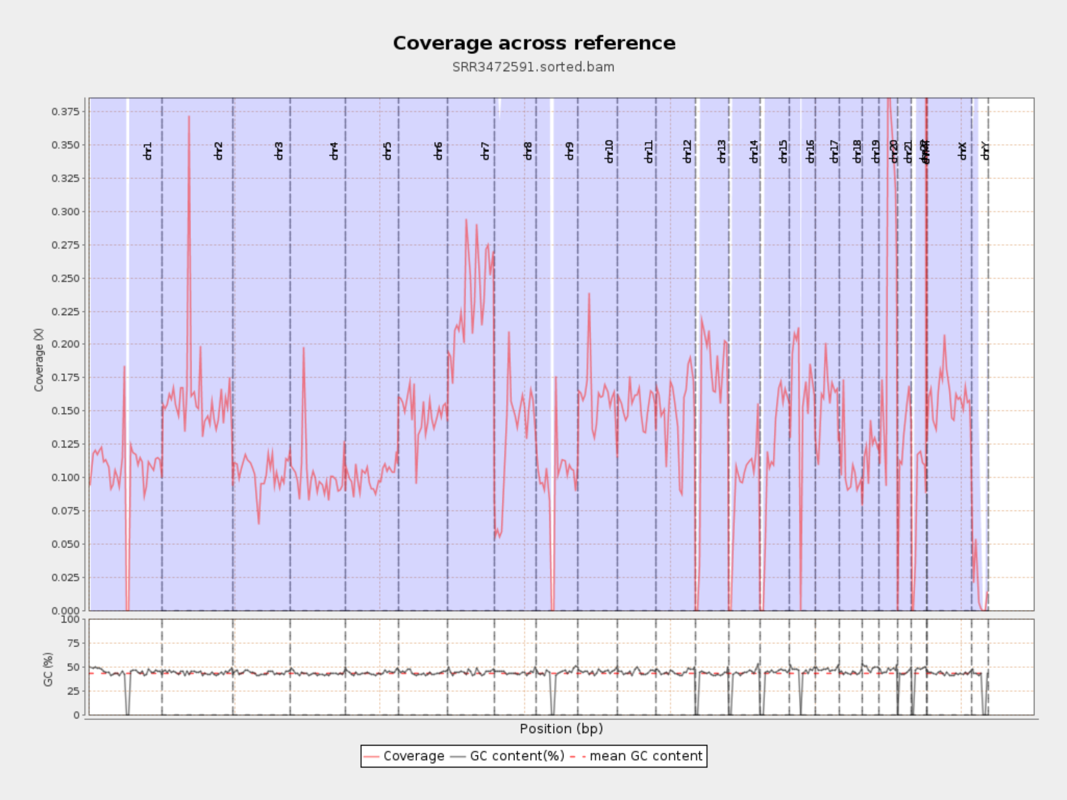
2.7. Chromosome stats

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

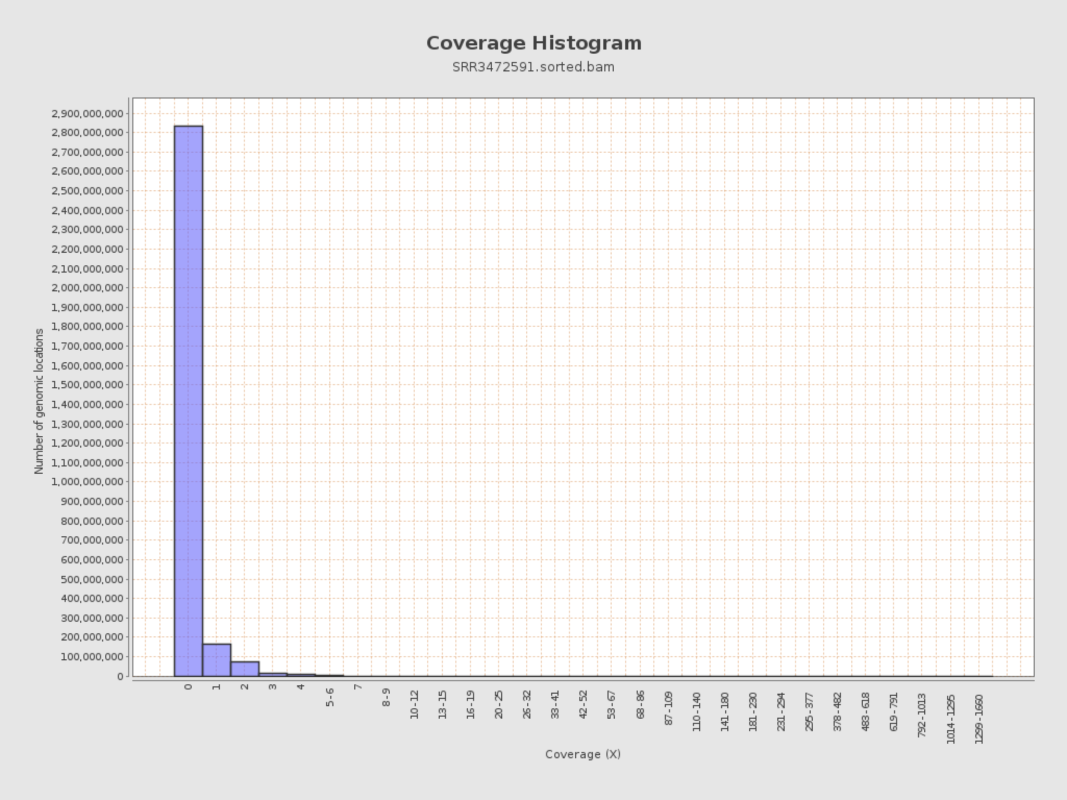
		bases	coverage	deviation
chr1	249250621	26110780	0.1048	1.4332
chr2	243199373	39310767	0.1616	1.7794
chr3	198022430	20467178	0.1034	0.4389
chr4	191154276	19466972	0.1018	0.6659
chr5	180915260	18268431	0.101	0.4471
chr6	171115067	25315973	0.1479	0.7213
chr7	159138663	37462105	0.2354	2.0094
chr8	146364022	19094359	0.1305	1.0637
chr9	141213431	13374764	0.0947	1.2758
chr10	135534747	21857430	0.1613	1.1661
chr11	135006516	20736897	0.1536	1.207
chr12	133851895	20217788	0.151	0.5509
chr13	115169878	18247833	0.1584	0.5703
chr14	107349540	9932290	0.0925	2.1619
chr15	102531392	11794754	0.115	0.479
chr16	90354753	14692833	0.1626	0.7526
chr17	81195210	12763082	0.1572	0.9585
chr18	78077248	8352803	0.107	2.0315
chr19	59128983	7110572	0.1203	1.0544
chr20	63025520	16057997	0.2548	0.8436
chr21	48129895	5965771	0.124	0.5982
chr22	51304566	3989183	0.0778	0.3865
chrMT	16571	228129	13.7668	8.9276
chrX	155270560	24906125	0.1604	0.7263

chrY	59373566	1010873	0.017	0.5173

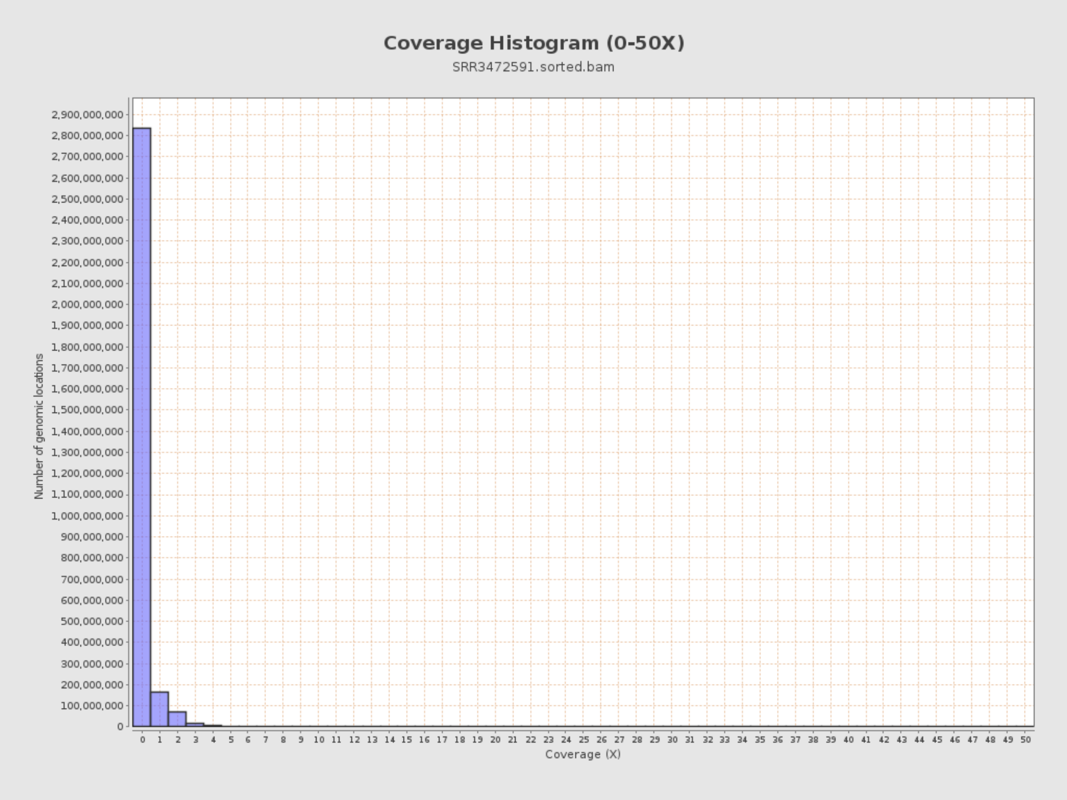
3. Results : Coverage across reference



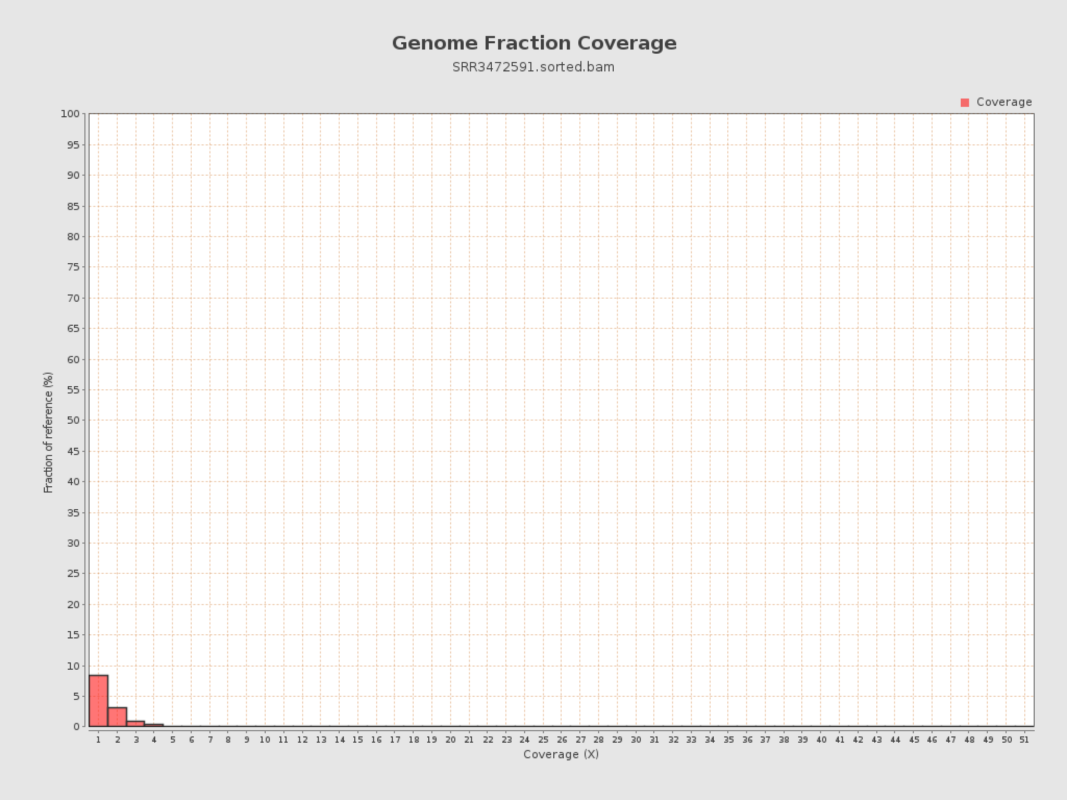
4. Results : Coverage Histogram



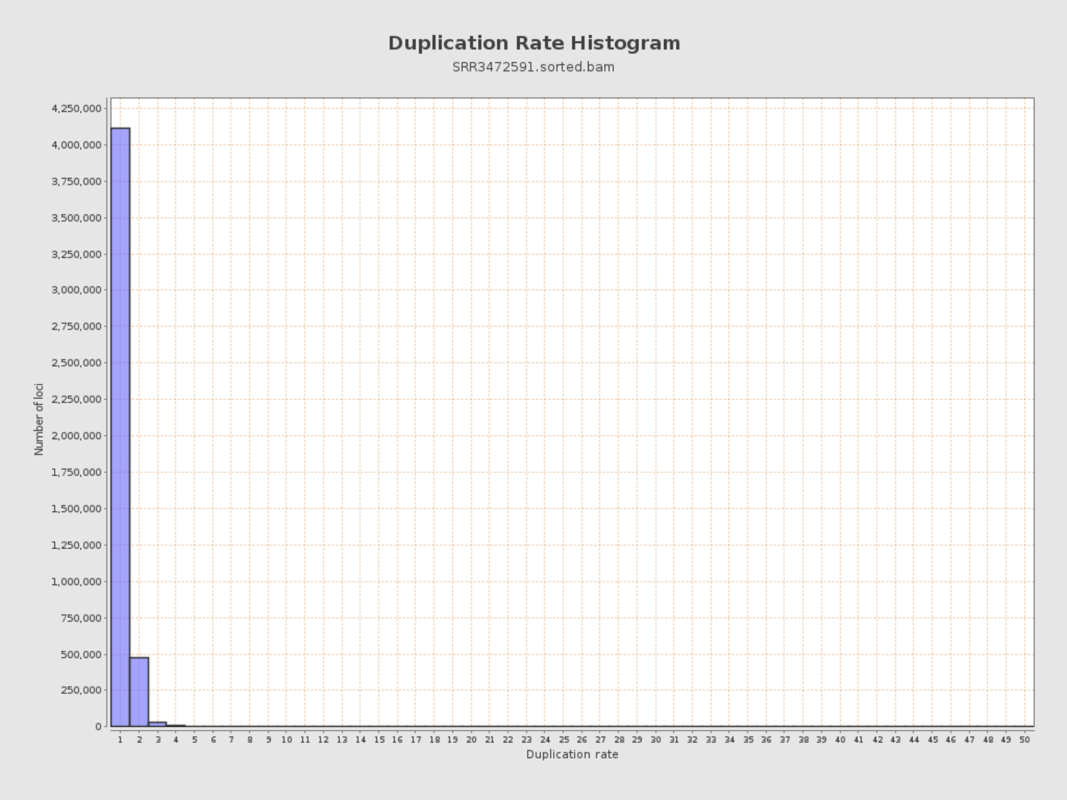
5. Results : Coverage Histogram (0-50X)



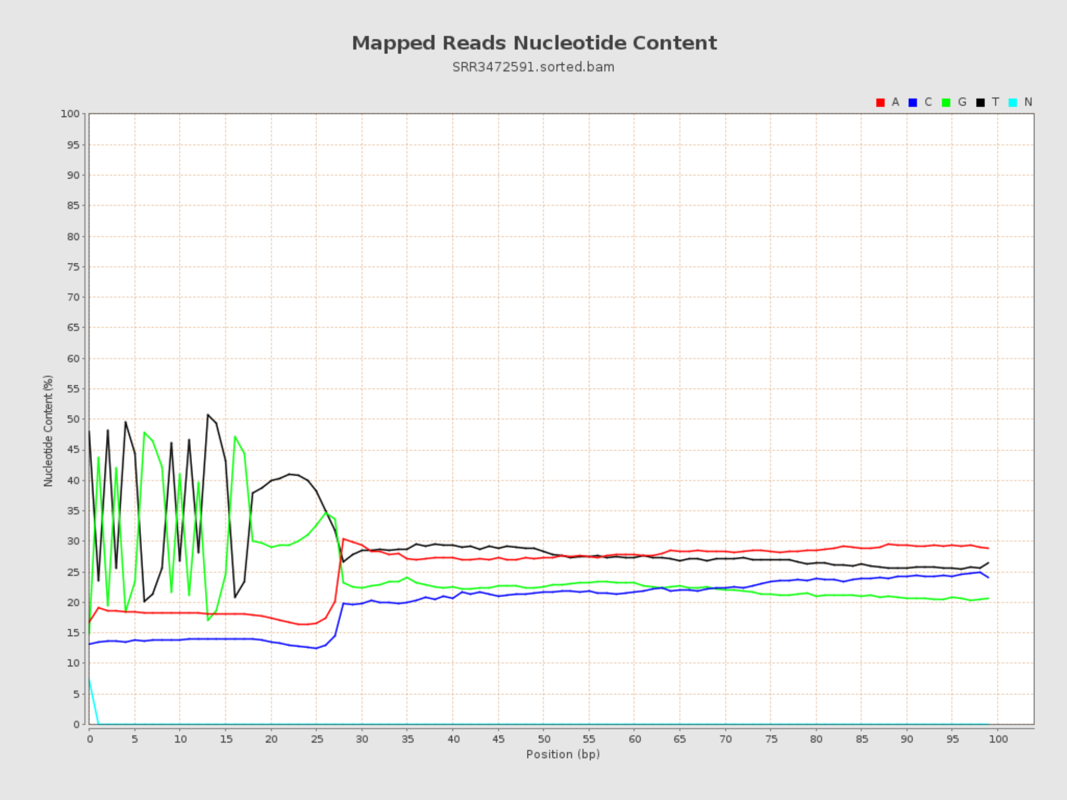
6. Results : Genome Fraction Coverage



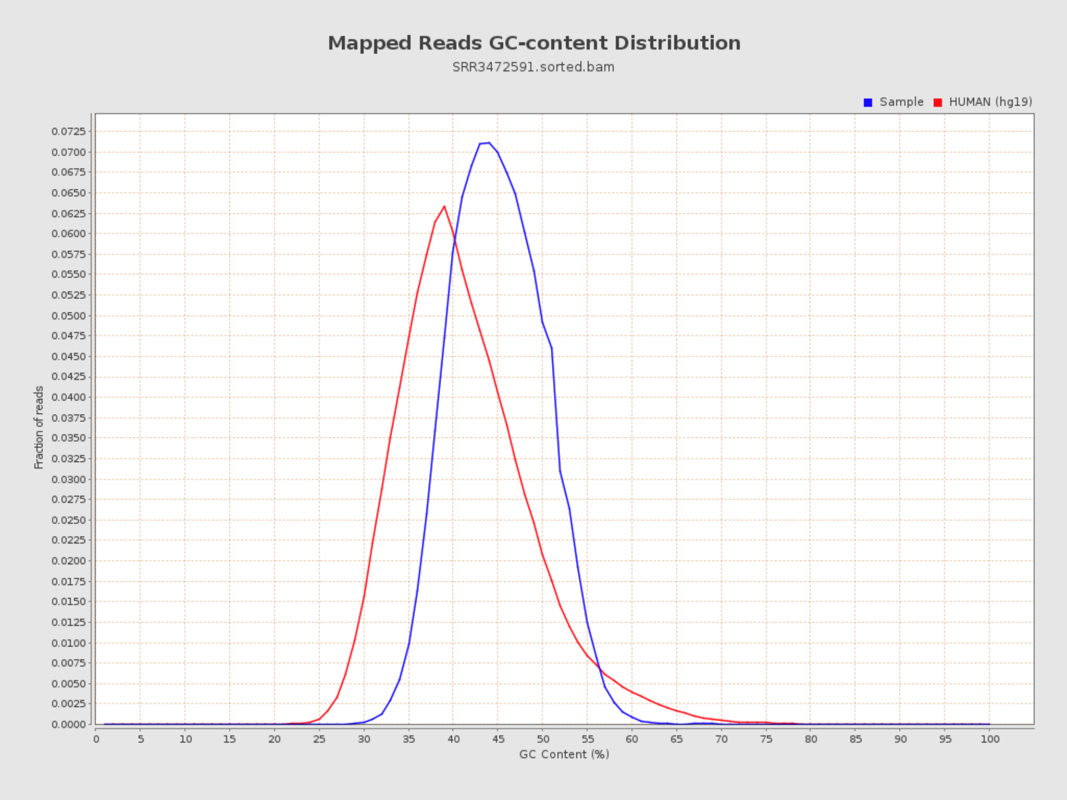
7. Results : Duplication Rate Histogram



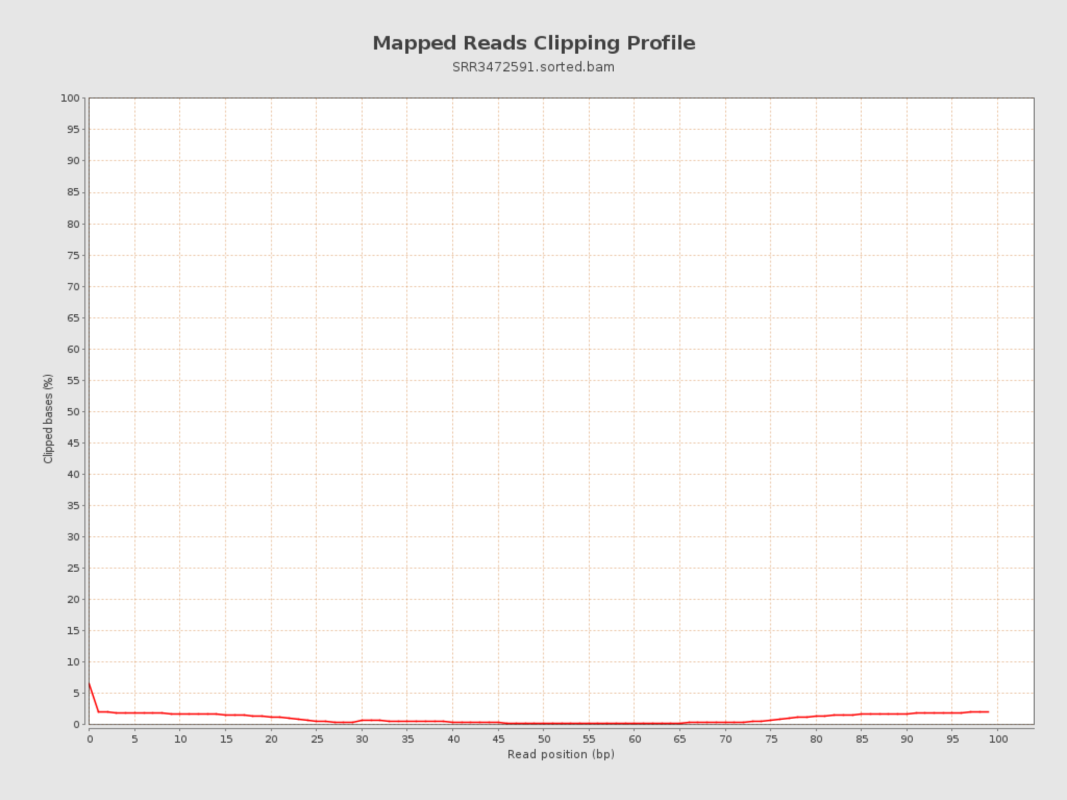
8. Results : Mapped Reads Nucleotide Content



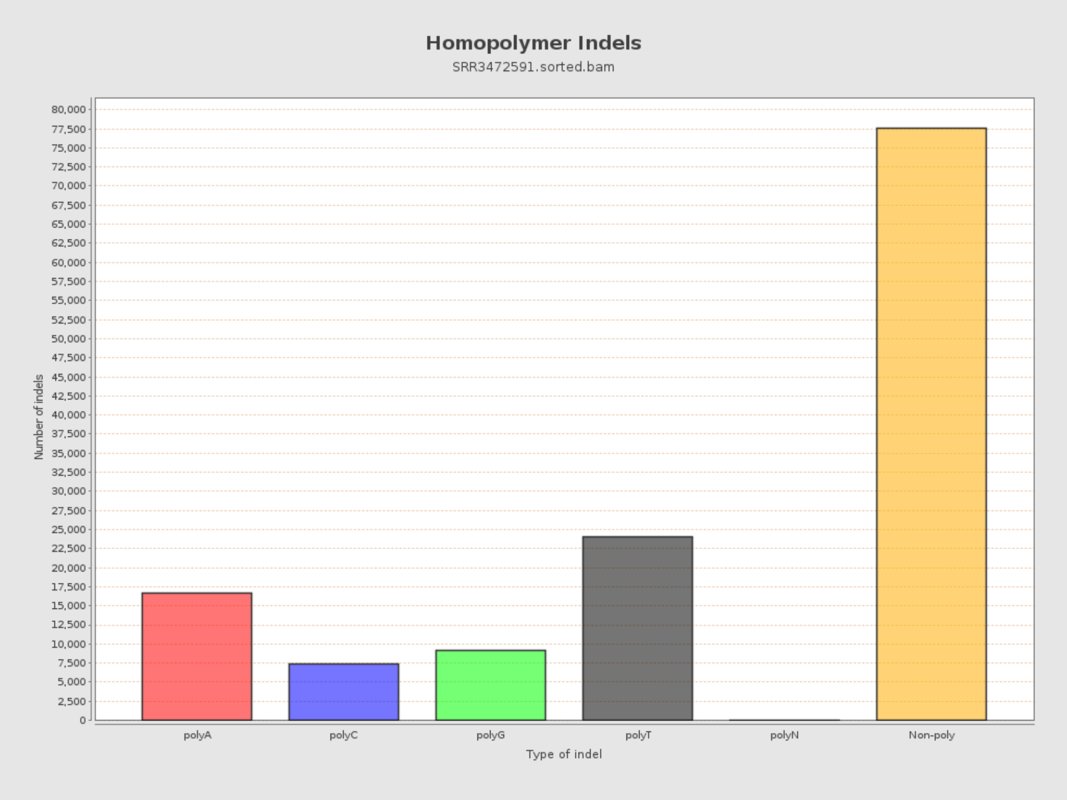
9. Results : Mapped Reads GC-content Distribution



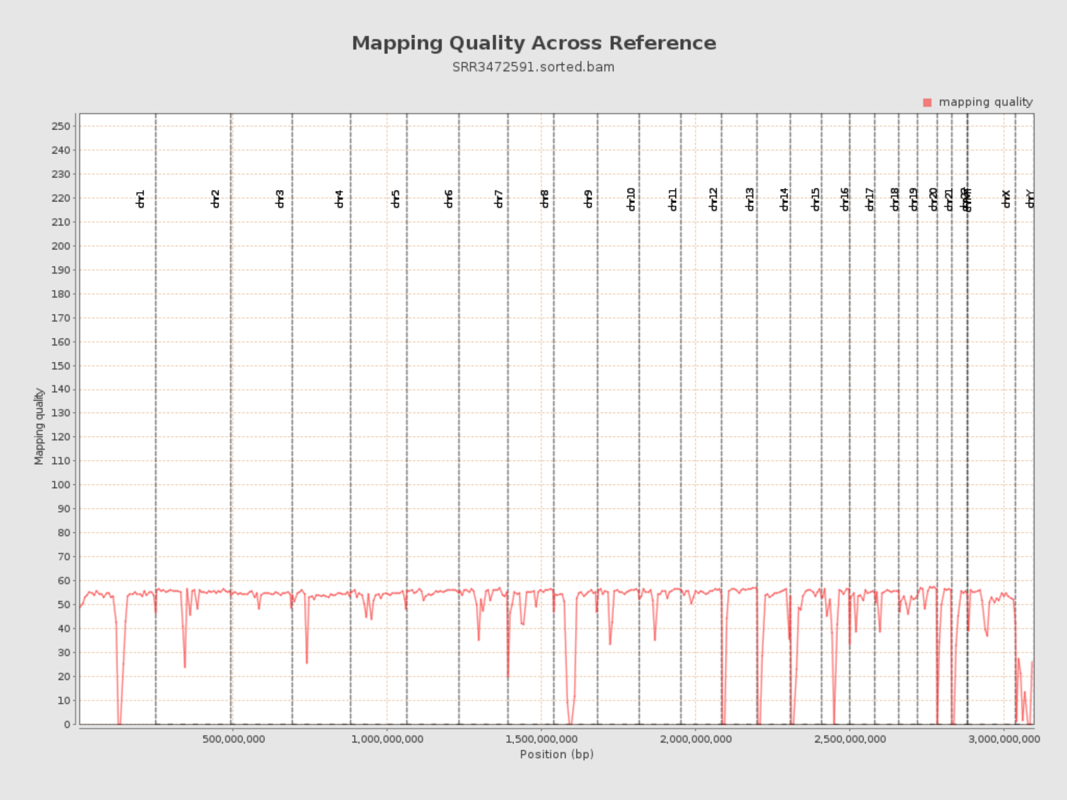
10. Results : Mapped Reads Clipping Profile



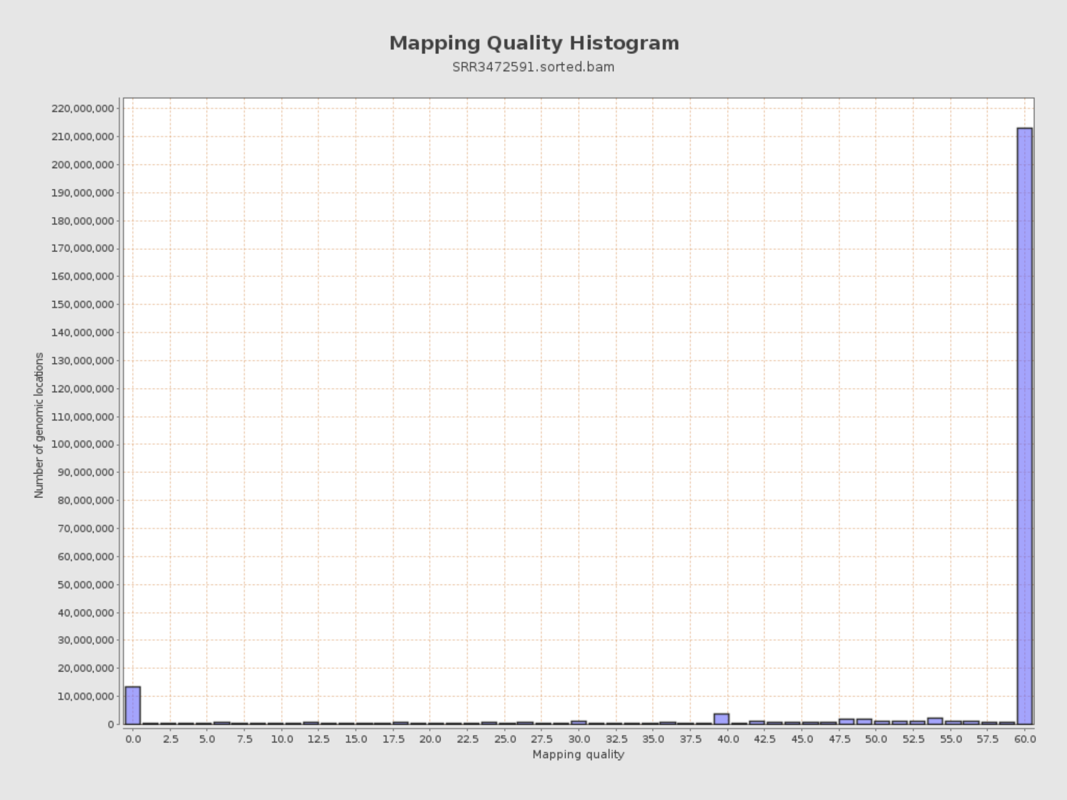
11. Results : Homopolymer Indels



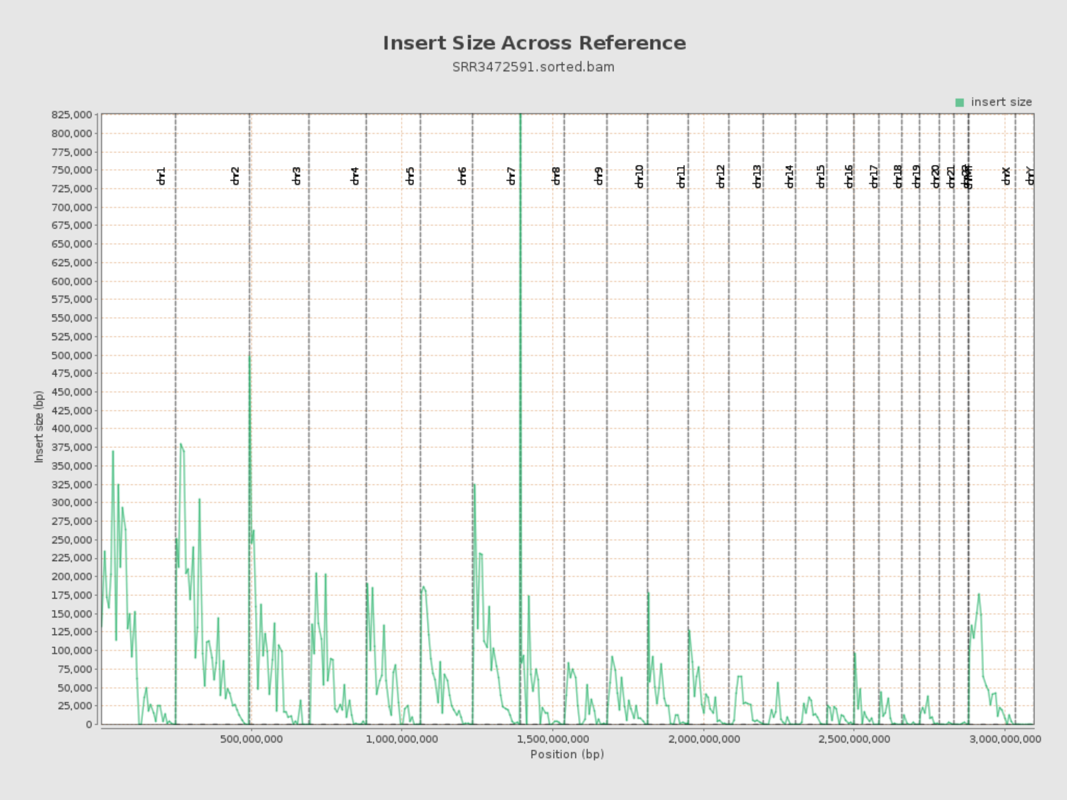
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram