Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 16:55:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472390.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_SRR3472390 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472390_1.fastq.gz SRR3472390_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 16:55:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472390.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,565,804
Mapped reads	22,391,043 / 99.23%
Unmapped reads	174,761 / 0.77%
Mapped paired reads	22,391,043 / 99.23%
Mapped reads, first in pair	11,231,655 / 49.77%
Mapped reads, second in pair	11,159,388 / 49.45%
Mapped reads, both in pair	22,281,832 / 98.74%
Mapped reads, singletons	109,211 / 0.48%
Secondary alignments	0
Supplementary alignments	115,530 / 0.51%
Read min/max/mean length	30 / 100 / 99.49
Duplicated reads (estimated)	14,446,896 / 64.02%
Duplication rate	48.22%
Clipped reads	1,639,844 / 7.27%

2.2. ACGT Content

Number/percentage of A's	601,239,870 / 27.36%
Number/percentage of C's	498,400,962 / 22.68%
Number/percentage of T's	601,346,067 / 27.37%
Number/percentage of G's	495,967,143 / 22.57%
Number/percentage of N's	275,654 / 0.01%

GC Percentage	45.26%

2.3. Coverage

Mean	0.7099
Standard Deviation	21.5872

2.4. Mapping Quality

Mean Mapping Quality	54.86

2.5. Insert size

Mean	23,073.38
Standard Deviation	1,472,522.06
P25/Median/P75	160 / 224 / 304

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	12,064,546
Insertions	136,313
Mapped reads with at least one insertion	0.6%
Deletions	117,832
Mapped reads with at least one deletion	0.52%
Homopolymer indels	45.84%

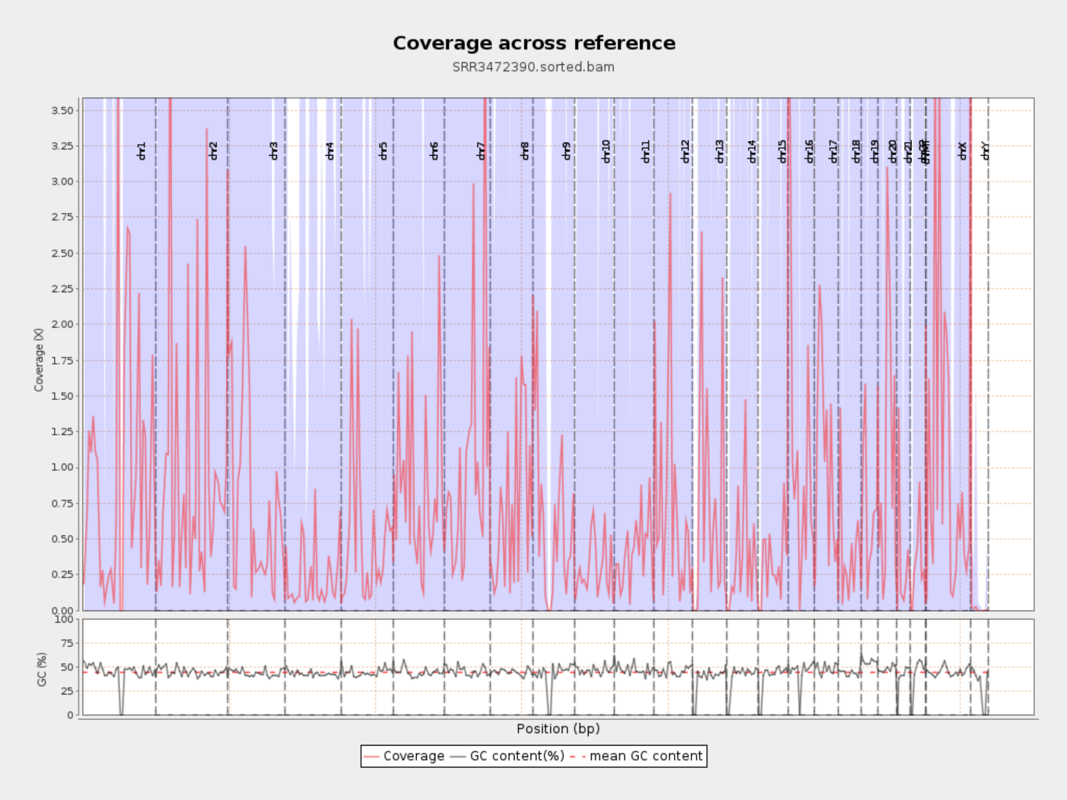
2.7. Chromosome stats

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

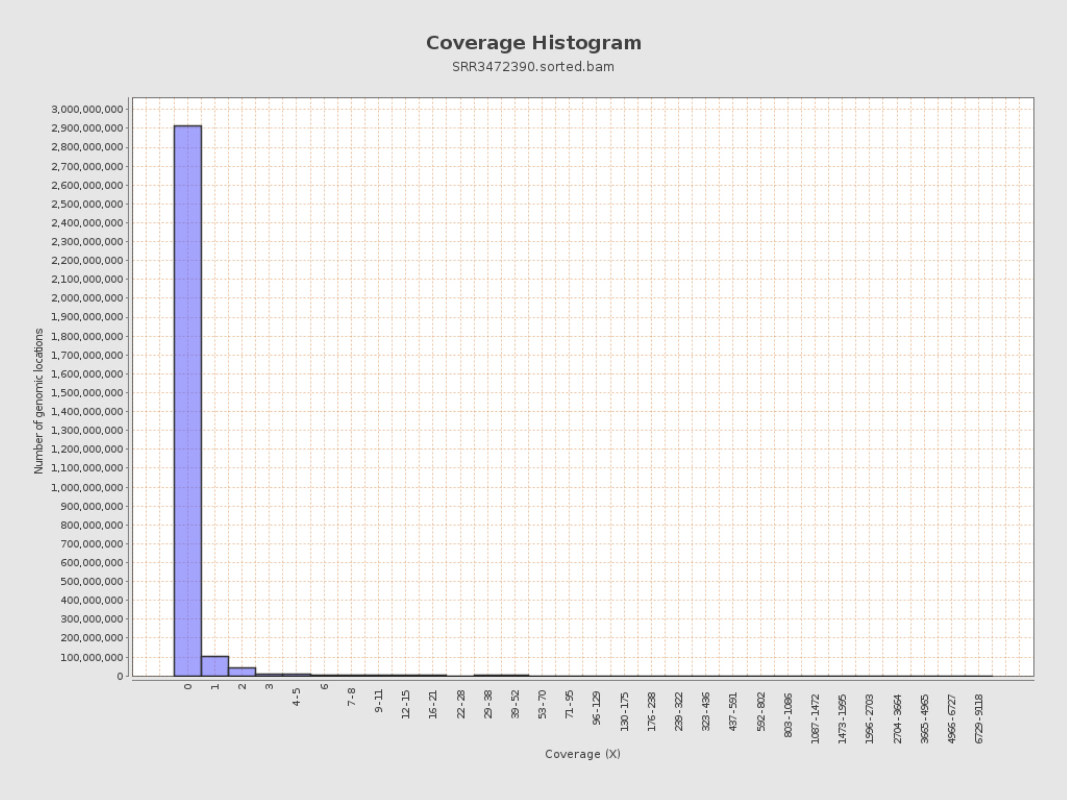
		bases	coverage	deviation
chr1	249250621	233243611	0.9358	25.1295
chr2	243199373	231700780	0.9527	35.5352
chr3	198022430	161114270	0.8136	19.7285
chr4	191154276	44816389	0.2345	7.3937
chr5	180915260	92837883	0.5132	16.2048
chr6	171115067	149800215	0.8754	21.3201
chr7	159138663	176047692	1.1063	30.0446
chr8	146364022	105905637	0.7236	19.6318
chr9	141213431	85319136	0.6042	14.5255
chr10	135534747	42577611	0.3141	9.7799
chr11	135006516	54467125	0.4034	9.7532
chr12	133851895	105453579	0.7878	20.6746
chr13	115169878	87890201	0.7631	26.4173
chr14	107349540	39208174	0.3652	10.3883
chr15	102531392	32207978	0.3141	10.1237
chr16	90354753	105975687	1.1729	27.6273
chr17	81195210	88366223	1.0883	24.442
chr18	78077248	31500375	0.4035	11.3585
chr19	59128983	42675419	0.7217	15.4094
chr20	63025520	69802652	1.1075	23.9934
chr21	48129895	18355614	0.3814	20.8445
chr22	51304566	16500464	0.3216	8.964
chrMT	16571	33095	1.9972	1.6604
chrX	155270560	181225810	1.1672	30.7413

chrY	59373566	491884	0.0083	0.642

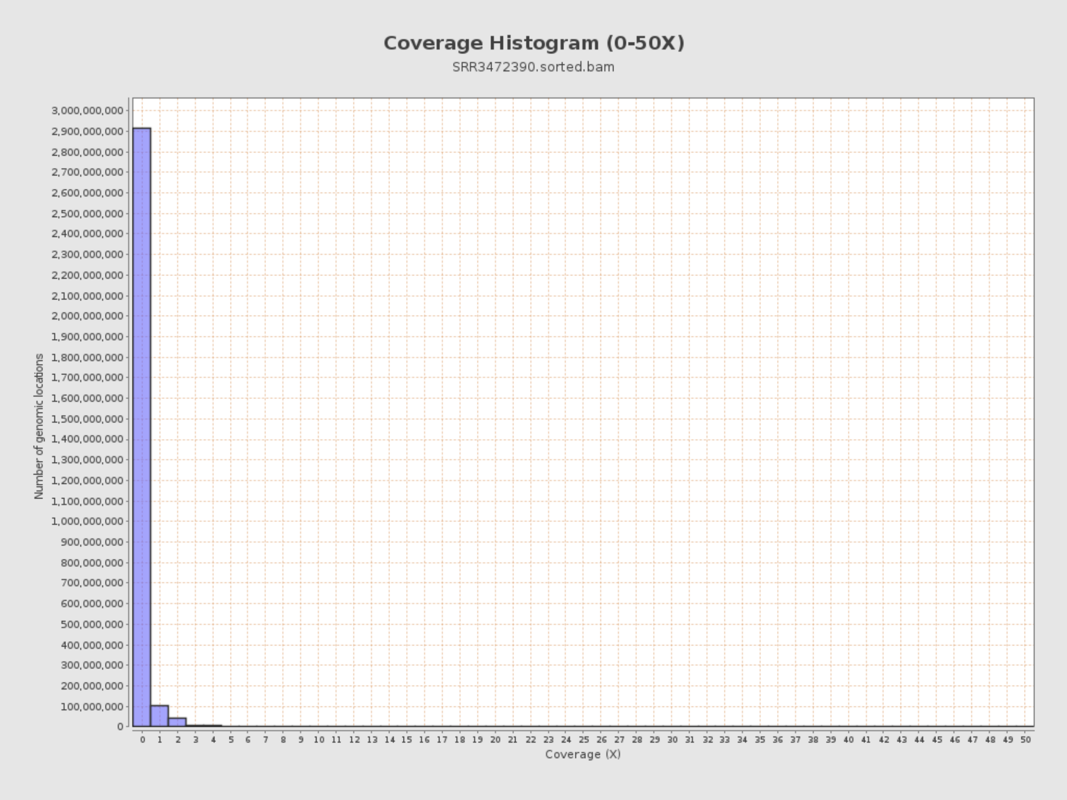
3. Results : Coverage across reference



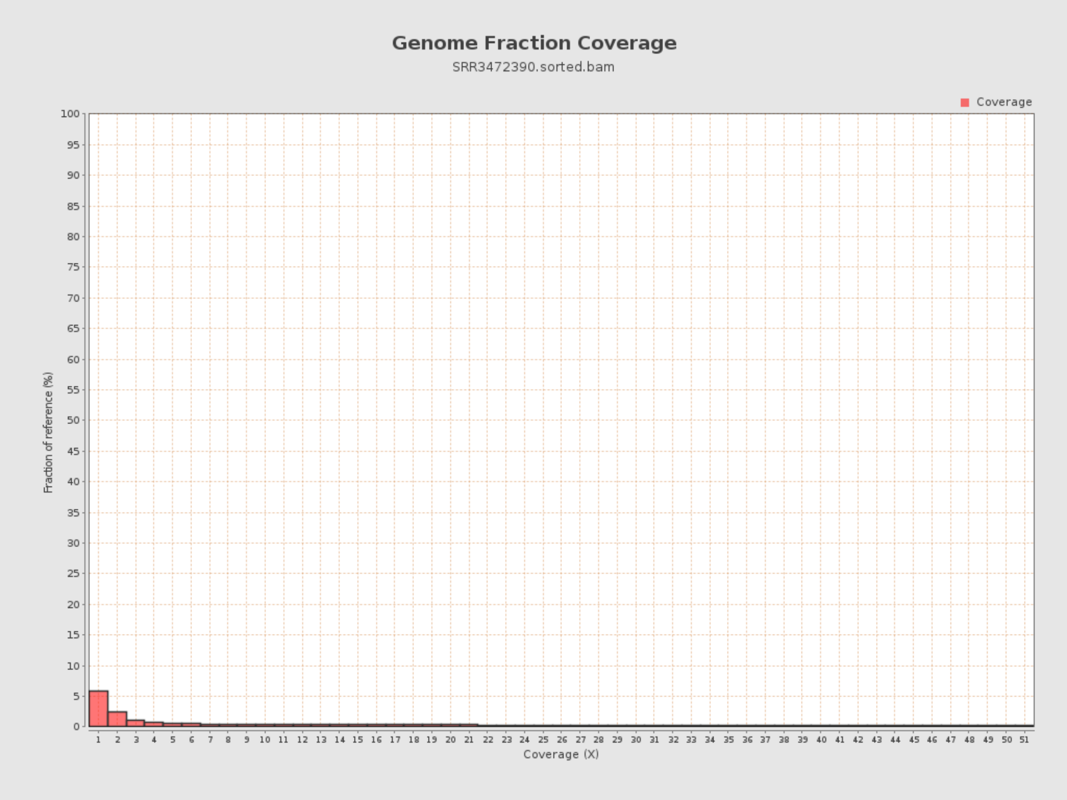
4. Results : Coverage Histogram



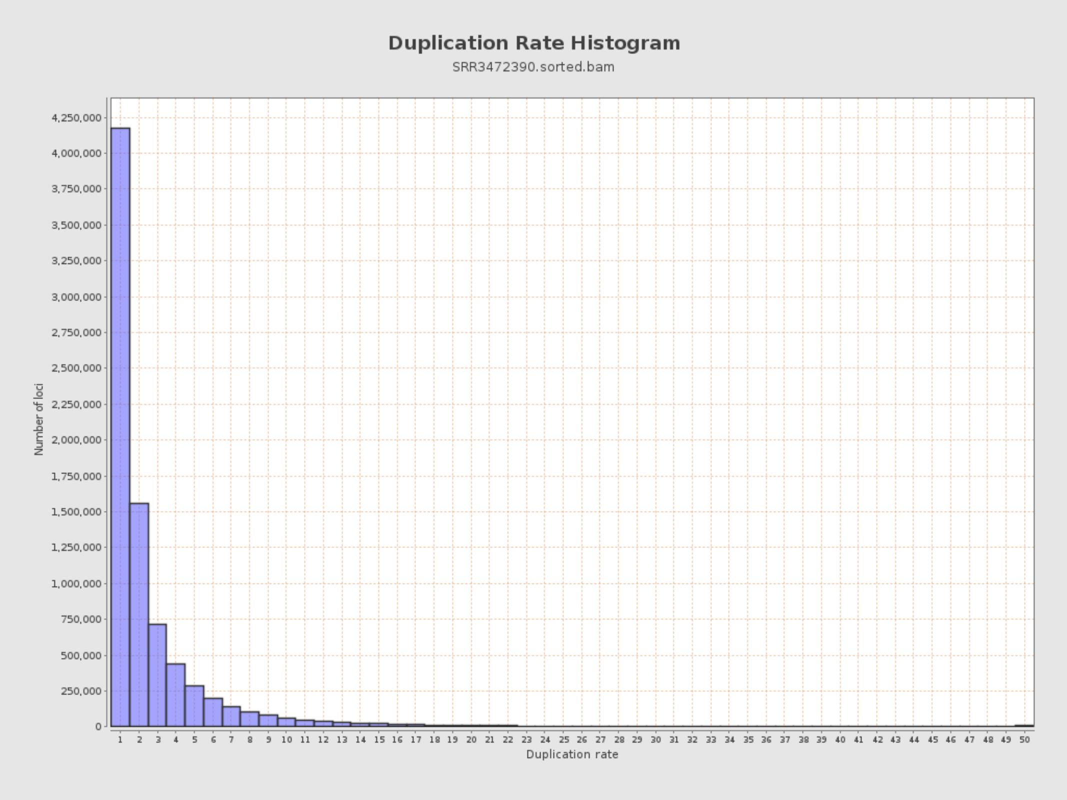
5. Results : Coverage Histogram (0-50X)



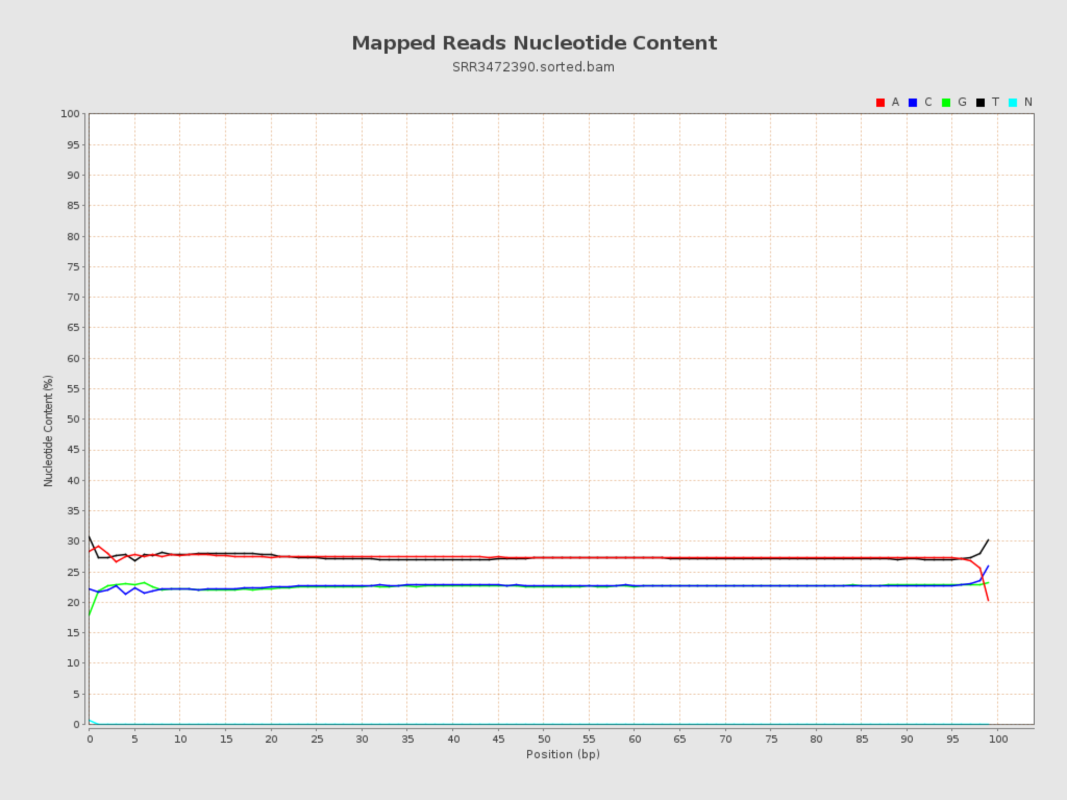
6. Results : Genome Fraction Coverage



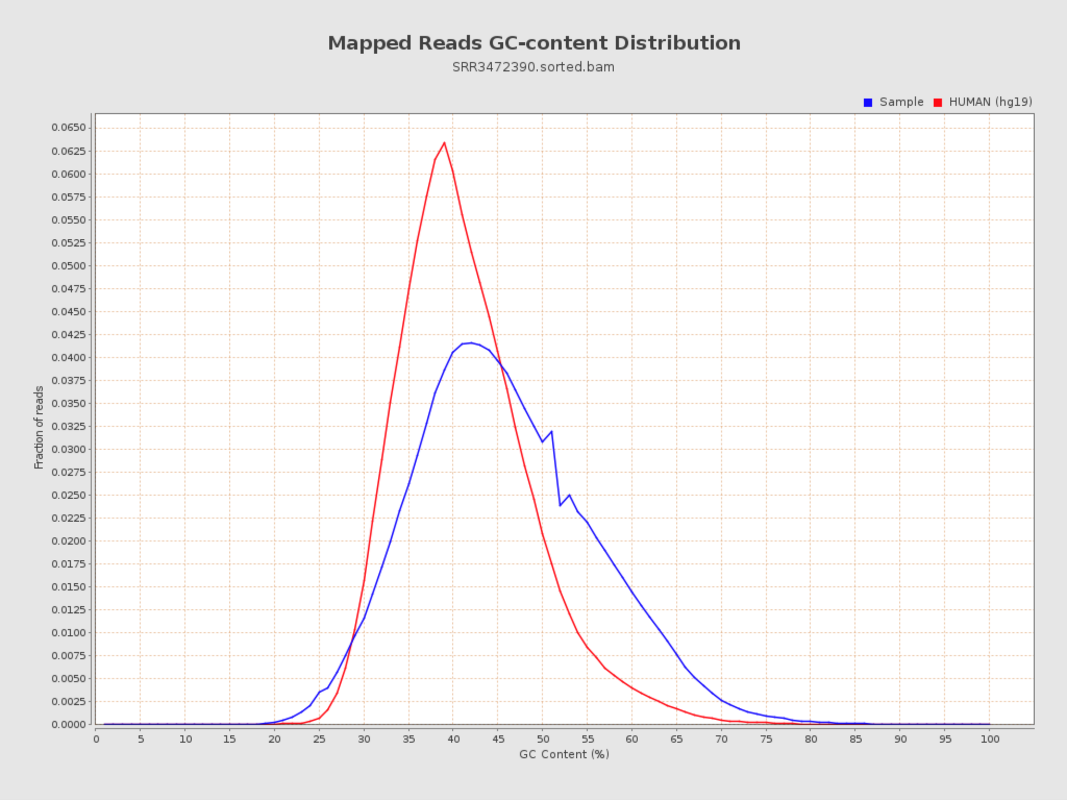
7. Results : Duplication Rate Histogram



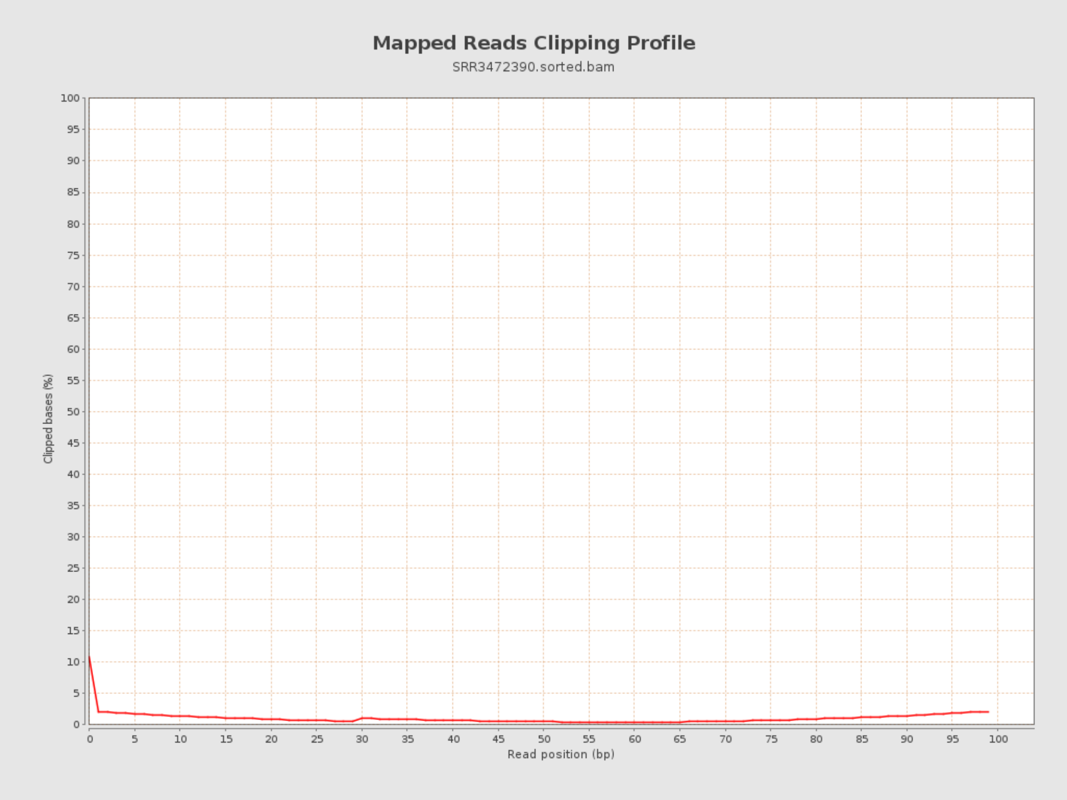
8. Results : Mapped Reads Nucleotide Content



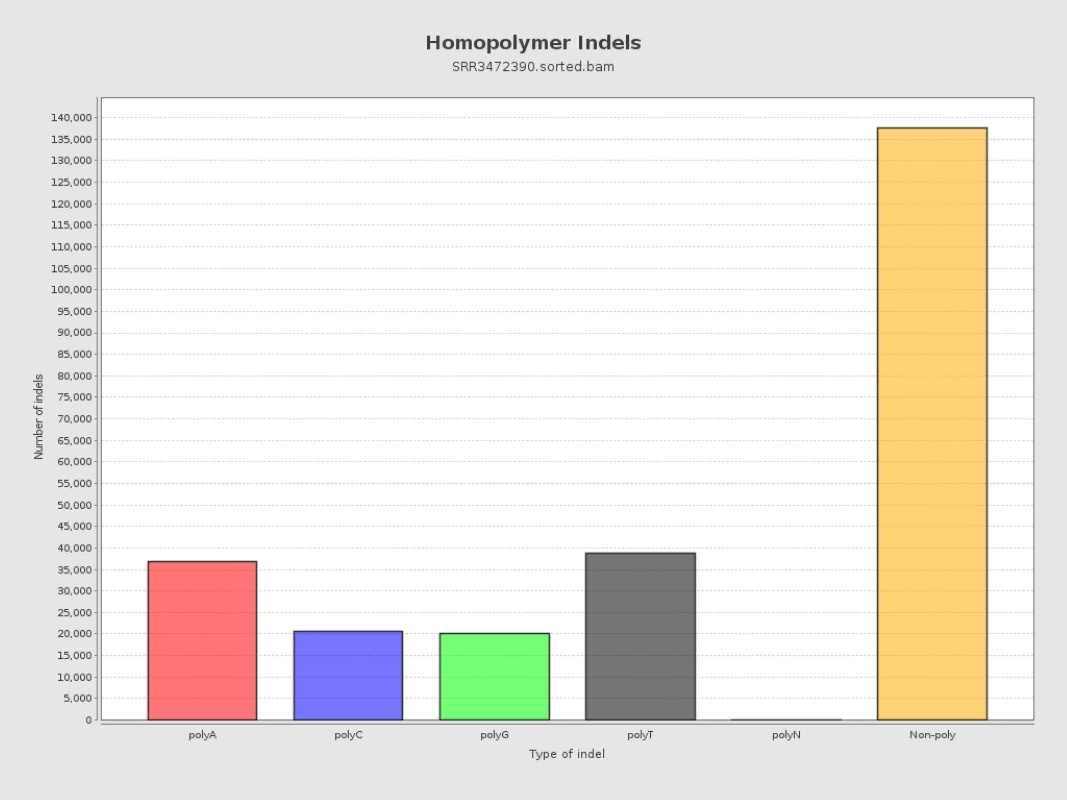
9. Results : Mapped Reads GC-content Distribution



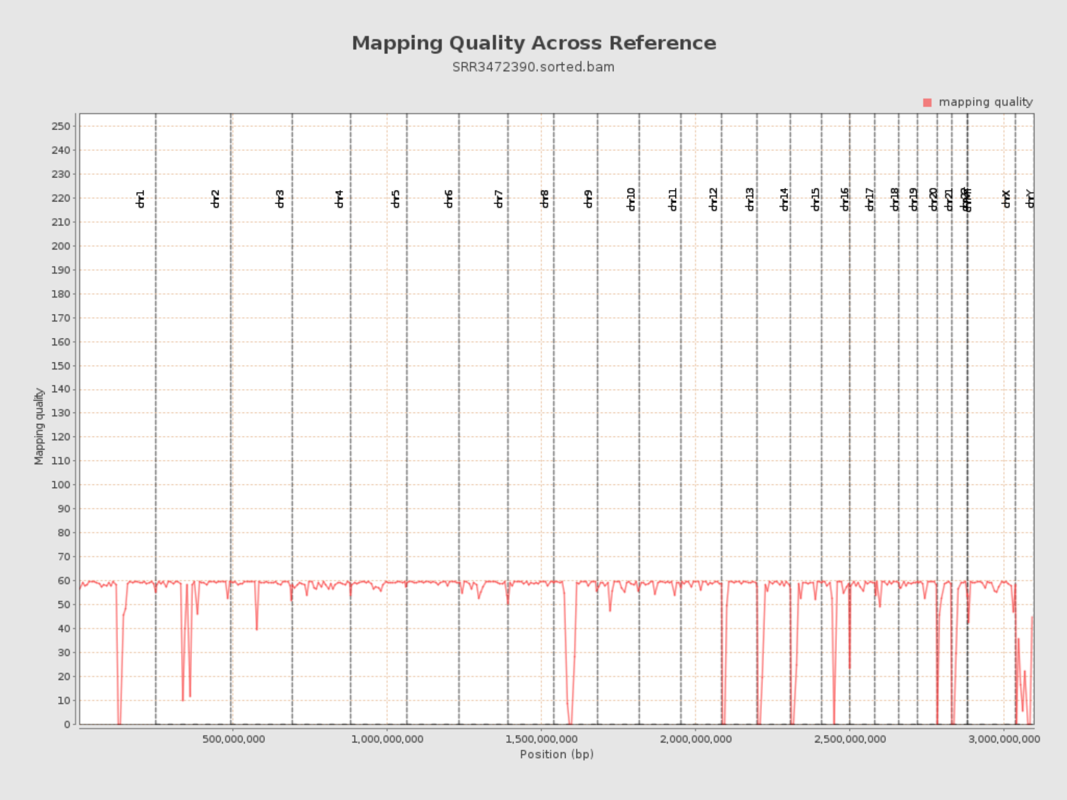
10. Results : Mapped Reads Clipping Profile



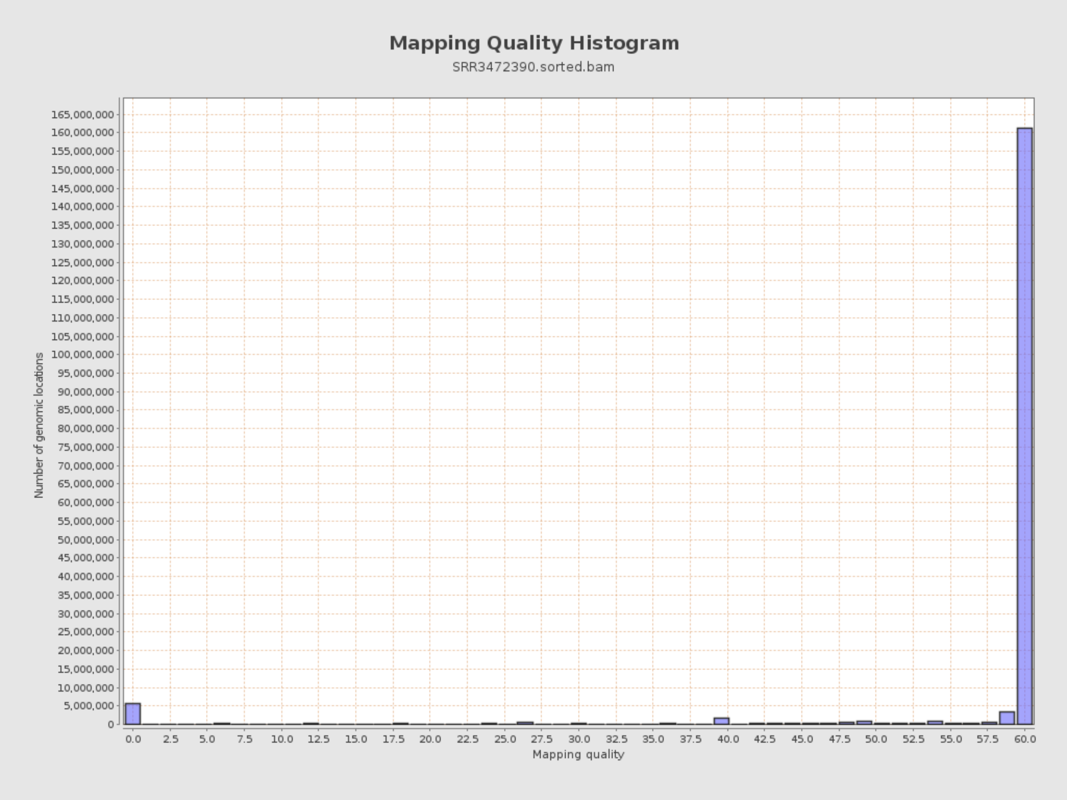
11. Results : Homopolymer Indels



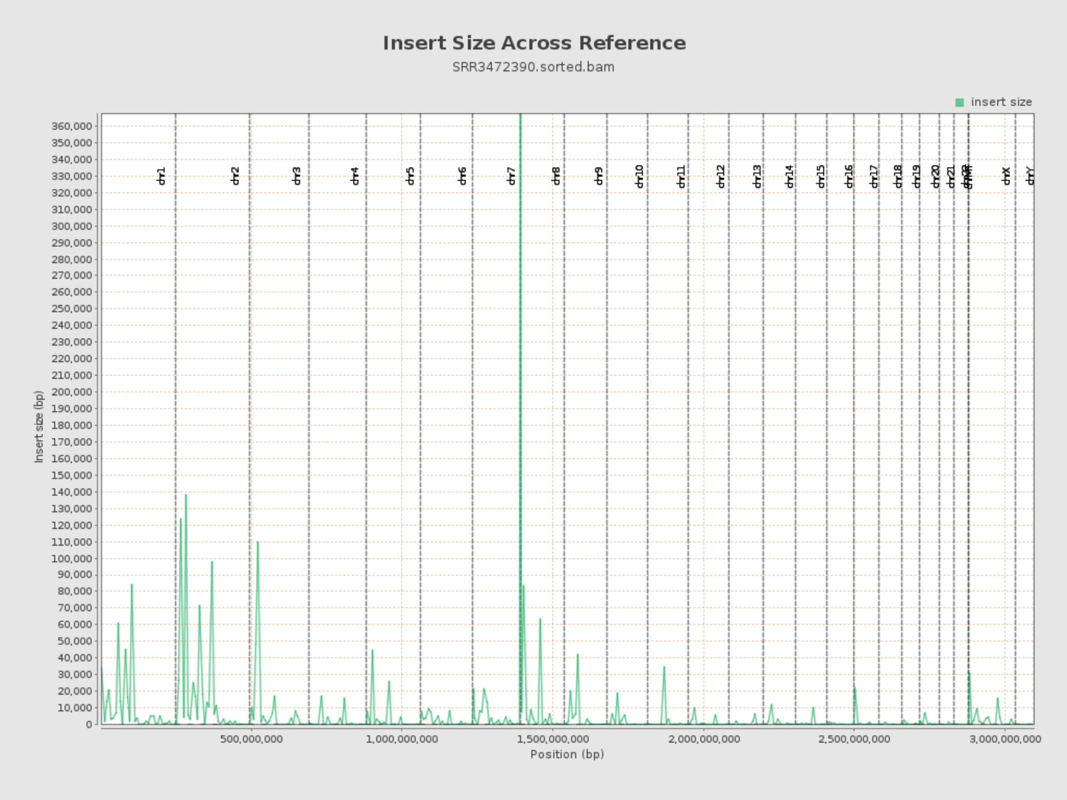
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram